Master's thesis

NTNU
Norwegian University of Science and Technology
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Department of Mathematical Sciences

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Delousing Effect and Welfare Implications of Non-Medicinal Delousing Methods

Master's thesis in Applied Physics and Mathematics
Supervisor: John Sølve Tyssedal
Co-supervisor: Anna Solvang Båtnes and Cecilie Miljeteig
March 2023

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Preface

This thesis was completed in the spring of 2023 and finalizes my Master of Science (M.Sc.) in Applied Physics and Mathematics at the Norwegian University of Science and Technology (NTNU). This thesis is written in collaboration with Taskforce Salmon Lice, a Research and Development project at NTNU.

I would like to express my gratitude to my supervisor John Sølve Tyssedal at the Department of Mathematical Sciences at NTNU and my co-supervisors Anna Solvang Båtnes and Cecilie Miljeteig at NTNU SeaLab. Thank you for valuable guidance, feedback and support throughout the work with this thesis.

Martine Middelthon
Trondheim, March 2023

Abstract

Lepeophtheirus salmonis, commonly referred to as the salmon louse, is a parasitic organism that affects the welfare of the Atlantic salmon. In recent years, there has been a growing interest in utilizing non-medicinal delousing methods, yet these have been linked to various welfare concerns. The group of non-medicinal delousing methods include freshwater treatment, thermal treatments and mechanical treatments. Several commercial delousing technologies have been developed based on these treatment principles, where the method called Optilicer is a thermal treatment, while Hydrolicer and SkaMik are two types of mechanical delousing methods. The objective of this thesis was to investigate and compare the impact of freshwater treatment, Optilicer, Hydrolicer and SkaMik on a selection of parameters regarding delousing effect and fish welfare. These parameters included the delousing effectiveness against adult female lice, salmon mortality 3 and 14 days post-treatment and the change in the score-based welfare indicators for skin haemorrhages (skin bleeding) and scale loss after treatment.

The provided data were from delousing operations on the cage level in production areas 5 and 6 from 2020 to the fall of 2022. The impact of the different delousing methods was analyzed by fitting generalized linear models and generalized linear mixed models to the data, including a range of explanatory variables to account for other factors that may influence the outcome.

For the delousing effect and mortalities, both quasi-binomial fixed-effects models and binomial mixed-effects models were fitted as two different ways to address the observed overdispersion. For analyzing the change in score evaluations for skin haemorrhages and scale loss after delousing treatment, linear mixed models were preferred and used. The fitted models indicated disparities in the impact of the different delousing methods on all the parameters considered, where most of the results were dependent on the sea temperature. However, there were no indications that the delousing methods associated with the highest delousing effect necessarily were better for the fish welfare.

Sammendrag

Lakselusen (*Lepeophtheirus salmonis*) er en parasitt som påvirker velferden til atlanterhavslaksen. De siste årene har det vært økende interesse for å bruke ikke-medikamentelle metoder for å bekjempe lus, men disse behandlingene har også blitt knyttet til ulike velferdsmessige problemer. Ikke-medikamentelle avlusingsmetoder omfatter ferskvannsbehandling, termiske behandlinger og mekaniske behandlinger. Ulike avlusingsmetoder har blitt utviklet basert på disse prinsippene, der Optilicer er en termisk behandling, mens Hydrolicer og SkaMik er to typer mekanisk behandling. Formålet med denne masteroppgaven var å undersøke og sammenligne effekten av ferskvannsbehandling, Optilicer, Hydrolicer og SkaMik på en rekke parametere for avlusingseffekt og fiskevelferd. De utvalgte parameterne inkluderte avlusingseffekt på voksne hunnlus, dødelighet for laksen 3 og 14 dager etter behandling og endring i skår-baserte velferdsindikatorer for rødbuk (hudblødning) og risttap (skjelltap) etter behandling.

Dataene som ble analysert var fra avlusingsbehandlinger på merd-nivå i produksjonsområdene 5 og 6 fra 2020 til høsten 2022. Effekten av de ulike avlusingsmetodene ble analysert ved bruk av generaliserte lineære modeller og generaliserte lineære mixed effekt modeller, der en rekke forklaringsvariabler var inkludert for å ta hensyn til andre faktorer som kunne tenkes å påvirke utfallet.

For analyse av avlusingseffekt og laksedødelighet ble både kvasi-binomiske fixed effekt modeller og binomiske mixed effekt modeller brukt som to forskjellige måter å håndtere den observerte overdispersjonen. For endringen i skårvurderinger for rødbuk og risttap etter avlusingsbehandling ble lineære mixed effekt modeller brukt. De tilpassede regresjonsmodellene indikerte at det var ulikheter i effekten av de ulike avlusingsbehandlingene på alle de undersøkte parameterne, der mesteparten av resultatene var avhengig av sjøtemperaturen. Det var derimot ingen indikasjoner på at avlusingsmetodene som var assosiert med størst avlusingseffekt nødvendigvis var bedre for fiskevelferden.

Table of Contents

Preface i

Abstract iii

Sammendrag v

Table of Contents vii

List of Figures x

List of Tables xiii

1 Introduction 1

1.1 Sea Lice . . . 1

1.2 Fish Welfare . . . 2

1.3 Lice Control . . . 3

1.4 Delousing Treatments . . . 4

1.4.1 Thermal Delousing Treatment . . . 4

1.4.2 Mechanical Delousing Treatment . . . 4

1.4.3 Freshwater Treatment . . . 5

1.5 Motivation and Objective . . . 5

1.5.1 Earlier Work . . . 6

1.5.2 Outline of the Thesis . . . 6

2 Theory 7

2.1 The Exponential Family . . . 7

2.2 Linear and Generalized Linear Models . . . 8

2.2.1 The Linear Model . . . 8

2.2.2 Generalized Linear Models . . . 9

2.2.3 Maximum Likelihood Estimation in GLMs . . . 9

2.2.4 Binomial GLM . . . 10

2.2.5 Overdispersion in Binomial GLM . . . 11

2.2.6 Hypothesis Tests . . . 12

2.2.7 Model Diagnostics . . . 13
2.3 Correlation-Inducing Data Structure . . . 14
2.3.1 Multilevel Data Structure . . . 14
2.4 Mixed Models . . . 16
2.4.1 The Linear Mixed Model . . . 16
2.4.2 A Linear Random Intercept Model . . . 18
2.4.3 Generalized Linear Mixed Models . . . 18
2.4.4 GLMMs for Data with Two Levels of Grouping . . . 18
2.4.5 General Form of GLMMs . . . 18
2.4.6 Parameter Estimation . . . 19
2.4.7 A Binomial Mixed Model . . . 20
2.4.8 Hypothesis Tests . . . 21
2.4.9 Model Diagnostics . . . 21
2.5 Model Selection . . . 22
2.6 Collinearity . . . 23
2.7 Variables and Model Interpretation . . . 24
2.7.1 Centering and Scaling of Covariates . . . 24
2.7.2 Categorical Explanatory Variables . . . 25
2.7.3 Interaction Terms . . . 25

3 Data Preparation and Exploration 26

3.1 Data Set and Preparation . . . 26
3.1.1 Explanatory Variables . . . 27
3.1.2 Random Explanatory Variables . . . 29
3.1.3 Response Variables and Creation of Data Sets . . . 30
3.2 Data Exploration . . . 31
3.2.1 Delousing Effect . . . 32
3.2.2 Salmon Mortality . . . 35
3.2.3 Score-Based Welfare Indicators . . . 39

4 Data Analysis 43

4.1 Delousing Effect . . . 47

4.1.1 Fixed Effects Binomial Regression 47
4.1.2 Mixed Effects Binomial Regression 51
4.2 Salmon Mortality 3 Days Post-Treatment 57
4.2.1 Fixed Effects Binomial Regression 57
4.2.2 Mixed Effects Binomial Regression 59
4.3 Salmon Mortality 14 Days Post-Treatment 64
4.3.1 Fixed Effects Binomial Regression 64
4.3.2 Mixed Effects Binomial Regression 64
4.4 Change in Skin Haemorrhages 66
4.5 Change in Scale Loss 69

5 Discussion **71**
5.1 Delousing Effect 71
5.2 Salmon Mortality 72
5.3 Score-Based Welfare Indicators 74
5.4 Conclusion and Recommendations for Further Work 75

Bibliography **77**

Appendix **80**

A Additional Figures **80**

B Additional Tables **87**

C R-code from Data Preparation **92**

D Model Output **104**

List of Figures

1.1 Developmental Stages of *Lepeophtheirus salmonis* 1

1.2 Morphological Scheme for Classifying External Injuries 3

2.1 Illustration of Nested Multilevel Structure 14

3.1 Map of Production Areas 26

3.2 Number of Observations from Different Locations (Data Set for Delousing Effect) 32

3.3 Correlation Plot (Data Set for Delousing Effect) 33

3.4 Proportion of Removed Lice for each Delousing Method 33

3.5 Proportion of Removed Lice and Sea Temperature against Season 34

3.6 Correlation Plots (Data Sets for Mortality after 3 and 14 Days) 36

3.7 Mortality Rates for the Delousing Methods 37

3.8 Mortality against Disease and Season 38

3.9 Correlation Plots (Data Sets for Skin Haemorrhages and Scale Loss) 40

3.10 Change in Skin Haemorrhages and Scale Loss against Delousing Method, Season and Disease 41

4.1 Illustration of the Difference in the Estimated Linear Predictor (Reduced Quasi-Binomial DE-FE Model) 50

4.2 Residual Plots for the Reduced Quasi-Binomial DE-FE Model 51

4.3 Illustration of the Difference in the Estimated Linear Predictor (Reduced DE-ME Model) 53

4.4 Residual Plots for the Reduced DE-ME Model 54

4.5 Fitted Random Effects in the Reduced DE-ME Model 55

4.6 Residual Plots for the Reduced Quasi-Binomial M3-FE Model 58

4.7 Illustration of the Difference in the Estimated Linear Predictor (Reduced M3-ME Model) 61

4.8 Residual Plots for the Reduced M3-ME Model 62

4.9 Fitted Random Effects in the Reduced M3-ME Model 63

4.10 Illustration of the Difference in the Estimated Linear Predictor (Reduced M14-ME Model) 65

4.11 Fitted Random Effects in the Reduced SH-ME Model 67

4.12 Residual Plots for the Reduced SH-ME Model 68

4.13 Illustration of the Difference in the Estimated Linear Predictor (Reduced SL-ME Model) 70

A.1 Sea Temperature against Season and Delousing Method (Tata Set for Delousing Effect) 80

A.2 Number of Observations from the Different Locations (Data Sets for Salmon Mortality after 3 and 14 Days) 80

A.3 Sea Temperature against Season and Method (Data Set for Mortality after 3 Days) 81

A.4 Sea Temperature against Season and Method (Data Set for Mortality after 14 Days) 81

A.5 Number of Observations from the Different Locations (Data Sets for Skin Haemorrhages and Scale Loss) 82

A.6 Sea Temperature against Season and Method (Data Set for Change in Skin Haemorrhages) 82

A.7 Sea Temperature against Season and Method (Data Set for Change in Scale Loss) 83

A.8 Residuals for each Delousing Method (Reduced DE-ME Model) 83

A.9 Distribution of Residuals from the Reduced M3-FE Model 83

A.10 Residuals for each Delousing Method (Reduced M3-ME Model) 84

A.11 Residual Plots for the Reduced Quasi-Binomial M14-FE Model 84

A.12 Residual Plots for the Reduced M14-ME Model 85

A.13 Fitted Random Effects from the Reduced M14-ME Model 85

A.14 Residual Plots for the Reduced SL-ME Model 86

A.15 Fitted Random Effects from the Reduced SL-ME Model 86

D.1 Model Output for the Full Binomial DE-FE Model 104

D.2 Model Output for the Full Quasi-Binomial DE-FE Model 105

D.3 Model Output for the Reduced Quasi-Binomial DE-FE Model 106

D.4 Model Output for the Reduced Quasi-Binomial DE-FE Model with a Different Intercept Value for the Sea Temperature 107

D.5 Model Output for the Full DE-ME Model 108

D.6 Model Output for the Full Quasi-Binomial M3-FE Model 109

D.7 Model Output for the Full M3-ME Model 110

D.8 Model Output for the Full Quasi-Binomial M14-FE Model 111

D.9 Model Output for the Reduced Quasi-Binomial M14-FE Model 112

D.10 Model Output for the Full M14-ME Model 113

D.11 Model Output for the Reduced M14-ME Model 114
D.12 Model Output for the Full SH-FE Model 115
D.13 Model Output for the Full SH-ME Model 116
D.14 Model Output for the Full SL-FE Model 117
D.15 Model Output for the Full SL-ME Model 118

List of Tables

2.1 Two-Level Data Structure 15

3.1 Description of the Variables Used in the Models 28

3.2 Mean Value and Standard Deviation of Numeric Explanatory Variables 29

3.3 Number of Observations in the Data Sets 31

3.4 Distribution of Observations for the Seasons (Data Set for Delousing Effect) . . . 35

3.5 Comparable GVIF (Data Set for Delousing Effect) 35

4.1 Models and Abbreviations 43

4.2 Variables Considered in the Models 45

4.3 Results from the LR Test for the Quasi-Binomial DE-FE Model 48

4.4 Model Summary for the Reduced Quasi-Binomial DE-FE Model 48

4.5 Additional Wald Tests for the Reduced Quasi-Binomial DE-FE Model 49

4.6 Model Summary for the Reduced DE-ME Model 53

4.7 Additional Wald Tests for the Reduced DE-ME Model 54

4.8 Model Summary for the Reduced Quasi-Binomial M3-FE Model 57

4.9 Additional Wald Tests for the Reduced M3-FE Model 58

4.10 Model Summary for the Reduced M3-ME Model 60

4.11 Additional Wald Tests for the Reduced M3-ME Model 61

4.12 Model Summary for the Reduced SH-ME Model 67

4.13 Model Summary for the Reduced SL-ME Model 70

B.1 Distribution of Observations for the Seasons (Data Sets for Mortality) 87

B.2 Comparable GVIF (Data Sets for Mortality) 87

B.3 Distribution of Observations for the Seasons (Data Sets for Skin Haemorrhages and Scale Loss) 88

B.4 Comparable GVIF (Data Sets for Skin Haemorrhages and Scale Loss) 88

B.5 Results from LR Tests for the DE-ME Model 88

B.6 Results from LR Tests for the Quasi-Binomial M3-FE Model 89

B.7 Results from LR Tests for the M3-ME Model 89

B.8 Results from LR tests for the Quasi-Binomial M14-FE Model 89

B.9 Additional Wald Tests for the Reduced M14-FE Model 89

B.10 Results from LR Tests for the M14-ME Model 90
B.11 Additional Wald Tests for the Reduced M14-ME Model 90
B.12 Results from LR Tests for the SH-ME Model 90
B.13 Wald Tests for the Reduced SH-ME Model 91
B.14 Results from LR Tests for the SL-ME Model 91
B.15 Wald Tests for the Reduced SL-ME Model 91

1 Introduction

1.1 Sea Lice

Lepeophtheirus salmonis (Krøyer 1837) and *Caligus elongatus* (Norrmann 1832) are two species of sea lice that affect the Atlantic salmon (Noble et al., 2018). These are parasites that attach to the salmon and feed on the skin, mucus and blood of the host (Overton et al., 2019). *L. salmonis*, also called the salmon louse, is more prevalent and persistent on the salmon, and therefore constitutes a greater health and welfare problem than *C. elongatus* (Costello, 2006; Noble et al., 2018). The salmon louse has been a serious problem for the aquaculture industry since the 1970s (Torrissen et al., 2013). With the intensive salmon farming, the density of hosts is high year-round, creating ideal conditions for the louse to survive and reproduce. This results in unnaturally high lice pressure for both farmed and wild salmon (Barrett et al., 2020; Torrissen et al., 2013). Lice infestations can lead to health and welfare problems such as physical damage, osmoregulatory problems, stress response, immunosuppression and secondary infections (Noble et al., 2018; Overton et al., 2019). Infestations of sea lice may even be lethal in severe cases. While wild salmon can have lice levels that may lead to welfare problems and increased mortality, the lice levels are controlled for farmed salmon. Thus, for farmed salmon, the frequent handling and treatment related to the delousing may be of greater concern for the welfare (Noble et al., 2018).

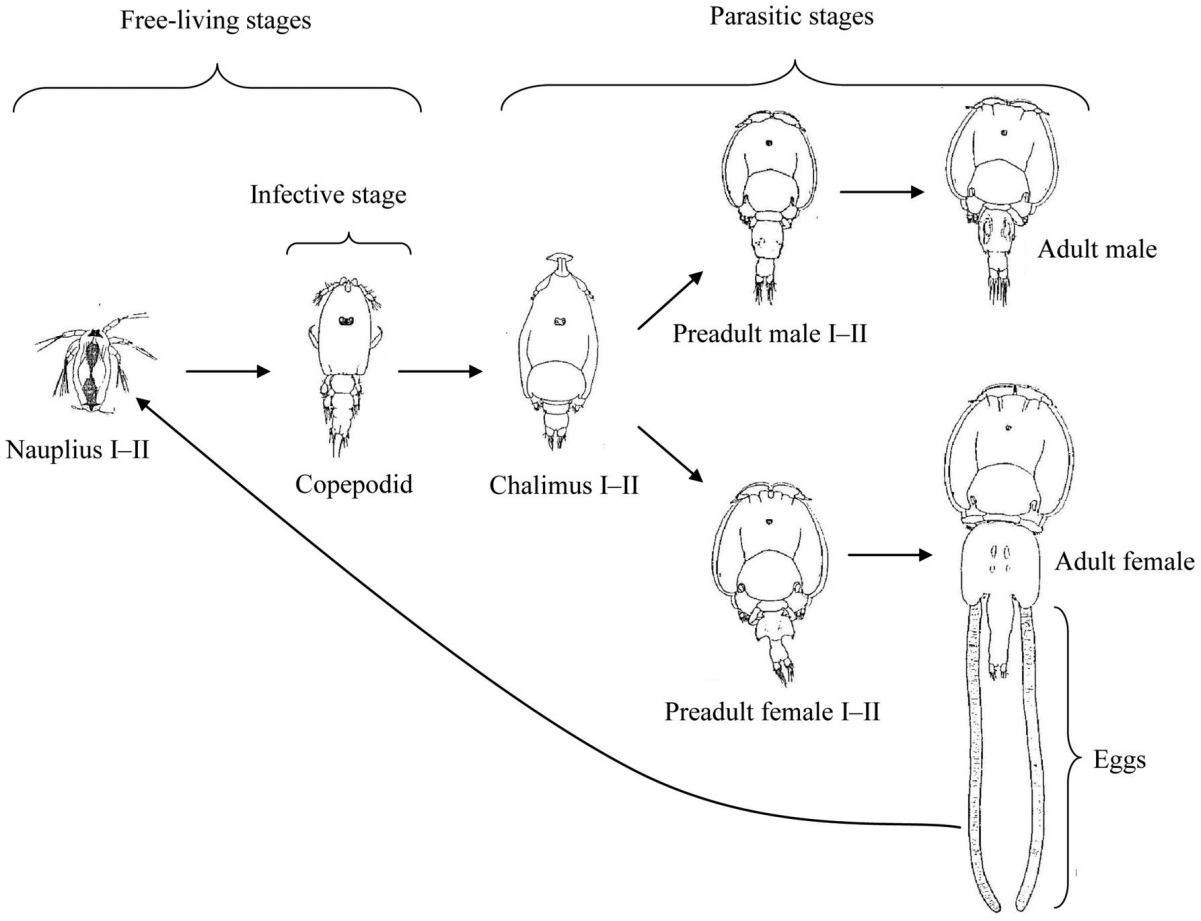


Figure 1.1: Developmental stages of *Lepeophtheirus salmonis*.

Source: Igboeli et al., 2014

L. salmonis goes through eight developmental stages during its life cycle, which are illustrated in Figure 1.1. The first two nauplius stages and the copepodid stage make up the free-living phase, where the louse flows in the water, before attaching to a host in the infective copepodid stage. The copepodid then molts into the first of the two chalimus stages. These are characterized by the development of a frontal filament that secures the attachment to the salmon, and the louse is then sessile. Two pre-adult stages then follow, before the louse reaches the adult male or female stage. In the pre-adult and adult stages, called the mobile stages, the louse is capable of temporarily detaching the frontal filament, allowing it to move freely on the host (Hamre et al., 2013; Igboeli et al., 2014). The adult female lice produce egg strings, which can contain hundreds of eggs (Brooker et al., 2018).

When lice are counted, the different life stages are categorized a little differently than what is described here. In concordance with the description, the term sessile is used for the two chalimus stages. In contrast, the term mobile lice typically refers to lice in the pre-adult and adult male stages. That means the adult female louse is excluded from this category, and instead makes up a category of its own. In the remaining part of this thesis, we will use these definitions of the terms unless otherwise specified.

1.2 Fish Welfare

Fish welfare is an important aspect in commercial farming. Welfare indicators (WIs) are measurements or observations that are used to assess the welfare status of the fish (Noble et al., 2018). Following Noble et al., 2018, where several welfare indicators are presented, we introduce a few of them here.

The mortality rate is an animal-based WI that is measured on a group of fish, and is probably the most used WI. If the mortality rate is higher than what is considered to be normal, it is an indication that a welfare problem exists. However, it is pointed out that a low mortality rate not necessarily means that there does not exist a welfare problem, because other problems may reduce the welfare without resulting in deaths. It is therefore beneficial to use various WIs to detect welfare problems.

Individual animal-based WIs are welfare indicators that can be measured on individual fish. Some examples of externally visible WIs are the number of sea lice on a salmon, fin damage, lesions, scale loss and skin haemorrhages. The latter two are indicators for skin condition, where scale loss concerns observed areas on the fish where scales are missing and skin haemorrhages are bleedings beneath the skin. The FISHWELL standard is suggested by Noble et al., 2018 as a measure for evaluating the severeness of 14 types of WIs like these. This is a standardized scoring system, where each indicator is evaluated with a score from 0 to 3. The score 0 indicates little to no evidence of the WI and the scores 1 to 3 indicate increasingly worse evidence of the WI. This grading system is illustrated in Figure 1.2 for scale loss and skin haemorrhages for scores from 1 to 3. This type of indicators can also be applied on the group level by quantifying the damage on a sample of fish from the group unit, and using it as an estimate for the whole group.

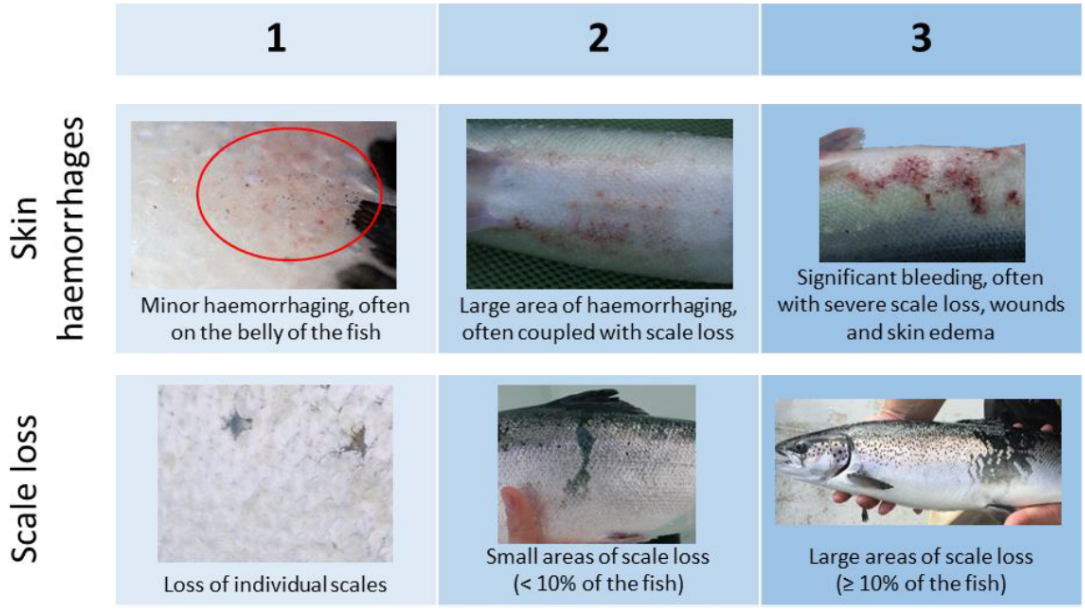


Figure 1.2: Morphological scheme for classifying injuries like skin haemorrhages and scale loss according to the FISHWELL standard.

Source: Noble et al., 2018, p. 65

1.3 Lice Control

To reduce the harm due to sea lice on both farmed and wild salmon populations, it is important to control the lice infestations. Preventing the spread of lice, which may lead to large infestations in wild salmon populations where the lice infestations are not controlled, is a motivating factor. Regulations regarding salmon lice control in the aquaculture facilities have therefore been established by *The Ministry of Trade, Industry and Fisheries* in Norway (Forskrift om lakselusbekjempelse, 2012). Depending on the sea temperature, the salmon farms are required to count and report the average number of salmon lice per fish every two weeks if the sea temperature is below 4°C or every week if the temperature is equal to or greater than 4°C. The average lice numbers have to be calculated from samples of a minimum of 10 or 20 arbitrary fish from each cage depending on the time of year and geographical location of the salmon farm. In addition, the average lice numbers should be reported for three categories of salmon lice based on the life cycle. The lice are categorized by sessile lice, adult female lice and mobile lice (where adult female lice are excluded).

In the regulations, there are specified allowed limits of adult female lice at a salmon farm. Most of the year the allowed limit is an average of 0.5 adult female lice. However, in 6 weeks during the spring, at the time of migration of wild salmon smolts, the limit is reduced to an average of 0.2 adult female lice. The specified weeks are different depending on the geographical location of the salmon farm. The salmon farms are required to initiate measures to reduce the lice pressure to ensure that the limits are not violated.

1.4 Delousing Treatments

There are many different delousing treatments that can be used in order to reduce the lice pressure. Medicinal delousing treatments, like chemotherapeutants as bath treatments or in-feed additives, have long been effective and predictable measures to prevent high lice pressure. However, the extensive use have resulted in sea lice developing resistance towards the drugs. The aquaculture industry has therefore developed non-medicinal alternatives to combat the problem (Aaen et al., 2015; Overton et al., 2019). The group of non-medicinal delousing treatments include mechanical, thermal and freshwater treatments (Overton et al., 2019).

The use of the technologies based on these non-medicinal delousing treatments all involve pumping the fish from the cage into the treatment system through a pipe. A process called *crowding* is necessary for the pipe to get access to all the fish in the cage. In this process, the fish density is increased by forcing the fish into a smaller volume closer to the pipe (Nersten, 2021). The crowding process is associated with higher risk of injuries and stress responses in the fish, and is therefore considered to be a risk factor for the fish welfare (Holan et al., 2017).

1.4.1 Thermal Delousing Treatment

Thermal delousing treatments are based on the concept of exposing the salmon to lukewarm sea water with a temperature of 28-34 °C for 20-30 seconds. Since the salmon are much bigger than the lice, and with a short exposure time, the heating is intended to mainly affect the lice. The sudden temperature difference paralyzes the lice, causing them to loose the ability of remaining attached to the dermis of the fish and falling off (Holan et al., 2017).

There exist two commercial delousing technologies based on this concept, and one of them is called Optilicer (Roth, 2016). This treatment system uses an open bath of heated sea water (Holan et al., 2017). After the fish are pumped from the cage into the treatment system, the water is drained and the fish are taken through the treatment water bath by paddle wheels. The exposure to the heated water can be adjusted to last for 21 seconds or longer. Thereafter, the water is drained again to remove any lice that may be in the water and the fish are sent back to a cage in the sea (Holan et al., 2017; Overton et al., 2019; Roth, 2016). This delousing method is effective for removing mobile and adult female lice. The effectiveness depends on the difference in temperature between the sea and the treatment water, where a greater difference gives better results. Therefore, the treatment water temperature is partly determined based on the sea temperature (Holan et al., 2017; Roth, 2016). However, fish experience a stress response when exposed to heated water, which increases with a greater temperature difference (Roth, 2016; Stien et al., 2022). Exposure to heated water may also increase the risk of various injuries like eye problems, scale loss, fin injuries and snout wounds (Moltumyr et al., 2022; Stien et al., 2022).

1.4.2 Mechanical Delousing Treatment

Mechanical delousing treatments use techniques like flushing and brushing to physically remove lice from the fish. There are three commercial delousing technologies that have been developed based on this approach to remove the lice, and two of them, called SkaMik and Hydrolicer, are presented here.

In the SkaMik treatment system (SkaMik 1.5), the water is drained before the fish are taken

through three different chambers. The first is a flushing chamber with adjustable pressure of around 4 bar, followed by a brushing chamber with rotating brushes. Then, the fish go through a final flushing chamber to flush any remaining lice off. The total treatment time inside the SkaMik treatment system is 1.5 seconds (SkaMik AS, n.d.). There are few studies regarding the effectiveness and impact on the fish welfare for the SkaMik treatment system. A study by Westgård et al., 2021, carried out at 4 different salmon farms, reported an effectiveness of 90-100% on mobile lice and 50-100% on adult female lice. Additionally, an increase in scale loss was found.

In the Hydrolicer treatment system, the fish are pumped through a pipe filled with water at a controlled speed. Inside the pipe, over- and under-pressure, which creates turbulence, is used to detach the lice, followed by low-pressure flushing to remove the lice (Antonsen, 2021; Erikson et al., 2018; Overton et al., 2019; Smir AS, n.d.). According to a study by Erikson et al., 2018, the effectiveness of Hydrolicer was reported to be 78-95% on mobile lice and 55-92% on adult female lice. In addition, use of Hydrolicer was associated with scale loss and moderate skin haemorrhages.

1.4.3 Freshwater Treatment

Another delousing method is the freshwater bath treatment. The fish are pumped into a well-boat, where they are exposed to freshwater for 4-8 hours. The exposure to freshwater causes disturbances in the osmotic balance of the lice, which become paralyzed and eventually die. After the treatment, the water is drained, and the fish are returned to a cage (Holan et al., 2017). A study by Reynolds, 2015 reported a reduction of 97% for mobile lice and 92% for adult female lice. There are few studies about how freshwater treatment affects the welfare, but longer treatment time, which means that the fish are crowded in the wells for a longer time, may increase the risk of injuries (Holan et al., 2017).

1.5 Motivation and Objective

Sea lice infestations are associated with various welfare problems for both farmed and wild salmon, and delousing treatments are used to manage the lice pressure in the aquaculture industry. With the development of resistance towards chemotherapeutants in the sea lice, the use of alternative non-medicinal delousing treatments has increased the recent years. It is of great interest to the industry to use delousing treatments that have a good delousing effect, while minimizing the harmful effects on the salmon. However, the knowledge of these methods is somewhat limited, so more and up to date information is of interest.

This thesis is a comparative investigation of four different non-medicinal delousing methods. These delousing methods are Optilicer, SkaMik, Hydrolicer and freshwater treatment. The objective of this thesis is to investigate the impact of these methods on a selection of parameters for delousing effect and fish welfare. In particular, these parameters are the delousing effectiveness against adult female lice, salmon mortality 3 and 14 days post-treatment and change in evaluation of the welfare indicators skin haemorrhages and scale loss after treatment.

1.5.1 Earlier Work

In Middelthon, 2022, the four delousing treatments Optilicer, Hydrolicer, SkaMik and freshwater treatment were compared with regards to different response variables concerning delousing effect and fish welfare. Binomial models were fitted for the delousing effectiveness against adult female lice and the salmon mortality 3 and 14 days post-treatment. These showed signs of overdispersion, a phenomenon which will be explained later, so quasi-binomial models were eventually used. In addition, linear models were fitted for the change in two welfare indicators (skin haemorrhages and scale loss) after delousing treatment. The data that were analysed were from several delousing treatments in 2021.

1.5.2 Outline of the Thesis

This thesis is a continuation of Middelthon, 2022, where several improvements are made. To begin with, larger data sets have been analysed in this thesis, and the data are from 2020 to the fall of 2022. For the binomial responses, two different models to handle overdispersion are fitted. These are the quasi-binomial model and a binomial mixed model based on the multilevel structure of the data. The linear models for the change in the welfare indicators have also been improved by considering possible cluster effects, extending the models to linear mixed models. In addition, more explanatory variables have been used in all the models. Throughout this thesis, we will use the term "delousing effect" for the delousing effectiveness against adult female lice.

The remaining part of the thesis is structured as follows. An explanation of the theory behind the statistical models that are used is given in Section 2. Section 3 provides a description of the data and the pre-processing, as well as an initial exploration of the data sets. The data analysis, with results and evaluation of the fitted models, is presented in Section 4. Finally, a summary and discussion of the results, as well as some recommendations for further work are given in Section 5.

2 Theory

This section provides an explanation of the theory behind the generalized linear models and generalized linear mixed models, which are used in the analysis of the delousing effect and fish welfare.

2.1 The Exponential Family

The density function of a variable y that comes from a distribution belonging to the exponential family can be written on the form

$$f(y \mid \theta_c) = \exp\left(\frac{y\theta_c - b(\theta_c)}{\phi} w + c(y, \phi, w)\right), \tag{2.1}$$

where θ_c is referred to as the canonical parameter, ϕ is the dispersion parameter and w is a weight with a known value. Additionally, $b(\cdot)$ and $c(\cdot)$ are functions. With this notation, the expectation of y is $\mathrm{E}(y) = b'(\theta_c)$ and the variance is $\mathrm{Var}(y) = \phi b''(\theta_c)/w$ (Fahrmeir et al., 2013).

For a normally distributed variable y with mean μ and variance σ^2, the probability density function is

$$\begin{aligned} f(y \mid \mu, \sigma^2) &= \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{(y-\mu)^2}{2\sigma^2}\right) \\ &= \exp\left(-\frac{y^2}{2\sigma^2} + \frac{y\mu}{\sigma^2} - \frac{\mu^2}{2\sigma^2} - \frac{1}{2}\log\left(2\pi\sigma^2\right)\right) \\ &= \exp\left(\frac{y\mu - \mu^2/2}{\sigma^2} - \frac{y^2}{2\sigma^2} - \frac{1}{2}\log\left(2\pi\sigma^2\right)\right). \end{aligned}$$

This is on the form of (2.1), with canonical parameter $\theta_c = \mu$, dispersion parameter $\phi = \sigma^2$, weight $w = 1$ and functions $b(\theta_c) = \theta_c^2/2$ and $c(y, \phi, w) = -(y^2/\phi + \log(2\pi\phi))/2$. Thus, the normal distribution belongs to the exponential family.

If the number of successes y is binomial with success probability p for a given number of trials n, the density function is

$$\begin{aligned} f(y \mid p) &= \binom{n}{y} p^y (1-p)^{n-y} \\ &= \exp\left(\log\binom{n}{y} + y\log(p) + n\log(1-p) - y\log(1-p)\right) \\ &= \exp\left(y\log\left(\frac{p}{1-p}\right) + n\log(1-p) + \log\binom{n}{y}\right). \end{aligned}$$

If we set $\theta_c = \log(p/(1-p))$, then $\log(1-p) = -\log(1+\exp(\theta_c))$, and the density can be written

$$f(y \mid p) = \exp\left(y\theta_c - n\log(1+\exp(\theta_c)) + \log\binom{n}{y}\right).$$

Hence, the binomial distribution belongs to the exponential family, with canonical parameter $\theta_c = \log(p/(1-p))$, dispersion parameter $\phi = 1$, weight $w = 1$ and functions $b(\theta_c) = n\log(1+\exp(\theta_c))$ and $c(y, \phi, w) = \log\binom{n}{y}$.

If we instead define the observed success probability $\bar{y} = y/n$, where $y \sim \text{Binomial}(n, p)$, then $\bar{y}$ has a scaled binomial distribution $\bar{y} \sim \text{Binomial}(n, p)/n$. The density function for the observed success probability is identical to that of the number of the number of successes and can be written

$$\begin{aligned} f(\bar{y} = y/n \mid p) &= \binom{n}{y} p^y (1-p)^{n-y} \\ &= \exp\left(y \log\left(\frac{p}{1-p} \right) + n \log(1-p) + \log\binom{n}{y} \right) \\ &= \exp\left(n\Big(\bar{y}\theta_c - \log(1 + \exp(\theta_c) \Big) + \log\binom{n}{n\bar{y}} \right), \end{aligned}$$

where we have used $\theta_c = \log(p/(1-p))$ and $y = n\bar{y}$ in the last step. This is then on the form of (2.1) with dispersion parameter $\phi = 1$, weight $w = n$ and functions $b(\theta_c) = \log(1 + \exp(\theta_c))$ and $c(\bar{y}, \phi, w) = \log\binom{n}{n\bar{y}}$. We notice that the weight now has the value n, as opposed to the value 1 for the binomial distribution.

2.2 Linear and Generalized Linear Models

In this section we will present a comprehensive theory of linear and generalized linear models as to apply in our analysis. The theory in this section follows Fahrmeir et al., 2013 if nothing else is specified. We first give a definition of the linear predictor, which will be extensively used throughout this section. Then, the linear model is introduced, which is later extended to generalized linear models.

Let the response variable for observations $i = 1, \ldots, n$ be y_i, and assume that there are k explanatory variables, $x_{i1}, x_{i2}, \ldots, x_{ik}$, measured for each outcome. The linear predictor is then defined as

$$\eta_i = \beta_0 + \beta_1 x_{i1} + \ldots + \beta_k x_{ik} = \mathbf{x}_i^\intercal \boldsymbol{\beta}, \tag{2.2}$$

where $\boldsymbol{\beta} = (\beta_0, \beta_1, \ldots, \beta_k)^\intercal$ is the vector of coefficients and $\mathbf{x}_i = (1, x_{i1}, \ldots, x_{ik})^\intercal$ is the vector of explanatory variables, also called covariates, for observation i. Notice that the first element in the covariate vector is 1 because the first element in the vector of coefficients is the "intercept" β_0, so these vectors have length $p = k + 1$.

2.2.1 The Linear Model

Consider responses y_i, $i = 1, \ldots, n$, that are assumed to be independently and normally distributed, with mean $E(y_i) = \mu_i$ and variance $Var(y_i) = \sigma^2$, and probability density function

$$f(y_i \mid \mu_i, \sigma^2) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\Big\{ -\frac{(y_i - \mu_i)^2}{2\sigma^2} \Big\}.$$

In the linear model, we assume that the mean μ_i is linked linearly to the covariates through the linear predictor in (2.2), resulting in

$$\mu_i = \eta_i = \mathbf{x}_i^\intercal \boldsymbol{\beta}. \tag{2.3}$$

The method of maximum likelihood (ML) can be used to estimate the coefficients $\boldsymbol{\beta}$ and the variance σ^2. Their ML estimates will be denoted by $\hat{\boldsymbol{\beta}} = (\hat{\beta}_0, \hat{\beta}_1, \ldots, \hat{\beta}_k)^\intercal$ and $\hat{\sigma}^2$, and the

following derivation of these estimates is from Myers et al., 2002, p. 32-33. With the assumption of independently and normally distributed responses, the likelihood function is given as

$$L(\boldsymbol{\beta}, \sigma^2) = \prod_{i=1}^{n} f(y_i \mid \boldsymbol{\beta}, \sigma^2) = \frac{1}{(2\pi\sigma^2)^{n/2}} \exp\Big\{ -\frac{1}{2\sigma^2}(\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^\intercal(\mathbf{y} - \mathbf{X}\boldsymbol{\beta})\Big\}.$$

Here, $\mathbf{y} = (y_1, y_2, \ldots, y_n)^\intercal$ is the vector of responses and $\mathbf{X} = (\mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_n)^\intercal$ is the design matrix of dimension $n \times p$, which we assume to have full column rank p. The log-likelihood is then calculated by taking the logarithm of the likelihood, which gives

$$l(\boldsymbol{\beta}, \sigma^2) = \log\left(L(\boldsymbol{\beta}, \sigma^2)\right) \propto -\frac{n}{2}\log\left(\sigma^2\right) - \frac{1}{2\sigma^2}(\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^\intercal(\mathbf{y} - \mathbf{X}\boldsymbol{\beta}).$$

Taking the derivative of the log-likelihood with respect to $\boldsymbol{\beta}$ yields the score function

$$\mathbf{s}(\boldsymbol{\beta}) = \frac{\partial l(\boldsymbol{\beta}, \sigma^2)}{\partial \boldsymbol{\beta}} = -\frac{1}{\sigma^2}\mathbf{X}^\intercal(\mathbf{y} - \mathbf{X}\boldsymbol{\beta}).$$

The ML estimator of $\boldsymbol{\beta}$ is then obtained by solving $\mathbf{s}(\boldsymbol{\beta}) = \mathbf{0}$, which gives $\hat{\boldsymbol{\beta}} = (\mathbf{X}^\intercal\mathbf{X})^{-1}\mathbf{X}^\intercal\mathbf{y}$. Similarly, the ML estimate of the variance is found by solving

$$\frac{\partial l(\boldsymbol{\beta}, \sigma^2)}{\partial \sigma^2} = -\frac{n}{2\sigma^2} - \frac{1}{2\sigma^4}(\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^\intercal(\mathbf{y} - \mathbf{X}\boldsymbol{\beta}) = 0,$$

resulting in $\hat{\sigma}^2 = \frac{1}{n}(\mathbf{y} - \mathbf{X}\hat{\boldsymbol{\beta}})^\intercal(\mathbf{y} - \mathbf{X}\hat{\boldsymbol{\beta}})$. Here we note that the ML estimate of $\boldsymbol{\beta}$ is used to compute the ML estimate of the variance.

It can be shown that the maximum likelihood estimator of the variance, $\hat{\sigma}^2$, is biased, and that an unbiased estimator is given by

$$\tilde{\sigma}^2 = \frac{n}{n-p}\hat{\sigma}^2.$$

Thus, the ML estimator is downwardly biased, but the bias reduces for large n (Fahrmeir et al., 2013; Myers et al., 2002).

2.2.2 Generalized Linear Models

The generalized linear model (GLM) is an extension of the linear model in that it allows for the response variable to have other distributions than the normal distribution. Specifically, it assumes that the response y_i has a distribution belonging to the exponential family. In addition, it is assumed that the expectation of the response, $E(y_i) = \mu_i$, can be modelled by connecting the expectation to a linear combination of the covariates (i.e. the linear predictor in (2.2)) through a response function h. We can write this relation as $\mu_i = h(\eta_i)$, where the response function has an inverse $g(\mu_i) = h^{-1}(\mu_i)$, called the link function (Fahrmeir et al., 2013).

2.2.3 Maximum Likelihood Estimation in GLMs

In Section 2.2.1, the ML estimates of the coefficients for the linear model were found by solving $\mathbf{s}(\boldsymbol{\beta}) = \mathbf{0}$ exactly. In contrast, the ML estimates $\hat{\boldsymbol{\beta}}$ of the coefficients in a GLM are computed numerically by using the Fisher scoring algorithm to solve $\mathbf{s}(\hat{\boldsymbol{\beta}}) = \mathbf{0}$ (Fahrmeir et al., 2013). We therefore present the expected Fisher information matrix, to be used in this algorithm. It is given by

$$\mathbf{F}(\boldsymbol{\beta}) = E\bigg(-\frac{\partial^2 l(\boldsymbol{\beta})}{\partial\boldsymbol{\beta}\partial\boldsymbol{\beta}^\intercal}\bigg),$$

where $l(\boldsymbol{\beta})$ is the log-likelihood (Fahrmeir et al., 2013).

Provided with starting values $\hat{\boldsymbol{\beta}}^{(0)}$ and using the score function and Fisher information matrix, the Fisher scoring algorithm iteratively updates the estimate by calculating

$$\hat{\boldsymbol{\beta}}^{(t+1)} = \hat{\boldsymbol{\beta}}^{(t)} + \mathbf{F}^{-1}\big(\hat{\boldsymbol{\beta}}^{(t)}\big)\mathbf{s}\big(\hat{\boldsymbol{\beta}}^{(t)}\big), \quad t = 0, 1, 2, \ldots \tag{2.4}$$

until a convergence criterion is met. However, the algorithm can only converge to the ML estimate if the design matrix $\mathbf{X}$ has full column rank. With a sufficiently large sample size n, the ML estimate $\hat{\boldsymbol{\beta}}$ has an approximate normal distribution

$$\hat{\boldsymbol{\beta}} \sim N(\boldsymbol{\beta}, \mathbf{F}^{-1}(\hat{\boldsymbol{\beta}})), \tag{2.5}$$

where the inverse expected Fisher information matrix, evaluated at the ML estimate $\hat{\boldsymbol{\beta}}$, i.e. $\mathbf{F}^{-1}(\hat{\boldsymbol{\beta}})$, is the estimated covariance matrix (Fahrmeir et al., 2013).

2.2.4 Binomial GLM

Here we describe the use of the generalized linear model for binomial responses. We begin by assuming that the response variables y_i are Bernoulli trials with success probability π_i, and define $y_i = 1$ as success and $y_i = 0$ as failure. If some of the covariate vectors of the observations $(y_i, \mathbf{x_i})$, $i = 1, \ldots, n$, are the same, the observations with identical covariates can be grouped. Then, the data are instead given by $(n_j, y_j, \mathbf{x_j})$, $j = 1, \ldots, G$. Here, G is the number of groups, n_j is the number of observations in group j that all have the same covariate vector $\mathbf{x}_j$, and y_j is the number of successes in group j. That is, $y_j \in [0, n_j]$ is the sum of the n_j individual binary responses belonging to group j, and this quantity is also referred to as the absolute frequency. We can then define the relative frequency $\bar{y}_j \in [0, 1]$ as the proportion of successes in group j, i.e. $\bar{y}_j = y_j/n_j$. Under the assumption of independence between the individual Bernoulli distributed responses y_i, the absolute frequencies follow a binomial distribution $y_j \sim Binomial(n_j, \pi_j)$. Equivalently, the relative frequencies have a scaled binomial distribution $\bar{y}_j \sim Binomial(n_j, \pi_j)/n_j$, with $E(\bar{y}_j) = \pi_j$ and $Var(\bar{y}_j) = \pi_j(1 - \pi_j)/n_j$.

The expectation π_j can be modeled using either the logit, probit or complementary log-log link function. Here we will use the former, i.e. the logit link function $g(\pi_j) = \log\left(\pi_j/(1 - \pi_j)\right)$, which takes the logarithm of what is called the odds, i.e. $\pi_j/(1 - \pi_j) = P(\bar{y}_j = 1 \mid \mathbf{x}_j)/P(\bar{y}_j = 0 \mid \mathbf{x}_j)$. As mentioned previously, this is used to link the expectation to the covariates through the linear predictor, so we get

$$\log\left(\frac{\pi_j}{1 - \pi_j}\right) = \eta_j = \mathbf{x}_j^\intercal \boldsymbol{\beta}. \tag{2.6}$$

The inverse of the link function is the response function, given by $\pi_j = h(\eta_j) = (1 + \exp(-\eta_j))^{-1}$ for the logit link function.

The log-likelihood, score function and the Fisher information matrix for the binomial logistic model can be derived by following a similar procedure as for the linear model. These formulas

are given in Fahrmeir et al., 2013, p. 283 as

$$l(\boldsymbol{\beta}) = \sum_{j=1}^{G} \{y_j \log(\pi_j) - y_j \log(1-\pi_j) + n_j \log(1-\pi_j)\}, \tag{2.7}$$

$$\mathbf{s}(\boldsymbol{\beta}) = \sum_{j=1}^{G} n_j \mathbf{x}_j (\bar{y}_j - \pi_j), \tag{2.8}$$

$$\mathbf{F}(\boldsymbol{\beta}) = \sum_{j=1}^{G} \mathbf{x}_j \mathbf{x}_j^{\intercal} n_j \pi_j (1-\pi_j), \tag{2.9}$$

where $\pi_j = \pi_j(\boldsymbol{\beta})$ as given by (2.6). The ML estimates of the coefficients $\boldsymbol{\beta}$ in the binomial logistic model can then be obtained by the Fisher scoring algorithm in (2.4), using the expressions for the score function and Fisher information matrix in (2.8) and (2.9).

2.2.5 Overdispersion in Binomial GLM

In this section, the concept of overdispersion in the binomial model is introduced and its possible causes and implications are presented. Overdispersion occurs when the empirical variance, i.e. the variance observed in the data, is much larger than the variance assumed by the model. In the case of the binomial model, this can occur because the variance of the model is a function of the predicted mean. There are two primary reasons for overdispersion in the binomial model. The first is unobserved heterogeneity, which the covariates fail to explain. The second reason is positive correlations between the responses of the individual observations that belong to the same group. Such correlation may arise if the individual observations within each group are not independent, a reason for which is that they might stem from a cluster (Dunn and Smyth, 2018; Fahrmeir et al., 2013).

Following Fahrmeir et al., 2013 the overdispersion parameter ϕ can be estimated as the average Pearson statistic or the average deviance. The Pearson residuals and the Pearson statistic are defined as

$$r_j = \frac{\bar{y}_j - \hat{\pi}_j}{\sqrt{\hat{\pi}_j(1-\hat{\pi}_j)/n_j}} \quad \text{and} \quad P = \sum_{j=1}^{G} r_j^2, \tag{2.10}$$

where $\hat{\pi}_j = h(\mathbf{x}_j^{\intercal}\hat{\boldsymbol{\beta}})$. In Collett, 1991, the deviance residuals and the deviance are given by

$$d_j = \text{sign}(\bar{y}_j - \hat{\pi}_j)\sqrt{2n_j\left\{\bar{y}_j \log\left(\frac{\bar{y}_j}{\hat{\pi}_j}\right) + (1-\bar{y}_j)\log\left(\frac{1-\bar{y}_j}{1-\hat{\pi}_j}\right)\right\}} \quad \text{and} \quad D = \sum_{j=1}^{G} d_j^2, \tag{2.11}$$

where $\text{sign}(\bar{y}_j - \hat{\pi}_j)$ equals 1 if $\bar{y}_j \geq \hat{\pi}_j$ and -1 if $\bar{y}_j < \hat{\pi}_j$. If the group sizes n_j are sufficiently large, both the Pearson statistic and the deviance are approximately chi-squared distributed with $G - p$ degrees of freedom, where $p = k + 1$ is the number of coefficients in the model (Fahrmeir et al., 2013). The estimates of the overdispersion parameter, based on the Pearson statistic and the deviance, are then given by

$$\hat{\phi}_P = \frac{P}{G-p} \quad \text{and} \quad \hat{\phi}_D = \frac{D}{G-p},$$

respectively. If the estimated dispersion parameter is significantly greater than 1, it indicates overdispersion (Fahrmeir et al., 2013). The presence of overdispersion leads to underestimated

standard errors for the coefficients in the model (Dunn and Smyth, 2018). Therefore, significance tests for the coefficients may suggest that the coefficients are more significant than they really are.

One possible way to address overdispersion is to introduce the overdispersion parameter, assuming that $Var(\bar{y}_j) = \phi\pi_j(1-\pi_j)/n_j$. This leads to what is called a quasi-binomial model. Another approach is to include random effects in the model in the case of possibly correlated responses (Fahrmeir et al., 2013). It is also possible to improve the model fit by including additional terms or interaction terms, thereby potentially reducing the unobserved heterogeneity (Collett, 1991).

2.2.6 Hypothesis Tests

In this section on hypothesis tests, we present several tests to assess the significance of explanatory variables. In order to test the significance of one of the regression coefficients β_j, $j = 0, 1, \ldots, k$, one can use the t-test based on the hypotheses

$$H_0 : \beta_j = 0 \quad \text{vs} \quad H_1 : \beta_j \neq 0,$$

which are referred to as the null hypothesis and alternative hypothesis, respectively. To perform this test, we calculate and evaluate the t-statistic

$$t_j = \frac{\hat{\beta}_j}{\sqrt{\hat{a}_{jj}}},$$

where $\hat{a}_{jj}$ is the estimated variance of the estimated coefficient $\hat{\beta}_j$. The estimated variance $\hat{a}_{jj}$ is the jth diagonal element of the estimated covariance matrix $\hat{\boldsymbol{A}} = \boldsymbol{F}^{-1}(\hat{\boldsymbol{\beta}})$, which follows from the asymptotic distribution of $\hat{\boldsymbol{\beta}}$ in (2.5). The statistic is t-distributed with $n - p$ ($G - p$ for the binomial model) degrees of freedom. The significance can be evaluated based on the p-value from the test, which is the probability of obtaining a more extreme value for the statistic than the observed value. If the p-value is smaller than a chosen significance level α, we can reject the null hypothesis.

The Wald test is a more general approach for testing linear hypotheses about the regression coefficients on the form

$$H_0 : \boldsymbol{C\beta} = \mathbf{d} \quad \text{vs} \quad H_1 : \boldsymbol{C\beta} \neq \mathbf{d}, \tag{2.12}$$

where $\mathbf{d}$ is a vector of length r and the matrix $\mathbf{C}$, of dimension $r \times p$, has full row rank $r \leq p$. The Wald test is based on the Wald statistic

$$W_S = (\mathbf{C}\hat{\boldsymbol{\beta}} - \mathbf{d})^\intercal [\mathbf{C}\hat{\mathbf{A}}\mathbf{C}^\intercal]^{-1} (\mathbf{C}\hat{\boldsymbol{\beta}} - \mathbf{d}),$$

where $\hat{\mathbf{A}}$ is the estimated covariance matrix of $\hat{\boldsymbol{\beta}}$. Since $\hat{\boldsymbol{\beta}}$ is approximately normally distributed according to (2.5), the Wald statistic has an asymptotic chi-squared distribution with r degrees of freedom under H_0. With appropriate choices of $\mathbf{C}$ and $\mathbf{d}$, one can test a wide range of hypotheses, for instance hypotheses such as $H_0 : \beta_1 = \beta_2$ against $H_1 : \beta_1 \neq \beta_2$.

The likelihood ratio (LR) test is a test based on likelihood calculations used to evaluate the hypotheses in (2.12). Let $\boldsymbol{\beta}$ be the coefficients under the full model and $\boldsymbol{\beta}_{alt}$ the coefficients for the alternative model subject to the constraints $\mathbf{C\beta} = \mathbf{d}$. The LR statistic is then given by

$$LR = -2\big(l(\hat{\boldsymbol{\beta}}_{alt}) - l(\hat{\boldsymbol{\beta}})\big), \tag{2.13}$$

where $l(\hat{\boldsymbol{\beta}})$ is the unrestricted maximum likelihood and $l(\hat{\boldsymbol{\beta}}_{alt})$ is the restricted maximum likelihood under H_0. The LR statistic has an asymptotic chi-squared distribution with r degrees of freedom under H_0.

The scaled deviance of a model with parameters $\boldsymbol{\beta}$ is defined in McCullagh and Nelder, 1989 as

$$D^*(\boldsymbol{\beta}) = 2l_s - 2l(\boldsymbol{\beta}),$$

where l_s is the maximized log-likelihood under the saturated model, i.e. where the fitted values coincide with the observed values. The scaled deviance is also given by $D^*(\boldsymbol{\beta}) = D(\boldsymbol{\beta})/\phi$, where ϕ is the dispersion parameter in the exponential family and D is the deviance. That is, ϕ represents σ^2 for the normal distribution or the overdispersion parameter ϕ in the quasi-binomial model. The deviance for the binomial model is given in (2.11) and for the Gaussian model the deviance is $\sum_{i=1}^{n}(y_i - \hat{\mu}_i)^2$. The scaled deviance is approximately or asymptotically chi square distributed with degrees of freedom equal to the difference between the number of observations and the number of coefficients (Fahrmeir et al., 2013; McCullagh and Nelder, 1989). Using the relation between the scaled deviance and the log-likelihood of the model, the LR statistic in (2.13) can be written as

$$\begin{aligned} LR &= -2l(\hat{\boldsymbol{\beta}}_{alt}) - [-2l(\hat{\boldsymbol{\beta}})] \\ &= D^*(\hat{\boldsymbol{\beta}}_{alt}) - 2l_s - [D^*(\hat{\boldsymbol{\beta}}) - 2l_s] \\ &= D^*(\hat{\boldsymbol{\beta}}_{alt}) - D^*(\hat{\boldsymbol{\beta}}). \end{aligned}$$

2.2.7 Model Diagnostics

Model misspecification can result in biased and inefficient estimates of the covariate coefficients and invalid variance estimates, which may lead to wrong conclusions (McCulloch et al., 2008). It is therefore essential to detect model misspecification, which can be done by evaluating the assumptions of the model.

As mentioned in Section 2.2.5, the Pearson and deviance statistics given in (2.10) and (2.11) can be used to indicate whether or not the variance in the data is captured by the fitted model. They are therefore considered goodness of fit measures for the binomial model.

Assessing the distribution of the residuals is an important step in model evaluation. The standardized residuals for the linear model are given in Fahrmeir et al., 2013 as

$$r_i = \frac{y_i - \mathbf{x}_i^\intercal \hat{\boldsymbol{\beta}}}{\hat{\sigma}\sqrt{1 - h_i}},$$

where h_i is the leverage of observation i, and is the ith diagonal element of the hat matrix $\mathbf{H} = \mathbf{X}(\mathbf{X}^\intercal\mathbf{X})^{-1}\mathbf{X}^\intercal$.

Accordingly, it is possible to standardize the Pearson and deviance residuals of the binomial model, given in (2.10) and (2.11), by dividing them by $\sqrt{1 - h_j}$ or with $\sqrt{\hat{\phi}(1 - h_j)}$ in the case of using a quasi-binomial model (Dunn and Smyth, 2018). Here, the hat matrix is $\mathbf{H} = \mathbf{W}^{1/2}\mathbf{X}(\mathbf{X}^\intercal\mathbf{W}\mathbf{X})^{-1}\mathbf{X}^\intercal\mathbf{W}^{1/2}$, where $\mathbf{W}$ is the diagonal matrix of working weights used in fitting the model. For the logistic model, the jth diagonal element is $w_j = n_j\hat{\pi}_j(1 - \hat{\pi}_j)$. When the model assumptions are correct, the standardized deviance residuals can be approximated by the standard normal distribution (Collett, 1991).

2.3 Correlation-Inducing Data Structure

In the generalized linear model, the responses y_i, $i = 1, \ldots, n$, were assumed to be independently distributed. However, there are some situations in which this assumption may not be reasonable. One such situation arises in the case of longitudinal data, where there are repeated measurements on the same subjects over time. The other situation is in the case of clustered data, where measurements are made on related subjects, e.g. subjects that belong to the same schools, locations, countries etc. Measurements on one individual in the case of longitudinal data or on a group of individuals within one cluster may be more alike than measurements on different individuals or clusters, which could result in correlated responses (Dobson and Barnett, 2008; Fahrmeir et al., 2013).

2.3.1 Multilevel Data Structure

Consider a multilevel data structure, as illustrated in Figure 2.1 for three levels. Imagine, for example, that measurements are made on individual salmon (level 3) that are grouped within different cages (level 2). The different cages, in turn, are located at different salmon farms (level 1). This is called a *nested* data structure, which points to the property that all observations from one cluster group on the second level belong to the same cluster group on the first level. In the context of the example, this means that all salmon that belong to the same cage also belong to the same salmon farm. The illustration in Figure 2.1 then represents this nested data structure for three salmon farms, each with five cages, where measurements are made on four salmon in each of the cages. In the illustration we also notice that the number of observations at the third level are equal for all level 2 clusters and within each level 1 cluster there are the same number of level 2 clusters.

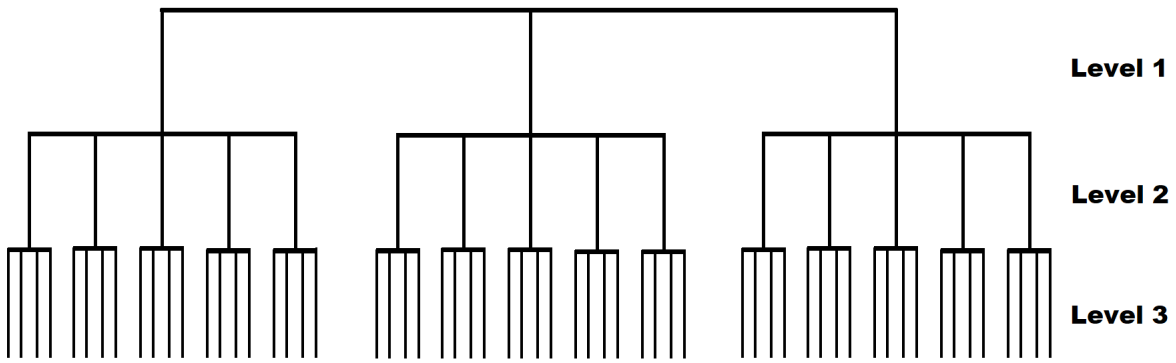


Figure 2.1: Illustration of nested multilevel structure.

Source: Inspiration from Dobson and Barnett, 2008, p. 208.

We generalize this data structure to other numbers of observations and clusters. Let N be the number of clusters at the first level. For each first-level cluster $i = 1, \ldots, N$, let n_i be the number of clusters at the second level, indexed by $j = 1, \ldots, n_i$. At the third level, the number of observations in cluster ij is n_{ij}, and the observations are indexed by $h = 1, \ldots, n_{ij}$. Each observed response is then denoted by y_{ijh} and we assume that there are k explanatory variables, $x_{ijh1}, \ldots, x_{ijhk}$, measured for the outcome. We define the covariate vector for observation ijh

as $\mathbf{x}_{ijh} = (1, x_{ijh1}, \ldots, x_{ijhk})^\intercal$. The observations in this 3-level data structure are then given by

$$(y_{ijh}, \mathbf{x}_{ijh}), \quad i = 1, \ldots, N, \quad j = 1, \ldots, n_i, \quad h = 1, \ldots, n_{ij}. \tag{2.14}$$

Imagine instead that some measurement is made on the cage level, i.e. the second level in Figure 2.1, so that the third level is irrelevant and we have a 2-level data structure. The observations are then given by cluster $i = 1, \ldots, N$ at the first level and the observation $j = 1, \ldots, n_i$ at the second level. The covariate vector associated with each observed response y_{ij} is denoted by $\mathbf{x}_{ij} = (1, x_{ij1}, \ldots, x_{ijk})^\intercal$, and the observations in the 2-level data structure are then given by

$$(y_{ij}, \mathbf{x}_{ij}), \quad i = 1, \ldots, N, \quad j = 1, \ldots, n_i. \tag{2.15}$$

The structure for this 2-level data is also visualized in Table 2.1.

Table 2.1: 2-level data structure.

Level 1 cluster	**Observation**	**Response**	**Covariates**
1	1	y_{11}	$x_{111}, \ldots, x_{11k}$
1	2	y_{12}	$x_{121}, \ldots, x_{12k}$
$\vdots$	$\vdots$	$\vdots$	$\vdots$
1	n_1	y_{1n_1}	$x_{1n_11}, \ldots, x_{1n_1k}$
$\vdots$	$\vdots$	$\vdots$	$\vdots$
N	1	y_{N1}	$x_{N11}, \ldots, x_{N1k}$
N	2	y_{N2}	$x_{N21}, \ldots, x_{N2k}$
$\vdots$	$\vdots$	$\vdots$	$\vdots$
N	n_N	y_{Nn_N}	$x_{Nn_N1}, \ldots, x_{Nn_Nk}$

2.4 Mixed Models

Mixed models takes correlation between observations into account by allowing for individual- or cluster-specific effects to be estimated. This is achieved by including *random* effects for the grouping variables in addition to the *fixed* effects $\boldsymbol{\beta} = (\beta_0, \beta_1, \ldots, \beta_k)^\intercal$ in the linear predictor in (2.2). Consider multilevel data with one grouping level, as given in (2.15). The linear predictor for observation ij is then given as

$$\eta_{ij} = \mathbf{x}_{ij}^\intercal \boldsymbol{\beta} + \mathbf{u}_{ij}^\intercal \boldsymbol{\gamma}_i, \tag{2.16}$$

where $\mathbf{u}_{ij}$ is the vector of random-effects variables, usually a subvector of the vector $\mathbf{x}_{ij} = (1, x_{ij1}, \ldots, x_{ijk})^\intercal$ of fixed-effects variables. Furthermore, $\boldsymbol{\gamma}_i$ is a vector of cluster-specific (or random) effects for cluster i. The random effects are assumed to be independent and identically normally distributed with $\boldsymbol{\gamma}_i \sim N(\mathbf{0}, \mathbf{Q})$, where $\mathbf{Q}$ is the covariance matrix. The name *mixed* models refers to this mixture of both fixed effects and random effects in the linear predictor (Fahrmeir et al., 2013).

2.4.1 The Linear Mixed Model

In this section, the linear mixed model (LMM) and an estimation procedure for the fixed and random effects is presented, following the theory in Fahrmeir et al., 2013 unless otherwise specified.

Consider observations $(y_{ij}, \mathbf{x}_{ij})$ resulting from data with one grouping level, which gives the linear predictor in (2.16). We assume that the responses are conditionally normally distributed with mean μ_{ij} and variance σ^2, given the random effect $\boldsymbol{\gamma}_i \sim N(\mathbf{0}, \mathbf{Q})$. Furthermore, we assume that the expectation can be linked linearly to the linear predictor through $\mu_{ij} = \eta_{ij} = \mathbf{x}_{ij}^\intercal \boldsymbol{\beta} + \mathbf{u}_{ij}^\intercal \boldsymbol{\gamma}_i$, resulting in the linear mixed model

$$y_{ij} = \mathbf{x}_{ij}^\intercal \boldsymbol{\beta} + \mathbf{u}_{ij}^\intercal \boldsymbol{\gamma}_i + \epsilon_{ij}, \tag{2.17}$$

where $\epsilon_{ij} \sim N(0, \sigma^2)$. By defining

$$\begin{aligned}
\mathbf{y}_i &= (y_{i1}, \ldots, y_{in_i})^\intercal, & \mathbf{y} &= (\mathbf{y}_1^\intercal, \ldots, \mathbf{y}_N^\intercal)^\intercal, \\
\mathbf{X}_i &= (\mathbf{x}_{i1}, \ldots, \mathbf{x}_{in_i})^\intercal, & \mathbf{X} &= (\mathbf{X}_1, \ldots, \mathbf{X}_N)^\intercal, \\
\mathbf{U}_i &= (\mathbf{u}_{i1}, \ldots, \mathbf{u}_{in_i})^\intercal, & \mathbf{U} &= \text{blockdiag}(\mathbf{U}_1, \ldots, \mathbf{U_N}), \\
\boldsymbol{\epsilon}_i &= (\epsilon_{i1}, \ldots, \epsilon_{in_i})^\intercal, & \boldsymbol{\epsilon} &= (\boldsymbol{\epsilon}_i^\intercal, \ldots, \boldsymbol{\epsilon}_N^\intercal)^\intercal,
\end{aligned}$$

and $\boldsymbol{\gamma} = (\boldsymbol{\gamma}_1^\intercal, \ldots, \boldsymbol{\gamma}_N^\intercal)^\intercal$, the linear mixed model in (2.17) can be written in the general form

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{U}\boldsymbol{\gamma} + \boldsymbol{\epsilon}. \tag{2.18}$$

Here, $\boldsymbol{\epsilon} \sim N(\mathbf{0}, \mathbf{R})$ and $\boldsymbol{\gamma} \sim N(\mathbf{0}, \mathbf{G})$, where $\mathbf{R} = \sigma^2 \mathbf{I}$ and $\mathbf{G} = \text{blockdiag}(\mathbf{Q}, \ldots, \mathbf{Q})$.

The model (2.24) can be written as either a conditional or marginal model. The conditional model formulation of $\mathbf{y}$ given the random effects is

$$\begin{aligned}
\mathbf{y} \mid \boldsymbol{\gamma} &\sim N(\mathbf{X}\boldsymbol{\beta} + \mathbf{U}\boldsymbol{\gamma}, \mathbf{R}), \\
\boldsymbol{\gamma} &\sim N(\mathbf{0}, \mathbf{G}).
\end{aligned} \tag{2.19}$$

If we instead define $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\epsilon}^*$ and $\boldsymbol{\epsilon}^* = \mathbf{U}\boldsymbol{\gamma} + \boldsymbol{\epsilon}$, the model can be written as the marginal model

$$\mathbf{y} \sim N(\mathbf{X}\boldsymbol{\beta}, \mathbf{U}\mathbf{G}\mathbf{U}^\intercal + \mathbf{R}). \tag{2.20}$$

Maximum Likelihood Estimation of Parameters

The maximum likelihood estimation of the variance and covariance parameters in the LMM is based on the marginal model in (2.20). In the following, we denote by $\boldsymbol{\psi}$ the unknown variance and covariance parameters in $\mathbf{R}$ and $\mathbf{G}$. Furthermore, we define

$$\mathbf{V}(\boldsymbol{\psi}) = \mathbf{U}\mathbf{G}(\boldsymbol{\psi})\mathbf{U}^\intercal + \mathbf{R}(\boldsymbol{\psi}).$$

The log-likelihood corresponding to the marginal model in (2.20), up to additive constants, is given by

$$l(\boldsymbol{\beta}, \boldsymbol{\psi}) = -\frac{1}{2}\Big(\log \big|\mathbf{V}(\boldsymbol{\psi})\big| + (\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^\intercal \mathbf{V}^{-1}(\boldsymbol{\psi})(\mathbf{y} - \mathbf{X}\boldsymbol{\beta})\Big),$$

where $|\cdot|$ denotes the determinant of a matrix. The maximization of the log-likelihood with respect to $\boldsymbol{\beta}$ results in $\hat{\boldsymbol{\beta}}(\boldsymbol{\psi}) = [\mathbf{X}^\intercal \mathbf{V}^{-1}(\boldsymbol{\psi})\mathbf{X}]^{-1}\mathbf{X}^\intercal \mathbf{V}^{-1}(\boldsymbol{\psi})\mathbf{y}$. The profile log-likelihood $l_P(\boldsymbol{\psi})$ is obtained by inserting the estimated fixed-effect coefficients into the marginal likelihood, i.e. $l_P(\boldsymbol{\psi}) = l(\hat{\boldsymbol{\beta}}(\boldsymbol{\psi}), \boldsymbol{\psi})$. The maximization of the profile log-likelihood with respect to $\boldsymbol{\psi}$ then results in the ML estimator $\hat{\boldsymbol{\psi}}_{ML}$ for the variance and covariance parameters.

The ML estimates of the fixed effects $\boldsymbol{\beta}$ and the random effects $\boldsymbol{\gamma}$ are then found by maximizing the joint log-likelihood of $\mathbf{y}$ and $\boldsymbol{\gamma}$ resulting from the conditional model formulation in (2.19) with the ML estimate $\hat{\boldsymbol{\psi}}_{ML}$ for the variance and covariance parameters. Thus, we write $\hat{\mathbf{R}} = \mathbf{R}(\hat{\boldsymbol{\psi}}_{ML})$, $\hat{\mathbf{G}} = \mathbf{G}(\hat{\boldsymbol{\psi}}_{ML})$ and $\hat{\mathbf{V}} = \mathbf{V}(\hat{\boldsymbol{\psi}}_{ML})$. The joint likelihood can then be written

$$\begin{aligned} L(\boldsymbol{\beta}, \boldsymbol{\gamma}) &= f(\mathbf{y} \mid \boldsymbol{\gamma}) f(\boldsymbol{\gamma}) \\ &\propto \exp\Big(-\frac{1}{2}\Big[(\mathbf{y} - \mathbf{X}\boldsymbol{\beta} - \mathbf{U}\boldsymbol{\gamma})^\intercal \hat{\mathbf{R}}^{-1}(\mathbf{y} - \mathbf{X}\boldsymbol{\beta} - \mathbf{U}\boldsymbol{\gamma}) + \boldsymbol{\gamma}^\intercal \hat{\mathbf{G}}^{-1}\boldsymbol{\gamma} \Big]\Big), \end{aligned}$$

and the log-likelihood, up to additive constants, is

$$l(\boldsymbol{\beta}, \boldsymbol{\gamma}) = \log L(\boldsymbol{\beta}, \boldsymbol{\gamma}) = -\frac{1}{2}\Big((\mathbf{y} - \mathbf{X}\boldsymbol{\beta} - \mathbf{U}\boldsymbol{\gamma})^\intercal \hat{\mathbf{R}}^{-1}(\mathbf{y} - \mathbf{X}\boldsymbol{\beta} - \mathbf{U}\boldsymbol{\gamma}) + \boldsymbol{\gamma}^\intercal \hat{\mathbf{G}}^{-1}\boldsymbol{\gamma} \Big).$$

It can be shown that maximizing this with respect to $\boldsymbol{\beta}$ and $\boldsymbol{\gamma}$ results in the ML estimates

$$\begin{aligned} \hat{\boldsymbol{\beta}}_{ML} &= (\mathbf{X}^\intercal \hat{\mathbf{V}}^{-1}\mathbf{X})^{-1}\mathbf{X}^\intercal \hat{\mathbf{V}}^{-1}\mathbf{y} \\ \hat{\boldsymbol{\gamma}}_{ML} &= \hat{\mathbf{G}}\mathbf{U}^\intercal \hat{\mathbf{V}}^{-1}(\mathbf{y} - \mathbf{X}\hat{\boldsymbol{\beta}}_{ML}). \end{aligned}$$

Bias in ML Estimates of Variance Parameters

It was pointed out in Section 2.2.1 that the maximum likelihood estimate of the variance parameter in the linear model is biased downwards. This can also be shown for the ML estimates of the variance parameters in mixed models. The ML estimates of the fixed effects are not so much impacted by the biased variance parameters, but their standard errors may be affected. However, if $n - p$, i.e. the difference between the number of observations and number of covariates, is relatively large the bias is negligible, but values of $n - p$ smaller than 100 may be of concern (Hedeker and Gibbons, 2006).

The bias can be corrected by an estimation procedure called *restricted* maximum likelihood (REML) that maximizes a restricted likelihood. This procedure is therefore generally preferred over ML estimation. However, the likelihood is modified for different numbers of covariates in the model under REML estimation, so it is not possible to use restricted likelihood ratio tests for comparison of models with different covariates (Hedeker and Gibbons, 2006). Due to this limitation, and since $n - p$ is relatively large for the data sets used in this thesis, the maximum likelihood estimation procedure will be used.

2.4.2 A Linear Random Intercept Model

In the special case where $\mathbf{u}_{ij} = 1$ in the model in (2.17), this defines a linear random intercept model, given by

$$y_{ij} = \mathbf{x}_{ij}^{\intercal}\boldsymbol{\beta} + \gamma_{0i} + \epsilon_{ij} \tag{2.21}$$

The random effect γ_{0i} is called the random intercept (hence the use of the subscript 0) because it allows the intercept of each cluster i to deviate randomly from the intercept β_0 with $\gamma_{0i} \sim N(0, \sigma_\gamma^2)$ (Fahrmeir et al., 2013).

2.4.3 Generalized Linear Mixed Models

The generalized linear mixed model (GLMM) is a generalization of the linear mixed model to models for responses that are assumed to have other distributions than the normal distribution (Fahrmeir et al., 2013). In particular, the responses are assumed to have a conditional distribution belonging to the exponential family. For 2-level data with response y_{ij}, the linear predictor in (2.16) still applies and we denote the conditional expectation given the random effects as $E(y_{ij} \mid \boldsymbol{\gamma}_i) = \mu_{ij}$. In the GLMM, the conditional expectation is assumed to be related to the linear predictor through a link function g, i.e. $g(\mu_{ij}) = \eta_{ij}$, resulting in the model

$$g(\mu_{ij}) = \mathbf{x}_{ij}^{\intercal}\boldsymbol{\beta} + \mathbf{u}_{ij}^{\intercal}\boldsymbol{\gamma}_i. \tag{2.22}$$

2.4.4 GLMMs for Data with Two Levels of Grouping

Mixed models can also be extended to data structures with more than one grouping level. Here we consider the 3-level data structure from (2.14), where each observation is given by $(y_{ijh}, \mathbf{x}_{ijh})$. Then the linear predictor for observation ijh is

$$\eta_{ijh} = \mathbf{x}_{ijh}^{\intercal}\boldsymbol{\beta} + \mathbf{u}_{ijh}^{\intercal}\boldsymbol{\gamma}_i + \mathbf{v}_{ijh}^{\intercal}\boldsymbol{\gamma}_{ij},$$

where $\mathbf{u}_{ijh}$ and $\mathbf{v}_{ijh}$ are vectors of random-effects variables, which usually are subvectors of the vector $\mathbf{x}_{ijh} = (1, x_{ijh1}, \ldots, x_{ijhk})^{\intercal}$ of fixed-effects variables. The random effects $\boldsymbol{\gamma}_i$ and $\boldsymbol{\gamma}_{ij}$ are vectors of cluster-specific effects for cluster i and ij, respectively. They are assumed to be normally distributed with $\boldsymbol{\gamma}_i \sim N(\mathbf{0}, \mathbf{Q}_1)$ and $\boldsymbol{\gamma}_{ij} \sim N(\mathbf{0}, \mathbf{Q}_2)$ (Fahrmeir et al., 2013; Pinheiro and Chao, 2006). Similar to the model with one grouping level, the conditional expectation $E(y_{ijh} \mid \boldsymbol{\gamma}_i, \boldsymbol{\gamma}_{ij}) = \mu_{ijh}$ given the random effects is then assumed to be related to the linear predictor through a link function, i.e. $g(\mu_{ijh}) = \eta_{ijh}$, or

$$g(\mu_{ijh}) = \mathbf{x}_{ijh}^{\intercal}\boldsymbol{\beta} + \mathbf{u}_{ijh}^{\intercal}\boldsymbol{\gamma}_i + \mathbf{v}_{ijh}^{\intercal}\boldsymbol{\gamma}_{ij}. \tag{2.23}$$

In the special case where $\mathbf{u}_{ijh} = \mathbf{v}_{ijh} = 1$, the model is a random intercept model for two grouping levels. It is given by $g(\mu_{ijh}) = \eta_{ijh} = \mathbf{x}_{ijh}^{\intercal}\boldsymbol{\beta} + \gamma_{0i} + \gamma_{0ij}$, where γ_{0i} and γ_{0ij} are the random intercepts for cluster i and ij, respectively.

2.4.5 General Form of GLMMs

The GLMMs in (2.22) and (2.23) can both be written in the general form

$$g(E(\mathbf{y} \mid \boldsymbol{\gamma})) = \boldsymbol{\eta} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\boldsymbol{\gamma}. \tag{2.24}$$

Here, $\boldsymbol{\gamma}$ is the vector of all random effects and is normally distributed with $\boldsymbol{\gamma} \sim N(\mathbf{0}, \mathbf{Q})$, where $\mathbf{Q}$ is a block-diagonal covariance matrix. Additionally, $\mathbf{y}$ is the vector of all responses, and $\mathbf{X}$ and $\mathbf{Z}$ are the design matrices of appropriate dimensions for the fixed-effects and random-effects variables, respectively (Fahrmeir et al., 2013).

2.4.6 Parameter Estimation

Maximum likelihood estimation is a popular method for parameter estimation for GLMMs. For the general GLMM in (2.24), it involves maximization of the likelihood function

$$L(\boldsymbol{\beta}, \mathbf{Q}) = \int f(\mathbf{y} \mid \boldsymbol{\gamma}, \boldsymbol{\beta}) f(\boldsymbol{\gamma} \mid \mathbf{Q}) d\boldsymbol{\gamma}. \tag{2.25}$$

This can not be solved analytically, except for the special case when the responses $\mathbf{y}$ are assumed to be conditionally normally distributed and the identity link is used, resulting in the linear mixed model described in Section 2.4.1. In other cases, it must be solved numerically (Raudenbush et al., 2000).

The likelihood function is an integral, and therefore it needs to be approximated numerically. When the dimension of the integral is small, the Gauss-Hermite quadrature method can be used (Agresti, 2013; Raudenbush et al., 2000). The method is applicable for integrals of the form $\int_{-\infty}^{\infty} f(x) \exp(-x^2) dx$, and approximates it as a weighted sum

$$\int_{-\infty}^{\infty} f(x) \exp(-x^2) dx \approx \sum_{r=1}^{N_{AGQ}} w_r f(x_r),$$

where N_{AGQ} is the number of (adaptive) quadrature points x_r, which are the roots of the Hermite polynomial $H_{N_{AGQ}}(x)$ of degree N_{AGQ} and are symmetric around zero. The weights are given by

$$w_r = \frac{2^{N_{AGQ}-1} N_{AGQ}! \sqrt{\pi}}{N_{AGQ}^2 [H_{N_{AGQ}-1}(x_r)]^2}$$

(McCulloch et al., 2008). If the function f is not centered around zero, many of the quadrature points x_r may be located outside of the integration region of interest. The adaptive Gauss-Hermite quadrature deals with this issue by centering the quadrature points around the mode of the integrand and scaling them based on the estimated curvature at the mode, which reduces the number of quadrature points needed to approximate the integral (Agresti, 2013). In the case of using one quadrature point, $N_{AGQ} = 1$, the adaptive Gauss-Hermite quadrature approximation is equivalent to the first-order Laplace approximation, which is based on a Taylor-series expansion of the log-likelihood around the mode.

The `glmer` function in the `R`-package `lme4` can approximate the integral (2.25) with the adaptive Gauss-Hermite quadrature with up to 25 quadrature points in the case of only one random effect. With more than one random effect, the method is only implemented for the use of one quadrature point (Handayani et al., 2017).

The likelihood approximation method described here can be used with different optimization algorithms to obtain ML estimates of $\boldsymbol{\beta}$ and $\mathbf{Q}$ (Agresti, 2013). The `glmer` function uses the Nelder-Mead and the Bounded Optimisation By Quadratic Approximation (BOBYQA) algorithms (Willis et al., 2020). These are described in more detail in Nelder and Mead, 1965 and Powell, 2009.

2.4.7 A Binomial Mixed Model

Consider the GLMM (2.23) resulting from observations $(y_{ijh}, \mathbf{x}_{ijh})$ from a data structure with two nested grouping levels, as described in Section 2.4.4. Assuming that $y_{ijh} \mid \boldsymbol{\gamma}_i, \boldsymbol{\gamma}_{ij} \sim Bernoulli(\pi_{ijh})$, the model in (2.23) becomes

$$g(\pi_{ijh}) = \mathbf{x}_{ijh}^\intercal \boldsymbol{\beta} + \mathbf{u}_{ijh}^\intercal \boldsymbol{\gamma}_i + \mathbf{v}_{ijh}^\intercal \boldsymbol{\gamma}_{ij}, \tag{2.26}$$

with an appropriate link function g, e.g. the logit link function $g(\pi) = \log(\pi/(1-\pi))$.

If the covariate vector (and the vectors of random-effect variables) is the same for all observations $h = 1, \ldots, n_{ij}$ within each group ij, the data can instead be given by $(n_{ij}, y_{ij}, \mathbf{x}_{ij})$, where $y_{ij} = \sum_{h=1}^{n_{ij}} y_{ijh}$ and $\mathbf{x}_{ij}$ is the covariate vector in common to all observations in group ij. It then follows that y_{ij} has a conditional binomial distribution, i.e. $y_{ij} \mid \boldsymbol{\gamma}_i, \boldsymbol{\gamma}_{ij} \sim Binomial(n_{ij}, \pi_{ij})$, with probability mass function

$$f(y_{ij} = k \mid \boldsymbol{\gamma}_i, \boldsymbol{\gamma}_{ij}) = \binom{n_{ij}}{k} \pi_{ij}^k (1-\pi_{ij})^{n_{ij}-k}, \qquad k = 0, \ldots, n_{ij}.$$

Equivalently, the relative frequency, $\bar{y}_{ij} = y_{ij}/n_{ij}$, has a conditionally scaled binomial distribution $\bar{y}_{ij} \mid \boldsymbol{\gamma}_i, \boldsymbol{\gamma}_{ij} \sim Binomial(n_{ij}, \pi_{ij})/n_{ij}$.

A model for the binomial response probability based on the model (2.26) for the Bernoulli-distributed responses can be written as $g(\pi_{ij}) = \mathbf{x}_{ij}^\intercal \boldsymbol{\beta} + \mathbf{u}_{ij}^\intercal \boldsymbol{\gamma}_i + \gamma_{0ij}$. Here, the subscript h in (2.26) has been omitted, and we have set $\mathbf{v}_{ij} = 1$, giving only a random intercept γ_{0ij} for the binomial grouping level.

The random effect γ_{0ij} on the binomial observation-level is (sometimes) referred to as the observation-level random effect (OLRE). The use of OLRE is a GLMM-specific way to account for overdispersion in a binomial regression model, where each observation is assigned to a unique level of a random effect to absorb the extra-binomial variation (Bolker, 2015; Harrison, 2015).

In the case of only a random intercept for the first grouping level i as well (i.e. setting $\mathbf{u}_{ij} = 1$), and assuming that the logit link function is appropriate, a random intercepts model for the binomial response probability is given by

$$\log\left(\frac{\pi_{ij}}{1-\pi_{ij}}\right) = \eta_{ij} = \mathbf{x}_{ij}^\intercal \boldsymbol{\beta} + \gamma_{0i} + \gamma_{0ij}. \tag{2.27}$$

where $\gamma_{0i} \sim N(0, \sigma_1^2)$ and $\gamma_{0ij} \sim N(0, \sigma_2^2)$.

The parameters in the model (2.27) can be estimated by maximizing the likelihood, which will be derived in the following. By integration over the second-level random intercept, we have

$$f(y_{ij} \mid \boldsymbol{\beta}, \gamma_{0i}, \sigma_2^2) = \int_{\gamma_{0ij}} f(y_{ij} \mid \boldsymbol{\beta}, \gamma_{0i}, \gamma_{0ij}) f(\gamma_{0ij} \mid \sigma_2^2) d\gamma_{0ij},$$

where

$$\begin{aligned} f(y_{ij} \mid \boldsymbol{\beta}, \gamma_{0i}, \gamma_{0ij}) &= \binom{n_{ij}}{y_{ij}} \pi_{ij}^{y_{ij}} (1-\pi_{ij})^{n_{ij}-y_{ij}} \\ &= \exp\left(y_{ij} \log\left(\frac{\pi_{ij}}{1-\pi_{ij}}\right) + n_{ij} \log(1-\pi_{ij}) + \log\binom{n_{ij}}{y_{ij}} \right), \end{aligned}$$

with $\pi_{ij} = \pi_{ij}(\boldsymbol{\beta}, \gamma_{0i}, \gamma_{0ij})$ as in (2.27). Again, let $\mathbf{y}_i = (y_{i1}, \ldots, y_{in_i})$ be the responses for first-level group i. Then the marginal distribution of $\mathbf{y}_i$ is

$$\begin{aligned} f(\mathbf{y}_i \mid \boldsymbol{\beta}, \sigma_1^2, \sigma_2^2) &= \int_{\gamma_{0i}} \prod_{j=1}^{n_i} f(y_{ij} \mid \boldsymbol{\beta}, \gamma_{0i}, \sigma_2^2) f(\gamma_{0i} \mid \sigma_1^2) d\gamma_{0i} \\ &= \int_{\gamma_{0i}} \prod_{j=1}^{n_i} \left[\int_{\gamma_{0ij}} f(y_{ij} \mid \boldsymbol{\beta}, \gamma_{0i}, \gamma_{0ij}) f(\gamma_{0ij} \mid \sigma_2^2) d\gamma_{0ij} \right] f(\gamma_{0i} \mid \sigma_1^2) d\gamma_{0i}, \end{aligned}$$

and the likelihood is given by

$$\begin{aligned} L(\boldsymbol{\beta}, \sigma_1^2, \sigma_2^2) &= \prod_{i=1}^{N} f(\mathbf{y}_i \mid \boldsymbol{\beta}, \sigma_1^2, \sigma_2^2) \\ &= \prod_{i=1}^{N} \left[\int_{\gamma_{0i}} \prod_{j=1}^{n_i} \left[\int_{\gamma_{0ij}} f(y_{ij} \mid \boldsymbol{\beta}, \gamma_{0i}, \gamma_{0ij}) f(\gamma_{0ij} \mid \sigma_2^2) d\gamma_{0ij} \right] f(\gamma_{0i} \mid \sigma_1^2) d\gamma_{0i} \right], \end{aligned}$$

which can be maximized with the parameter estimation procedure described in Section 2.4.6 to obtain ML estimates.

2.4.8 Hypothesis Tests

Hypothesis tests for the fixed effects in GLMMs can be carried out like the tests described in Section 2.2.6 (Fahrmeir et al., 2013).

For testing the significance of a random effect, the likelihood ratio test can be used (Fahrmeir et al., 2013). Consider the model in (2.21) with parameters $\boldsymbol{\theta} = (\boldsymbol{\beta}^\mathsf{T}, \sigma_\gamma^2)$. For testing the significance of a single random effect, in this case the random intercept γ_{0i}, we formulate the hypotheses

$$H_0 : \sigma_\gamma^2 = 0 \quad \text{vs} \quad H_1 : \sigma_\gamma^2 > 0.$$

The LR statistic is calculated as

$$LR = -2\big(l(\hat{\boldsymbol{\theta}}_0) - l(\hat{\boldsymbol{\theta}})\big),$$

where $l(\hat{\boldsymbol{\theta}})$ is the unrestricted maximum log-likelihood and $l(\hat{\boldsymbol{\theta}}_0)$ is the restricted maximum log-likelihood under H_0. When performing a significance test on a single random intercept compared to a model with no random effects, the LR statistic has an asymptotic distribution that is an equal mixture of a chi-square distribution with zero degrees of freedom and a chi-square distribution with one degree of freedom under H_0. We write this kind of mixture distribution as $0.5\chi_0^2 : 0.5\chi_1^2$. However, for testing one scalar random slope in the presence of a random intercept, the LR statistic attains an asymptotic $0.5\chi_1^2 : 0.5\chi_2^2$ mixture distribution (Fahrmeir et al., 2013). Hypothesis tests regarding random effects in models with other random effects structures can be carried out e.g. with a parametric bootstrap likelihood ratio test, as explained in Halekoh and Højsgaard, 2014.

2.4.9 Model Diagnostics

Model diagnostics for GLMMs involve assessing the model assumptions. Since random effects are included in GLMMs, their distributional assumptions should be evaluated (McCulloch et

al., 2008). For the fitted random effects, one should only worry about extreme deviations from normality, since little is known about how non-normal distributions of fitted random effects may affect a GLMM (Bolker, 2015).

Residuals are more difficult to interpret for GLMMs than for GLMs, partly because the expected distribution of the observations changes with the fitted values. A simulation-based approach for creating easily interpretable residuals for GLMMs is proposed by Hartig, 2022. The procedure can be used for the models in (2.17) and (2.27), and follows the steps:

1. Simulate m new responses from the fitted model for each observation $(y_{ij,obs}, \mathbf{x}_{ij})$.
2. For each observation, calculate the empirical cumulative density function $\hat{F}_{ij}$ from the m simulated responses. Assuming that the fitted model is correct, $\hat{F}_{ij}$ then describes the possible values (and their probability) of the response at the predictor combination $\mathbf{x}_{ij}$ of the observed value.
3. Define the residual r_{ij} as the value of the empirical density function at the value of the observed response, i.e. $\hat{F}_{ij}(y_{ij,obs})$. Then a residual $r_{ij} = 0$ means that all simulated values are larger than the observed value, and a residual $r_{ij} = 0.5$ means that half of the simulated values are larger than the observed value.

The residuals are expected to have a uniform distribution on the interval $[0, 1]$ if the model is correct (Hartig, 2022).

2.5 Model Selection

In selecting a model, there needs to be a compromise between a good fit to the data and model complexity, since including too many and irrelevant parameters may result in overfitting (Fahrmeir et al., 2013). Besides the use of hypothesis tests such as the ones presented in Section 2.2.6 and Section 2.4.8 to exclude insignificant parameters, there are other criteria that can also be used.

The Akaike information criterion (AIC) is a popular measure used to compare different models. Let $\boldsymbol{\theta} = (\theta_1, \ldots, \theta_q)$ be the parameter vector of dimension q of the model under consideration. The AIC is then defined as

$$AIC = -2l(\hat{\boldsymbol{\theta}}) + 2q,$$

where $l(\hat{\boldsymbol{\theta}})$ is the maximized log-likelihood. The effect of the term $2q$ is to penalize more complex models. When using this measure in model selection, models with small AIC values are favored (Fahrmeir et al., 2013).

2.6 Collinearity

The problem of collinearity arises when some of the explanatory variables in a model have a near-linear dependence. This can cause the estimated coefficients to be highly dependent on other explanatory variables and their estimated standard errors to become large. Collinearity is therefore mainly a problem when interpretation, rather than prediction, is the goal (Dunn and Smyth, 2018).

Following Montgomery et al., 2012, the easiest way to detect collinearity is to compute the correlations between pairs of variables, where correlations close to one in absolute value are of concern. However, when there is a near-linear dependence involving more than two covariates, pairwise correlations may not be enough to detect collinearity. In such cases, the variance inflation factor (VIF), which is a measure for the dependency between several covariates, can be used instead. For the jth explanatory variable, the VIF is defined as

$$\text{VIF}_j = \frac{1}{1 - R_j^2},$$

where R_j^2 is the coefficient of determination obtained by regressing this explanatory variable on the rest of the explanatory variables. A VIF above 5 or 10 indicates collinearity and the corresponding regression coefficient is likely to be poorly estimated (Montgomery et al., 2012). According to Fahrmeir et al., 2013, there exists a serious collinearity problem if any of the VIFs exceed 10.

To assess the dependency of a categorical explanatory variable on the other variables, the generalized variance inflation factor (GVIF) must be calculated instead. Following Fox and Monette, 1992, the design matrix $\mathbf{X}$ of the p explanatory variables is first partitioned into $\mathbf{X} = (\mathbf{X}_0, \mathbf{X}_1, \mathbf{X}_2)$, where $\mathbf{X}_0$ is the column that contains the constant, $\mathbf{X}_1$ contains the set of indicator variables for the different categories of the categorical variable of interest and $\mathbf{X}_2$ contains all other explanatory variables. Each column of $\mathbf{X}_1$ and $\mathbf{X}_2$ is then centered with mean 0 and scaled to length 1. Further, let $\mathbf{R}$ be the correlation matrix for all the columns in $\mathbf{X}_1$ and $\mathbf{X}_2$, and let $\mathbf{R}_{11}$ and $\mathbf{R}_{22}$ be the correlation matrices for $\mathbf{X}_1$ and $\mathbf{X}_2$, respectively. The generalized variance inflation factor for the categorical variable of interest in $\mathbf{X}_1$ is then

$$\text{GVIF}_1 = \frac{|\mathbf{R}_{11}|\,|\mathbf{R}_{22}|}{|\mathbf{R}|},$$

where $|\cdot|$ denotes the determinant of a matrix. For the GVIF to be comparable for categorical variables with differing number of categories, one can calculate the quantity $\text{GVIF}^{1/(2df)}$, where *df* is the number of categories. The GVIF can also be compared with the VIF for numeric variables by squaring this quantity, i.e. $\left(\text{GVIF}^{1/(2df)}\right)^2$. Throughout this thesis, we will refer to this as the comparable GVIF.

2.7 Variables and Model Interpretation

Consider responses y_i, $i = 1, \ldots, n$, with k corresponding explanatory variables x_{ij}, $j = 1, \ldots, k$. The linear regression model (2.3) fitted to this data, where a variable $x_{i0} = 1$ is included for all observations (thus including an intercept), results in the estimated model for the mean μ_i

$$\hat{\mu}_i = \hat{\beta}_0 + \hat{\beta}_1 x_{i1} + \ldots + \hat{\beta}_j x_{ij} + \ldots + \hat{\beta}_k x_{ik}. \tag{2.28}$$

Here, $\hat{\beta}_j$, $j = 1, \ldots, k$, is the estimated regression coefficient of the jth explanatory variables and $\hat{\beta}_0$ is the estimated regression coefficient for the intercept. In the case where all the explanatory variables are numeric, the intercept represents the estimated mean when all the variables have the value zero. However, if the range of the explanatory variables do not include zero, the intercept has no practical interpretation (Montgomery and Peck, 1982). If, for example, measurements are made on adults, and one of the explanatory variables is the height of the individual measured in meters, this will never have the value zero. Thus, the intercept will represent the estimated mean for a height of 0 meters, which is not of particular interest. For a numeric variable x_{ij}, the regression coefficient $\hat{\beta}_j$ represents the change in the estimated mean $\hat{\mu}_i$ by a unit change in x_{ij}. This type of regression coefficient is also referred to as the slope of x_{ij}.

2.7.1 Centering and Scaling of Covariates

A popular scaling technique for numerical explanatory variables is the unit normal scaling. Consider the jth explanatory variable x_{ij} for each observation $i = 1, \ldots, n$. The unit normal scaling of the variable is obtained by subtracting the sample mean $\bar{x}_j = \sum_{i=1}^{n} x_{ij}/n$ of the covariate and dividing by the sample standard deviation $s_j = \sqrt{\sum_{i=1}^{n}(x_{ij} - \bar{x}_j)^2/(n-1)}$. The centered and scaled variable is then given by

$$x_{ij}^* = \frac{x_{ij} - \bar{x}_j}{s_j} \tag{2.29}$$

for each observation $i = 1, \ldots, n$ (Montgomery and Peck, 1982). With this transformation, the new covariate $\mathbf{x}_j^* = (x_{1j}^*, \ldots, x_{nj}^*)^\intercal$ has mean $\bar{x}_j^* = 0$ instead of the mean $\bar{x}_j$ for the untransformed variable. With the unit normal scaling of the jth explanatory variable as in (2.29), we have $x_{ij} = s_j x_{ij}^* + \bar{x}_j$, and the model in (2.28) can be written as

$$\begin{aligned}
\hat{\mu}_i &= \hat{\beta}_0 + \hat{\beta}_1 x_{i1} + \ldots + \hat{\beta}_j x_{ij} + \ldots + \hat{\beta}_k x_{ik} \\
&= \hat{\beta}_0 + \hat{\beta}_1 x_{i1} + \ldots + \hat{\beta}_j (s_j x_{ij}^* + \bar{x}_j) + \ldots + \hat{\beta}_k x_{ik} \\
&= (\hat{\beta}_0 + \hat{\beta}_j \bar{x}_j) + \hat{\beta}_1 x_{i1} + \ldots + \hat{\beta}_j s_j x_{ij}^* + \ldots + \hat{\beta}_k x_{ik} \\
&= \hat{\beta}_0^* + \hat{\beta}_1 x_{i1} + \ldots + \hat{\beta}_j^* x_{ij}^* + \ldots + \hat{\beta}_k x_{ik}.
\end{aligned} \tag{2.30}$$

Here we observe that the regression coefficients for the intercept and the jth covariate (which is now centered and scaled) also are changed. A unit increase in x_{ij}^* is now represented by the new coefficient $\hat{\beta}_j^* = \hat{\beta}_j s_j$. In addition, it was mentioned that the intercept $\hat{\beta}_0$ in (2.28) represents the estimated mean when all variables are numeric and have the value zero. In (2.30), we now observe that there is another constant in addition to the original intercept coefficient $\hat{\beta}_0$, i.e. the term $\hat{\beta}_j \bar{x}_j$. Thus, the new intercept becomes $\hat{\beta}_0^* = \hat{\beta}_0 + \hat{\beta}_j \bar{x}_j$. This new intercept now represents the estimated mean when x_{ij} attains its mean value $\bar{x}_j$ (corresponding to $x_{ij}^* = 0$) and the other variables have values of zero.

2.7.2 Categorical Explanatory Variables

A categorical variable does not have a natural measurement scale, but the effect of the variable must be connected to the different categories of the variable. This is achieved with the use of indicator variables (Montgomery and Peck, 1982). Consider the model in (2.28) with $k = 2$, i.e.

$$\hat{\mu}_i = \hat{\beta}_0 + \hat{\beta}_1 x_{i1} + \hat{\beta}_2 x_{i2}, \tag{2.31}$$

where x_{i1} is a numerical variable and x_{i2} is a categorical variable with two different categories A and B. The variable x_{i2} can then be used to represent the two different categories if it is expressed as an indicator variable

$$x_{i2} = \begin{cases} 0 & \text{if observation } i \text{ belongs to category A} \\ 1 & \text{if observation } i \text{ belongs to category B.} \end{cases} \tag{2.32}$$

If observation i belongs to category A, then $x_{i2} = 0$, and the model in (2.31) becomes $\hat{\mu}_i = \hat{\beta}_0 + \hat{\beta}_1 x_{i1}$. For category B, with $x_{i2} = 1$, the model becomes $\hat{\mu}_i = \hat{\beta}_0 + \hat{\beta}_1 x_{i1} + \hat{\beta}_2 = (\hat{\beta}_0 + \hat{\beta}_2) + \hat{\beta}_1 x_{i1}$. That is, the slope $\hat{\beta}_1$ for the numeric variable is the same for the two categories, but the intercept for category B differs by $\hat{\beta}_2$ compared to category A.

The representation of a categorical variable can be extended to one with a different categories. In this case, representing the different categories involves $a-1$ indicator variables (Montgomery and Peck, 1982). Let $a = 3$ be the number of categories. Then the model in (2.31) must be extended to include two indicator variables x_{i2} and x_{i3}, resulting in $\hat{\mu}_i = \hat{\beta}_0 + \hat{\beta}_1 x_{i1} + \hat{\beta}_2 x_{i2} + \hat{\beta}_3 x_{i3}$, where the two indicator variables are now defined as

$$x_{i2} = \begin{cases} 0 & \text{if observation } i \text{ does not belong to category B} \\ 1 & \text{if observation } i \text{ belongs to category B} \end{cases}$$

$$x_{i3} = \begin{cases} 0 & \text{if observation } i \text{ does not belong to category C} \\ 1 & \text{if observation } i \text{ belongs to category C.} \end{cases}$$

For category B, we have $x_{i2} = 1$ and $x_{i3} = 0$, while $x_{i2} = 0$ and $x_{i3} = 1$ for category C. This results in intercepts $\hat{\beta}_0 + \hat{\beta}_2$ and $\hat{\beta}_0 + \hat{\beta}_3$, for category B and C, respectively. However, for category A, both indicator variables are zero, which gives the intercept $\hat{\beta}_0$. Thus, we call A the *reference* category, since the effect of category B and C are given compared to the intercept $\hat{\beta}_0$ for A.

2.7.3 Interaction Terms

Consider the model (2.31), where x_{i1} is a numeric variable and x_{i2} is an indicator variable, as given in (2.32), for a category with two levels A and B. Suppose that the effect of the numeric variable x_{i1} in reality varies for the two categories, as opposed to the assumption of the same effect for the two categories in model (2.31). This can be modeled by including an interaction term between x_{i1} and x_{i2} in (2.31), i.e.

$$\hat{\mu}_i = \hat{\beta}_0 + \hat{\beta}_1 x_{i1} + \hat{\beta}_2 x_{i2} + \hat{\beta}_3 x_{i1} x_{i2}.$$

Thus, for category A, the model becomes $\hat{\mu}_i = \hat{\beta}_0 + \hat{\beta}_1 x_{i1}$. For category B, it is $\hat{\mu}_i = (\hat{\beta}_0 + \hat{\beta}_2) + (\hat{\beta}_1 + \hat{\beta}_3) x_{i1}$. We notice that the intercept for B differs with $\hat{\beta}_2$ from A, and the slope for x_{i1} for B differs by $\hat{\beta}_3$, compared to A.

3 Data Preparation and Exploration

In this section, a description of the provided data and the data preparation are given, followed by an initial exploration of the data.

3.1 Data Set and Preparation

The provided data that were analysed in this thesis were collected from 2020 to the fall of 2022, and contain information about the use of four delousing methods, namely freshwater treatment, Optilicer, Hydrolicer, and SkaMik. More specifically, the data were from delousing treatments at the cage-level from different salmon farms located in production areas 5 and 6 along the Norwegian coast (Figure 3.1).

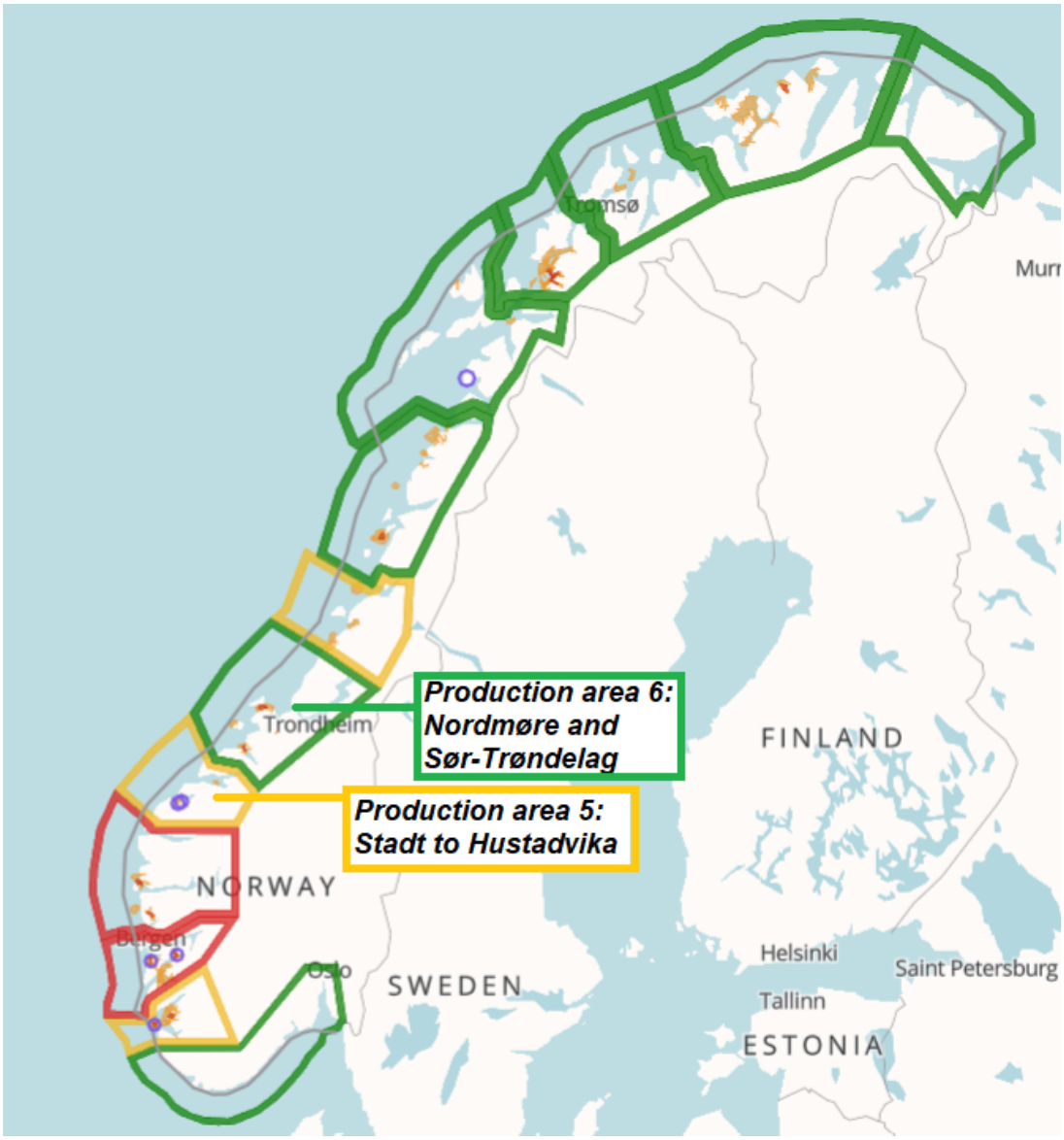


Figure 3.1: Map of production areas along the Norwegian coast. The data were collected from delousing treatments at salmon farms located in production areas 5 and 6.

Source: Modified from BarentsWatch, 2023

The provided data were given in different Excel documents, one for each delousing method per year. An exception is Optilicer, for which there were no observations from 2022. Each observation in the documents represents the delousing of one cage of salmon on a salmon farm location on a specified date. To compare the four delousing methods, the relevant information that was reported for all of the methods was selected and combined to create data sets.

The selected information included the date of treatment, crowding time during handling of the salmon, average weight of the salmon in the cage, the total biomass in the cage and the sea temperature, which were considered possible explanatory variables. In some of the analyses, information about disease at the location and the score of some welfare indicators before treatment were also included as explanatory variables. The location of the farm was also reported for the observations. Since there were several observations from each location, this induced a natural hierarchic structure in the data, which is taken into account. Additionally, the provided data contained information about the average lice number before and after treatment, the cumulative mortality in the following days after treatment, as well as score evaluations for a number of different welfare indicators for the salmon. This information is the basis of the response variables. The variables used in the analysis are described in more detail in the subsequent sections, and a summary of them is given in Table 3.1.

3.1.1 Explanatory Variables

When combining the data from the different documents, the observations were categorized based on the delousing methods used. The categorical variable *Method* was created to keep track of the different delousing methods. The observations where the fish had undergone treatments by use of freshwater treatment, SkaMik, Hydrolicer or Optilicer, were labeled as *Freshwater*, *SkaMik*, *Hydrolicer* and *Optilicer*. The categorical variable was automatically converted into indicator variables when fitting the models in `R`, and these are called *MethodFreshwater*, *MethodSkaMik*, *MethodHydrolicer* and *MethodOptilicer*.

In order to gain a better understanding of the factors influencing the response variables, other explanatory variables than the delousing method were included in the analysis. The reported date of treatment was the basis for the creation of the categorical variable *Season* with four levels, namely *Winter* (December-February), *Spring* (March-May), *Summer* (June-August) and *Fall* (September-November). These categories were also converted to indicator variables, called *SeasonWinter*, *SeasonSpring*, *SeasonSummer* and *SeasonFall*.

The sea temperature, given by *SeaTemp* in degrees Celsius, at the time of the delousing treatment is also included as an explanatory variable. In some cases, *SeaTemp* was the only explanatory variable missing, and an effort was then made to restore the values. The sea temperature that was reported for the location the same week as the date of the delousing was found at BarentsWatch, 2022a and used as an estimate. When using different delousing methods, some precautions are taken to not harm the salmon. The thermal delousing method Optilicer is typically avoided when the sea temperature is high since it requires the use of higher temperatures for the treatment water to obtain a good delousing effect. The use of mechanical delousing methods (Hydrolicer and SkaMik), on the other hand, is often avoided at lower sea temperatures due to slower wound healing when the temperature is lower. As a consequence, there are times of the year where these methods are seldom used, which influences the data sets.

Table 3.1: Description of the variables used in the models.

Variable	Description
Explanatory variables	
Method	Treatment method used: Freshwater, SkaMik, Hydrolicer, Optilicer
Season	Time of year of the treatment: Winter, Spring, Summer, Fall
Disease	Variable indicating whether there was an ongoing pancreas disease (PD) case on the location at the time of the delousing (values: PD or None)
SeaTemp	Temperature in the sea, in °C
SeaTempSc	Centered and scaled value of SeaTemp
AvCrowding	Average crowding time, in minutes
AvCrowdingSc	Centered and scaled value of AvCrowding
AvWeight	Average weight of the salmon in the cage, in kg
AvWeightSc	Centered and scaled value of AvWeight
Biomass	Total biomass in the cage, in metric ton
BiomassSc	Centered and scaled value of Biomass
HaemorrBefore	Degree of skin haemorrhages before treatment (value from 0-3)
ScalelossBefore	Degree of scale loss before treatment (value from 0-3)
Explanatory random variables	
LocNumber	The different locations (salmon farms) Each assigned to a different number (1-31)
Cage	The different cages of salmon treated Each assigned to a different number
Response variables	
CountFemalesBefore	Number of adult female lice before treatment in a sample of 20 fish
CountFemalesAfter	Number of adult female lice after treatment in a sample of 20 fish
NumBefore	Number of salmon before treatment Calculated as (Biomass · 1000 / AverageWeight), rounded to integer
NumDeaths3	Total number of dead salmon during the first 3 days after treatment
NumDeaths14	Total number of dead salmon during the first 14 days after treatment
HaemorrhagesChange	Difference in degree of skin haemorrhages after and before treatment Possible values are in the range -3 to 3
ScalelossChange	Difference in degree of scale loss after and before treatment Possible values are in the range -3 to 3

Before the fish are transferred into the treatment systems, they are crowded in the cage, a process that is often repeated several times on groups of fish to collect all the fish from the cage. The average crowding time before treatment, reported in minutes, is given by the variable *AvCrowding*. This is calculated by dividing the total crowding time by the number of times the crowding procedure was repeated to collect all the fish for treatment. In some observations, a number was written followed by a question mark in the provided data. In these cases, the

observations were inspected more closely, and better estimates were set for the average crowding time. Additionally, the observations with the most extreme values (either very large or small values) for this variable were also inspected more closely, and some typographical errors and calculation mistakes were identified and corrected.

Moreover, two additional variables, namely the average weight of all the salmon in the cage in kilogram (*AvWeight*) and the total biomass in the cage in metric tons (*Biomass*) were included as explanatory variables. In some cases, the average weight was not reported, but information about biomass and the number of fish before treatment was given. For these observations, *AvWeight* was calculated from these quantities.

After the data preparation process described thus far, observations where any of the numeric variables *SeaTemp*, *AvCrowding*, *Biomass* and *AvWeight* had missing values were removed and not used in further analyses. These numeric variables were thereafter centered and scaled by subtracting the mean value of the variable and dividing by the standard deviation, as described in Section 2.7.1. Namely, the centering and scaling process was done before elimination of observations due to invalid response values in the creation of the different data sets. The centering and scaling values are given in Table 3.2 in the same unit as each of the variables. The resulting scaled and centered variables are called *SeaTempSc*, *AvCrowdingSc*, *BiomassSc* and *AvWeightSc*, respectively.

Table 3.2: Mean value and standard deviation of numeric variables used in the centering and scaling process. These values were found before removing any observations due to invalid response values in the creation of the data sets.

Explanatory variable	**Mean**	**Standard deviation**
SeaTemp	11.7	3.30
AvCrowding	62.6	17.97
AvWeight	3.15	1.475
Biomass	438.5	167.00

In addition, information about reported incidences of diseases such as pancreas disease (PD) and infectious salmon anemia was found at BarentsWatch, 2022b. The data provide information about disease cases on salmon farms and the time period for the duration of the cases. This does not necessarily mean that all fish on the farm had the disease in the reported time period, but only that there were discovered cases. Only the time periods from the date of demonstrated cases (not from the date of suspected cases) to the end date of the case were considered here. This information was then merged with the other data based on location and date. There were no observations in the data where cases of infectious salmon anemia had been reported, so there were only reported PD cases. Therefore, the categorical variable *Disease* was created with the levels *PD* and *None*, which resulted in the creation of the indicator variables *DiseasePD* and *DiseaseNone*.

3.1.2 Random Explanatory Variables

Salmon in the same cage may have more in common compared to salmon from other cages, and the same can be said for salmon from different farms. This hierarchic nature of the data motivated the creation of two additional variables, which will be used in some of the models. The salmon farms (locations) were assigned to different numbers from 1 to 31 to maintain

confidentiality. The information of the salmon farms for the observations was stored in the variable *LocNumber*. Similarly, each observation (cage) was assigned to a different number, represented by the variable *Cage*.

3.1.3 Response Variables and Creation of Data Sets

In this section, the response variables are presented and the creation of the data sets for the different responses of interest is described.

One of the aims of this thesis was to compare the delousing effect of the different delousing methods, with particular emphasis on the reduction of adult female lice since they can produce egg strings containing hundreds of eggs. The variables used to evaluate the delousing effect were based on the reported average number of adult female lice from a sample of fish before and after treatment, which were contained in the variables *FemalesBefore* and *FemalesAfter*, respectively. The standard practice is to use a sample size of 20 fish, but smaller sample sizes may occasionally have been used for unknown reasons. Since fitting a binomial model requires integer data, the average lice numbers were multiplied by 20. However, for some observations, multiplying by 20 resulted in non-integer values, which may be due to human errors in the reporting process or due to the use of smaller sample sizes. Since it was not possible to know which was the reason, these numbers were also multiplied by 20 and then rounded to integer values. The variables called *CountFemalesBefore* and *CountFemalesAfter* were created from this count data, representing the total count of adult female lice in a sample of 20 fish before and after treatment, respectively. Initially, there were some observations with missing values for these variables, which were removed from the data set. Observations with zero counts for *CountFemalesBefore* were also removed since they could not provide any information about the effectiveness of the methods. Furthermore, observations with *CountFemalesBefore* less than 5 were removed, because such small values could give very inaccurate estimates of the delousing effect. In cases where the count after treatment was greater than the count before treatment, *CountFemalesAfter* was set to the number of *CountFemalesBefore* due to model requirements, indicating that the treatment had no effect. One observation, with an especially large value of 289 for *CountFemalesBefore*, was also detected and removed, since this was considered a very unlikely value and was more likely to be due to some human mistake. This pre-processing of the data resulted in a data set which was used for modelling the delousing effectiveness against adult female lice. In the following, this data set will be referred to as the delousing effect data set.

Another objective was to investigate the effect of the delousing methods on the salmon, and some welfare indicators (WIs) were considered. The score-based WIs skin haemorrhages and scale loss were selected among other welfare indicators because they were reported for a larger number of observations. The severity of these indicators was evaluated from the sample of fish before and after treatment and reported on a scale of 0-3, which was contained in the variables *HaemorrBefore*, *HaemorrAfter*, *ScalelossBefore* and *ScalelossAfter*. Both of these welfare indicators before treatment were also used as explanatory variables in the analyses concerning fish welfare, as they can provide information about the health status of the fish prior to treatment. When creating data sets with these variables, any observations with missing values or values outside the possible range of 0-3 were removed. However, the response variables of interest were the changes in these indicators after treatment. To capture this, the variables *HaemorrChange* and *ScalelossChange* were created, representing the difference between the value after treatment and before treatment for the skin haemorrhages and scale loss indicators, respectively. These variables can range from -3 to 3, and a positive value indicates a worsening of the condition of

the salmon. Separate data sets were created for the change in skin haemorrhages and the change in scale loss, where also observations with invalid values for *HaemorrAfter* and *ScalelossAfter*, respectively, were removed.

It was also of interest to examine how different delousing methods affect the mortality rate of salmon. To assess the short-term impact, the mortality 3 days after delousing was selected, while mortality after 14 days was used as an indicator for the longer-term effects on mortality. The variable *NumBefore* was created, representing the number of salmon in the cage before the treatment. This number was only reported for two of the delousing methods, and the variable was therefore created by dividing the biomass by the average weight of the salmon in the cage and rounding this quantity to an integer value. The variables *NumDeaths3* and *NumDeaths14* represent the cumulative number of salmon from the cage that had died during the first 3 and 14 days after treatment, respectively. Since these quantities were not always reported for the same observations, two separate data sets for salmon mortality were created, one for mortality after 3 days and one for mortality after 14 days. Observations without reported values for *NumDeaths3* or *NumDeaths14* were excluded from the respective data sets. For four observations, it was reported that some of the fish were slaughtered after the treatment. Due to this, *NumDeaths3* and *NumDeaths14* were considered to be inaccurate, so these observations were not included in either of the mortality data sets. In addition to the explanatory variables presented in Section 3.1.1, the variables *HaemorrBefore* and *ScalelossBefore* were included as explanatory variables in the analyses of salmon mortality. Hence, any observations with missing or invalid values for these variables were also excluded from the data sets.

3.2 Data Exploration

The `R`-code from the data preparation described in the previous section is given in Appendix C. The data preparation resulted in five separate data sets; one for delousing effect, two for salmon mortality after 3 and 14 days, and two for the change in skin haemorrhages and scale loss. The creation of separate data sets for the different responses was done in order to obtain the maximal number of observations for each of the responses. The total number of observations in each of the data sets, as well as the number of observations for the different delousing methods used, is given in Table 3.3. SkaMik constitutes the majority of the observations, while there are fewer observations for the other delousing methods. These data sets are explored further in what follows.

Table 3.3: Number of observations in each of the data sets with number of observations for each delousing method.

Data set	Number of observations for each method				Total number of observations
	Freshwater	Optilicer	Hydrolicer	SkaMik	
Delousing effect	104 (13%)	125 (15%)	162 (20%)	431 (52%)	822
Mortality (3 days)	92 (13%)	99 (14%)	145 (20%)	389 (54%)	725
Mortality (14 days)	85 (13%)	98 (15%)	99 (15%)	369 (57%)	651
Skin haemorrhages	98 (13%)	102 (14%)	148 (20%)	390 (53%)	738
Scale loss	98 (13%)	102 (14%)	148 (20%)	391 (53%)	739

3.2.1 Delousing Effect

An initial data exploration of the data set for delousing effectiveness against adult female lice (delousing effect) is given in this section. Since this data set was used to model the delousing effect, i.e. the probability of removal of a louse when exposed to a delousing method, a variable for the estimated proportion of removed lice after treatment was created for the visualization of the data. In the figures that follow, this proportion is called *PropRemoved*, and it is calculated by dividing (*CountFemalesBefore*-*CountFemalesAfter*) by *CountFemalesBefore* for each observation.

The explanatory variables considered in the analysis of delousing effect are those mentioned in Section 3.1.1, except for the *Disease* variable, which is considered unlikely to affect the delousing effect.

The 822 observations in the delousing effect data set are from 31 locations. The number of observations for the different locations is shown in Figure 3.2, where the different colors distinguish between the number of observations for the different delousing methods. The locations varies a lot in number of observations, ranging from 2 to 60. The distribution of observations over location for each of the methods is also highly variable, and none of the methods are present for all 31 locations. Naturally, as SkaMik accounts for $\sim 52\%$ of the observations, it is also the method that is represented from the most locations compared to the other methods.

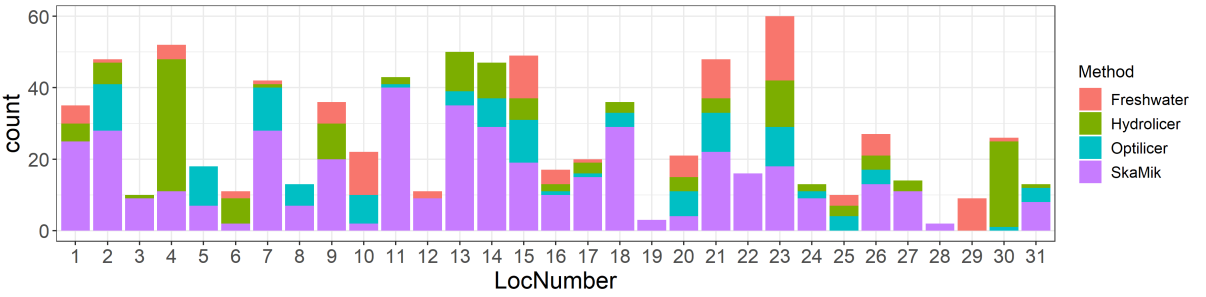


Figure 3.2: Number of observations from the different locations for the data set for delousing effect. The different colors distinguish between the number of observations for the different delousing methods.

The correlation between pairs of numeric variables in the data set was investigated and the results are displayed in Figure 3.3. Scatter plots for each variable pair are shown to the left of the diagonal, the Pearson correlation coefficients are shown to the right of the diagonal, and density plots for each variable are displayed on the diagonal. Some correlation between certain variables is observed, but none of them are found to be highly correlated, i.e. with absolute values close to one. In particular, the variables *AvWeightSc* and *BiomassSc* seem to be moderately correlated, which is a natural consequence of biomass being a product of the number and average weight of the salmon in a cage. The correlation coefficient between these variables was calculated to be 0.473, and is the largest correlation between any pair of variables.

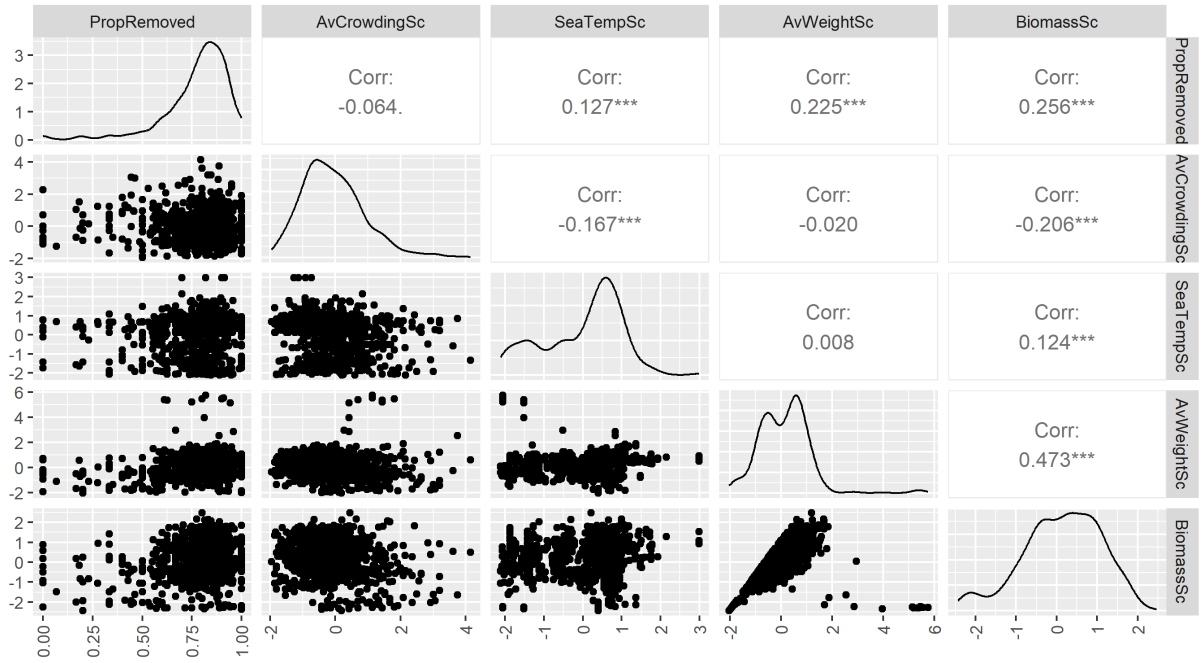
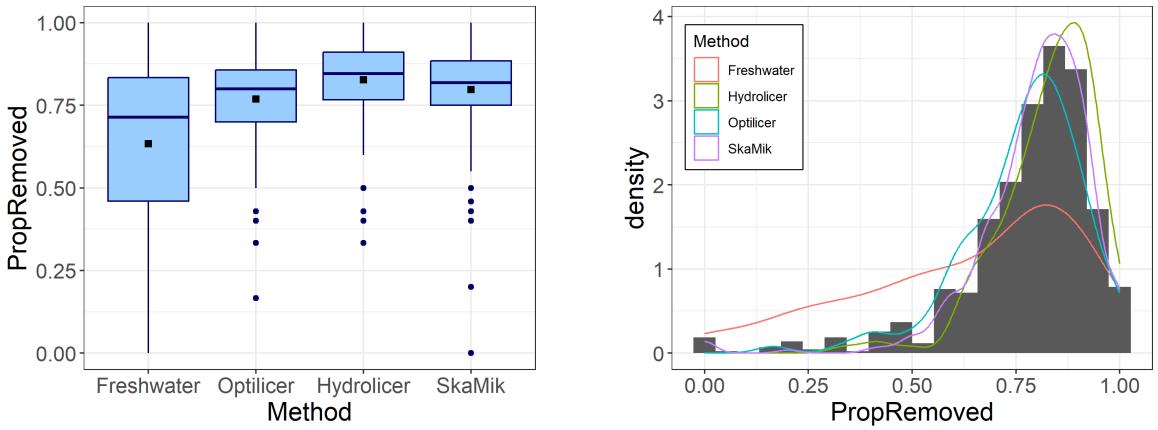


Figure 3.3: Correlations of the numeric variables in the data set for delousing effect. Scatterplots between each pair of numeric variables are displayed on the left side of the diagonal, while the Pearson correlation is shown on the right side. Distribution plots for the variables are shown on the diagonal.



(a) **(b)**

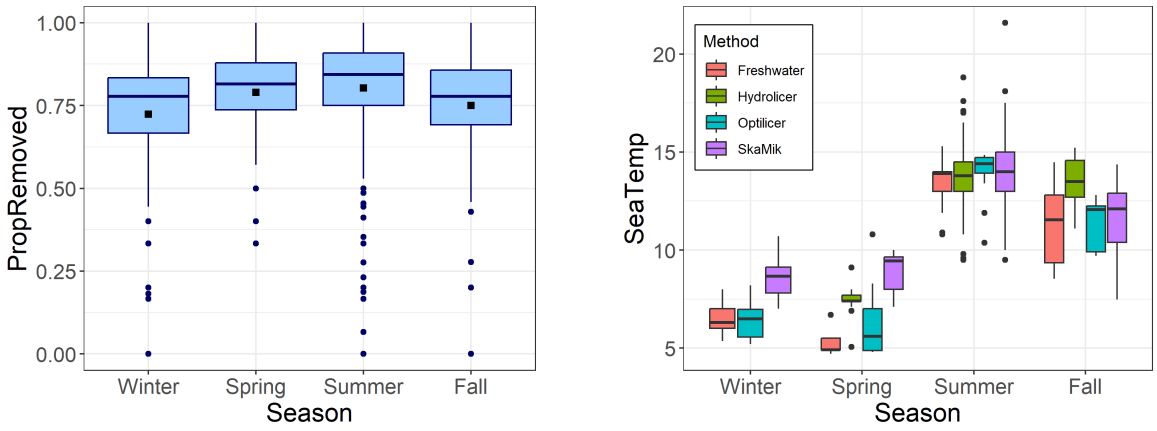
Figure 3.4: **(a):** Box plot of the proportion of adult female lice removed after the treatment for each delousing method. The average values are shown by the black squares. **(b):** Density plot for the proportion of removed lice. The grey histogram shows the density for all the observations. Density curves for each of the different methods are shown with different colors.

A box plot of the proportion of removed adult female lice against delousing method is displayed in Figure 3.4a. The blue boxes mark the interval of the observed values that are between the lower and upper quartiles, i.e. half of the observations are in this interval, which is called the interquartile range. The blue line inside the box shows the median value, while the black square shows the average. From the plot one can observe some differences between the methods, where freshwater seems to have the smallest proportion of removed lice. It is also noticeable that the interquartile range is much larger for the freshwater treatment than for the other methods,

meaning that the observations are more variable for this delousing method. There are smaller differences between the other methods, but Hydrolicer seems to have the highest proportion of removed lice.

The density of the proportion of removed adult female lice is also illustrated in Figure 3.4b. Here, the grey histogram is the density of all observations, and the colored density curves are for each of the delousing methods. All methods have a spike in approximately the same area, around 0.8 to 0.9. However, freshwater seems to have relatively more small values compared to the other methods, and the shape of its density curve stands out from the rest.

Figure 3.5a shows a box plot of the proportion of removed female lice against the season. It indicates that the lice might have a lower probability of surviving the treatment in the summer and spring, but the differences are quite small. However, it is important to keep in mind that some of the methods are rarely or not used at all for certain temperatures or seasons, which is illustrated in Figure 3.5b. It shows a box plot of *SeaTemp* against *Season* for each of the delousing methods. We notice that the sea temperature is lowest in the winter and spring and higher in the summer and fall. Table 3.4 gives the number of observations from the different delousing methods in the different seasons. It also lists the minimum and maximum temperature, as well as the interquartile range, for which the different delousing methods have been used. In the spring and winter, when the temperature is at the lowest, Hydrolicer has been used few times, and has not been used at all in the winter according to this data set. The lowest temperature registered when Hydrolicer was used was 5.1°C, but it has only been used three times at temperatures below 7.4°C, and its interquartile range is from 12.4 to 14.4°C. On the other hand, the second mechanical delousing method, SkaMik, has been used in winter as well. It has been used at temperatures as low as 7°C, but not at any lower temperatures. SkaMik has been used the most during summer and fall, and has an interquartile range from 10.7 to 14.4°C. In contrast, Optilicer is typically avoided when the sea temperature is high, so its interquartile range is from 5.6 to 10.4°C. The highest registered temperature when Optilicer was used was 14.9°C and this was in the summer.



(a) **(b)**

Figure 3.5: (a): Box plot of the proportion of adult female lice removed after the treatment against season. The average values are shown by the black squares. **(b):** Box plot of sea temperature against season for each delousing method.

Table 3.4: Number of observations for the seasons for each delousing method (data set for delousing effect). Additionally, the interquartile range, as well as the minimum and maximum value of the sea temperature for which the different delousing methods have been used is given.

	Number of observations in seasons				Temperature		
Method	Winter	Spring	Summer	Fall	Min	Max	IQR
Freshwater	30	16	43	15	4.7	15.3	6.2-13.9
Optilicer	62	29	26	8	4.8	14.9	5.6-10.4
Hydrolicer	0	21	122	19	5.1	18.8	12.4-14.4
SkaMik	29	20	240	142	7.0	21.6	10.7-14.4

The relation between the sea temperature and the season is even clearer in Figure A.1a in Appendix A. As discussed, the sea temperature is somewhat related to the choice of delousing method, which is more apparent in Figure A.1b. It therefore seems necessary to further assess the severity of the dependency between the explanatory variables in the data set by calculating the comparable generalized variance inflation factor. The function `vif` from the `car`-package (Fox and Weisberg, 2019) in `R` was used to compute these quantities, given in Table 3.5. Here, an interaction effect between *Method* and *SeaTemp* is included, since, by the nature of the different delousing methods, the sea temperature may have different effects depending on the delousing method used. We notice that the value for *SeaTemp* is quite high, with a value of 5.83. However, the value does not exceed 10, in which case there would be a collinearity problem of concern.

Table 3.5: Comparable generalized variance inflation factor for the explanatory variables in the data set for delousing effect. An interaction between delousing method and sea temperature has been included here.

Explanatory variable	df	$\left(\text{GVIF}^{1/(2df)}\right)^2$
Method	3	1.64
SeaTempSc	1	5.83
SeaTempSc:Method	3	2.00
AvWeightSc	1	1.44
AvCrowdingSc	1	1.23
BiomassSc	1	1.81
Season	3	1.95

3.2.2 Salmon Mortality

In this section, an initial data exploration and visualization of the two data sets for salmon mortality after 3 and 14 days is presented. Variables for the proportion of salmon that had died 3 and 14 days after treatment was created for the visualization of the data. The variable for the mortality rate after 3 days is called *Mortality3*, and it is calculated by dividing *NumDeaths3* by *NumBefore* for each observation. Likewise, *Mortality14* is calculated by dividing *NumDeaths14* by *NumBefore*.

In the analyses of salmon mortality, all the explanatory variables introduced in Section 3.1.1 are included. In addition, *HaemorrBefore* and *ScalelossBefore* are considered as possible explanatory variables.

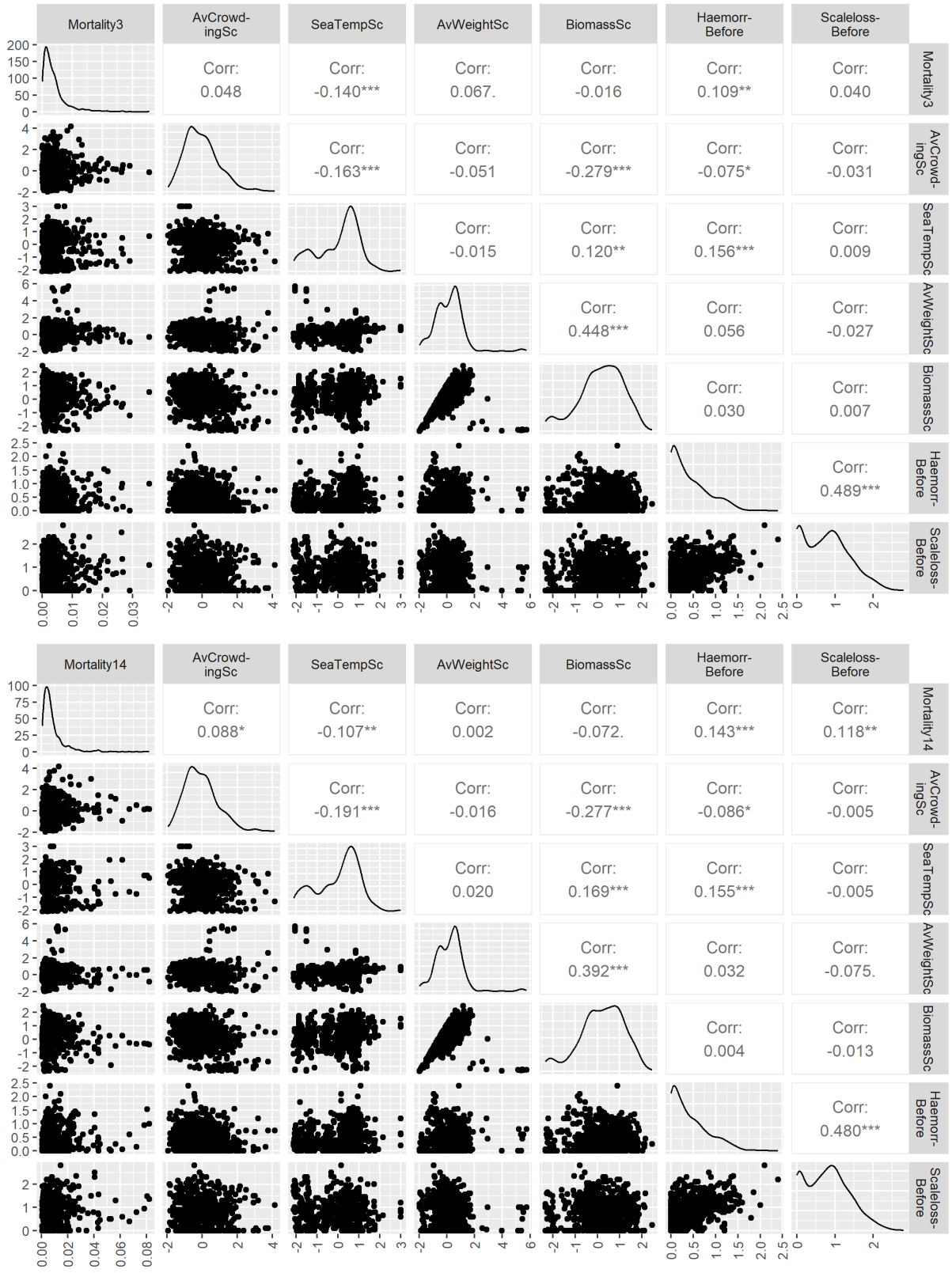
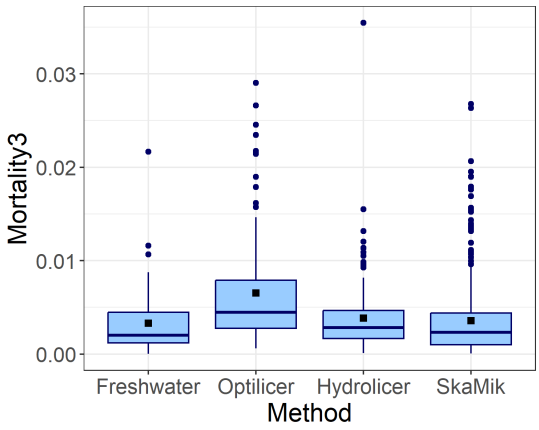


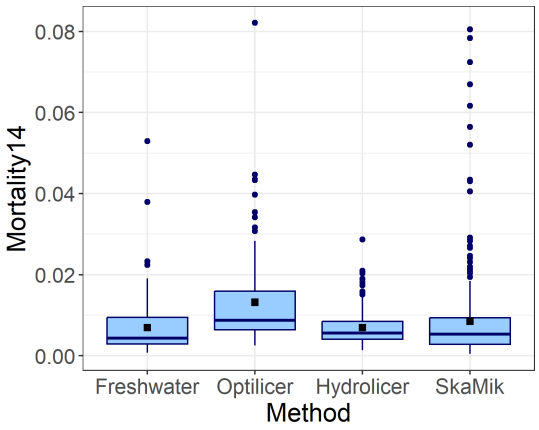
Figure 3.6: Correlations of the numeric variables in the data sets for mortality after 3 days (top) and 14 days (bottom). Scatterplots between each pair of numeric variables are displayed on the left side of the diagonal, while the Pearson correlation is shown on the right side. Distribution plots for the variables are shown on the diagonal.

In both the data sets for mortality, the observations are from 31 locations. The locations varies a lot in number of observations, ranging from 1 to 60 for mortality after 3 days and 1 to 48 for mortality after 14 days (Figure A.2), due to a smaller data set for mortality after 14 days. There is also an uneven distribution of observations over the locations for each of the methods, where none of the methods are present for all the locations.

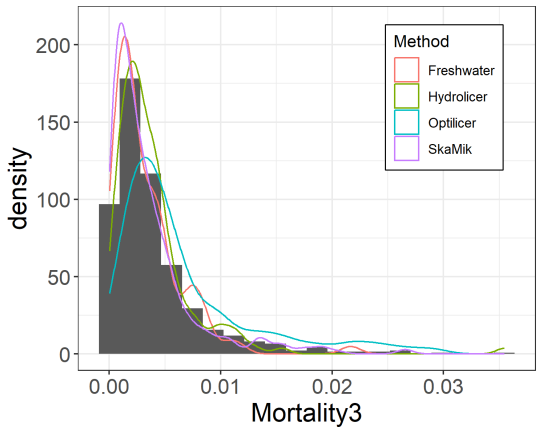
In Figure 3.6, the correlation between each pair of the numeric variables is displayed. The figure in the top and bottom panels show the correlations in the data set for mortality after 3 and 14 days, respectively. As mentioned, the variables *AvWeightSc* and *BiomassSc* are naturally correlated. This is evident in both data sets for salmon mortality, where the Pearson correlation is 0.448 and 0.392, respectively. There is also some correlation between *HaemorrBefore* and *ScalelossBefore*, with values of 0.489 and 0.480 for the two data sets. Both skin haemorrhages and scale loss are probably associated with rough treatment, which may result from earlier delousing treatments or other factors, so this may explain the correlation.



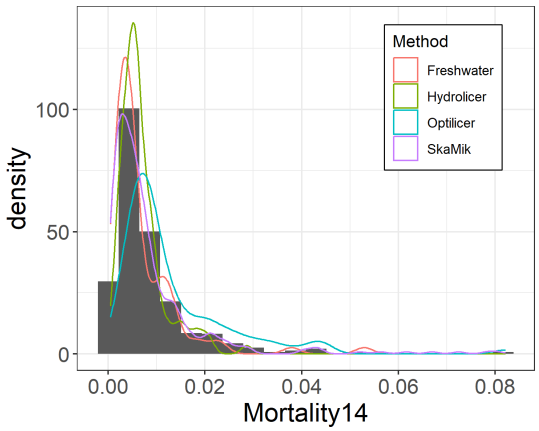
(a) Mortality after 3 days for each delousing method.



(b) Mortality after 14 days for each delousing method.



(c) Density plot for mortality rate after 3 days.

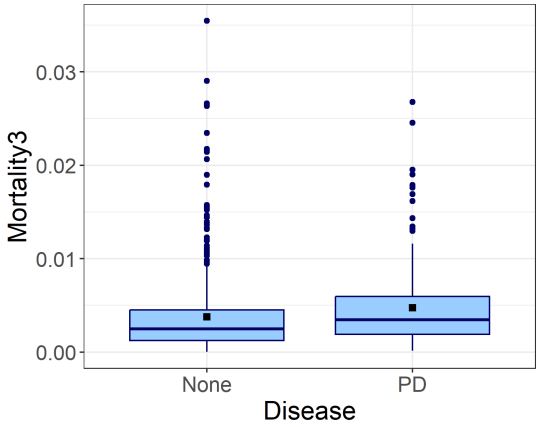


(d) Density plot for mortality rate after 14 days.

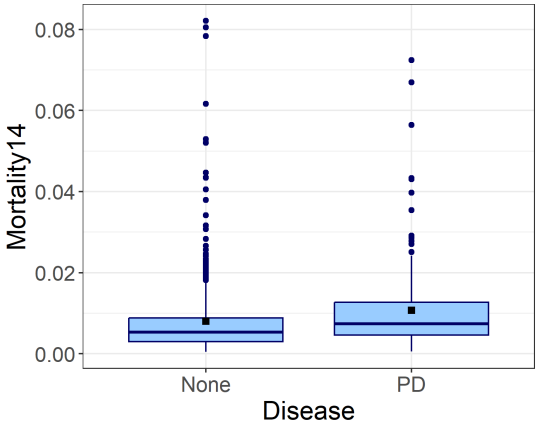
Figure 3.7: Salmon mortality (proportion of fish that had died after 3 and 14 days). **(a)-(b)**: Box plots of mortality rate for each delousing method. The average values are shown by the black squares. **(c)-(d)**: Density plots for mortality rate. The grey histogram shows the density for all observations. Density curves for each of the different delousing methods are shown with different colors. Note the different axis values for mortality after 3 and 14 days.

The mortality rate after 3 and 14 days against the delousing method used is shown in Figure 3.7a and Figure 3.7b, respectively. Comparing the plots for 3 and 14 days, we notice that the mortality rate seems to increase from 3 to 14 days (note the different values on the y-axis), which is expected. We also observe that Optilicer has a noticeably higher median and average value than the other methods both after 3 and 14 days. Optilicer also has a larger interquartile range than the other methods, that is more skewed towards higher mortality rates. This can also be seen in Figure 3.7c and Figure 3.7d, which show the distribution of the mortality rates for the different delousing methods.

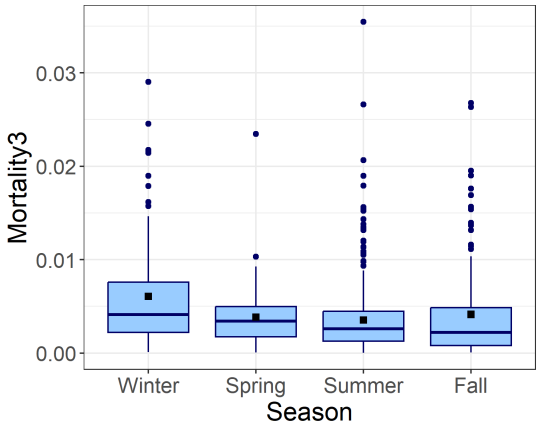
The mortality after 3 and 14 days is also plotted against *Disease*, shown in Figure 3.8a and Figure 3.8b, respectively. In both plots, the mortalities seem to be higher for observations where there has been a PD case on the location at the time of delousing. However, in both data sets for mortality, only 176 observations belonged to the PD group, which make up 24% and 27% of the observations in the data sets for mortality after 3 and 14 days, respectively. Out of these observations, 45 stem from the use of Optilicer, 16 from freshwater, 12 from Hydrolicer and 103 from SkaMik.



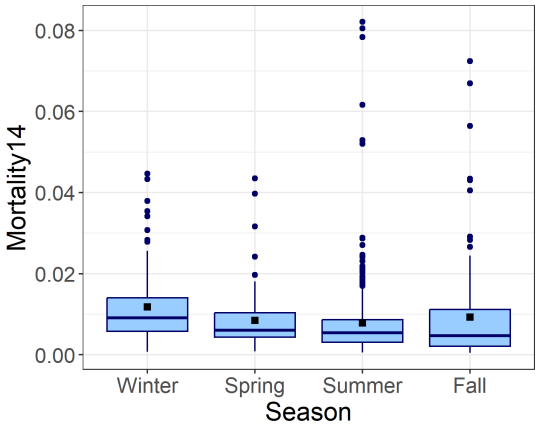
(a) Mortality after 3 days against *Disease*



(b) Mortality after 14 days against *Disease*



(c) Mortality after 3 days for each season



(d) Mortality after 14 days for each season

Figure 3.8: Salmon mortality (proportion of fish that had died after 3 and 14 days) against *Disease* and *Season*. Note the different axis values for mortality after 3 and 14 days.

Figure 3.8c and Figure 3.8d show the mortality rate after 3 and 14 days for each season, respectively. For both 3 and 14 days, the mortality seems to be higher in the winter compared to the

other seasons. However, this is also the time of year when Optilicer, which was associated with higher mortality, is used the most according to these data sets. About $\sim 63\%$ of the observations in the winter are from delousing operations using Optilicer (Table B.1 in Appendix B).

The relation between delousing method, the sea temperature and the season in these data sets is similar to what was described in the previous section. The sea temperature is lowest in the winter and spring (Figure A.3a and A.4a in Appendix A), and the different delousing methods seem to be preferred to be used at different temperatures (Figure A.3b and A.4b), as pointed out in the previous section. This induces a relation between the season and method, where most seasons are dominated by observations from one or two delousing methods (Table B.1). An exception is the spring, which has a more even distribution of observations from all four methods.

The comparable GVIF for the explanatory variables in the data sets for mortality were calculated, and are given in Table B.2. An interaction between *Method* and *SeaTempSc* has been included, since the effect of the different delousing methods on the mortality may vary differently with this variable. In the data sets for mortality after 3 days and 14 days, the variable *SeaTempSc* obtained values of 7.42 and 6.65, respectively. These values are somewhat high, but do not exceed 10.

3.2.3 Score-Based Welfare Indicators

An initial data exploration for the two data sets for change in skin haemorrhages and scale loss is given in this section. In the analyses of the change in WIs, all explanatory variables presented in Section 3.1.1, as well as *HaemorrBefore* and *ScalelossBefore* are considered possible explanatory variables. The latter ones are included since they may contain information about the health status of the salmon prior to the delousing treatment. In addition, since the score of the WIs are limited to the interval 0-3, one can imagine that the change may be smaller if the fish exhibit a higher score of the particular WI in consideration before treatment.

As for the data sets described earlier, the observations in the data sets for change in WIs are from 31 different locations, and the distributions are shown in Figure A.5 in Appendix A. The number of observations for each location varies from 1 to 59 for both data sets. The distribution of the number of observations from each delousing method is also highly variable.

In Figure 3.9, the correlation between each pair of numeric variables is displayed for the two data sets. The figure in the top panel shows the correlations in the data set for change in skin haemorrhages and the figure in the bottom panel shows the correlations in the data set for change in scale loss. As pointed out earlier, the variables *AvWeightSc* and *BiomassSc* are moderately correlated, with values of 0.452 for both data sets. In addition, *HaemorrBefore* and *ScalelossBefore* have moderate correlations of 0.491 and 0.490 for the two data sets. We also notice that *HaemorrBefore* is moderately correlated with *HaemorrChange*, with a value of -0.443, meaning that observations with a smaller degree of skin haemorrhages before treatment tend to have a higher positive change in skin haemorrhages after treatment. The same applies to *ScalelossBefore* and *ScalelossChange*, which are strongly correlated, with a value of -0.614, in the data set for change in scale loss.

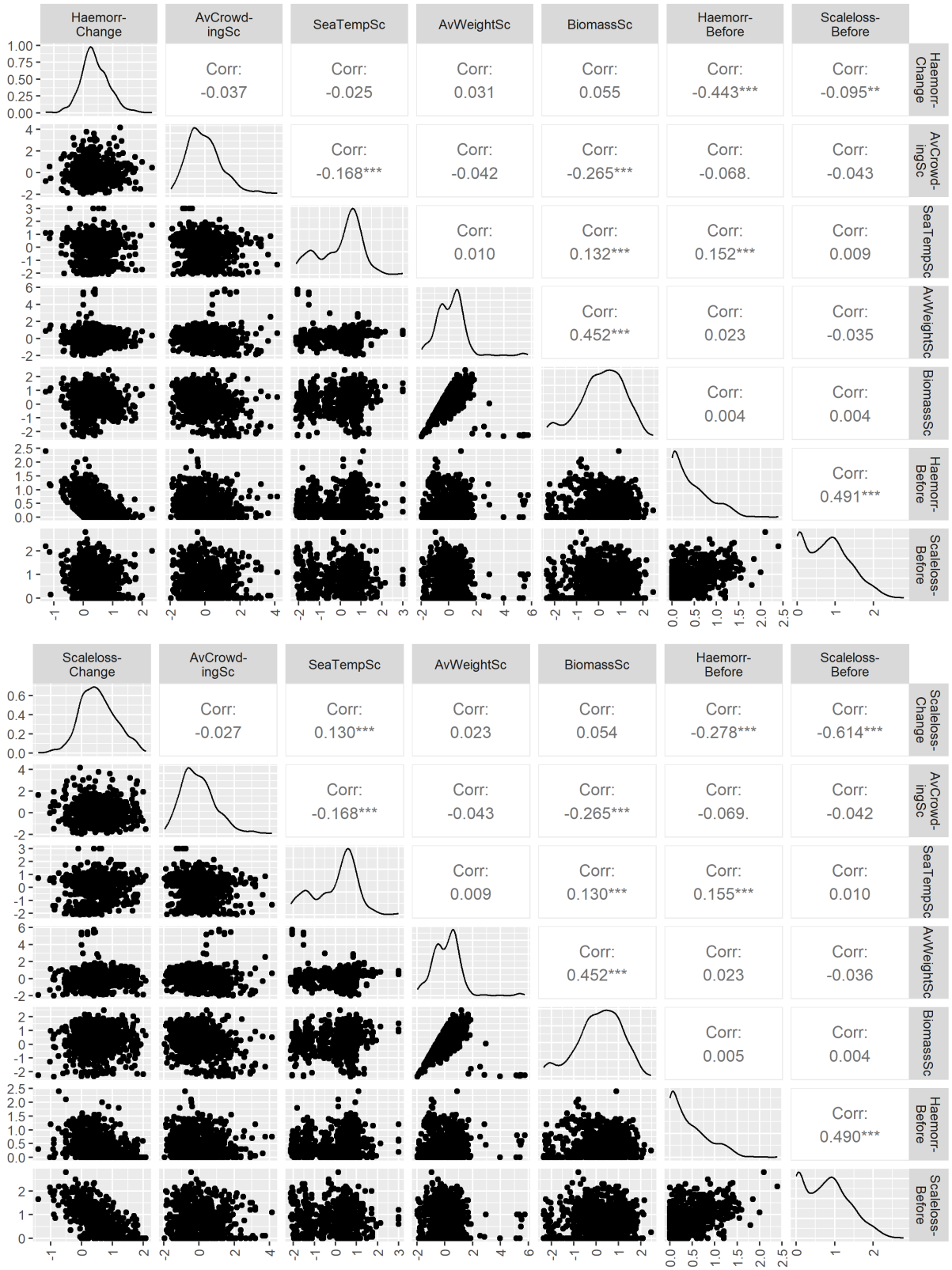
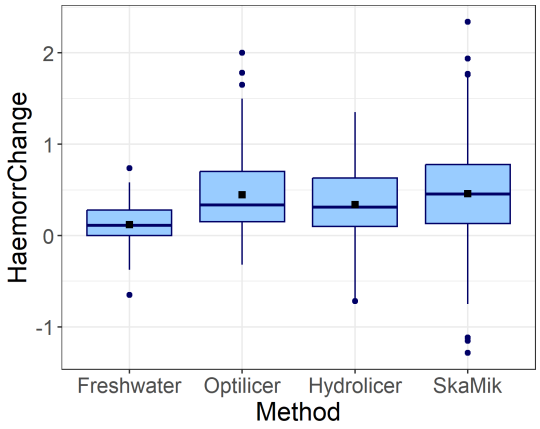
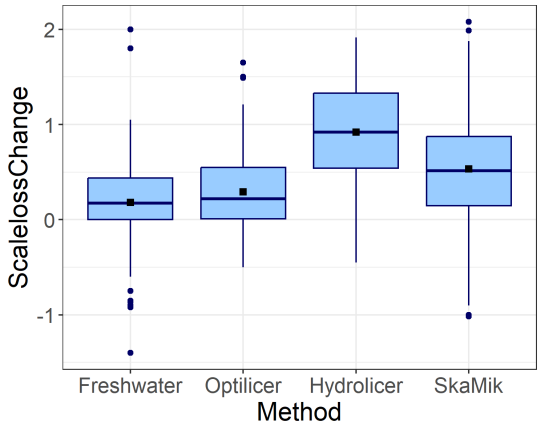


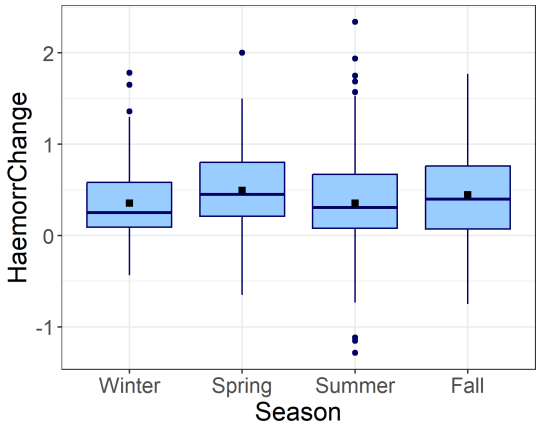
Figure 3.9: Correlations of the numeric variables in the data sets for skin haemorrhages (top) and scale loss (bottom). Scatterplots between each pair of numeric variables are displayed on the left side of the diagonal, while the Pearson correlation is shown on the right side. Distribution plots for the variables are shown on the diagonal.



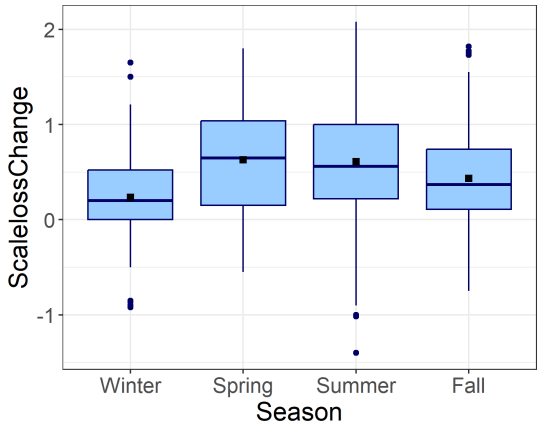
(a) Change in skin haemorrhages for each delousing method



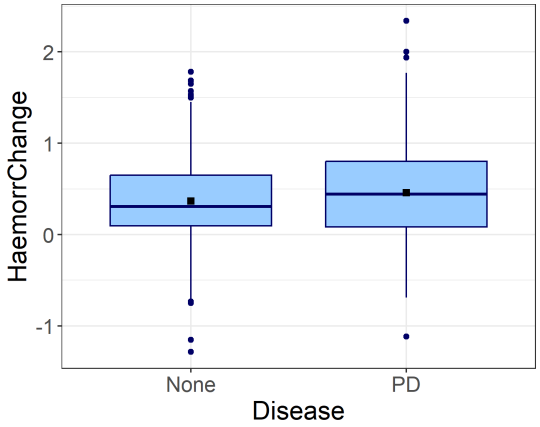
(b) Change in scale loss for each delousing method



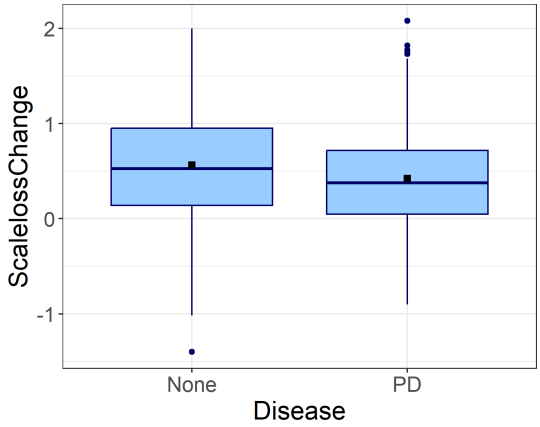
(c) Change in skin haemorrhages for each season



(d) Change in scale loss for each season



(e) Change in skin haemorrhages against *Disease*



(f) Change in scale loss against *Disease*

Figure 3.10: Box plots of change in skin haemorrhages and scale loss against delousing method, season and disease. The average values are shown by the black squares.

The change in skin haemorrhages plotted against the categorical variables *Method*, *Season* and

Disease is shown in the left panels in Figure 3.10. Freshwater seems to be associated with a smaller change in skin haemorrhages compared to the other delousing methods (Figure 3.10a). The differences between the seasons seem to be small (Figure 3.10c), and the observations with a PD case at the location are associated with only a slightly larger change in skin haemorrhages (Figure 3.10e). In this data set for change in skin haemorrhages, 179 ($\sim$ 24%) observations belong to the PD group, of which 20 are from freshwater, 46 from Optilicer, 12 from Hydrolicer and 101 from SkaMik.

The change in scale loss plotted against the categorical variables is shown in the right panels in Figure 3.10. We notice that the mechanical delousing methods, i.e. Hydrolicer and SkaMik, seem to be associated with a larger change than freshwater and Optilicer (Figure 3.10b). Hydrolicer also seems to be related to a larger change than SkaMik. The spring and summer are associated with a larger change in scale loss than the fall and the winter (Figure 3.10d). The observations with a PD case at the location are associated with a slightly smaller change in scale loss than the observations for which PD was not reported (Figure 3.10f), which seems counter-intuitive. In this data set, 180 ($\sim$ 24%) observations belong to the PD group, of which 20 are from freshwater, 46 from Optilicer, 12 from Hydrolicer and 102 from SkaMik. That is, relatively few observations in this group are from Hydrolicer, which seems to be associated with the largest change in scale loss, so this may explain the smaller change in scale loss for the PD group.

The relation between the delousing method, sea temperature and season has the same tendencies as pointed out for the data sets for delousing effect and salmon mortality (Figure A.6, Figure A.7 and Table B.3). The comparable GVIF for the explanatory variables in the data sets for change in skin haemorrhages and scale loss are given in Table B.4. An interaction between the delousing method and sea temperature has been included here as well. We notice that the variable *SeaTempSc* obtain a somewhat high value of 5.80 for both data sets.

4 Data Analysis

In this section, models are fitted for delousing effectiveness against adult female lice (delousing effect), salmon mortality after 3 and 14 days, as well as change in skin haemorrhages and scale loss. The analysis presented in this section was done in `R`, so all functions and packages referred to throughout this section are from `R`. For each of the responses of interest, two different models are fitted. First, a GLM is fitted using the function `glm` from the `stats`-package (R Core Team, 2022). In these models, only fixed effects are used, so these models are called fixed effects models. Then a GLMM, that aims at also taking the hierarchical structure of the observations into account, is fitted by using the function `glmer` or `lmer` from the `lme4`-package (Bates et al., 2015). These models include both fixed and random effects, and are therefore referred to as mixed effects models. For a more clear distinction between and easier referral to the models, the abbreviations in Table 4.1 will be used in the following.

Table 4.1: Models and their abbreviations.

Model for	**Regression type**	**Model abbreviation**
Delousing effect	Fixed effects	DE-FE
	Mixed effects	DE-ME
Mortality after 3 days	Fixed effects	M3-FE
	Mixed effects	M3-ME
Mortality after 14 days	Fixed effects	M14-FE
	Mixed effects	M14-ME
Change in skin haemorrhages	Fixed effects	SH-FE
	Mixed effects	SH-ME
Change in scale loss	Fixed effects	SL-FE
	Mixed effects	SL-ME

The delousing effect and mortality after 3 and 14 days are modelled with binomial models. If only fixed effects are used, these models suffer from overdispersion, which will be pointed out in the following presentation of the analysis. As discussed in Section 2, there are different ways of dealing with overdispersion in binomial models. One of them is to use a quasi-binomial model in the case of only fixed effects. Another possibility is to include random effects, where especially the inclusion of an observation-level random effect is effective to model overdispersion. Since it is not as straight forward to compare quasi-binomial models with models including random effects, both a fixed effects quasi-binomial model and a mixed effects binomial model is fitted. Thus, the results from both types of models will be presented for the delousing effect and the mortalities.

On the other hand, the change in skin haemorrhages and scale loss are assumed to have a normal distribution, which does not have the same limitation as the binomial distribution regarding the estimated variance. Thus, the fixed and mixed effects linear models are more easily comparable. The significance of the random effect will therefore be evaluated, and based on this, either a fixed or mixed effects model will be preferred and presented.

Model Selection

Different explanatory variables are considered in the different models, and an overview of these are presented in Table 4.2. As mentioned, the fixed effects models use only fixed effects, while the mixed effects models consider both fixed effects and random effects from the hierarchical structure of the data. All the explanatory variables in Section 3.1.1, in addition to *HaemorrBefore* and *ScalelossBefore*, are considered in the models for salmon mortality and change in WIs. In the models for delousing effect, the same explanatory variables, except for *Disease*, *HaemorrBefore* and *ScalelossBefore*, are included. The mixed effects models include, in addition to the fixed effects, random effects in the form of random intercepts. The mixed effects models for delousing effect and salmon mortality consider random intercepts for *Cage* and *LocNumber*. Since each observation stems from the delousing of an entire cage, the random intercept for *Cage* is what we have referred to as an observation-level random effect for the binomial mixed model. For the mixed effects models for change in WIs, however, only a random intercept for *LocNumber* is included.

The models where all the corresponding variables in Table 4.2 are included will be referred to as full models. However, a model selection may be preferred if there are insignificant explanatory variables. For the fixed effects models, the significance of a covariate can be evaluated by comparing the larger model including the covariate with a smaller model without it with a LR test, which was covered in Section 2.2.6. A backward step-wise selection procedure based on the LR test will be applied for the models. The procedure is carried out by starting with the full model containing all explanatory variables and eliminating the variable that obtains the largest p-value above the 0.05 significance level from the LR test. For the LR tests, we use the function `drop1` from the `stats`-package (R Core Team, 2022). Then, the model without the insignificant variable is refitted and the elimination step is performed again. This process is repeated until no more variables are considered insignificant. We emphasize that, since the delousing method used is the variable of interest in this thesis, it will not be removed regardless. In addition, *SeaTempSc* should not be removed if the interaction *Method:SeaTempSc* is considered significant.

When it comes to model selection for the mixed effects models, the random effects structure will be evaluated first. The significance of the random effects are also evaluated with the LR test, which is described in Section 2.4.8 in the context of testing random effects. This will also be done in a backward manner, where the starting point is the full model, containing all fixed and random effects. For testing one random intercept in the presence of another, which applies for the models considering random intercepts for both *Cage* and *LocNumber*, there is no known distribution for the LR test statistic, so parametric bootstrap LR tests are performed for evaluating the significances. The function `PBmodcomp` from the `pbkrtest`-package (Halekoh and Højsgaard, 2014) is used for this, with 1000 simulated bootstrap values. However, for testing a single random intercept, where one compares the model with the random intercept with the model without any random effects, the asymptotic mixture distribution of the LR statistic (see Section 2.4.8) will be assumed. This is especially relevant for the SH-ME and SL-ME models that only consider a random intercept for *LocNumber*. The AIC, where each random effect counts as one parameter, will also be used as a supplementary measure in the evaluation of the random effects structure. After deciding on the random effects structure, the fixed effects will be determined. For assessing the fixed effects structure in the mixed effects models, the same procedure as described above for the fixed effects models will be used.

Table 4.2: Variables considered in the models.

Model	Variables
DE-FE	
Fixed effects:	Method, SeaTempSc, Method:SeaTempSc, AvWeightSc, AvCrowdingSc, BiomassSc, Season
DE-ME	
Fixed effects:	Method, SeaTempSc, Method:SeaTempSc, AvWeightSc, AvCrowdingSc, BiomassSc, Season
Random intercepts:	Cage, LocNumber
M3-FE	
Fixed effects:	Method, SeaTempSc, Method:SeaTempSc, AvWeightSc, AvCrowdingSc, BiomassSc, Season, Disease, HaemorrBefore, ScalelossBefore
M3-ME	
Fixed effects:	Method, SeaTempSc, Method:SeaTempSc, AvWeightSc, AvCrowdingSc, BiomassSc, Season, Disease, HaemorrBefore, ScalelossBefore
Random intercepts:	Cage, LocNumber
M14-FE	
Fixed effects:	Method, SeaTempSc, Method:SeaTempSc, AvWeightSc, AvCrowdingSc, BiomassSc, Season, Disease, HaemorrBefore, ScalelossBefore
M14-ME	
Fixed effects:	Method, SeaTempSc, Method:SeaTempSc, AvWeightSc, AvCrowdingSc, BiomassSc, Season, Disease, HaemorrBefore, ScalelossBefore
Random intercepts:	Cage, LocNumber
SH-FE	
Fixed effects:	Method, SeaTempSc, Method:SeaTempSc, AvWeightSc, AvCrowdingSc, BiomassSc, Season, Disease, HaemorrBefore, ScalelossBefore
SH-ME	
Fixed effects:	Method, SeaTempSc, Method:SeaTempSc, AvWeightSc, AvCrowdingSc, BiomassSc, Season, Disease, HaemorrBefore, ScalelossBefore
Random intercepts:	LocNumber
SL-FE	
Fixed effects:	Method, SeaTempSc, Method:SeaTempSc, AvWeightSc, AvCrowdingSc, BiomassSc, Season, Disease, HaemorrBefore, ScalelossBefore
SL-ME	
Fixed effects:	Method, SeaTempSc, Method:SeaTempSc, AvWeightSc, AvCrowdingSc, BiomassSc, Season, Disease, HaemorrBefore, ScalelossBefore
Random intercepts:	LocNumber

Residuals for Fixed and Mixed Effects Models

Residuals are used for model diagnostic purposes for both fixed and mixed effects models. For the fixed effects models, standardized residuals (see Section 2.2.7) are calculated with the function `rstandard` from the `stats`-package (R Core Team, 2022) and evaluated based on their expected standard normal distribution. For the mixed effects models, however, we simulate scaled residuals, as described in Section 2.4.9. To obtain these simulated residuals, the function `simulateResiduals` from the `DHARMa`-package (Hartig, 2022) is used with $m = 1000$ simulations for each observation. The simulations are done unconditional on the fitted random effects, meaning that new random effects are simulated from their estimated distributions in the first step in the procedure. It was pointed out in Section 2.4.9 that these residuals should have a uniform distribution on the interval $[0, 1]$.

4.1 Delousing Effect

4.1.1 Fixed Effects Binomial Regression

In this section, the results of a model for the proportion of lice that were removed after treatment is presented. This is a model with only fixed effects, so the hierarchical structure of the data is not accounted for. The proportions of removed lice $\bar{y}_j = (n_j - \mathit{CountFemalesAfter}_j)/n_j$ for each observation j, where $n_j = \mathit{CountFemalesBefore}_j$, were assumed to follow a scaled binomial distribution $\bar{y}_j \sim \mathit{Binomial}(n_j, \pi_j)/n_j$, and the logistic regression model in (2.6) was fitted to the data.

The model output from the full binomial DE-FE model fitted initially is given in Figure D.1 in Appendix D. The summary gives the estimated regression coefficients with corresponding standard errors, t values and p-values. The Pearson statistic is found to be $P = 1736.387$ and should have an asymptotic χ^2_{808}-distribution. Further, the estimated overdispersion parameter is $\hat{\phi}_P = 2.149$. To find out if the overdispersion is significant, the p-value is calculated and found to be $\sim 7.28 \cdot 10^{-70}$, so the variability in the data is significantly greater than the variability assumed by the binomial model. As pointed out in Section 2.2.5, this may lead to deflated standard errors, and as a result, significance tests for the regression coefficients may become unreliable.

To avoid overly significant coefficients, a quasi-binomial model is fitted instead. All explanatory variables to be considered are included initially, and the resulting model output for the full quasi-binomial model is given in Figure D.2. As expected, the coefficient estimates remain the same, but the standard errors have increased for all the coefficients, resulting in increased p-values. In particular, we observe that the standard errors for all coefficients are relatively equally inflated with a factor of $\hat{\phi}^{1/2}$ compared to the full binomial model in Figure D.1. By performing Wald tests for each numerical and categorical variable for the full quasi-binomial model, the variables *SeaTempSc*, *AvCrowdingSc*, *BiomassSc* and *Season* with p-values 0.133, 0.087, 0.580 and 0.061, respectively, were considered insignificant at the 0.05 significance level.

A backward stepwise selection procedure based on the LR test was then applied to reduce the model. Table 4.3 shows the variables removed at each step in order in a top-down manner. The procedure begins with the full model, and in the first step, the model without *BiomassSc* obtains the largest p-value from the LR test. Hence, this is the first variable to be removed. Thereafter, *Season* obtained the largest p-value above the 0.05 level. However, the p-value was only 0.067 which is not that large. Wald tests were also computed for each of the variables at this step, and they supported the conclusion from the LR test, so *Season* was removed. In the last step, *AvCrowding* was eliminated since it obtained a p-value of 0.076 from the LR test, a conclusion which was also supported by the calculation of Wald tests at this step. We notice that the step-wise elimination removed all the variables that were considered insignificant in the initial full model by the Wald tests, except for *SeaTempSc* which was included since its interaction with delousing method was significant.

Table 4.3: Results from the LR tests for the quasi-binomial DE-FE model. The dropped terms of the initial full model are listed sequentially in a top-down manner, so that each line represents the model from the previous line with the additional dropped term given.

Dropped	**Df**	**Deviance**	**Scaled deviance difference**	**Pr(>Chi)**
None (full model)		1790.6		
BiomassSc	1	1791.2	0.3062	0.580
Season	3	1806.6	7.1646	0.067
AvCrowdingSc	1	1813.4	3.1533	0.076

The model selection resulted in the reduced model

$$\begin{aligned}\log\left(\frac{\hat{\pi}_j}{1-\hat{\pi}_j}\right) &= \hat{\eta}_j \\ &= \hat{\beta}_0 + \hat{\beta}_1 \cdot \text{MethodFreshwater}_j + \hat{\beta}_2 \cdot \text{MethodHydrolicer}_j + \hat{\beta}_3 \cdot \text{MethodOptilicer}_j \\ &+ \hat{\beta}_4 \cdot \text{SeaTempSc}_j + \hat{\beta}_5 \cdot \text{AvWeightSc}_j + \hat{\beta}_6 \cdot \text{MethodFreshwater:SeaTempSc}_j \\ &+ \hat{\beta}_7 \cdot \text{MethodHydrolicer:SeaTempSc}_j + \hat{\beta}_8 \cdot \text{MethodOptilicer:SeaTempSc}_j,\end{aligned} \tag{4.1}$$

where the estimated coefficients are given in Table 4.4, and the full model output is given in Figure D.3. Note that *MethodSkaMik* is used as the reference category. In this model, $\hat{\pi}_j$ is the estimated probability of removal of a louse, and the estimated odds for removing a louse is $\frac{\hat{\pi}_j}{1-\hat{\pi}_j} = \exp(\hat{\eta}_j)$. A high probability of removal means that the delousing effect is good, and a higher probability $\hat{\pi}_j$ corresponds to a larger value for the odds. Hence, larger positive values of the coefficients means that the associated delousing effect is better. For SkaMik the estimated coefficient for *SeaTempSc* has a value of $\hat{\beta}_4 \approx 0.19$. For Hydrolicer, the estimated coefficient for *SeaTempSc* is $\hat{\beta}_4 + \hat{\beta}_7 = 0.1903 - 0.0091 \approx 0.18$. This means that a better delousing effect is associated with higher sea temperatures for these two methods. The estimated coefficients for *SeaTempSc* for freshwater and optilicer are -0.09 and -0.12, respectively. These values are negative, which implies that a better delousing effect is associated with lower sea temperatures.

Table 4.4: Model summary for the reduced quasi-binomial DE-FE model. Estimated coefficients with corresponding standard error, t value and p-value are given. *MethodSkamik* is used as reference category.

Coefficient	**Estimate**	**Standard error**	**t value**	**p-value**
Intercept	1.3869	0.0474	32.45	$< 2 \cdot 10^{-16}$
MethodFreshwater	-0.6918	0.0876	-7.90	$9.12 \cdot 10^{-15}$
MethodHydrolicer	0.2946	0.0894	3.30	$1.03 \cdot 10^{-3}$
MethodOptilicer	-0.1350	0.0957	-1.41	0.159
SeaTempSc	0.1903	0.0546	3.49	$5.14 \cdot 10^{-4}$
AvWeightSc	0.1494	0.0275	5.42	$7.73 \cdot 10^{-8}$
MethodFreshwater:SeaTempSc	-0.2848	0.0874	-3.26	$1.17 \cdot 10^{-3}$
MethodHydrolicer:SeaTempSc	-0.0091	0.1125	-0.08	0.936
MethodOptilicer:SeaTempSc	-0.3106	0.0828	-3.75	$1.87 \cdot 10^{-4}$
Dispersion parameter taken to be 2.169				

When interpreting the results it is important to keep in mind that the model was fitted with

the average sea temperature of 11.7°C as the intercept value. This was due to the centering of the variable *SeaTemp*, where the average temperature of 11.7°C was subtracted in the centering and scaling procedure, resulting in the transformed variable *SeaTempSc*. This means that the temperature 11.7°C for *SeaTemp* corresponds to the value 0 for *SeaTempSc*. The centering and scaling procedure and the effects on the regression coefficients is covered in Section 2.7.1.

Since the estimated coefficient for *SeaTempSc* is different for the different delousing methods, the estimated coefficients for the delousing methods in Table 4.4 give information about how the different delousing methods perform in comparison to one another for $SeaTempSc = 0$ (corresponding to $SeaTemp = 11.7$°C). Looking at the estimated coefficients for the delousing methods, Hydrolicer seems to have the best delousing effect, followed by SkaMik and Optilicer, whereas freshwater is associated with the least effect of the methods for a sea temperature of 11.7°C. From the p-values in Table 4.4, both freshwater and Hydrolicer have a significantly different effect than SkaMik, but Optilicer is not considered significantly different from SkaMik. Some additional Wald tests were performed to compare the effects of the different delousing methods, and these are given in Table 4.5 for the intercept temperature of 11.7°C. Not surprisingly, Hydrolicer is significantly different from freshwater and Optilicer. Additionally, freshwater is significantly different from Optilicer.

Table 4.5: Results from additional Wald tests from the reduced quasi-binomial DE-FE model. The tests are done for two models fitted with the same covariates, but with two different sea temperatures defined as intercept values.

Sea temperature as intercept	**Null hypothesis**	**df**	**Wald statistic**	**p-value**
11.7°C	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodHydrolicer}}$	1	13.714	$2.13 \cdot 10^{-4}$
	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodFreshwater}}$	1	23.942	$9.93 \cdot 10^{-7}$
	$\beta_{\text{MethodFreshwater}} = \beta_{\text{MethodHydrolicer}}$	1	80.802	$2.49 \cdot 10^{-19}$
7°C	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodHydrolicer}}$	1	1.319	0.997
	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodFreshwater}}$	1	19.750	$8.82 \cdot 10^{-6}$
	$\beta_{\text{MethodFreshwater}} = \beta_{\text{MethodHydrolicer}}$	1	7.315	$6.84 \cdot 10^{-3}$
	$\beta_{\text{MethodFreshwater}} = 0$	1	4.060	0.044
	$\beta_{\text{MethodHydrolicer}} = 0$	1	1.921	0.166
	$\beta_{\text{MethodOptilicer}} = 0$	1	5.190	0.023

The performance of the different delousing methods for different sea temperatures according to the fitted model is illustrated in Figure 4.1. From the estimated coefficients in Table 4.4 for the model (4.1), only the part of the linear predictor that varies for the different delousing methods is plotted as a function of the untransformed sea temperature. That is, for each delousing method X we have plotted $\hat{\beta}_{MethodX} + (\hat{\beta}_{SeaTempSc} + \hat{\beta}_{MethodX:SeaTempSc}) \cdot SeaTempSc$ against the corresponding values of *SeaTemp*. For SkaMik, which is used as the reference category, $\hat{\beta}_{SeaTempSc} \cdot SeaTempSc$ is plotted. Note that at the sea temperature 11.7°C, marked by the second vertical dotted line, SkaMik attains the value 0. In addition, we emphasize that the lines for each of the delousing methods are plotted only for sea temperatures within the range of the observations for that particular method.

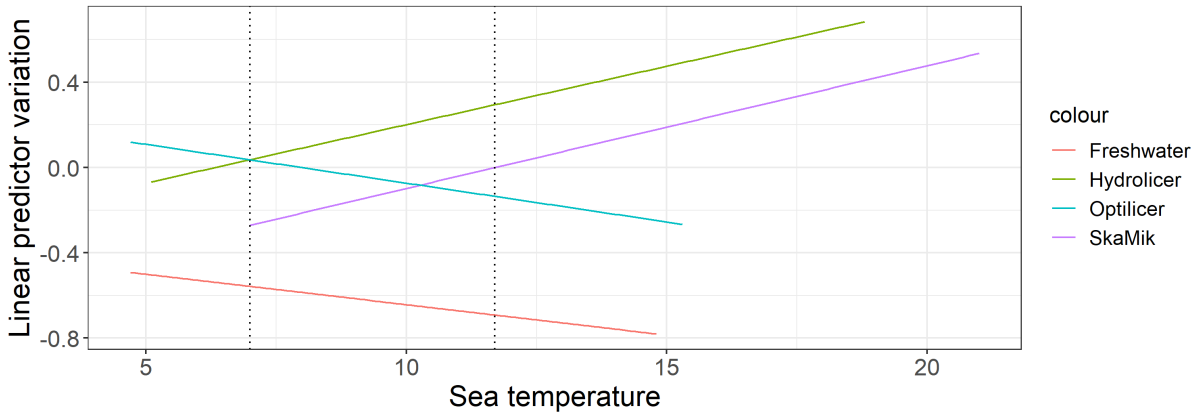


Figure 4.1: Illustration of the difference in the estimated linear predictor (from the reduced quasi-binomial DE-FE model) for the different delousing methods at different sea temperatures. For each delousing method X we have plotted $\hat{\beta}_{MethodX} + (\hat{\beta}_{SeaTempSc} + \hat{\beta}_{MethodX:SeaTempSc}) \cdot SeaTempSc$ against the corresponding sea temperature. For SkaMik, $\hat{\beta}_{SeaTempSc} \cdot SeaTempSc$ is plotted. Note that these are plotted only for sea temperatures within the range of the observations for each of the methods. The dotted lines mark the temperatures 7°C and 11.7°C (intercept value in the fitted model).

The important aspect of this plot is not the values at the different sea temperatures, but rather the difference between the values for the delousing methods at different sea temperatures, since it is preferable to use the best method. For higher temperatures than 11.7°C, the differences between freshwater and Optilicer compared to the mechanical delousing methods seem to increase. For lower temperatures, however, the differences between freshwater and Optilicer compared to the mechanical methods decrease. It is therefore of interest to do significance tests at a lower temperature as well. The temperature 7°C is chosen, and we fit the same model with this as the intercept value for the sea temperature. This results in the model output in Figure D.4, where we observe that the estimated coefficients for the intercept and the delousing methods have changed. In addition, the standard errors have increased for these coefficients, likely because there are fewer observations with lower temperatures. Although the coefficient values have changed, the differences between the estimated coefficients for the delousing methods remain the same as the differences observed in Figure 4.1 for the temperature 7°C, marked by the first dotted vertical line. At this temperature, Hydrolicer and Optilicer are considered to have best delousing effect and have almost the same estimated coefficients. Freshwater, on the other hand, is considered to have the lowest delousing effect. Wald tests are performed again for this model, and these are given in Table 4.5 for the sea temperature 7°C. From these tests, freshwater and Optilicer are considered significantly different from SkaMik, but Hydrolicer is not. The fact that Optilicer is significantly different from SkaMik, but Hydrolicer is not, although they have almost the same estimated coefficient is likely due to the fact that Optilicer have more observations around this temperature, which may result in less uncertainty. Additionally, Optilicer and Hydrolicer are significantly different from freshwater, but Optilicer and Hydrolicer are not significantly different.

In Figure 4.2, the standardized deviance residuals are plotted against the fitted values and the theoretical quantiles of the normal distribution. Looking at the plot against fitted values, there does not appear to be any obvious pattern in the residuals, but there are some residuals with quite large absolute values. In addition, it may seem like freshwater has more large residuals compared to the other methods, even though it is one of the methods with fewer observations. From the plot against the theoretical quantiles of the normal distribution, the residuals seem to follow the dotted line quite well, indicating a standard normal distribution. However, there

seem to be some larger values in the tails than what is expected. Observations with standardized deviance residuals larger than 3 in absolute value were inspected to detect any irregular observations. There were found six observations with residuals values smaller than -3. These were from 4 treatments with freshwater and 2 with SkaMik. They all had very small registered proportions of removed lice. Specifically, five of them had a proportion of 0 and the last one had a proportion of 0.067. There were three observations with residual values greater than 3, which were from freshwater, Optilicer and SkaMik. These had quite large registered proportions of removed lice of 0.959, 0.988 and 0.972. In addition, they had quite high values of *CountFemalesBefore* of 170, 80 and 108. However, this was not considered evidence enough to exclude any of the observations.

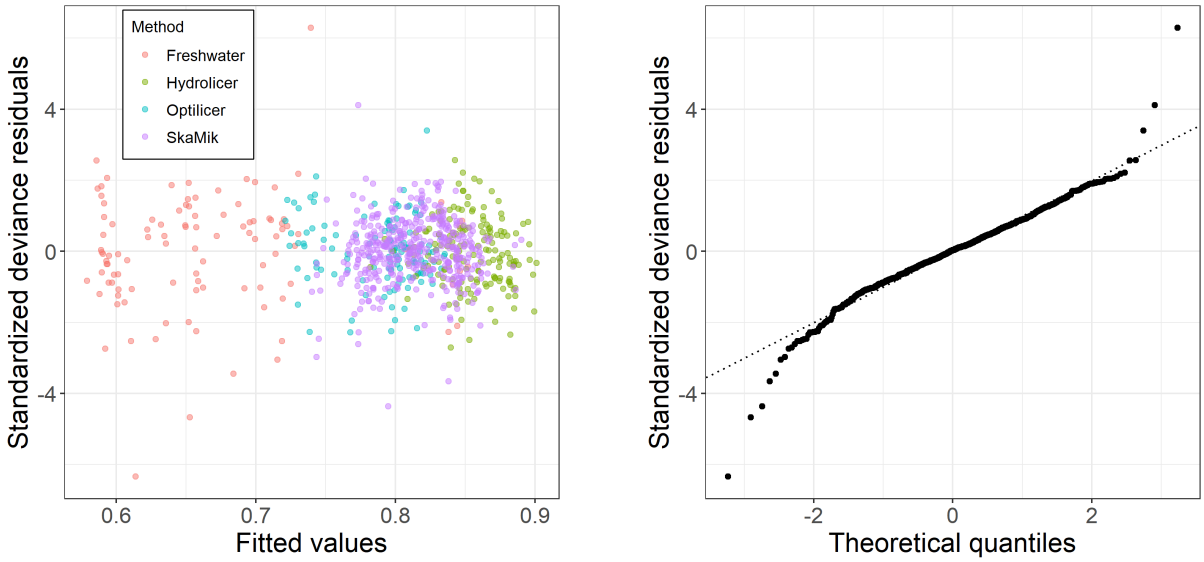


Figure 4.2: Model diagnostic plots for the reduced quasi-binomial DE-FE model. Standardized deviance residuals plotted against fitted values and the theoretical quantiles of the normal distribution.

4.1.2 Mixed Effects Binomial Regression

A model for the proportion of lice that were removed after treatment that also takes the hierarchical structure of the data into account was also fitted. In the following, all individual binomial observations are indexed by ij, and these represent observations from different cages, indexed by j, nested within different locations, indexed by i. The proportions of removed lice $\bar{y}_{ij} = (n_{ij} - \mathit{CountFemalesAfter}_{ij})/n_{ij}$ for each observation ij, where $n_{ij} = \mathit{CountFemalesBefore}_{ij}$, were assumed to have a conditional scaled binomial distribution $\bar{y}_{ij} \sim \mathit{Binomial}(n_{ij}, \pi_{ij})/n_{ij}$ given the random effects. The logistic mixed-effect model in (2.27), with random intercepts for *Cage* and *LocNumber* in addition to the fixed effects, was initially fitted to the data. The random intercept for *Cage* on the binomial observation-level is then an observation-level random effect. The fitting of the model is done using the Laplace approximation (corresponding to nAGQ = 1 adaptive quadrature point) since the adaptive Gaussian quadrature with more quadrature points is not implemented for models with more than one random effect for the function `glmer`.

This resulted in the full model in Figure D.5, where the estimated variance for the random intercepts for *Cage* and *LocNumber* is 0.3167 and 0.0089, respectively. We also observe that the standard errors of the fixed effects coefficients have increased compared to the full binomial fixed effects model in Figure D.1. However, in contrast to the quasi-binomial model, the standard

errors are not inflated by the same factor.

The estimated variance for the intercept for *LocNumber* is rather small compared to *Cage* in the full DE-ME model. In any case, the random effects structure is decided with a backward step-wise elimination based on likelihood ratio tests. A parametric bootstrap likelihood ratio test is performed to test the null hypothesis that the variance of the intercept for *LocNumber* is zero in the presence of a random intercept for *Cage*. As mentioned, the test is performed using the `PBmodcomp`-function from the package `pbkrtest` (Halekoh and Højsgaard, 2014), with 1000 simulated bootstrap values. This results in a p-value of 0.0360. A similar test is also performed for the variance of the intercept for *Cage* in the presence of random intercept for *LocNumber*, which gives a p-value of 0.0029. Since both p-values are smaller than the chosen significance level 0.05, the null hypotheses are rejected and both random effects are considered significant. Additionally, the smaller models without *Cage* and *LocNumber* obtained AIC values of 3984.8 and 3662.5, respectively. The full model obtained a value of 3663.4, which was slightly larger than for the model without *LocNumber*. Since the random intercept for *LocNumber* was considred significant by the parametric bootstrap LR test and the difference in the AIC between the full model and the model without *LocNumber* was relatively small, both random effects were included.

After deciding the random effects structure, the fixed effects structure was decided by a backward stepwise elimination based on the LR test, and the results are shown in Table B.5. Both *BiomassSc* and *AvCrowdingSc* were removed from the model, since their contributions to the model fit were considered insignificant. The model selection procedure resulted in the reduced model

$$\begin{aligned}
\log\left(\frac{\hat{\pi}_{ij}}{1-\hat{\pi}_{ij}}\right) &= \hat{\eta}_{ij} \\
&= (\hat{\beta}_0 + \hat{\gamma}_{0i} + \hat{\gamma}_{0ij}) + \hat{\beta}_1 \cdot \text{MethodFreshwater}_{ij} + \hat{\beta}_2 \cdot \text{MethodHydrolicer}_{ij} \\
&+ \hat{\beta}_3 \cdot \text{MethodOptilicer}_{ij} + \hat{\beta}_4 \cdot \text{SeaTempSc}_{ij} + \hat{\beta}_5 \cdot \text{AvWeightSc}_{ij} \\
&+ \hat{\beta}_6 \cdot \text{SeasonFall}_{ij} + \hat{\beta}_7 \cdot \text{SeasonSpring}_{ij} + \hat{\beta}_8 \cdot \text{SeasonWinter}_{ij} \\
&+ \hat{\beta}_9 \cdot \text{MethodFreshwater:SeaTempSc}_{ij} + \hat{\beta}_{10} \cdot \text{MethodHydrolicer:SeaTempSc}_{ij} \\
&+ \hat{\beta}_{11} \cdot \text{MethodOptilicer:SeaTempSc}_{ij},
\end{aligned} \tag{4.2}$$

conditional on the random effects. The estimated fixed effects coefficients are given in Table 4.6. In this model for delousing effect, the interaction between delousing method and sea temperature was also considered significant. The estimated coefficient for *SeaTempSc* for SkaMik, Hydrolicer, Optilicer and freshwater was 0.04, 0.03, -0.22 and -0.33, respectively. The expected difference in the log odds (or the linear predictor) in (4.2) for the different delousing methods for different sea temperatures is illustrated in Figure 4.3. For the sea temperature 11.7°C (marked by the second dotted line), we notice that Hydrolicer is associated with the highest delousing effect, followed by SkaMik and Optilicer, while freshwater is associated with the least effect. For inference about the difference in delousing effect for a sea temperature of 11.7°C, t-tests and Wald tests are performed. Based on the p-values in Table 4.6 and the additional Wald tests in Table 4.7, all methods are considered significantly different for this sea temperature, except for the difference between Optilicer and SkaMik. This is the same conclusion as obtained by the reduced DE-FE model.

For the sea temperature 7°C, marked by the first dotted line in Figure 4.3, we observe that Optilicer is associated with the best delousing effect, followed by Hydrolicer, SkaMik and then freshwater. For inference about the differences for this temperature, the model (4.2) was fitted

with a sea temperature of 7°C as the intercept value instead. Wald tests were then performed, and they are given in Table 4.7. The results show that freshwater is considered significantly different from the three other delousing methods for the sea temperature 7°C, but there is no significant difference between Optilicer, Hydrolicer and SkaMik. The conclusions from the DE-FE model only differs from the DE-ME model in that Optilicer was considered significantly different from SkaMik.

Table 4.6: Model summary for the reduced DE-ME model. Estimated coefficients with corresponding standard error, t value and p-value are given. *MethodSkamik* and *SeasonSummer* are used as reference categories.

Coefficient	**Estimate**	**Standard error**	**t value**	**p-value**
Intercept	1.6439	0.0722	22.78	$< 2 \cdot 10^{-16}$
MethodFreshwater	-0.8496	0.1073	-7.92	$9.12 \cdot 10^{-15}$
MethodHydrolicer	0.1823	0.0974	1.87	0.061
MethodOptilicer	-0.1352	0.1199	-1.13	0.259
SeaTempSc	0.0428	0.0729	0.59	0.558
AvWeightSc	0.1064	0.0351	3.04	$2.40 \cdot 10^{-3}$
SeasonFall	-0.3269	0.0867	-3.77	$1.62 \cdot 10^{-4}$
SeasonSpring	-0.3339	0.1802	-1.85	0.064
SeasonWinter	-0.4938	0.1631	-3.03	$2.46 \cdot 10^{-3}$
MethodFreshwater:SeaTempSc	-0.3699	0.1028	-3.599	$3.20 \cdot 10^{-4}$
MethodHydrolicer:SeaTempSc	-0.0102	0.1115	-0.09	0.927
MethodOptilicer:SeaTempSc	-0.2602	0.1010	-2.58	$9.99 \cdot 10^{-3}$
Estimated variance				
Cage (Intercept):	0.3175			
LocNumber (Intercept):	0.0096			

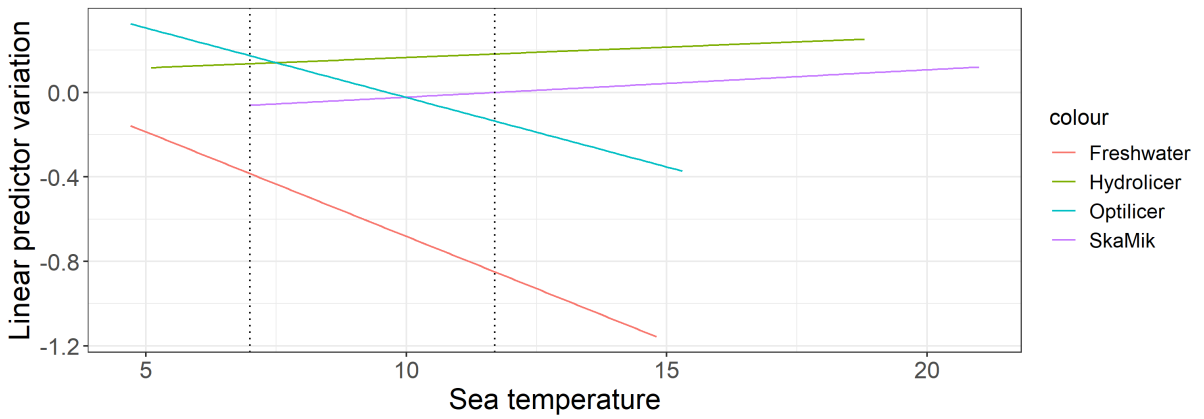
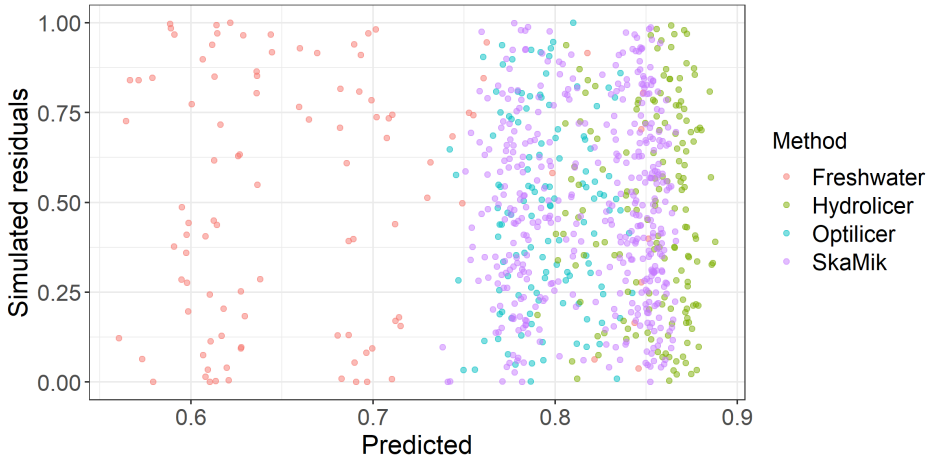


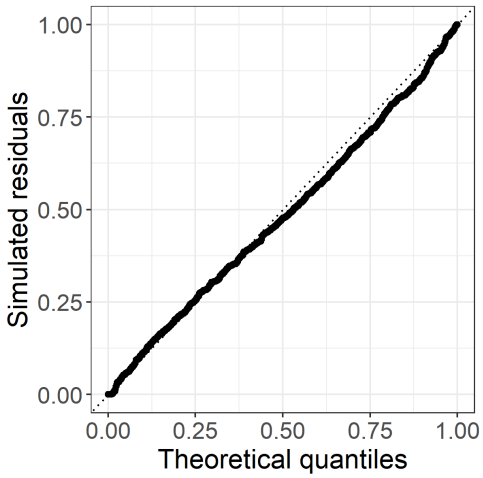
Figure 4.3: Illustration of the difference in the estimated linear predictor (from the reduced DE-ME model) for the different delousing methods at different sea temperatures. For each delousing method X we have plotted $\hat{\beta}_{MethodX} + (\hat{\beta}_{SeaTempSc} + \hat{\beta}_{MethodX:SeaTempSc}) \cdot SeaTempSc$ against the corresponding sea temperature. For SkaMik, $\hat{\beta}_{SeaTempSc} \cdot SeaTempSc$ is plotted. Note that these are plotted only for sea temperatures within the range of the observations for each of the methods. The dotted lines mark the temperatures 7°C and 11.7°C (intercept value in the fitted model).

Table 4.7: Additional Wald tests from the reduced DE-ME model. The tests are done for two models fitted with the same variables, but with two different sea temperatures defined as intercept values.

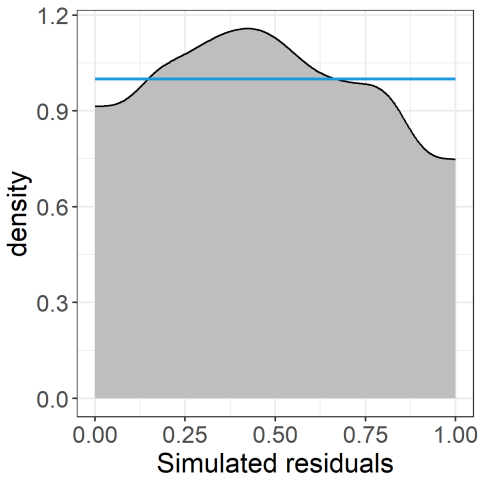
Sea temperature as intercept	Null hypothesis	df	Wald statistic	p-value
11.7°C	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodHydrolicer}}$	1	5.326	0.021
	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodFreshwater}}$	1	25.848	$3.69 \cdot 10^{-7}$
	$\beta_{\text{MethodFreshwater}} = \beta_{\text{MethodHydrolicer}}$	1	68.184	$1.49 \cdot 10^{-16}$
7°C	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodHydrolicer}}$	1	0.032	0.859
	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodFreshwater}}$	1	16.093	$6.03 \cdot 10^{-5}$
	$\beta_{\text{MethodFreshwater}} = \beta_{\text{MethodHydrolicer}}$	1	5.502	0.019
	$\beta_{\text{MethodFreshwater}} = 0$	1	4.105	0.043
	$\beta_{\text{MethodHydrolicer}} = 0$	1	0.764	0.382
	$\beta_{\text{MethodOptilicer}} = 0$	1	2.462	0.117



(a) Simulated residuals against predicted values.



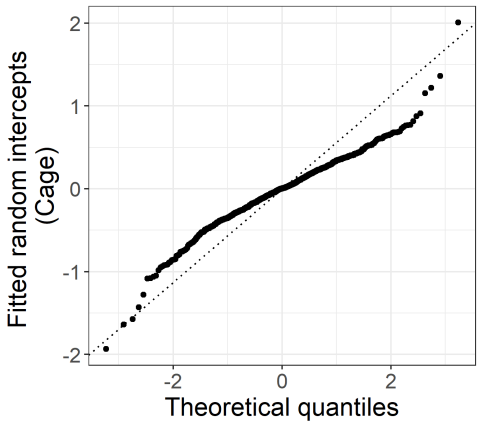
(b) Simulated residuals against the theoretical quantiles of the uniform distribution.



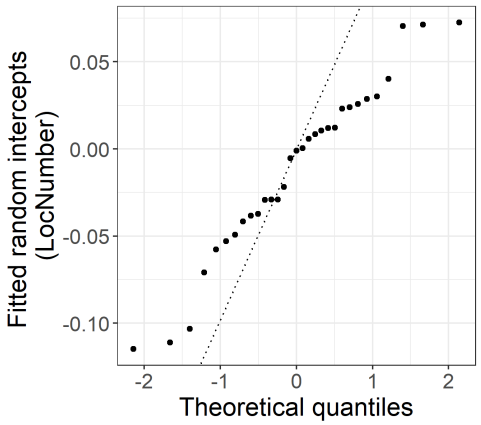
(c) Distribution of simulated residuals. The blue line indicates the uniform distribution.

Figure 4.4: Model diagnostic plots for the reduced DE-ME model.

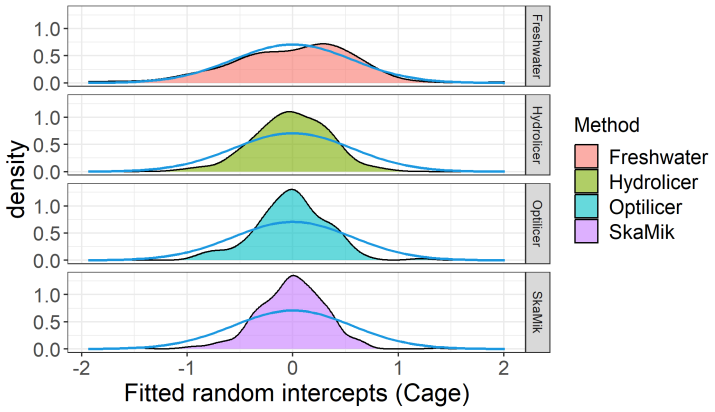
In Figure 4.4a, the simulated residuals for the DE-ME model are plotted against predicted values (i.e. the predictions based on fixed effects only). Since the simulated residuals theoretically should have a uniform distribution if the model is correct, we look at the distribution in the y-direction. The distribution seems to be quite even. However, it may seem like SkaMik, Hydrolicer and Optilicer have slightly more residuals centered around 0.5, while freshwater seems to have less residuals in the middle. This is further confirmed by the box plot of simulated residuals for each delousing method in Figure A.8, where we observe that the interquartile range is smaller than 0.5 for SkaMik, Hydrolicer and Optilicer, but larger than 0.5 for freshwater. The simulated residuals are plotted against the theoretical quantiles of the uniform distribution, shown in Figure 4.4b. The plot shows a slightly inverted s-shape when compared to the dotted line that shows the expected relation. The distribution of the simulated residuals is further shown in Figure 4.4c. The blue line indicates the uniform distribution, and we observe that there are more residuals in the middle and fewer in the extremes compared to the uniform distribution.



(a) Quantile plot for fitted random intercepts for *Cage*.



(b) Quantile plot for fitted random intercepts for *LocNumber*.



(c) Density plot of fitted random intercepts for *Cage* for each delousing method.

Figure 4.5: Model diagnostic plots for the reduced DE-ME model. **(a)-(b):** Fitted random intercepts for *Cage* and *LocNumber* plotted against the theoretical quantiles of the normal distribution. The straight dotted lines indicate the expected distribution based on the estimated variances $\hat{\sigma}_2^2$ and $\hat{\sigma}_1^2$. **(c):** Distribution of the fitted random intercepts for *Cage* for each delousing method. The blue lines indicate the expected distribution based on the estimated variance $\hat{\sigma}_2^2$.

The random intercepts γ_{0i} and γ_{0ij} were assumed to be normally distributed with mean 0 and

variance σ_1^2 and σ_2^2, respectively. The fitted random intercepts for *Cage* and *LocNumber* are plotted against the theoretical quantiles of the normal distribution, shown in Figure 4.5a and Figure 4.5b, where the expected relations (based on the estimated variances) are shown by the straight dotted lines. The plots seem to indicate that the fitted random intercepts have smaller variance than what is expected. Since the simulated residuals seemed to be slightly different for freshwater, the distribution of the fitted observation-level random effects (i.e. the fitted random intercepts for *Cage*) is plotted for each delousing method. This is shown in Figure 4.5c, where the blue lines indicate the expected distribution based on the estimated variance $\hat{\sigma}_2^2$. We notice that the distribution for freshwater is closest to the expected, and it has some large values in the tails. As opposed to this, the distributions for the other delousing methods are more peaked in the middle and have smaller tails compared to the expectation. It seems like freshwater obtains more of the larger fitted values for the random intercept for *Cage* compared to the other three delousing methods. Thus, one may suspect that the estimated variance $\hat{\sigma}_2^2$ is higher due to more variable observations for freshwater, and this would explain the pattern in the simulated residuals.

4.2 Salmon Mortality 3 Days Post-Treatment

4.2.1 Fixed Effects Binomial Regression

In this section, a fixed-effects model for the salmon mortality three days after delousing treatment is presented. The proportions of dead salmon $\bar{y}_j = \textit{NumDeaths3}/n_j$ for each observation j, where $n_j = \textit{NumBefore}_j$, were assumed to follow a scaled binomial distribution $\bar{y}_j \sim \textit{Binomial}(n_j, \pi_j)/n_j$, and the logistic regression model in (2.6) was fitted to the data. The estimated overdispersion parameter for the full M3-FE model was $\hat{\phi}_P = 603.0$, and, not surprisingly, it was found to be highly significant. Hence, a quasi-binomial model was fitted instead, given in Figure D.6. Many of the explanatory variables were not considered significant then, so a backward step-wise model selection based on the LR test was applied. The variables listed in Table B.6 were sequentially dropped, so only the variables *Method*, *AvWeightSc*, *Season* and *HaemorrBefore* were considered significant and were included in the final model.

Specifically, the model selection resulted in the reduced model

$$\begin{aligned}\log\Big(\frac{\hat{\pi}_j}{1-\hat{\pi}_j}\Big) &= \hat{\eta}_j \\ &= \hat{\beta}_0 + \hat{\beta}_1 \cdot \text{MethodFreshwater}_j + \hat{\beta}_2 \cdot \text{MethodHydrolicer}_j \\ &+ \hat{\beta}_3 \cdot \text{MethodOptilicer}_j + \hat{\beta}_4 \cdot \text{AvWeightSc}_j + \hat{\beta}_5 \cdot \text{SeasonFall}_j \\ &+ \hat{\beta}_6 \cdot \text{SeasonSpring}_j + \hat{\beta}_7 \cdot \text{SeasonWinter}_j + \hat{\beta}_8 \cdot \text{HaemorrBefore}_j,\end{aligned} \tag{4.3}$$

where the estimated cofficients are given in Table 4.8. The estimated mortality rate is given by $\hat{\pi}_j$ for this model.

Table 4.8: Model summary for the reduced quasi-binomial M3-FE model. Estimated coefficients with corresponding standard error, t value and p-value are given. *MethodSkamik* and *SeasonSummer* are used as reference categories.

Coefficient	**Estimate**	**Standard error**	**t value**	**p-value**
Intercept	-5.8805	0.0879	-66.91	$< 2 \cdot 10^{-16}$
MethodFreshwater	-0.0568	0.1627	-0.35	0.727
MethodHydrolicer	0.2780	0.1058	2.63	$8.76 \cdot 10^{-3}$
MethodOptilicer	0.6061	0.1427	4.25	$2.44 \cdot 10^{-5}$
AvWeightSc	0.1086	0.0550	1.98	0.049
SeasonFall	0.2250	0.1073	2.10	0.036
SeasonSpring	-0.1666	0.1504	-1.11	0.268
SeasonWinter	0.2186	0.1403	1.56	0.120
HaemorrBefore	0.2419	0.0902	2.68	$7.51 \cdot 10^{-3}$
Dispersion parameter taken to be 612.1				

From (4.3) it can be seen that larger and positive coefficients mean that the expected mortality rate is higher. Based on the estimated coefficients for the delousing methods in Table 4.8, Optilicer is associated with the highest mortality, followed by Hydrolicer, SkaMik and freshwater. Compared to SkaMik, the odds for mortality is expected to decrease with a factor of $\exp(\hat{\beta}_1) = \exp(-0.0568) \approx 0.94$ if freshwater is used instead and the other variables are the same. If Optilicer and Hydrolicer are used, the odds for mortality is expected to increase with factors

$\exp(0.6061) \approx 1.83$ and $\exp(0.2780) \approx 1.32$, respectively, when compared to SkaMik. Based on the t-tests in Table 4.8 and the additional Wald tests in Table 4.9, the differences between all delousing methods are considered significant at the 0.05 significance level, except for the difference between freshwater and SkaMik.

Table 4.9: Results from additional Wald tests from the reduced quasi-binomial M3-FE model.

Null hypothesis	**df**	**Wald statistic**	**p-value**
$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodHydrolicer}}$	1	4.554	0.033
$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodFreshwater}}$	1	16.057	$6.15 \cdot 10^{-5}$
$\beta_{\text{MethodFreshwater}} = \beta_{\text{MethodHydrolicer}}$	1	3.940	0.047

The standardized deviance residuals from the M3-FE model are plotted against the fitted values and the theoretical quantiles of the normal distribution in Figure 4.6. The residuals may seem to have somewhat smaller variance for the smaller fitted values. In addition, there seems to be more large positive than negative residuals, but more small negative than positive residuals. In the quantile plot, we observe that the residuals deviate quite strongly from the standard normal distribution. It is more apparent in Figure A.9 that the distribution of the residuals is right skewed, with median and mean values of -0.29 and -0.12, respectively, shown by the brown and purple dashed lines. Furthermore, the distribution of the residuals shows signs of having smaller variance compared to the standard normal distribution. The deviating distribution may be explained by the fact that the observed mortality rates are very close to zero, which makes deviations towards zero relatively limited, but not in the opposite direction. This would explain why there are more small negative residuals and more large positive residuals.

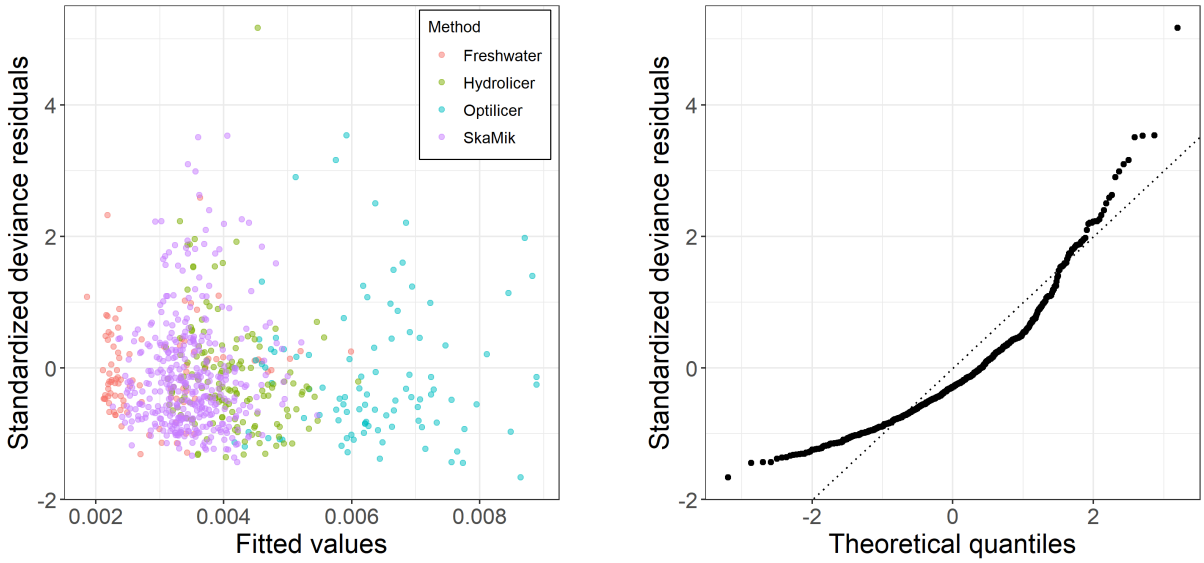


Figure 4.6: Model diagnostics for the reduced quasi-binomial M3-FE model. Standardized deviance residuals plotted against fitted values and the theoretical quantiles of the normal distribution. The dotted line in the quantile plot indicates the standard normal distribtution.

4.2.2 Mixed Effects Binomial Regression

A model for the mortality rate that also considers random intercepts for *Cage* and *LocNumber* was then fitted. The individual binomial observations are indexed by ij, where the index j represent observations from different cages that are nested within different locations, indexed by i. The proportions of dead salmon after 3 days $\bar{y}_{ij} = \mathit{NumDeaths3}_{ij}/n_{ij}$, where $n_{ij} = \mathit{NumBefore}_{ij}$, were assumed to have a conditional scaled binomial distribution $\bar{y}_{ij} \sim \mathit{Binomial}(n_{ij}, \pi_{ij})/n_{ij}$ given the random effects.

The full M3-ME model was fitted according to (2.27) and the model output is given in Figure D.7. The significance of the random effects was evaluated with parametric bootstrap likelihood ratio tests by comparing the smaller models with the full model. This resulted in p-values of 0.0031 and 0.0026 for *Cage* and *LocNumber*, respectively. In addition, the smaller models without *Cage* and *LocNumber* obtained AIC values of 247698 and 10554, while the full model had a value 10429, which was the smallest. Hence, both random intercepts were included in the model, and the fixed effects structure was then decided by a backward step-wise elimination based on the LR test. Only *ScalelossBefore* and *HaemorrBefore* were considered insignificant (Table B.7), and were therefore eliminated from the model. This resulted in the model

$$\begin{aligned}
\log\left(\frac{\hat{\pi}_{ij}}{1-\hat{\pi}_{ij}}\right) &= \hat{\eta}_{ij} \\
&= (\hat{\beta}_0 + \hat{\gamma}_{0i} + \hat{\gamma}_{0ij}) + \hat{\beta}_1 \cdot \text{MethodFreshwater}_{ij} + \hat{\beta}_2 \cdot \text{MethodHydrolicer}_{ij} \\
&+ \hat{\beta}_3 \cdot \text{MethodOptilicer}_{ij} + \hat{\beta}_4 \cdot \text{SeaTempSc}_{ij} + \hat{\beta}_5 \cdot \text{AvCrowdingSc}_{ij} \\
&+ \hat{\beta}_6 \cdot \text{AvWeightSc}_{ij} + \hat{\beta}_7 \cdot \text{BiomassSc}_{ij} + \hat{\beta}_8 \cdot \text{SeasonSpring}_{ij} \\
&+ \hat{\beta}_9 \cdot \text{SeasonFall}_{ij} + \hat{\beta}_{10} \cdot \text{SeasonWinter}_{ij} + \hat{\beta}_{11} \cdot \text{DiseasePD}_{ij} \\
&+ \hat{\beta}_{12} \cdot \text{MethodFreshwater:SeaTempSc}_{ij} + \hat{\beta}_{13} \cdot \text{MethodHydrolicer:SeaTempSc}_{ij} \\
&+ \hat{\beta}_{14} \cdot \text{MethodOptilicer:SeaTempSc}_{ij},
\end{aligned} \tag{4.4}$$

conditional on the random effects. The estimated coefficients are given in Table 4.10. The estimated variance is $\hat{\sigma}_1^2 = 0.29$ for *LocNumber* and $\hat{\sigma}_2^2 = 0.73$ for *Cage*. The interaction between delousing method and sea temperature was significant, and thus included in this model. The estimated slope for *SeaTempSc* was 0.11, -0.06, -0.28 and 0.08 for SkaMik, Hydrolicer, Optilicer and freshwater, respectively. A higher value for the slope means that the delousing method is associated with a higher mortality for higher temperatures. The slope for Optilicer is significantly different from those of SkaMik and freshwater.

It is a little surprising that Optilicer has a negative slope. However, it should be noted that only 25% of the observations from Optilicer have *SeaTemp* $> 7.4^\circ$ C, which also could explain why the estimated coefficient $\hat{\beta}_{14}$ has the largest estimated standard error compared to the other estimated slope parameters for *SeaTempSc*. In addition to the scarce data for Optilicer for higher sea temperatures, another possible explanation for this unexpected result is that the industry may be particularly careful when using Optilicer when the sea temperature is high, since they then have to use higher temperatures for the treatment water to obtain a good delousing effect. The industry may be inclined to reduce the use of Optilicer for bigger fish or fish with poor health when the sea temperature is high. The data was therefore inspected, and the observations from delousing operations using Optilicer for sea temperatures less than or equal to 7.4°C had a mean of 3.0 kg for *AvWeight*. However, for observations where Optilicer had been used for sea temperatures greater than 7.4°C, *AvWeight* had a mean of 2.1 kg. For the observations with *SeaTemp* > 10°C, the mean of was even smaller, with a value of 1.86 kg.

The correlation between *AvWeightSc* and *SeaTempSc* was calculated and found to be -0.435 for the observations for Optilicer, so the sea temperature and average weight may be somewhat confounded for Optilicer.

Table 4.10: Model summary for the reduced M3-ME model. Estimated coefficients with corresponding standard error, t value and p-value are given. *MethodSkamik* and *SeasonSummer* are used as reference categories.

Coefficient	**Estimate**	**Standard error**	**t value**	**p-value**
Intercept	-6.5154	0.1315	-49.56	$< 2 \cdot 10^{-16}$
MethodFreshwater	0.1785	0.1465	1.22	0.223
MethodHydrolicer	0.5544	0.1151	4.82	$1.45 \cdot 10^{-6}$
MethodOptilicer	0.3553	0.1818	1.96	0.051
SeaTempSc	0.1096	0.0822	1.33	0.1824
AvCrowdingSc	0.0865	0.0385	2.24	0.025
AvWeightSc	0.2733	0.0623	4.39	$1.14 \cdot 10^{-5}$
BiomassSc	-0.1299	0.0575	-2.26	0.024
SeasonSpring	-0.0746	0.1903	-0.39	0.695
SeasonFall	-0.0027	0.1164	-0.023	0.982
SeasonWinter	0.4339	0.2069	2.10	0.036
DiseasePD	0.3610	0.1207	2.991	$2.78 \cdot 10^{-3}$
MethodFreshwater:SeaTempSc	-0.0323	0.1184	-0.27	0.785
MethodHydrolicer:SeaTempSc	-0.1661	0.1221	-1.36	0.174
MethodOptilicer:SeaTempSc	-0.3854	0.1448	-2.66	$7.78 \cdot 10^{-3}$
Estimated variance				
Cage (Intercept):	0.7300			
LocNumber (Intercept):	0.2885			

The difference in the linear predictor in (4.4) between the different delousing methods for different sea temperatures is illustrated in Figure 4.7. For a sea temperature of 11.7°C, Hydrolicer is associated with the highest mortality, followed by Optilicer, freshwater and SkaMik. From the t-tests in Table 4.10 and the additional Wald tests in Table 4.11 the only significant differences is between Hydrolicer, which is significantly different from freshwater and SkaMik at a 0.05 significance level. The difference between Optilicer and SkaMik has a significance level just above this, with a p-value of 0.051.

For a sea temperature of 7°C, Optilicer is associated with the highest mortality, followed by Hydrolicer, freshwater and SkaMik, as can be seen in Figure 4.7. Both Optilicer and Hydrolicer are significantly different from both freshwater and SkaMik for this temperature.

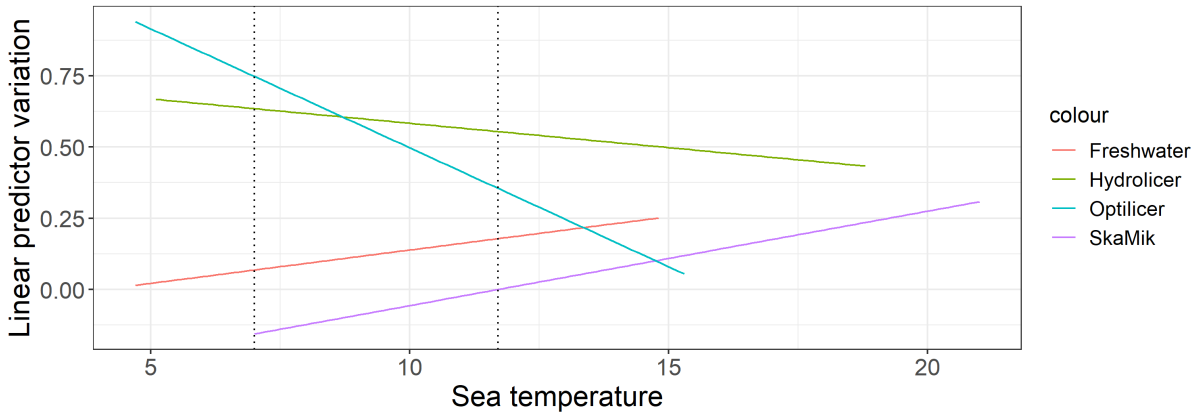


Figure 4.7: Illustration of the difference in the estimated linear predictor (from the reduced M3-ME model) for the different delousing methods at different sea temperatures. For each delousing method X we have plotted $\hat{\beta}_{MethodX} + (\hat{\beta}_{SeaTempSc} + \hat{\beta}_{MethodX:SeaTempSc}) \cdot SeaTempSc$ against the corresponding sea temperature. For SkaMik, $\hat{\beta}_{SeaTempSc} \cdot SeaTempSc$ is plotted. Note that these are plotted only for sea temperatures within the range of the observations for each of the methods. The dotted lines mark the temperatures 7°C and 11.7°C (intercept value in the fitted model).

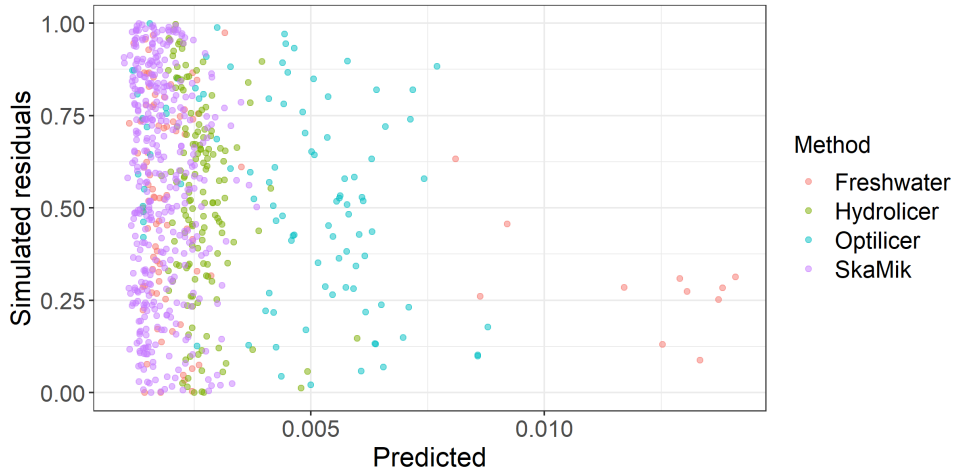
Table 4.11: Results from additional Wald tests from the reduced M3-ME model. The tests are done for two models fitted with the same variables, but with two different sea temperatures defined as intercept values.

Sea temperature as intercept	**Null hypothesis**	**df**	**Wald statistic**	**p-value**
11.7°C	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodHydrolicer}}$	1	0.997	0.325
	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodFreshwater}}$	1	0.697	0.404
	$\beta_{\text{MethodFreshwater}} = \beta_{\text{MethodHydrolicer}}$	1	5.588	0.018
7°C	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodHydrolicer}}$	1	0.216	0.642
	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodFreshwater}}$	1	14.805	$1.19 \cdot 10^{-4}$
	$\beta_{\text{MethodFreshwater}} = \beta_{\text{MethodHydrolicer}}$	1	5.076	0.024
	$\beta_{\text{MethodFreshwater}} = 0$	1	1.230	0.268
	$\beta_{\text{MethodHydrolicer}} = 0$	1	10.813	$1.01 \cdot 10^{-3}$
	$\beta_{\text{MethodOptilicer}} = 0$	1	25.824	$3.74 \cdot 10^{-7}$

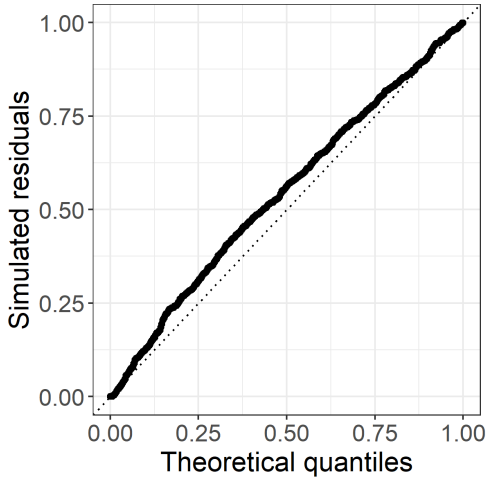
The simulated residuals for the M3-ME model are plotted against predicted values, shown in Figure 4.8a. It seems like there is a somewhat uneven distribution in the y-direction, with more residuals with larger values. This is especially evident for SkaMik, which is more apparent in Figure A.10. We observe that SkaMik has a residual mean that is a little higher than for the other methods. Thus, it is possible that the model may underestimate the mortality for SkaMik more than for the other delousing methods.

We also notice from the plot against predicted values that there are some observations from freshwater with high predicted values and small residuals with quite similar values. The residuals with predicted values larger than 0.01 all stem from observations from the same location, where freshwater was used. In addition, they have an unusual high weight in the range 10.7-11.3 kg, as well as quite similar covariate values, and mortality rates in the range 0.0034-0.0088.

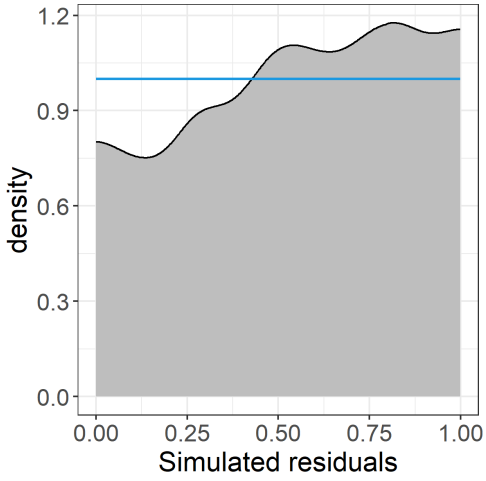
In Figure 4.8b, the simulated residuals are plotted against the theoretical quantiles of the uniform distribution, and there is some deviation from the expectation (shown by the dotted line). From the distribution plot in Figure 4.8c, we see that there are more residuals with values from around 0.45 to 1 than expected for the uniform distribution, indicated by the blue line.



(a) Simulated residuals against predicted values.



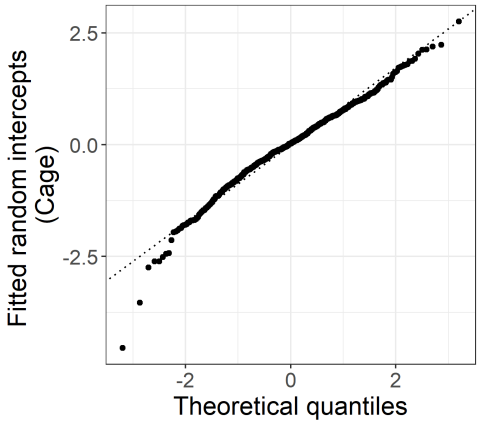
(b) Simulated residuals against the theoretical quantiles of the uniform distribution.



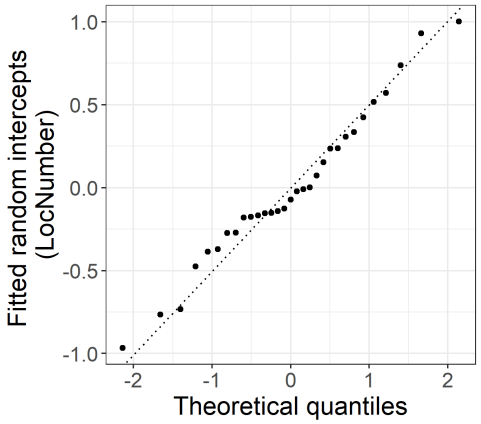
(c) Distribution of simulated residuals. The blue line indicates the uniform distribution.

Figure 4.8: Model diagnostic plots for the reduced M3-ME model.

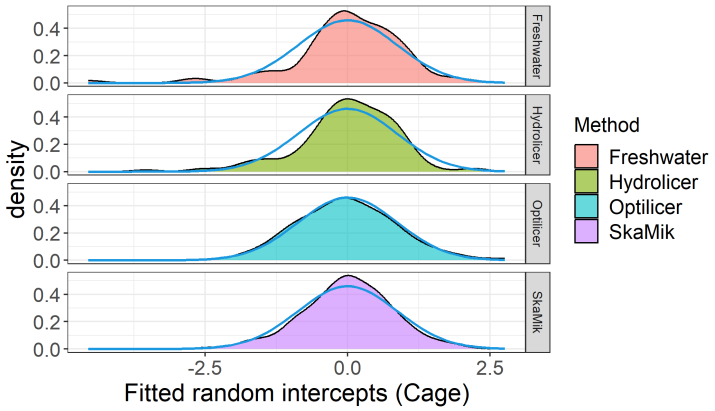
The fitted random intercepts for *Cage* and *LocNumber* are plotted against the theoretical quantiles of the normal distribution, shown in Figure 4.9a and Figure 4.9b, respectively. The straight dotted lines indicate the expected relations based on the estimated variances $\hat{\sigma}_2^2$ and $\hat{\sigma}_1^2$. The fitted random effects seem to follow the expected lines quite well. In addition, the distribution of the fitted random intercepts for *Cage* is plotted for each delousing method, shown in Figure 4.9c. There does not seem to be any large deviations from the expected distribution and the distributions for the delousing methods do not seem to be too different.



(a) Quantile plot for fitted random intercepts for *Cage*.



(b) Quantile plot for fitted random intercepts for *LocNumber*.



(c) Density plot of fitted random intercepts for *Cage* for each delousing method.

Figure 4.9: Model diagnostic plots for the reduced M3-ME model. **(a)-(b):** Fitted random intercepts for *Cage* and *LocNumber* plotted against the theoretical quantiles of the normal distribution. The straight dotted lines indicate the expected distribution based on the estimated variances $\hat{\sigma}_2^2$ and $\hat{\sigma}_1^2$. **(c):** Distribution of the fitted random intercepts for *Cage* for each delousing method. The blue lines indicate the expected distribution based on the estimated variance $\hat{\sigma}_2^2$.

4.3 Salmon Mortality 14 Days Post-Treatment

4.3.1 Fixed Effects Binomial Regression

Similar to the M3-FE model presented in Section 4.2.1, a fixed-effects model was fitted for the proportion of dead salmon 14 days after delousing treatment. Since the overdispersion was highly significant for this as well, a quasi-binomial model was fitted. The full quasi-binomial M14-FE model is given in Figure D.8. Many of the explanatory variables were then considered insignificant, so the model was reduced with a backward step-wise elimination based on the LR test. The dropped terms in each of the steps are given in Table B.8, and only *Method*, *AvCrowdingSc* and *HaemorrBefore* were considered significant. This resulted in the model in Figure D.9, with estimated overdispersion parameter $\hat{\phi} = 1433$, which is even higher than for the M3-FE model.

According to the model, Optilicer is associated with the highest mortality, followed by SkaMik, Hydrolicer and Freshwater. Based on the t-tests in Figure D.9 and the Wald tests in Table B.9, the delousing methods are considered to have different effects, except for Hydrolicer, which is not significantly different from SkaMik or freshwater.

The standardized deviance residuals are plotted against the fitted values and theoretical quantiles of the normal distribution, shown in Figure A.11. The residuals exhibit quite similar patterns as the residuals from the M3-FE model.

4.3.2 Mixed Effects Binomial Regression

Similar to the M3-ME model, a mixed-effects model for the proportion of dead salmon after 14 days was also fitted. The full model was initially fitted (see Figure D.10) and the significance of the random effects were evaluated. Based on a parametric bootstrap LR test, the random intercept for *LocNumber* was considered significant with a p-value of 0.0013. In the attempt of doing a similar test for *Cage*, the model with only a random intercept for *LocNumber* could not be fitted, even with different optimizers or scaling of the variables. However, since the random intercept for *Cage* was significant compared to the model with no random effects and the random intercept for *Cage* was considered significant in the M3-ME model, it was kept in the M14-ME model as well. The decision was further supported by computation of the AIC. The full model, the model with only a random intercept for *Cage* and the model without any random effects obtained AIC values of 10172, 10347 and 614840, respectively. That is, the model with only *Cage* as random intercept has a substantially smaller AIC than the model without random effects, and should therefore be included in the model. In addition, the model with random intercepts for both *LocNumber* and *Cage* has an even smaller AIC, and it is therefore preferred.

The fixed effects structure was then decided with a backward step-wise elimination based on the LR test. This procedure found *HaemorrBefore* and *BiomassSc* to be insignificant, as given in Table B.10, so these were eliminated from the model. The resulting model is given in Figure D.11. The estimated variance is $\hat{\sigma}_1^2 = 0.28$ for *LocNumber* and $\hat{\sigma}_2^2 = 0.48$ for *Cage*. The interaction between delousing method and sea temperature was significant to the model fit, and the estimated slope for *SeaTempSc* for SkaMik, Hydrolicer, Optilicer and freshwater are 0.07, 0.06, -0.38 and -0.01, respectively. As for the M3-ME model, we notice that Optilicer has a quite large negative slope, meaning that larger temperatures are associated with a lower mortality. We suspect the same possible reasons for this unexpected result as was pointed out in Section

4.2.2.

The difference in the estimated linear predictor for the different delousing methods at different sea temperatures is illustrated in Figure 4.10. For a sea temperature of 11.7°C, Hydrolicer is associated with the highest mortality, followed by freshwater, Optilicer and SkaMik. The only significant difference for this temperature is between Hydrolicer and SkaMik (see Figure D.11 and Table B.11).

In contrast, for a sea temperature of 7°C, Optilicer is associated with the highest mortality, followed by Hydrolicer, freshwater and SkaMik. Optilicer differs significantly from freshwater and SkaMik for this temperature (see Table B.11).

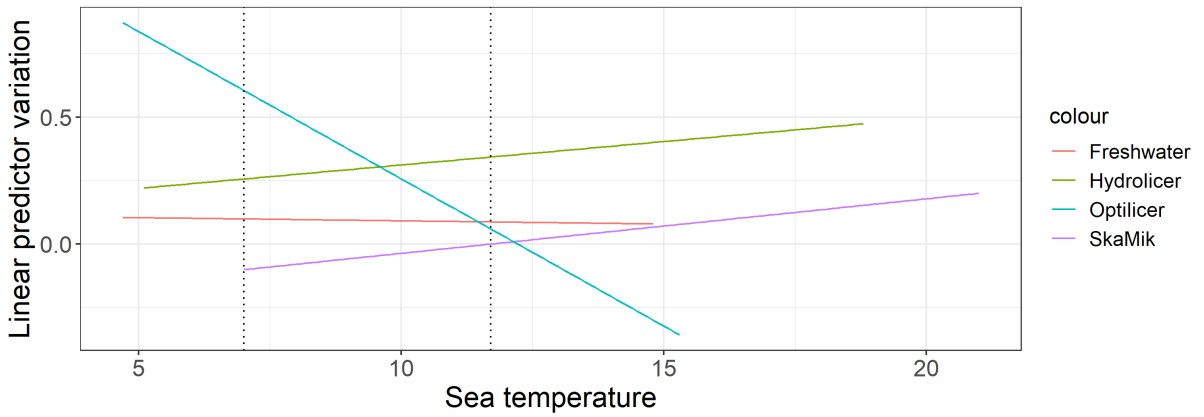


Figure 4.10: Illustration of the difference in the estimated linear predictor (from the reduced M14-ME model) for the different delousing methods at different sea temperatures. For each delousing method X we have plotted $\hat{\beta}_{MethodX} + (\hat{\beta}_{SeaTempSc} + \hat{\beta}_{MethodX:SeaTempSc}) \cdot SeaTempSc$ against the corresponding sea temperature. For SkaMik, $\hat{\beta}_{SeaTempSc} \cdot SeaTempSc$ is plotted. Note that these are plotted only for sea temperatures within the range of the observations for each of the methods. The dotted lines mark the temperatures 7°C and 11.7°C (intercept value in the fitted model).

The simulated residuals from the M14-ME model exhibit quite similar features as the residuals from the M3-ME model (Figure A.12). The fitted random effects are plotted against the theoretical quantiles of the uniform distribution and seem to follow the expected line quite closely (Figure A.13).

4.4 Change in Skin Haemorrhages

The results from a model for change in skin haemorrhages after delousing treatment is presented in this section. The full SH-FE model (Figure D.12) was obtained by fitting the linear model in (2.3) to the data with all the explanatory variables included initially. The model relies on the assumption of the change in skin haemorrhages to be independent and normally distributed. The full SH-ME model was then obtained by fitting the linear random intercept model in (2.21) to the data using the `lmer` function, and is given in Figure D.13. This model initially includes the same explanatory variables, but also an additional random intercept for *LocNumber*. The SH-ME model then accounts for possible correlation between observations from the same location, modelled through a random intercept.

Since the SH-FE model is nested within the SH-ME model, these were compared by evaluating the significance of the random intercept with a LR test. The LR statistic was calculated to be 34.031, and with an asymptotic $0.5\chi^2_0 : 0.5\chi^2_1$ mixture distribution, the p-value was found to be $2.71 \cdot 10^{-9}$, so the random intercept was considered significant and the SH-ME model was preferred. The AIC supported this conclusion, with values of 699 and 731 for the SH-ME and SH-FE model, respectively.

The fixed effects structure of the SH-ME was then decided with a backward step-wise elimination that excluded the variables listed in Table B.12. In the end, only *Method*, *SeaTempSc*, *Season*, *HaemorrBefore* and *ScalelossBefore* were considered significant by the LR test, resulting in the model

$$\begin{aligned}\hat{\mu}_{ij} = (\hat{\beta}_0 + \hat{\gamma}_{0i}) &+ \hat{\beta}_1 \cdot \text{MethodFreshwater}_{ij} + \hat{\beta}_2 \cdot \text{MethodHydrolicer}_{ij} + \hat{\beta}_3 \cdot \text{MethodOptilicer}_{ij} \\ &+ \hat{\beta}_4 \cdot \text{SeaTempSc}_{ij} + \hat{\beta}_5 \cdot \text{SeasonFall}_{ij} + \hat{\beta}_6 \cdot \text{SeasonSpring}_{ij} + \hat{\beta}_7 \cdot \text{SeasonWinter}_{ij} \\ &+ \hat{\beta}_8 \cdot \text{HaemorrBefore}_{ij} + \hat{\beta}_9 \cdot \text{ScalelossBefore}_{ij},\end{aligned} \tag{4.5}$$

where the estimated coefficients are given in Table 4.12, with corresponding standard errors and t-values. Note that p-values are not given here, since this was not provided in the model output when using the `lmer` function. However, a t-value outside the interval $(t_{0.025,n-p}, t_{0.975,n-p}) = (-1.963, 1.963)$ indicates that the variable is significant at the 0.05 significance level. The residual variance for this model was estimated to be $\hat{\sigma}^2 = 0.137$ and the estimated random intercept variance was $\hat{\sigma}^2_\gamma = 0.020$.

In the model (4.5), $\hat{\mu}_{ij}$ is the estimated change in skin haemorrhages for the salmon after delousing treatment. Hence, larger estimated coefficients mean that the associated change in skin haemorrhages is greater, which corresponds to a worsened condition for the salmon. Based on the estimated coefficients, Optilicer is associated with the greatest change in skin haemorrhages, followed by SkaMik, Hydrolicer and freshwater. According to the Wald tests in Table B.13, the differences between all delousing methods are significant, except for the one between Optilicer and SkaMik. Based on the model, the change in skin haemorrhages (i.e. the change in the evaluation of the degree of skin haemorrhages after delousing treatment based on a score from 0-3) is expected to increase with $\hat{\beta}_2 - \hat{\beta}_1 = 0.20$, $-\hat{\beta}_1 = 0.33$ and $\hat{\beta}_3 - \hat{\beta}_1 = 0.42$ for Hydrolicer, SkaMik and Optilicer, respectively, if these are used instead of freshwater and all other variables are constant.

The simulated residuals plotted against the predicted values are shown in Figure 4.12a, and show no obvious pattern. The quantile plot and the distribution plot in Figure 4.12b and Figure 4.12c do not show signs of any large deviations from uniformity. The fitted random intercepts for *LocNumber* are plotted against the theoretical quantiles of the normal distribution, shown

in Figure 4.11, and they seem to follow the expected line quite well.

Table 4.12: Model summary for the reduced SH-ME model. Estimated coefficients with corresponding standard error and t value are given. A t value outside the interval $(t_{0.025,n-p}, t_{0.975,n-p}) = (-1.963, 1.963)$ indicates that the variable is significant at the 0.05 significance level. *MethodSkamik* and *SeasonSummer* are used as reference categories.

Coefficient	**Estimate**	**Standard error**	**t value**
Intercept	0.6151	0.0484	12.723
MethodFreshwater	-0.3284	0.0513	-6.407
MethodHydrolicer	-0.1250	0.0462	-2.706
MethodOptilicer	0.0879	0.0571	1.540
SeaTempSc	0.0870	0.0297	2.936
SeasonFall	0.0221	0.0466	0.475
SeasonSpring	0.2279	0.0752	3.031
SeasonWinter	0.1016	0.0811	1.252
HaemorrBefore	-0.6694	0.0414	-16.180
ScalelossBefore	0.0891	0.0308	2.891
Estimated variance			
Residual:	0.1366		
LocNumber (Intercept):	0.0203		

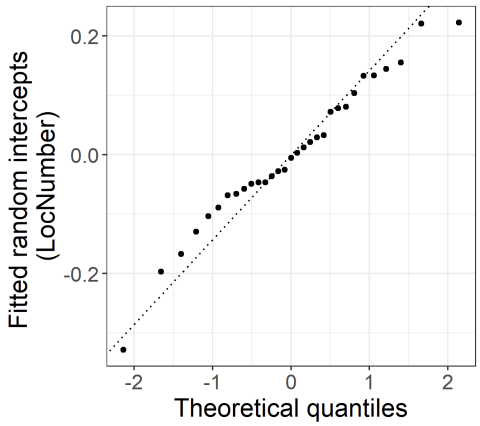
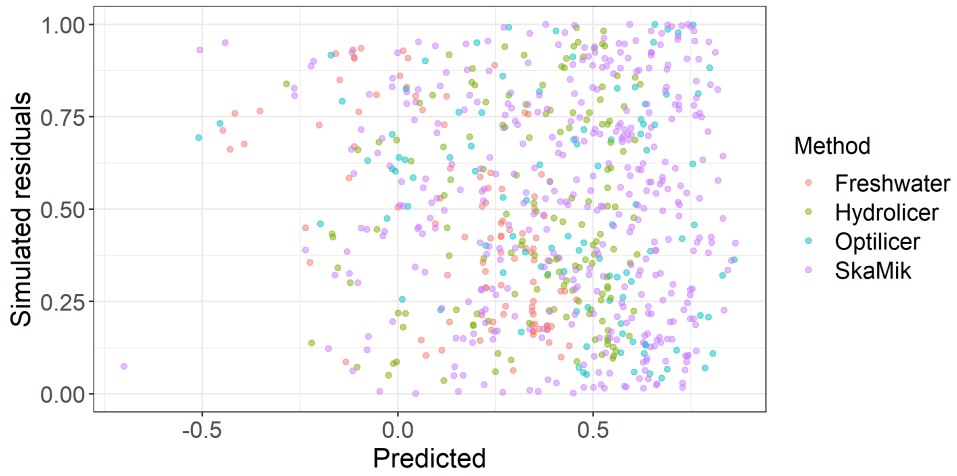
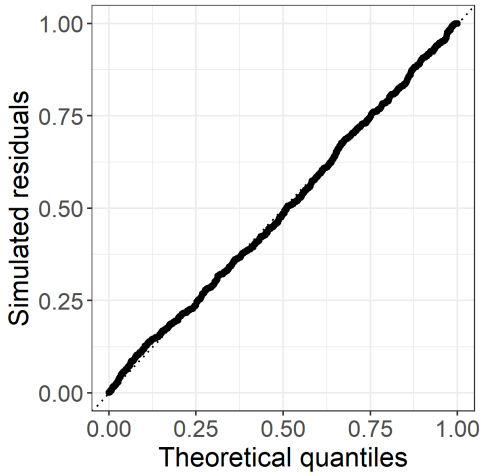


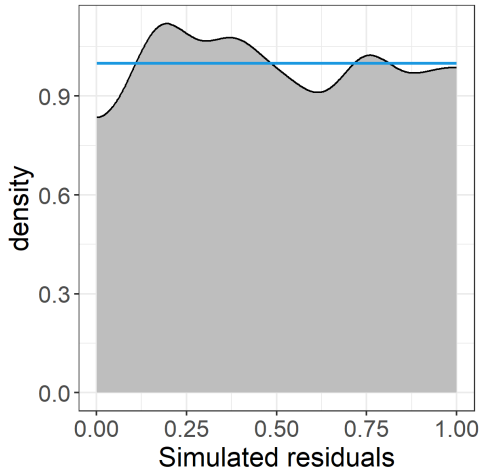
Figure 4.11: Fitted random intercepts for *LocNumber* from the reduced SH-ME model against the theoretical quantiles of the normal distribution. The straight dotted line indicates the expected distribution based on the estimated variance $\hat{\sigma}_\gamma^2$.



(a) Simulated residuals against predicted values.



(b) Simulated residuals against the theoretical quantiles of the uniform distribution.



(c) Distribution of the residuals. The blue line indicates the uniform distribution.

Figure 4.12: Model diagnostic plots for the reduced SH-ME model.

4.5 Change in Scale Loss

The full SL-FE (Figure D.14) and SL-ME (Figure D.15) models for the change in scale loss were fitted similarly as the SH-FE and SH-ME models, with all explanatory variables included initially. The SL-ME model, with a random intercept for *LocNumber*, was compared to the SL-FE model without any random effects by a LR test to evaluate the significance of the random effect. The random intercept was found to be significant, with a p-value of $3.02 \cdot 10^{-34}$, and the SL-ME model was therefore preferred. AIC calculations also supported the inclusion of the random intercept, with values of 573 and 718 for the model with the random intercept and the model without it, respectively.

A backward step-wise elimination of insignificant fixed effects based on the LR test resulted in the elimination of the variables in Table B.14. The reduced model was then given by

$$\begin{aligned}\hat{\mu}_{ij} = (\hat{\beta}_0 + \hat{\gamma}_{0i}) &+ \hat{\beta}_1 \cdot \text{MethodFreshwater}_{ij} + \hat{\beta}_2 \cdot \text{MethodHydrolicer}_{ij} + \hat{\beta}_3 \cdot \text{MethodOptilicer}_{ij} \\ &+ \hat{\beta}_4 \cdot \text{SeaTempSc}_{ij} + \hat{\beta}_4 \cdot \text{AvWeightSc}_{ij} + \hat{\beta}_4 \cdot \text{BiomassSc}_{ij} + \hat{\beta}_5 \cdot \text{SeasonFall}_{ij} \\ &+ \hat{\beta}_6 \cdot \text{SeasonSpring}_{ij} + \hat{\beta}_7 \cdot \text{SeasonWinter}_{ij} + \hat{\beta}_9 \cdot \text{ScalelossBefore}_{ij} \\ &+ \hat{\beta}_8 \cdot \text{MethodFreshwater:SeaTempSc}_{ij} + \hat{\beta}_8 \cdot \text{MethodHydrolicer:SeaTempSc}_{ij} \\ &+ \hat{\beta}_8 \cdot \text{MethodOptilicer:SeaTempSc}_{ij},\end{aligned} \tag{4.6}$$

where the estimated coefficients are given in Table 4.13. For this model, the estimated residual variance was $\hat{\sigma}^2 = 0.111$ and the estimated variance for the random intercept for *LocNumber* was $\hat{\sigma}^2_\gamma = 0.049$.

The interaction between the delousing method and sea temperature was considered significant to the model fit. The slopes for *SeaTempSc* for SkaMik, Hydrolicer, Optilicer and freshwater are 0.07, 0.18, -0.02 and 0.08, respectively. The difference in the expected mean in (4.6) for the different delousing methods for different sea temperatures, when all other variables are the same, is illustrated in Figure 4.13. Wald tests for the difference between the delousing methods for sea temperatures of 7°C and 11.7°C are presented in Table B.15.

For a sea temperature of 11.7°C, SkaMik is associated with the greatest change in scale loss, followed by Hydrolicer, Optilicer and freshwater. Compared to freshwater, which is associated with the smallest change, the change in scale loss after delousing treatment is expected to increase with 0.13, 0.60 and 0.68 for Optilicer, Hydrolicer and SkaMik, respectively, if these are used instead. Based on the Wald tests, SkaMik and Hydrolicer are both significantly different from both Optilicer and freshwater. However, SkaMik is not significantly different from Hydrolicer, and neither is the difference between Optilicer and freshwater.

For a sea temperature of 7°C, the delousing methods are ranked in the same order from worst to best. SkaMik is associated with the greatest change in scale loss, followed by Hydrolicer, Optilicer and freshwater. However, the magnitude of the differences between the methods have changed for this sea temperature. The change in scale loss after delousing treatment is expected to increase with 0.27, 0.46 and 0.69 for Optilicer, Hydrolicer and SkaMik, respectively, if these are used instead of freshwater. The differences between all four delousing methods are considered significant for this sea temperature.

Plots of the simulated residuals from the SL-ME model against predicted values and the theoretical quantiles of the uniform distribution, as well as a distribution plot of the residuals, are shown in Figure A.14. A quantile plot for the fitted random intercepts is shown in Figure A.15. No obvious patterns or deviations are detected from these.

Table 4.13: Model summary for the reduced SL-ME model. Estimated coefficients with corresponding standard error and t value are given. A t value outside the interval $(t_{0.025,n-p}, t_{0.975,n-p}) = (-1.963, 1.963)$ indicates that the variable is significant at the 0.05 significance level. *MethodSkamik* and *SeasonSummer* are used as reference categories.

Coefficient	**Estimate**	**Standard error**	**t value**
Intercept	1.2389	0.0553	22.413
MethodFreshwater	-0.6832	0.0565	-12.084
MethodHydrolicer	-0.0842	0.0459	-1.833
MethodOptilicer	-0.5574	0.0682	-8.177
SeaTempSc	0.0689	0.0317	2.173
AvWeightSc	-0.0661	0.0234	-2.822
BiomassSc	-0.0568	0.0218	-2.606
SeasonFall	-0.0837	0.0438	-1.914
SeasonSpring	0.2732	0.0726	3.765
SeasonWinter	-0.0023	0.0778	-0.030
ScalelossBefore	-0.6942	0.0258	-26.873
MethodFreshwater:SeaTempSc	0.0076	0.0470	0.161
MethodHydrolicer:SeaTempSc	0.1071	0.0458	2.340
MethodOptilicer:SeaTempSc	-0.0920	0.0540	-1.703
Estimated variance			
Residual:	0.1105		
LocNumber (Intercept):	0.0489		

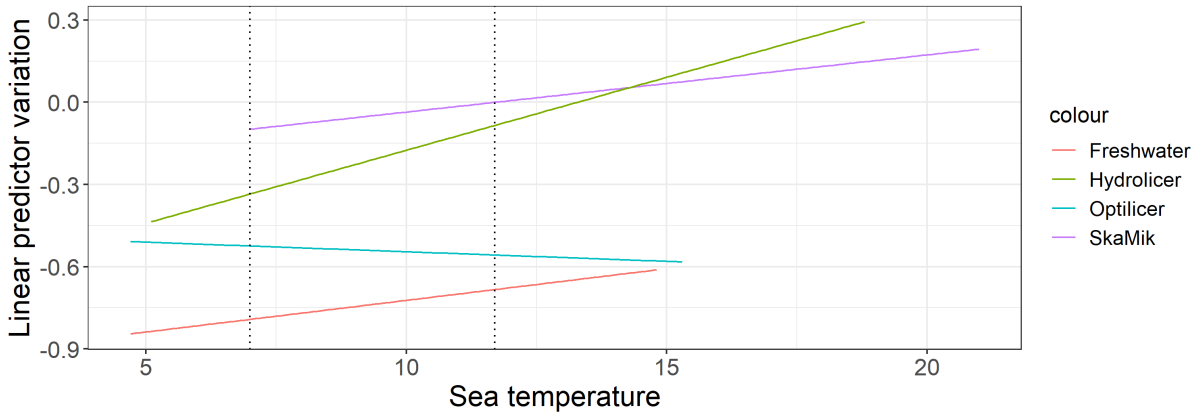


Figure 4.13: Illustration of the difference in the estimated linear predictor (from the reduced SL-ME model) for the different delousing methods at different sea temperatures. For each delousing method X we have plotted $\hat{\beta}_{MethodX} + (\hat{\beta}_{SeaTempSc} + \hat{\beta}_{MethodX:SeaTempSc}) \cdot SeaTempSc$ for the corresponding sea temperature. For SkaMik, $\hat{\beta}_{SeaTempSc} \cdot SeaTempSc$ is plotted. Note that these are plotted only for sea temperatures within the range of the observations for each of the methods. The dotted lines mark the temperatures 7°C and 11.7°C (intercept value in the fitted model).

5 Discussion

Different models were fitted for different responses in order to compare the impact that the delousing methods freshwater, Optilicer, Hydrolicer and SkaMik have on delousing effect and fish welfare. Here, we present a comparison of the models and the results for the different responses of interest. The significance level 0.05 has been used in all significance tests mentioned in the following discussion.

5.1 Delousing Effect

When fitting a binomial fixed effects model to the data set for delousing effectiveness against adult female lice (delousing effect), the model showed signs of significant overdispersion, which indicates a lack of fit. In addition, overdispersion is a problem when performing significance tests, since it causes the coefficients to seemingly be more significant than they actually are.

One way of dealing with overdispersion is to use the quasi-binomial model, where one simply adjusts the assumed variance of the binomial model with the estimated overdispersion. In essence, this approach then adjusts the estimated standard errors of the coefficients by the same multiplicative factor (the square root of the estimated overdispersion parameter), thus reducing the perceived significance of the coefficients from the Wald test.
A weakness of this approach is that the sources of overdispersion is not actually modelled. Instead, the significance of the parameters are simply corrected with the same multiplying factor. The assumption that the standard errors of all explanatory variables are equally biased may not be appropriate (Harrison, 2015).

Another way to model overdispersion is by including random effects. A random effect on the binomial observation-level can be used to "soak up" the extra-binomial variation. By fitting a binomial mixed model for the delousing effect, it was observed that the standard errors of the coefficients were inflated compared to the binomial model. However, the inflation factor for the binomial mixed model compared to the binomial model was not constant for all coefficients, like it was for the quasi-binomial model. This shows that the two types of models model overdispersion differently, which motivated the use of both types of models for comparison purposes. If both models reach the same conclusion, we consider it to be more certain.

In both the reduced quasi-binomial DE-FE model (Table 4.4) and the reduced DE-ME model (Table 4.6), the interaction between delousing method and sea temperature was considered significant. Thus, the comparison of the delousing methods had to be done for specific temperatures, and the sea temperatures 7°C and 11.7°C were chosen. All four delousing methods have observations in this interval, but SkaMik and Hydrolicer have quite few observations with $SeaTemp \leq 7°C$.

For a sea temperature of 11.7°C, both models agree that Hydrolicer was associated with the best delousing effect, followed by SkaMik, Optilicer and freshwater. In addition, significance tests from both models suggested that freshwater was significantly different from the three other delousing methods and that Hydrolicer was significantly different from Optilicer. For a sea temperature of 7°C, the models agree that freshwater is associated with the lowest delousing effect, and is significantly different from the three other delousing methods.

Although significance tests have only been performed for the two temperatures, we emphasize that for both models, freshwater is considered to have the lowest delousing effect for all tem-

peratures for which it has been used when all other variables are constant. Figure 3.4, from the initial data exploration, also indicated that freshwater had the lowest delousing effect. From this figure it also seemed like the delousing effect from freshwater was subject to more uncertainty than the other delousing methods. Although the binomial logistic model (with variance $n\pi(1-\pi) \propto \pi(1-\pi)$) allows for larger variance for proportions closer to 0.5 and smaller variance for proportions close to 0 or 1, it did not seem like this was enough to capture the larger variance for freshwater. In both the DE-FE and DE-ME model, the residuals seemed to have higher variance for freshwater compared to the other delousing methods. For freshwater treatment, it has been suspected that the lice may be strongly affected by the osmotic shock and immobilized, while still remaining attached to the fish for a variable amount of time, which may be an explanation for the larger uncertainty.
As a consequence of the delayed response to the freshwater treatment, there may be a further reduction in lice numbers after the fish are returned back into the sea after freshwater treatment (Holan et al., 2017). In Gaasø, 2019, there seemed to be a tendency of smaller lice numbers in the week after treatment than what was counted during the unloading of the fish from the treatment vessel into the cage. Although the models for delousing effect in this thesis indicated that freshwater had a smaller reduction in adult female lice than the other methods when the lice were counted immediately after treatment, the more long-term effect after the fish had been returned to the sea for some time should ideally also have been investigated. Unfortunately, this kind of data were not available.

A drawback of the response data for delousing effect is that lice are counted on different samples of fish before and after treatment. This means that there are different lice that are counted before and after treatment. Thus, one relies on the assumption that the lice are evenly distributed on all the fish in the cage both before and after. This is not necessarily the case, which became evident in the data preparation where there were instances where the number of lice reported after treatment was greater than before treatment. In a binomial setting where the same lice were measured before and after treatment this would not have been possible. In addition, one assumes that the lice are similar in all ways and respond to the treatment in the same way. Thus, one can argue that there are other sources of variation in the measurements other than the variance in the simple binomial setting, so the observed overdispersion is quite reasonable.

5.2 Salmon Mortality

Like the delousing effect, the mortality rates for salmon 3 and 14 days after delousing were modelled with binomial models, and the problem with overdispersion applied to these as well. Thus, both quasi-binomial fixed effects models and binomial mixed effects models were fitted for comparison reasons. We first summarize the results for the models for mortality after 3 and 14 days separately, before a comparison and discussion of the two follows.

Mortality 3 Days Post-Treatment

After the model selection of the quasi-binomial M3-FE model and the M3-ME model, the two models ended up including different explanatory variables. In particular, the interaction between delousing method and sea temperature was considered significant, and was therefore included, in the reduced M3-ME model (Table 4.10). However, this was not the case in the reduced M3-FE model (Table 4.8).

According to the results of the reduced M3-FE model, Optilicer was associated with the highest

mortality, followed by Hydrolicer, SkaMik and freshwater. The differences between all delousing methods were considered significant, except for the difference between freshwater and SkaMik. For the reduced M3-ME model, Hydrolicer was associated with a significantly higher mortality than both freshwater and SkaMik at a sea temperature of 11.7°C. For a sea temperature of 7°C, both Optilicer and Hydrolicer are associated with a significantly higher mortality than both freshwater and SkaMik.

To summarize, the models suggest that, 3 days after delousing treatment, Hydrolicer has a significantly higher mortality than freshwater and SkaMik for both these temperatures, and that Optilicer has a significantly higher mortality than freshwater and SkaMik for a sea temperature of 7°C.

Mortality 14 Days Post-Treatment

Like the models for mortality after 3 days, the interaction between delousing method and sea temperature was considered significant in the mixed effects model for mortality after 14 days, but not in the fixed effects model. In the reduced quasi-binomial M14-FE model (Figure D.9), Optilicer was associated with the highest mortality, followed by SkaMik, Hydrolicer and Freshwater. The differences are significant, except for Hydrolicer, which is not significantly different from SkaMik or freshwater.
The reduced M14-ME model (Figure D.11) suggests that Hydrolicer has a significantly higher mortality than SkaMik for a sea temperature of 11.7°C. For a sea temperature of 7°C, Optilicer has significantly higher mortality than both freshwater and SkaMik.

Thus, both models seem to agree that Optilicer has a significantly higher mortality 14 days after treatment than freshwater and SkaMik for a sea temperature of 7°C.

Comparison and Discussion

The mortality rate after 3 days was chosen as a measure for the short-term mortality, while the mortality rate after 14 days was used for long-term mortality. The models for mortality after 3 days had more significant results than the models for mortality after 14 days. However, they all concluded that Optilicer has a significantly higher mortality than freshwater and SkaMik for a sea temperature of 7°C. Hence, it seems like this may be both an short-term and a long-term effect. The long-term effect on the mortality could be further investigated by considering longer periods of time.

The full binomial M3-FE and M14-FE models had estimated overdispersion parameters of 603 and 1386, respectively. This is an indication that the models for mortality after 3 days may fit better than the models after 14 days. It is not surprising that the variability after 14 days seemingly is greater than after 3 days, since more time after delousing to measurement of mortality means that there is more time for other factors, possibly unrelated to the delousing, to influence the mortality. The models for mortality after 3 and 14 days were also fit to different data sets, where the data set for mortality after 3 days was bigger than that for 14 days.

An advantage of the mortality data is that the mortality is measured for the entire group of fish in the cage, rather than for small and different samples of fish. However, a weakness with using the mortality as a welfare indicator is that welfare problems may result in mortality after a period of time (Noble et al., 2018). In other words, there may have been other causes happening before the treatment that could result in increased mortality in the period after treatment as

well. Therefore, the health status of the salmon prior to the delousing treatment is an important factor to take into consideration. With the available data, it was attempted to take this into consideration by including the welfare indicator scores for skin haemorrhages and scale loss before treatment. However, these are only indicators for skin condition, and were calculated from a sample of the fish. Other welfare indicators could have been included, but these were less frequently reported, so inclusion of these would have resulted in a smaller data set. It would likely be more beneficial to use the mortality rate in a time period prior to the delousing treatment as an explanatory variable, as this would provide a more direct comparison to the mortality rate after treatment. Unfortunately, this kind of information was not available. By including this, it would probably become more clear whether the delousing treatments were the actual cause of higher mortality or not.

5.3 Score-Based Welfare Indicators

The change in the score of the welfare indicators skin haemorrhages and scale loss after delousing was assumed to be normally distributed and was therefore modelled with linear mixed models with a random intercept for *LocNumber*. The mixed effects models were compared with the fixed effects models with LR tests, and the mixed effects models were preferred for both welfare indicators.

According to the reduced SH-ME model (Table 4.12), Optilicer is associated with the greatest change in skin haemorrhages, followed by SkaMik, Hydrolicer and freshwater. Compared to freshwater, which was associated with the smallest change after delousing treatment, the change was expected to increase with 0.20, 0.3 and 0.42 for Hydrolicer, SkaMik and Optilicer, respectively, if these were used instead and all other variables were constant. The differences between all delousing methods were considered significant, except for the difference between Optilicer and SkaMik.

In the reduced SL-ME model (Table 4.13) for change in scale loss, the interaction between delousing method and sea temperature was included. Comparisons between the delousing methods were therefore done for the two temperatures 11.7°C and 7°C. For both these temperatures, SkaMik was associated with the greatest change in scale loss, followed by Hydrolicer, Optilicer and freshwater. For a sea temperature of 7°C, the change in scale loss is expected to increase with 0.27, 0.46 and 0.69 for Optilicer, Hydrolicer and SkaMik, respectively, if these are used instead of freshwater. The differences between all four delousing methods are considered significant for this sea temperature. However, for a sea temperature of 11.7°C, the change is expected to increase with 0.13, 0.60 and 0.68 for Optilicer, Hydrolicer and SkaMik, respectively, if these are used instead of freshwater. The mechanical delousing methods (SkaMik and Hydrolicer) are significantly different from both Optilicer and freshwater for this temperature.

Similar to the delousing effect responses, the responses for the welfare indicators, i.e. the reported scores before and after delousing for each cage, were based on evaluations of different samples of fish for practical reasons. One can imagine that this could be an extra source of uncertainty, and more reliable results could probably have been obtained if measurements were made on the same sample. That being said, the linear mixed models seem to capture the uncertainty well, with residuals that appeared to follow the assumed distribution.

5.4 Conclusion and Recommendations for Further Work

Significant overdispersion was observed in the binomial models for the delousing effectiveness against adult female lice and mortality for salmon 3 and 14 days after delousing treatment. Therefore, both quasi-binomial and binomial mixed models, which handle the overdispersion differently, were fitted for comparison reasons.
According to both models for the delousing effectiveness against adult female lice, Hydrolicer had a significantly better delousing effect than Optilicer for a sea temperature of 11.7°C. In addition, both types of models indicated that freshwater had a lower delousing effect than the three other methods for all sea temperatures for which it had been used. The result was tested for two sea temperatures of 7°C and 11.7°C, and was found to be significant for both temperatures. However, this way of measuring the delousing effect, where the reduction in lice immediately after treatment is considered, may not be accurate for freshwater treatment. It has been observed that freshwater treatment may lead to further reduction in lice after the fish are returned to the sea, so this aspect should be further investigated.

According to the models for mortality 3 days after delousing treatment, which was chosen as a measure for short-term mortality, Hydrolicer had a significantly higher mortality than freshwater and SkaMik for sea temperatures of 7°C and 11.7°C. In addition, Optilicer has a significantly higher mortality than freshwater and SkaMik for a sea temperature of 7°C.
According to the models for mortality after 14 days, which was chosen for the long-term mortality, Optilicer had a significantly higher mortality than freshwater and SkaMik for a sea temperature of 7°C. This result is in concordance with the models for short-term mortality.
For further analyses of the mortality, an improvement would be to include an explanatory variable for the mortality before the treatment as well. In this way, one could obtain more information about the actual cause of mortality.

For further analysis of the delousing effect and mortality with binomial models, where overdispersion is present, one could also consider more complex mixed models with the inclusion of random slopes or other random effects. On the other hand, more complex models in general require more data and the chance of the model not converging to a stable solution may increase. Another method for modelling overdispersion in binomial data is the hierarchical beta-binomial model. This is an alternative to the inclusion of an observation-level random effect in the binomial mixed model (Harrison, 2015). In this model, one assumes that the probability of success in each binomial trial varies with a beta distribution (Collett, 2003). It would be interesting to see if this type of model could handle the overdispersion better.

The change in score evaluations for skin haemorrhages and scale loss after delousing treatment was modelled using linear mixed models. Optilicer was then associated with the greatest change in score for skin haemorrhages, followed by SkaMik, Hydrolicer and freshwater. The differences between the delousing methods were considered significant, except for the difference between Optilicer and SkaMik.
Regarding the change in scale loss after delousing, SkaMik was associated with the greatest change, followed by Hydrolicer, Optilicer and freshwater for sea temperatures up to approximately 14°C. All four methods are significantly different for a sea temperature of 7°C. However, for a sea temperature of 11.7°C, only the mechanical delousing methods (SkaMik and Hydrolicer) are significantly different from both Optilicer and freshwater.

In this thesis, only a selection of parameters have been investigated for a comparison of the delousing methods. In order to get a broader picture of the impacts of the different delousing methods, more parameters should be looked into. Regarding the delousing effect, only the effect

on adult female lice was considered in this thesis, but it could also be analysed for mobile and sessile lice. As pointed out, the more long-term effect of the delousing methods on the lice numbers should also be investigated. To evaluate the fish welfare, it was argued in Section 1.2 that one should consider several different welfare indicators. In this thesis, only the mortality, in addition to skin haemorrhages and scale loss, were investigated. However, many more welfare indicators could be considered (see Noble et al., 2018).

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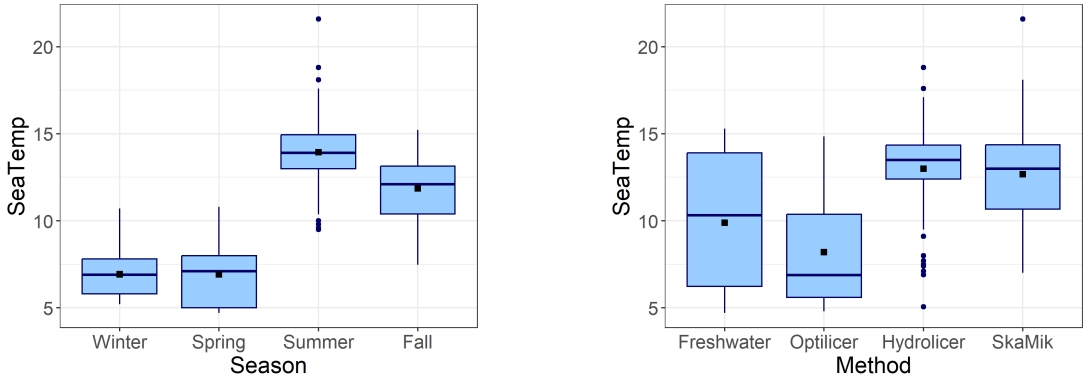
Appendix

A Additional Figures



(a) *SeaTemp* against *Season*

(b) *SeaTemp* against *Method*

Figure A.1: Additional box plots from the data set for delousing effect on adult female lice.

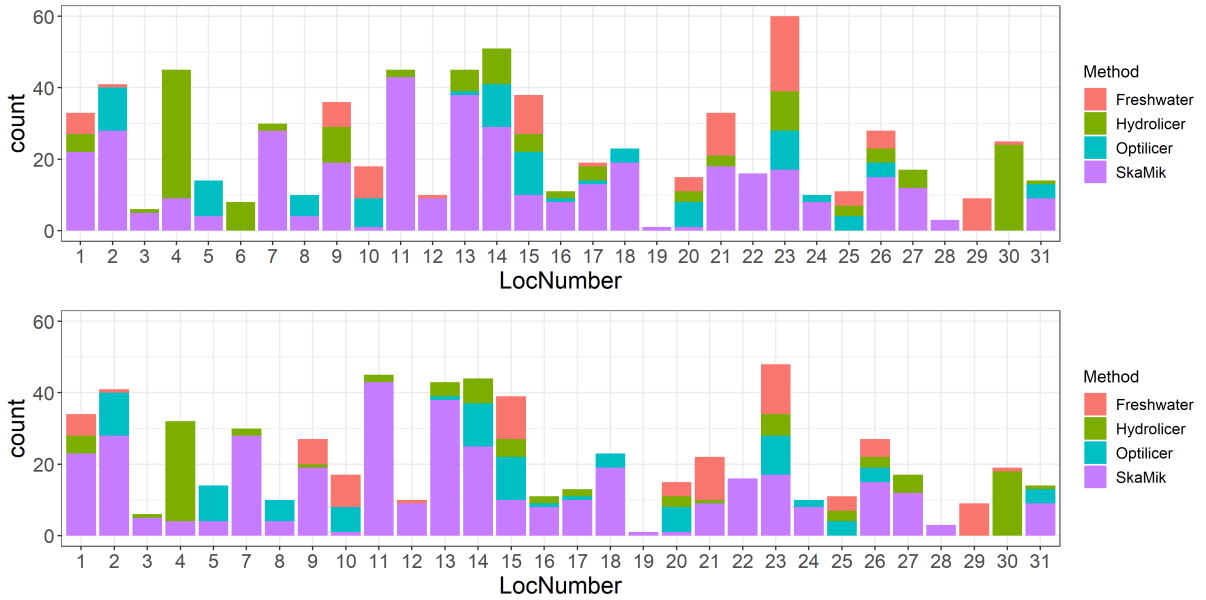
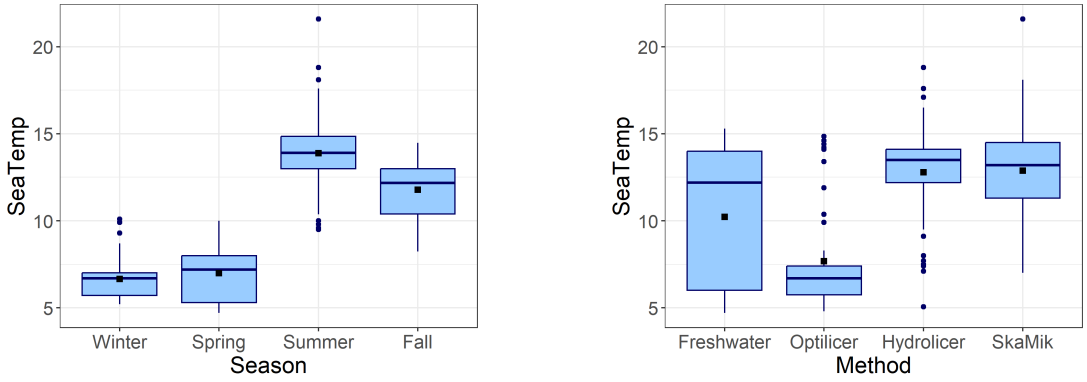
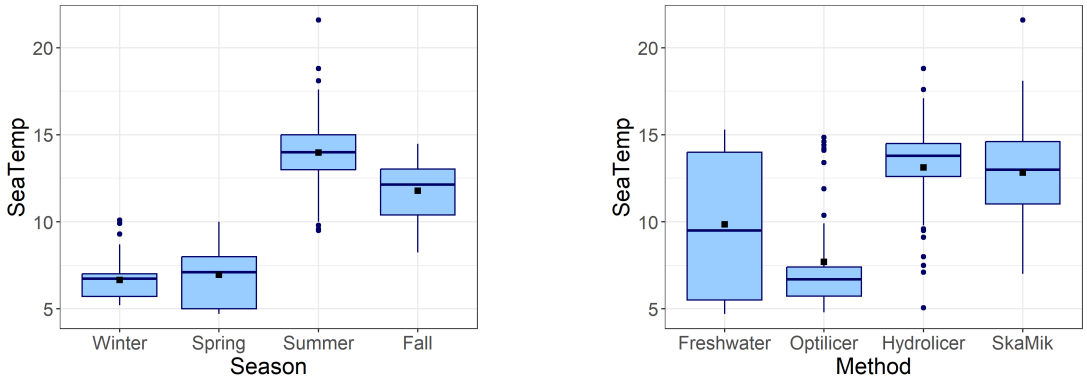


Figure A.2: Number of observations from the different locations for the data sets for salmon mortality after 3 days (top) and 14 days (bottom). The different colors distinguish between the number of observations for the different delousing methods.



(a) *SeaTemp* against *Season* **(b)** *SeaTemp* against *Method*

Figure A.3: Additional box plots from the data set for mortality after 3 days.



(a) *SeaTemp* against *Season* **(b)** *SeaTemp* against *Method*

Figure A.4: Additional box plots from the data set for mortality after 14 days.

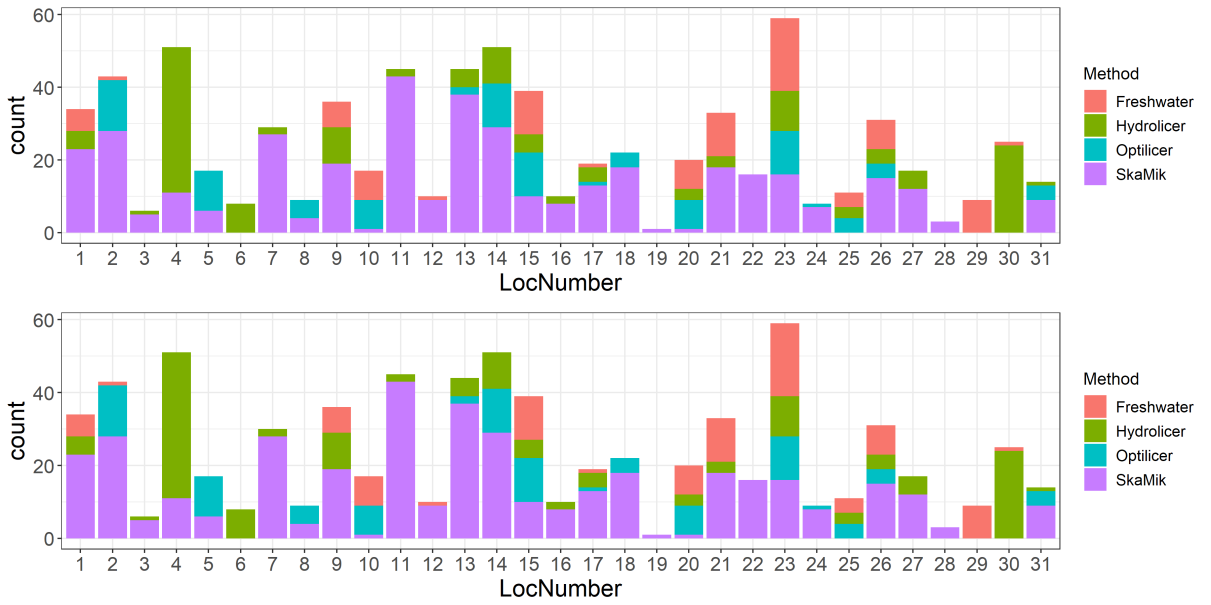
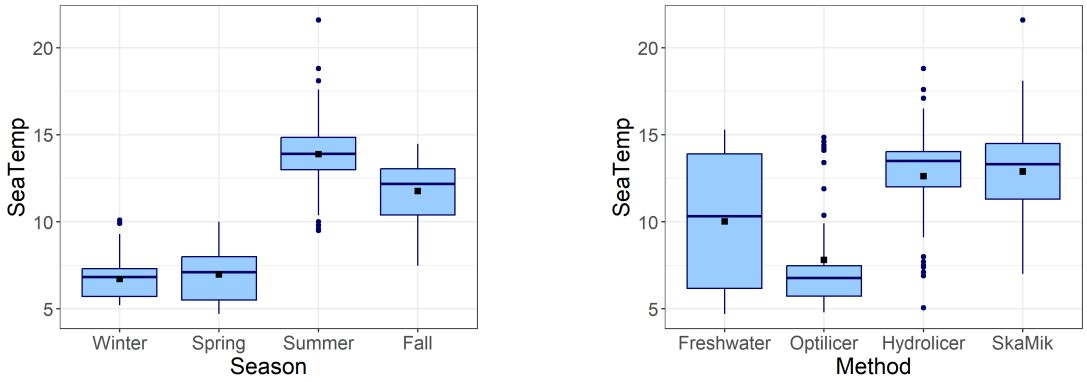
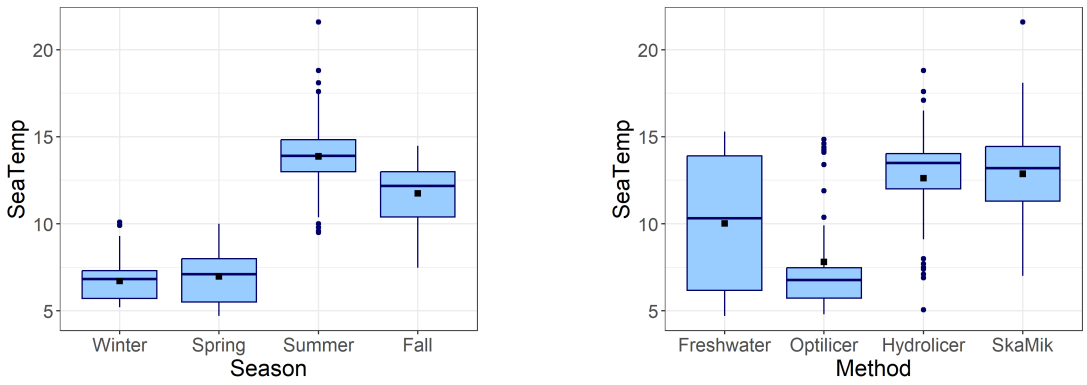


Figure A.5: Number of observations from the different locations for the data sets for skin haemorrhages (top) and scale loss (bottom). The different colors distinguish between the number of observations for the different delousing methods.



(a) *SeaTemp* against *Season* **(b)** *SeaTemp* against *Method*

Figure A.6: Additional box plots from the data set for change in skin haemorrhages.



(a) *SeaTemp* against *Season* **(b)** *SeaTemp* against *Method*

Figure A.7: Additional box plots from the data set for change in scale loss.

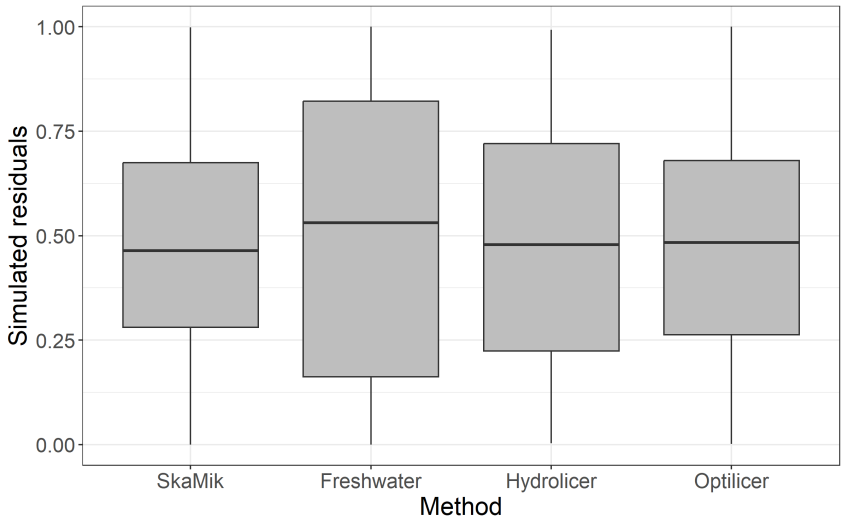


Figure A.8: Box plot of simulated residuals for each delousing method for the reduced DE-ME model.

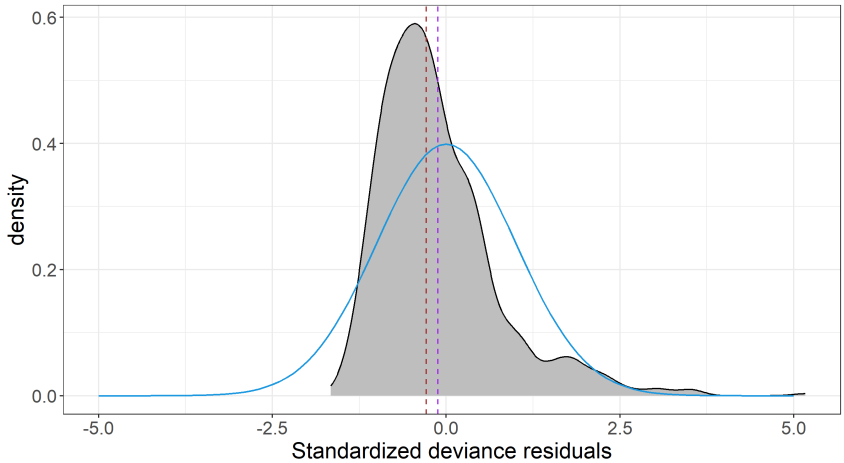


Figure A.9: Distribution of standardized deviance residuals from the M3-FE model (gray). The brown and purple dashed lines show the median and mean values, respectively. The blue density curve shows the standard normal distribution.

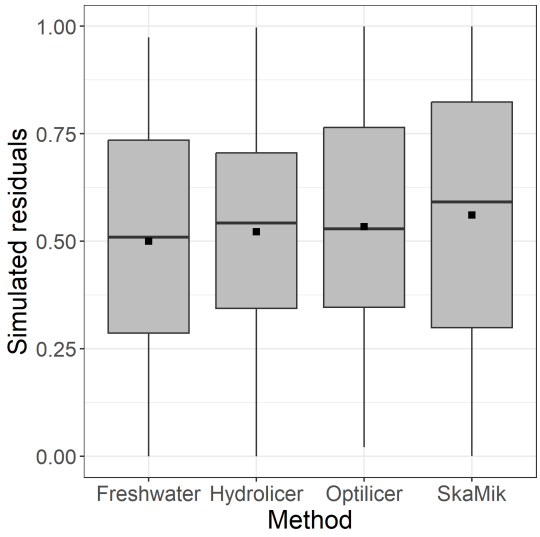


Figure A.10: Box plot of simulated residuals for each delousing method for the reduced M3-ME model. The mean values are marked by the black squares.

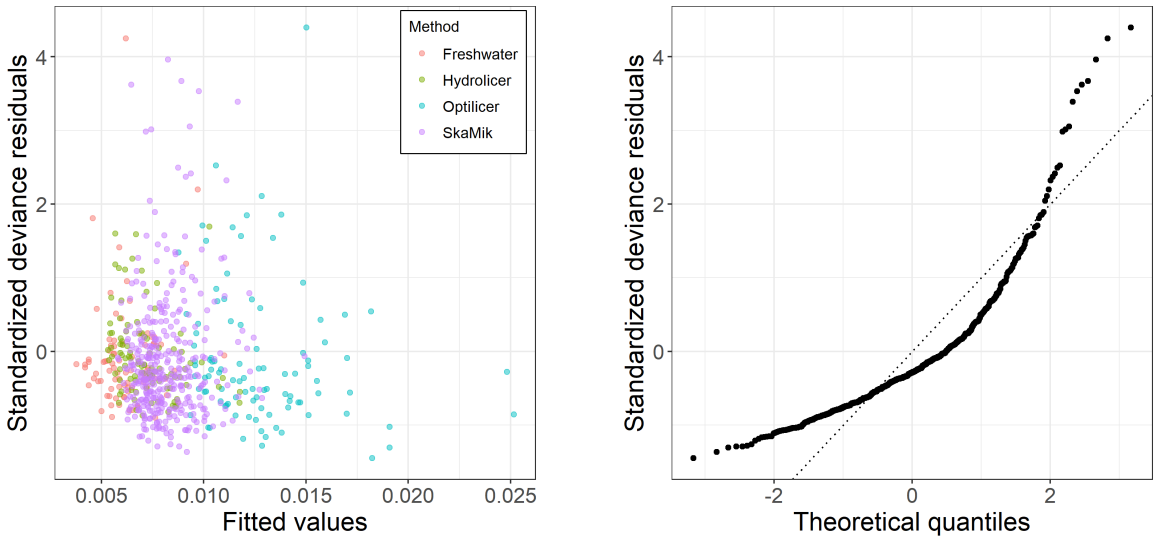
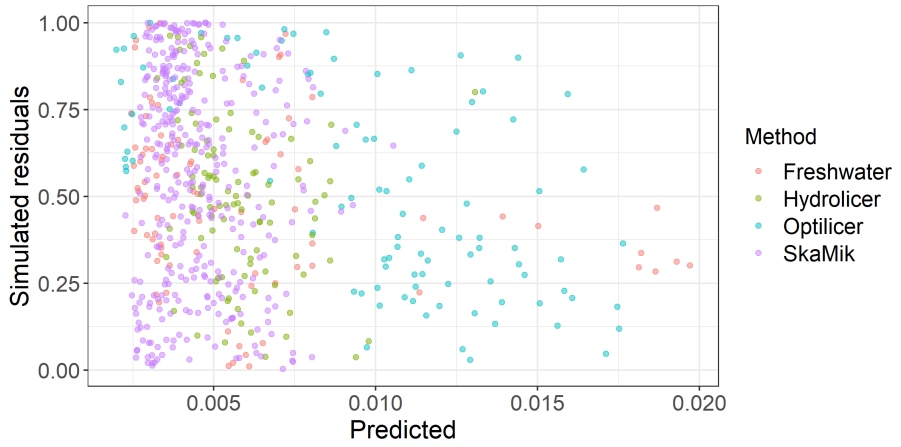
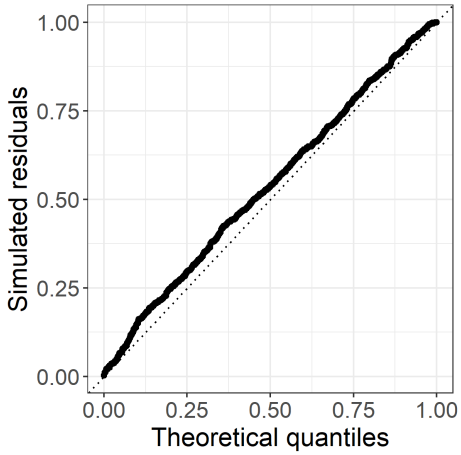


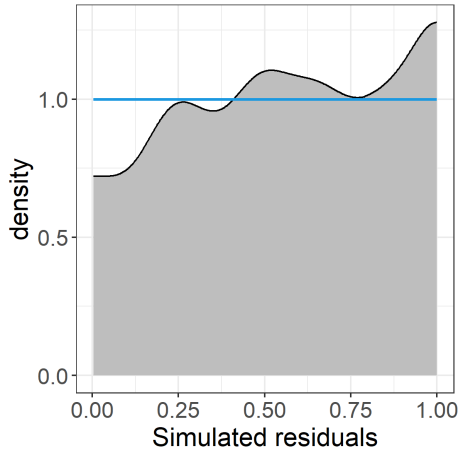
Figure A.11: Model diagnostics for the reduced quasi-binomial M14-FE model. Standardized deviance residuals plotted against fitted values and the theoretical quantiles of the normal distribution.



(a) Simulated residuals against predicted values.

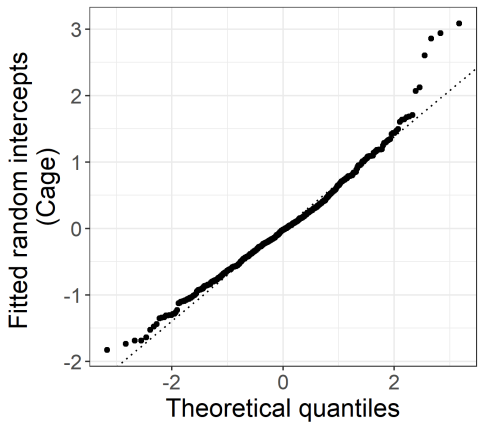


(b) Simulated residuals against the theoretical quantiles of the uniform distribution.



(c) Distribution of simulated residuals. The blue line indicates the uniform distribution.

Figure A.12: Model diagnostic plots for the reduced M14-ME model.



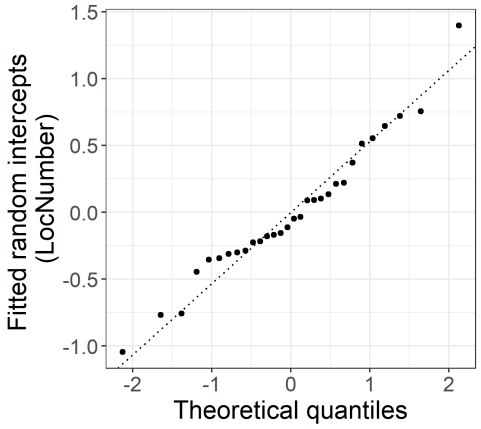
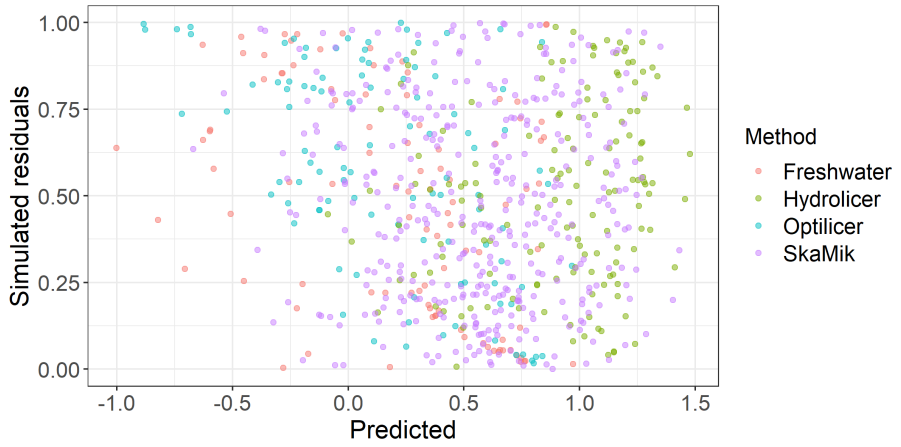
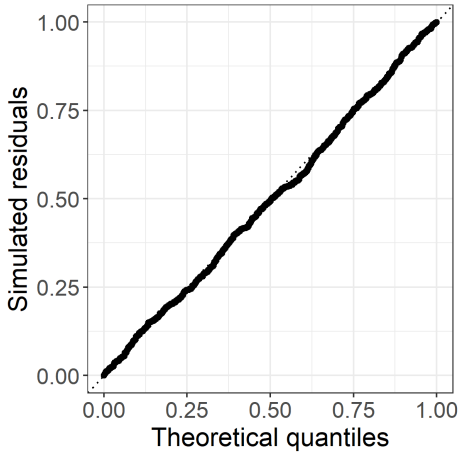


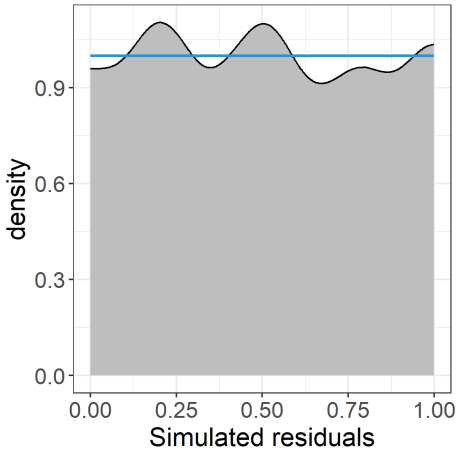
Figure A.13: Model diagnostic plots for the reduced M14-ME model. The fitted random intercepts for *Cage* and *LocNumber* are plotted against the theoretical quantiles of the normal distribution. The straight dotted lines indicate the expected distribution based on the estimated variances $\hat{\sigma}_2^2$ and $\hat{\sigma}_1^2$.



(a) Simulated residuals against predicted values.



(b) Simulated residuals against the theoretical quantiles of the uniform distribution



(c) Distribution of simulated residuals. The blue line indicates the uniform distribution.

Figure A.14: Model diagnostic plots for the reduced SL-ME model.

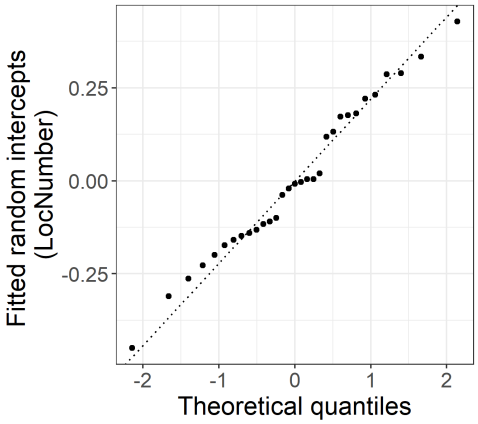


Figure A.15: Fitted random intercepts for *LocNumber* from the reduced SL-ME model plotted against the theoretical quantiles of the normal distribution. The straight dotted line indicates the expected distribution based on the estimated variance $\hat{\sigma}^2_\gamma$.

B Additional Tables

Table B.1: Number of observations for the seasons for each delousing method in the data sets for mortality. Additionally, the interquartile range, as well as the minimum and maximum value of the sea temperature for which the different delousing methods have been used is given. This information is given for both the data sets for mortality (after 3 and 14 days), as given by the first column.

		Number of observations in seasons				Temperature		
Data set	Method	Winter	Spring	Summer	Fall	Min	Max	IQR
3 days	Freshwater	18	20	45	9	4.7	15.3	6.0-14.0
	Optilicer	58	21	18	2	4.8	14.9	5.8-7.4
	Hydrolicer	0	21	115	9	5.1	18.8	12.2-14.1
	SkaMik	15	19	238	117	7.0	21.6	11.3-14.5
14 days	Freshwater	19	20	38	8	4.7	15.3	5.5-14.0
	Optilicer	58	20	18	2	4.8	14.9	5.7-7.4
	Hydrolicer	0	13	77	9	5.1	18.8	12.6-14.5
	SkaMik	15	19	218	117	7.0	21.6	11.0-14.6

Table B.2: Comparable generalized variance inflation factor for the explanatory variables in the data sets for mortality after 3 and 14 days. An interaction between delousing method and sea temperature is included.

Explanatory variable	df	3 days $\left(\text{GVIF}^{1/(2df)}\right)^2$	14 days $\left(\text{GVIF}^{1/(2df)}\right)^2$
Method	3	2.11	2.12
SeaTempSc	1	7.42	6.65
SeaTempSc:Method	3	2.58	2.50
AvWeightSc	1	2.79	2.70
AvCrowdingSc	1	1.18	1.20
BiomassSc	1	2.86	2.75
Season	3	2.15	2.08
Disease	1	1.20	1.17
HaemorrBefore	1	1.59	1.61
ScalelossBefore	1	1.62	1.51

Table B.3: Number of observations for the seasons for each delousing method in the data sets for skin haemorrhages and scale loss. Additionally, the interquartile range, as well as the minimum and maximum value of the sea temperature for which the different delousing methods have been used is given.

		Number of observations in seasons				Temperature		
Data set	Method	Winter	Spring	Summer	Fall	Min	Max	IQR
Skin haemorrhages	Freshwater	23	20	42	13	4.7	15.3	6.2-13.9
	Optilicer	57	23	20	2	4.8	14.9	5.7-7.5
	Hydrolicer	0	25	114	9	5.1	18.8	12.0-14.0
	SkaMik	13	19	239	119	7.0	21.6	11.3-14.5
Scale loss	Freshwater	23	20	42	13	4.7	15.3	6.2-13.9
	Optilicer	57	23	20	2	4.8	14.9	5.7-7.5
	Hydrolicer	0	25	114	9	5.1	18.8	12.0-14.0
	SkaMik	13	19	238	121	7.0	21.6	11.3-14.5

Table B.4: Comparable generalized variance inflation factor for the explanatory variables in the data sets for change in skin haemorrhages and scale loss. An interaction between delousing method and sea temperature is included.

Explanatory variable	df	Skin haemorrhages $\left(\text{GVIF}^{1/(2df)}\right)^2$	Scale loss $\left(\text{GVIF}^{1/(2df)}\right)^2$
Method	3	1.99	1.99
SeaTempSc	1	5.80	5.80
SeaTempSc:Method	3	2.40	2.40
AvWeightSc	1	1.69	1.69
AvCrowdingSc	1	1.21	1.21
BiomassSc	1	1.79	1.79
Season	3	2.01	2.01
Disease	1	1.18	1.18
HaemorrBefore	1	1.51	1.52
ScalelossBefore	1	1.62	1.62

Table B.5: Results from the LR tests for the DE-ME model. The dropped fixed effects terms of the initial full model are listed sequentially in a top-down manner, so that each line represents the model from the previous line with the additional dropped term given.

Dropped	**Df**	**Log likelihood**	**LR**	**Pr(>Chi)**
None (full model)		-1815.679		
BiomassSc	1	-1815.831	0.3040	0.5814
AvCrowdingSc	1	-1816.396	1.1299	0.2878

Table B.6: Results from the LR tests for the quasi-binomial M3-FE model. The dropped terms of the initial full model are listed sequentially in a top-down manner, so that each line represents the model from the previous line with the additional dropped term given.

Dropped	Df	Deviance	Scaled deviance difference	Pr(>Chi)
None (full model)		326310		
ScalelossBefore	1	326343	0.0546	0.815
Disease	1	326437	0.1556	0.693
Method:SeaTempSc	3	328154	2.8572	0.414
SeaTempSc	1	328846	1.1483	0.284
BiomassSc	1	329494	1.0674	0.302
AvCrowdingSc	1	331367	3.0776	0.079

Table B.7: Results from the LR tests for the M3-ME model. The dropped fixed effects terms of the initial full model are listed sequentially in a top-down manner, so that each line represents the model from the previous line with the additional dropped term given.

Dropped	Df	Log likelihood	LR	Pr(>Chi)
None (full model)		-5195.298		
ScalelossBefore	1	-5195.299	0.0020	0.964
HaemorrBefore	1	-5195.661	0.7229	0.395

Table B.8: Results from the LR tests for the quasi-binomial M14-FE model. The dropped terms of the initial full model are listed sequentially in a top-down manner, so that each line represents the model from the previous line with the additional dropped term given.

Dropped	Df	Deviance	Scaled deviance difference	Pr(>Chi)
None (full model)		609264		
Season	3	611683	1.7453	0.627
Method:SeaTempSc	3	616143	3.2105	0.360
SeaTempSc	1	617411	0.9136	0.339
ScalelossBefore	1	619872	1.7878	0.181
AvWeightSc	1	622420	1.8483	0.174
BiomassSc	1	624657	1.6046	0.205
Disease	1	629255	3.2231	0.073

Table B.9: Results from additional Wald tests from the reduced M14-FE model.

Null hypothesis	df	Wald statistic	p-value
$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodHydrolicer}}$	1	12.632	$3.79 \cdot 10^{-4}$
$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodFreshwater}}$	1	21.221	$4.09 \cdot 10^{-6}$
$\beta_{\text{MethodFreshwater}} = \beta_{\text{MethodHydrolicer}}$	1	1.952	0.162

Table B.10: Results from the LR tests for the M14-ME model. The dropped fixed effects terms of the initial full model are listed sequentially in a top-down manner, so that each line represents the model from the previous line with the additional dropped term given.

Dropped	**Df**	**Log likelihood**	**LR**	**Pr(>Chi)**
None (full model)		-5066.781		
HaemorrBefore	1	-5067.553	1.5450	0.214
BiomassSc	1	-5069.135	3.1642	0.075

Table B.11: Results from additional Wald tests from the reduced M14-ME model. The tests are done for two models fitted with the same variables, but with two different sea temperatures defined as intercept values.

Sea temperature as intercept	**Null hypothesis**	**df**	**Wald statistic**	**p-value**
11.7°C	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodHydrolicer}}$	1	2.541	0.111
	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodFreshwater}}$	1	0.023	0.878
	$\beta_{\text{MethodFreshwater}} = \beta_{\text{MethodHydrolicer}}$	1	2.998	0.083
7°C	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodHydrolicer}}$	1	2.321	0.128
	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodFreshwater}}$	1	12.434	$4.22 \cdot 10^{-4}$
	$\beta_{\text{MethodFreshwater}} = \beta_{\text{MethodHydrolicer}}$	1	0.465	0.495
	$\beta_{\text{MethodFreshwater}} = 0$	1	1.464	0.226
	$\beta_{\text{MethodHydrolicer}} = 0$	1	2.509	0.113
	$\beta_{\text{MethodOptilicer}} = 0$	1	23.523	$1.23 \cdot 10^{-6}$

Table B.12: Results from the LR tests for the SH-ME model. The dropped fixed effects terms of the initial full model are listed sequentially in a top-down manner, so that each line represents the model from the previous line with the additional dropped term given.

Dropped	**Df**	**Log likelihood**	**LR**	**Pr(>Chi)**
None (full model)		-330.5468		
Disease	1	-330.5949	0.096	0.756
AvCrowdingSc	1	-330.6479	0.106	0.745
AvWeightSc	1	-330.7410	0.186	0.666
Method:SeaTempSc	3	-333.2657	5.049	0.168
BiomassSc	1	-333.9229	1.314	0.252

Table B.13: Results from Wald tests from the reduced SH-ME model.

Null hypothesis	df	Wald statistic	p-value
$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodHydrolicer}}$	1	10.688	$1.08 \cdot 10^{-3}$
$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodFreshwater}}$	1	48.421	$3.44 \cdot 10^{-12}$
$\beta_{\text{MethodFreshwater}} = \beta_{\text{MethodHydrolicer}}$	1	12.376	$4.34 \cdot 10^{-4}$
$\beta_{\text{MethodFreshwater}} = 0$	1	41.045	$1.49 \cdot 10^{-10}$
$\beta_{\text{MethodHydrolicer}} = 0$	1	7.322	$6.81 \cdot 10^{-3}$
$\beta_{\text{MethodOptilicer}} = 0$	1	2.371	0.124

Table B.14: Results from the LR tests for the SL-ME model. The dropped fixed effects terms of the initial full model are listed sequentially in a top-down manner, so that each line represents the model from the previous line with the additional dropped term given.

Dropped	Df	Log likelihood	LR	Pr(>Chi)
None (full model)		-267.2923		
AvCrowdingSc	1	-267.3167	0.05	0.825
HaemorrBefore	1	-267.5329	0.43	0.511
Disease	1	-269.2801	3.49	0.062

Table B.15: Results from Wald tests from the reduced SL-ME model. The tests are done for two models fitted with the same variables, but with two different sea temperatures defined as intercept values.

Sea temperature as intercept	Null hypothesis	df	Wald statistic	p-value
11.7°C	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodHydrolicer}}$	1	38.230	$6.29 \cdot 10^{-10}$
	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodFreshwater}}$	1	2.501	0.114
	$\beta_{\text{MethodFreshwater}} = \beta_{\text{MethodHydrolicer}}$	1	96.939	$7.15 \cdot 10^{-23}$
	$\beta_{\text{MethodFreshwater}} = 0$	1	146.020	$1.29 \cdot 10^{-33}$
	$\beta_{\text{MethodHydrolicer}} = 0$	1	3.358	0.067
	$\beta_{\text{MethodOptilicer}} = 0$	1	66.861	$2.91 \cdot 10^{-16}$
7°C	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodHydrolicer}}$	1	4.538	0.033
	$\beta_{\text{MethodOptilicer}} = \beta_{\text{MethodFreshwater}}$	1	18.092	$2.11 \cdot 10^{-5}$
	$\beta_{\text{MethodFreshwater}} = \beta_{\text{MethodHydrolicer}}$	1	23.075	$1.56 \cdot 10^{-6}$
	$\beta_{\text{MethodFreshwater}} = 0$	1	81.805	$1.50 \cdot 10^{-19}$
	$\beta_{\text{MethodHydrolicer}} = 0$	1	6.654	$9.89 \cdot 10^{-3}$
	$\beta_{\text{MethodOptilicer}} = 0$	1	39.226	$3.78 \cdot 10^{-10}$

C R-code from Data Preparation

R-code from the preparation of the data and creation of the data sets. Salmon farm names and treatment dates have been replaced by "..." to maintain confidentiality.

```
####### Loading packages #############
library("readxl")
library("writexl")
library("dplyr")
library("stringr")

############## Load data ###############
# Freshwater
df.ferskDod20 = read_excel("Ferskvann_2020.xlsx",
                           sheet = "D delighet", skip = 1, n_max = 41)
df.ferskEff20 = read_excel("Ferskvann_2020.xlsx",
                           sheet = "Effekt", skip = 1, n_max = 41)

df.ferskDod21 = read_excel("Ferskvann_2021.xlsx",
                           sheet = "D delighet", skip = 1, n_max = 81)
df.ferskEff21 = read_excel("Ferskvann_2021.xlsx",
                           sheet = "Effekt", skip = 1, n_max = 81)

df.ferskDod22 = read_excel("Ferskvann_2022.xlsx",
                           sheet = "D delighet", skip = 1, n_max = 100)
df.ferskEff22 = read_excel("Ferskvann_2022.xlsx",
                           sheet = "Effekt", skip = 1, n_max = 100)

# Optilicer
df.optDod20 = read_excel("Optilicer_2020.xlsx",
                         sheet = "D delighet", skip = 1, n_max = 107)
df.optEff20 = read_excel("Optilicer_2020.xlsx",
                         sheet = "Effekt", skip = 1, n_max = 107)

df.optDod21 = read_excel("Optilicer_2021.xlsx",
                         sheet = "D delighet", skip = 1, n_max = 73)
df.optEff21 = read_excel("Optilicer_2021.xlsx",
                         sheet = "Effekt", skip = 1, n_max = 73)

# Hydrolicer
df.hydDod20 = read_excel("Hydrolicer_2020.xlsx",
                         sheet = "D delighet", skip = 1, n_max = 31)
df.hydEff20 = read_excel("Hydrolicer_2020.xlsx",
                         sheet = "Effekt", skip = 1, n_max = 31)

df.hydDod21 = read_excel("Hydrolicer_2021.xlsx",
                         sheet = "D delighet", skip = 1, n_max = 45)
df.hydEff21 = read_excel("Hydrolicer_2021.xlsx",
                         sheet = "Effekt", skip = 1, n_max = 45)

df.hydDod22 = read_excel("Hydrolicer_2022.xlsx",
                         sheet = "D delighet", skip = 1, n_max = 126)
df.hydEff22 = read_excel("Hydrolicer_2022.xlsx",
                         sheet = "Effekt", skip = 1, n_max = 126)
```

```
# SkaMik
df.skamikDod20 = read_excel("SkaMik_2020.xlsx",
                            sheet = "D delighet", skip = 1, n_max = 139)
df.skamikEff20 = read_excel("SkaMik_2020.xlsx",
                            sheet = "Effekt", skip = 1, n_max = 139)

df.skamikDod21 = read_excel("SkaMik_2021.xlsx",
                            sheet = "D delighet", skip = 1, n_max = 253)
df.skamikEff21 = read_excel("SkaMik_2021.xlsx",
                            sheet = "Effekt", skip = 1, n_max = 253)

df.skamikDod22 = read_excel("SkaMik_2022.xlsx",
                            sheet = "D delighet", skip = 1, n_max = 110)
df.skamikEff22 = read_excel("SkaMik_2022.xlsx",
                            sheet = "Effekt", skip = 1, n_max = 110)


####### Check consistency between excel sheets #######
# Freshwater
stopifnot(df.ferskDod20$Behandlingsdato == df.ferskEff20$`Beh. dato`)
stopifnot(df.ferskDod20$Anlegg == df.ferskEff20$Anlegg)

stopifnot(df.ferskDod21$Behandlingsdato == df.ferskEff21$`Beh. dato`)
stopifnot(df.ferskDod21$Anlegg == df.ferskEff21$Anlegg)

stopifnot(df.ferskDod22$Behandlingsdato == df.ferskEff22$`Beh. dato`)
df.ferskDod22$Behandlingsdato[21] = df.ferskEff22$`Beh. dato`[21]
df.ferskEff22$`Beh. dato`[27] = df.ferskDod22$Behandlingsdato[27]
stopifnot(df.ferskDod22$Anlegg == df.ferskEff22$Anlegg)

# Optilicer
stopifnot(df.optDod20$Behandlingsdato == df.optEff20$`Beh. dato`)
df.optEff20 = df.optEff20[-c(74), ] # delete treatment with no information
temp = df.optDod20[83,]             # inconsistent order of the treatments
df.optDod20[83,] = df.optDod20[84,]
df.optDod20[84,] = temp
stopifnot(df.optDod20$Anlegg == df.optEff20$Anlegg)

stopifnot(df.optDod21$Behandlingsdato == df.optEff21$`Beh. dato`)
stopifnot(df.optDod21$Anlegg == df.optEff21$Anlegg)

# Hydrolicer
stopifnot(df.hydDod20$Beh.dato == df.hydEff20$`Beh. dato`)
stopifnot(df.hydDod20$Anlegg == df.hydEff20$Anlegg)

stopifnot(df.hydDod21$Beh.dato == df.hydEff21$`Beh. dato`)
stopifnot(df.hydDod21$Anlegg == df.hydEff21$Anlegg)

stopifnot(df.hydDod22$Beh.dato == df.hydEff22$`Beh. dato`)
stopifnot(df.hydDod22$Anlegg == df.hydEff22$Anlegg)

# SkaMik
stopifnot(df.skamikDod20$Beh.dato == df.skamikEff20$`Beh. dato`)
stopifnot(df.skamikDod20$Anlegg == df.skamikEff20$Anlegg)

stopifnot(df.skamikDod21$Beh.dato == df.skamikEff21$`Beh. dato`)
```

```
# rearrange obs that was not in effect sheet
df.skamikDod21 = rbind(df.skamikDod21, df.skamikDod21[114, ])
df.skamikDod21 = df.skamikDod21[-c(114), ]
df.skamikEff21[253, ]$`Beh. dato` = df.skamikDod21[253, ]$Beh.dato
df.skamikEff21[253, ]$Anlegg = df.skamikDod21[253, ]$Anlegg
stopifnot(df.skamikDod21$Anlegg == df.skamikEff21$Anlegg)

stopifnot(df.skamikDod22$Beh.dato == df.skamikEff22$`Beh. dato`)
stopifnot(df.skamikDod22$Anlegg == df.skamikEff22$Anlegg)


########## Extract relevant data ################

# Season variable function
makeSeasonVariables = function(liste){
  chars = as.character(liste) %>% strsplit(split = "-")
  seasonList = rep("", length(liste))
  for (i in (1:length(liste))){
    month = chars[[i]][2]
    if (month %in% c("12", "01", "02")){
      seasonList[i] = "Winter"
    }
    else if (month %in% c("03", "04", "05")){
      seasonList[i] = "Spring"
    }
    else if (month %in% c("06", "07", "08")){
      seasonList[i] = "Summer"
    }
    else if (month %in% c("09", "10", "11")){
      seasonList[i] = "Fall"
    }
    else {print('Error in treatment date.')}
  }
  return(seasonList)
}

# Function for extracting data
extractData = function(dfDod, dfEff, methodString, year){
  len = length(dfEff$Anlegg)
  df = data.frame(Date = as.character(dfEff$`Beh. dato`),
                  Location = dfEff$Anlegg,
                  Cage = dfEff$Merd,
                  Method = rep(methodString, len),
                  Season = makeSeasonVariables(dfEff$`Beh. dato`),
                  Slaughter = rep(0, len),
                  FemalesBefore = dfEff$Kj.modn...6,
                  stringsAsFactors = FALSE)
  if (methodString == "Optilicer"){
    df = cbind(df, AvWeight = dfDod$`Snittvekt (g)`,
               Biomass = dfDod$`Biomasse (kg)`,
               NumFish = dfDod$`Antall (stk)`,
               SeaTemp = dfDod$`Temp i sj `,
               AvCrowding = dfDod$`Gj.snitt trengetid`,
               NumDeaths3 = dfDod$`3 dager  stk`,
               NumDeaths14 = dfDod$`Dag 14 (stk)`,
               Disease = dfDod$`Sykdom p  lokalitet`,
```

```
                FemalesAfter = dfEff$Kj.modn...16,
                HaemorrBefore = dfEff$Rdbuk...10,
                HaemorrAfter = dfEff$Rdbuk...20,
                ScalelossBefore = dfEff$Risttap...11,
                ScalelossAfter = dfEff$Risttap...21)
  }
  else if (methodString == "Freshwater"){
    df = cbind(df, AvWeight = dfDod$Snittvekt,
                Biomass = dfDod$`Biomasse (KG)`,
                NumFish = dfDod$`Antall (stk)`,
                SeaTemp = dfDod$ R sjsj ,
                AvCrowding = dfDod$`Gj.snitt trengetid (min)`,
                NumDeaths3 = dfDod$`Etter 3 dager (stk)`,
                NumDeaths14 = dfDod$`Etter 14 dager (stk)`,
                Disease = rep(as.character(NA), len),
                FemalesAfter = dfEff$Kj.modn...16,
                HaemorrBefore = dfEff$Rdbuk...10,
                HaemorrAfter = dfEff$Rdbuk...20,
                ScalelossBefore = dfEff$Risttap...11,
                ScalelossAfter = dfEff$Risttap...21)
  }
  else if (methodString == "Hydrolicer") {
    df = cbind(df, AvWeight = dfDod$Snittvekt,
                Biomass = dfDod$`Biomasse (kg)`,
                NumFish = rep(NA, len),
                SeaTemp = dfDod$`Temp i sj `,
                AvCrowding = dfDod$`Gj.snitt trengetid per kast (min)`,
                NumDeaths3 = dfDod$`3 dager (stk)`,
                NumDeaths14 = dfDod$`Dag 14 (stk)`,
                Disease = dfDod$`Sykdom p lokalitet`)
    if (year == "2022") {
      df = cbind(df, FemalesAfter = dfEff$Kj.modn...17,
                  HaemorrBefore = dfEff$Rdbuk...8,
                  HaemorrAfter = dfEff$Rdbuk...19,
                  ScalelossBefore = dfEff$Risttap...9,
                  ScalelossAfter = dfEff$Risttap...20)
    }
    else {
      df = cbind(df, FemalesAfter = dfEff$Kj.modn...16,
                  HaemorrBefore = dfEff$Rdbuk...7,
                  HaemorrAfter = dfEff$Rdbuk...17,
                  ScalelossBefore = dfEff$Risttap...8,
                  ScalelossAfter = dfEff$Risttap...18)
    }
  }
  else if (methodString == "SkaMik") {
    df = cbind(df, AvWeight = dfDod$Snittvekt,
                Biomass = dfDod$`Biomasse (kg)`,
                NumFish = rep(NA, len),
                SeaTemp = dfDod$`Temp i sj `,
                AvCrowding = dfDod$...13,
                NumDeaths3 = dfDod$`3 dager (stk)`,
                NumDeaths14 = dfDod$`Dag 14 (stk)`,
                Disease = dfDod$`Sykdom p lokalitet`)
    if (year == "2022") {
      df = cbind(df, FemalesAfter = dfEff$Kj.modn...17,
```

```
                    HaemorrBefore = dfEff$Rdbuk...8,
                    HaemorrAfter = dfEff$Rdbuk...19,
                    ScalelossBefore = dfEff$Risttap...9,
                    ScalelossAfter = dfEff$Risttap...20)
    }
    else {
      df = cbind(df, FemalesAfter = dfEff$Kj.modn...16,
                    HaemorrBefore = dfEff$Rdbuk...7,
                    HaemorrAfter = dfEff$Rdbuk...17,
                    ScalelossBefore = dfEff$Risttap...8,
                    ScalelossAfter = dfEff$Risttap...18)
    }
  }
  return(df)
}

# Combine to one data frame
df = rbind(extractData(df.ferskDod20, df.ferskEff20, "Freshwater", "2020"),
           extractData(df.ferskDod21, df.ferskEff21, "Freshwater", "2021"),
           extractData(df.ferskDod22, df.ferskEff22, "Freshwater", "2022"),
           extractData(df.optDod20, df.optEff20, "Optilicer", "2020"),
           extractData(df.optDod21, df.optEff21, "Optilicer", "2021"),
           extractData(df.hydDod20, df.hydEff20, "Hydrolicer", "2020"),
           extractData(df.hydDod21, df.hydEff21, "Hydrolicer", "2021"),
           extractData(df.hydDod22, df.hydEff22, "Hydrolicer", "2022"),
           extractData(df.skamikDod20, df.skamikEff20, "SkaMik", "2020"),
           extractData(df.skamikDod21, df.skamikEff21, "SkaMik", "2021"),
           extractData(df.skamikDod22, df.skamikEff22, "SkaMik", "2022"))


######## Manually go through comments in excel sheets #########
######## and make changes in data set                 #########

# Slaughter of fish
df = df %>% mutate(Slaughter = ifelse(Location == "..." & Cage =="6"
                                      & Date == "...", 1, Slaughter))
df = df %>% mutate(Slaughter = ifelse(Location == "..." & Cage =="7"
                                      & Date == "...", 1, Slaughter))
df = df %>% mutate(Slaughter = ifelse(Location == "..." & Cage =="12"
                                      & Date == "...", 1, Slaughter))
df = df %>% mutate(Slaughter = ifelse(Location == "..." & Cage =="13"
                                      & Date == "...", 1, Slaughter))
# Only half the cage was treated
df = filter(df, !(Location == "..." & Cage == "10" & Date == "..."))
# Observation where Freshwater was used first and then Hydrolicer
df = filter(df, !(Location == "..." & Cage == "4" & Date == "..."))
# Early termination of treatment
df = filter(df, !(Location == "..." & Date == "..."))
df = filter(df, !(Location == "..." & Date == "..."))
df = filter(df, !(Location == "..." & Date == "..."))
df = filter(df, !(Location == "..." & Date == "..."))
df = filter(df, !(Location == "..." & Date == "..."))
df = filter(df, !(Location == "..." & Date == "..."))


############## Pre-processing of variables #################
```

```
# Convert Biomass to numerical variable
strRemove = substr(df$Biomass[50],4,4)
df = df %>% mutate(Biomass = str_remove_all(Biomass, strRemove))
df$Biomass = as.double(df$Biomass)

# Convert NumFish to numerical variable
df = df %>% mutate(NumFish = str_remove_all(NumFish, strRemove))
df$NumFish = as.double(df$NumFish)


# Convert AvWeight to numerical variable
df = df %>% mutate(AvWeight = str_remove_all(AvWeight, strRemove))
df = df %>% mutate(AvWeight = gsub(",", ".", AvWeight))
df$AvWeight = as.double(df$AvWeight)
df$AvWeight = df$AvWeight / 1000          # in kg
df = df %>% mutate(AvWeight = ifelse(is.na(AvWeight) & !is.na(NumFish)
                                     & !is.na(Biomass),
                                     Biomass/NumFish, AvWeight))

# Create variable NumBefore
df = cbind(df, NumBefore = df$Biomass / df$AvWeight)

# Biomass in metric ton
df$Biomass = df$Biomass / 1000

# Convert SeaTemp to numerical variable
df = df %>% mutate(SeaTemp = ifelse(SeaTemp == "-", NA, SeaTemp))
df$SeaTemp = as.double(df$SeaTemp)

# Convert NumDeaths3 to numerical variable
df = df %>% mutate(NumDeaths3 = ifelse(NumDeaths3 == "-", NA, NumDeaths3))
df$NumDeaths3 = as.double(df$NumDeaths3)

# Factorize categorical variables
df$Method = as.factor(df$Method)
df$Season = as.factor(df$Season)
df$Slaughter = as.factor(df$Slaughter)

# Correct typos for Location
df = df %>% mutate(Location = ifelse(Location == "...", "...", Location))
# .... Chunk of similar code skipped for confidentiality

# Remove observations where fish were moved to another
# location after treatment
df = filter(df, Location != "...")

# Convert FemalesBefore to numerical variables
df = mutate(df, FemalesBefore = ifelse(FemalesBefore == "?",
                                       NA, FemalesBefore))
df = mutate(df, FemalesBefore = gsub(",", ".", FemalesBefore))
df = mutate(df, FemalesBefore = gsub(" ", "", FemalesBefore))
df$FemalesBefore = as.double(df$FemalesBefore)

# Convert HaemorrBefore and HaemorrAfter to numerical variables
df = mutate(df, HaemorrBefore = ifelse(HaemorrBefore == "-",
```

```
                                          NA, HaemorrBefore))
df = mutate(df, HaemorrBefore = ifelse(HaemorrBefore == "?",
                                          NA, HaemorrBefore))
df$HaemorrBefore = as.double(df$HaemorrBefore)
df = mutate(df, HaemorrAfter = ifelse(HaemorrAfter == "-", NA, HaemorrAfter))
df = mutate(df, HaemorrAfter = ifelse(HaemorrAfter == "?", NA, HaemorrAfter))
df$HaemorrAfter = as.double(df$HaemorrAfter)

# Convert ScalelossBefore and ScalelossAfter to numerical variables
df = mutate(df, ScalelossBefore = ifelse(ScalelossBefore == "-",
                                          NA, ScalelossBefore))
df = mutate(df, ScalelossBefore = ifelse(ScalelossBefore == "?",
                                          NA, ScalelossBefore))
df$ScalelossBefore = as.double(df$ScalelossBefore)
df = mutate(df, ScalelossAfter = ifelse(ScalelossAfter == "-",
                                          NA, ScalelossAfter))
df = mutate(df, ScalelossAfter = ifelse(ScalelossAfter == "?",
                                          NA, ScalelossAfter))
df$ScalelossAfter = as.double(df$ScalelossAfter)


# AvCrowding
filter(df, grepl("?", AvCrowding, fixed = TRUE))
# better estimates after looking at the treatments
df = mutate(df,
            AvCrowding = ifelse(AvCrowding == "40,63?", "44.7", AvCrowding))
df = mutate(df,
            AvCrowding = ifelse(AvCrowding == "49,16?", "59", AvCrowding))
df = mutate(df, AvCrowding = ifelse(AvCrowding == "60?", "72", AvCrowding))
df = mutate(df,
            AvCrowding = ifelse(AvCrowding == "53,42?", "62.3", AvCrowding))
# converting to numerical variable
df = mutate(df, AvCrowding = ifelse(AvCrowding == "?", NA, AvCrowding))
df = mutate(df, AvCrowding = gsub(",", ".", AvCrowding))
df$AvCrowding = as.double(df$AvCrowding)
# Correct calculation mistakes
df = mutate(df, AvCrowding = ifelse(AvCrowding == 636.7, 63.67, AvCrowding))
df = mutate(df, AvCrowding = ifelse(AvCrowding == 212.5, 106.25, AvCrowding))
df = mutate(df, AvCrowding = ifelse(AvCrowding == 199, 99.5, AvCrowding))
df = mutate(df, AvCrowding = ifelse(AvCrowding == 180, 120, AvCrowding))
df = mutate(df, AvCrowding = ifelse(AvCrowding == 160, 120, AvCrowding))
df = mutate(df, AvCrowding = ifelse(AvCrowding == 25, 50, AvCrowding))
df = mutate(df, AvCrowding = ifelse(AvCrowding == 50 & Date == "...",
                                    100, AvCrowding))
df = mutate(df, AvCrowding = ifelse(AvCrowding == 20.2, 32.2, AvCrowding))
df$AvCrowding = round(df$AvCrowding, 2)
df = mutate(df, AvCrowding = ifelse(AvCrowding == 26.67, 46.67, AvCrowding))
df = mutate(df, AvCrowding = ifelse(AvCrowding == 139.2, 91.67, AvCrowding))


# Disease data from BarentsWatch
df.disease = read_excel("ila_pd_barentswatch.xlsx",
                        sheet = "ILA_og_PD", n_max = 33093,
                        col_types = c("numeric", "numeric", "numeric",
                                      "text", "text", "text", "text", "text",
                                      "skip", "skip", "skip", "skip", "skip",
```

```
                                        "skip", "text","skip", "text", "text",
                                        "date", "date", "date", "date"))

# Function for date format
dateFunk = function(DateList){
  newList = rep("", length(DateList))
  for (i in (1:length(DateList))){
    newList[i] = strsplit(DateList[i], split = " ")[[1]][1]
  }
  return(newList)
}

# Function for date format
dateFunk2 = function(date){
  chars = strsplit(date, split = "/")
  month = ifelse(nchar(chars[[1]][1]) == 1,
                 paste("0",chars[[1]][1], sep = ""), chars[[1]][1])
  day = ifelse(nchar(chars[[1]][2]) == 1,
               paste("0",chars[[1]][2], sep = ""), chars[[1]][2])
  year = chars[[1]][3]
  newDate = paste(year, month, day, sep = "-")
  return(newDate)
}

df.disease$`Til dato` = dateFunk(df.disease$`Til dato`)
df.disease$`Fra dato` = dateFunk(df.disease$`Fra dato`)
df.disease$` P vist -dato` = as.character(df.disease$` P vist -dato`)
df.disease$`Avsluttet-dato` = as.character(df.disease$`Avsluttet-dato`)
df.disease$` P vist -dato` = dateFunk(df.disease$` P vist -dato`)
df.disease$`Avsluttet-dato` = dateFunk(df.disease$`Avsluttet-dato`)

df.disease = cbind(df.disease, ToDate = df.disease$`Avsluttet-dato`)
for (i in (1:length(df.disease$Uke))){
  if (is.na(df.disease$ToDate[i]) & !is.na(df.disease$`Til dato`[i])){
    df.disease$ToDate[i] = dateFunk2(df.disease$`Til dato`[i])
  }
}

df.disease = cbind(df.disease, FromDate = df.disease$` P vist -dato`)
for (i in (1:length(df.disease$Uke))){
  if (is.na(df.disease$FromDate[i]) & !is.na(df.disease$`Fra dato`[i])){
    df.disease$FromDate[i] = dateFunk2(df.disease$`Fra dato`[i])
  }
}

# Filtering out relevant locations
# Code skipped for confidentiality

# Filter out relevant data
df.disease = cbind(df.disease, Out = rep(0, length(df.disease$Uke)))
df.disease = filter(df.disease, Status== " P vist ")
df.disease = df.disease %>%
  mutate(ToDate = ifelse(is.na(ToDate) & r == 2022, "2022-10-22", ToDate))
df.disease = filter(df.disease, !is.na(ToDate))
df.disease = mutate(df.disease,
                    Out = ifelse(!(ymd(ToDate) %within%
```

```
                                        interval(ymd("2020-01-01"),
                                                 ymd("2022-10-22"))),1, Out))
df.disease = filter(df.disease, Out == 0)
df.disease$Lokalitetsnavn = droplevels(df.disease$Lokalitetsnavn)


# Exclude CMS from disease because of information only for one data sheet
df = mutate(df, Disease = ifelse(Disease == "CMS", NA, Disease))

# Extract disease information from BW data
for (i in (1:length(df$Date))){
  if (df$Location[i] %in% levels(df.disease$Lokalitetsnavn)
      & is.na(df$Disease[i])) {
    diseaseDF = filter(df.disease, Lokalitetsnavn == df$Location[i])
    for (j in (1:length(diseaseDF$ r ))){
      int = interval(ymd(diseaseDF$FromDate[j]), ymd(diseaseDF$ToDate[j]))
      if (ymd(df$Date[i]) %within% int){
        df$Disease[i] = diseaseDF$Sykdom[j]
        break
      }
    }
  }
}

# Disease variable
df = mutate(df, Disease = ifelse(is.na(Disease), "None", Disease))
df$Disease = as.factor(df$Disease)

# Combine nearby location I and II to one location
df = mutate(df, Location = ifelse(Location %in% c("...", "..."),
                                  "...", Location))
df = mutate(df, Location = ifelse(Location %in% c("...", "..."),
                                  "...", Location))
df = mutate(df, Location = ifelse(Location %in% c("...", "..."),
                                  "...", Location))
df$Location = as.factor(df$Location)

# Manually find estimates for missing SeaTemp
# from BW data
filter(df, is.na(SeaTemp) & !is.na(AvWeight) & !is.na(AvCrowding))

df = mutate(df, SeaTemp = ifelse(Location == "..." & is.na(SeaTemp)
                                 & ymd(Date) %within%
                                   interval(ymd("..."), ymd("...")),
                                 13.9, SeaTemp))
df = mutate(df, SeaTemp = ifelse(Location == "..." & is.na(SeaTemp)
                                 & ymd(Date) %within%
                                   interval(ymd("..."), ymd("...")),
                                 14.8, SeaTemp))
# .... Skipped chunk of similar code for confidentiality

# Variable LocNumber
# Assign numbers belonging to different locations for all observations
df = cbind(df, LocNumber = rep(NA, length(df$Location)))
names = levels(df$Location)
for (i in (1:length(df$Location))){
```

```
  for (j in (1:length(names))){
    if (df$Location[i] == names[j]){
      df$LocNumber[i] = j
      break
    }
  }
}

# Remove observations with missing explanatory variables
df = filter(df, !is.na(Biomass))
df = filter(df, !is.na(AvWeight))
df = filter(df, !is.na(SeaTemp))
df = filter(df, !is.na(AvCrowding))

# Scale/center numeric explanatory variables
numVarStats = data.frame(Vars = c("AvWeight", "AvCrowding",
                                  "Biomass", "SeaTemp"))
numVarStats = cbind(numVarStats, Mean = c(mean(df$AvWeight),
                                          mean(df$AvCrowding),
                                          mean(df$Biomass),
                                          mean(df$SeaTemp)))
numVarStats = cbind(numVarStats, SD = c(sd(df$AvWeight),
                                        sd(df$AvCrowding),
                                        sd(df$Biomass),
                                        sd(df$SeaTemp)))

df = cbind(df,
           AvWeightSc = as.double(scale(df$AvWeight)),
           AvCrowdingSc = as.double(scale(df$AvCrowding)),
           BiomassSc = as.double(scale(df$Biomass)),
           SeaTempSc = as.double(scale(df$SeaTemp)))

write_xlsx(numVarStats,"NumVarStats.xlsx")


#########################################################
# Data set for delousing effect (adult female lice)
#########################################################
df.Effect = df

# CountFemalesBefore, CountFemalesAfter
df.Effect = cbind(df.Effect,
                  CountFemalesBefore = round(df.Effect$FemalesBefore * 20))
df.Effect = cbind(df.Effect,
                  CountFemalesAfter = round(df.Effect$FemalesAfter * 20))
df.Effect = filter(df.Effect, !is.na(CountFemalesBefore))
df.Effect = filter(df.Effect, !is.na(CountFemalesAfter))
df.Effect = filter(df.Effect, CountFemalesBefore>0)
df.Effect = df.Effect %>%
  mutate(CountFemalesAfter = ifelse(CountFemalesAfter > CountFemalesBefore,
                                    CountFemalesBefore, CountFemalesAfter))
# Estimated proportion of removed adult female lice
df.Effect =
  cbind(df.Effect, PropRemoved =
          (df.Effect$CountFemalesBefore-df.Effect$CountFemalesAfter)/
          df.Effect$CountFemalesBefore)
```

```
# Small count,  drop CountFemalesBefore < 5
df.Effect = filter(df.Effect, CountFemalesBefore >= 5)

# Drop observation with count of 289
df.Effect = filter(df.Effect, CountFemalesBefore < 289)

# Index observations - New variable Cage
df.Effect = subset(df.Effect, select = -c(Cage))
df.Effect = cbind(df.Effect, Cage = seq(1:length(df.Effect$Date)))
df.Effect$Cage = as.factor(df.Effect$Cage)

write_xlsx(df.Effect,"Data_delousingEffect.xlsx")


########################################
# Data set for mortality after 3 days
########################################
df.Mort3 = df
df.Mort3 = filter(df.Mort3, !is.na(NumDeaths3))
df.Mort3 = filter(df.Mort3, Slaughter == "0")
df.Mort3$NumDeaths3 = round(df.Mort3$NumDeaths3)
df.Mort3 = cbind(df.Mort3,
                 Mortality3 = df.Mort3$NumDeaths3/df.Mort3$NumBefore)

# Remove observations with invalid wi scores for explanatory variables
df.Mort3 = filter(df.Mort3, !is.na(HaemorrBefore))
df.Mort3 = filter(df.Mort3, !is.na(ScalelossBefore))
df.Mort3 = filter(df.Mort3, ScalelossBefore <= 3)

# Index observations - New variable Cage
df.Mort3 = subset(df.Mort3, select = -c(Cage))
df.Mort3 = cbind(df.Mort3, Cage = seq(1:length(df.Mort3$Date)))
df.Mort3$Cage = as.factor(df.Mort3$Cage)

write_xlsx(df.Mort3,"Data_mortality3.xlsx")

########################################
# Data set for mortality after 14 days
########################################
df.Mort14 = df
df.Mort14 = filter(df.Mort14, !is.na(NumDeaths14))
df.Mort14 = filter(df.Mort14, Slaughter == "0")
df.Mort14 = cbind(df.Mort14,
                  Mortality14 = df.Mort14$NumDeaths14/df.Mort14$NumBefore)

# Remove observations with invalid wi scores for explanatory variables
df.Mort14 = filter(df.Mort14, !is.na(HaemorrBefore))
df.Mort14 = filter(df.Mort14, !is.na(ScalelossBefore))
df.Mort14 = filter(df.Mort14, ScalelossBefore <= 3)

# Index observations - New variable Cage
df.Mort14 = subset(df.Mort14, select = -c(Cage))
df.Mort14 = cbind(df.Mort14, Cage = seq(1:length(df.Mort14$Date)))
df.Mort14$Cage = as.factor(df.Mort14$Cage)
```

```
write_xlsx(df.Mort14,"Data_mortality14.xlsx")


##############################################
# Data set for change in skin haemorrhages
##############################################
df.Haemorr = df
df.Haemorr = filter(df.Haemorr, !is.na(HaemorrBefore))
df.Haemorr = filter(df.Haemorr, !is.na(ScalelossBefore))
df.Haemorr = filter(df.Haemorr, ScalelossBefore <= 3)
df.Haemorr = filter(df.Haemorr, !is.na(HaemorrAfter))
df.Haemorr = filter(df.Haemorr, HaemorrAfter <= 3)
df.Haemorr = cbind(df.Haemorr,
                   HaemorrChange = df.Haemorr$HaemorrAfter -
                                   df.Haemorr$HaemorrBefore)

write_xlsx(df.Haemorr,"Data_changeHaemorr.xlsx")

##############################################
# Data set for change in scaleloss
##############################################
df.Scaleloss = df
df.Scaleloss = filter(df.Scaleloss, !is.na(ScalelossBefore))
df.Scaleloss = filter(df.Scaleloss, !is.na(HaemorrBefore))
df.Scaleloss = filter(df.Scaleloss, !is.na(ScalelossAfter))
df.Scaleloss = filter(df.Scaleloss, ScalelossBefore <= 3)
df.Scaleloss = cbind(df.Scaleloss,
                     ScalelossChange = df.Scaleloss$ScalelossAfter -
                                       df.Scaleloss$ScalelossBefore)

write_xlsx(df.Scaleloss,"Data_changeScaleloss.xlsx")
```

D Model Output

DE-FE

```
Call:
glm(formula = cbind(CountFemalesBefore - CountFemalesAfter, CountFemalesAfter) ~
    Method * SeaTempSc + AvWeightSc + AvCrowdingSc + BiomassSc +
        Season, family = binomial(link = "logit"), data = df.effect)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-8.9213  -0.8621   0.0395   0.8773   8.1582

Coefficients:
                           Estimate Std. Error z value Pr(>|z|)
(Intercept)                1.528658   0.045896  33.307  < 2e-16 ***
MethodFreshwater          -0.755112   0.070781 -10.668  < 2e-16 ***
MethodHydrolicer           0.238062   0.065531   3.633 0.000280 ***
MethodOptilicer           -0.142454   0.072057  -1.977 0.048047 *
SeaTempSc                  0.105096   0.047709   2.203 0.027605 *
AvWeightSc                 0.158944   0.020953   7.586 3.31e-14 ***
AvCrowdingSc               0.054307   0.021595   2.515 0.011911 *
BiomassSc                 -0.020741   0.025582  -0.811 0.417487
SeasonFall                -0.208463   0.053970  -3.863 0.000112 ***
SeasonSpring              -0.282741   0.128369  -2.203 0.027625 *
SeasonWinter              -0.272899   0.109032  -2.503 0.012317 *
MethodFreshwater:SeaTempSc -0.276274   0.063316  -4.363 1.28e-05 ***
MethodHydrolicer:SeaTempSc -0.007591   0.080596  -0.094 0.924965
MethodOptilicer:SeaTempSc  -0.321171   0.060057  -5.348 8.90e-08 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 2214.5  on 821  degrees of freedom
Residual deviance: 1790.6  on 808  degrees of freedom
AIC: 4035.7

Number of Fisher Scoring iterations: 4
```

Figure D.1: Model output for the full binomial DE-FE model.

```
Call:
glm(formula = cbind(CountFemalesBefore - CountFemalesAfter, CountFemalesAfter) ~
    Method * SeaTempSc + AvWeightSc + AvCrowdingSc + BiomassSc +
        Season, family = quasibinomial(link = "logit"), data = df.effect)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-8.9213  -0.8621   0.0395   0.8773   8.1582

Coefficients:
                            Estimate Std. Error t value Pr(>|t|)
(Intercept)                 1.528658   0.067281  22.720  < 2e-16 ***
MethodFreshwater           -0.755112   0.103762  -7.277 8.07e-13 ***
MethodHydrolicer            0.238062   0.096065   2.478 0.013411 *
MethodOptilicer            -0.142454   0.105633  -1.349 0.177851
SeaTempSc                   0.105096   0.069939   1.503 0.133314
AvWeightSc                  0.158944   0.030716   5.175 2.88e-07 ***
AvCrowdingSc                0.054307   0.031658   1.715 0.086645 .
BiomassSc                  -0.020741   0.037502  -0.553 0.580363
SeasonFall                 -0.208463   0.079118  -2.635 0.008579 **
SeasonSpring               -0.282741   0.188182  -1.502 0.133363
SeasonWinter               -0.272899   0.159835  -1.707 0.088136 .
MethodFreshwater:SeaTempSc -0.276274   0.092819  -2.976 0.003003 **
MethodHydrolicer:SeaTempSc -0.007591   0.118150  -0.064 0.948791
MethodOptilicer:SeaTempSc  -0.321171   0.088041  -3.648 0.000281 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 2.149024)

    Null deviance: 2214.5  on 821  degrees of freedom
Residual deviance: 1790.6  on 808  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4
```

Figure D.2: Model output for the full quasi-binomial DE-FE model.

```
Call:
glm(formula = cbind(CountFemalesBefore - CountFemalesAfter, CountFemalesAfter) ~
    Method + SeaTempSc + AvWeightSc + Method:SeaTempSc, family = quasibinomial(link = "logit"),
    data = df.effect)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-9.0045  -0.8883   0.0461   0.9001   7.6727

Coefficients:
                           Estimate Std. Error t value Pr(>|t|)
(Intercept)                1.386906   0.042743  32.447  < 2e-16 ***
MethodFreshwater          -0.691790   0.087580  -7.899 9.12e-15 ***
MethodHydrolicer           0.294639   0.089429   3.295 0.001028 **
MethodOptilicer           -0.134984   0.095726  -1.410 0.158889
SeaTempSc                  0.190263   0.054561   3.487 0.000514 ***
AvWeightSc                 0.149440   0.027557   5.423 7.73e-08 ***
MethodFreshwater:SeaTempSc -0.284800   0.087435  -3.257 0.001172 **
MethodHydrolicer:SeaTempSc -0.009056   0.112532  -0.080 0.935877
MethodOptilicer:SeaTempSc  -0.310630   0.082759  -3.753 0.000187 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 2.168904)

    Null deviance: 2214.5  on 821  degrees of freedom
Residual deviance: 1813.4  on 813  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4
```

Figure D.3: Model output for the reduced quasi-binomial DE-FE model.

```
Call:
glm(formula = cbind(CountFemalesBefore - CountFemalesAfter, CountFemalesAfter) ~
    Method * scale(SeaTempSc, center = -1.422, scale = F) + AvWeightSc,
    family = quasibinomial(link = "logit"), data = df.effect)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-9.0045  -0.8883   0.0461   0.9001   7.6727

Coefficients:
                                                                 Estimate Std. Error t value Pr(>|t|)
(Intercept)                                                      1.116352   0.101816  10.964  < 2e-16 ***
MethodFreshwater                                                -0.286805   0.142338  -2.015 0.044237 *
MethodHydrolicer                                                 0.307517   0.221884   1.386 0.166146
MethodOptilicer                                                  0.306732   0.134635   2.278 0.022970 *
scale(SeaTempSc, center = -1.422, scale = F)                     0.190263   0.054561   3.487 0.000514 ***
AvWeightSc                                                       0.149440   0.027557   5.423 7.73e-08 ***
MethodFreshwater:scale(SeaTempSc, center = -1.422, scale = F) -0.284800   0.087435  -3.257 0.001172 **
MethodHydrolicer:scale(SeaTempSc, center = -1.422, scale = F) -0.009056   0.112532  -0.080 0.935877
MethodOptilicer:scale(SeaTempSc, center = -1.422, scale = F)  -0.310630   0.082759  -3.753 0.000187 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 2.168904)

    Null deviance: 2214.5  on 821  degrees of freedom
Residual deviance: 1813.4  on 813  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4
```

Figure D.4: Model output for the reduced quasi-binomial DE-FE model with sea temperature of 7°C (corresponding to *SeaTempSc*=-1.422) as the intercept value.

DE-ME

```
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
 Family: binomial  ( logit )
Formula: cbind(CountFemalesBefore - CountFemalesAfter, CountFemalesAfter) ~
    Method * SeaTempSc + AvCrowdingSc + AvWeightSc + BiomassSc +          Season + (1 | LocNumber/Cage)
   Data: df.effect
Control: glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 1e+05))

     AIC      BIC   logLik deviance df.resid
  3663.4   3738.7  -1815.7   3631.4      806

Scaled residuals:
    Min      1Q  Median      3Q     Max
-3.1953 -0.4293  0.0017  0.4470  1.8485

Random effects:
 Groups         Name        Variance Std.Dev.
 Cage:LocNumber (Intercept) 0.316717 0.56278
 LocNumber      (Intercept) 0.008937 0.09454
Number of obs: 822, groups:  Cage:LocNumber, 822; LocNumber, 31

Fixed effects:
                            Estimate Std. Error z value Pr(>|z|)
(Intercept)                  1.64101    0.07281  22.539  < 2e-16 ***
MethodFreshwater            -0.84273    0.11957  -7.048 1.82e-12 ***
MethodHydrolicer             0.17071    0.09763   1.749 0.080367 .
MethodOptilicer             -0.10486    0.12291  -0.853 0.393556
SeaTempSc                    0.04781    0.07331   0.652 0.514311
AvCrowdingSc                 0.03878    0.03374   1.149 0.250402
AvWeightSc                   0.09853    0.03734   2.639 0.008326 **
BiomassSc                    0.02330    0.04205   0.554 0.579476
SeasonFall                  -0.32812    0.08645  -3.795 0.000147 ***
SeasonSpring                -0.30894    0.18132  -1.704 0.088409 .
SeasonWinter                -0.50361    0.16382  -3.074 0.002111 **
MethodFreshwater:SeaTempSc  -0.36416    0.10287  -3.540 0.000400 ***
MethodHydrolicer:SeaTempSc   0.00220    0.11227   0.020 0.984364
MethodOptilicer:SeaTempSc   -0.25479    0.10121  -2.517 0.011822 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Figure D.5: Model output for the full DE-ME model.

M3-FE

```
Call:
glm(formula = cbind(NumDeaths3, NumBefore) ~ Method * SeaTempSc +
    AvCrowdingSc + AvWeightSc + BiomassSc + Season + Disease +
    HaemorrBefore + ScalelossBefore, family = quasibinomial(link = "logit"),
    data = df.mort3)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-39.713  -17.182   -7.096    6.072  127.444

Coefficients:
                           Estimate Std. Error t value Pr(>|t|)
(Intercept)                -5.79033    0.11519 -50.266   <2e-16 ***
MethodFreshwater           -0.19005    0.18172  -1.046   0.2960
MethodHydrolicer            0.22227    0.13117   1.694   0.0906 .
MethodOptilicer             0.47177    0.17316   2.724   0.0066 **
SeaTempSc                  -0.06613    0.09846  -0.672   0.5020
AvCrowdingSc                0.06321    0.04100   1.542   0.1236
AvWeightSc                  0.17201    0.07747   2.220   0.0267 *
BiomassSc                  -0.08514    0.07016  -1.214   0.2253
SeasonSpring               -0.35632    0.23435  -1.520   0.1288
SeasonFall                  0.16156    0.12101   1.335   0.1823
SeasonWinter               -0.06245    0.22844  -0.273   0.7846
DiseasePD                   0.03823    0.09388   0.407   0.6840
HaemorrBefore               0.27460    0.10656   2.577   0.0102 *
ScalelossBefore            -0.01853    0.07932  -0.234   0.8154
MethodFreshwater:SeaTempSc -0.12368    0.14894  -0.830   0.4066
MethodHydrolicer:SeaTempSc  0.08713    0.14847   0.587   0.5575
MethodOptilicer:SeaTempSc  -0.14274    0.13497  -1.058   0.2906
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 602.962)

    Null deviance: 370751  on 724  degrees of freedom
Residual deviance: 326310  on 708  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 5
```

Figure D.6: Model output for the full quasi-binomial M3-FE model.

M3-ME

```
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
 Family: binomial  ( logit )
Formula: cbind(NumDeaths3, NumBefore) ~ Method + SeaTempSc + AvCrowdingSc +
    AvWeightSc + BiomassSc + Season + Disease + HaemorrBefore +
    ScalelossBefore + (1 | LocNumber/Cage) + Method:SeaTempSc
   Data: df.mort3
Control: glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 1e+05))

     AIC      BIC   logLik deviance df.resid
 10428.6  10515.7  -5195.3  10390.6      706

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.05242 -0.04219  0.00203  0.02833  0.09416

Random effects:
 Groups         Name        Variance Std.Dev.
 Cage:LocNumber (Intercept) 0.7302   0.8545
 LocNumber      (Intercept) 0.2786   0.5278
Number of obs: 725, groups:  Cage:LocNumber, 725; LocNumber, 31

Fixed effects:
                            Estimate Std. Error z value Pr(>|z|)
(Intercept)                -6.5397550  0.1416696 -46.162  < 2e-16 ***
MethodFreshwater            0.1874419  0.1501378   1.248  0.21186
MethodHydrolicer            0.5583435  0.1213909   4.600 4.23e-06 ***
MethodOptilicer             0.3242058  0.1869233   1.734  0.08284 .
SeaTempSc                   0.0995509  0.0831838   1.197  0.23140
AvCrowdingSc                0.0863413  0.0386274   2.235  0.02540 *
AvWeightSc                  0.2677406  0.0623787   4.292 1.77e-05 ***
BiomassSc                  -0.1231979  0.0578164  -2.131  0.03310 *
SeasonSpring               -0.0767144  0.1907366  -0.402  0.68754
SeasonFall                  0.0005438  0.1165835   0.005  0.99628
SeasonWinter                0.4174118  0.2077220   2.009  0.04449 *
DiseasePD                   0.3561121  0.1206422   2.952  0.00316 **
HaemorrBefore               0.0792569  0.1025900   0.773  0.43978
ScalelossBefore            -0.0034293  0.0757702  -0.045  0.96390
MethodFreshwater:SeaTempSc -0.0265060  0.1200714  -0.221  0.82529
MethodHydrolicer:SeaTempSc -0.1650890  0.1226508  -1.346  0.17830
MethodOptilicer:SeaTempSc  -0.3980218  0.1462563  -2.721  0.00650 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Figure D.7: Model output for the full M3-ME model.

M14-FE

```
Call:
glm(formula = cbind(NumDeaths14, NumBefore) ~ Method * SeaTempSc +
    AvCrowdingSc + AvWeightSc + BiomassSc + Season + Disease +
    HaemorrBefore + ScalelossBefore, family = quasibinomial(link = "logit"),
    data = df.mort14)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-48.267  -23.424  -10.733    5.737  183.700

Coefficients:
                           Estimate Std. Error t value Pr(>|t|)
(Intercept)                -4.96856    0.12548 -39.597  < 2e-16 ***
MethodFreshwater           -0.45569    0.20404  -2.233  0.02587 *
MethodHydrolicer           -0.07243    0.16382  -0.442  0.65855
MethodOptilicer             0.25670    0.17866   1.437  0.15128
SeaTempSc                  -0.04862    0.10015  -0.486  0.62749
AvCrowdingSc                0.12817    0.04483   2.859  0.00439 **
AvWeightSc                  0.12567    0.08335   1.508  0.13213
BiomassSc                  -0.16765    0.07569  -2.215  0.02712 *
SeasonFall                  0.06583    0.12962   0.508  0.61172
SeasonSpring               -0.20698    0.24915  -0.831  0.40643
SeasonWinter               -0.05234    0.23755  -0.220  0.82567
DiseasePD                   0.13350    0.09621   1.388  0.16576
HaemorrBefore               0.26534    0.11475   2.312  0.02108 *
ScalelossBefore             0.08139    0.08487   0.959  0.33797
MethodFreshwater:SeaTempSc -0.14669    0.15247  -0.962  0.33637
MethodHydrolicer:SeaTempSc  0.14286    0.17577   0.813  0.41666
MethodOptilicer:SeaTempSc  -0.10159    0.13718  -0.741  0.45926
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 1385.9)

    Null deviance: 700421  on 650  degrees of freedom
Residual deviance: 609264  on 634  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 5
```

Figure D.8: Model output for the full quasi-binomial M14-FE model.

```
Call:
glm(formula = cbind(NumDeaths14, NumBefore) ~ Method + AvCrowdingSc +
    HaemorrBefore, family = quasibinomial(link = "logit"), data = df.mort14)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-53.589  -23.655  -10.815    5.312  164.772

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)      -4.90972    0.07415 -66.215  < 2e-16 ***
MethodFreshwater -0.36822    0.15692  -2.347 0.019248 *
MethodHydrolicer -0.10959    0.13163  -0.833 0.405414
MethodOptilicer   0.41342    0.10301   4.014 6.68e-05 ***
AvCrowdingSc      0.15060    0.04296   3.505 0.000487 ***
HaemorrBefore     0.28664    0.09420   3.043 0.002438 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 1432.58)

    Null deviance: 700421  on 650  degrees of freedom
Residual deviance: 629255  on 645  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 5
```

Figure D.9: Model output for the reduced quasi-binomial M14-FE model.

M14-ME

```
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
 Family: binomial  ( logit )
Formula: cbind(NumDeaths14, NumBefore) ~ Method + SeaTempSc + AvCrowdingSc +
    AvWeightSc + BiomassSc + Season + Disease + HaemorrBefore +
    ScalelossBefore + (1 | LocNumber/Cage) + Method:SeaTempSc
   Data: df.mort14
Control: glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 1e+05))

     AIC      BIC   logLik deviance df.resid
 10171.6  10256.7  -5066.8  10133.6      632

Scaled residuals:
     Min       1Q   Median       3Q      Max
-0.41640 -0.04072 -0.00190  0.02320  0.09181

Random effects:
 Groups         Name        Variance Std.Dev.
 Cage:LocNumber (Intercept) 0.4769   0.6906
 LocNumber      (Intercept) 0.3004   0.5481
Number of obs: 651, groups:  Cage:LocNumber, 651; LocNumber, 30

Fixed effects:
                            Estimate Std. Error z value Pr(>|z|)
(Intercept)                -5.698134   0.135670 -42.000  < 2e-16 ***
MethodFreshwater           -0.004878   0.134989  -0.036 0.971176
MethodHydrolicer            0.338844   0.114589   2.957 0.003106 **
MethodOptilicer            -0.020074   0.154430  -0.130 0.896574
SeaTempSc                   0.064699   0.068321   0.947 0.343642
AvCrowdingSc                0.115480   0.033908   3.406 0.000660 ***
AvWeightSc                  0.217792   0.055729   3.908 9.30e-05 ***
BiomassSc                  -0.082726   0.051636  -1.602 0.109137
SeasonFall                 -0.148137   0.097383  -1.521 0.128216
SeasonSpring               -0.015475   0.163074  -0.095 0.924399
SeasonWinter                0.340257   0.172554   1.972 0.048623 *
DiseasePD                   0.385959   0.104752   3.685 0.000229 ***
HaemorrBefore               0.110892   0.089209   1.243 0.213845
ScalelossBefore             0.086256   0.065351   1.320 0.186876
MethodFreshwater:SeaTempSc -0.120702   0.102958  -1.172 0.241061
MethodHydrolicer:SeaTempSc -0.015082   0.108594  -0.139 0.889541
MethodOptilicer:SeaTempSc  -0.488478   0.120605  -4.050 5.12e-05 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Figure D.10: Model output for the full M14-ME model.

```
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation)
glmerMod]
 Family: binomial  ( logit )
Formula: cbind(NumDeaths14, NumBefore) ~ Method * SeaTempSc + AvCrowdingSc +
    AvWeightSc + Season + Disease + ScalelossBefore + (1 | LocNumber/Cage)
   Data: df.mort14
Control: glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 1e+05))

     AIC      BIC   logLik deviance df.resid
 10172.3  10248.4  -5069.1  10138.3      634

Scaled residuals:
     Min       1Q   Median       3Q      Max
-0.41160 -0.04065 -0.00146  0.02267  0.14245

Random effects:
 Groups         Name        Variance Std.Dev.
 Cage:LocNumber (Intercept) 0.4818   0.6941
 LocNumber      (Intercept) 0.2833   0.5323
Number of obs: 651, groups:  Cage:LocNumber, 651; LocNumber, 30

Fixed effects:
                            Estimate Std. Error z value Pr(>|z|)
(Intercept)                -5.708645   0.133262 -42.838  < 2e-16 ***
MethodFreshwater            0.086853   0.125978   0.689 0.490552
MethodHydrolicer            0.343250   0.114916   2.987 0.002818 **
MethodOptilicer             0.059653   0.149235   0.400 0.689361
SeaTempSc                   0.071073   0.068312   1.040 0.298145
AvCrowdingSc                0.121554   0.033703   3.607 0.000310 ***
AvWeightSc                  0.176609   0.046782   3.775 0.000160 ***
SeasonFall                 -0.146954   0.097465  -1.508 0.131616
SeasonSpring               -0.006904   0.163549  -0.042 0.966331
SeasonWinter                0.359002   0.172574   2.080 0.037500 *
DiseasePD                   0.398645   0.104476   3.816 0.000136 ***
ScalelossBefore             0.131565   0.058113   2.264 0.023576 *
MethodFreshwater:SeaTempSc -0.079352   0.100807  -0.787 0.431185
MethodHydrolicer:SeaTempSc -0.010104   0.108873  -0.093 0.926055
MethodOptilicer:SeaTempSc  -0.454892   0.119552  -3.805 0.000142 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Figure D.11: Model output for the reduced M14-ME model.

SH-FE

```
Call:
glm(formula = HaemorrChange ~ Method * SeaTempSc + AvCrowdingSc +
    AvWeightSc + BiomassSc + Season + Disease + HaemorrBefore +
    ScalelossBefore, family = gaussian(link = "identity"), data = df.haemorr)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.21193  -0.24581  -0.01187   0.25742   1.56231

Coefficients:
                            Estimate Std. Error t value Pr(>|t|)
(Intercept)                 0.631520   0.041641  15.166  < 2e-16 ***
MethodFreshwater           -0.480551   0.060460  -7.948 7.29e-15 ***
MethodHydrolicer           -0.119590   0.046890  -2.550  0.01096 *
MethodOptilicer             0.147165   0.074367   1.979  0.04821 *
SeaTempSc                   0.103298   0.034376   3.005  0.00275 **
AvCrowdingSc                0.013673   0.016294   0.839  0.40166
AvWeightSc                  0.006619   0.018703   0.354  0.72351
BiomassSc                  -0.045457   0.019837  -2.291  0.02222 *
SeasonFall                  0.023479   0.044817   0.524  0.60051
SeasonSpring                0.173919   0.081834   2.125  0.03390 *
SeasonWinter                0.068813   0.084923   0.810  0.41804
DiseasePD                   0.054106   0.036591   1.479  0.13967
HaemorrBefore              -0.636000   0.041840 -15.201  < 2e-16 ***
ScalelossBefore             0.077477   0.031006   2.499  0.01268 *
MethodFreshwater:SeaTempSc -0.085424   0.049897  -1.712  0.08732 .
MethodHydrolicer:SeaTempSc -0.104373   0.051480  -2.027  0.04298 *
MethodOptilicer:SeaTempSc   0.032378   0.054814   0.591  0.55491
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for gaussian family taken to be 0.1537128)

    Null deviance: 165.85  on 737  degrees of freedom
Residual deviance: 110.83  on 721  degrees of freedom
AIC: 731.12

Number of Fisher Scoring iterations: 2
```

Figure D.12: Model output for the full SH-FE model.

SH-ME

```
Linear mixed model fit by maximum likelihood  ['lmerMod']
Formula: HaemorrChange ~ Method * SeaTempSc + AvCrowdingSc + AvWeightSc +
    BiomassSc + Season + Disease + HaemorrBefore + ScalelossBefore +      (1 | LocNumber)
   Data: df.haemorr

     AIC      BIC   logLik deviance df.resid
   699.1    786.6   -330.5    661.1      719

Scaled residuals:
    Min      1Q  Median      3Q     Max
-3.5831 -0.6117 -0.0494  0.6611  4.3290

Random effects:
 Groups    Name        Variance Std.Dev.
 LocNumber (Intercept) 0.01834  0.1354
 Residual              0.13577  0.3685
Number of obs: 738, groups:  LocNumber, 31

Fixed effects:
                            Estimate Std. Error t value
(Intercept)                 0.617232   0.049429  12.487
MethodFreshwater           -0.376859   0.062321  -6.047
MethodHydrolicer           -0.097105   0.050402  -1.927
MethodOptilicer             0.116681   0.076402   1.527
SeaTempSc                   0.117251   0.034644   3.384
AvCrowdingSc               -0.005361   0.016161  -0.332
AvWeightSc                  0.008409   0.022548   0.373
BiomassSc                  -0.034578   0.022045  -1.569
SeasonFall                  0.028321   0.047117   0.601
SeasonSpring                0.181230   0.080255   2.258
SeasonWinter                0.089577   0.084607   1.059
DiseasePD                   0.014721   0.047104   0.313
HaemorrBefore              -0.680002   0.042002 -16.190
ScalelossBefore             0.087819   0.031563   2.782
MethodFreshwater:SeaTempSc -0.089089   0.050827  -1.753
MethodHydrolicer:SeaTempSc -0.084841   0.050467  -1.681
MethodOptilicer:SeaTempSc  -0.012579   0.058965  -0.213
```

Figure D.13: Model output for the full SH-ME model.

SL-FE

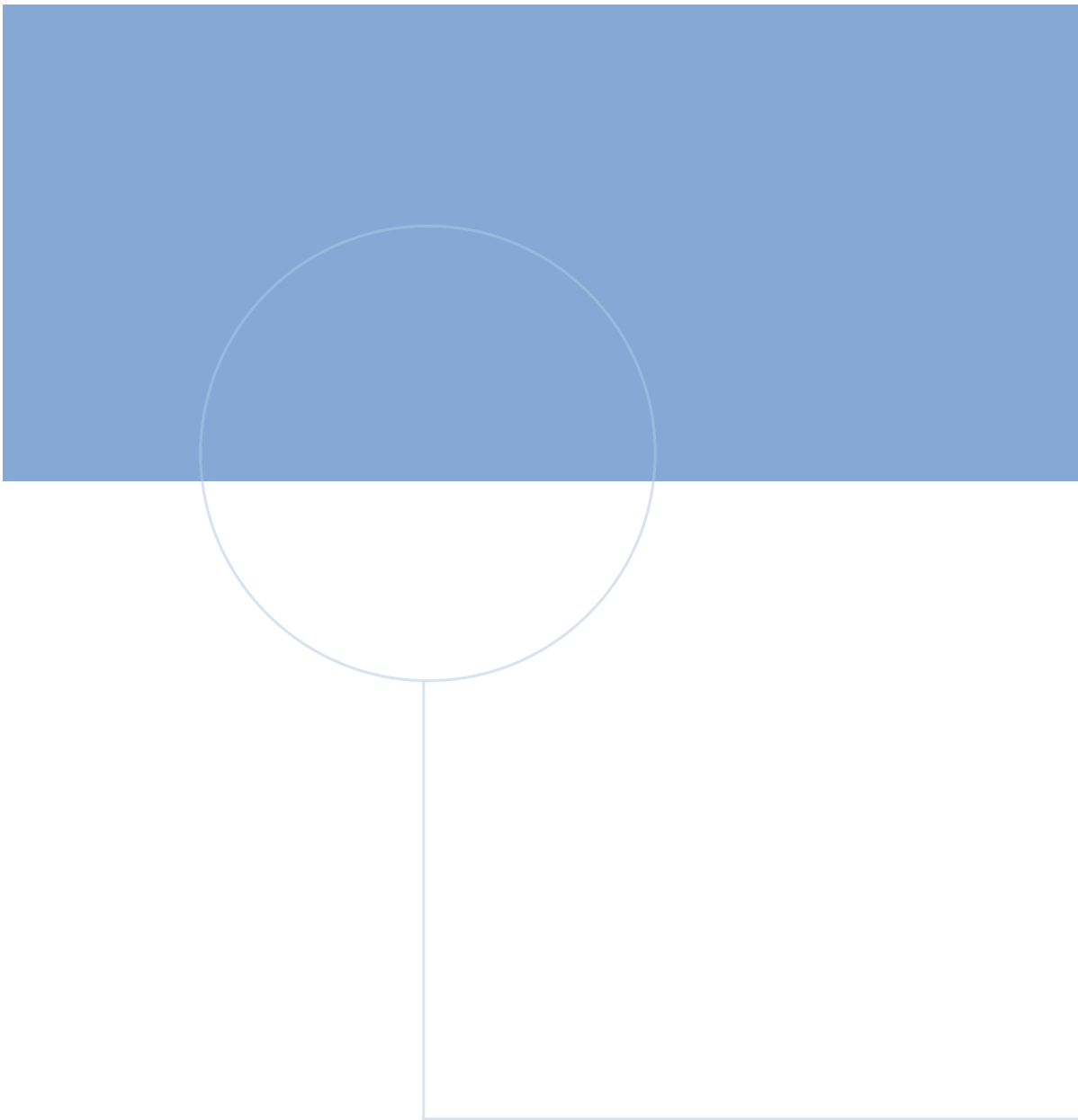
```
Call:
glm(formula = ScalelossChange ~ Method * SeaTempSc + AvCrowdingSc +
    AvWeightSc + BiomassSc + Season + Disease + HaemorrBefore +
    ScalelossBefore, family = gaussian(link = "identity"), data = df.scaleloss)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.31321  -0.25661  -0.00694   0.25271   1.40723

Coefficients:
                          Estimate Std. Error t value Pr(>|t|)
(Intercept)                1.16833    0.04122  28.346  < 2e-16 ***
MethodFreshwater          -0.74097    0.05986 -12.378  < 2e-16 ***
MethodHydrolicer          -0.01999    0.04643  -0.430 0.667022
MethodOptilicer           -0.27818    0.07366  -3.776 0.000172 ***
SeaTempSc                 -0.04852    0.03410  -1.423 0.155222
AvCrowdingSc               0.02478    0.01611   1.538 0.124410
AvWeightSc                -0.04153    0.01851  -2.244 0.025164 *
BiomassSc                 -0.06230    0.01965  -3.170 0.001588 **
SeasonFall                -0.05095    0.04424  -1.152 0.249816
SeasonSpring               0.23708    0.08106   2.925 0.003555 **
SeasonWinter              -0.05055    0.08411  -0.601 0.548076
DiseasePD                  0.00467    0.03616   0.129 0.897288
HaemorrBefore              0.02689    0.04148   0.648 0.516917
ScalelossBefore           -0.63215    0.03067 -20.609  < 2e-16 ***
MethodFreshwater:SeaTempSc  0.05723    0.04945   1.157 0.247553
MethodHydrolicer:SeaTempSc  0.15988    0.05101   3.135 0.001791 **
MethodOptilicer:SeaTempSc   0.11952    0.05430   2.201 0.028042 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for gaussian family taken to be 0.1508317)

    Null deviance: 241.26  on 738  degrees of freedom
Residual deviance: 108.90  on 722  degrees of freedom
AIC: 718.11

Number of Fisher Scoring iterations: 2
```

Figure D.14: Model output for the full SL-FE model.

SL-ME

```
Linear mixed model fit by maximum likelihood  ['lmerMod']
Formula: ScalelossChange ~ Method * SeaTempSc + AvCrowdingSc + AvWeightSc +
    BiomassSc + Season + Disease + HaemorrBefore + ScalelossBefore +      (1 | LocNumber)
   Data: df.scaleloss

     AIC      BIC   logLik deviance df.resid
   572.6    660.1   -267.3    534.6      720

Scaled residuals:
    Min      1Q  Median      3Q     Max
-4.8797 -0.6248  0.0183  0.6066  3.6881

Random effects:
 Groups    Name        Variance Std.Dev.
 LocNumber (Intercept) 0.05271  0.2296
 Residual              0.10958  0.3310
Number of obs: 739, groups:  LocNumber, 31

Fixed effects:
                            Estimate Std. Error t value
(Intercept)                 1.261404   0.057480  21.945
MethodFreshwater           -0.686242   0.057334 -11.969
MethodHydrolicer           -0.093108   0.046734  -1.992
MethodOptilicer            -0.559563   0.070298  -7.960
SeaTempSc                   0.072254   0.031833   2.270
AvCrowdingSc               -0.003240   0.014667  -0.221
AvWeightSc                 -0.056147   0.024180  -2.322
BiomassSc                  -0.057746   0.022126  -2.610
SeasonFall                 -0.077247   0.043866  -1.761
SeasonSpring                0.282791   0.072953   3.876
SeasonWinter                0.011925   0.077966   0.153
DiseasePD                  -0.087514   0.047185  -1.855
HaemorrBefore              -0.025523   0.038492  -0.663
ScalelossBefore            -0.687637   0.029094 -23.635
MethodFreshwater:SeaTempSc  0.007548   0.046960   0.161
MethodHydrolicer:SeaTempSc  0.106063   0.045871   2.312
MethodOptilicer:SeaTempSc  -0.103298   0.054932  -1.880
```

Figure D.15: Model output for the full SL-ME model.



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