Mysis Preservation – Length-Weight Analysis for Manuscript

January 5, 2008

1 Length Analysis

1.1 Initialization

1.1.1 Data entry and cleaning

```
> mysis <- read.xls("Mysis_Data_Master.xls", sheet = "Mysis", colClasses = c("logical",
+     "logical", "factor", "logical", "logical", "factor", "factor", "numeric",
+     "factor", "factor", "isodate", "isotime", "factor", "factor", "factor",
+     "numeric", "numeric", "numeric", "numeric", "numeric", "numeric",
+     "numeric", "numeric", "factor"))
> mysisL <- mysis[mysis$include.L, ]
> mysis.len <- mysisL[mysisL$use.l, ]
> mysis.len$tx <- factor(mysis.len$tx)
> mysis.len$stage <- factor(mysis.len$stage)
> mysis.len$group <- mysis.len$stage:mysis.len$tx
> mysis.len$loss.p2w <- mysis.len$len.p2w - mysis.len$len.fr
> mysis.len$loss.p2m <- mysis.len$len.p2m - mysis.len$len.fr
> mysis.len$ploss.p2w <- mysis.len$loss.p2w/mysis.len$len.fr
> mysis.len$ploss.p2m <- mysis.len$loss.p2m/mysis.len$len.fr
```

Getting rid of juveniles – decided this from length-weight work – see below.

```
> mysis.len2 <- subset(mysis.len, stage != "Juv")
> mysis.len2$stage <- factor(mysis.len2$stage)
> mysis.len2$group <- factor(mysis.len2$group)
```

1.2 Sample Summaries

These results form Table R1 in the manuscript.

```
> attach(mysis.len2)
> ftable(xtabs(~tx + stage))
```

```
     stage Fem Male
tx
8BF          24   18
8SBF         15    8
```

```
> tapply(len.fr, stage:tx, Summary, na.rm = T)
```

```
$`Fem:8BF`
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.     StDev
 9.200000 10.000000 11.300000 12.200000 14.400000 16.000000  2.458964

$`Fem:8SBF`
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.     StDev
 8.300000  9.200000  9.600000 10.290000 10.400000 16.100000  1.974287

$`Male:8BF`
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.     StDev
10.400000 12.830000 13.150000 13.110000 14.170000 14.500000  1.277815

$`Male:8SBF`
      Min.    1st Qu.     Median       Mean    3rd Qu.       Max.      StDev
12.2000000 13.0200000 13.5500000 13.3100000 13.7000000 13.9000000  0.5792544
```

```
> tapply(loss.p2w, stage:tx, Summary, na.rm = T)
```

```
$`Fem:8BF`
      Min.    1st Qu.     Median       Mean    3rd Qu.       Max.      StDev
-0.6000000 -0.3250000 -0.2000000 -0.2125000 -0.1000000  0.2000000  0.1872281

$`Fem:8SBF`
      Min.    1st Qu.     Median       Mean    3rd Qu.       Max.      StDev
-0.3000000 -0.2000000 -0.1000000 -0.1000000  0.0000000  0.1000000  0.1362770

$`Male:8BF`
      Min.    1st Qu.     Median       Mean    3rd Qu.       Max.      StDev
-0.3000000 -0.2000000 -0.1000000 -0.1000000  0.0000000  0.1000000  0.1283378

$`Male:8SBF`
      Min.    1st Qu.     Median       Mean    3rd Qu.       Max.      StDev
-0.5000000 -0.2000000  0.0000000 -0.1000000  0.0250000  0.2000000  0.2618615
```

1.3 Results on Length After 2 Weeks Preservation

Most (63.1%) Mysids were shorter after two weeks of , while a small number (10.8%) actually appeared to be longer after preservation.

```
> p <- prop.table(table(round(loss.p2w, 1)))
> p
```

```
      -0.6       -0.5       -0.4       -0.3       -0.2       -0.1          0        0.1
0.01538462 0.04615385 0.06153846 0.13846154 0.20000000 0.16923077 0.26153846 0.07692308
       0.2
0.03076923
```

```
> sum(p[1:6])
```

```
[1] 0.6307692
```

```
> sum(p[8:9])
```

```
[1] 0.1076923
```

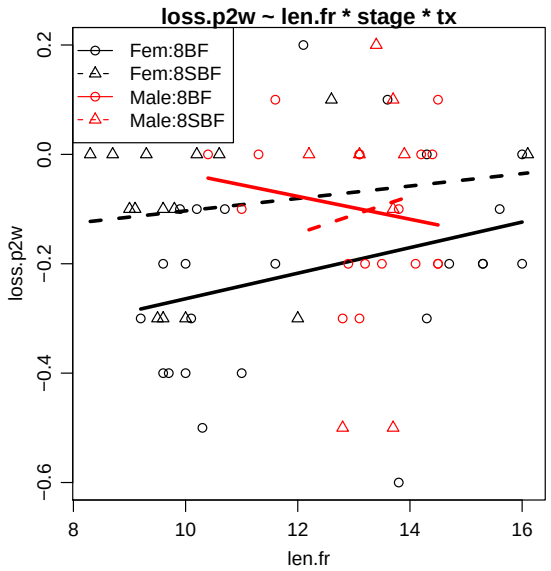
The change in standard length after two weeks of preservation was not significantly related to the fresh standard length measurement (p=0.2001) nor did it differ between male and female Mysids (p=0.1732). There was weak but insignificant evidence (p=0.0638) that Mysids preserved in 8% buffered formalin lost more length than Mysids preserved in 8% sugar-buffered formalin.

```
> lm2 <- lm(loss.p2w ~ len.fr * stage * tx)
> Anova(lm2)
```

```
Anova Table (Type II tests)

Response: loss.p2w
                Sum Sq Df F value  Pr(>F)
len.fr          0.05080  1  1.6752 0.20078
stage           0.05768  1  1.9023 0.17321
tx              0.10837  1  3.5740 0.06378 .
len.fr:stage    0.03731  1  1.2305 0.27196
len.fr:tx       0.00300  1  0.0988 0.75445
stage:tx        0.03503  1  1.1551 0.28701
len.fr:stage:tx 0.00920  1  0.3036 0.58381
Residuals       1.72835 57
---
Signif. codes:  0 Ś***Š 0.001 Ś**Š 0.01 Ś*Š 0.05 Ś.Š 0.1 Ś Š 1
```

The folowing plot is NOT in the manuscript.

```
> fit.plot(lm2, legend = "topleft")
```



Thus, regardless of fresh standard length, life stage or preservation type, Mysids lost an average of 0.14 mm (95% CI: 0.10,0.19).

```
> t.test(loss.p2w)


        One Sample t-test

data:  loss.p2w
t = -6.4265, df = 64, p-value = 1.865e-08
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.18553658 -0.09754035
sample estimates:
 mean of x
-0.1415385


> detach(mysis.len2)
```

2 Length-Weight Analysis

2.1 Initialization

2.1.1 Data entry and cleaning

```
> mysis <- read.xls("Mysis_Data_Master.xls", sheet = "Mysis")
> mysis$c.wt <- mysis$c.wt * 1000
> mysis1 <- mysis[mysis$include.LW, ]
> mysis2 <- mysis1[mysis1$use.lw == TRUE, ]
> mysis2$logwt <- log10(mysis2$c.wt)
> mysis2$loglen <- log10(mysis2$len)
> mysis2$treat <- mysis2$tx:mysis2$stage
```

`mysis2` is now the cleaned and ready data frame.

2.1.2 declare some labels

```
> xlbl1 <- "Standard Length (mm)"
> xlbl2 <- "log(Standard Length (mm))"
> ylbl1 <- "Dry Weight (mg)"
> ylbl2 <- "log(Dry Weight (mg))"
```

2.2 EDA

2.2.1 Original data

None of this section is in the manuscript. Note (1) that gravid-8BF are missing and (2) increased variance at small lengths on log-log scale. This led to the exclusion of juveniles – problem with weights of small specimens.

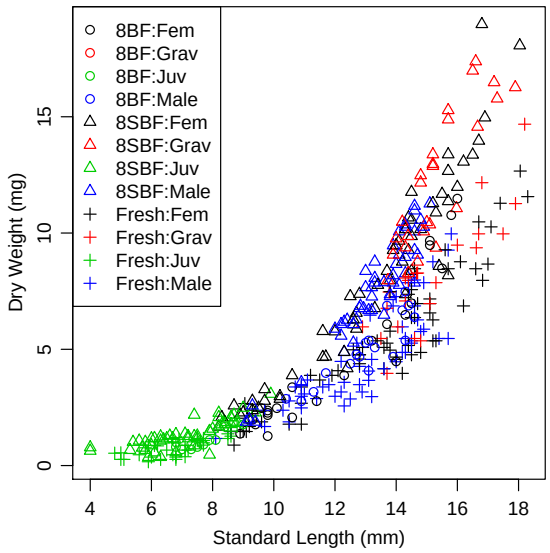
```
> attach(mysis2)
> ftable(xtabs(~tx + stage + len.bin))
```

```
            len.bin  3  5  7  9 11 13 15 17
tx    stage
8BF   Fem            0  0  1 11  2  5  5  0
      Grav           0  0  0  0  0  0  0  0
      Juv            0  2  9  1  0  0  0  0
      Male           0  0  0  2  5 11  0  0
8SBF  Fem            0  0  4 10 12 19 14  1
      Grav           0  0  0  0  0 12 12  3
      Juv            2 20 23  3  0  0  0  0
      Male           0  0  0  5 12 32  1  0
Fresh Fem            0  0  3 11 10 19 13  5
      Grav           0  0  0  0  1 12  6  3
      Juv            1 19 16  0  0  0  0  0
      Male           0  0  2  9 15 23  5  0
```

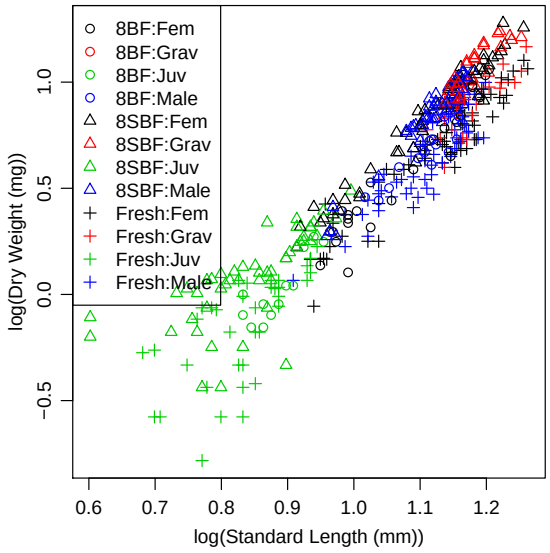
```
> ftable(xtabs(~tx + stage))
```

```
      stage Fem Grav Juv Male
tx
8BF            24    0  12   18
8SBF           60   27  48   50
Fresh          61   22  37   54
```

```
> plot(c.wt ~ len, pch = as.numeric(tx), col = as.numeric(stage), xlab = xlbl1,
+     ylab = ylbl1)
> legend(x = "topleft", legend = levels(tx:stage), col = rep(seq(1, 4),
+     3), pch = rep(seq(1, 4), each = 4))
```



```
> plot(logwt ~ loglen, pch = as.numeric(tx), col = as.numeric(stage),
+     xlab = xlbl2, ylab = ylbl2)
> legend(x = "topleft", legend = levels(tx:stage), col = rep(seq(1, 4),
+     3), pch = rep(seq(1, 4), each = 4))
> detach(mysis2)
```



2.2.2 Permanently Remove Juveniles

```
> mysis3 <- mysis2[mysis2$stage != "Juv", ]
> mysis3$stage <- factor(mysis3$stage)
> mysis3$treat <- factor(mysis3$treat)
> attach(mysis3)
```

`mysis3` is now the cleaned and ready data frame

These results are not in the manuscript – just double-checking that juveniles have been removed.

```
> ftable(xtabs(~tx + stage + len.bin))
```

```
             len.bin  7  9 11 13 15 17
tx    stage
8BF   Fem            1 11  2  5  5  0
      Grav           0  0  0  0  0  0
      Male           0  2  5 11  0  0
8SBF  Fem            4 10 12 19 14  1
      Grav           0  0  0 12 12  3
      Male           0  5 12 32  1  0
Fresh Fem            3 11 10 19 13  5
      Grav           0  0  1 12  6  3
      Male           2  9 15 23  5  0
```

The following results form Table R2 in the manuscript.

```
> ftable(xtabs(~tx + stage))
```

```
      stage Fem Grav Male
tx
8BF          24    0   18
8SBF         60   27   50
Fresh        61   22   54
```

```
> tapply(len, stage:tx, Summary, na.rm = T)
```

```
$`Fem:8BF`
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.     StDev
 8.900000  9.800000 11.000000 11.990000 14.350000 16.000000  2.522752

$`Fem:8SBF`
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.     StDev
 8.200000 11.600000 13.850000 13.150000 14.900000 18.040000  2.541817

$`Fem:Fresh`
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.     StDev
 8.600000 11.500000 13.800000 13.420000 15.100000 18.300000  2.611002

$`Grav:8BF`
NULL

$`Grav:8SBF`
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.     StDev
13.730000 14.390000 15.100000 15.280000 15.840000 17.890000  1.125171

$`Grav:Fresh`
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.     StDev
12.900000 14.110000 14.680000 15.160000 16.460000 18.200000  1.517133

$`Male:8BF`
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.     StDev
10.400000 12.550000 13.100000 13.010000 14.120000 14.600000  1.257396

$`Male:8SBF`
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.     StDev
 9.100000 12.620000 13.300000 13.180000 14.250000 15.100000  1.473647

$`Male:Fresh`
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.     StDev
 8.100000 11.450000 13.100000 12.870000 14.470000 15.800000  1.890991
```

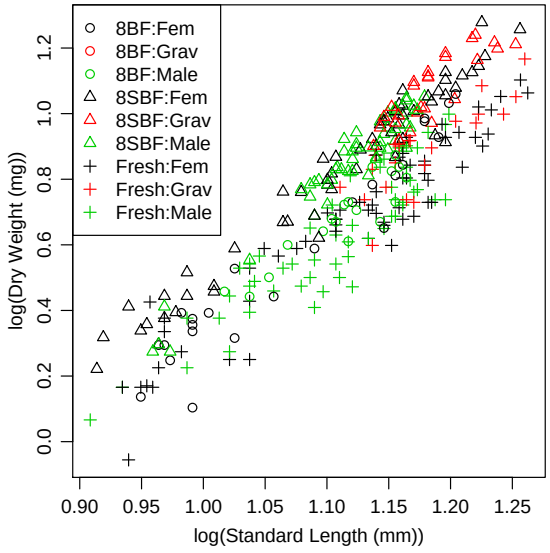
```
> tapply(c.wt, stage:tx, Summary, na.rm = T)
```

```
$`Fem:8BF`
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.     StDev
 1.270000  2.145000  3.070000  4.644000  6.605000 11.480000  3.246756

$`Fem:8SBF`
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.     StDev
 1.665000  4.544000  8.073000  7.877000 10.590000 18.980000  4.141679
```

```
$`Fem:Fresh`
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.     StDev
 0.880000  3.880000  5.080000  5.456000  7.165000 12.660000  2.783356

$`Grav:8BF`
NULL

$`Grav:8SBF`
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.     StDev
 7.965000  9.615000 11.060000 12.070000 14.720000 17.380000  2.952271

$`Grav:Fresh`
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.     StDev
 3.965000  6.165000  7.915000  8.081000  9.451000 14.680000  2.512076

$`Male:8BF`
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max.    StDev
2.770000 4.155000 4.930000 5.045000 6.130000 7.480000 1.407255

$`Male:8SBF`
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.     StDev
 1.880000  6.269000  7.715000  7.445000  9.040000 11.270000  2.344641

$`Male:Fresh`
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max.    StDev
1.165000 3.005000 4.215000 4.628000 5.840000 9.965000 2.098266
```

The following figure is NOT in the manuscript.

```
> plot(logwt ~ loglen, pch = as.numeric(tx), col = as.numeric(stage),
+     xlab = xlbl2, ylab = ylbl2)
> legend(x = "topleft", legend = levels(tx:stage), col = rep(seq(1, 3),
+     3), pch = rep(seq(1, 3), each = 3))
> detach(mysis3)
```



2.3 First Length-Weight Model Analysis

The first model examined the effect of all three preservation treatments and two life stages (males and females) on the L-W relationship.

2.3.1 Temporarily excludes gravids

None of these results are in the manuscript.

```
> mysis3.nograv <- mysis3[mysis3$stage != "Grav", ]
> mysis3.nograv$stage <- factor(mysis3.nograv$stage)
> mysis3.nograv$treat <- factor(mysis3.nograv$treat)
> attach(mysis3.nograv)
> ftable(xtabs(~tx + stage + len.bin))
```

```
            len.bin  7  9 11 13 15 17
tx    stage
8BF   Fem            1 11  2  5  5  0
      Male           0  2  5 11  0  0
8SBF  Fem            4 10 12 19 14  1
      Male           0  5 12 32  1  0
Fresh Fem            3 11 10 19 13  5
      Male           2  9 15 23  5  0
```

2.3.2 Fitting The Model

```
> lm1 <- lm(logwt ~ loglen * tx * stage)
```

Assumption Checking

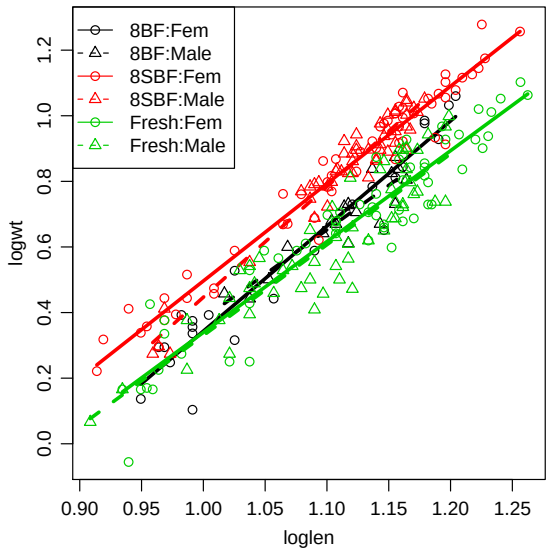
None of these results are in the manuscript. The normality test and non-constant variance test both indicate assumption violations. However, the residual plot shows a general homoscedasticity (with the exception of two minor outliers and a small narrowing at large lengths) and the histogram is largely symmetric.

```
> fit.plot(lm1, leg = "topleft", main = "")
> ad.test(lm1$residuals)
```

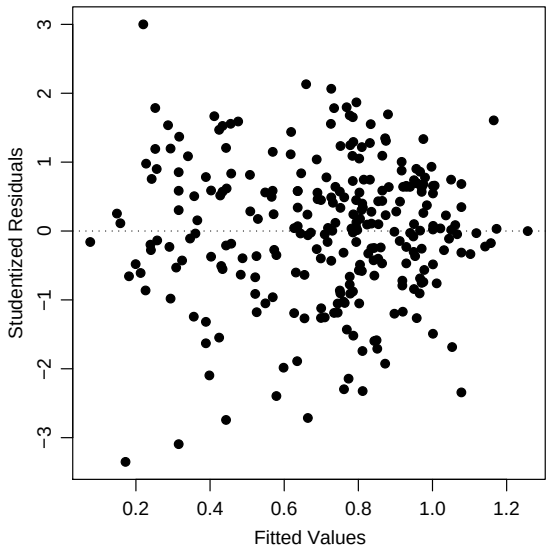
```
        Anderson-Darling normality test

data:  lm1$residuals
A = 0.8453, p-value = 0.02923
```

```
> ncv.test(lm1)
```

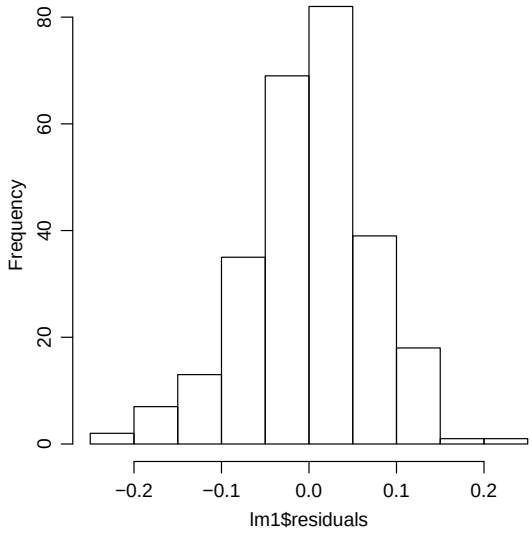
```
Non-constant Variance Score Test
Variance formula: ~ fitted.values
Chisquare = 10.80524    Df = 1     p = 0.00101213
```




```
> residual.plot(lm1, main = "")
```




```
> hist(lm1$residuals, main = "")
```



Results

The first linear model fit to males and females and all three preservation treatments showed that there was a significant difference in slope among the three preservation treatments (p=0.0213) but not among the two life-stages (p=0.4457).

The mean log(weight) adjusted for log(length) did not differ among male and females (p=0.4038).

```
> Anova(lm1)


Anova Table (Type II tests)

Response: logwt
                Sum Sq  Df   F value  Pr(>F)
loglen          13.5407   1 2593.5986 < 2e-16 ***
tx               1.9385   2  185.6499 < 2e-16 ***
stage            0.0037   1    0.6992 0.40382
loglen:tx        0.0408   2    3.9089 0.02128 *
loglen:stage     0.0030   1    0.5835 0.44567
tx:stage         0.0010   2    0.0943 0.91005
loglen:tx:stage  0.0215   2    2.0626 0.12923
Residuals        1.3313 255
---
Signif. codes:  0 Ś***Š 0.001 Ś**Š 0.01 Ś*Š 0.05 Ś.Š 0.1 Ś Š 1
```

Post hoc multiple comparisons indicated that the 8% buffered formalin and 8% sugar-buffered formalin treatments had statistically similar slopes (p=0.7974) that were significantly steeper than the slope of the fresh preserved treatment (p<0.0798).

```
> comp.slopes(lm1)


Multiple comparison control procedures used: fdr
```

```
Multiple Slope Comparisons
  comparison     diff      lwr      upr   raw.p   adj.p
1   8SBF-8BF -0.04466 -0.38690  0.29758 0.79743 0.79743
2  Fresh-8BF -0.33003 -0.66463  0.00456 0.05318 0.07977
3 Fresh-8SBF -0.28538 -0.53023 -0.04053 0.02253 0.06759

Slope Information
  level  slopes     lwr     upr raw.p adj.p
3 Fresh 2.77462 2.60912 2.94011     0     0
2  8SBF 3.06000 2.87954 3.24045     0     0
1   8BF 3.10465 2.81385 3.39545     0     0
```

Removed fresh treatment and fit a model with males and females combined to see if there was a difference in intercepts between the 8% buffered formalin and 8% sugar buffered formalin group.

```
> detach(mysis3.nograv)
> mysis3.nograv.nofresh <- mysis3.nograv[mysis3.nograv$tx != "Fresh",
+     ]
> mysis3.nograv.nofresh$tx <- factor(mysis3.nograv.nofresh$tx)
> attach(mysis3.nograv.nofresh)
> lm1a <- lm(logwt ~ loglen + tx)
```

Further comparisons indicated that the 8% sugar-buffered formalin treatment had a larger mean log(weight) than the 8% buffered formalin treatment for all values of log(length) ($p<0.0005$).

```
> anova(lm1a)


Analysis of Variance Table

Response: logwt
           Df Sum Sq Mean Sq F value    Pr(>F)
loglen      1 8.9499  8.9499 2647.80 < 2.2e-16 ***
tx          1 0.5505  0.5505  162.86 < 2.2e-16 ***
Residuals 149 0.5036  0.0034
---
Signif. codes:  0 Ś***Š 0.001 Ś**Š 0.01 Ś*Š 0.05 Ś.Š 0.1 Ś Š 1


> comp.intercepts(lm1a)


Tukey HSD on adjusted means assuming parallel lines.
  comparison      diff       lwr       upr p.adj
1   8SBF-8BF 0.1360738 0.1153065 0.1568411     0

Mean adjusted values at a covariate value of 1.10621751474566
      8BF      8SBF
0.6738179 0.8098917


> detach(mysis3.nograv.nofresh)
```

2.4 Second Length-Weight Model Analysis

The second model examined the effect of two preservation treatments (fresh preserved and 8

2.4.1 Temporarily Excludes 8% Buffered Formaling Treatment

```
> mysis3.no8BF <- mysis3[mysis3$tx != "8BF", ]
> mysis3.no8BF$stage <- factor(mysis3.no8BF$stage)
> mysis3.no8BF$tx <- factor(mysis3.no8BF$tx)
> mysis3.no8BF$treat <- factor(mysis3.no8BF$treat)
> attach(mysis3.no8BF)
> ftable(xtabs(~tx + stage + len.bin))
```

```
            len.bin  7  9 11 13 15 17
tx    stage
8SBF  Fem            4 10 12 19 14  1
      Grav           0  0  0 12 12  3
      Male           0  5 12 32  1  0
Fresh Fem            3 11 10 19 13  5
      Grav           0  0  1 12  6  3
      Male           2  9 15 23  5  0
```

2.4.2 Fitting The Model

```
> lm2 <- lm(logwt ~ loglen * tx * stage)
```

Assumption Checking

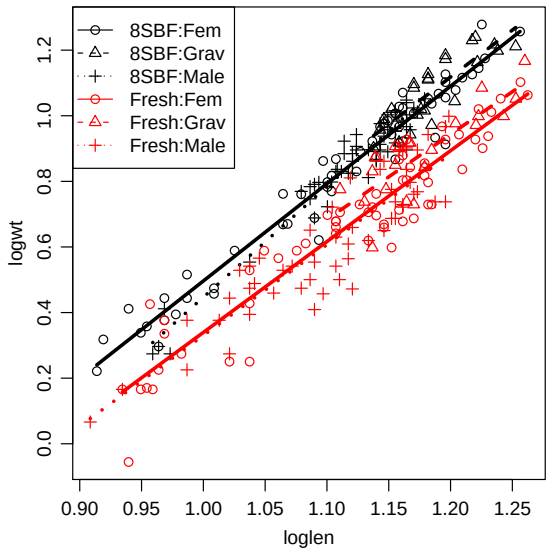
None of these results are in the manuscript. The normality test and non-constant variance test both indicate assumption violations. However, the residual plot shows a general homoscedasticity (with the exception of two minor outliers and a small narrowing at large lengths) and the histogram is largely symmetric.

```
> fit.plot(lm2, leg = "topleft", main = "")
> ad.test(lm2$residuals)
```

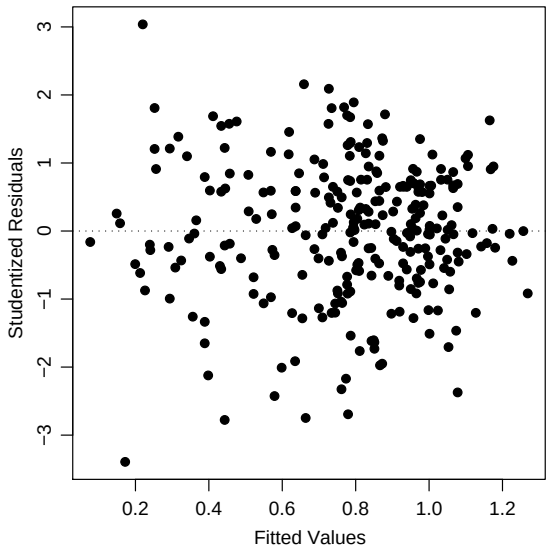
```
        Anderson-Darling normality test

data:  lm2$residuals
A = 0.6848, p-value = 0.07297
```

```
> ncv.test(lm2)
```

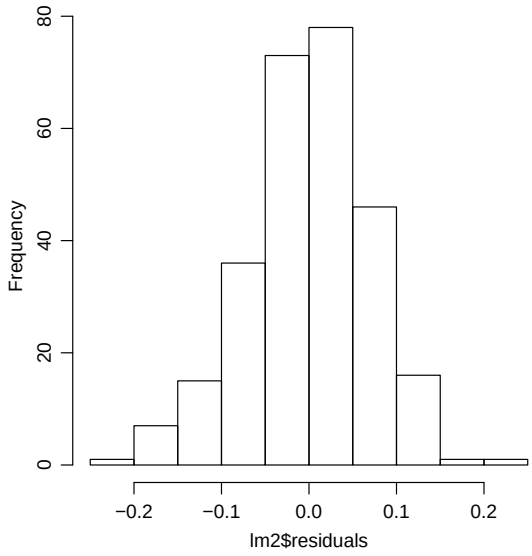
```
Non-constant Variance Score Test
Variance formula: ~ fitted.values
Chisquare = 13.57363    Df = 1     p = 0.0002293850
```




```
> residual.plot(lm2, main = "")
```




```
> hist(lm2$residuals, main = "")
```



Results

The second linear model fit to all three life-stages and the fresh preserved and 8% sugar-buffered formalin treatments showed that there was a significantly steeper slope for the 8% sugar-buffered formalin treatment (p=0.012) but no difference in slope among the three life-stages (0.4124).

```
> Anova(lm2)


Anova Table (Type II tests)

Response: logwt
               Sum Sq  Df   F value    Pr(>F)
loglen         11.8507   1 2326.8062 < 2.2e-16 ***
tx              2.1941   1  430.7889 < 2.2e-16 ***
stage           0.0605   2    5.9392  0.003002 **
loglen:tx       0.0326   1    6.4052  0.011965 *
loglen:stage    0.0091   2    0.8888  0.412395
tx:stage        0.0103   2    1.0138  0.364265
loglen:tx:stage 0.0108   2    1.0634  0.346778
Residuals       1.3344 262
---
Signif. codes:  0 Ś***Š 0.001 Ś**Š 0.01 Ś*Š 0.05 Ś.Š 0.1 Ś Š 1


> comp.slopes(lm2)


Multiple comparison control procedures used: fdr

Multiple Slope Comparisons
  comparison     diff      lwr      upr   raw.p   adj.p
1 Fresh-8SBF -0.25238 -0.47839 -0.02638 0.02876 0.02876
```

```
Slope Information
  level  slopes     lwr     upr raw.p adj.p
2 Fresh 2.84961 2.69511 3.00411     0     0
1  8SBF 3.10199 2.93705 3.26694     0     0
```

Within a preservation treatment there was a significant difference in mean log(weight) adjusted for log(length) (0.0241) with gravid females being significantly heavier than male or non-gravid females for all values of log(length) (p<0.0336).

```
> lm2a <- lm(logwt ~ loglen + stage)
> anova(lm2a)


Analysis of Variance Table

Response: logwt
           Df  Sum Sq Mean Sq   F value  Pr(>F)
loglen      1 14.4866 14.4866 1085.5607 < 2e-16 ***
stage       2  0.1009  0.0504    3.7795 0.02405 *
Residuals 270  3.6031  0.0133
---
Signif. codes:  0 Ś***Š 0.001 Ś**Š 0.01 Ś*Š 0.05 Ś.Š 0.1 Ś Š 1


> comp.intercepts(lm2a)


Tukey HSD on adjusted means assuming parallel lines.
  comparison         diff          lwr          upr      p.adj
1   Grav-Fem  0.049036498  0.003022977  0.095050020 0.03361352
2   Male-Fem -0.007539737 -0.043875446  0.028795972 0.87659483
3  Male-Grav -0.056576235 -0.103661253 -0.009491217 0.01375084

Mean adjusted values at a covariate value of 1.12492564403163
      Fem      Grav      Male
0.7755453 0.8245818 0.7680056


> detach(mysis3.no8BF)
```

2.5 Length-Weight Regressions for Different Groups

2.5.1 Males and Females in Fresh Group

This isolates just the fresh treatment and creates a stage variable that has gravid females and males/females combined. It then fits a model with a common slope and separate intercepts by the new stage variable.

```
> mysis3.fresh <- mysis3[mysis3$tx == "Fresh", ]
> mysis3.fresh$stage1 <- factor(ifelse(mysis3.fresh$stage == "Grav", "Grav",
+     "MF"))
> mysis3.fresh$tx <- factor(mysis3.fresh$tx)
> attach(mysis3.fresh)
> lm3.fresh <- lm(logwt ~ loglen + stage1)
> summary(lm3.fresh)
```

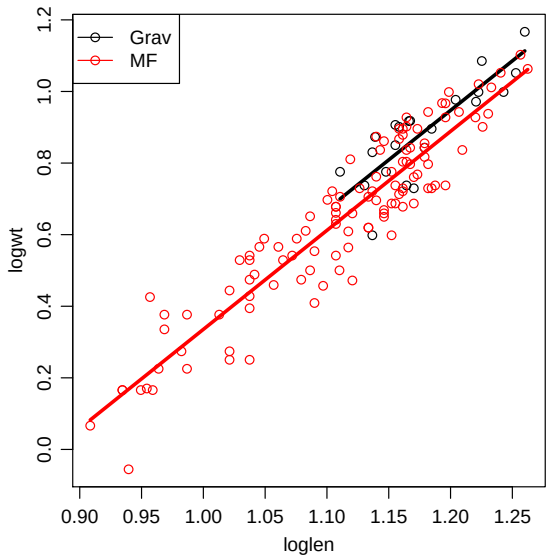
```
Call:
lm(formula = logwt ~ loglen + stage1)

Residuals:
      Min        1Q    Median        3Q       Max
-0.223649 -0.059177  0.007352  0.063210  0.209712

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -2.37190    0.11558 -20.522  < 2e-16 ***
loglen       2.76585    0.09684  28.562  < 2e-16 ***
stage1MF    -0.05854    0.02087  -2.806  0.00577 **
---
Signif. codes:  0 Ś***Š 0.001 Ś**Š 0.01 Ś*Š 0.05 Ś.Š 0.1 Ś Š 1

Residual standard error: 0.0853 on 134 degrees of freedom
Multiple R-Squared: 0.878,        Adjusted R-squared: 0.8762
F-statistic: 482.4 on 2 and 134 DF,  p-value: < 2.2e-16
```

Thus, the equations of the lines are (these are in the manuscript)...

- Fresh,MF: $log_{10}(W)$ = -2.4304 + 2.7659$log_{10}(L)$
- Fresh,Gravid: $log_{10}(W)$ = -2.3719 + 2.7659$log_{10}(L)$

The following is not in the manuscript – just a visual check

```
> fit.plot(lm3.fresh, main = "", leg = "topleft")
```




```
> detach(mysis3.fresh)
```

2.5.2 Males and Females in Fresh Group

This isolates the 8BF and 8SBF groups (excludes fresh) and combines males and females as above. It then fits the linear model with a common slope and separate intercepts.

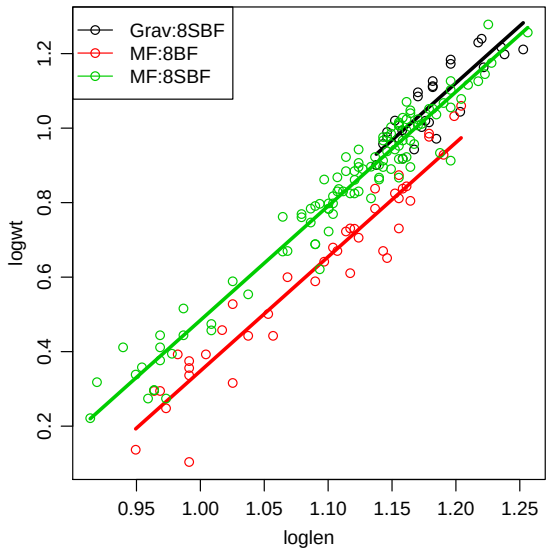
```
> mysis3.nfresh <- mysis3[mysis3$tx != "Fresh", ]
> mysis3.nfresh$stage1 <- factor(ifelse(mysis3.nfresh$stage == "Grav",
+     "Grav", "MF"))
> mysis3.fresh$tx <- factor(mysis3.fresh$tx)
> mysis3.nfresh$treat1 <- factor(mysis3.nfresh$stage1:mysis3.nfresh$tx)
> attach(mysis3.nfresh)
> lm3.nfresh <- lm(logwt ~ loglen + treat1)
> summary(lm3.nfresh)


Call:
lm(formula = logwt ~ loglen + treat1)

Residuals:
      Min        1Q    Median        3Q       Max
-0.217285 -0.029277  0.003547  0.043603  0.112868

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)   -2.55867    0.07330 -34.906   <2e-16 ***
loglen         3.06650    0.06124  50.071   <2e-16 ***
treat1MF:8BF  -0.15985    0.01536 -10.406   <2e-16 ***
treat1MF:8SBF -0.02362    0.01310  -1.804    0.073 .
---
Signif. codes:  0 Ś***Š 0.001 Ś**Š 0.01 Ś*Š 0.05 Ś.Š 0.1 Ś Š 1

Residual standard error: 0.05762 on 175 degrees of freedom
Multiple R-Squared: 0.9528,        Adjusted R-squared: 0.952
F-statistic:  1178 on 3 and 175 DF,  p-value: < 2.2e-16
```

Thus, the equations of the lines are (these are in the manuscript)...

- 8BF,MF: $log_{10}(W)$ = -2.7185 + 3.0665$log_{10}(L)$
- 8SBF,MF: $log_{10}(W)$ = -2.5823 + 3.0665$log_{10}(L)$
- 8SBF,Gravid: $log_{10}(W)$ = -2.5587 + 3.0665$log_{10}(L)$

The following is not in the manuscript, it is just a visual and computational check.

```
> comp.intercepts(lm3.nfresh, 0)


Tukey HSD on adjusted means assuming parallel lines.
         comparison        diff        lwr          upr        p.adj
1  MF:8BF-Grav:8SBF -0.15984574 -0.1933487 -0.126342799 6.061818e-14
2 MF:8SBF-Grav:8SBF -0.02362329 -0.0527940  0.005547414 1.376686e-01
3    MF:8SBF-MF:8BF  0.13622245  0.1115867  0.160858192 4.918288e-14

Mean adjusted values at a covariate value of 0
Grav:8SBF    MF:8BF   MF:8SBF
-2.558665 -2.718511 -2.582288


> fit.plot(lm3.nfresh, main = "", leg = "topleft")
```




```
> detach(mysis3.nfresh)
```

2.5.3 R-square For Above Equations

The R^2 for the above equations can be computed easily by exploiting the fact that the R^2 for an equation can be computed with the R^2 between the observed response values and the predicted response values from the equation.

Begin by isolating the data for each of the five different groups.

```
> mysis4 <- mysis3
> mysis4$stage1 <- factor(ifelse(mysis4$stage == "Grav", "Grav", "MF"))
> data.Fmf <- subset(mysis4, stage1 == "MF" & tx == "Fresh")
> data.Fg <- subset(mysis4, stage1 == "Grav" & tx == "Fresh")
> data.8Bmf <- subset(mysis4, stage1 == "MF" & tx == "8BF")
> data.8Smf <- subset(mysis4, stage1 == "MF" & tx == "8SBF")
> data.8Sg <- subset(mysis4, stage1 == "Grav" & tx == "8SBF")
```

Then find predicted $\log_{10}(W)$ for each group

```
> pred.Fmf <- 2.7659 * data.Fmf$loglen - 2.4304
> pred.Fg <- 2.7659 * data.Fg$loglen - 2.3719
> pred.8Bmf <- 3.0665 * data.8Bmf$loglen - 2.7185
> pred.8Smf <- 3.0665 * data.8Smf$loglen - 2.5823
> pred.8Sg <- 3.0665 * data.8Sg$loglen - 2.5587
```

Then compute regressions

```
> lm.Fmf <- lm(pred.Fmf ~ data.Fmf$logwt)
> lm.Fg <- lm(pred.Fg ~ data.Fg$logwt)
> lm.8Bmf <- lm(pred.8Bmf ~ data.8Bmf$logwt)
> lm.8Smf <- lm(pred.8Smf ~ data.8Smf$logwt)
> lm.8Sg <- lm(pred.8Sg ~ data.8Sg$logwt)
```

And then extract R^2 values

```
> summary(lm.Fmf)$r.squared
```

```
[1] 0.8688818
```

```
> summary(lm.Fg)$r.squared
```

```
[1] 0.6865749
```

```
> summary(lm.8Bmf)$r.squared
```

```
[1] 0.9206869
```

```
> summary(lm.8Smf)$r.squared
```

```
[1] 0.9501737
```

```
> summary(lm.8Sg)$r.squared
```

```
[1] 0.7329088
```

For comparison purposes, the following is the R^2 from the fit of the linear model just to the Fresh,MF group. This is on the raw data, as if the model was fit to just this group, and is not used in the manuscript.

```
> lm.Fmf1 <- lm(data.Fmf$logwt ~ data.Fmf$loglen)
> coef(lm.Fmf1)
```

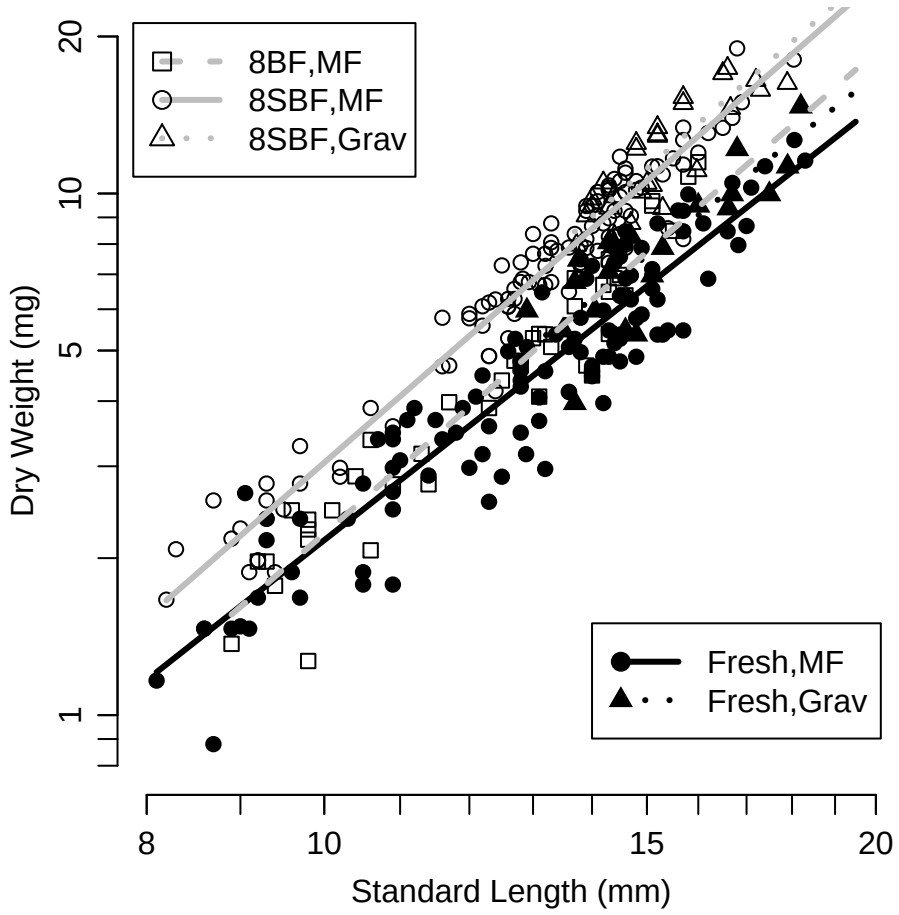
```
    (Intercept) data.Fmf$loglen
      -2.440190        2.774618
```

```
> summary(lm.Fmf1)$r.squared
```

```
[1] 0.8688818
```

2.5.4 The Plot for the Manuscript

```
> plot(mysis4$c.wt ~ mysis4$len, log = "xy", col = "white", axes = FALSE,
+     xlab = xlbl1, ylab = ylbl1, xlim = c(8, 20), ylim = c(0.8, 20))
> axis(2, at = c(0.8, 0.9, seq(1, 10, by = 1), 20), labels = F)
> axis(2, at = c(1, 5, 10, 20), labels = T)
> axis(1, at = c(8:20), labels = F)
> axis(1, at = c(8, 10, 15, 20), labels = T)
> points(data.Fmf$c.wt ~ data.Fmf$len, col = "black", pch = 19)
> points(data.Fg$c.wt ~ data.Fg$len, col = "black", pch = 17, cex = 1.25)
> points(data.8Bmf$c.wt ~ data.8Bmf$len, col = "black", pch = 0)
> points(data.8Smf$c.wt ~ data.8Smf$len, col = "black", pch = 1)
> points(data.8Sg$c.wt ~ data.8Sg$len, col = "black", pch = 2)
> lines(c(8.1, 19.5), 10^c(2.7659 * log10(8.1) - 2.4304, 2.7659 * log10(19.5) -
+     2.4304), lwd = 3, col = "black", lty = 1)
> lines(c(12.9, 19.5), 10^c(2.7659 * log10(12.9) - 2.3719, 2.7659 * log10(19.5) -
+     2.3719), lwd = 3, col = "black", lty = 3)
> lines(c(8.9, 19.5), 10^c(3.0665 * log10(8.9) - 2.7185, 3.0665 * log10(19.5) -
+     2.7185), lwd = 3, col = "gray", lty = 2)
> lines(c(8.2, 19.5), 10^c(3.0665 * log10(8.2) - 2.5823, 3.0665 * log10(19.5) -
+     2.5823), lwd = 3, col = "gray", lty = 1)
> lines(c(13.7, 19.5), 10^c(3.0665 * log10(13.7) - 2.5587, 3.0665 * log10(19.5) -
+     2.5587), lwd = 3, col = "gray", lty = 3)
> legend(x = 14, y = 1.5, legend = c("Fresh,MF", "Fresh,Grav"), lty = c(1,
+     3), lwd = 3, inset = 0.02)
> legend(x = 14, y = 1.5, legend = c("", ""), pch = c(19, 17), pt.cex = 1.25,
+     inset = 0.02, bty = "n")
> legend("topleft", legend = c("8BF,MF", "8SBF,MF", "8SBF,Grav"), lty = c(2,
+     1, 3), lwd = 3, col = "gray", inset = 0.02)
> legend("topleft", legend = c("", "", ""), pch = c(0, 1, 2), pt.cex = 1.25,
+     inset = 0.02, bty = "n")
```


8BF,MF
8SBF,MF
8SBF,Grav
Fresh,MF
Fresh,Grav
Dry Weight (mg)
1
5
10
20
8
10
15
20
Standard Length (mm)