

# Supplementary Materials: Seasonal Variations in the Use of Profundal Habitat among Freshwater Fishes in Lake Norsjø, Southern Norway, and Subsequent Effects on Fish Mercury Concentrations

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## 1. R-Code and Outputs

### 1.1. A. Charr (*Salvelinus alpinus*)

```
> Charr <- read.csv2("E:/Dokumenter/R/PublicationModel/A.Charr/Charr.csv")
> View(Charr)
> Charr$LogAge <- Charr$LogAge - mean(Charr$LogAge)
> Charr$LogLength <- Charr$LogLength - mean(Charr$LogLength)
> Charr$LogWeight <- Charr$LogWeight - mean(Charr$LogWeight)
> Charr$d13C <- Charr$d13CVPDB - mean(Charr$d13CVPDB)
> Charr$d15N <- Charr$d15NAIR - mean(Charr$d15NAIR)
> library(nlme)
> M1.A <- gls(LogHg ~ cAge, data = Charr, method = "ML")
> M1.L <- gls(LogHg ~ cLength, data = Charr, method = "ML")
> M1.W <- gls(LogHg ~ cWeight, data = Charr, method = "ML")
> M1.C <- gls(LogHg ~ cd13C, data = Charr, method = "ML")
> M1.N <- gls(LogHg ~ cd15N, data = Charr, method = "ML")
> M1.S <- gls(LogHg ~ Season, data = Charr, method = "ML")
> AIC(M1.A, M1.L, M1.W, M1.C, M1.N, M1.S)
      df      AIC
M1.A  3 136.67816
M1.L  3  92.52365
M1.W  3 103.20169
M1.C  3 163.55179
M1.N  3 160.47540
M1.S  5 163.32387
> M2.Simp <- M1.L
> M2.A <- gls(LogHg ~ cLength + cAge, data = Charr, method = "ML")
> M2.W <- gls(LogHg ~ cLength + cWeight, data = Charr, method = "ML")
> M2.C <- gls(LogHg ~ cLength + cd13C, data = Charr, method = "ML")
> M2.N <- gls(LogHg ~ cLength + cd15N, data = Charr, method = "ML")
> M2.S <- gls(LogHg ~ cLength + Season, data = Charr, method = "ML")
> anova(M2.Simp, M2.A)
      Model df      AIC      BIC  logLik  Test  L.Ratio p-value
M2.Simp   1  3 92.52365 99.55507 -43.26183
M2.A      2  4 94.46959 103.84481 -43.23479 1 vs 2 0.05406256 0.8161
> anova(M2.Simp, M2.W)
      Model df      AIC      BIC  logLik  Test  L.Ratio p-value
M2.Simp   1  3 92.52365 99.55507 -43.26183
M2.W      2  4 88.75169 98.12691 -40.37585 1 vs 2 5.771961 0.0163
> anova(M2.Simp, M2.C)
      Model df      AIC      BIC  logLik  Test  L.Ratio p-value
M2.Simp   1  3 92.52365 99.55507 -43.26183
M2.C      2  4 90.51702 99.89225 -41.25851 1 vs 2 4.006626 0.0453
```

```

> anova(M2.Simp, M2.N)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M2.Simp   1  3 92.52365 99.55507 -43.26183
M2.N      2  4 88.99440 98.36962 -40.49720 1 vs 2 5.529253 0.0187
> anova(M2.Simp, M2.S)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M2.Simp   1  3 92.52365 99.55507 -43.26183
M2.S      2  6 85.84356 99.90639 -36.92178 1 vs 2 12.6801 0.0054
> M3.Simp <- M2.S
> M3.A <- gls(LogHg ~ cLength + Season + cAge, data = Charr, method = "ML")
> M3.W <- gls(LogHg ~ cLength + Season + cWeight, data = Charr, method = "ML")
> M3.C <- gls(LogHg ~ cLength + Season + cd13C, data = Charr, method = "ML")
> M3.N <- gls(LogHg ~ cLength + Season + cd15N, data = Charr, method = "ML")
> M3.LS <- gls(LogHg ~ cLength + Season + cLength:Season, data = Charr, method = "ML")
> anova(M3.Simp, M3.A)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M3.Simp   1  6 85.84356 99.90639 -36.92178
M3.A      2  7 87.83269 104.23933 -36.91635 1 vs 2 0.01086453 0.917
> anova(M3.Simp, M3.W)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M3.Simp   1  6 85.84356 99.90639 -36.92178
M3.W      2  7 84.12894 100.53558 -35.06447 1 vs 2 3.714616 0.0539
> anova(M3.Simp, M3.C)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M3.Simp   1  6 85.84356 99.90639 -36.92178
M3.C      2  7 87.41860 103.82524 -36.70930 1 vs 2 0.4249522 0.5145
> anova(M3.Simp, M3.N)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M3.Simp   1  6 85.84356 99.90639 -36.92178
M3.N      2  7 86.00564 102.41228 -36.00282 1 vs 2 1.837913 0.1752
> anova(M3.Simp, M3.LS)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M3.Simp   1  6 85.84356 99.90639 -36.92178
M3.LS     2  9 90.18268 111.27692 -36.09134 1 vs 2 1.660879 0.6457
> M.Fixed <- gls(LogHg ~ cLength + Season, data = Charr, method = "REML")
> E.Fixed <- residuals(M.Fixed, type = "normalized")
> Fit.Fixed <- fitted(M.Fixed)
> op <- par(mfrow = c(2,2))
> plot(E.Fixed ~ Fit.Fixed, col = c("black", "green", "red", "blue")[as.numeric = Charr$Season], main =
"Residuals vs Fitted", xlab = "", ylab = "", las = 1)
> abline (0,0)
> hist(E.Fixed, main = "Residuals", xlab = "", ylab = "", las = 1)
> qqnorm(E.Fixed, main = "Residuals", xlab = "", ylab = "", las = 1)
> boxplot(E.Fixed ~ Charr$Season, main = "Residuals", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E.Fixed ~ Charr$cAge, col = c("black", "green", "red", "blue")[as.numeric = Charr$Season], main =
"Residuals vs Age", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E.Fixed ~ Charr$cLength, col = c("black", "green", "red", "blue")[as.numeric = Charr$Season],
main = "Residuals vs Length", xlab = "", ylab = "", las = 1)
> abline (0,0)

```

```

> plot(E.Fixed ~ Charr$cWeight, col = c("black", "green", "red", "blue")[as.numeric = Charr$Season],
main = "Residuals vs Weight", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E.Fixed ~ Charr$cd13C, col = c("black", "green", "red", "blue")[as.numeric = Charr$Season],
main = expression(paste("Residuals vs ", delta^{13}, "C")), xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E.Fixed ~ Charr$cd15N, col = c("black", "green", "red", "blue")[as.numeric = Charr$Season],
main = expression(paste("Residuals vs ", delta^{15}, "N")), xlab = "", ylab = "", las = 1)
> abline (0,0)
> M2.Fixed <- gls(LogHg ~ cLength + Season + cd15N, data = Charr, method = "REML")
> par(op)
> E2.Fixed <- residuals(M2.Fixed, type = "normalized")
> Fit2.Fixed <- fitted(M2.Fixed)
> op <- par(mfrow = c(2,2))
> plot(E2.Fixed ~ Fit2.Fixed, col = c("black", "green", "red", "blue")[as.numeric = Charr$Season], main =
"Residuals vs Fitted", xlab = "", ylab = "", las = 1)
> abline (0,0)
> hist(E2.Fixed, main = "Residuals", xlab = "", ylab = "", las = 1)
> qqnorm(E2.Fixed, main = "Residuals", xlab = "", ylab = "", las = 1)
> boxplot(E2.Fixed ~ Charr$Season, main = "Residuals vs Season", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E2.Fixed ~ Charr$cAge, col = c("black", "green", "red", "blue")[as.numeric = Charr$Season],
main = "Residuals vs Age", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E2.Fixed ~ Charr$cLength, col = c("black", "green", "red", "blue")[as.numeric = Charr$Season],
main = "Residuals vs Length", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E2.Fixed ~ Charr$cWeight, col = c("black", "green", "red", "blue")[as.numeric = Charr$Season],
main = "Residuals vs Weight", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E2.Fixed ~ Charr$cd13C, col = c("black", "green", "red", "blue")[as.numeric = Charr$Season],
main = expression(paste("Residuals vs ", delta^{13}, "C")), xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E2.Fixed ~ Charr$cd15N, col = c("black", "green", "red", "blue")[as.numeric = Charr$Season],
main = expression(paste("Residuals vs ", delta^{15}, "N")), xlab = "", ylab = "", las = 1)
> abline (0,0)
> par(op)
> M2.VarN <- gls(LogHg ~ cLength + Season + cd15N, weights = varExp(form =~ cd15N), data =
Charr, method = "REML")
> M2.VarS <- gls(LogHg ~ cLength + Season + cd15N, weights = varIdent(form =~ 1|Season), data =
Charr, method = "REML")
> M2.VarSN <- gls(LogHg ~ cLength + Season + cd15N, weights = varComb(varIdent(form =~
1|Season), varExp(form =~ cd15N)), data = Charr, method = "REML")
> anova(M2.Fixed, M2.VarN)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M2.Fixed   1  7 104.4192 120.2580 -45.20962
M2.VarN    2  8 105.0119 123.1133 -44.50594 1 vs 2 1.407367 0.2355
> anova(M2.Fixed, M2.VarS)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M2.Fixed   1  7 104.4192 120.2580 -45.20962
M2.VarS    2 10 103.2906 125.9174 -41.64529 1 vs 2 7.128654 0.0679
> anova(M2.Fixed, M2.VarSN)

```

```

      Model df    AIC    BIC  logLik Test L.Ratio p-value
M2.Fixed   1 7 104.4192 120.2580 -45.20962
M2.VarSN   2 11 102.9150 127.8045 -40.45752 1 vs 2 9.504206 0.0497
> M.Var <- M2.VarSN
> E.Var <- residuals(M.Var, type = "normalized")
> Fit.Var <- fitted(M.Var)
> op <- par(mfrow = c(2,2))
> plot(E.Var ~ Fit.Var, col = c("black", "green", "red", "blue")[as.numeric = Charr$Season], main =
"Residuals vs Fitted", xlab = "", ylab = "", las = 1)
> abline (0,0)
> hist(E.Var, main = "Residuals", xlab = "", ylab = "", las = 1)
> qqnorm(E.Var, main = "Residuals", xlab = "", ylab = "", las = 1)
> boxplot(E.Var ~ Charr$Season, main = "Residuals vs Season", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E.Var ~ Charr$cAge, col = c("black", "green", "red", "blue")[as.numeric = Charr$Season], main =
"Residuals vs Age", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E.Var ~ Charr$cLength, col = c("black", "green", "red", "blue")[as.numeric = Charr$Season],
main = "Residuals vs Length", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E.Var ~ Charr$cWeight, col = c("black", "green", "red", "blue")[as.numeric = Charr$Season],
main = "Residuals vs Weight", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E.Var ~ Charr$cd13C, col = c("black", "green", "red", "blue")[as.numeric = Charr$Season], main =
expression(paste("Residuals vs ", delta^{13}, "C")), xlab = "", ylab = "", las = 1)
> abline (0,0)
> par(op)
> plot(E.Var ~ Charr$cd15N, col = c("black", "green", "red", "blue")[as.numeric = Charr$Season],
main = expression(paste("Residuals vs ", delta^{15}, "N")), xlab = "", ylab = "", las = 1)
> abline (0,0)
> summary(M.Var)
Generalized least squares fit by REML
Model: LogHg ~ cLength + Season + cd15N
Data: Charr
      AIC    BIC  logLik
102.915 127.8045 -40.45752

```

Combination of variance functions:

Structure: Different standard deviations per stratum

Formula: ~1 | Season

Parameter estimates:

```

Winter Spring Summer Autumn
1.0000000 0.4173003 0.8846567 0.7615738

```

Structure: Exponential of variance covariate

Formula: ~cd15N

Parameter estimates:

```

expon
0.1543219

```

Coefficients:

```

      Value Std.Error t-value p-value
(Intercept) -1.8250198 0.06958365 -26.227709 0.0000

```

```

cLength    1.5921231 0.13052101 12.198213 0.0000
SeasonSpring 0.3553162 0.10017704 3.546882 0.0007
SeasonSummer -0.0239671 0.10883908 -0.220207 0.8263
SeasonWinter 0.2970098 0.16661214 1.782642 0.0789
cd15N       0.0163011 0.02981476 0.546747 0.5863

```

Correlation:

```

(Intr) cLngth SsnSpr SsnSmm SsnWnt
cLength    -0.006
SeasonSpring -0.755 0.142
SeasonSummer -0.540 -0.048 0.375
SeasonWinter -0.450 -0.038 0.343 0.231
cd15N       0.428 -0.145 -0.455 -0.040 -0.248

```

Standardized residuals:

```

      Min      Q1      Med      Q3      Max
-2.0410733    -0.9249228          0.1162202    0.7262981    1.7113298

```

Residual standard error: 0.498476

Degrees of freedom: 77 total; 71 residual

```

> library(rgl)
> library(rglwidget)
> with(Charr, plot3d(cLength, cd15N, LogHg, type = "s", col = c("black", "green", "red",
"blue"))[as.numeric(Season)]))
> fit <- gls(LogHg ~ cLength + Season + cd15N, weights = varComb(varIdent(form =~ 1|Season),
varExp(form =~ cd15N)), data = Charr, method = "REML")
> coefs <- coef(fit)
> View(coefs)
> a <- 1.59212311
> b <- 0.01630114
> c <- -1
> d <- -1.82501976
> planes3d(a, b, c, d, col = "blue")
> d <- -1.82501976 + 0.35531618
> planes3d(a, b, c, d, col = "green")
> d <- -1.82501976 - 0.02396713
> planes3d(a, b, c, d, col = "red")
> d <- -1.82501976 + 0.29700981
> planes3d(a, b, c, d, col = "black")
> filename <- writeWebGL(dir = file.path(tempdir(), "WebGL"), width = 750, reuse = TRUE)
> if(interactive()) browseURL(paste0("file://", filename))
> MPlot.LHg <- gls(LogHg ~ Season + cd15N, weights = varComb(varIdent(form =~ 1|Season),
varExp(form =~ cd15N)), data = Charr, method = "REML")
> MPlot.L <- gls(cLength ~ Season + cd15N, weights = varComb(varIdent(form =~ 1|Season),
varExp(form =~ cd15N)), data = Charr, method = "REML")
> Charr$PlotLHg <- residuals(MPlot.LHg, type = "normalized")
> Charr$PlotL <- residuals(MPlot.L, type = "normalized")
> MPlot.NHg <- gls(LogHg ~ cLength + Season, weights = varIdent(form =~ 1|Season), data = Charr,
method = "REML")
> MPlot.N <- gls(cd15N ~ cLength + Season, weights = varIdent(form =~ 1|Season), data = Charr,
method = "REML")
> Charr$PlotNHg <- residuals(MPlot.NHg, type = "normalized")
> Charr$PlotN <- residuals(MPlot.N, type = "normalized")

```

```
> write.csv(Charr, file = "PlotCharr.csv", row.names = FALSE)
```

### 1.2. E. Smelt (*Osmerus eperlanus*)

```
> Smelt <- read.csv2("E:/Dokumenter/R/PublicationModel/Smelt/Smelt.csv")
```

```
> View(Smelt)
```

```
> Smelt$Age <- Smelt$LogAge - mean(Smelt$LogAge)
```

```
> Smelt$Length <- Smelt$LogLength - mean(Smelt$LogLength)
```

```
> Smelt$Weight <- Smelt$LogWeight - mean(Smelt$LogWeight)
```

```
> Smelt$d13C <- Smelt$d13CVPDB - mean(Smelt$d13CVPDB)
```

```
> Smelt$d15N <- Smelt$d15NAIR - mean(Smelt$d15NAIR)
```

```
> library(nlme)
```

```
> M1.A <- gls(LogHg ~ cAge, data = Smelt, method = "ML")
```

```
> M1.L <- gls(LogHg ~ cLength, data = Smelt, method = "ML")
```

```
> M1.W <- gls(LogHg ~ cWeight, data = Smelt, method = "ML")
```

```
> M1.C <- gls(LogHg ~ cd13C, data = Smelt, method = "ML")
```

```
> M1.N <- gls(LogHg ~ cd15N, data = Smelt, method = "ML")
```

```
> M1.S <- gls(LogHg ~ Season, data = Smelt, method = "ML")
```

```
> AIC(M1.A, M1.L, M1.W, M1.C, M1.N, M1.S)
```

```
df    AIC
```

```
M1.A 3 44.02234
```

```
M1.L 3 58.75371
```

```
M1.W 3 62.11697
```

```
M1.C 3 55.07796
```

```
M1.N 3 61.74562
```

```
M1.S 5 65.87988
```

```
> M2.Simp <- M1.A
```

```
> M2.L <- gls(LogHg ~ cAge + cLength, data = Smelt, method = "ML")
```

```
> M2.W <- gls(LogHg ~ cAge + cWeight, data = Smelt, method = "ML")
```

```
> M2.C <- gls(LogHg ~ cAge + cd13C, data = Smelt, method = "ML")
```

```
> M2.N <- gls(LogHg ~ cAge + cd15N, data = Smelt, method = "ML")
```

```
> M2.S <- gls(LogHg ~ cAge + Season, data = Smelt, method = "ML")
```

```
> anova(M2.Simp, M2.L)
```

```
Model df    AIC    BIC  logLik  Test  L.Ratio p-value
```

```
M2.Simp  1 3 44.02234 51.80770 -19.01117
```

```
M2.L      2 4 45.98906 56.36954 -18.99453 1 vs 2 0.03328313 0.8552
```

```
> anova(M2.Simp, M2.W)
```

```
Model df    AIC    BIC  logLik  Test  L.Ratio p-value
```

```
M2.Simp  1 3 44.02234 51.80770 -19.01117
```

```
M2.W      2 4 37.73471 48.11519 -14.86736 1 vs 2 8.287629 0.004
```

```
> anova(M2.Simp, M2.C)
```

```
Model df    AIC    BIC  logLik  Test  L.Ratio p-value
```

```
M2.Simp  1 3 44.02234 51.80770 -19.01117
```

```
M2.C      2 4 39.86640 50.24688 -15.93320 1 vs 2 6.155939 0.0131
```

```
> anova(M2.Simp, M2.N)
```

```
Model df    AIC    BIC  logLik  Test  L.Ratio p-value
```

```
M2.Simp  1 3 44.02234 51.8077 -19.01117
```

```
M2.N      2 4 44.35002 54.7305 -18.17501 1 vs 2 1.672325 0.1959
```

```
> anova(M2.Simp, M2.S)
```

```
Model df    AIC    BIC  logLik  Test  L.Ratio p-value
```

```
M2.Simp  1 3 44.02234 51.80770 -19.01117
```

```
M2.S      2 6 43.98924 59.55996 -15.99462 1 vs 2 6.033096 0.11
```

```
> M3.Simp <- M2.W
```

```

> M3.L <- gls(LogHg ~ cAge + cWeight + cLength, data = Smelt, method = "ML")
> M3.C <- gls(LogHg ~ cAge + cWeight + cd13C, data = Smelt, method = "ML")
> M3.N <- gls(LogHg ~ cAge + cWeight + cd15N, data = Smelt, method = "ML")
> M3.S <- gls(LogHg ~ cAge + cWeight + Season, data = Smelt, method = "ML")
> M3.AW <- gls(LogHg ~ cAge + cWeight + cAge:cWeight, data = Smelt, method = "ML")
> anova(M3.Simp, M3.L)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M3.Simp   1  4 37.73471 48.11519 -14.86736
M3.L      2  5 32.07755 45.05315 -11.03877 1 vs 2 7.657165 0.0057
> anova(M3.Simp, M3.C)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M3.Simp   1  4 37.73471 48.11519 -14.86736
M3.C      2  5 31.57148 44.54708 -10.78574 1 vs 2 8.163228 0.0043
> anova(M3.Simp, M3.N)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M3.Simp   1  4 37.73471 48.11519 -14.86736
M3.N      2  5 36.46050 49.43610 -13.23025 1 vs 2 3.274211 0.0704
> anova(M3.Simp, M3.S)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M3.Simp   1  4 37.73471 48.11519 -14.86736
M3.S      2  7 38.49459 56.66043 -12.24729 1 vs 2 5.240124 0.155
> anova(M3.Simp, M3.AW)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M3.Simp   1  4 37.73471 48.11519 -14.86736
M3.AW     2  5 39.68562 52.66122 -14.84281 1 vs 2 0.04908747 0.8247
> M4.Simp <- M3.C
> M4.L <- gls(LogHg ~ cAge + cWeight + cd13C + cLength, data = Smelt, method = "ML")
> M4.N <- gls(LogHg ~ cAge + cWeight + cd13C + cd15N, data = Smelt, method = "ML")
> M4.S <- gls(LogHg ~ cAge + cWeight + cd13C + Season, data = Smelt, method = "ML")
> M4.AW <- gls(LogHg ~ cAge + cWeight + cd13C + cAge:cWeight, data = Smelt, method = "ML")
> M4.AC <- gls(LogHg ~ cAge + cWeight + cd13C + cAge:cd13C, data = Smelt, method = "ML")
> M4.WC <- gls(LogHg ~ cAge + cWeight + cd13C + cWeight:cd13C, data = Smelt, method = "ML")
> anova(M4.Simp, M4.L)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M4.Simp   1  5 31.57148 44.54708 -10.78574
M4.L      2  6 23.94682 39.51754 -5.97341 1 vs 2 9.624663 0.0019
> anova(M4.Simp, M4.N)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M4.Simp   1  5 31.57148 44.54708 -10.78574
M4.N      2  6 32.29739 47.86811 -10.14869 1 vs 2 1.274097 0.259
> anova(M4.Simp, M4.S)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M4.Simp   1  5 31.57148 44.54708 -10.78574
M4.S      2  8 33.27205 54.03300 -8.636023 1 vs 2 4.299439 0.2309
> anova(M4.Simp, M4.AW)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M4.Simp   1  5 31.57148 44.54708 -10.78574
M4.AW     2  6 33.51857 49.08929 -10.75928 1 vs 2 0.0529148 0.8181
> anova(M4.Simp, M4.AC)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M4.Simp   1  5 31.57148 44.54708 -10.78574
M4.AC     2  6 32.92661 48.49733 -10.46330 1 vs 2 0.6448753 0.422

```

```

> anova(M4.Simp, M4.WC)
      Model df   AIC    BIC  logLik  Test  L.Ratio p-value
M4.Simp   1  5 31.57148 44.54708 -10.78574
M4.WC     2  6 33.43266 49.00338 -10.71633 1 vs 2 0.1388203 0.7095
> M5.Simp <- M4.L
> M5.N <- gls(LogHg ~ cAge + cWeight + cd13C + cLength + cd15N, data = Smelt, method = "ML")
> M5.S <- gls(LogHg ~ cAge + cWeight + cd13C + cLength + Season, data = Smelt, method = "ML")
> M5.AW <- gls(LogHg ~ cAge + cWeight + cd13C + cLength + cAge:cWeight, data = Smelt, method =
"ML")
> M5.AC <- gls(LogHg ~ cAge + cWeight + cd13C + cLength + cAge:cd13C, data = Smelt, method =
"ML")
> M5.AL <- gls(LogHg ~ cAge + cWeight + cd13C + cLength + cAge:cLength, data = Smelt, method =
"ML")
> M5.WC <- gls(LogHg ~ cAge + cWeight + cd13C + cLength + cWeight:cd13C, data = Smelt, method =
"ML")
> M5.LW <- gls(LogHg ~ cAge + cWeight + cd13C + cLength + cLength:cWeight, data = Smelt, method =
"ML")
> M5.LC <- gls(LogHg ~ cAge + cWeight + cd13C + cLength + cLength:cd13C, data = Smelt, method =
"ML")
> anova(M5.Simp, M5.N)
      Model df   AIC    BIC  logLik  Test  L.Ratio p-value
M5.Simp   1  6 23.94682 39.51754 -5.973410
M5.N      2  7 25.49394 43.65978 -5.746968 1 vs 2 0.4528835 0.501
> anova(M5.Simp, M5.S)
      Model df   AIC    BIC  logLik  Test  L.Ratio p-value
M5.Simp   1  6 23.94682 39.51754 -5.973410
M5.S      2  9 23.93689 47.29297 -2.968444 1 vs 2 6.009933 0.1111
> anova(M5.Simp, M5.AW)
      Model df   AIC    BIC  logLik  Test  L.Ratio p-value
M5.Simp   1  6 23.94682 39.51754 -5.973410
M5.AW     2  7 25.88967 44.05551 -5.944834 1 vs 2 0.05715189 0.8111
> anova(M5.Simp, M5.AC)
      Model df   AIC    BIC  logLik  Test  L.Ratio p-value
M5.Simp   1  6 23.94682 39.51754 -5.973410
M5.AC     2  7 25.68684 43.85268 -5.843419 1 vs 2 0.259983 0.6101
> anova(M5.Simp, M5.AL)
      Model df   AIC    BIC  logLik  Test  L.Ratio p-value
M5.Simp   1  6 23.94682 39.51754 -5.973410
M5.AL     2  7 25.43064 43.59648 -5.715318 1 vs 2 0.5161839 0.4725
> anova(M5.Simp, M5.WC)
      Model df   AIC    BIC  logLik  Test  L.Ratio p-value
M5.Simp   1  6 23.94682 39.51754 -5.973410
M5.WC     2  7 25.67972 43.84556 -5.839859 1 vs 2 0.2671035 0.6053
> anova(M5.Simp, M5.LW)
      Model df   AIC    BIC  logLik  Test  L.Ratio p-value
M5.Simp   1  6 23.94682 39.51754 -5.97341
M5.LW     2  7 24.80744 42.97328 -5.40372 1 vs 2 1.13938 0.2858
> anova(M5.Simp, M5.LC)
      Model df   AIC    BIC  logLik  Test  L.Ratio p-value
M5.Simp   1  6 23.94682 39.51754 -5.973410
M5.LC     2  7 25.50969 43.67553 -5.754847 1 vs 2 0.4371264 0.5085
> M0.Var <- gls(LogHg ~ cAge + cLength + cWeight + cd13C, data = Smelt, method = "REML")

```

```

> E0.Var <- residuals(M0.Var, type = "normalized")
> Fit0.Var <- fitted(M0.Var)
> op <- par(mfrow = c(2,2))
> plot(E0.Var ~ Fit0.Var, col = c("black", "green", "red", "blue")[as.numeric = Smelt$Season], main =
"Residuals vs Fitted", xlab = "", ylab = "", las = 1)
> abline (0,0)
> hist(E0.Var, main = "Residuals", xlab = "", ylab = "", las = 1)
> qqnorm(E0.Var, main = "Residuals", xlab = "", ylab = "", las = 1)
> boxplot(E0.Var ~ Smelt$Season, main = "Residuals vs Season", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E0.Var ~ Smelt$cAge, col = c("black", "green", "red", "blue")[as.numeric = Smelt$Season], main =
"Residuals vs Age", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E0.Var ~ Smelt$cLength, col = c("black", "green", "red", "blue")[as.numeric = Smelt$Season],
main = "Residuals vs Length", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E0.Var ~ Smelt$cWeight, col = c("black", "green", "red", "blue")[as.numeric = Smelt$Season],
main = "Residuals vs Weight", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E0.Var ~ Smelt$cd13C, col = c("black", "green", "red", "blue")[as.numeric = Smelt$Season], main =
expression(paste("Residuals vs ", delta^{13}, "C")), xlab = "", ylab = "", las = 1)
> abline (0,0)
> par(op)
> plot(E0.Var ~ Smelt$cd15N, col = c("black", "green", "red", "blue")[as.numeric = Smelt$Season], main =
expression(paste("Residuals vs ", delta^{15}, "N")), xlab = "", ylab = "", las = 1)
> abline (0,0)
> summary(M0.Var)
Generalized least squares fit by REML
Model: LogHg ~ cAge + cLength + cWeight + cd13C
Data: Smelt
      AIC      BIC    logLik
39.94647 55.20624 -13.97324

```

## Coefficients:

|             | Value      | Std.Error | t-value   | p-value |
|-------------|------------|-----------|-----------|---------|
| (Intercept) | -1.5525078 | 0.0265096 | -58.56399 | 0.0000  |
| cAge        | 0.1856882  | 0.0601804 | 3.08552   | 0.0027  |
| cLength     | 1.9269519  | 0.6220007 | 3.09799   | 0.0026  |
| cWeight     | -0.5321774 | 0.1163744 | -4.57298  | 0.0000  |
| cd13C       | -0.1569987 | 0.0493315 | -3.18252  | 0.0020  |

## Correlation:

|         | (Intr) | cAge   | cLngth | cWeght |
|---------|--------|--------|--------|--------|
| cAge    | 0.000  |        |        |        |
| cLength | 0.000  | -0.491 |        |        |
| cWeight | 0.000  | 0.173  | -0.645 |        |
| cd13C   | 0.000  | 0.176  | -0.066 | 0.106  |

## Standardized residuals:

| Min         | Q1 | Med         | Q3          | Max                   |
|-------------|----|-------------|-------------|-----------------------|
| -2.09731219 |    | -0.67514227 | -0.04802533 | 0.78028875 2.53300846 |

Residual standard error: 0.2637672

Degrees of freedom: 99 total; 94 residual

```
> MPlot.AHg <- gls(LogHg ~ cLength + cWeight + cd13C, data = Smelt, method = "REML")
> MPlot.A <- gls(cAge ~ cLength + cWeight + cd13C, data = Smelt, method = "REML")
> MPlot.LHg <- gls(LogHg ~ cAge + cWeight + cd13C, data = Smelt, method = "REML")
> MPlot.L <- gls(cLength ~ cAge + cWeight + cd13C, data = Smelt, method = "REML")
> MPlot.WHg <- gls(LogHg ~ cAge + cLength + cd13C, data = Smelt, method = "REML")
> MPlot.W <- gls(cWeight ~ cAge + cLength + cd13C, data = Smelt, method = "REML")
> MPlot.CHg <- gls(LogHg ~ cAge + cLength + cWeight, data = Smelt, method = "REML")
> MPlot.C <- gls(cd13C ~ cAge + cLength + cWeight, data = Smelt, method = "REML")
> Smelt$PlotAHg <- residuals(MPlot.AHg, type = "normalized")
> Smelt$PlotA <- residuals(MPlot.A, type = "normalized")
> Smelt$PlotLHg <- residuals(MPlot.LHg, type = "normalized")
> Smelt$PlotL <- residuals(MPlot.L, type = "normalized")
> Smelt$PlotWHg <- residuals(MPlot.WHg, type = "normalized")
> Smelt$PlotW <- residuals(MPlot.W, type = "normalized")
> Smelt$PlotCHg <- residuals(MPlot.CHg, type = "normalized")
> Smelt$PlotC <- residuals(MPlot.C, type = "normalized")
> write.csv(Smelt, file = "PlotSmelt.csv", row.names = FALSE)
```

### 1.3. Whitefish (*Coregonus lavaretus*)

```
> Whitefish <- read.csv2("E:/Dokumenter/R/PublicationModel/White/Whitefish.csv")
> View(Whitefish)
> Whitefish$cAge <- Whitefish$LogAge - mean(Whitefish$LogAge)
> Whitefish$cLength <- Whitefish$LogLength - mean(Whitefish$LogLength)
> Whitefish$cWeight <- Whitefish$LogWeight - mean(Whitefish$LogWeight)
> Whitefish$cd13C <- Whitefish$d13CVPDB - mean(Whitefish$d13CVPDB)
> Whitefish$cd15N <- Whitefish$d15NAIR - mean(Whitefish$d15NAIR)
> library(nlme)
> M1.A <- gls(LogHg ~ cAge, data = Whitefish, method = "ML")
> M1.L <- gls(LogHg ~ cLength, data = Whitefish, method = "ML")
> M1.W <- gls(LogHg ~ cWeight, data = Whitefish, method = "ML")
> M1.C <- gls(LogHg ~ cd13C, data = Whitefish, method = "ML")
> M1.N <- gls(LogHg ~ cd15N, data = Whitefish, method = "ML")
> M1.S <- gls(LogHg ~ Season, data = Whitefish, method = "ML")
> AIC(M1.A, M1.L, M1.W, M1.C, M1.N, M1.S)
      df      AIC
M1.A 3 63.10259
M1.L 3 49.15772
M1.W 3 65.74765
M1.C 3 103.79593
M1.N 3 84.59179
M1.S 4 106.86325
> M2.Simp <- M1.L
> M2.A <- gls(LogHg ~ cLength + cAge, data = Whitefish, method = "ML")
> M2.W <- gls(LogHg ~ cLength + cWeight, data = Whitefish, method = "ML")
> M2.C <- gls(LogHg ~ cLength + cd13C, data = Whitefish, method = "ML")
> M2.N <- gls(LogHg ~ cLength + cd15N, data = Whitefish, method = "ML")
> M2.S <- gls(LogHg ~ cLength + Season, data = Whitefish, method = "ML")
> anova(M2.Simp, M2.A)
      Model df      AIC      BIC logLik Test L.Ratio p-value
M2.Simp  1 3 49.15772 56.14992 -21.57886
```

```

M2.A      2 4 37.10706 46.42999 -14.55353 1 vs 2 14.05067 2e-04
> anova(M2.Simp, M2.W)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M2.Simp   1 3 49.15772 56.14992 -21.57886
M2.W      2 4 36.07216 45.39509 -14.03608 1 vs 2 15.08556 1e-04
> anova(M2.Simp, M2.C)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M2.Simp   1 3 49.15772 56.14992 -21.57886
M2.C      2 4 47.18977 56.51270 -19.59488 1 vs 2 3.967956 0.0464
> anova(M2.Simp, M2.N)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M2.Simp   1 3 49.15772 56.14992 -21.57886
M2.N      2 4 42.40075 51.72368 -17.20037 1 vs 2 8.756976 0.0031
> anova(M2.Simp, M2.S)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M2.Simp   1 3 49.15772 56.14992 -21.57886
M2.S      2 5 52.16745 63.82112 -21.08373 1 vs 2 0.9902746 0.6095
> M3.Simp <- M2.W
> M3.A <- gls(LogHg ~ cLength + cWeight + cAge, data = Whitefish, method = "ML")
> M3.C <- gls(LogHg ~ cLength + cWeight + cd13C, data = Whitefish, method = "ML")
> M3.N <- gls(LogHg ~ cLength + cWeight + cd15N, data = Whitefish, method = "ML")
> M3.S <- gls(LogHg ~ cLength + cWeight + Season, data = Whitefish, method = "ML")
> M3.LW <- gls(LogHg ~ cLength + cWeight + cLength:cWeight, data = Whitefish, method = "ML")
> anova(M3.Simp, M3.A)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M3.Simp   1 4 36.07216 45.39509 -14.03608
M3.A      2 5 22.18879 33.84245 -6.094393 1 vs 2 15.88337 1e-04
> anova(M3.Simp, M3.C)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M3.Simp   1 4 36.07216 45.39509 -14.03608
M3.C      2 5 35.44823 47.10190 -12.72411 1 vs 2 2.62393 0.1053
> anova(M3.Simp, M3.N)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M3.Simp   1 4 36.07216 45.39509 -14.03608
M3.N      2 5 27.34135 38.99502 -8.670676 1 vs 2 10.73081 0.0011
> anova(M3.Simp, M3.S)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M3.Simp   1 4 36.07216 45.39509 -14.03608
M3.S      2 6 33.85548 47.83988 -10.92774 1 vs 2 6.216682 0.0447
> anova(M3.Simp, M3.LW)
      Model df   AIC    BIC  logLik  Test L.Ratio p-value
M3.Simp   1 4 36.07216 45.39509 -14.03608
M3.LW     2 5 35.87748 47.53114 -12.93874 1 vs 2 2.194683 0.1385
> M4.Simp <- M3.A
> M4.C <- gls(LogHg ~ cLength + cWeight + cAge + cd13C, data = Whitefish, method = "ML")
> M4.N <- gls(LogHg ~ cLength + cWeight + cAge + cd15N, data = Whitefish, method = "ML")
> M4.S <- gls(LogHg ~ cLength + cWeight + cAge + Season, data = Whitefish, method = "ML")
> M4.AL <- gls(LogHg ~ cLength + cWeight + cAge + cAge:cLength, data = Whitefish, method =
"ML")
> M4.AW <- gls(LogHg ~ cLength + cWeight + cAge + cAge:cWeight, data = Whitefish, method =
"ML")

```

```

> M4.LW <- gls(LogHg ~ cLength + cWeight + cAge + cLength:cWeight, data = Whitefish, method =
"ML")
> anova(M4.Simp, M4.C)
      Model df   AIC    BIC logLik Test L.Ratio p-value
M4.Simp   1  5 22.18879 33.84245 -6.094393
M4.C      2  6 22.90913 36.89353 -5.454565 1 vs 2 1.279656 0.258
> anova(M4.Simp, M4.N)
      Model df   AIC    BIC logLik Test L.Ratio p-value
M4.Simp   1  5 22.18879 33.84245 -6.094393
M4.N      2  6 21.75438 35.73878 -4.877189 1 vs 2 2.434408 0.1187
> anova(M4.Simp, M4.S)
      Model df   AIC    BIC logLik Test L.Ratio p-value
M4.Simp   1  5 22.18879 33.84245 -6.094393
M4.S      2  7 24.13467 40.44981 -5.067337 1 vs 2 2.054112 0.3581
> anova(M4.Simp, M4.AL)
      Model df   AIC    BIC logLik Test L.Ratio p-value
M4.Simp   1  5 22.18879 33.84245 -6.094393
M4.AL     2  6 23.06528 37.04968 -5.532642 1 vs 2 1.123502 0.2892
> anova(M4.Simp, M4.AW)
      Model df   AIC    BIC logLik Test L.Ratio p-value
M4.Simp   1  5 22.18879 33.84245 -6.094393
M4.AW     2  6 23.05784 37.04224 -5.528920 1 vs 2 1.130946 0.2876
> anova(M4.Simp, M4.LW)
      Model df   AIC    BIC logLik Test L.Ratio p-value
M4.Simp   1  5 22.18879 33.84245 -6.094393
M4.LW     2  6 23.95844 37.94284 -5.979218 1 vs 2 0.2303509 0.6313
> M0.Var <- gls(LogHg ~ cLength + cWeight + cAge, data = Whitefish, method = "REML")
> E0.Var <- residuals(M0.Var, type = "normalized")
> Fit0.Var <- fitted(M0.Var)
> op <- par(mfrow = c(2,2))
> plot(E0.Var ~ Fit0.Var, col = c("black", "green", "blue")[as.numeric = Whitefish$Season], main =
"Residuals vs Fitted", xlab = "", ylab = "", las = 1)
> abline (0,0)
> hist(E0.Var, main = "Residuals", xlab = "", ylab = "", las = 1)
> qqnorm(E0.Var, main = "Residuals", xlab = "", ylab = "", las = 1)
> boxplot(E0.Var ~ Whitefish$Season, main = "Residuals vs Season", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E0.Var ~ Whitefish$cAge, col = c("black", "green", "blue")[as.numeric = Whitefish$Season], main =
"Residuals vs Age", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E0.Var ~ Whitefish$cLength, col = c("black", "green", "blue")[as.numeric = Whitefish$Season],
main = "Residuals vs Length", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E0.Var ~ Whitefish$cWeight, col = c("black", "green", "blue")[as.numeric = Whitefish$Season],
main = "Residuals vs Weight", xlab = "", ylab = "", las = 1)
> abline (0,0)
> plot(E0.Var ~ Whitefish$cd13C, col = c("black", "green", "blue")[as.numeric = Whitefish$Season],
main = expression(paste("Residuals vs ", delta^{13}, "C")), xlab = "", ylab = "", las = 1)
> abline (0,0)
> par(op)
> plot(E0.Var ~ Whitefish$cd15N, col = c("black", "green", "blue")[as.numeric = Whitefish$Season],
main = expression(paste("Residuals vs ", delta^{15}, "N")), xlab = "", ylab = "", las = 1)

```

```
> abline (0,0)
> summary(M0.Var)
Generalized least squares fit by REML
Model: LogHg ~ cLength + cWeight + cAge
Data: Whitefish
      AIC   BIC logLik
33.66095 45.04428 -11.83047
```

Coefficients:

|             | Value     | Std.Error | t-value   | p-value |
|-------------|-----------|-----------|-----------|---------|
| (Intercept) | -1.702532 | 0.0308974 | -55.10272 | 0e+00   |
| cLength     | 4.943859  | 0.8510078 | 5.80942   | 0e+00   |
| cWeight     | -1.081176 | 0.2551769 | -4.23697  | 1e-04   |
| cAge        | 0.237659  | 0.0580948 | 4.09088   | 1e-04   |

Correlation:

|         | (Intr) | cLngth | cWeght |
|---------|--------|--------|--------|
| cLength | 0.000  |        |        |
| cWeight | 0.000  | -0.962 |        |
| cAge    | 0.000  | -0.202 | 0.042  |

Standardized residuals:

| Min         | Q1          | Med         | Q3         | Max        |
|-------------|-------------|-------------|------------|------------|
| -2.56004691 | -0.67445338 | -0.01991938 | 0.63648974 | 2.42606592 |

Residual standard error: 0.2693576

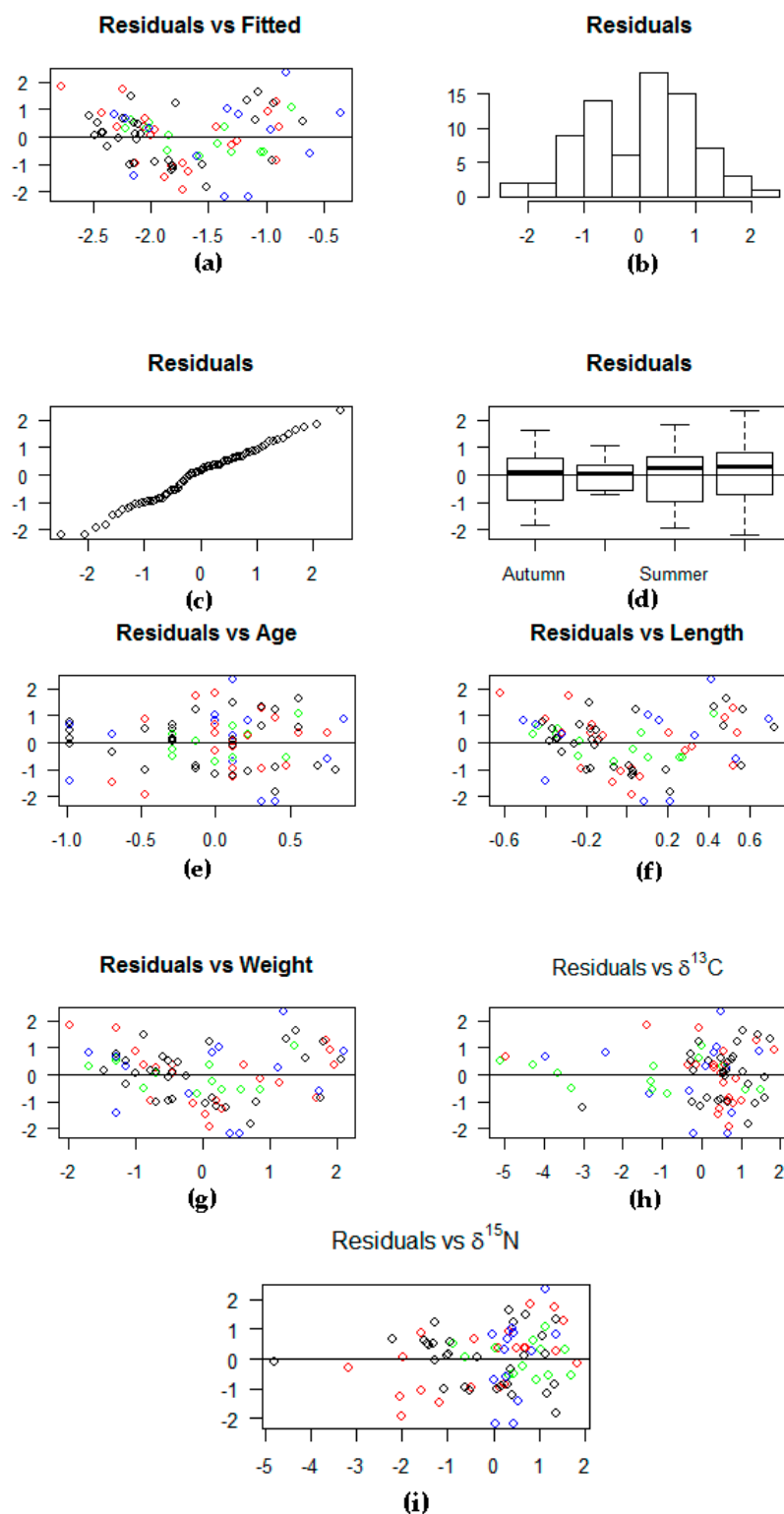
Degrees of freedom: 76 total; 72 residual

```
> MPlot.LHg <- gls(LogHg ~ cWeight + cAge, data = Whitefish, method = "REML")
> MPlot.L <- gls(cLength ~ cWeight + cAge, data = Whitefish, method = "REML")
> MPlot.WHg <- gls(LogHg ~ cLength + cAge, data = Whitefish, method = "REML")
> MPlot.W <- gls(cWeight ~ cLength + cAge, data = Whitefish, method = "REML")
> MPlot.AHg <- gls(LogHg ~ cLength + cWeight, data = Whitefish, method = "REML")
> MPlot.A <- gls(cAge ~ cLength + cWeight, data = Whitefish, method = "REML")
> Whitefish$PlotLHg <- residuals(MPlot.LHg, type = "normalized")
> Whitefish$PlotL <- residuals(MPlot.L, type = "normalized")
> Whitefish$PlotWHg <- residuals(MPlot.WHg, type = "normalized")
> Whitefish$PlotW <- residuals(MPlot.W, type = "normalized")
> Whitefish$PlotAHg <- residuals(MPlot.AHg, type = "normalized")
> Whitefish$PlotA <- residuals(MPlot.A, type = "normalized")
> write.csv(Whitefish, file = "PlotWhitefish.csv", row.names = FALSE)
```

## 2. Residual Graphs and Discussion

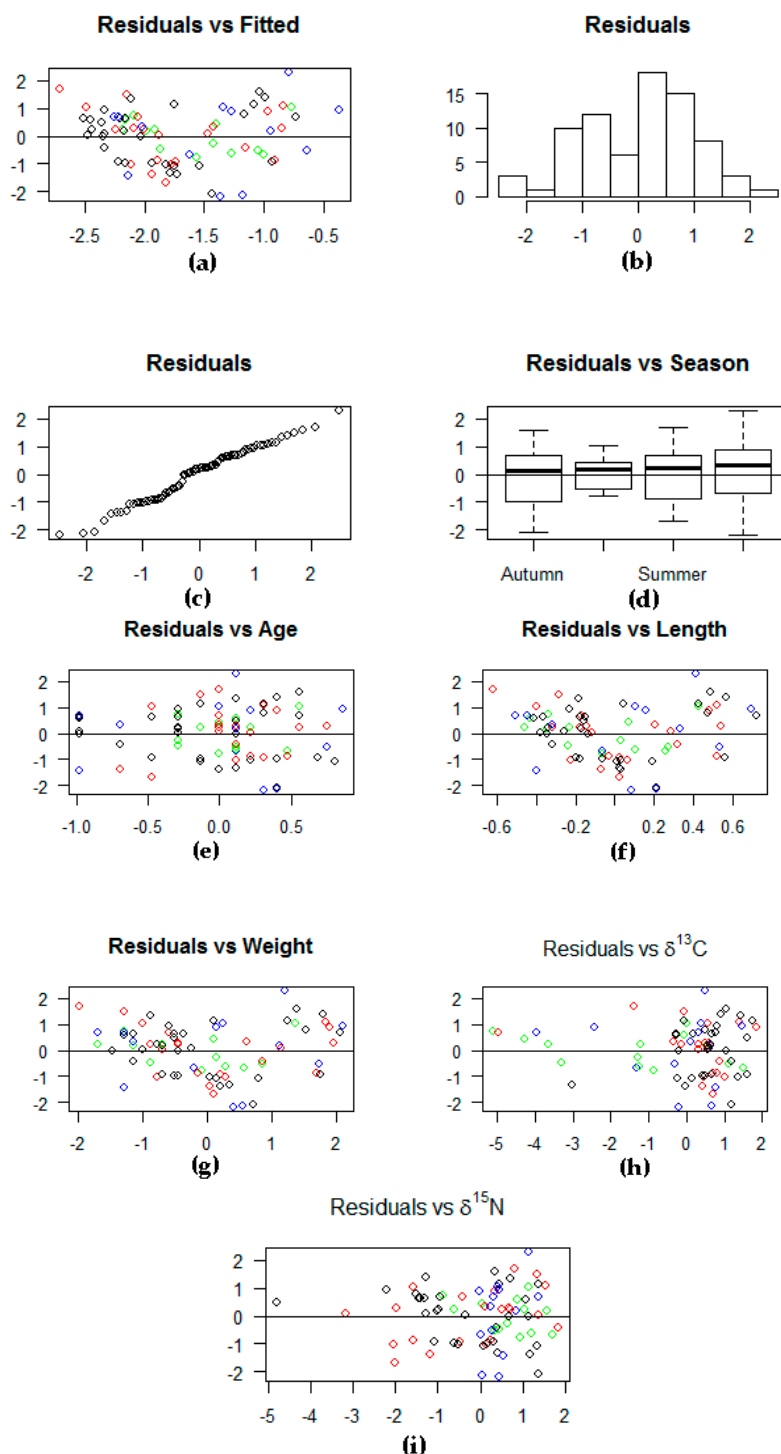
### 2.1. A. Charr Model

In the first model selection step, choosing significant predictors for Tot-Hg by likelihood ratio tests using ML estimation, only length and season are included in the model. The residuals of this basic model are close to normal distribution (Figure S2), and show no correlation to age, length or season. However, the variance increases with increasing  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$ , and different seasons exhibit different variances. The differences in seasonal means are appropriately accounted for in the model.



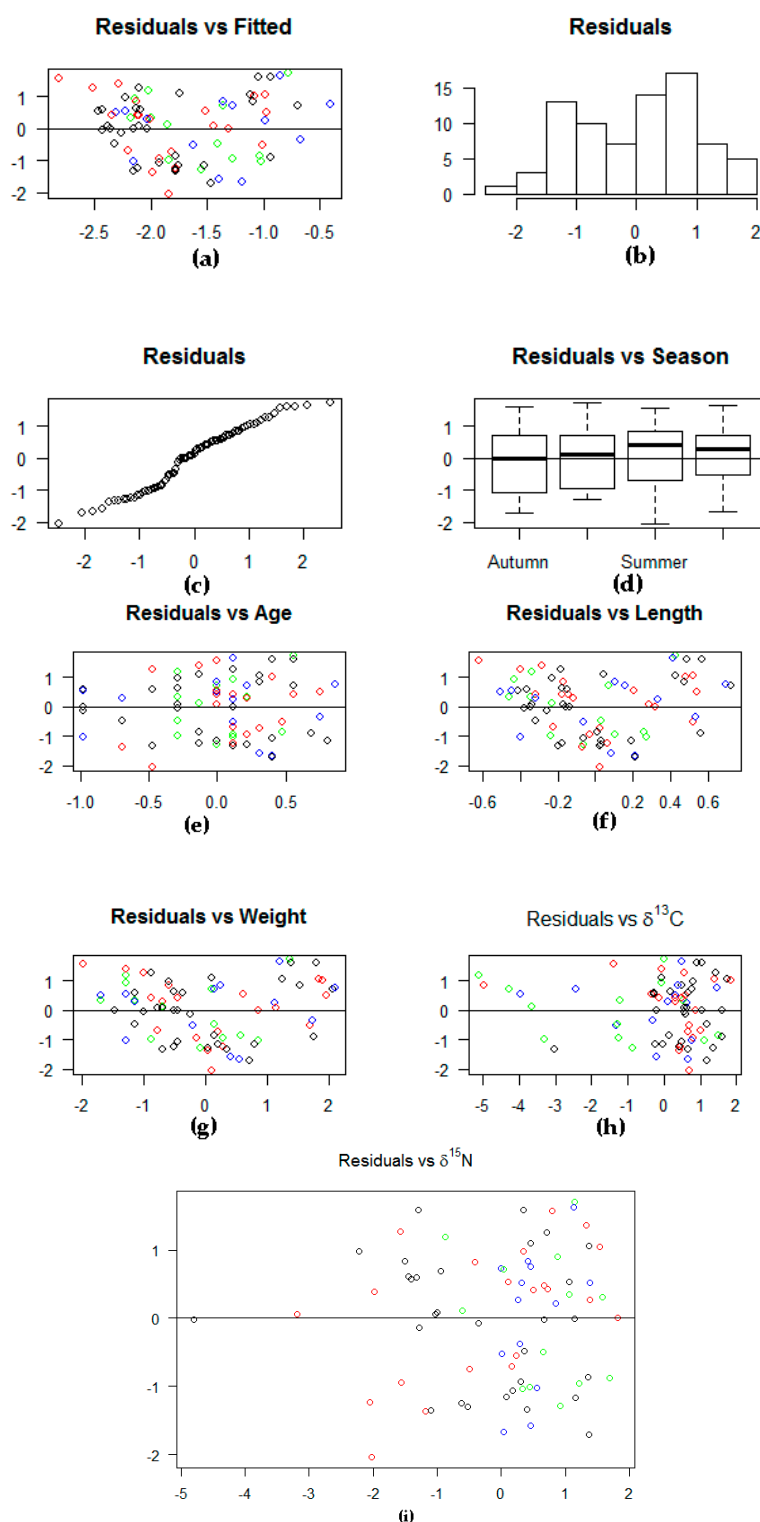
**Figure S2.** Residuals of the basic *A. charr* model not including  $\delta^{15}\text{N}$  as an explanatory variable. (a) Residuals plotted against fitted values show no sign of violation of the assumptions; (b) histogram showing resemblance to a normal distribution; (c) quantile comparison plot resembling a straight line, proving no serious divergence from a normal distribution; (d) residuals per season, indicating different variances per season, but proving adequately modelled seasonal means; (e) residuals show no correlation with age; (f) no correlation or residual pattern in relation to length; (g) no residual pattern or correlation in relation to weight; (h) residual pattern in relation to  $\delta^{13}\text{C}$ , as the residual variance increases with increasing  $\delta^{13}\text{C}$ ; (i) increasing residual variance was also found in relation to  $\delta^{15}\text{N}$ .

As similar residual patterns were detected for both stable isotope ratios, only  $\delta^{15}\text{N}$  was included as an additional explanatory variable at first. The partial linear regression between  $\delta^{15}\text{N}$  and Tot-Hg, however, was not significant. Adding  $\delta^{15}\text{N}$  to the model as a fixed effect results in similar residual patterns as for the model not including  $\delta^{15}\text{N}$  (Figure S3), but it also allows using  $\delta^{15}\text{N}$  as a variance-covariate in subsequent steps.



**Figure S3.** Residuals of the *A. charr* model including  $\delta^{15}\text{N}$  as explanatory variable; (a) plotted against fitted values, the residuals do not exhibit patterns; (b) the histogram resembles a normal distribution; (c) no serious divergence from a normal distribution was detected in the quantile comparison plot; (d) different residual variances per season can still be detected; (e) there is no residual pattern related to age; (f) length; (g) or weight; (h) residual variance is still increasing with increasing  $\delta^{13}\text{C}$  and; (i)  $\delta^{15}\text{N}$ .

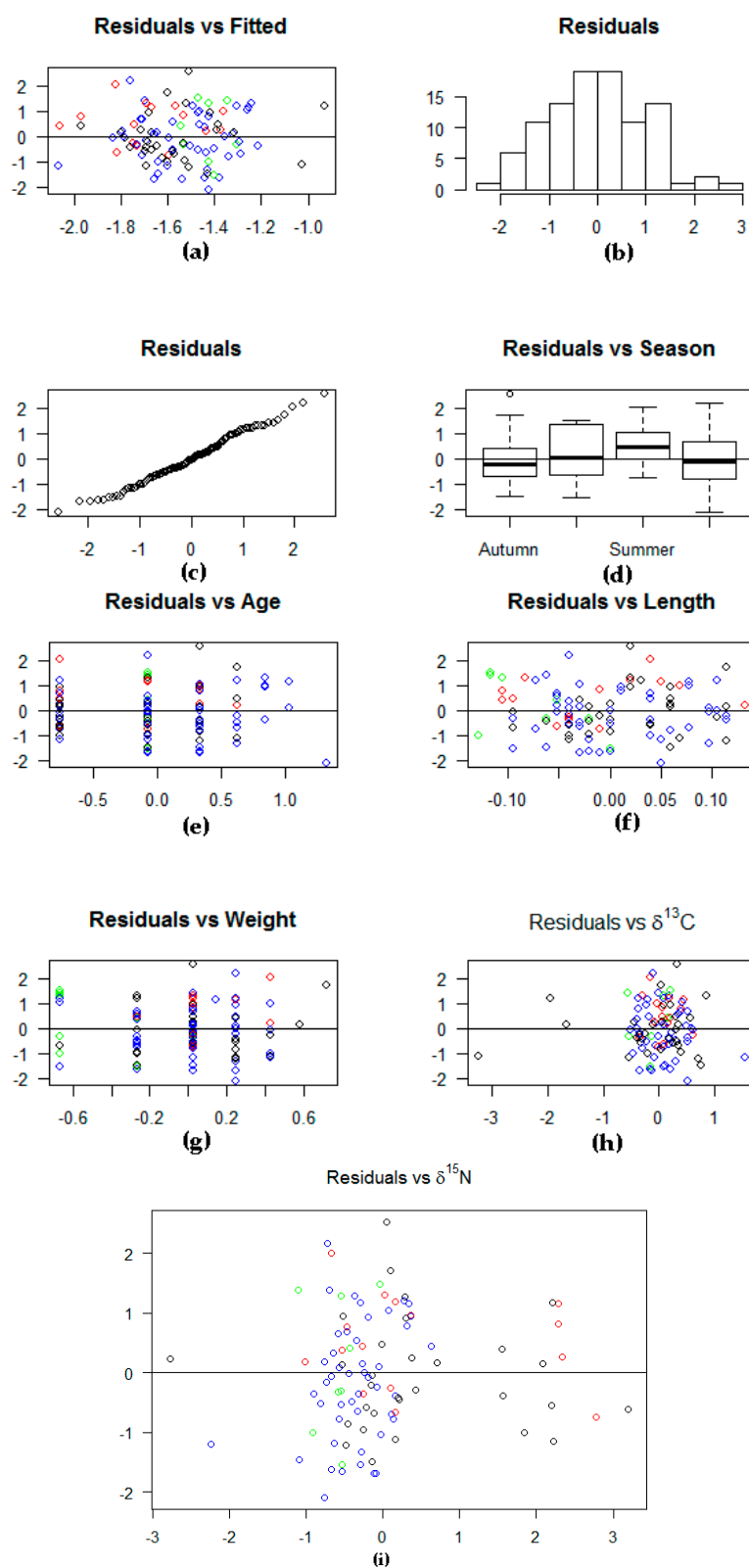
Including  $\delta^{15}\text{N}$  as a variance-covariate and allowing for different variances per season results in a superior model fit according to the AIC and likelihood ratio test, using REML-estimation. Both issues linked to different variances per season, and increasing residual variances with increasing  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$  are resolved (Figure S4).



**Figure S4.** Implementing a variance-covariate structure improves the A. charr model; (a) there is no residual pattern linked to fitted values; (b,c) the residual distribution does not seriously depart from a normal distribution; (d) all seasons exhibit similar residual variances; (e–g) there are no residual patterns linked to age, length and weight; (h,i) residual variances do not increase substantially with increasing  $\delta^{13}\text{C}$  or  $\delta^{15}\text{N}$ .

## 2.2. *E. Smelt Model*

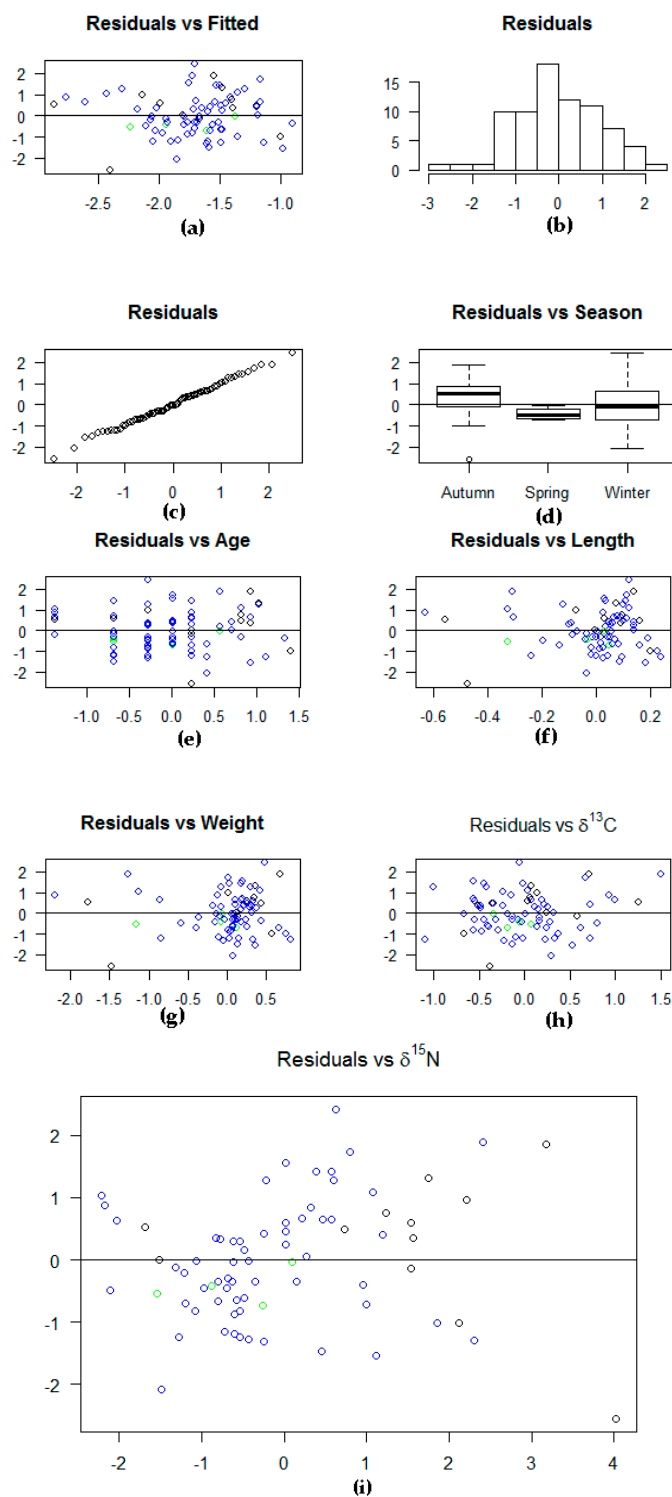
The basic model for *E. smelt*, including age, length, weight and  $\delta^{13}\text{C}$  as explanatory variables, exhibited no residual patterns of concern (Figure S5).



**Figure S5.** The residual patterns of the basic *E. smelt* models show no residual patterns of concern related to; (a) the fitted values; (b,c) normal distribution; (d) seasonal variance; (e–i) any of the possible explanatory variables.

### 2.3. Whitefish Model

The basic model for whitefish, including length, age and weight as explanatory variables, exhibited no serious residual issues (Figure S6). However, variances differ per season, as sample sizes are substantially different. This was not included in the model, as no seasonal differences in Tot-Hg-concentrations were detected for whitefish.



**Figure S6.** Residuals for the basic whitefish model reveal no concerns related to; (a) fitted values and; (b,c) normal distribution; (d) The variances differ with season, based on vastly different sample sizes; (e–i) exhibit no clear residual patterns in relation to any of the explanatory variables.

## Abbreviations

The following abbreviations are used in this manuscript:

|      |                               |
|------|-------------------------------|
| ML   | maximum likelihood            |
| REML | restricted maximum likelihood |



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