Statistical analyses for ‘Characterization of a Southern Ocean deep chlorophyll maximum: response of phytoplankton to light, iron, and manganese enrichment’

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Contents

```r
setwd("C:/Users/platour/OneDrive - University of Tasmania/PhD/SOLACE/2SOLTEE analysis/Rmarkdown")
library(tidyverse)
library(lme4)
library(MuMIn)
library(ggplot2)
```

```
library(report)
library(kableExtra)
library(sjPlot)
library(emmeans)
library(visreg)
```

1 Background

This R markdown document shows the detailed results of the statistical analyses on our manuscript: ‘Characterization of a Southern Ocean deep chlorophyll maximum: response of phytoplankton to light, iron, and manganese enrichment’. To study the effect of changing iron, manganese and light conditions on deep phytoplankton communities, we performed linear mixed effect models on R. We then used the function ‘drop1’ to choose the best model fit. All data were log-transformed before analyses in order to normalize model residuals. The R code and output results can be found below.

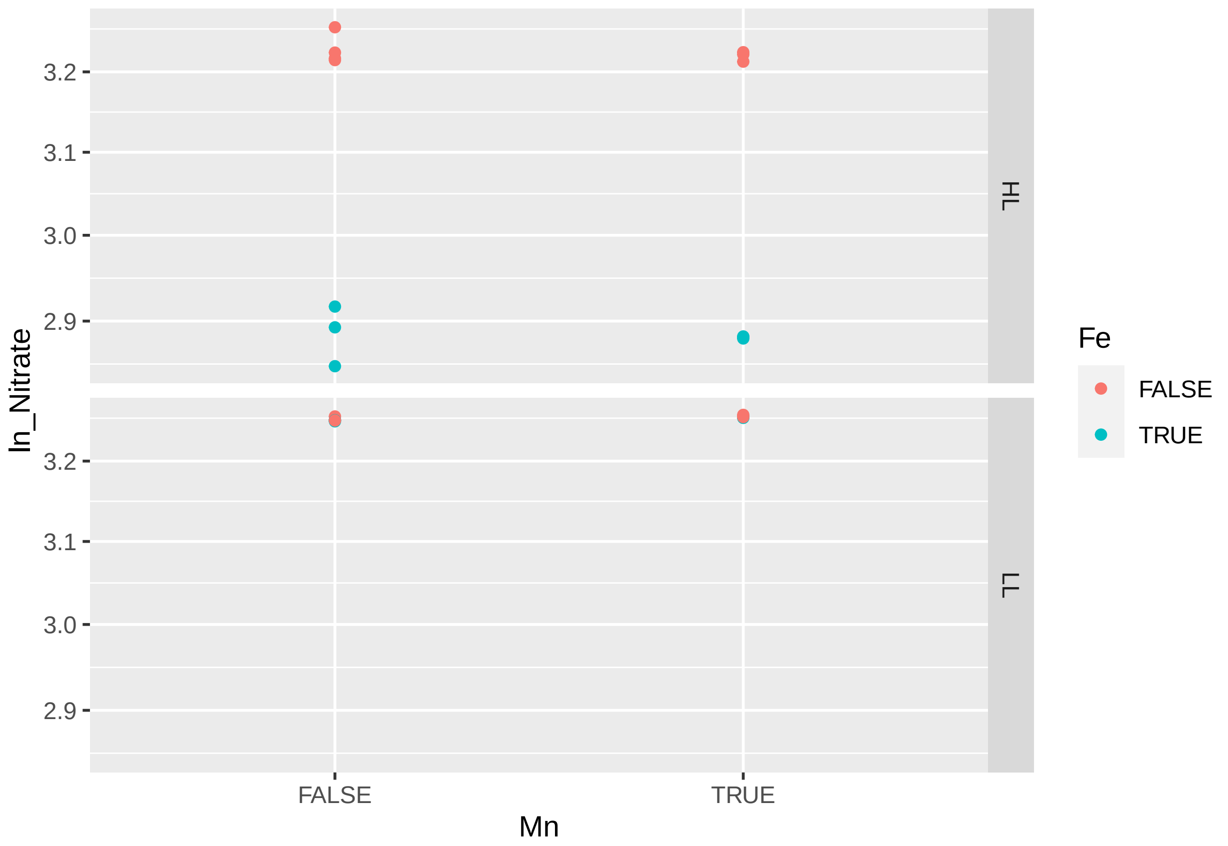
2 Macronutrients

2.1 Nitrate

```
physio <- read.csv("2SOLTEE_final_sampling_macronutrients_Chl_POC_BSi_photophysiology.csv")
physio <- physio[sample(1:nrow(physio)),] #randomize the order of the data for lmer analyses
```

```
physio$ln_Nitrate <- log(physio$Nitrate)   #data log-transformed
```

```
#Plot using ggplot2
ggplot(physio) +
  geom_point(aes(x = Mn, y = ln_Nitrate, col = Fe)) +
  facet_grid(Light ~ .) +
  scale_y_log10()
```



```r
#first model fit with all factors (Mn, Fe and Light)
fit_nitrate <- lmer(ln_Nitrate ~ Mn + Fe + Light +
               Mn:Fe + Mn:Light + Fe:Light + (1|Bottle),
             data = physio, na.action=na.fail, REML = FALSE)

summary(fit_nitrate)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_Nitrate ~ Mn + Fe + Light + Mn:Fe + Mn:Light + Fe:Light +
##     (1 | Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##   -139.2   -127.9     78.6   -157.2       17
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.90002 -0.06623 -0.00751  0.10765  2.28845
##
## Random effects:
##  Groups   Name        Variance  Std.Dev.
##  Bottle   (Intercept) 2.628e-05 0.005126
##  Residual             1.125e-04 0.010608
## Number of obs: 26, groups:  Bottle, 25
##
```

```
## Fixed effects:
##                  Estimate Std. Error t value
## (Intercept)     3.227911   0.005597 576.679
## MnTRUE         -0.007276   0.007907  -0.920
## FeTRUE         -0.341167   0.007907 -43.147
## LightLL         0.024404   0.007283   3.351
## MnTRUE:FeTRUE   0.001349   0.009353   0.144
## MnTRUE:LightLL  0.011661   0.009234   1.263
## FeTRUE:LightLL  0.339684   0.009234  36.786
##
## Correlation of Fixed Effects:
##              (Intr) MnTRUE FeTRUE LghtLL MTRUE:F MTRUE:L
## MnTRUE      -0.608
## FeTRUE      -0.608  0.260
## LightLL     -0.651  0.307  0.307
## MTRUE:FTRUE  0.345 -0.557 -0.557  0.000
## MnTRUE:LgLL  0.342 -0.584  0.050 -0.526  0.000
## FTRUE:LghLL  0.342  0.050 -0.584 -0.526  0.000  -0.085
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_nitrate, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## ln_Nitrate ~ Mn + Fe + Light + Mn:Fe + Mn:Light + Fe:Light +
##     (1 | Bottle)
##          npar      AIC     LRT Pr(Chi)
## <none>        -139.195
## Mn:Fe       1 -141.175   0.020  0.8870
## Mn:Light    1 -139.737   1.458  0.2273
## Fe:Light    1  -38.347 102.847  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#it shows that only the Fe:light interaction is significant
#non-significant interactions are removed from the model

#second model fit
fit_nitrate2 <- lmer(ln_Nitrate ~ Mn + Fe + Light + Fe:Light + (1|Bottle),
                  data = physio, na.action=na.fail, REML = FALSE)
summary(fit_nitrate2)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_Nitrate ~ Mn + Fe + Light + Fe:Light + (1 | Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##   -141.7   -132.9     77.9   -155.7       19
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.83221 -0.26085 -0.09375  0.20485  2.58406
```

```
##
## Random effects:
##  Groups   Name        Variance  Std.Dev.
##  Bottle   (Intercept) 9.619e-06 0.003101
##  Residual             1.372e-04 0.011714
## Number of obs: 26, groups:  Bottle, 25
##
## Fixed effects:
##                   Estimate Std. Error t value
## (Intercept)       3.225214   0.005025 641.851
## MnTRUE           -0.001036   0.004788  -0.216
## FeTRUE           -0.340916   0.006748 -50.518
## LightLL           0.029917   0.006445   4.642
## FeTRUE:LightLL    0.340003   0.009512  35.745
##
## Correlation of Fixed Effects:
##              (Intr) MnTRUE FeTRUE LghtLL
## MnTRUE       -0.412
## FeTRUE       -0.598 -0.048
## LightLL      -0.641  0.000  0.478
## FTRUE:LghLL   0.434  0.000 -0.705 -0.678
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_nitrate2, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## ln_Nitrate ~ Mn + Fe + Light + Fe:Light + (1 | Bottle)
##          npar      AIC     LRT Pr(Chi)
## <none>         -141.702
## Mn          1 -143.657   0.045  0.8318
## Fe:Light    1  -42.073 101.629  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#it shows that Mn does not influence nitrate concentrations
#Mn is removed from the model

#best model identified by drop
fit_best_nitrate <- lmer(ln_Nitrate ~ Fe + Light + Fe:Light + (1|Bottle),
                  data = physio, na.action=na.fail, REML = FALSE)
summary(fit_best_nitrate)
```

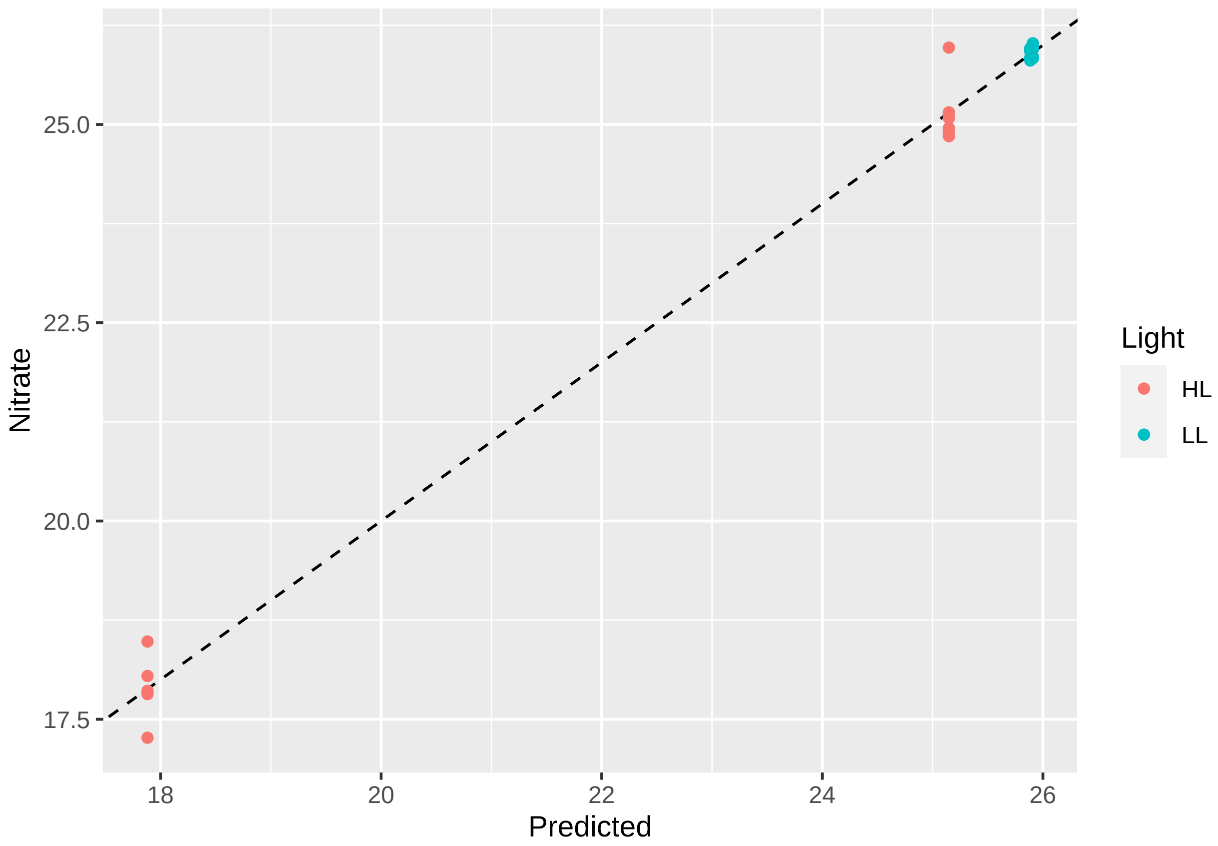
```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_Nitrate ~ Fe + Light + Fe:Light + (1 | Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##   -143.7   -136.1     77.8   -155.7       20
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
```

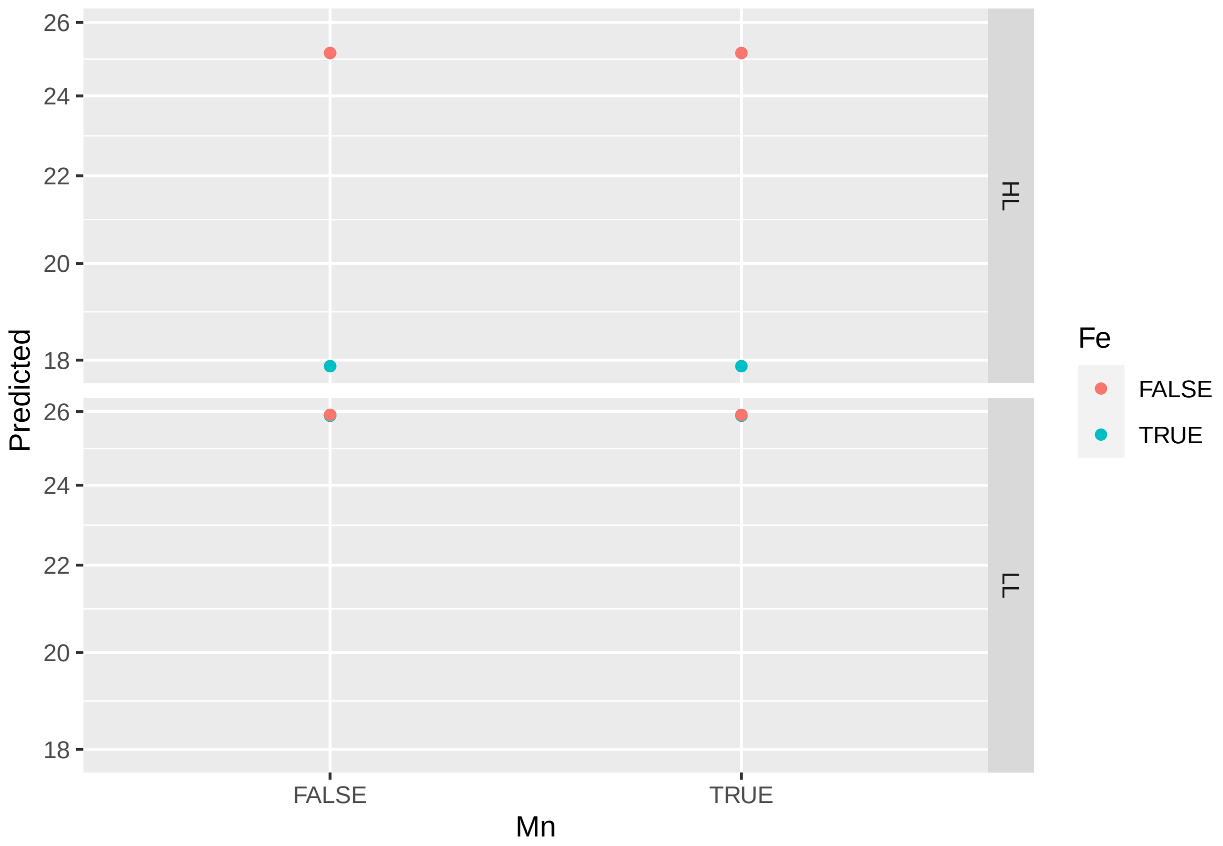
```
## -2.7612 -0.2272 -0.1179  0.1628  2.5974
##
## Random effects:
##  Groups   Name        Variance  Std.Dev.
##  Bottle   (Intercept) 0.0000123 0.003507
##  Residual             0.0001348 0.011610
## Number of obs: 26, groups:  Bottle, 25
##
## Fixed effects:
##                 Estimate Std. Error t value
## (Intercept)     3.224772   0.004582 703.771
## FeTRUE         -0.340992   0.006746 -50.545
## LightLL         0.029827   0.006441   4.631
## FeTRUE:LightLL  0.340092   0.009514  35.746
##
## Correlation of Fixed Effects:
##             (Intr) FeTRUE LghtLL
## FeTRUE      -0.679
## LightLL     -0.703  0.477
## FTRUE:LghLL  0.476 -0.705 -0.677
```

```
#Report results
report(fit_best_nitrate)
```

```
## We fitted a linear mixed model (estimated using ML and nloptwrap optimizer) to
## predict ln_Nitrate with Fe and Light (formula: ln_Nitrate ~ Fe + Light +
## Fe:Light). The model included Bottle as random effect (formula: ~1 | Bottle).
## The model's total explanatory power is substantial (conditional R2 = 0.99) and
## the part related to the fixed effects alone (marginal R2) is of 0.99. The
## model's intercept, corresponding to Fe = [?] and Light = HL, is at 3.22 (95% CI
## [3.22, 3.23], t(20) = 703.77, p < .001). Within this model:
##
##   - The effect of FeTRUE is statistically significant and negative (beta = -0.34,
## 95% CI [-0.36, -0.33], t(20) = -50.55, p < .001; Std. beta = -2.19, 95% CI
## [-2.28, -2.10])
##   - The effect of Light [LL] is statistically significant and positive (beta =
## 0.03, 95% CI [0.02, 0.04], t(20) = 4.63, p < .001; Std. beta = 0.19, 95% CI
## [0.11, 0.28])
##   - The effect of FeTRUE × Light [LL] is statistically significant and positive
## (beta = 0.34, 95% CI [0.32, 0.36], t(20) = 35.75, p < .001; Std. beta = 2.18,
## 95% CI [2.06, 2.31])
##
## Standardized parameters were obtained by fitting the model on a standardized
## version of the dataset. 95% Confidence Intervals (CIs) and p-values were
## computed using a Wald t-distribution approximation.
```

```
#Represent data predicted by the model vs real data
physio$Predicted <- exp(predict(fit_best_nitrate, re.form = NA))
```


25.0
22.5
20.0
17.5
Nitrate
18
20
22
24
26
Predicted
Light
HL
LL



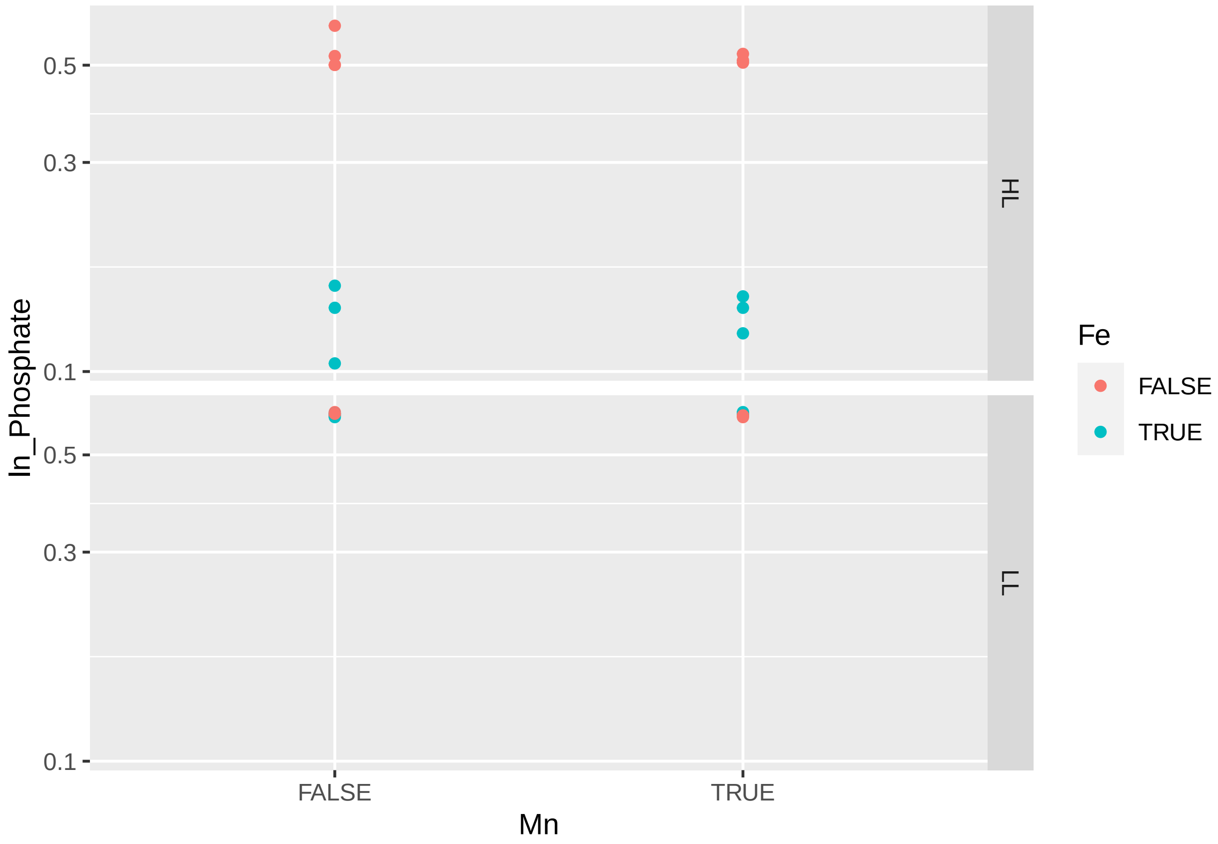
```
#Pairwise comparison
emmeans(fit_best_nitrate, pairwise ~ Fe + Light, adjust = "tukey")
```

```
## $emmeans
##  Fe    Light emmean       SE    df lower.CL upper.CL
##  FALSE HL     3.225 0.005763 30.63    3.213    3.237
##   TRUE HL     2.884 0.005383 30.71    2.873    2.895
##  FALSE LL     3.255 0.005763 30.63    3.243    3.266
##   TRUE LL     3.254 0.005383 30.71    3.243    3.265
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $contrasts
##  contrast            estimate      SE   df t.ratio p.value
##  FALSE HL - TRUE HL    0.3410 0.00789 30.7  43.240  <.0001
##  FALSE HL - FALSE LL  -0.0298 0.00833 22.2  -3.582  0.0083
##  FALSE HL - TRUE LL   -0.0289 0.00789 30.7  -3.668  0.0048
##  TRUE HL - FALSE LL   -0.3708 0.00789 30.7 -47.022  <.0001
##  TRUE HL - TRUE LL    -0.3699 0.00761 30.7 -48.595  <.0001
##  FALSE LL - TRUE LL    0.0009 0.00789 30.7   0.114  0.9995
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 4 estimates
```

2.2 Phosphate

```
physio$ln_Phosphate <- log(physio$Phosphate)    #data log-transformed
```

```
#Plot using ggplot2
ggplot(physio) +
  geom_point(aes(x = Mn, y = ln_Phosphate, col = Fe)) +
  facet_grid(Light ~ .) +
  scale_y_log10()
```



```
#model fit with all factors (Mn, Fe and Light)
fit_phosphate <- lmer(ln_Phosphate ~ Mn + Fe + Light +
               Mn:Fe + Mn:Light + Fe:Light + (1|Bottle),
             data = physio, na.action=na.fail, REML = FALSE)

summary(fit_phosphate)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_Phosphate ~ Mn + Fe + Light + Mn:Fe + Mn:Light + Fe:Light +
##     (1 | Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##   -109.5    -98.2     63.7   -127.5       17
```

```
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.5984 -0.3069 -0.0606  0.2528  3.8901
##
## Random effects:
##  Groups   Name        Variance  Std.Dev.
##  Bottle   (Intercept) 0.0000000 0.00000
##  Residual             0.0004345 0.02085
## Number of obs: 26, groups:  Bottle, 25
##
## Fixed effects:
##                 Estimate Std. Error t value
## (Intercept)     0.534095   0.009888  54.016
## MnTRUE         -0.015643   0.013940  -1.122
## FeTRUE         -0.398691   0.013940 -28.600
## LightLL         0.087746   0.013184   6.656
## MnTRUE:FeTRUE   0.015344   0.016480   0.931
## MnTRUE:LightLL  0.007283   0.016443   0.443
## FeTRUE:LightLL  0.390331   0.016443  23.739
##
## Correlation of Fixed Effects:
##             (Intr) MnTRUE FeTRUE LghtLL MTRUE:F MTRUE:L
## MnTRUE      -0.604
## FeTRUE      -0.604  0.255
## LightLL     -0.667  0.315  0.315
## MTRUE:FTRUE  0.333 -0.552 -0.552  0.000
## MnTRUE:LgLL  0.356 -0.590  0.042 -0.535  0.000
## FTRUE:LghLL  0.356  0.042 -0.590 -0.535  0.000  -0.071
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_phosphate, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## ln_Phosphate ~ Mn + Fe + Light + Mn:Fe + Mn:Light + Fe:Light +
##     (1 | Bottle)
##          npar      AIC    LRT Pr(Chi)
## <none>        -109.488
## Mn:Fe       1 -110.635  0.853  0.3558
## Mn:Light    1 -111.293  0.195  0.6584
## Fe:Light    1  -30.337 81.152  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#it shows that only the Fe:light interaction is significant
#non-significant interactions are removed from the model

#second model fit
fit_phosphate2 <- lmer(ln_Phosphate ~ Mn + Fe + Light + Fe:Light + (1|Bottle),
```

```
                  data = physio, na.action=na.fail, REML = FALSE)
summary(fit_phosphate2)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_Phosphate ~ Mn + Fe + Light + Fe:Light + (1 | Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##   -112.4   -103.6     63.2   -126.4       19
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.5665 -0.4068  0.0115  0.2575  4.0307
##
## Random effects:
##  Groups   Name        Variance  Std.Dev.
##  Bottle   (Intercept) 0.0000000 0.00000
##  Residual             0.0004523 0.02127
## Number of obs: 26, groups:  Bottle, 25
##
## Fixed effects:
##                 Estimate Std. Error t value
## (Intercept)     0.529465   0.008805  60.130
## MnTRUE         -0.004841   0.008388  -0.577
## FeTRUE         -0.391791   0.011847 -33.071
## LightLL         0.090867   0.011368   7.993
## FeTRUE:LightLL  0.390851   0.016733  23.358
##
## Correlation of Fixed Effects:
##             (Intr) MnTRUE FeTRUE LghtLL
## MnTRUE      -0.408
## FeTRUE      -0.599 -0.051
## LightLL     -0.645  0.000  0.480
## FTRUE:LghLL  0.439  0.000 -0.706 -0.679
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_phosphate2, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## ln_Phosphate ~ Mn + Fe + Light + Fe:Light + (1 | Bottle)
##          npar      AIC    LRT Pr(Chi)
## <none>        -112.446
## Mn          1 -114.115  0.331  0.5651
## Fe:Light    1  -34.097 80.349  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#it shows that Mn does not influence phosphate concentrations
#Mn is removed from the model

#best model identified by drop
fit_best_phosphate <- lmer(ln_Phosphate ~  Fe + Light + Fe:Light + (1|Bottle),
                 data = physio, na.action=na.fail, REML = FALSE)
summary(fit_best_phosphate)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_Phosphate ~ Fe + Light + Fe:Light + (1 | Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##   -114.1   -106.6     63.1   -126.1       20
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.4435 -0.3818 -0.0835  0.2001  4.1020
##
## Random effects:
##  Groups   Name        Variance  Std.Dev.
##  Bottle   (Intercept) 0.0000000 0.0000
##  Residual             0.0004581 0.0214
## Number of obs: 26, groups:  Bottle, 25
##
## Fixed effects:
##                 Estimate Std. Error t value
## (Intercept)      0.52739    0.00809  65.194
## FeTRUE          -0.39214    0.01191 -32.932
## LightLL          0.09087    0.01144   7.943
## FeTRUE:LightLL  0.39085    0.01684  23.210
##
## Correlation of Fixed Effects:
##             (Intr) FeTRUE LghtLL
## FeTRUE      -0.679
## LightLL     -0.707  0.480
## FTRUE:LghLL  0.480 -0.707 -0.679
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

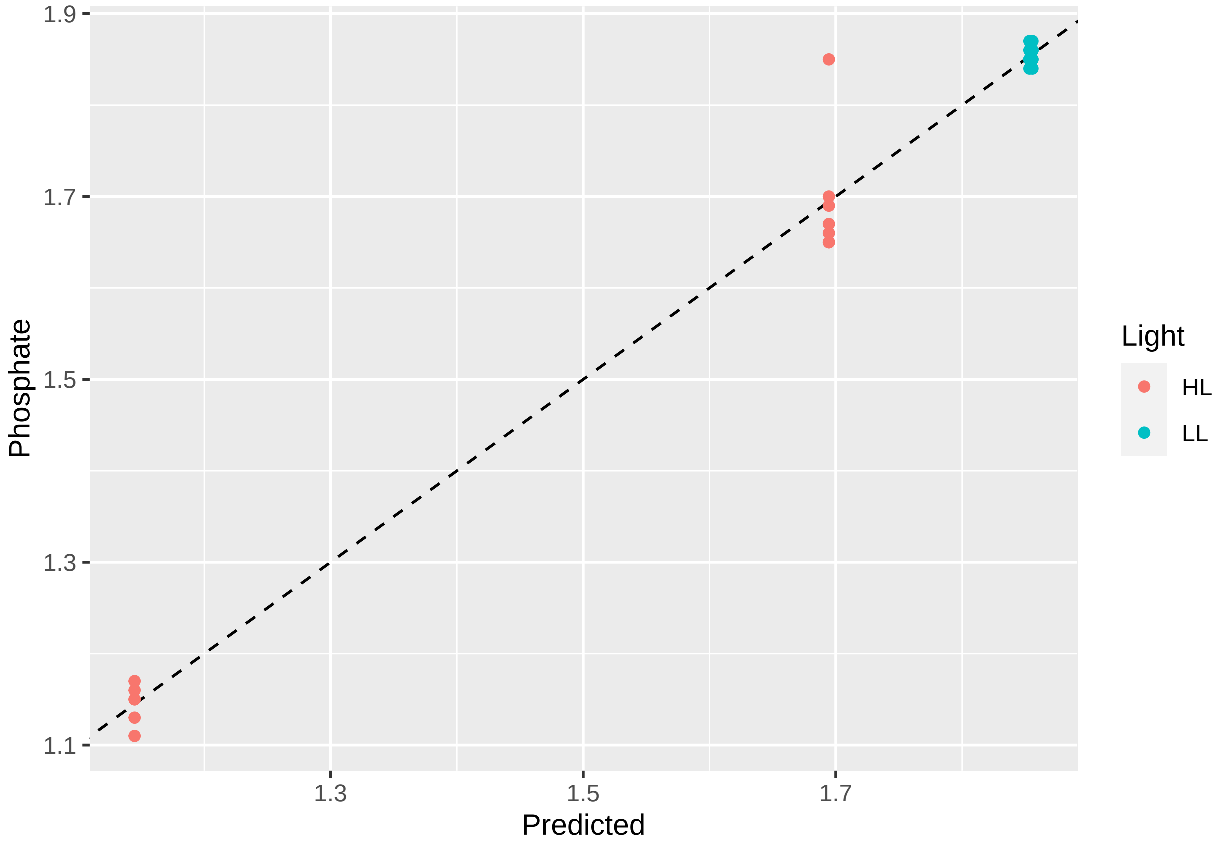
```r
#Report results
report(fit_best_phosphate)
```

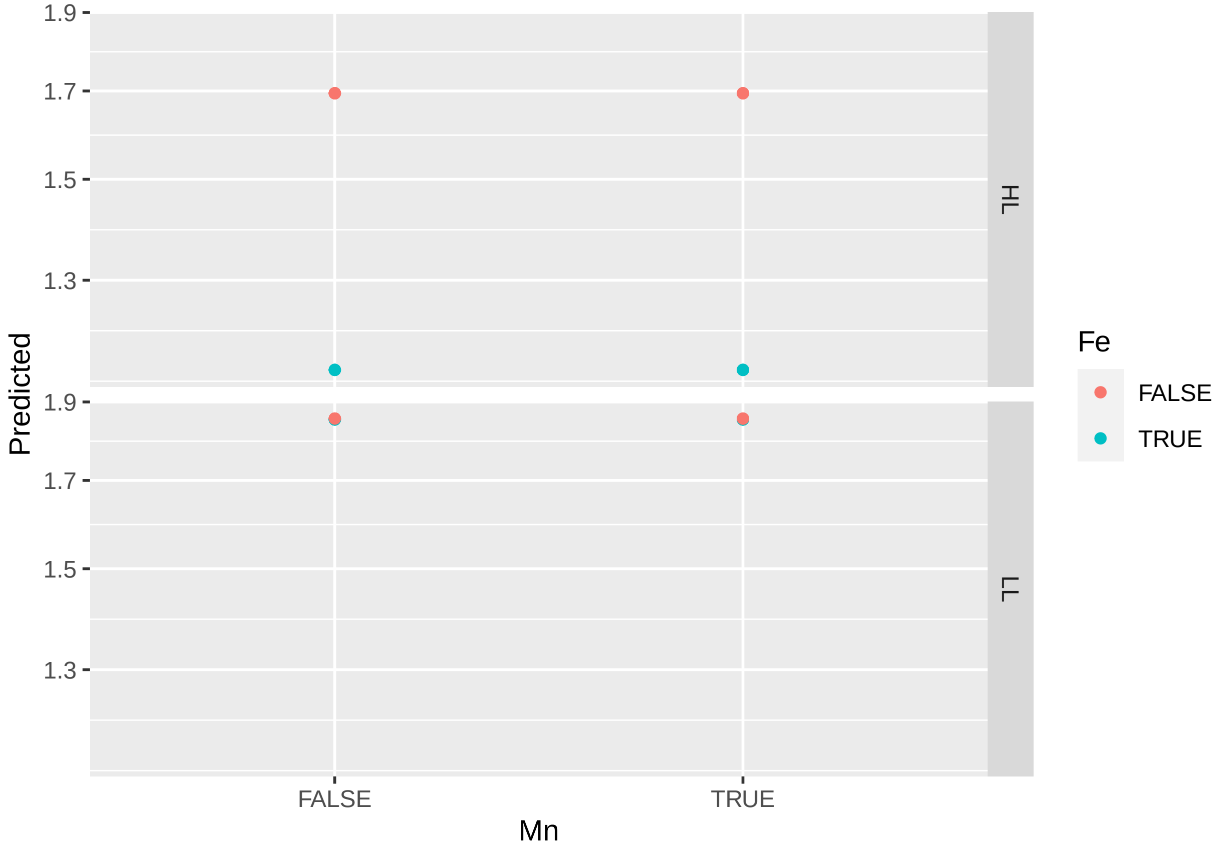
```
## Random effect variances not available. Returned R2 does not account for random effects.
## Random effect variances not available. Returned R2 does not account for random effects.
```

```
## We fitted a linear mixed model (estimated using ML and nloptwrap optimizer) to
## predict ln_Phosphate with Fe and Light (formula: ln_Phosphate ~ Fe + Light +
## Fe:Light). The model included Bottle as random effect (formula: ~1 | Bottle).
## The model's explanatory power related to the fixed effects alone (marginal R2)
## is 0.99. The model's intercept, corresponding to Fe = [?] and Light = HL, is at
## 0.53 (95% CI [0.51, 0.54], t(20) = 65.19, p < .001). Within this model:
```

```
##
##   - The effect of FeTRUE is statistically significant and negative (beta = -0.39,
## 95% CI [-0.42, -0.37], t(20) = -32.93, p < .001; Std. beta = -1.97, 95% CI
## [-2.10, -1.85])
##   - The effect of Light [LL] is statistically significant and positive (beta =
## 0.09, 95% CI [0.07, 0.11], t(20) = 7.94, p < .001; Std. beta = 0.46, 95% CI
## [0.34, 0.58])
##   - The effect of FeTRUE × Light [LL] is statistically significant and positive
## (beta = 0.39, 95% CI [0.36, 0.43], t(20) = 23.21, p < .001; Std. beta = 1.97,
## 95% CI [1.79, 2.14])
##
## Standardized parameters were obtained by fitting the model on a standardized
## version of the dataset. 95% Confidence Intervals (CIs) and p-values were
## computed using a Wald t-distribution approximation.
```

```
#Represent data predicted by the model vs real data
physio$Predicted <- exp(predict(fit_best_phosphate, re.form = NA))
```





```r
emmeans (fit_best_phosphate, pairwise ~ Fe + Light, adjust = "tukey")
```

```
## boundary (singular) fit: see help('isSingular')

## $emmeans
##  Fe    Light emmean     SE   df lower.CL upper.CL
##  FALSE HL     0.527 0.0102 30.7    0.507    0.548
##   TRUE HL     0.135 0.0095 30.7    0.116    0.155
##  FALSE LL     0.618 0.0102 30.7    0.598    0.639
##   TRUE LL     0.617 0.0095 30.7    0.598    0.636
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $contrasts
##  contrast             estimate     SE   df t.ratio p.value
##  FALSE HL - TRUE HL    0.39214 0.0139 30.7  28.201  <.0001
##  FALSE HL - FALSE LL -0.09087 0.0144 23.5  -6.327  <.0001
##  FALSE HL - TRUE LL  -0.08958 0.0139 30.7  -6.442  <.0001
##  TRUE HL - FALSE LL  -0.48300 0.0139 30.7 -34.736  <.0001
##  TRUE HL - TRUE LL   -0.48172 0.0134 30.7 -35.860  <.0001
##  FALSE LL - TRUE LL   0.00128 0.0139 30.7   0.092  0.9997
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 4 estimates
```

2.3 Silicate

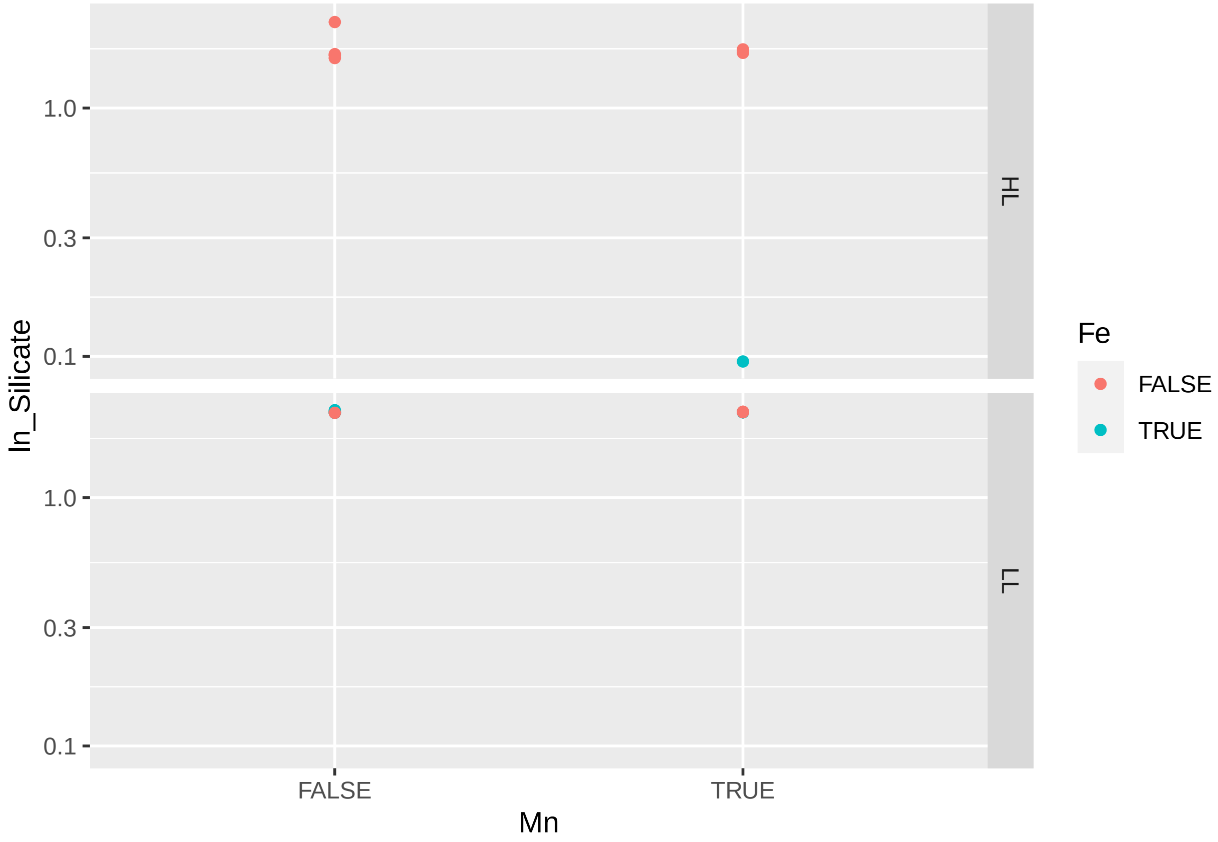
```
physio$ln_Silicate <- log(physio$Silicate)   #data log-transformed
```

```
#Plot using ggplot2
ggplot(physio) +
  geom_point(aes(x = Mn, y = ln_Silicate, col = Fe)) +
  facet_grid(Light ~ .) +
  scale_y_log10()
```

```
## Warning in self$trans$transform(x): NaNs produced
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

```
## Warning: Removed 5 rows containing missing values (`geom_point()`).
```



```
#model fit with all factors (Mn, Fe and Light)
fit_silicate <- lmer(ln_Silicate ~ Mn + Fe + Light +
               Mn:Fe + Mn:Light + Fe:Light + (1|Bottle),
             data = physio, na.action=na.fail, REML = FALSE)

summary(fit_silicate)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_Silicate ~ Mn + Fe + Light + Mn:Fe + Mn:Light + Fe:Light +
##     (1 | Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##     11.0     22.3      3.5     -7.0       17
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.5849 -0.3075 -0.1944  0.3118  2.3471
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.00000  0.0000
##  Residual             0.04473  0.2115
## Number of obs: 26, groups:  Bottle, 25
##
## Fixed effects:
##                  Estimate Std. Error t value
## (Intercept)       1.72281    0.10032  17.173
## MnTRUE            0.04063    0.14144   0.287
## FeTRUE           -2.16860    0.14144 -15.333
## LightLL           0.53145    0.13376   3.973
## MnTRUE:FeTRUE     0.22314    0.16720   1.335
## MnTRUE:LightLL   -0.14436    0.16683  -0.865
## FeTRUE:LightLL    2.06824    0.16683  12.397
##
## Correlation of Fixed Effects:
##              (Intr) MnTRUE FeTRUE LghtLL MTRUE:F MTRUE:L
## MnTRUE       -0.604
## FeTRUE       -0.604  0.255
## LightLL      -0.667  0.315  0.315
## MTRUE:FTRUE   0.333 -0.552 -0.552  0.000
## MnTRUE:LgLL   0.356 -0.590  0.042 -0.535  0.000
## FTRUE:LghLL   0.356  0.042 -0.590 -0.535  0.000  -0.071
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_silicate, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## ln_Silicate ~ Mn + Fe + Light + Mn:Fe + Mn:Light + Fe:Light +
##     (1 | Bottle)
##          npar    AIC    LRT   Pr(Chi)
## <none>        11.000
## Mn:Fe       1 10.720  1.720    0.1897
## Mn:Light    1  9.738  0.738    0.3902
## Fe:Light    1 59.262 50.262 1.345e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#it shows that only the Fe:light interaction is significant
#non-significant interactions are removed from the model

#second model fit
fit_silicate2 <- lmer(ln_Silicate ~ Mn + Fe + Light + Fe:Light + (1|Bottle),
                      data = physio, na.action=na.fail, REML = FALSE)
summary(fit_silicate2)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_Silicate ~ Mn + Fe + Light + Fe:Light + (1 | Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##      9.4     18.2      2.3     -4.6       19
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -3.602 -0.233 -0.079  0.209  2.170
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.006044 0.07774
##  Residual             0.042969 0.20729
## Number of obs: 26, groups:  Bottle, 25
##
## Fixed effects:
##                 Estimate Std. Error t value
## (Intercept)      1.70756    0.09189  18.583
## MnTRUE           0.07670    0.08760   0.876
## FeTRUE          -2.05982    0.12325 -16.713
## LightLL          0.46033    0.11717   3.929
## FeTRUE:LightLL  2.06718    0.17339  11.922
##
## Correlation of Fixed Effects:
##             (Intr) MnTRUE FeTRUE LghtLL
## MnTRUE      -0.415
## FeTRUE      -0.598 -0.046
## LightLL     -0.638  0.000  0.475
## FTRUE:LghLL  0.431  0.000 -0.703 -0.676
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_silicate2, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## ln_Silicate ~ Mn + Fe + Light + Fe:Light + (1 | Bottle)
##          npar    AIC    LRT   Pr(Chi)
## <none>          9.362
## Mn          1  8.092  0.730    0.3927
## Fe:Light    1 55.519 48.157 3.935e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#it shows that Mn does not influence silicate concentrations
#Mn is removed from the model

#best model identified by drop
fit_best_silicate <- lmer(ln_Silicate ~  Fe + Light + Fe:Light + (1|Bottle),
                    data = physio, na.action=na.fail, REML = FALSE)
summary(fit_best_silicate)
```

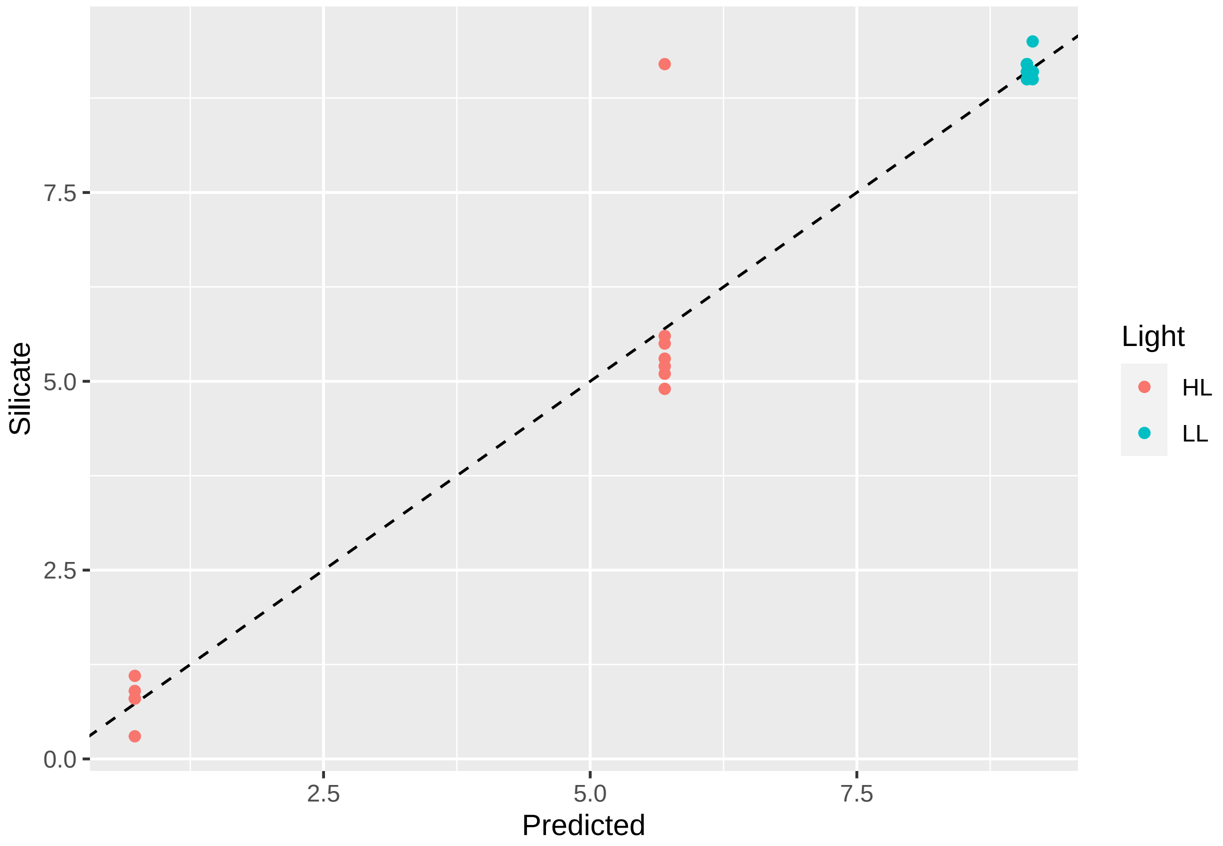
```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_Silicate ~ Fe + Light + Fe:Light + (1 | Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##      8.1     15.6      2.0     -3.9       20
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.9039 -0.0754 -0.0234  0.1366  2.1012
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.001551 0.03939
##  Residual             0.048830 0.22098
## Number of obs: 26, groups:  Bottle, 25
##
## Fixed effects:
##                 Estimate Std. Error t value
## (Intercept)      1.74024    0.08483  20.514
## FeTRUE          -2.05415    0.12487 -16.450
## LightLL          0.46746    0.11971   3.905
## FeTRUE:LightLL  2.06005    0.17642  11.677
##
## Correlation of Fixed Effects:
##             (Intr) FeTRUE LghtLL
## FeTRUE      -0.679
## LightLL     -0.706  0.479
## FTRUE:LghLL  0.479 -0.706 -0.679
```

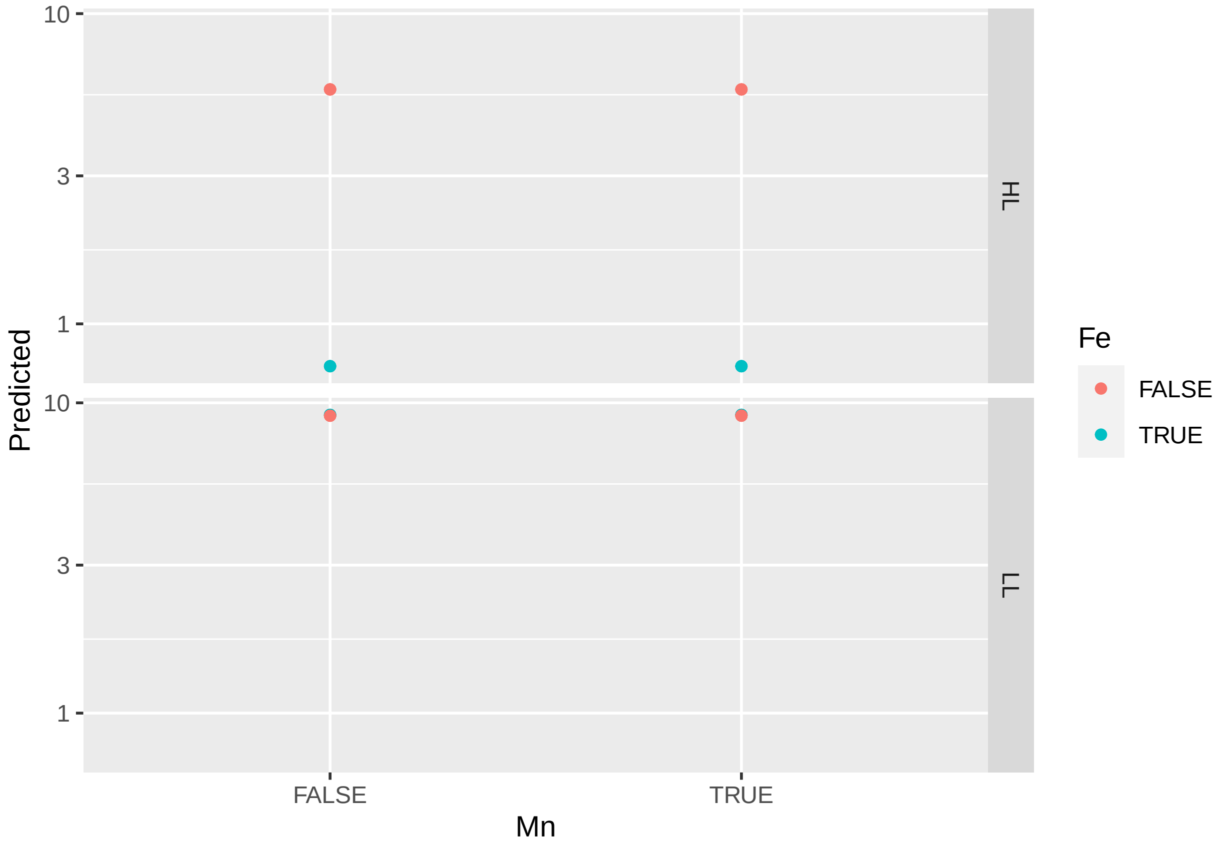
```
#Report results
report(fit_best_silicate)
```

```
## We fitted a linear mixed model (estimated using ML and nloptwrap optimizer) to
## predict ln_Silicate with Fe and Light (formula: ln_Silicate ~ Fe + Light +
## Fe:Light). The model included Bottle as random effect (formula: ~1 | Bottle).
## The model's total explanatory power is substantial (conditional R2 = 0.96) and
## the part related to the fixed effects alone (marginal R2) is of 0.95. The
## model's intercept, corresponding to Fe = [?] and Light = HL, is at 1.74 (95% CI
## [1.56, 1.92], t(20) = 20.51, p < .001). Within this model:
##
##   - The effect of FeTRUE is statistically significant and negative (beta = -2.05,
## 95% CI [-2.31, -1.79], t(20) = -16.45, p < .001; Std. beta = -1.94, 95% CI
## [-2.19, -1.69])
##   - The effect of Light [LL] is statistically significant and positive (beta =
```

```
## 0.47, 95% CI [0.22, 0.72], t(20) = 3.91, p < .001; Std. beta = 0.44, 95% CI
## [0.21, 0.68])
##   - The effect of FeTRUE × Light [LL] is statistically significant and positive
## (beta = 2.06, 95% CI [1.69, 2.43], t(20) = 11.68, p < .001; Std. beta = 1.95,
## 95% CI [1.60, 2.29])
##
## Standardized parameters were obtained by fitting the model on a standardized
## version of the dataset. 95% Confidence Intervals (CIs) and p-values were
## computed using a Wald t-distribution approximation.
```

```
#Represent data predicted by the model vs real data
physio$Predicted <- exp(predict(fit_best_silicate, re.form = NA))
```





```r
#Pairwise comparison
emmeans (fit_best_silicate, pairwise ~ Fe + Light, adjust = "tukey")
```

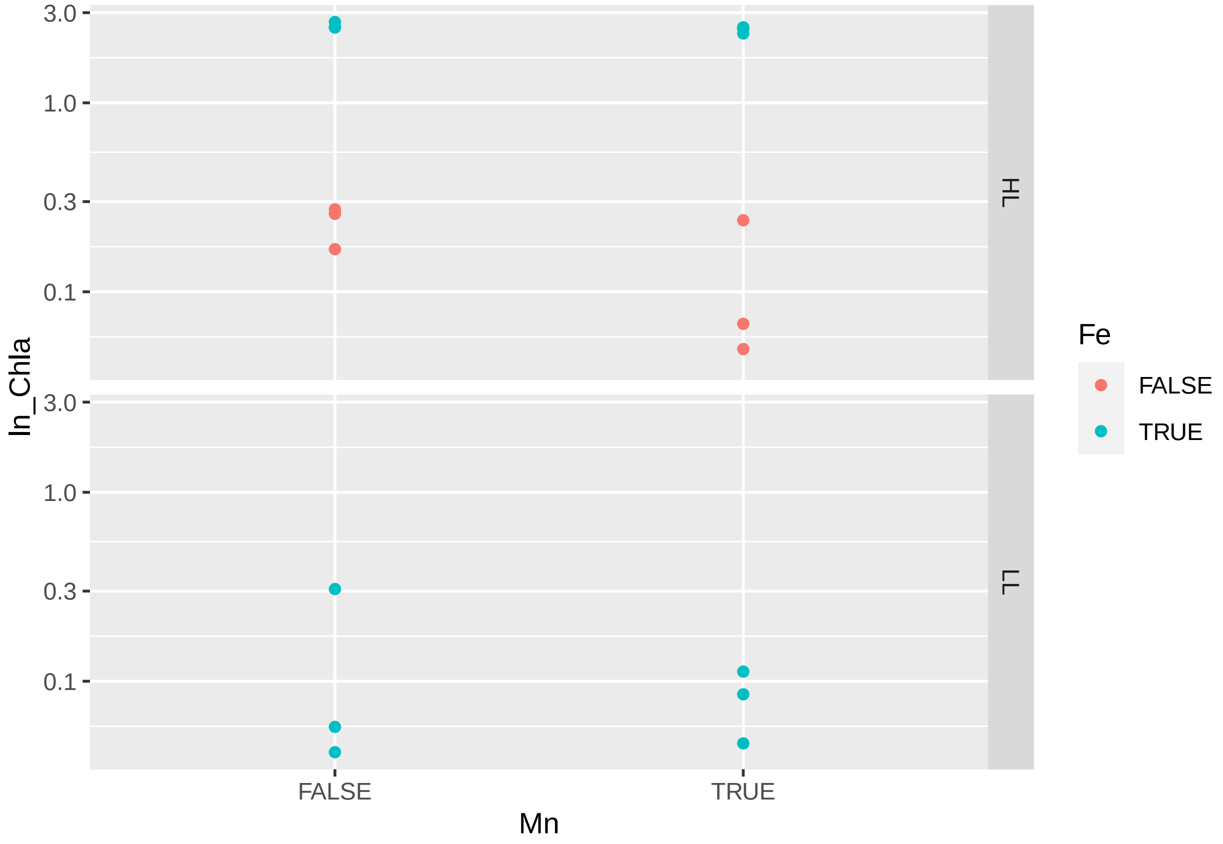
```
## $emmeans
##  Fe    Light emmean     SE   df lower.CL upper.CL
##  FALSE HL     1.740 0.1065 30.7    1.523    1.958
##   TRUE HL    -0.314 0.0996 30.7   -0.517   -0.111
##  FALSE LL     2.208 0.1065 30.7    1.990    2.425
##   TRUE LL     2.214 0.0996 30.7    2.010    2.417
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $contrasts
##  contrast            estimate    SE   df t.ratio p.value
##  FALSE HL - TRUE HL   2.05415 0.146 30.7  14.085  <.0001
##  FALSE HL - FALSE LL -0.46746 0.152 23.1  -3.079  0.0253
##  FALSE HL - TRUE LL  -0.47337 0.146 30.7  -3.246  0.0142
##  TRUE HL - FALSE LL  -2.52160 0.146 30.7 -17.290  <.0001
##  TRUE HL - TRUE LL   -2.52751 0.141 30.7 -17.941  <.0001
##  FALSE LL - TRUE LL  -0.00591 0.146 30.7  -0.041  1.0000
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 4 estimates
```

3 Physiological responses

3.1 Chlorophyll-a production

```
physio$ln_Chla <- log(physio$Chla_mg.m3)    #data log-transformed
```

```
#Plot using ggplot2
ggplot(physio) +
  geom_point(aes(x = Mn, y = ln_Chla, col = Fe)) +
  facet_grid(Light ~ .) +
  scale_y_log10()
```



```
#model fit with all factors (Mn, Fe and Light)
fit_Chla <- lmer(ln_Chla ~ Mn + Fe + Light +
               Mn:Fe + Mn:Light + Fe:Light + (1|Bottle),
             data = physio, na.action=na.fail, REML = FALSE)

summary(fit_Chla)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_Chla ~ Mn + Fe + Light + Mn:Fe + Mn:Light + Fe:Light + (1 |
##     Bottle)
##    Data: physio
```

```
##
##      AIC      BIC   logLik deviance df.resid
##     -0.1     11.3      9.0    -18.1       17
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.04613 -0.10870  0.06089  0.30703  1.01929
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.01355  0.1164
##  Residual             0.01594  0.1263
## Number of obs: 26, groups:  Bottle, 25
##
## Fixed effects:
##                Estimate Std. Error t value
## (Intercept)     0.03496    0.08076   0.433
## MnTRUE          0.04489    0.11539   0.389
## FeTRUE          2.49251    0.11539  21.600
## LightLL        -0.39766    0.10042  -3.960
## MnTRUE:FeTRUE  -0.09723    0.13693  -0.710
## MnTRUE:LightLL -0.07967    0.13263  -0.601
## FeTRUE:LightLL -1.95523    0.13263 -14.742
##
## Correlation of Fixed Effects:
##              (Intr) MnTRUE FeTRUE LghtLL MTRUE:F MTRUE:L
## MnTRUE       -0.610
## FeTRUE       -0.610  0.262
## LightLL      -0.622  0.290  0.290
## MTRUE:FTRUE   0.362 -0.564 -0.564  0.000
## MnTRUE:LgLL   0.314 -0.575  0.068 -0.505  0.000
## FTRUE:LghLL   0.314  0.068 -0.575 -0.505  0.000  -0.118
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_Chla, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## ln_Chla ~ Mn + Fe + Light + Mn:Fe + Mn:Light + Fe:Light + (1 |
##     Bottle)
##          npar    AIC    LRT  Pr(Chi)
## <none>        -0.064
## Mn:Fe       1 -1.572  0.491   0.4833
## Mn:Light    1 -1.736  0.328   0.5669
## Fe:Light    1 54.522 56.586 5.38e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#it shows that only the Fe:light interaction is significant
#non-significant interactions are removed from the model

#second model fit
```

```
fit_Chla2 <- lmer(ln_Chla ~ Mn + Fe + Light + Fe:Light + (1|Bottle),
                  data = physio, na.action=na.fail, REML = FALSE)
summary(fit_Chla2)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_Chla ~ Mn + Fe + Light + Fe:Light + (1 | Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##     -3.2      5.6      8.6    -17.2       19
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.2085 -0.0925  0.0871  0.2641  0.8922
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.01334  0.1155
##  Residual             0.01710  0.1308
## Number of obs: 26, groups:  Bottle, 25
##
## Fixed effects:
##                Estimate Std. Error t value
## (Intercept)     0.07174    0.07210   0.995
## MnTRUE         -0.04044    0.06945  -0.582
## FeTRUE          2.44979    0.09652  25.382
## LightLL        -0.43194    0.08846  -4.883
## FeTRUE:LightLL -1.96078    0.13406 -14.626
##
## Correlation of Fixed Effects:
##             (Intr) MnTRUE FeTRUE LghtLL
## MnTRUE      -0.432
## FeTRUE      -0.592 -0.037
## LightLL     -0.613  0.000  0.458
## FTRUE:LghLL  0.405  0.000 -0.694 -0.660
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_Chla2, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## ln_Chla ~ Mn + Fe + Light + Fe:Light + (1 | Bottle)
##          npar    AIC    LRT   Pr(Chi)
## <none>         -3.220
## Mn          1 -4.888  0.332    0.5646
## Fe:Light    1 50.820 56.040 7.101e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#it shows that Mn does not influence chlorophyll-a concentrations
#Mn is removed from the model
```

```r
#best model identified by drop
fit_best_Chla <- lmer(ln_Chla ~  Fe + Light + Fe:Light + (1|Bottle),
                  data = physio, na.action=na.fail, REML = FALSE)
summary(fit_best_Chla)
```

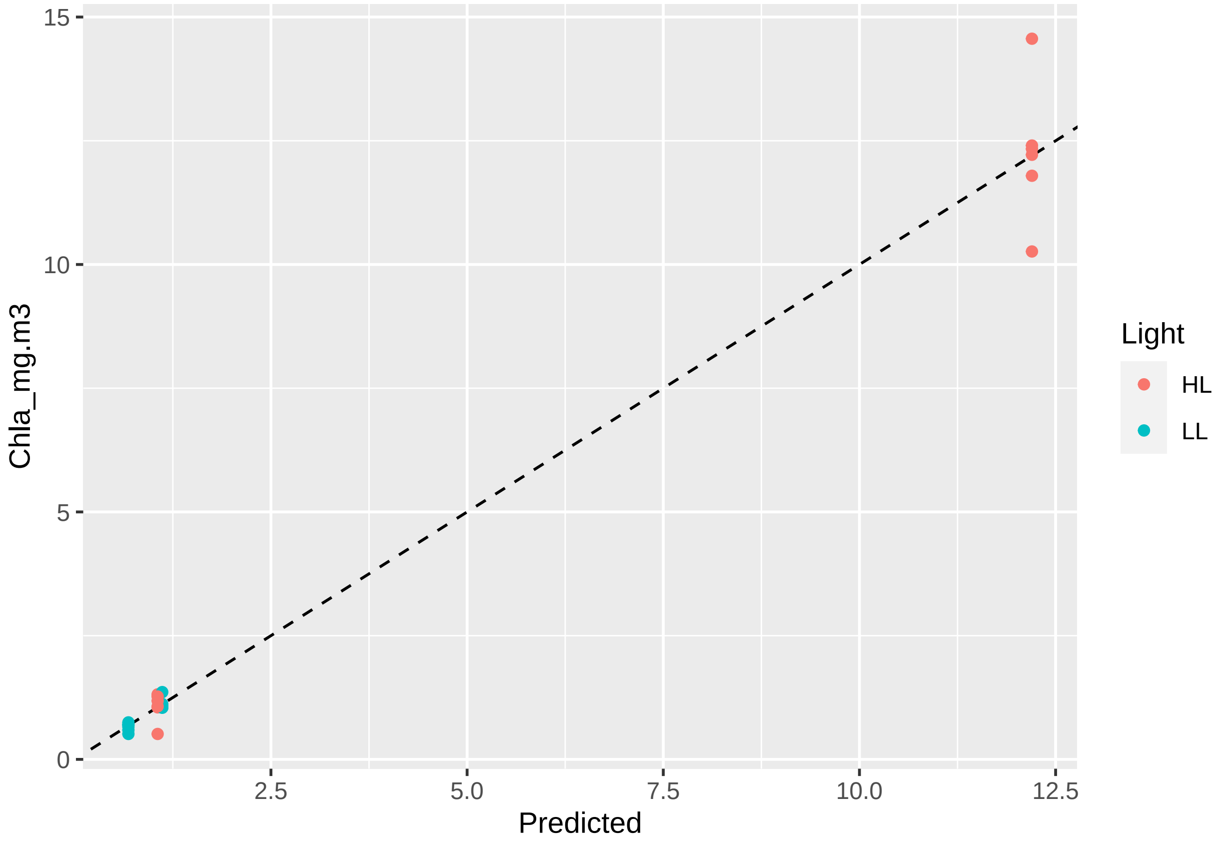
```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_Chla ~ Fe + Light + Fe:Light + (1 | Bottle)
##    Data: physio
## 
##      AIC      BIC   logLik deviance df.resid 
##     -4.9      2.7      8.4    -16.9       20 
## 
## Scaled residuals: 
##      Min       1Q   Median       3Q      Max 
## -3.16204 -0.17523  0.05109  0.34058  0.94797 
## 
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.01296  0.1138  
##  Residual             0.01785  0.1336  
## Number of obs: 26, groups:  Bottle, 25
## 
## Fixed effects:
##                Estimate Std. Error t value
## (Intercept)     0.05449    0.06551   0.832
## FeTRUE          2.44681    0.09709  25.201
## LightLL        -0.43501    0.08931  -4.871
## FeTRUE:LightLL -1.95772    0.13508 -14.493
## 
## Correlation of Fixed Effects:
##             (Intr) FeTRUE LghtLL
## FeTRUE      -0.675              
## LightLL     -0.682  0.460       
## FTRUE:LghLL  0.451 -0.696 -0.661
```

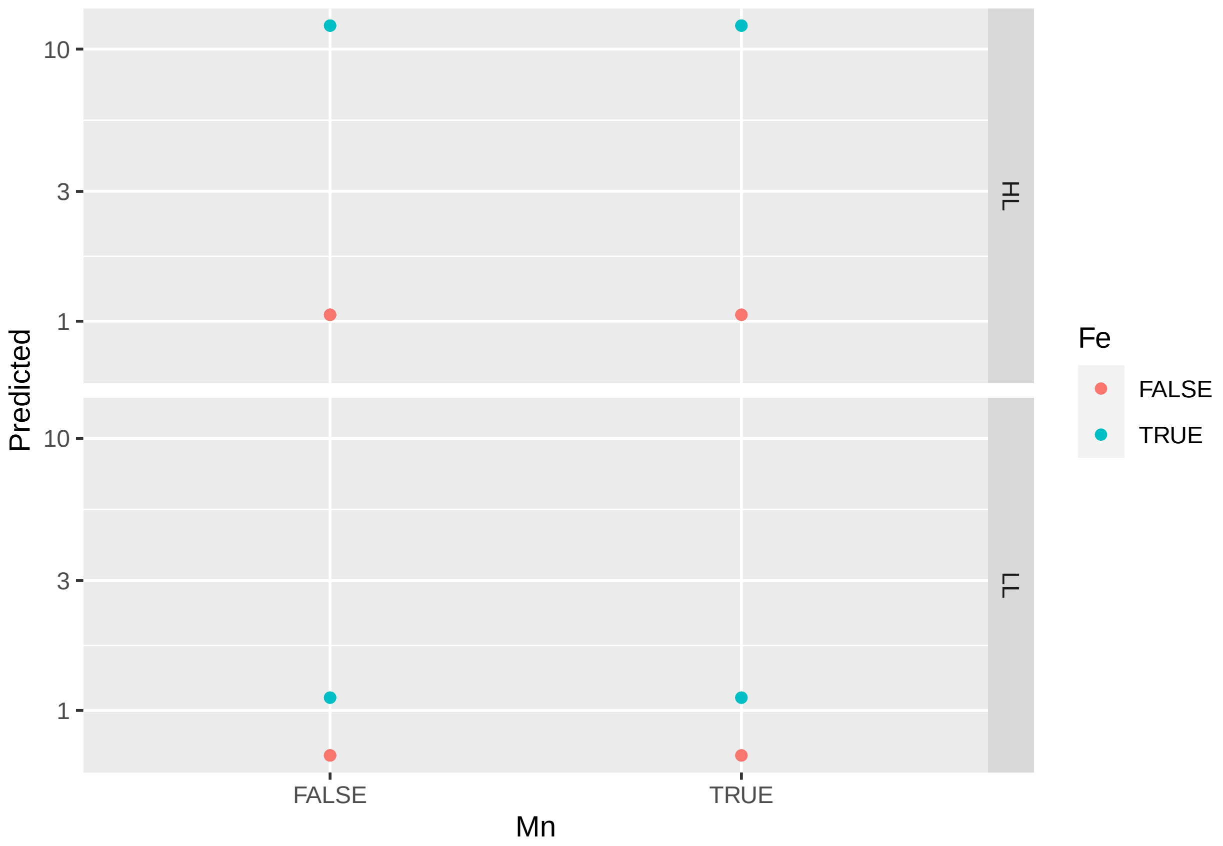
```r
#Report results
report(fit_best_Chla)
```

```
## We fitted a linear mixed model (estimated using ML and nloptwrap optimizer) to
## predict ln_Chla with Fe and Light (formula: ln_Chla ~ Fe + Light + Fe:Light).
## The model included Bottle as random effect (formula: ~1 | Bottle). The model's
## total explanatory power is substantial (conditional R2 = 0.99) and the part
## related to the fixed effects alone (marginal R2) is of 0.98. The model's
## intercept, corresponding to Fe = [?] and Light = HL, is at 0.05 (95% CI [-0.08,
## 0.19], t(20) = 0.83, p = 0.415). Within this model:
## 
##   - The effect of FeTRUE is statistically significant and positive (beta = 2.45,
## 95% CI [2.24, 2.65], t(20) = 25.20, p < .001; Std. beta = 2.12, 95% CI [1.95,
## 2.30])
##   - The effect of Light [LL] is statistically significant and negative (beta =
## -0.44, 95% CI [-0.62, -0.25], t(20) = -4.87, p < .001; Std. beta = -0.38, 95%
## CI [-0.54, -0.22])
```

```
##   - The effect of FeTRUE × Light [LL] is statistically significant and negative
## (beta = -1.96, 95% CI [-2.24, -1.68], t(20) = -14.49, p < .001; Std. beta =
## -1.70, 95% CI [-1.94, -1.45])
##
## Standardized parameters were obtained by fitting the model on a standardized
## version of the dataset. 95% Confidence Intervals (CIs) and p-values were
## computed using a Wald t-distribution approximation.
```

```
#Represent data predicted by the model vs real data
physio$Predicted <- exp(predict(fit_best_Chla, re.form = NA))
```





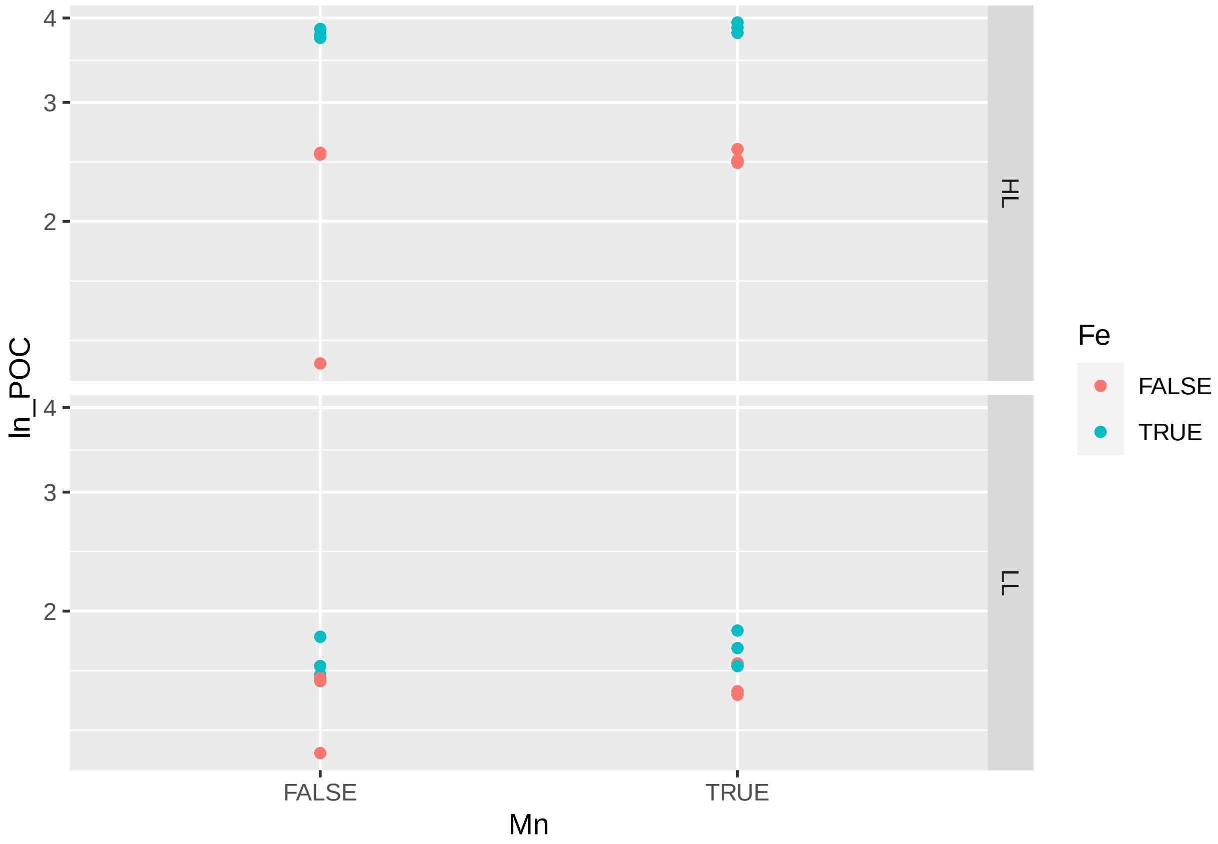
```r
#Pairwise comparison
emmeans (fit_best_Chla, pairwise ~ Fe + Light, adjust = "tukey")
```

```
## $emmeans
##  Fe    Light  emmean     SE   df lower.CL upper.CL
##  FALSE HL     0.0545 0.0868 27.7  -0.1233    0.232
##   TRUE HL     2.5013 0.0779 30.4   2.3423    2.660
##  FALSE LL    -0.3805 0.0868 27.7  -0.5584   -0.203
##   TRUE LL     0.1086 0.0779 30.4  -0.0504    0.268
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $contrasts
##  contrast             estimate    SE   df t.ratio p.value
##  FALSE HL - TRUE HL    -2.4468 0.117 30.4 -20.984  <.0001
##  FALSE HL - FALSE LL    0.4350 0.135 13.8   3.215  0.0286
##  FALSE HL - TRUE LL    -0.0541 0.117 30.4  -0.464  0.9664
##  TRUE HL - FALSE LL     2.8818 0.117 30.4  24.714  <.0001
##  TRUE HL - TRUE LL      2.3927 0.110 30.4  21.721  <.0001
##  FALSE LL - TRUE LL    -0.4891 0.117 30.4  -4.194  0.0012
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 4 estimates
```

3.2 Particulate Organic Carbon production

```
physio$ln_POC <- log(physio$POC_uM)   #data log-transformed
```

```
#Plot using ggplot2
ggplot(physio) +
  geom_point(aes(x = Mn, y = ln_POC, col = Fe)) +
  facet_grid(Light ~ .) +
  scale_y_log10()
```



```
#model fit with all factors (Mn, Fe and Light)
fit_POC <- lmer(ln_POC ~ Mn + Fe + Light +
               Mn:Fe + Mn:Light + Fe:Light + (1|Bottle),
             data = physio, na.action=na.fail, REML = FALSE)

summary(fit_POC)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_POC ~ Mn + Fe + Light + Mn:Fe + Mn:Light + Fe:Light + (1 |
##     Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##     15.3     26.6      1.4     -2.7       17
```

```
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.4796 -0.2044  0.0698  0.3089  1.0310
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.01921  0.1386
##  Residual             0.03382  0.1839
## Number of obs: 26, groups:  Bottle, 25
##
## Fixed effects:
##                Estimate Std. Error t value
## (Intercept)     2.22846    0.10891  20.461
## MnTRUE          0.21814    0.15474   1.410
## FeTRUE          1.51921    0.15474   9.818
## LightLL        -0.65397    0.13801  -4.739
## MnTRUE:FeTRUE  -0.05279    0.18334  -0.288
## MnTRUE:LightLL -0.18421    0.17897  -1.029
## FeTRUE:LightLL -1.35198    0.17897  -7.554
##
## Correlation of Fixed Effects:
##             (Intr) MnTRUE FeTRUE LghtLL MTRUE:F MTRUE:L
## MnTRUE      -0.610
## FeTRUE      -0.610  0.262
## LightLL     -0.634  0.297  0.297
## MTRUE:FTRUE  0.356 -0.562 -0.562  0.000
## MnTRUE:LgLL  0.326 -0.578  0.060 -0.514  0.000
## FTRUE:LghLL  0.326  0.060 -0.578 -0.514  0.000  -0.104
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_POC, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## ln_POC ~ Mn + Fe + Light + Mn:Fe + Mn:Light + Fe:Light + (1 |
##     Bottle)
##          npar    AIC     LRT   Pr(Chi)
## <none>         15.282
## Mn:Fe       1 13.364  0.0813    0.7756
## Mn:Light    1 14.250  0.9679    0.3252
## Fe:Light    1 42.334 29.0516 7.048e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#it shows that only the Fe:light interaction is significant
#non-significant interactions are removed from the model

#second model fit
fit_POC2 <- lmer(ln_POC ~ Mn + Fe + Light + Fe:Light + (1|Bottle),
                 data = physio, na.action=na.fail, REML = FALSE)
summary(fit_POC2)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_POC ~ Mn + Fe + Light + Fe:Light + (1 | Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##     12.3     21.2      0.8     -1.7       19
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.7193 -0.1278  0.1201  0.3053  0.8782
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.01700  0.1304
##  Residual             0.03816  0.1954
## Number of obs: 26, groups:  Bottle, 25
##
## Fixed effects:
##                Estimate Std. Error t value
## (Intercept)     2.27778    0.09743  23.378
## MnTRUE          0.10389    0.09328   1.114
## FeTRUE          1.50062    0.13039  11.508
## LightLL        -0.73895    0.12173  -6.071
## FeTRUE:LightLL -1.35909    0.18222  -7.459
##
## Correlation of Fixed Effects:
##             (Intr) MnTRUE FeTRUE LghtLL
## MnTRUE      -0.425
## FeTRUE      -0.595 -0.040
## LightLL     -0.625  0.000  0.467
## FTRUE:LghLL  0.417  0.000 -0.699 -0.668
```

```r
#drop function perform valid likelihood ratio tests
drop1(fit_POC2, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## ln_POC ~ Mn + Fe + Light + Fe:Light + (1 | Bottle)
##          npar    AIC     LRT   Pr(Chi)
## <none>         12.349
## Mn          1 11.536  1.1865    0.276
## Fe:Light    1 38.940 28.5909 8.94e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

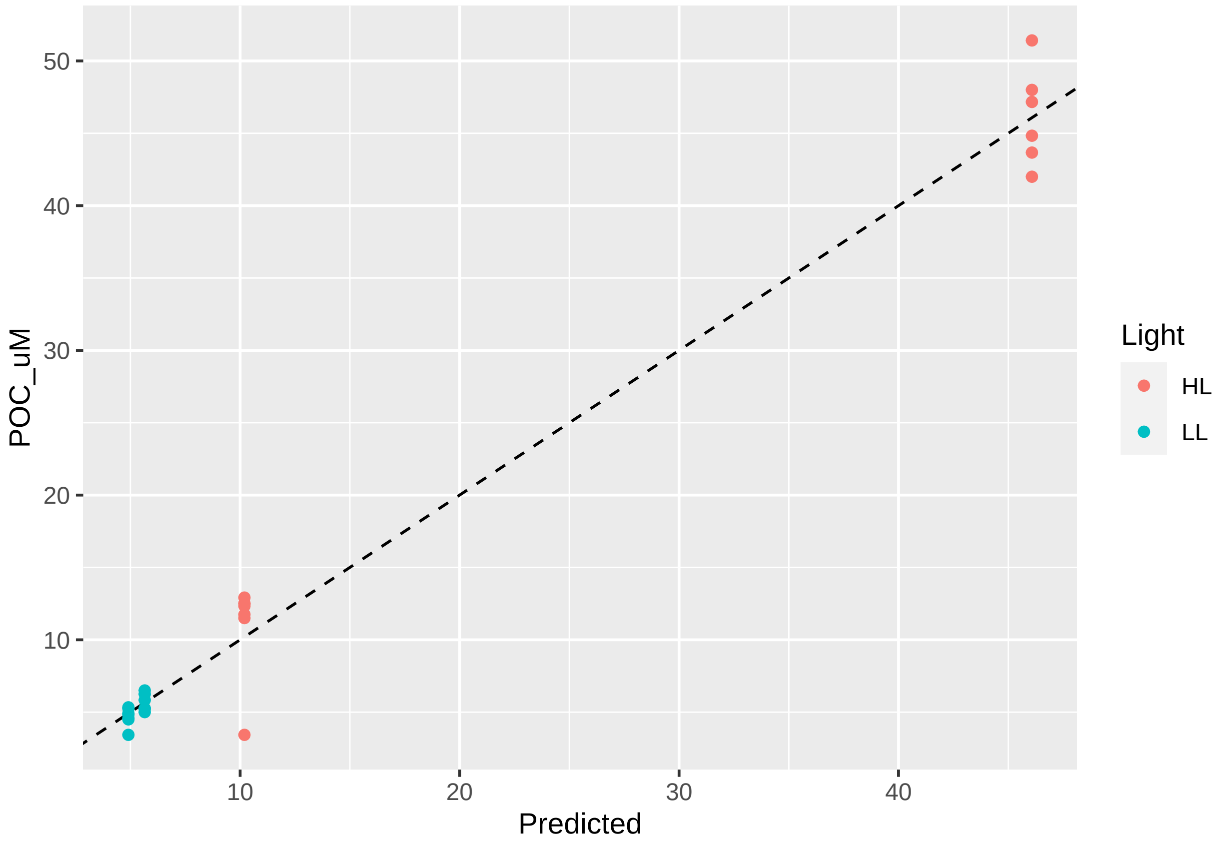
```r
#it shows that Mn does not influence particulate organic carbon concentrations
#Mn is removed from the model

#best model identified by drop
fit_best_POC <- lmer(ln_POC ~  Fe + Light + Fe:Light + (1|Bottle),
                  data = physio, na.action=na.fail, REML = FALSE)
summary(fit_best_POC)
```

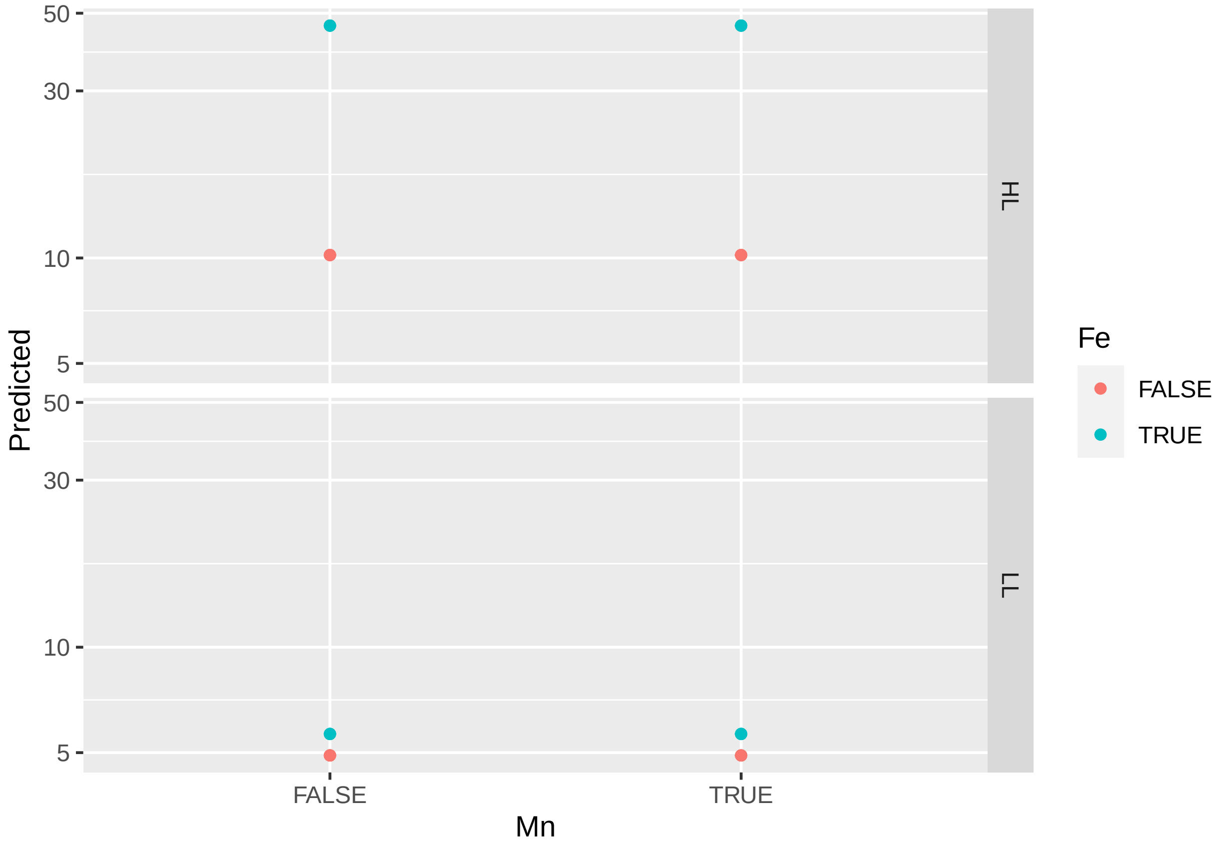
```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_POC ~ Fe + Light + Fe:Light + (1 | Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##     11.5     19.1      0.2     -0.5       20
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.6882 -0.2191  0.0918  0.3958  0.7957
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.01997  0.1413
##  Residual             0.03782  0.1945
## Number of obs: 26, groups:  Bottle, 25
##
## Fixed effects:
##                 Estimate Std. Error t value
## (Intercept)      2.32207    0.09013  25.762
## FeTRUE           1.50828    0.13326  11.319
## LightLL         -0.73083    0.12391  -5.898
## FeTRUE:LightLL -1.36722    0.18606  -7.348
##
## Correlation of Fixed Effects:
##              (Intr) FeTRUE LghtLL
## FeTRUE      -0.676
## LightLL     -0.687  0.465
## FTRUE:LghLL  0.458 -0.698 -0.666
```

```
#Report results
report(fit_best_POC)
```

```
## We fitted a linear mixed model (estimated using ML and nloptwrap optimizer) to
## predict ln_POC with Fe and Light (formula: ln_POC ~ Fe + Light + Fe:Light). The
## model included Bottle as random effect (formula: ~1 | Bottle). The model's
## total explanatory power is substantial (conditional R2 = 0.95) and the part
## related to the fixed effects alone (marginal R2) is of 0.93. The model's
## intercept, corresponding to Fe = [?] and Light = HL, is at 2.32 (95% CI [2.13,
## 2.51], t(20) = 25.76, p < .001). Within this model:
##
##   - The effect of FeTRUE is statistically significant and positive (beta = 1.51,
## 95% CI [1.23, 1.79], t(20) = 11.32, p < .001; Std. beta = 1.62, 95% CI [1.32,
## 1.92])
##   - The effect of Light [LL] is statistically significant and negative (beta =
## -0.73, 95% CI [-0.99, -0.47], t(20) = -5.90, p < .001; Std. beta = -0.79, 95%
## CI [-1.06, -0.51])
##   - The effect of FeTRUE × Light [LL] is statistically significant and negative
## (beta = -1.37, 95% CI [-1.76, -0.98], t(20) = -7.35, p < .001; Std. beta =
## -1.47, 95% CI [-1.89, -1.05])
##
## Standardized parameters were obtained by fitting the model on a standardized
## version of the dataset. 95% Confidence Intervals (CIs) and p-values were
## computed using a Wald t-distribution approximation.
```

```
#Represent data predicted by the model vs real data
physio$Predicted <- exp(predict(fit_best_POC, re.form = NA))
```





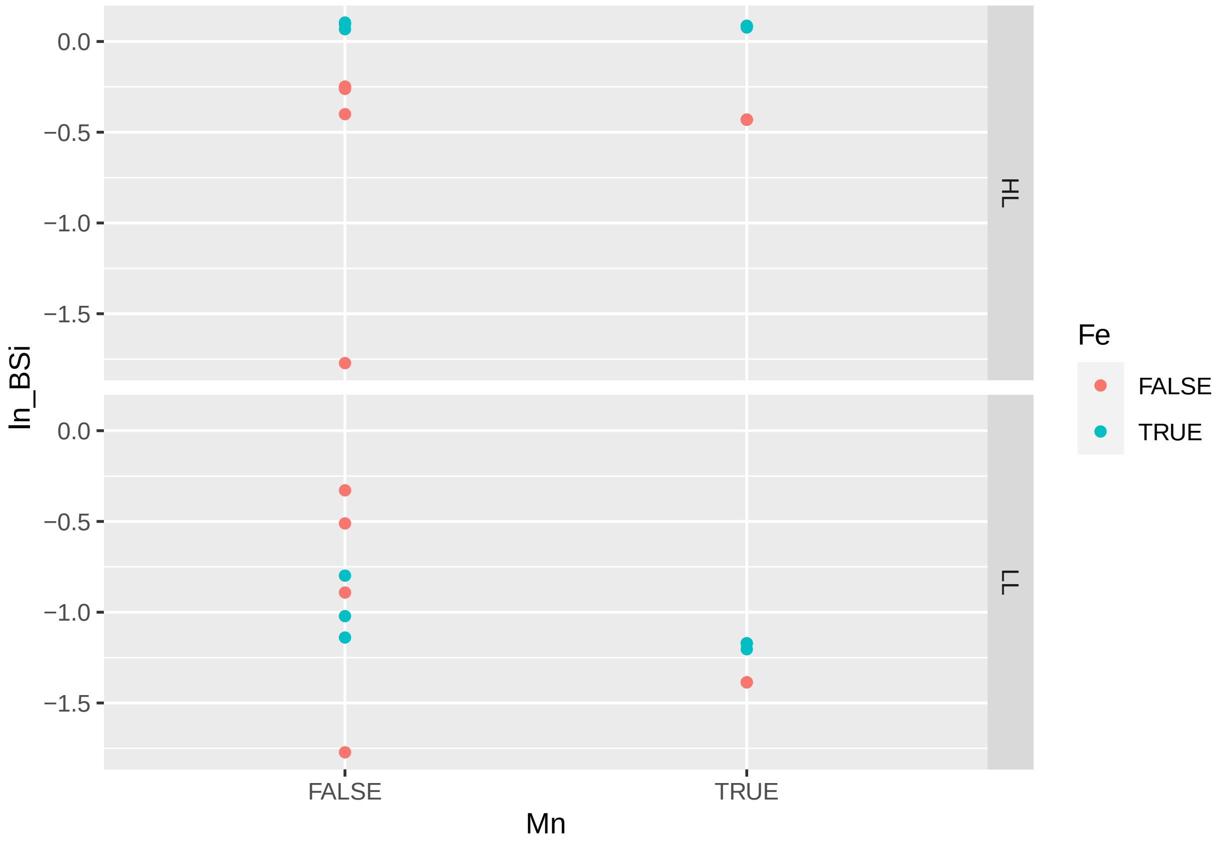
```
#Pairwise comparison
emmeans (fit_best_POC, pairwise ~ Fe + Light, adjust = "tukey")
```

```
## $emmeans
##  Fe    Light emmean    SE   df lower.CL upper.CL
##  FALSE HL      2.32 0.117 28.8     2.08     2.56
##   TRUE HL      3.83 0.107 30.5     3.61     4.05
##  FALSE LL      1.59 0.117 28.8     1.35     1.83
##   TRUE LL      1.73 0.107 30.5     1.51     1.95
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $contrasts
##  contrast            estimate    SE   df t.ratio p.value
##  FALSE HL - TRUE HL    -1.508 0.159 30.6  -9.513  <.0001
##  FALSE HL - FALSE LL    0.731 0.180 16.0   4.058  0.0046
##  FALSE HL - TRUE LL     0.590 0.159 30.6   3.720  0.0042
##  TRUE HL - FALSE LL     2.239 0.159 30.6  14.122  <.0001
##  TRUE HL - TRUE LL      2.098 0.151 30.5  13.905  <.0001
##  FALSE LL - TRUE LL    -0.141 0.159 30.6  -0.890  0.8102
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 4 estimates
```

3.3 Biogenic Silica

```
physio$ln_BSi <- log(physio$BSi_uM)   #data log-transformed
```

```
#Plot using ggplot2
ggplot(physio) +
  geom_point(aes(x = Mn, y = ln_BSi, col = Fe)) +
  facet_grid(Light ~ .)
```



```
#model fit with all factors (Mn, Fe and Light)
fit_BSi <- lmer(ln_BSi ~ Mn + Fe + Light +
               Mn:Fe + Mn:Light + Fe:Light + (1|Bottle),
             data = physio, na.action=na.fail, REML = FALSE)

summary(fit_BSi)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_BSi ~ Mn + Fe + Light + Mn:Fe + Mn:Light + Fe:Light + (1 |
##     Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##     -2.9      8.4     10.5    -20.9       17
##
```

```
## Scaled residuals:
##        Min         1Q     Median         3Q        Max
## -1.098e-06 -9.551e-08  7.951e-08  1.007e-07  2.946e-07
##
## Random effects:
##  Groups   Name        Variance  Std.Dev.
##  Bottle   (Intercept) 8.256e-02 2.873e-01
##  Residual             4.376e-15 6.615e-08
## Number of obs: 26, groups:  Bottle, 25
##
## Fixed effects:
##                  Estimate Std. Error t value
## (Intercept)    -6.169e-01  1.084e-01  -5.689
## MnTRUE          6.515e-02  1.862e-01   0.350
## FeTRUE          5.903e-01  1.862e-01   3.170
## LightLL        -8.407e-14  9.355e-08   0.000
## MnTRUE:FeTRUE   1.602e-01  2.301e-01   0.696
## MnTRUE:LightLL -6.523e-01  1.913e-01  -3.410
## FeTRUE:LightLL -8.441e-01  1.913e-01  -4.412
##
## Correlation of Fixed Effects:
##             (Intr) MnTRUE FeTRUE LghtLL MTRUE:F MTRUE:L
## MnTRUE      -0.582
## FeTRUE      -0.582  0.206
## LightLL      0.000  0.000  0.000
## MTRUE:FTRUE  0.471 -0.595 -0.595  0.000
## MnTRUE:LgLL  0.000 -0.515  0.258  0.000  0.001
## FTRUE:LghLL  0.000  0.258 -0.515  0.000  0.001  -0.500
## optimizer (nloptwrap) convergence code: 0 (OK)
## Model is nearly unidentifiable: very large eigenvalue
##  - Rescale variables?
```

```r
#drop function perform valid likelihood ratio tests
drop1(fit_BSi, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## ln_BSi ~ Mn + Fe + Light + Mn:Fe + Mn:Light + Fe:Light + (1 |
##     Bottle)
##          npar    AIC    LRT   Pr(Chi)
## <none>        -2.941
## Mn:Fe       1 -5.216 -0.275         1
## Mn:Light    1 29.851 34.792 3.669e-09 ***
## Fe:Light    1 33.758 38.700 4.943e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#it shows that Fe:light and Mn:Light interactions are significant
#all single factors: Fe, Mn and light are important for BSi concentrations

#best model identified by drop
fit_best_BSi <- lmer(ln_BSi ~ Fe + Mn + Light + Fe:Light + Mn:Light +
```

```
                       Mn:Fe + (1|Bottle),
                  data = physio, na.action=na.fail, REML = FALSE)
summary(fit_best_BSi)
```

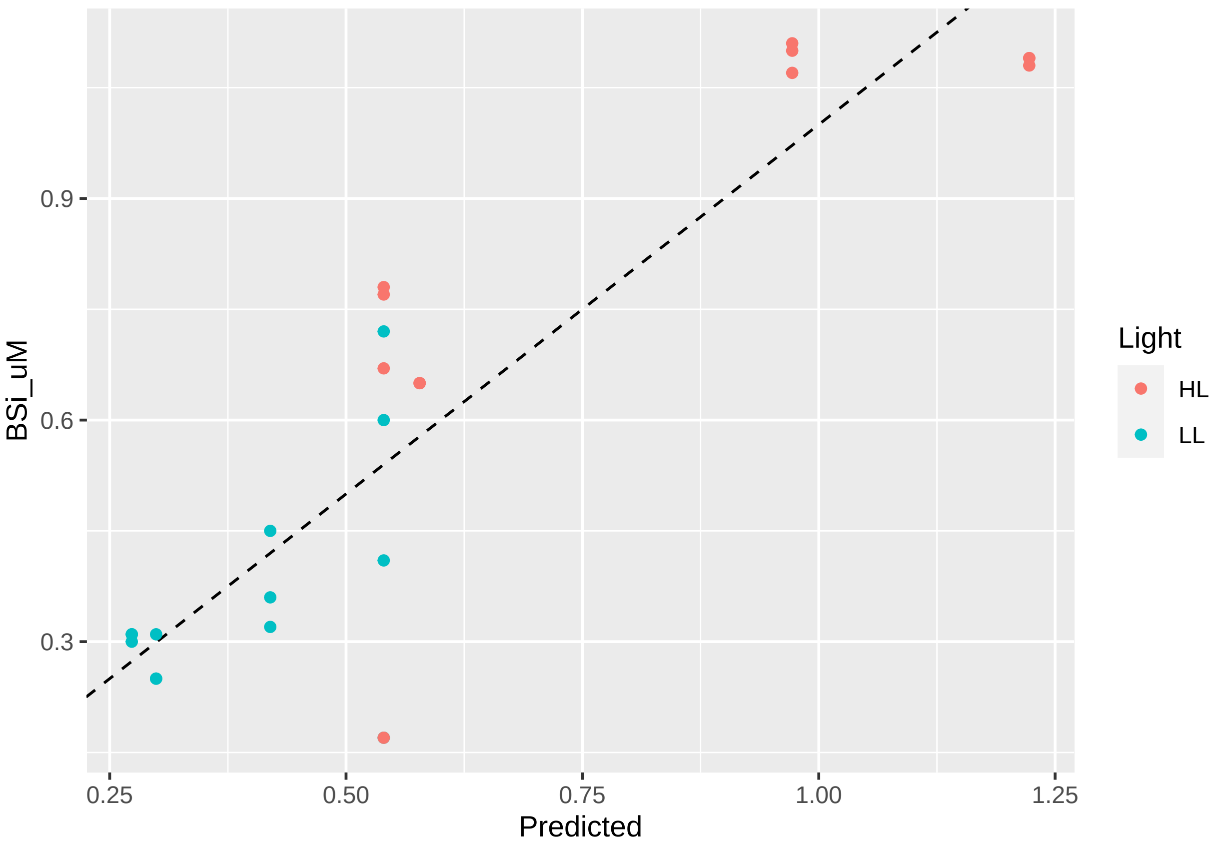
```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_BSi ~ Fe + Mn + Light + Fe:Light + Mn:Light + Mn:Fe + (1 |
##     Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##     -3.0      8.4     10.5    -21.0       17
##
## Scaled residuals:
##        Min         1Q     Median         3Q        Max
## -1.145e-06 -9.528e-08  7.982e-08  1.016e-07  2.905e-07
##
## Random effects:
##  Groups   Name        Variance  Std.Dev.
##  Bottle   (Intercept) 8.256e-02 2.873e-01
##  Residual             4.296e-15 6.554e-08
## Number of obs: 26, groups:  Bottle, 25
##
## Fixed effects:
##                   Estimate Std. Error t value
## (Intercept)    -6.165e-01  1.067e-01  -5.779
## FeTRUE          5.880e-01  1.855e-01   3.169
## MnTRUE          6.802e-02  1.855e-01   0.367
## LightLL        -9.030e-14  9.269e-08   0.000
## FeTRUE:LightLL -8.395e-01  1.922e-01  -4.367
## MnTRUE:LightLL -6.586e-01  1.922e-01  -3.426
## FeTRUE:MnTRUE   1.615e-01  2.301e-01   0.702
##
## Correlation of Fixed Effects:
##             (Intr) FeTRUE MnTRUE LghtLL FTRUE:L MTRUE:
## FeTRUE      -0.575
## MnTRUE      -0.575  0.197
## LightLL      0.000  0.000  0.000
## FTRUE:LghLL  0.000 -0.517  0.258  0.000
## MnTRUE:LgLL  0.000  0.258 -0.517  0.000 -0.500
## FTRUE:MTRUE  0.464 -0.590 -0.590  0.000 -0.001  -0.001
## optimizer (nloptwrap) convergence code: 0 (OK)
## Model is nearly unidentifiable: very large eigenvalue
##  - Rescale variables?
```

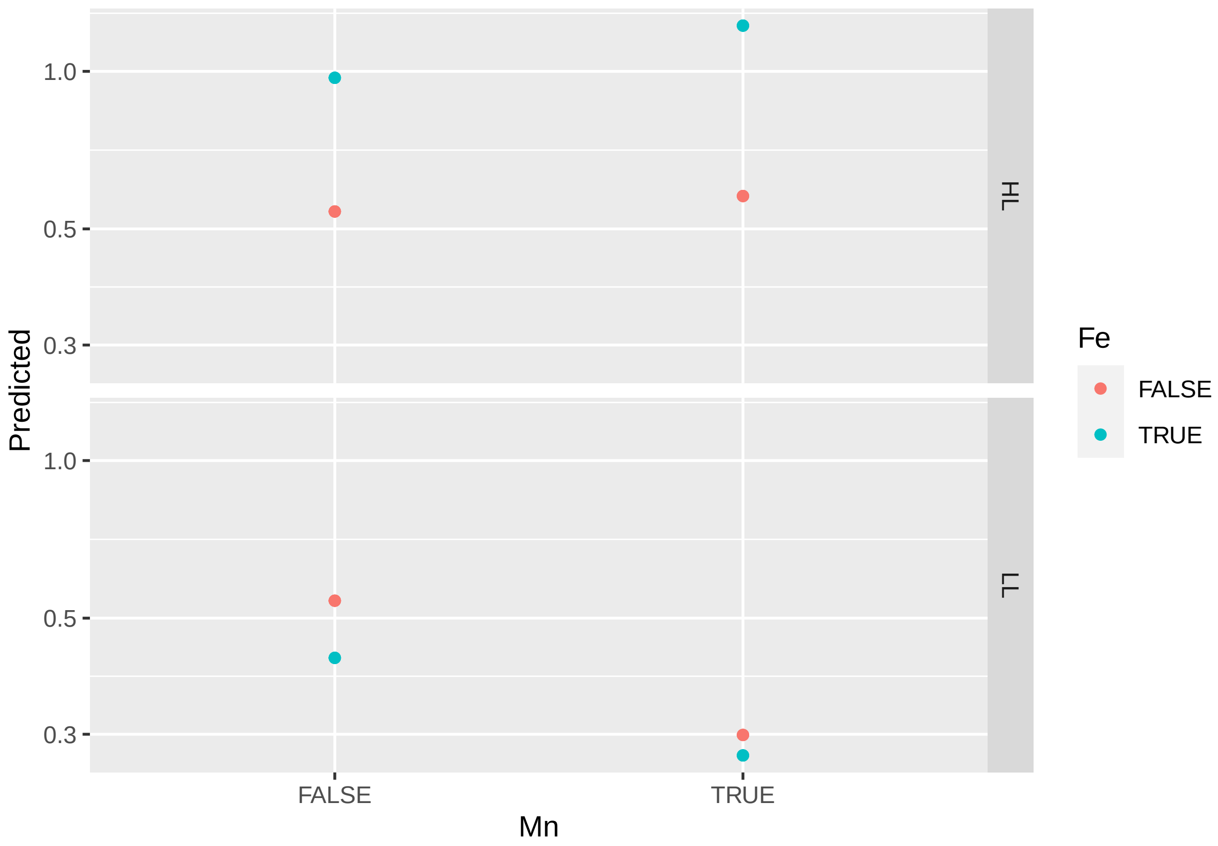
```
#Report results
report(fit_best_BSi)
```

```
## We fitted a linear mixed model (estimated using ML and nloptwrap optimizer) to
## predict ln_BSi with Fe, Mn and Light (formula: ln_BSi ~ Fe + Mn + Light +
## Fe:Light + Mn:Light + Mn:Fe). The model included Bottle as random effect
## (formula: ~1 | Bottle). The model's total explanatory power is substantial
## (conditional R2 = 1.00) and the part related to the fixed effects alone
```

```
## (marginal R2) is of 0.73. The model's intercept, corresponding to Fe = [?], Mn
## = [?] and Light = HL, is at -0.62 (95% CI [-0.84, -0.39], t(17) = -5.78, p <
## .001). Within this model:
##
##   - The effect of FeTRUE is statistically significant and positive (beta = 0.59,
## 95% CI [0.20, 0.98], t(17) = 3.17, p = 0.006; Std. beta = 0.96, 95% CI [0.33,
## 1.59])
##   - The effect of MnTRUE is statistically non-significant and positive (beta =
## 0.07, 95% CI [-0.32, 0.46], t(17) = 0.37, p = 0.718; Std. beta = 0.15, 95% CI
## [-0.48, 0.78])
##   - The effect of Light [LL] is statistically non-significant and negative (beta
## = -9.03e-14, 95% CI [-1.96e-07, 1.96e-07], t(17) = -9.74e-07, p > .999; Std.
## beta = -2.16e-14, 95% CI [-1.42e-07, 1.42e-07])
##   - The effect of FeTRUE × Light [LL] is statistically significant and negative
## (beta = -0.84, 95% CI [-1.25, -0.43], t(17) = -4.37, p < .001; Std. beta =
## -1.35, 95% CI [-2.02, -0.69])
##   - The effect of MnTRUE × Light [LL] is statistically significant and negative
## (beta = -0.66, 95% CI [-1.06, -0.25], t(17) = -3.43, p = 0.003; Std. beta =
## -1.12, 95% CI [-1.78, -0.46])
##   - The effect of FeTRUE × MnTRUE is statistically non-significant and positive
## (beta = 0.16, 95% CI [-0.32, 0.65], t(17) = 0.70, p = 0.492; Std. beta = 0.29,
## 95% CI [-0.50, 1.08])
##
## Standardized parameters were obtained by fitting the model on a standardized
## version of the dataset. 95% Confidence Intervals (CIs) and p-values were
## computed using a Wald t-distribution approximation.
```

```r
#Represent data predicted by the model vs real data
physio$Predicted <- exp(predict(fit_best_BSi, re.form = NA))
```


BSi_uM
0.9
0.6
0.3
0.25
0.50
0.75
1.00
1.25
Predicted
Light
HL
LL



```
#Pairwise comparison
emmeans (fit_best_BSi, pairwise ~ Fe + Mn + Light, adjust = "tukey")
```

```
## $emmeans
##  Fe    Mn    Light  emmean    SE   df lower.CL upper.CL
##  FALSE FALSE HL    -0.6165 0.268 34.9   -1.161  -0.0715
##   TRUE FALSE HL    -0.0285 0.194 33.6   -0.422   0.3652
##  FALSE  TRUE HL    -0.5485 0.194 33.6   -0.942  -0.1548
##   TRUE  TRUE HL     0.2010 0.194 33.3   -0.193   0.5948
##  FALSE FALSE LL    -0.6165 0.268 34.9   -1.161  -0.0715
##   TRUE FALSE LL    -0.8679 0.194 33.3   -1.262  -0.4742
##  FALSE  TRUE LL    -1.2070 0.194 33.3   -1.601  -0.8132
##   TRUE  TRUE LL    -1.2970 0.194 33.6   -1.691  -0.9034
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $contrasts
##  contrast                         estimate    SE  df t.ratio p.value
##  FALSE FALSE HL - TRUE FALSE HL     -0.588 0.269  34  -2.187  0.3843
##  FALSE FALSE HL - FALSE TRUE HL     -0.068 0.269  34  -0.253  1.0000
##  FALSE FALSE HL - TRUE TRUE HL      -0.817 0.383  34  -2.134  0.4148
##  FALSE FALSE HL - FALSE FALSE LL     0.000 0.473 Inf   0.000  1.0000
##  FALSE FALSE HL - TRUE FALSE LL      0.251 0.383  34   0.656  0.9976
##  FALSE FALSE HL - FALSE TRUE LL      0.591 0.383  34   1.542  0.7798
##  FALSE FALSE HL - TRUE TRUE LL       0.681 0.269  34   2.531  0.2171
```

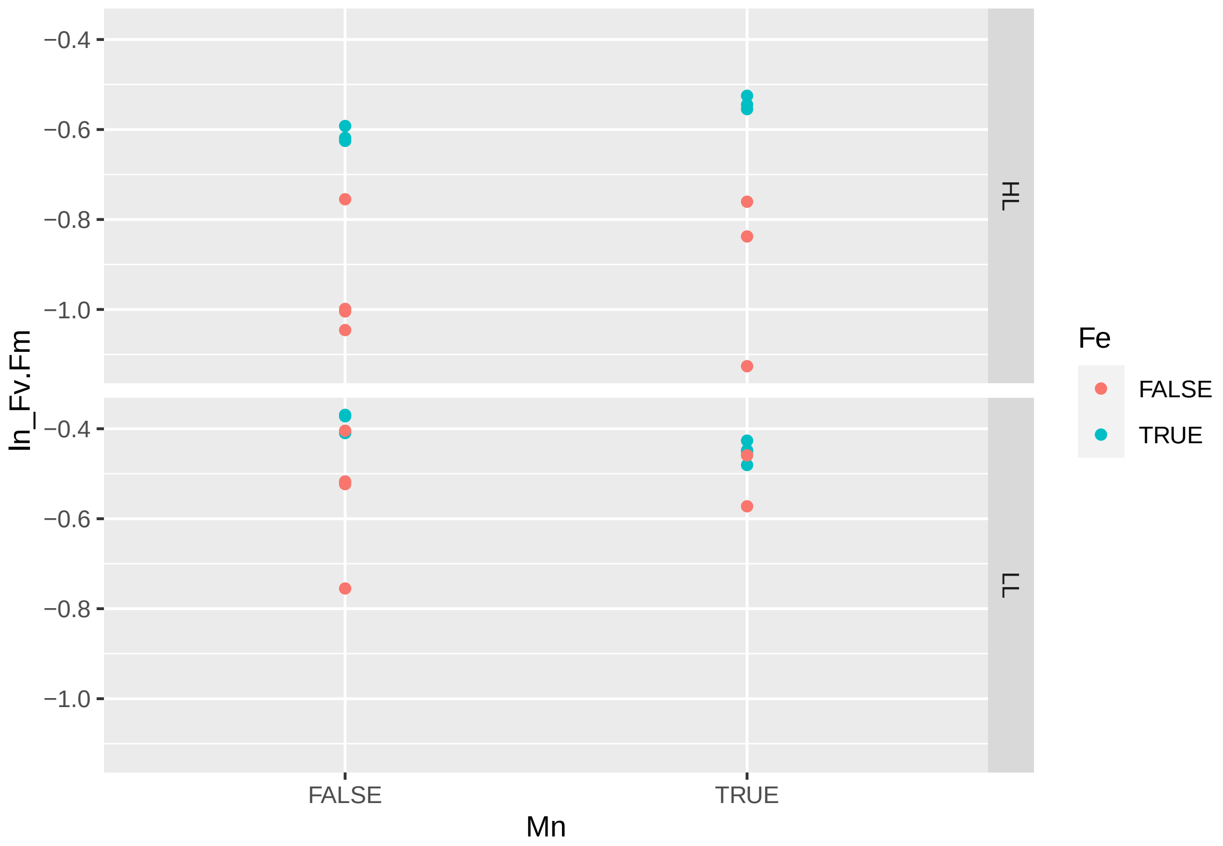
```
##  TRUE FALSE HL - FALSE TRUE HL      0.520 0.274  34   1.898  0.5616
##  TRUE FALSE HL - TRUE TRUE HL      -0.229 0.274  33  -0.839  0.9894
##  TRUE FALSE HL - FALSE FALSE LL     0.588 0.383  34   1.535  0.7834
##  TRUE FALSE HL - TRUE FALSE LL      0.839 0.274  33   3.068  0.0729
##  TRUE FALSE HL - FALSE TRUE LL      1.179 0.274  33   4.308  0.0031
##  TRUE FALSE HL - TRUE TRUE LL       1.269 0.274  34   4.630  0.0012
##  FALSE TRUE HL - TRUE TRUE HL      -0.749 0.274  33  -2.739  0.1465
##  FALSE TRUE HL - FALSE FALSE LL     0.068 0.383  34   0.178  1.0000
##  FALSE TRUE HL - TRUE FALSE LL      0.319 0.274  33   1.168  0.9355
##  FALSE TRUE HL - FALSE TRUE LL      0.659 0.274  33   2.407  0.2713
##  FALSE TRUE HL - TRUE TRUE LL       0.749 0.274  34   2.732  0.1476
##  TRUE TRUE HL - FALSE FALSE LL      0.817 0.269  34   3.040  0.0767
##  TRUE TRUE HL - TRUE FALSE LL       1.069 0.274  33   3.902  0.0094
##  TRUE TRUE HL - FALSE TRUE LL       1.408 0.274  33   5.139  0.0003
##  TRUE TRUE HL - TRUE TRUE LL        1.498 0.274  33   5.475  0.0001
##  FALSE FALSE LL - TRUE FALSE LL     0.251 0.269  34   0.935  0.9802
##  FALSE FALSE LL - FALSE TRUE LL     0.591 0.269  34   2.196  0.3790
##  FALSE FALSE LL - TRUE TRUE LL      0.681 0.383  34   1.777  0.6392
##  TRUE FALSE LL - FALSE TRUE LL      0.339 0.274  33   1.238  0.9144
##  TRUE FALSE LL - TRUE TRUE LL       0.429 0.274  33   1.568  0.7649
##  FALSE TRUE LL - TRUE TRUE LL       0.090 0.274  33   0.329  1.0000
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 8 estimates
```

4 Photophysiological responses

4.1 Fv/Fm

```r
physio$ln_Fv.Fm <- log(physio$Fv.Fm)   #data log-transformed
```

```r
#Plot using ggplot2
ggplot(physio) +
  geom_point(aes(x = Mn, y = ln_Fv.Fm, col = Fe)) +
  facet_grid(Light ~ .)
```



```
#model fit with all factors (Mn, Fe and Light)
fit_Fv.Fm <- lmer(ln_Fv.Fm ~ Mn + Fe + Light +
               Mn:Fe + Mn:Light + Fe:Light + (1|Bottle),
             data = physio, na.action=na.fail, REML = FALSE)

summary(fit_Fv.Fm)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_Fv.Fm ~ Mn + Fe + Light + Mn:Fe + Mn:Light + Fe:Light + (1 |
##     Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##    -33.0    -21.7     25.5    -51.0       17
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.62651 -0.36697  0.06611  0.39913  2.32821
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.000000 0.00000
##  Residual             0.008223 0.09068
## Number of obs: 26, groups:  Bottle, 25
##
```

```
## Fixed effects:
##                  Estimate Std. Error t value
## (Intercept)    -0.96615    0.04301 -22.461
## MnTRUE          0.07824    0.06064   1.290
## FeTRUE          0.37434    0.06064   6.173
## LightLL         0.43136    0.05735   7.521
## MnTRUE:FeTRUE  -0.04810    0.07169  -0.671
## MnTRUE:LightLL -0.05770    0.07153  -0.807
## FeTRUE:LightLL -0.24344    0.07153  -3.403
##
## Correlation of Fixed Effects:
##             (Intr) MnTRUE FeTRUE LghtLL MTRUE:F MTRUE:L
## MnTRUE      -0.604
## FeTRUE      -0.604  0.255
## LightLL     -0.667  0.315  0.315
## MTRUE:FTRUE  0.333 -0.552 -0.552  0.000
## MnTRUE:LgLL  0.356 -0.590  0.042 -0.535  0.000
## FTRUE:LghLL  0.356  0.042 -0.590 -0.535  0.000  -0.071
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_Fv.Fm, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## ln_Fv.Fm ~ Mn + Fe + Light + Mn:Fe + Mn:Light + Fe:Light + (1 |
##     Bottle)
##          npar     AIC    LRT  Pr(Chi)
## <none>        -33.036
## Mn:Fe       1 -34.589 0.4463 0.504075
## Mn:Light    1 -34.393 0.6426 0.422760
## Fe:Light    1 -25.456 9.5795 0.001968 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#it shows that only the Fe:light interaction is significant
#non-significant interactions are removed from the model

#second model fit
fit_Fv.Fm2 <- lmer(ln_Fv.Fm ~ Mn + Fe + Light + Fe:Light + (1|Bottle),
                  data = physio, na.action=na.fail, REML = FALSE)
summary(fit_Fv.Fm2)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_Fv.Fm ~ Mn + Fe + Light + Fe:Light + (1 | Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##    -36.0    -27.2     25.0    -50.0       19
##
## Scaled residuals:
```

```
##     Min      1Q  Median      3Q     Max 
## -2.3491 -0.5605  0.1240  0.6156  2.0430 
## 
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.000000 0.00000 
##  Residual             0.008571 0.09258 
## Number of obs: 26, groups:  Bottle, 25
## 
## Fixed effects:
##                Estimate Std. Error t value
## (Intercept)    -0.94417    0.03833 -24.631
## MnTRUE          0.02695    0.03651   0.738
## FeTRUE          0.35395    0.05157   6.863
## LightLL         0.40663    0.04949   8.217
## FeTRUE:LightLL -0.24756    0.07284  -3.399
## 
## Correlation of Fixed Effects:
##             (Intr) MnTRUE FeTRUE LghtLL
## MnTRUE      -0.408                     
## FeTRUE      -0.599 -0.051              
## LightLL     -0.645  0.000  0.480       
## FTRUE:LghLL  0.439  0.000 -0.706 -0.679
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_Fv.Fm2, test = "Chisq")
```

```
## Single term deletions
## 
## Model:
## ln_Fv.Fm ~ Mn + Fe + Light + Fe:Light + (1 | Bottle)
##          npar     AIC    LRT   Pr(Chi)   
## <none>        -35.957                    
## Mn          1 -37.419 0.5389 0.462888   
## Fe:Light    1 -28.400 9.5573 0.001992 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#it shows that Mn does not influence Fv/Fm
#Mn is removed from the model

#best model identified by drop
fit_best_Fv.Fm <- lmer(ln_Fv.Fm ~  Fe + Light + Fe:Light + (1|Bottle),
                  data = physio, na.action=na.fail, REML = FALSE)
summary(fit_best_Fv.Fm)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_Fv.Fm ~ Fe + Light + Fe:Light + (1 | Bottle)
##    Data: physio
## 
##      AIC      BIC   logLik deviance df.resid
```

```
##    -37.4    -29.9     24.7    -49.4       20
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.44834 -0.51321  0.05801  0.54455  1.89847
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.000000 0.00000
##  Residual             0.008751 0.09355
## Number of obs: 26, groups:  Bottle, 25
##
## Fixed effects:
##                Estimate Std. Error t value
## (Intercept)    -0.93262    0.03536 -26.377
## FeTRUE          0.35588    0.05204   6.838
## LightLL         0.40663    0.05000   8.132
## FeTRUE:LightLL -0.24756    0.07360  -3.364
##
## Correlation of Fixed Effects:
##             (Intr) FeTRUE LghtLL
## FeTRUE      -0.679
## LightLL     -0.707  0.480
## FTRUE:LghLL  0.480 -0.707 -0.679
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
#Report results
report(fit_best_Fv.Fm)
```

```
## Random effect variances not available. Returned R2 does not account for random effects.
## Random effect variances not available. Returned R2 does not account for random effects.
```

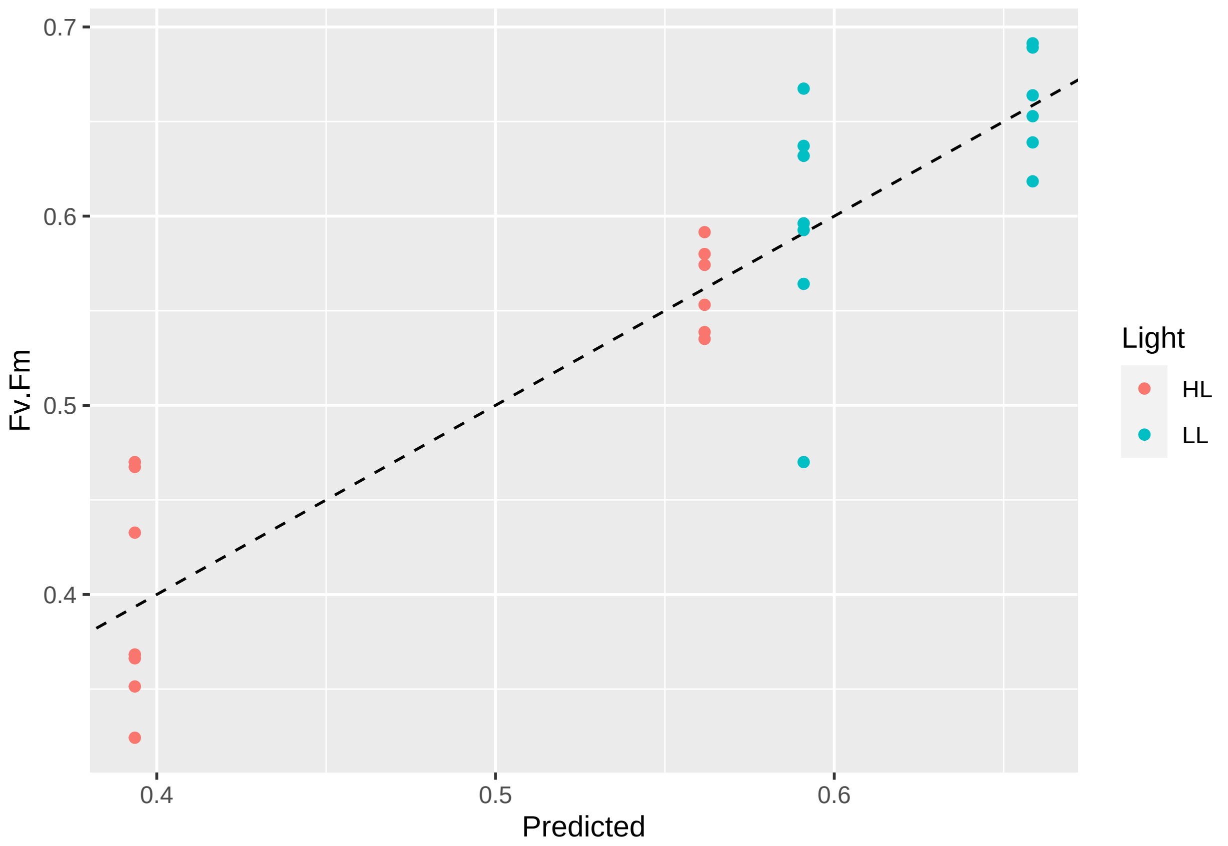
```
## We fitted a linear mixed model (estimated using ML and nloptwrap optimizer) to
## predict ln_Fv.Fm with Fe and Light (formula: ln_Fv.Fm ~ Fe + Light + Fe:Light).
## The model included Bottle as random effect (formula: ~1 | Bottle). The model's
## explanatory power related to the fixed effects alone (marginal R2) is 0.82. The
## model's intercept, corresponding to Fe = [?] and Light = HL, is at -0.93 (95%
## CI [-1.01, -0.86], t(20) = -26.38, p < .001). Within this model:
##
##   - The effect of FeTRUE is statistically significant and positive (beta = 0.36,
## 95% CI [0.25, 0.46], t(20) = 6.84, p < .001; Std. beta = 1.60, 95% CI [1.11,
## 2.09])
##   - The effect of Light [LL] is statistically significant and positive (beta =
## 0.41, 95% CI [0.30, 0.51], t(20) = 8.13, p < .001; Std. beta = 1.83, 95% CI
## [1.36, 2.30])
##   - The effect of FeTRUE × Light [LL] is statistically significant and negative
## (beta = -0.25, 95% CI [-0.40, -0.09], t(20) = -3.36, p = 0.003; Std. beta =
## -1.12, 95% CI [-1.81, -0.42])
##
## Standardized parameters were obtained by fitting the model on a standardized
## version of the dataset. 95% Confidence Intervals (CIs) and p-values were
## computed using a Wald t-distribution approximation.
```

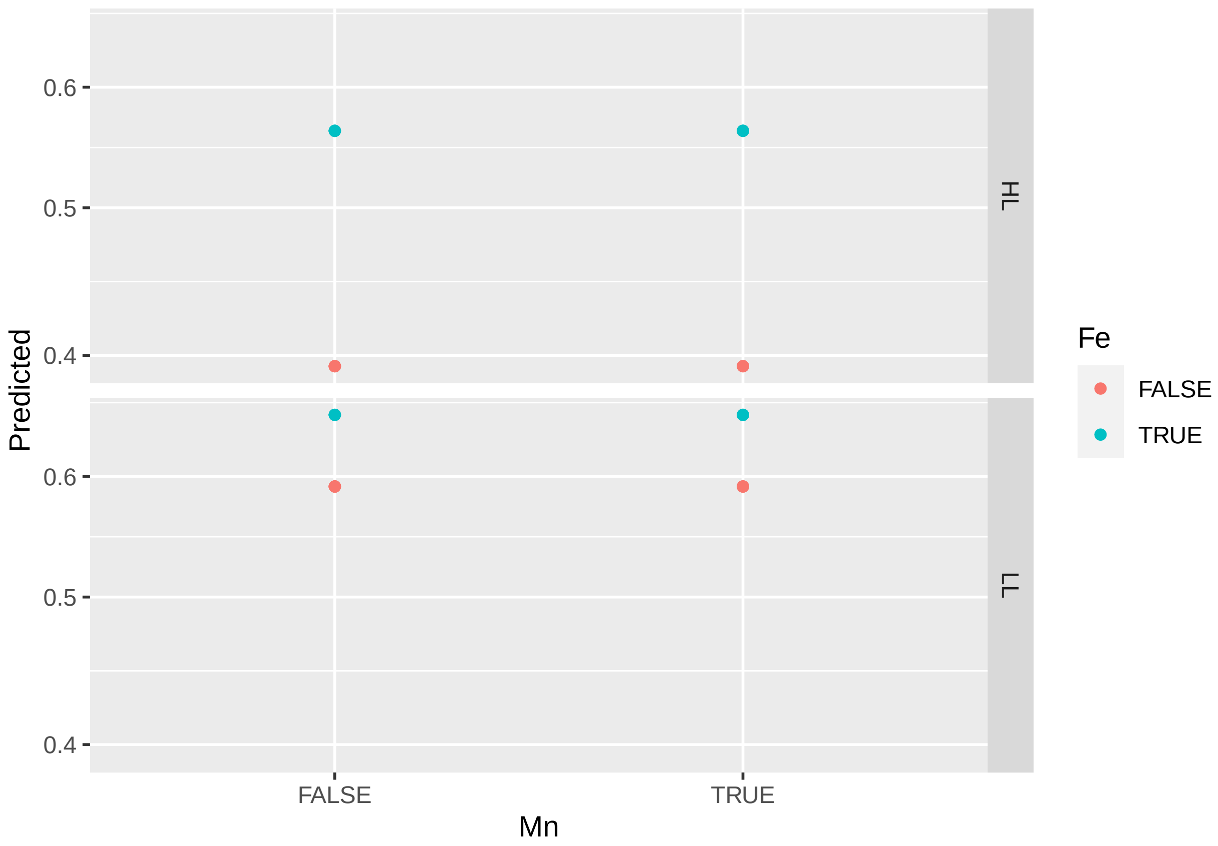
```
#Represent data predicted by the model vs real data
physio$Predicted <- exp(predict(fit_best_Fv.Fm, re.form = NA))
```

```
#Pairwise comparison
emmeans (fit_best_Fv.Fm, pairwise ~ Fe + Light, adjust = "tukey")
```

```
## boundary (singular) fit: see help('isSingular')
```

```
## $emmeans
##  Fe    Light emmean     SE   df lower.CL upper.CL
##  FALSE HL    -0.933 0.0444 30.7   -1.023   -0.842
##   TRUE HL    -0.577 0.0415 30.7   -0.661   -0.492
##  FALSE LL    -0.526 0.0444 30.7   -0.617   -0.435
##   TRUE LL    -0.418 0.0415 30.7   -0.502   -0.333
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $contrasts
##  contrast            estimate     SE   df t.ratio p.value
##  FALSE HL - TRUE HL   -0.3559 0.0608 30.7  -5.856  <.0001
##  FALSE HL - FALSE LL  -0.4066 0.0628 23.5  -6.478  <.0001
##  FALSE HL - TRUE LL   -0.5149 0.0608 30.7  -8.473  <.0001
##  TRUE HL - FALSE LL   -0.0508 0.0608 30.7  -0.835  0.8374
##  TRUE HL - TRUE LL    -0.1591 0.0587 30.7  -2.709  0.0507
##  FALSE LL - TRUE LL   -0.1083 0.0608 30.7  -1.782  0.3010
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 4 estimates
```

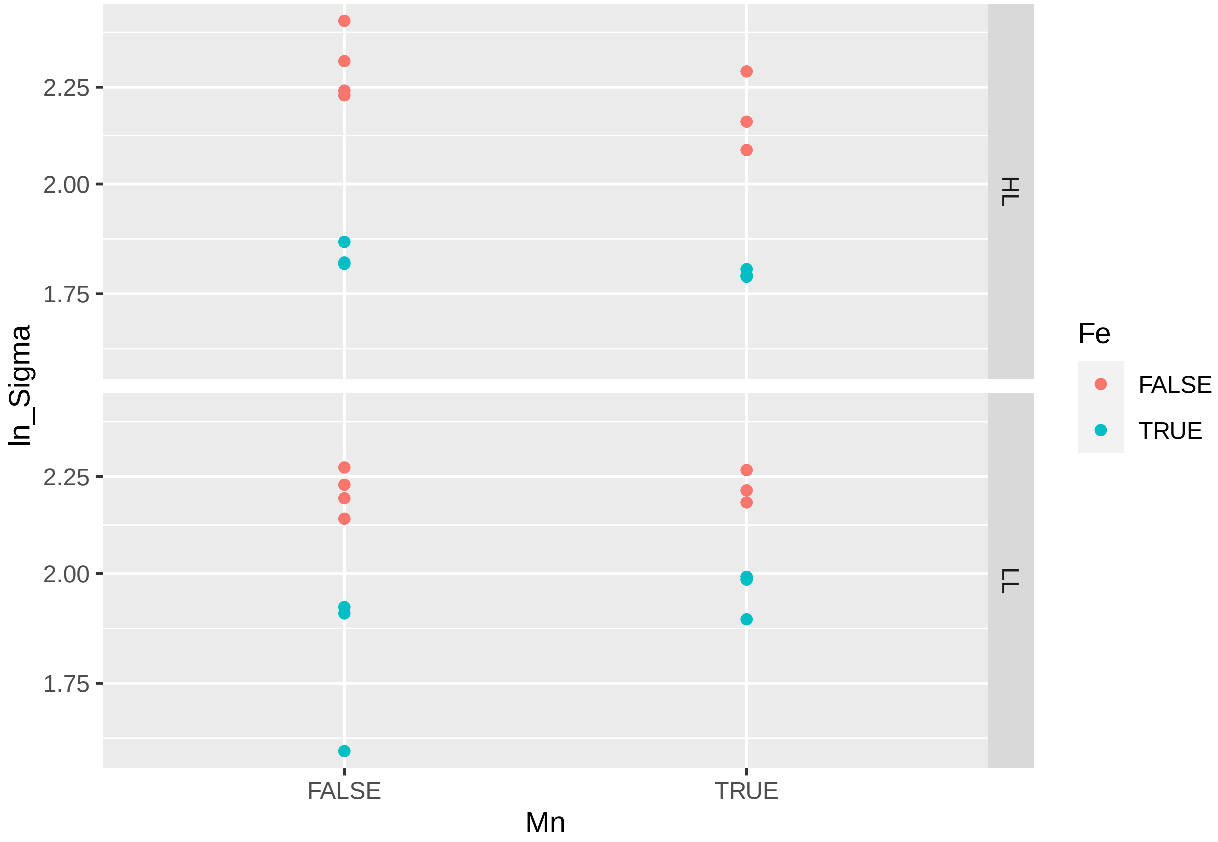

0.7
0.6
0.5
0.4
Fv.Fm
0.4
0.5
0.6
Predicted
Light
HL
LL



4.2 Sigma

```
physio$ln_Sigma <- log(physio$sigma_nm2.quanta.1)   #data log-transformed
```

```
#Plot using ggplot2
ggplot(physio) +
  geom_point(aes(x = Mn, y = ln_Sigma, col = Fe)) +
  facet_grid(Light ~ .) +
  scale_y_log10()
```



```
#model fit with all factors (Mn, Fe and Light)
fit_Sigma <- lmer(ln_Sigma ~ Mn + Fe + Light +
               Mn:Fe + Mn:Light + Fe:Light + (1|Bottle),
             data = physio, na.action=na.fail, REML = FALSE)

summary(fit_Sigma)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_Sigma ~ Mn + Fe + Light + Mn:Fe + Mn:Light + Fe:Light + (1 |
##     Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##    -45.2    -33.9     31.6    -63.2       17
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.8729 -0.5290 -0.1223  0.5616  1.7719
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.000000 0.0000
##  Residual             0.005155 0.0718
## Number of obs: 26, groups:  Bottle, 25
##
```

```
## Fixed effects:
##                 Estimate Std. Error t value
## (Intercept)      2.31164    0.03406  67.875
## MnTRUE          -0.13871    0.04802  -2.889
## FeTRUE          -0.48489    0.04802 -10.099
## LightLL         -0.10771    0.04541  -2.372
## MnTRUE:FeTRUE    0.11094    0.05676   1.954
## MnTRUE:LightLL   0.16072    0.05664   2.838
## FeTRUE:LightLL   0.09867    0.05664   1.742
##
## Correlation of Fixed Effects:
##              (Intr) MnTRUE FeTRUE LghtLL MTRUE:F MTRUE:L
## MnTRUE       -0.604
## FeTRUE       -0.604  0.255
## LightLL      -0.667  0.315  0.315
## MTRUE:FTRUE   0.333 -0.552 -0.552  0.000
## MnTRUE:LgLL   0.356 -0.590  0.042 -0.535  0.000
## FTRUE:LghLL   0.356  0.042 -0.590 -0.535  0.000  -0.071
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_Sigma, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## ln_Sigma ~ Mn + Fe + Light + Mn:Fe + Mn:Light + Fe:Light + (1 |
##     Bottle)
##          npar     AIC     LRT Pr(Chi)
## <none>        -45.177
## Mn:Fe       1 -43.613   3.564 0.05904 .
## Mn:Light    1 -67.659 -20.482 1.00000
## Fe:Light    1 -70.401 -23.224 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#it shows none of the interactions are significant
#all interactions are removed from the model

#second model fit
fit_Sigma2 <- lmer(ln_Sigma ~ Mn + Fe + Light + (1|Bottle),
                  data = physio, na.action=na.fail, REML = FALSE)
summary(fit_Sigma2)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: ln_Sigma ~ Mn + Fe + Light + (1 | Bottle)
##    Data: physio
##
##      AIC      BIC   logLik deviance df.resid
##    -67.4    -59.8     39.7    -79.4       20
##
## Scaled residuals:
```

```
##        Min         1Q     Median         3Q        Max 
## -1.145e-06 -2.638e-07 -2.792e-08  2.918e-07  9.716e-07 
## 
## Random effects:
##  Groups   Name        Variance  Std.Dev. 
##  Bottle   (Intercept) 8.300e-03 9.111e-02
##  Residual             1.581e-15 3.977e-08
## Number of obs: 26, groups:  Bottle, 25
## 
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept)  2.233e+00  3.028e-02  73.765
## MnTRUE      -4.253e-03  3.646e-02  -0.117
## FeTRUE      -3.834e-01  3.646e-02 -10.517
## LightLL      5.291e-14  5.624e-08   0.000
## 
## Correlation of Fixed Effects:
##         (Intr) MnTRUE FeTRUE
## MnTRUE  -0.553              
## FeTRUE  -0.553 -0.041       
## LightLL  0.000  0.000  0.000
## optimizer (nloptwrap) convergence code: 0 (OK)
## Model is nearly unidentifiable: very large eigenvalue
##  - Rescale variables?
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_Sigma2, test = "Chisq")
```

```
## Single term deletions
## 
## Model:
## ln_Sigma ~ Mn + Fe + Light + (1 | Bottle)
##        npar     AIC    LRT   Pr(Chi)    
## <none>      -67.389                     
## Mn        1 -68.904  0.485    0.4862    
## Fe        1 -26.779 42.610 6.683e-11 ***
## Light     1 -68.701  0.688    0.4069    
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
```

```
#only Fe significantly influences sigma
#no pairwise comparison will be performed due to only 1 factor identified

#best model identified by drop
fit_best_Sigma <- lmer(ln_Sigma ~ Fe + (1|Bottle),
                  data = physio, na.action=na.fail, REML = FALSE)
summary(fit_best_Sigma)
```

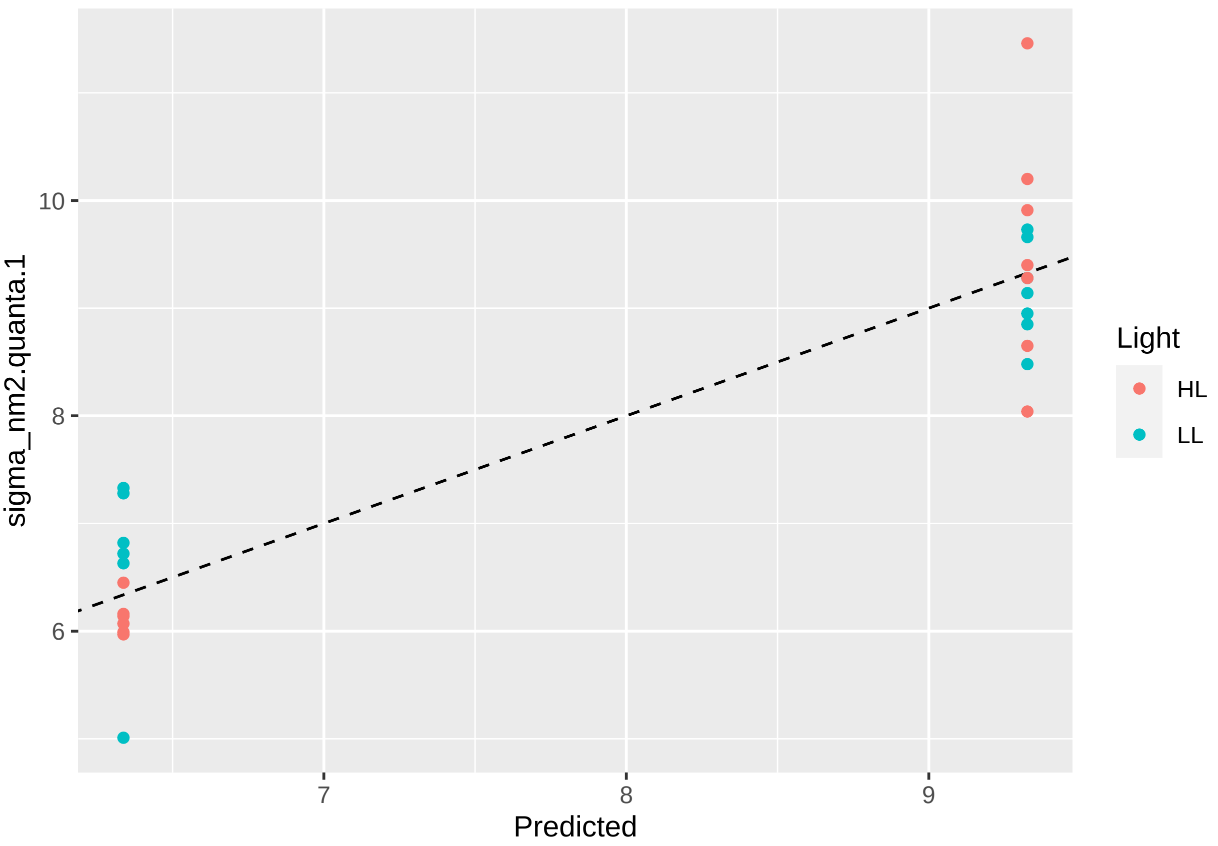
```
## Linear mixed model fit by maximum likelihood  [’lmerMod’]
## Formula: ln_Sigma ~ Fe + (1 | Bottle)
##    Data: physio
## 
##      AIC      BIC   logLik deviance df.resid
```

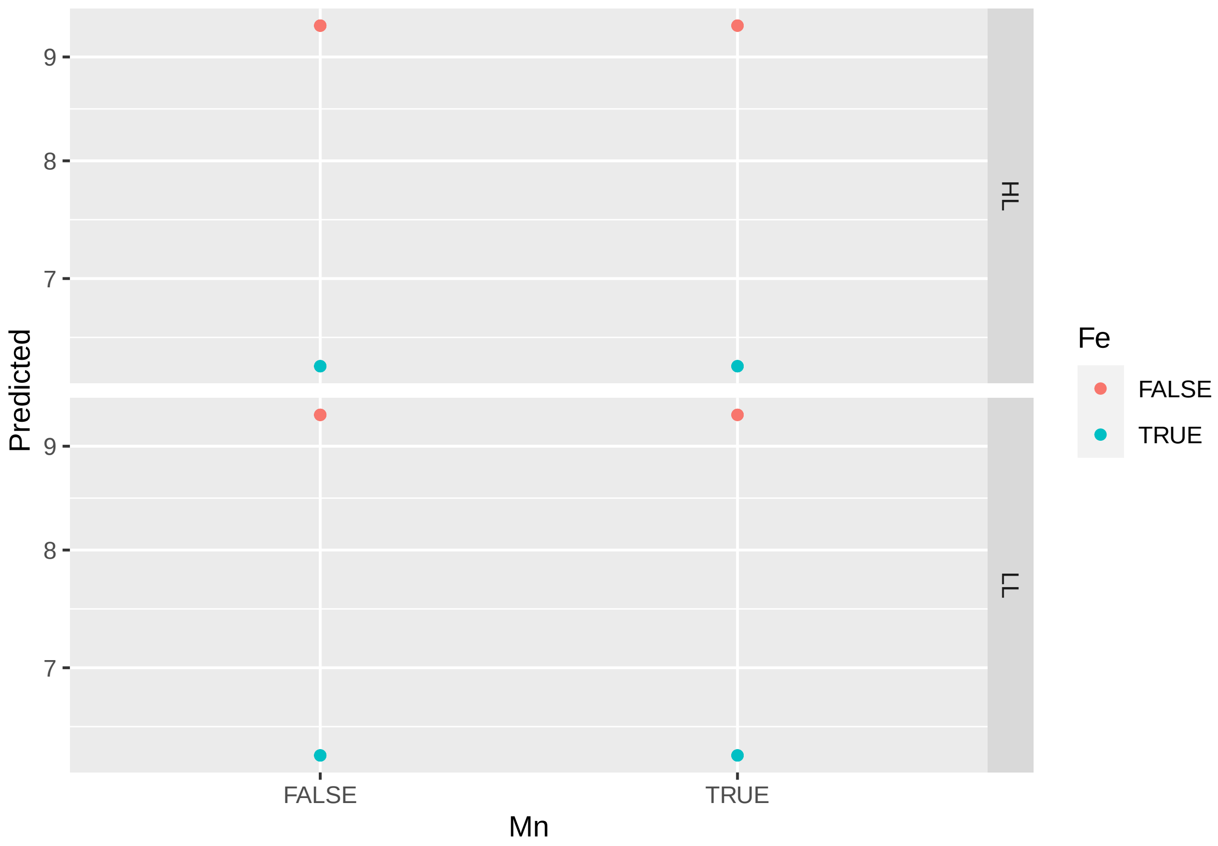
```
##    -71.0    -66.0     39.5    -79.0       22
##
## Scaled residuals:
##        Min         1Q     Median         3Q        Max
## -1.345e-06 -2.860e-07 -9.380e-09  3.164e-07  1.172e-06
##
## Random effects:
##  Groups   Name        Variance  Std.Dev.
##  Bottle   (Intercept) 8.311e-03 9.116e-02
##  Residual             2.243e-15 4.736e-08
## Number of obs: 26, groups:  Bottle, 25
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  2.23279    0.02528   88.32
## FeTRUE      -0.38630    0.03649  -10.59
##
## Correlation of Fixed Effects:
##        (Intr)
## FeTRUE -0.693
## optimizer (nloptwrap) convergence code: 0 (OK)
## Model failed to converge with max|grad| = 0.0315041 (tol = 0.002, component 1)
## Model is nearly unidentifiable: very large eigenvalue
##  - Rescale variables?
```

```
#Report results
report(fit_best_Sigma)
```

```
## We fitted a linear mixed model (estimated using ML and nloptwrap optimizer) to
## predict ln_Sigma with Fe (formula: ln_Sigma ~ Fe). The model included Bottle as
## random effect (formula: ~1 | Bottle). The model's total explanatory power is
## substantial (conditional R2 = 1.00) and the part related to the fixed effects
## alone (marginal R2) is of 0.82. The model's intercept, corresponding to Fe =
## [?], is at 2.23 (95% CI [2.18, 2.29], t(22) = 88.32, p < .001). Within this
## model:
##
##   - The effect of FeTRUE is statistically significant and negative (beta = -0.39,
## 95% CI [-0.46, -0.31], t(22) = -10.59, p < .001; Std. beta = -1.75, 95% CI
## [-2.09, -1.40])
##
## Standardized parameters were obtained by fitting the model on a standardized
## version of the dataset. 95% Confidence Intervals (CIs) and p-values were
## computed using a Wald t-distribution approximation.
```

```
#Represent data predicted by the model vs real data
physio$Predicted <- exp(predict(fit_best_Sigma, re.form = NA))
```


sigma_nm2.quanta.1
10
8
6
7
8
9
Predicted
Light
HL
LL



5 Phytoplankton community shift

```
FC <- read.csv("2SOLTEE_FC.csv")

#Calculation of Fpop using the equation of Bach et al. 2018
populations  <- c("Picoeukaryotes", "Nanoeukaryotes", "Microeukaryotes", "all_fluo")
addition_treatments <- c("Initial", "Control", "+Mn", "+Fe", "+FeMn")
light_conditions  <- c("HL", "LL")

# Create an empty data frame to store the results
results_df <- data.frame(Light = character(0), Treatment = character(0),
                         Replicate = integer(0), Pop = character(0),
                         Fpop = numeric(0), Fpop_percent = numeric(0),
                         Mn = logical(0), Fe = logical(0))

# Iterate through light conditions
for (light_condition in light_conditions) {
  # Iterate through addition treatments
  for (addition_treatment in addition_treatments) {
    # Determine Mn and Fe conditions based on treatment name
    is_Mn <- grepl("\\+Mn|FeMn", addition_treatment, ignore.case = TRUE)
    is_Fe <- grepl("\\+Fe|FeMn", addition_treatment)
```

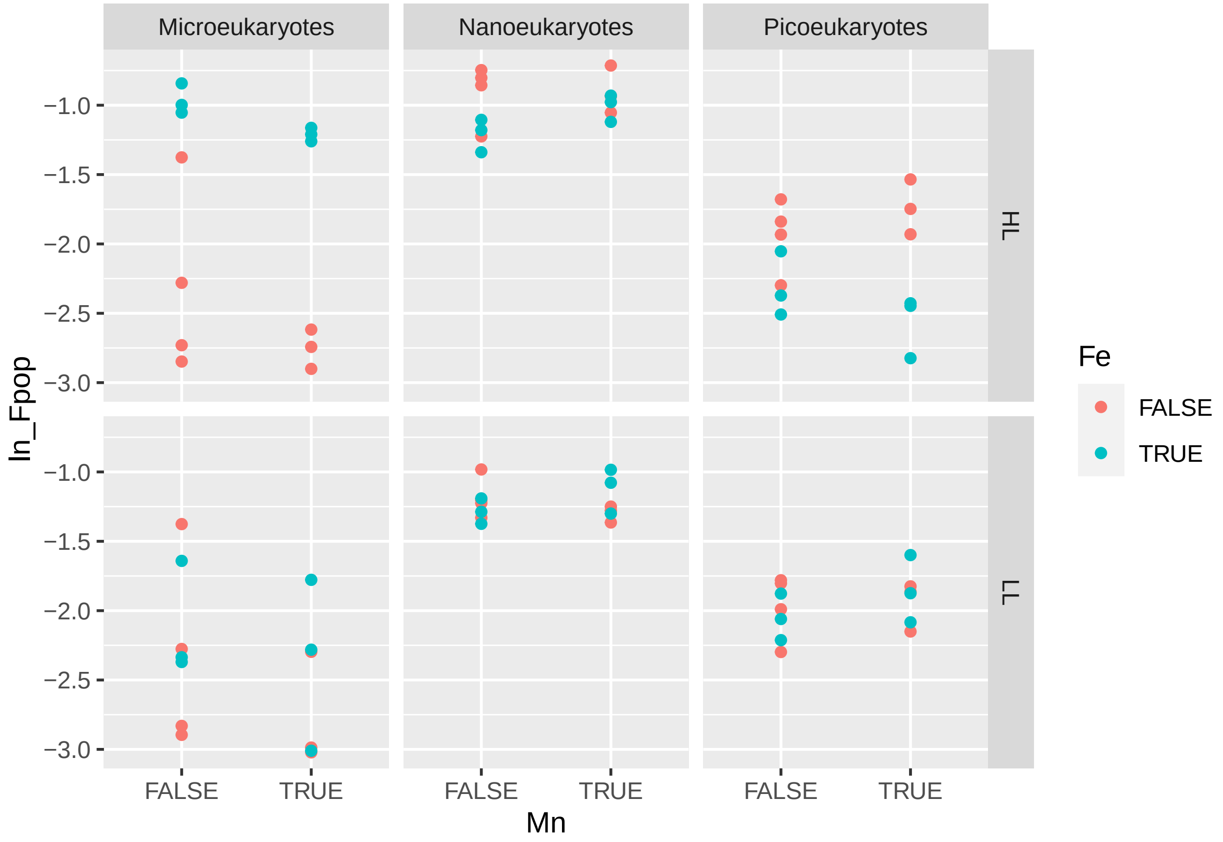
```r
    #Subset the data for the current combination of light and addition treatments
    subset_data <- subset(FC, Treatment == addition_treatment &
                           Light == light_condition)

    #Iterate through replicates within the current combination
    replicates <- unique(subset_data$Replicate)

    for (replicate in replicates) {
      #Subset the data for the current replicate
      replicate_data <- subset(subset_data, Replicate == replicate)

      #Calculate the abundance and biovolume for the "all phyto" population
      #specific to this replicate
      all_phyto_abundance <- sum(replicate_data$cell.count_ml[
        replicate_data$Pop == "all_fluo"])
      all_phyto_biovolume <- sum(replicate_data$FSC_biovolume[
        replicate_data$Pop == "all_fluo"])

      #Iterate through populations
      for (population in populations) {
        #Subset the data for the current population within the replicate
        population_data <- subset(replicate_data, Pop == population)

        #Calculate the size importance (Fpop) using the "all phyto" values specific
        #to this replicate
        size_importance <- (sum(population_data$cell.count_ml * population_data$FSC_biovolume) /
                          (all_phyto_abundance * all_phyto_biovolume))

        #Convert Fpop to percentage by multiplying by 100
        importance_percentage <- size_importance * 100

        # Store the results in the results_df data frame
        results_df <- rbind(results_df, data.frame(Light = light_condition,
                                                   Treatment = addition_treatment,
                                                   Replicate = replicate,
                                                   Population = population,
                                                   Fpop = size_importance,
                                                   Fpop_percent = importance_percentage,
                                                   Mn = is_Mn, Fe = is_Fe))
      }
    }
  }
}


#Print results
head(results_df)
```

```
##   Light Treatment Replicate      Population      Fpop Fpop_percent    Mn    Fe
## 1    HL   Initial         1  Picoeukaryotes 0.1004469     10.04469 FALSE FALSE
## 2    HL   Initial         1  Nanoeukaryotes 0.2937831     29.37831 FALSE FALSE
## 3    HL   Initial         1 Microeukaryotes 0.2525894     25.25894 FALSE FALSE
## 4    HL   Initial         1        all_fluo 1.0000000    100.00000 FALSE FALSE
```

```
## 5    HL   Control         1  Picoeukaryotes 0.1589756     15.89756 FALSE FALSE
## 6    HL   Control         1  Nanoeukaryotes 0.4247859     42.47859 FALSE FALSE
```

```
#Adding the bottle column of FC to the new dataframe for the stats analyses
#Add a unique identifier column using mutate
results_df <- results_df %>%
  mutate(identifier = paste0(as.character(results_df$Treatment),"_",
                             as.character(results_df$Replicate),"_",
                             as.character(results_df$Light),"_",
                             as.character(results_df$Population)))

#Do the same for original file
FC <- FC %>%
  mutate(identifier = paste0(as.character(results_df$Treatment),"_",
                             as.character(results_df$Replicate),"_",
                             as.character(results_df$Light),"_",
                             as.character(results_df$Population)))

Bottle <- FC$Bottle

results_df_joined <- results_df %>%
  left_join(select(FC, identifier, Bottle), by = "identifier")

#Select only population of interest
pop <- c("Microeukaryotes","Nanoeukaryotes", "Picoeukaryotes")
FC_stat <- results_df_joined[results_df_joined$Population %in% pop,]

FC_stat$ln_Fpop <- log(FC_stat$Fpop)  #data log-transformed for analyses
```

```
#Plot using ggplot2
ggplot(FC_stat) +
  geom_point(aes(x = Mn, y = ln_Fpop, col = Fe)) +
  facet_grid(Light ~ Population)     #for FC we use population instead of size class
```



```
#model fit with all factors (Mn, Fe, Light and Size)
fit_FC <- lmer(ln_Fpop ~ Mn + Fe + Light + Population +
               Mn:Fe + Mn:Light + Fe:Light + Mn:Population +
                 Fe:Population + Light:Population + (1|Bottle),
             data = FC_stat, na.action=na.fail, REML = FALSE)
summary(fit_FC)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula:
## ln_Fpop ~ Mn + Fe + Light + Population + Mn:Fe + Mn:Light + Fe:Light +
##     Mn:Population + Fe:Population + Light:Population + (1 | Bottle)
##    Data: FC_stat
##
##      AIC      BIC   logLik deviance df.resid
##     83.3    123.4    -24.7     49.3       61
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.7311 -0.5651 -0.0455  0.6143  3.6849
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.0000   0.0000
##  Residual             0.1102   0.3319
## Number of obs: 78, groups:  Bottle, 26
```

```
##
## Fixed effects:
##                                    Estimate Std. Error t value
## (Intercept)                        -2.09237    0.13578 -15.410
## MnTRUE                             -0.39805    0.16689  -2.385
## FeTRUE                              0.88031    0.16689   5.275
## LightLL                            -0.50679    0.16122  -3.143
## PopulationNanoeukaryotes            1.10956    0.17468   6.352
## PopulationPicoeukaryotes            0.08423    0.17468   0.482
## MnTRUE:FeTRUE                       0.09512    0.15151   0.628
## MnTRUE:LightLL                      0.01667    0.15117   0.110
## FeTRUE:LightLL                     -0.09848    0.15117  -0.651
## MnTRUE:PopulationNanoeukaryotes     0.40155    0.18515   2.169
## MnTRUE:PopulationPicoeukaryotes     0.39084    0.18515   2.111
## FeTRUE:PopulationNanoeukaryotes    -0.96605    0.18515  -5.218
## FeTRUE:PopulationPicoeukaryotes    -1.16848    0.18515  -6.311
## LightLL:PopulationNanoeukaryotes    0.32436    0.18413   1.762
## LightLL:PopulationPicoeukaryotes    0.71184    0.18413   3.866
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_FC, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## ln_Fpop ~ Mn + Fe + Light + Population + Mn:Fe + Mn:Light + Fe:Light +
##     Mn:Population + Fe:Population + Light:Population + (1 | Bottle)
##                    npar     AIC    LRT   Pr(Chi)
## <none>                   83.319
## Mn:Fe                 1  81.713  0.393  0.530642
## Mn:Light              1  81.332  0.012  0.912216
## Fe:Light              1  81.743  0.423  0.515357
## Mn:Population         2  85.201  5.881  0.052832 .
## Fe:Population         2 115.162 35.843 1.648e-08 ***
## Light:Population      2  93.026 13.707  0.001056 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#it shows that both Fe:Pop and Light:Pop interactions are significant
#all other interactions are removed from the model

#second model fit
fit_FC2 <- lmer(ln_Fpop ~ Mn + Fe + Light + Population + Fe:Population +
                  Light:Population + (1|Bottle),
                  data = FC_stat, na.action=na.fail, REML = FALSE)
summary(fit_FC2)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula:
## ln_Fpop ~ Mn + Fe + Light + Population + Fe:Population + Light:Population +
##     (1 | Bottle)
```

```
##    Data: FC_stat
##
##      AIC      BIC   logLik deviance df.resid
##     80.0    108.2    -28.0     56.0       66
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.9889 -0.4902 -0.0177  0.5527  3.9675
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.00     0.0000
##  Residual             0.12     0.3464
## Number of obs: 78, groups:  Bottle, 26
##
## Fixed effects:
##                                  Estimate Std. Error t value
## (Intercept)                      -2.20572    0.11970 -18.428
## MnTRUE                           -0.08120    0.07887  -1.029
## FeTRUE                            0.85659    0.13638   6.281
## LightLL                          -0.54454    0.13586  -4.008
## PopulationNanoeukaryotes          1.28165    0.16238   7.893
## PopulationPicoeukaryotes          0.25173    0.16238   1.550
## FeTRUE:PopulationNanoeukaryotes  -0.93737    0.19271  -4.864
## FeTRUE:PopulationPicoeukaryotes  -1.14056    0.19271  -5.919
## LightLL:PopulationNanoeukaryotes  0.32436    0.19214   1.688
## LightLL:PopulationPicoeukaryotes  0.71184    0.19214   3.705
##
## Correlation of Fixed Effects:
##             (Intr) MnTRUE FeTRUE LghtLL PpltnN PpltnP FTRUE:PN FTRUE:PP LLL:PN
## MnTRUE      -0.282
## FeTRUE      -0.513 -0.041
## LightLL     -0.568  0.000  0.000
## PpltnNnkryt -0.678  0.000  0.387  0.418
## PpltnPckryt -0.678  0.000  0.387  0.418  0.500
## FTRUE:PpltN  0.372  0.000 -0.707  0.000 -0.548 -0.274
## FTRUE:PpltP  0.372  0.000 -0.707  0.000 -0.274 -0.548  0.500
## LghtLL:PplN  0.401  0.000  0.000 -0.707 -0.592 -0.296  0.000    0.000
## LghtLL:PplP  0.401  0.000  0.000 -0.707 -0.296 -0.592  0.000    0.000    0.500
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_FC2, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## ln_Fpop ~ Mn + Fe + Light + Population + Fe:Population + Light:Population +
##     (1 | Bottle)
##                   npar     AIC    LRT   Pr(Chi)
## <none>                  79.960
## Mn                   1  79.012  1.053  0.304889
## Fe:Population        2 108.163 32.203 1.017e-07 ***
```

```
## Light:Population    2  88.634 12.674  0.001769 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#it shows that Mn does not significantly influence community composition
#Mn is removed from the model

#best model identified by drop
fit_best_FC <- lmer(ln_Fpop ~ Fe + Light + Population + Fe:Population +
                      Light:Population + (1|Bottle),
                    data = FC_stat, na.action=na.fail, REML = FALSE)
summary(fit_best_FC)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula:
## ln_Fpop ~ Fe + Light + Population + Fe:Population + Light:Population +
##     (1 | Bottle)
##    Data: FC_stat
##
##      AIC      BIC   logLik deviance df.resid
##     79.0    104.9    -28.5     57.0       67
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.0852 -0.4822 -0.0655  0.5582  4.0406
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.0000   0.0000
##  Residual             0.1216   0.3487
## Number of obs: 78, groups:  Bottle, 26
##
## Fixed effects:
##                                  Estimate Std. Error t value
## (Intercept)                       -2.2405     0.1156 -19.381
## FeTRUE                             0.8508     0.1372   6.202
## LightLL                           -0.5445     0.1368  -3.981
## PopulationNanoeukaryotes           1.2817     0.1635   7.840
## PopulationPicoeukaryotes           0.2517     0.1635   1.540
## FeTRUE:PopulationNanoeukaryotes   -0.9374     0.1940  -4.832
## FeTRUE:PopulationPicoeukaryotes   -1.1406     0.1940  -5.879
## LightLL:PopulationNanoeukaryotes   0.3244     0.1934   1.677
## LightLL:PopulationPicoeukaryotes   0.7118     0.1934   3.680
##
## Correlation of Fixed Effects:
##             (Intr) FeTRUE LghtLL PpltnN PpltnP FTRUE:PN FTRUE:PP LLL:PN
## FeTRUE      -0.548
## LightLL     -0.592  0.000
## PpltnNnkryt -0.707  0.387  0.418
## PpltnPckryt -0.707  0.387  0.418  0.500
## FTRUE:PpltN  0.387 -0.707  0.000 -0.548 -0.274
## FTRUE:PpltP  0.387 -0.707  0.000 -0.274 -0.548  0.500
## LghtLL:PplN  0.418  0.000 -0.707 -0.592 -0.296  0.000    0.000
## LghtLL:PplP  0.418  0.000 -0.707 -0.296 -0.592  0.000    0.000    0.500
```

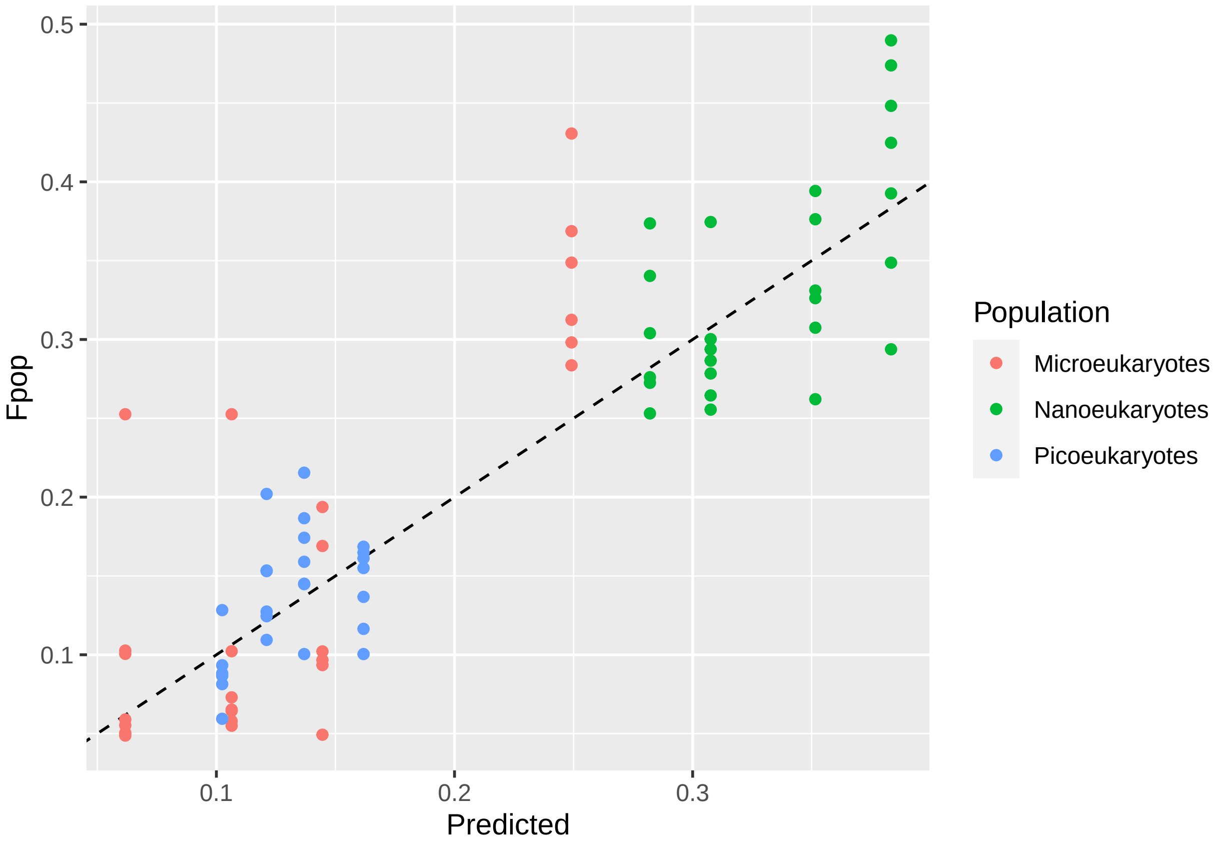
```
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```r
#Report results
report(fit_best_FC)
```

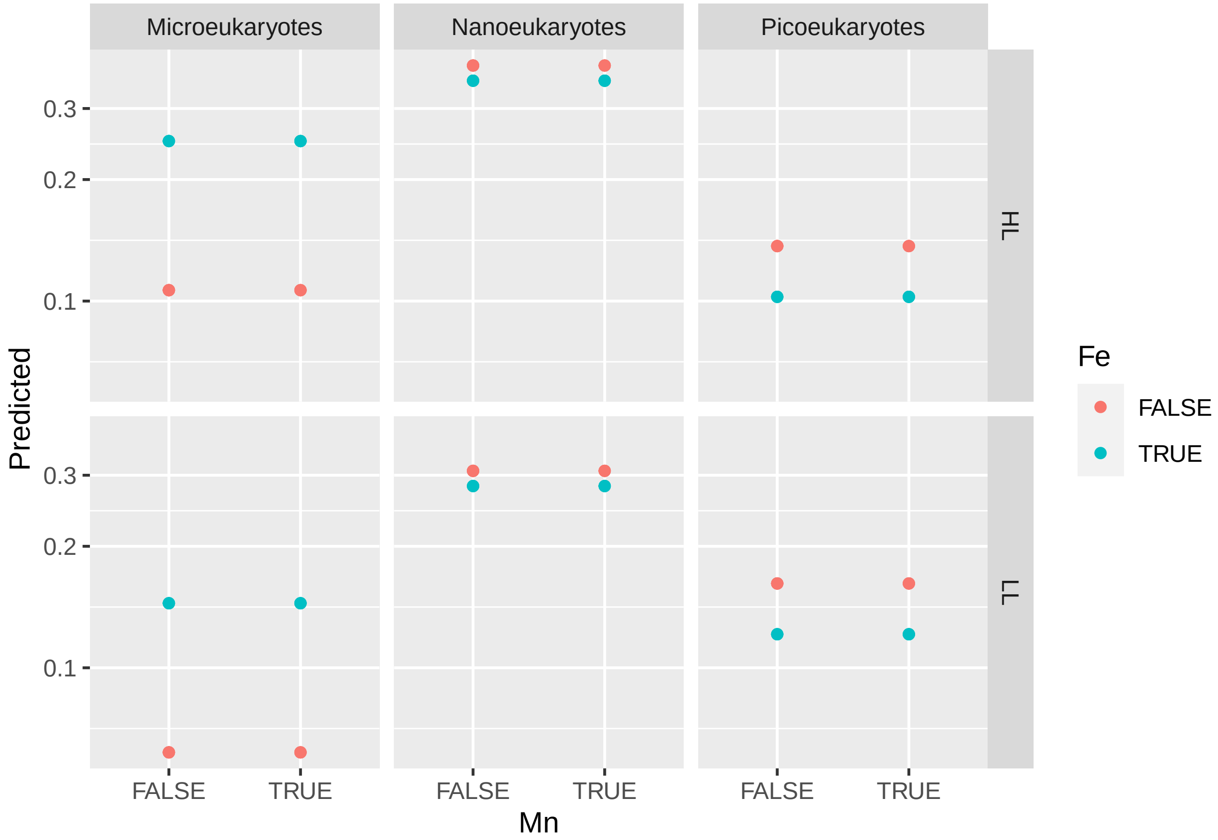
```
## Random effect variances not available. Returned R2 does not account for random effects.
## Random effect variances not available. Returned R2 does not account for random effects.
```

```
## We fitted a linear mixed model (estimated using ML and nloptwrap optimizer) to
## predict ln_Fpop with Fe, Light and Population (formula: ln_Fpop ~ Fe + Light +
## Population + Fe:Population + Light:Population). The model included Bottle as
## random effect (formula: ~1 | Bottle). The model's explanatory power related to
## the fixed effects alone (marginal R2) is 0.72. The model's intercept,
## corresponding to Fe = [?], Light = HL and Population = Microeukaryotes, is at
## -2.24 (95% CI [-2.47, -2.01], t(67) = -19.38, p < .001). Within this model:
##
##   - The effect of FeTRUE is statistically significant and positive (beta = 0.85,
## 95% CI [0.58, 1.12], t(67) = 6.20, p < .001; Std. beta = 1.29, 95% CI [0.87,
## 1.70])
##   - The effect of Light [LL] is statistically significant and negative (beta =
## -0.54, 95% CI [-0.82, -0.27], t(67) = -3.98, p < .001; Std. beta = -0.82, 95%
## CI [-1.24, -0.41])
##   - The effect of Population [Nanoeukaryotes] is statistically significant and
## positive (beta = 1.28, 95% CI [0.96, 1.61], t(67) = 7.84, p < .001; Std. beta =
## 1.94, 95% CI [1.45, 2.43])
##   - The effect of Population [Picoeukaryotes] is statistically non-significant
## and positive (beta = 0.25, 95% CI [-0.07, 0.58], t(67) = 1.54, p = 0.128; Std.
## beta = 0.38, 95% CI [-0.11, 0.88])
##   - The effect of FeTRUE × Population [Nanoeukaryotes] is statistically
## significant and negative (beta = -0.94, 95% CI [-1.32, -0.55], t(67) = -4.83, p
## < .001; Std. beta = -1.42, 95% CI [-2.01, -0.83])
##   - The effect of FeTRUE × Population [Picoeukaryotes] is statistically
## significant and negative (beta = -1.14, 95% CI [-1.53, -0.75], t(67) = -5.88, p
## < .001; Std. beta = -1.73, 95% CI [-2.31, -1.14])
##   - The effect of Light [LL] × Population [Nanoeukaryotes] is statistically
## non-significant and positive (beta = 0.32, 95% CI [-0.06, 0.71], t(67) = 1.68,
## p = 0.098; Std. beta = 0.49, 95% CI [-0.09, 1.08])
##   - The effect of Light [LL] × Population [Picoeukaryotes] is statistically
## significant and positive (beta = 0.71, 95% CI [0.33, 1.10], t(67) = 3.68, p <
## .001; Std. beta = 1.08, 95% CI [0.49, 1.66])
##
## Standardized parameters were obtained by fitting the model on a standardized
## version of the dataset. 95% Confidence Intervals (CIs) and p-values were
## computed using a Wald t-distribution approximation.
```

```r
#Represent data predicted by the model vs real data
FC_stat$Predicted <- exp(predict(fit_best_FC, re.form = NA))
```



0.5
0.4
0.3
0.2
0.1
Fpop
0.1
0.2
0.3
Predicted
Population
Microeukaryotes
Nanoeukaryotes
Picoeukaryotes



```r
#Pairwise comparison
emmeans (fit_best_FC, pairwise ~ Fe + Light + Population, adjust = "tukey")
```

```
## boundary (singular) fit: see help('isSingular')

## $emmeans
##  Fe    Light Population      emmean    SE   df lower.CL upper.CL
##  FALSE HL    Microeukaryotes -2.241 0.123 88.2    -2.48   -1.996
##   TRUE HL    Microeukaryotes -1.390 0.129 88.2    -1.65   -1.133
##  FALSE LL    Microeukaryotes -2.785 0.123 88.2    -3.03   -2.541
##   TRUE LL    Microeukaryotes -1.934 0.129 88.2    -2.19   -1.677
##  FALSE HL    Nanoeukaryotes  -0.959 0.123 88.2    -1.20   -0.715
##   TRUE HL    Nanoeukaryotes  -1.045 0.129 88.2    -1.30   -0.788
##  FALSE LL    Nanoeukaryotes  -1.179 0.123 88.2    -1.42   -0.935
##   TRUE LL    Nanoeukaryotes  -1.266 0.129 88.2    -1.52   -1.008
##  FALSE HL    Picoeukaryotes  -1.989 0.123 88.2    -2.23   -1.745
##   TRUE HL    Picoeukaryotes  -2.279 0.129 88.2    -2.54   -2.021
##  FALSE LL    Picoeukaryotes  -1.821 0.123 88.2    -2.07   -1.577
##   TRUE LL    Picoeukaryotes  -2.111 0.129 88.2    -2.37   -1.854
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $contrasts
##  contrast                                          estimate    SE   df
```

```
##  FALSE HL Microeukaryotes - TRUE HL Microeukaryotes   -0.8508 0.146 88.2
##  FALSE HL Microeukaryotes - FALSE LL Microeukaryotes   0.5445 0.145 88.2
##  FALSE HL Microeukaryotes - TRUE LL Microeukaryotes   -0.3063 0.206 88.2
##  FALSE HL Microeukaryotes - FALSE HL Nanoeukaryotes   -1.2817 0.174 58.8
##  FALSE HL Microeukaryotes - TRUE HL Nanoeukaryotes    -1.1951 0.178 83.6
##  FALSE HL Microeukaryotes - FALSE LL Nanoeukaryotes   -1.0615 0.174 84.4
##  FALSE HL Microeukaryotes - TRUE LL Nanoeukaryotes    -0.9749 0.178 83.6
##  FALSE HL Microeukaryotes - FALSE HL Picoeukaryotes   -0.2517 0.174 58.8
##  FALSE HL Microeukaryotes - TRUE HL Picoeukaryotes     0.0380 0.178 83.6
##  FALSE HL Microeukaryotes - FALSE LL Picoeukaryotes   -0.4190 0.174 84.4
##  FALSE HL Microeukaryotes - TRUE LL Picoeukaryotes    -0.1293 0.178 83.6
##  TRUE HL Microeukaryotes - FALSE LL Microeukaryotes    1.3953 0.206 88.2
##  TRUE HL Microeukaryotes - TRUE LL Microeukaryotes     0.5445 0.145 88.2
##  TRUE HL Microeukaryotes - FALSE HL Nanoeukaryotes    -0.4309 0.178 83.6
##  TRUE HL Microeukaryotes - TRUE HL Nanoeukaryotes     -0.3443 0.183 58.8
##  TRUE HL Microeukaryotes - FALSE LL Nanoeukaryotes    -0.2107 0.178 83.6
##  TRUE HL Microeukaryotes - TRUE LL Nanoeukaryotes     -0.1241 0.183 82.6
##  TRUE HL Microeukaryotes - FALSE HL Picoeukaryotes     0.5991 0.178 83.6
##  TRUE HL Microeukaryotes - TRUE HL Picoeukaryotes      0.8888 0.183 58.8
##  TRUE HL Microeukaryotes - FALSE LL Picoeukaryotes     0.4318 0.178 83.6
##  TRUE HL Microeukaryotes - TRUE LL Picoeukaryotes      0.7215 0.183 82.6
##  FALSE LL Microeukaryotes - TRUE LL Microeukaryotes   -0.8508 0.146 88.2
##  FALSE LL Microeukaryotes - FALSE HL Nanoeukaryotes   -1.8262 0.174 84.4
##  FALSE LL Microeukaryotes - TRUE HL Nanoeukaryotes    -1.7396 0.178 83.6
##  FALSE LL Microeukaryotes - FALSE LL Nanoeukaryotes   -1.6060 0.174 58.8
##  FALSE LL Microeukaryotes - TRUE LL Nanoeukaryotes    -1.5194 0.178 83.6
##  FALSE LL Microeukaryotes - FALSE HL Picoeukaryotes   -0.7963 0.174 84.4
##  FALSE LL Microeukaryotes - TRUE HL Picoeukaryotes    -0.5065 0.178 83.6
##  FALSE LL Microeukaryotes - FALSE LL Picoeukaryotes   -0.9636 0.174 58.8
##  FALSE LL Microeukaryotes - TRUE LL Picoeukaryotes    -0.6738 0.178 83.6
##  TRUE LL Microeukaryotes - FALSE HL Nanoeukaryotes    -0.9754 0.178 83.6
##  TRUE LL Microeukaryotes - TRUE HL Nanoeukaryotes     -0.8888 0.183 82.6
##  TRUE LL Microeukaryotes - FALSE LL Nanoeukaryotes    -0.7552 0.178 83.6
##  TRUE LL Microeukaryotes - TRUE LL Nanoeukaryotes     -0.6686 0.183 58.8
##  TRUE LL Microeukaryotes - FALSE HL Picoeukaryotes     0.0545 0.178 83.6
##  TRUE LL Microeukaryotes - TRUE HL Picoeukaryotes      0.3443 0.183 82.6
##  TRUE LL Microeukaryotes - FALSE LL Picoeukaryotes    -0.1128 0.178 83.6
##  TRUE LL Microeukaryotes - TRUE LL Picoeukaryotes      0.1770 0.183 58.8
##  FALSE HL Nanoeukaryotes - TRUE HL Nanoeukaryotes      0.0866 0.146 88.2
##  FALSE HL Nanoeukaryotes - FALSE LL Nanoeukaryotes     0.2202 0.145 88.2
##  FALSE HL Nanoeukaryotes - TRUE LL Nanoeukaryotes      0.3068 0.206 88.2
##  FALSE HL Nanoeukaryotes - FALSE HL Picoeukaryotes     1.0299 0.174 58.8
##  FALSE HL Nanoeukaryotes - TRUE HL Picoeukaryotes      1.3197 0.178 83.6
##  FALSE HL Nanoeukaryotes - FALSE LL Picoeukaryotes     0.8626 0.174 84.4
##  FALSE HL Nanoeukaryotes - TRUE LL Picoeukaryotes      1.1524 0.178 83.6
##  TRUE HL Nanoeukaryotes - FALSE LL Nanoeukaryotes      0.1336 0.206 88.2
##  TRUE HL Nanoeukaryotes - TRUE LL Nanoeukaryotes       0.2202 0.145 88.2
##  TRUE HL Nanoeukaryotes - FALSE HL Picoeukaryotes      0.9433 0.178 83.6
##  TRUE HL Nanoeukaryotes - TRUE HL Picoeukaryotes       1.2331 0.183 58.8
##  TRUE HL Nanoeukaryotes - FALSE LL Picoeukaryotes      0.7760 0.178 83.6
##  TRUE HL Nanoeukaryotes - TRUE LL Picoeukaryotes       1.0658 0.183 82.6
##  FALSE LL Nanoeukaryotes - TRUE LL Nanoeukaryotes      0.0866 0.146 88.2
##  FALSE LL Nanoeukaryotes - FALSE HL Picoeukaryotes     0.8097 0.174 84.4
##  FALSE LL Nanoeukaryotes - TRUE HL Picoeukaryotes      1.0995 0.178 83.6
```

```
##  FALSE LL Nanoeukaryotes - FALSE LL Picoeukaryotes     0.6424 0.174 58.8
##  FALSE LL Nanoeukaryotes - TRUE LL Picoeukaryotes      0.9322 0.178 83.6
##  TRUE LL Nanoeukaryotes - FALSE HL Picoeukaryotes      0.7232 0.178 83.6
##  TRUE LL Nanoeukaryotes - TRUE HL Picoeukaryotes       1.0129 0.183 82.6
##  TRUE LL Nanoeukaryotes - FALSE LL Picoeukaryotes      0.5559 0.178 83.6
##  TRUE LL Nanoeukaryotes - TRUE LL Picoeukaryotes       0.8456 0.183 58.8
##  FALSE HL Picoeukaryotes - TRUE HL Picoeukaryotes      0.2898 0.146 88.2
##  FALSE HL Picoeukaryotes - FALSE LL Picoeukaryotes    -0.1673 0.145 88.2
##  FALSE HL Picoeukaryotes - TRUE LL Picoeukaryotes      0.1225 0.206 88.2
##  TRUE HL Picoeukaryotes - FALSE LL Picoeukaryotes     -0.4571 0.206 88.2
##  TRUE HL Picoeukaryotes - TRUE LL Picoeukaryotes      -0.1673 0.145 88.2
##  FALSE LL Picoeukaryotes - TRUE LL Picoeukaryotes      0.2898 0.146 88.2
##  t.ratio p.value
##   -5.833  <.0001
##    3.744  0.0159
##   -1.487  0.9404
##   -7.373  <.0001
##   -6.696  <.0001
##   -6.107  <.0001
##   -5.463  <.0001
##   -1.448  0.9483
##    0.213  1.0000
##   -2.411  0.4106
##   -0.724  0.9999
##    6.774  <.0001
##    3.744  0.0159
##   -2.414  0.4085
##   -1.881  0.7655
##   -1.180  0.9891
##   -0.678  0.9999
##    3.357  0.0508
##    4.857  0.0005
##    2.419  0.4052
##    3.943  0.0087
##   -5.833  <.0001
##  -10.506  <.0001
##   -9.748  <.0001
##   -9.240  <.0001
##   -8.514  <.0001
##   -4.581  0.0009
##   -2.838  0.1836
##   -5.544  <.0001
##   -3.776  0.0147
##   -5.465  <.0001
##   -4.857  0.0003
##   -4.232  0.0032
##   -3.654  0.0251
##    0.305  1.0000
##    1.881  0.7669
##   -0.632  1.0000
##    0.967  0.9979
##    0.594  1.0000
##    1.514  0.9328
##    1.489  0.9397
```

```
##    5.925  <.0001
##    7.395  <.0001
##    4.963  0.0002
##    6.457  <.0001
##    0.649  1.0000
##    1.514  0.9328
##    5.286  0.0001
##    6.739  <.0001
##    4.348  0.0022
##    5.824  <.0001
##    0.594  1.0000
##    4.659  0.0007
##    6.161  <.0001
##    3.696  0.0222
##    5.223  0.0001
##    4.052  0.0060
##    5.535  <.0001
##    3.115  0.0961
##    4.621  0.0012
##    1.987  0.7010
##   -1.150  0.9912
##    0.595  1.0000
##   -2.219  0.5408
##   -1.150  0.9912
##    1.987  0.7010
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 12 estimates
```

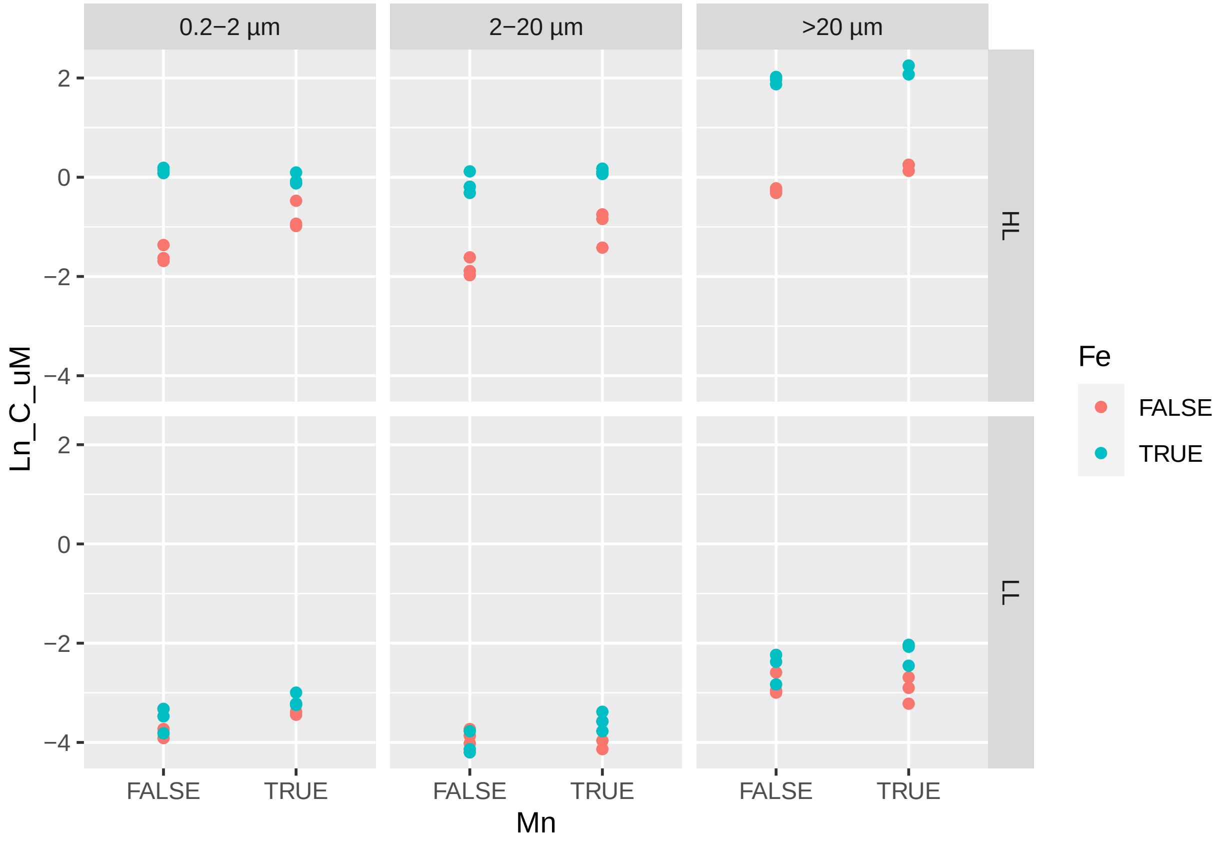
6 Net primary productivity and iron uptake

6.1 Carbon uptake

```
Uptake <- read.csv(file = "2SOLTEE_iron_carbon_uptake.csv")
```

```
Uptake$Size <- factor(Uptake$Size, levels = c("0.2-2 µm", "2-20 µm", ">20 µm"))
Uptake$Bottle <- factor(Uptake$Bottle)
Uptake.na <- Uptake[!is.na(Uptake$C_uM), ]
Uptake.na$Ln_C_uM <- log(Uptake.na$C_uM)   #data log-transformed
```

```
#Plot using ggplot2
ggplot(Uptake.na) +
  geom_point(aes(x = Mn, y = Ln_C_uM, col = Fe)) +
  facet_grid(Light ~ Size)
```



```
#model fit with all factors (Mn, Fe, Light and Size)
fit_C <- lmer(Ln_C_uM ~ Mn + Fe + Light + Size +
               Mn:Fe + Mn:Light + Fe:Light + Mn:Size + Fe:Size + Light:Size + (1|Bottle),
             data = Uptake.na, na.action=na.fail, REML = FALSE)

summary(fit_C)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: Ln_C_uM ~ Mn + Fe + Light + Size + Mn:Fe + Mn:Light + Fe:Light +
##     Mn:Size + Fe:Size + Light:Size + (1 | Bottle)
##    Data: Uptake.na
##
##      AIC      BIC   logLik deviance df.resid
##      2.6     41.1     15.7    -31.4       54
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.86055 -0.44023  0.05629  0.58543  2.18217
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.02599  0.1612
##  Residual             0.02289  0.1513
## Number of obs: 71, groups:  Bottle, 24
##
```

```
## Fixed effects:
##                     Estimate Std. Error t value
## (Intercept)         -1.47325    0.11116 -13.253
## MnTRUE               0.47402    0.13912   3.407
## FeTRUE               1.42042    0.13912  10.210
## LightLL             -2.13083    0.13953 -15.271
## Size2-20 µm         -0.19874    0.08736  -2.275
## Size>20 µm           1.31200    0.08736  15.019
## MnTRUE:FeTRUE       -0.15285    0.15010  -1.018
## MnTRUE:LightLL      -0.15557    0.15010  -1.036
## FeTRUE:LightLL      -1.30124    0.15010  -8.669
## MnTRUE:Size2-20 µm   0.05679    0.08736   0.650
## MnTRUE:Size>20 µm   -0.11426    0.08884  -1.286
## FeTRUE:Size2-20 µm   0.04786    0.08736   0.548
## FeTRUE:Size>20 µm    0.61306    0.08884   6.901
## LightLL:Size2-20 µm -0.27350    0.08736  -3.131
## LightLL:Size>20 µm  -0.75023    0.08884  -8.445
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_C, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## Ln_C_uM ~ Mn + Fe + Light + Size + Mn:Fe + Mn:Light + Fe:Light +
##     Mn:Size + Fe:Size + Light:Size + (1 | Bottle)
##            npar    AIC    LRT   Pr(Chi)
## <none>           2.620
## Mn:Fe         1  1.637  1.017    0.3132
## Mn:Light      1  1.669  1.049    0.3057
## Fe:Light      1 34.602 33.983 5.561e-09 ***
## Mn:Size       2  2.278  3.658    0.1606
## Fe:Size       2 37.118 38.499 4.367e-09 ***
## Light:Size    2 43.220 44.600 2.066e-10 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
```

```
#it shows that Fe:Light, Fe:Size and Light:Size interactions are significant
#all other interactions are removed from the model

#second model fit
fit_C2 <- lmer(Ln_C_uM ~ Mn + Fe + Light + Size + Fe:Light + Fe:Size + Light:Size + (1|Bottle),
                  data = Uptake.na, na.action=na.fail, REML = FALSE)
summary(fit_C2)
```

```
## Linear mixed model fit by maximum likelihood  [’lmerMod’]
## Formula: Ln_C_uM ~ Mn + Fe + Light + Size + Fe:Light + Fe:Size + Light:Size +
##     (1 | Bottle)
##    Data: Uptake.na
##
##      AIC      BIC   logLik deviance df.resid
##      0.3     29.7     12.8    -25.7       58
##
```

```
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.8791 -0.4846  0.1089  0.5183  2.2736
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.02801  0.1674
##  Residual             0.02486  0.1577
## Number of obs: 71, groups:  Bottle, 24
##
## Fixed effects:
##                     Estimate Std. Error t value
## (Intercept)         -1.38862    0.09830 -14.126
## MnTRUE               0.30271    0.07797   3.882
## FeTRUE               1.34605    0.12203  11.030
## LightLL             -2.20656    0.12203 -18.082
## Size2-20 µm         -0.17034    0.07883  -2.161
## Size>20 µm           1.25795    0.07926  15.872
## FeTRUE:LightLL      -1.30535    0.15595  -8.371
## FeTRUE:Size2-20 µm   0.04786    0.09103   0.526
## FeTRUE:Size>20 µm    0.61923    0.09249   6.695
## LightLL:Size2-20 µm -0.27350    0.09103  -3.005
## LightLL:Size>20 µm  -0.75640    0.09249  -8.178
##
## Correlation of Fixed Effects:
##             (Intr) MnTRUE FeTRUE LghtLL S2-20µ Sz>20µ FTRUE: FTRUE:S2µ
## MnTRUE      -0.399
## FeTRUE      -0.622  0.003
## LightLL     -0.622  0.003  0.408
## Size2-20 µm -0.401  0.000  0.215  0.215
## Size>20 µm  -0.405  0.007  0.219  0.219  0.497
## FTRUE:LghLL  0.399 -0.005 -0.639 -0.639  0.000 -0.007
## FTRUE:S2-2µ  0.231  0.000 -0.373  0.000 -0.577 -0.287  0.000
## FTRUE:S>20µ  0.218  0.012 -0.359  0.008 -0.284 -0.547 -0.012  0.492
## LgLL:S2-20µ  0.231  0.000  0.000 -0.373 -0.577 -0.287  0.000  0.000
## LghLL:S>20µ  0.238 -0.012 -0.008 -0.375 -0.284 -0.583  0.012  0.000
##             FTRUE:S>µ LLL:S2µ
## MnTRUE
## FeTRUE
## LightLL
## Size2-20 µm
## Size>20 µm
## FTRUE:LghLL
## FTRUE:S2-2µ
## FTRUE:S>20µ
## LgLL:S2-20µ  0.000
## LghLL:S>20µ -0.031     0.492
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_C2, test = "Chisq")
```

```
## Single term deletions
##
## Model:
```

```
## Ln_C_uM ~ Mn + Fe + Light + Size + Fe:Light + Fe:Size + Light:Size +
##     (1 | Bottle)
##            npar    AIC    LRT   Pr(Chi)
## <none>           0.332
## Mn            1 10.000 11.669 0.0006356 ***
## Fe:Light      1 31.078 32.746 1.050e-08 ***
## Fe:Size       2 33.200 36.869 9.864e-09 ***
## Light:Size    2 39.039 42.708 5.323e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#it shows that Mn alone does influence carbon uptake

#best model identified by drop
fit_best_C <- lmer(Ln_C_uM ~ Fe + Mn + Light + Size + Fe:Light + Fe:Size + Light:Size + (1|Bottle),
                  data = Uptake.na, na.action=na.fail, REML = FALSE)
summary(fit_best_C)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: Ln_C_uM ~ Fe + Mn + Light + Size + Fe:Light + Fe:Size + Light:Size +
##     (1 | Bottle)
##    Data: Uptake.na
##
##      AIC      BIC   logLik deviance df.resid
##      0.3     29.7     12.8    -25.7       58
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.8791 -0.4846  0.1089  0.5183  2.2736
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.02801  0.1674
##  Residual             0.02486  0.1577
## Number of obs: 71, groups:  Bottle, 24
##
## Fixed effects:
##                     Estimate Std. Error t value
## (Intercept)         -1.38862    0.09830 -14.126
## FeTRUE               1.34605    0.12203  11.030
## MnTRUE               0.30271    0.07797   3.882
## LightLL             -2.20656    0.12203 -18.082
## Size2-20 µm         -0.17034    0.07883  -2.161
## Size>20 µm           1.25795    0.07926  15.872
## FeTRUE:LightLL      -1.30535    0.15595  -8.371
## FeTRUE:Size2-20 µm   0.04786    0.09103   0.526
## FeTRUE:Size>20 µm    0.61923    0.09249   6.695
## LightLL:Size2-20 µm -0.27350    0.09103  -3.005
## LightLL:Size>20 µm  -0.75640    0.09249  -8.178
##
## Correlation of Fixed Effects:
##              (Intr) FeTRUE MnTRUE LghtLL S2-20µ Sz>20µ FTRUE: FTRUE:S2µ
## FeTRUE       -0.622
## MnTRUE       -0.399  0.003
```

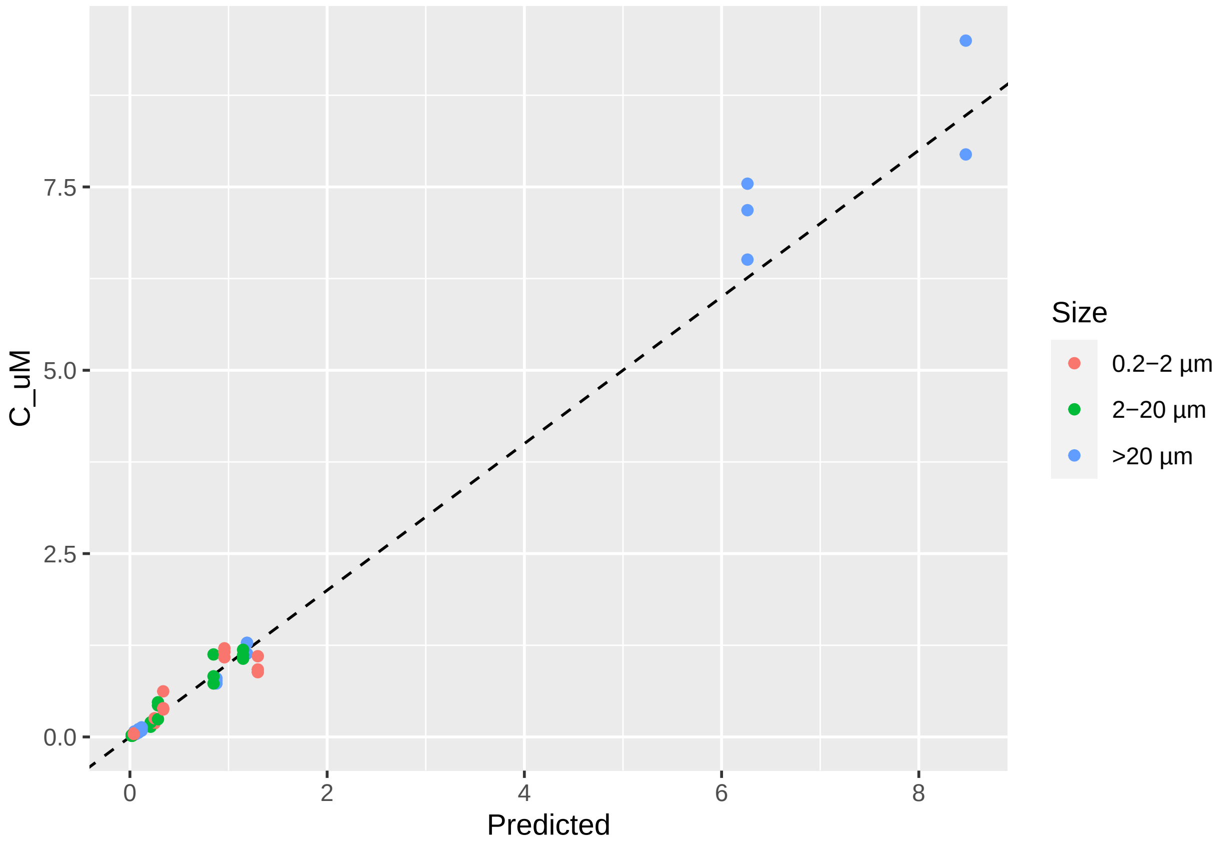
```
## LightLL     -0.622  0.408  0.003
## Size2-20 µm -0.401  0.215  0.000  0.215
## Size>20 µm  -0.405  0.219  0.007  0.219  0.497
## FTRUE:LghLL  0.399 -0.639 -0.005 -0.639  0.000 -0.007
## FTRUE:S2-2µ  0.231 -0.373  0.000  0.000 -0.577 -0.287  0.000
## FTRUE:S>20µ  0.218 -0.359  0.012  0.008 -0.284 -0.547 -0.012  0.492
## LgLL:S2-20µ  0.231  0.000  0.000 -0.373 -0.577 -0.287  0.000  0.000
## LghLL:S>20µ  0.238 -0.008 -0.012 -0.375 -0.284 -0.583  0.012  0.000
##             FTRUE:S>µ LLL:S2µ
## FeTRUE
## MnTRUE
## LightLL
## Size2-20 µm
## Size>20 µm
## FTRUE:LghLL
## FTRUE:S2-2µ
## FTRUE:S>20µ
## LgLL:S2-20µ  0.000
## LghLL:S>20µ -0.031     0.492
```

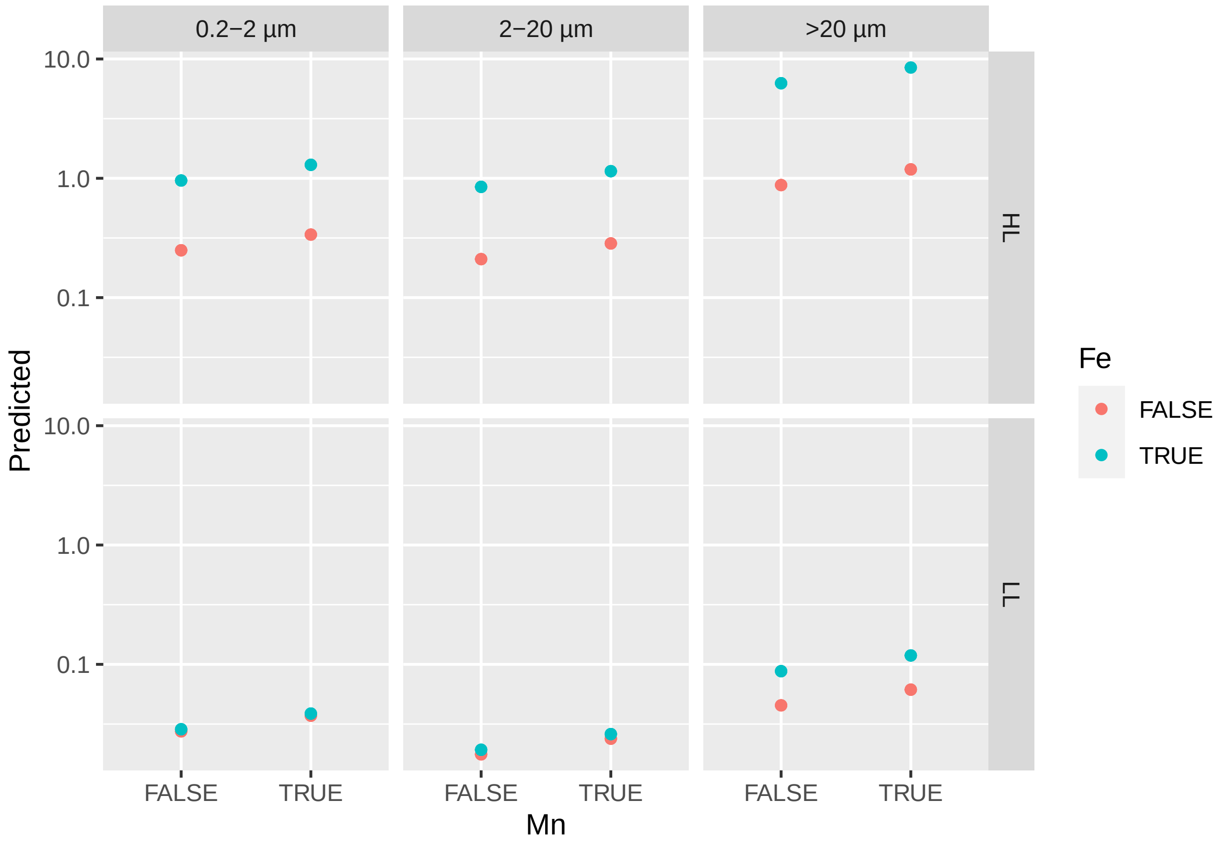
```
#Report results
report(fit_best_C)
```

```
## We fitted a linear mixed model (estimated using ML and nloptwrap optimizer) to
## predict Ln_C_uM with Fe, Mn, Light and Size (formula: Ln_C_uM ~ Fe + Mn + Light
## + Size + Fe:Light + Fe:Size + Light:Size). The model included Bottle as random
## effect (formula: ~1 | Bottle). The model's total explanatory power is
## substantial (conditional R2 = 0.99) and the part related to the fixed effects
## alone (marginal R2) is of 0.98. The model's intercept, corresponding to Fe =
## [?], Mn = [?], Light = HL and Size = 0.2-2 µm, is at -1.39 (95% CI [-1.59,
## -1.19], t(58) = -14.13, p < .001). Within this model:
##
##   - The effect of FeTRUE is statistically significant and positive (beta = 1.35,
## 95% CI [1.10, 1.59], t(58) = 11.03, p < .001; Std. beta = 0.74, 95% CI [0.61,
## 0.87])
##   - The effect of MnTRUE is statistically significant and positive (beta = 0.30,
## 95% CI [0.15, 0.46], t(58) = 3.88, p < .001; Std. beta = 0.17, 95% CI [0.08,
## 0.25])
##   - The effect of Light [LL] is statistically significant and negative (beta =
## -2.21, 95% CI [-2.45, -1.96], t(58) = -18.08, p < .001; Std. beta = -1.21, 95%
## CI [-1.35, -1.08])
##   - The effect of Size [2-20 µm] is statistically significant and negative (beta
## = -0.17, 95% CI [-0.33, -0.01], t(58) = -2.16, p = 0.035; Std. beta = -0.09,
## 95% CI [-0.18, -6.90e-03])
##   - The effect of Size [>20 µm] is statistically significant and positive (beta =
## 1.26, 95% CI [1.10, 1.42], t(58) = 15.87, p < .001; Std. beta = 0.69, 95% CI
## [0.60, 0.78])
##   - The effect of FeTRUE × Light [LL] is statistically significant and negative
## (beta = -1.31, 95% CI [-1.62, -0.99], t(58) = -8.37, p < .001; Std. beta =
## -0.72, 95% CI [-0.89, -0.55])
##   - The effect of FeTRUE × Size [2-20 µm] is statistically non-significant and
## positive (beta = 0.05, 95% CI [-0.13, 0.23], t(58) = 0.53, p = 0.601; Std. beta
## = 0.03, 95% CI [-0.07, 0.13])
##   - The effect of FeTRUE × Size [>20 µm] is statistically significant and
```

```
## positive (beta = 0.62, 95% CI [0.43, 0.80], t(58) = 6.70, p < .001; Std. beta =
## 0.34, 95% CI [0.24, 0.44])
##   - The effect of Light [LL] × Size [2-20 µm] is statistically significant and
## negative (beta = -0.27, 95% CI [-0.46, -0.09], t(58) = -3.00, p = 0.004; Std.
## beta = -0.15, 95% CI [-0.25, -0.05])
##   - The effect of Light [LL] × Size [>20 µm] is statistically significant and
## negative (beta = -0.76, 95% CI [-0.94, -0.57], t(58) = -8.18, p < .001; Std.
## beta = -0.42, 95% CI [-0.52, -0.31])
##
## Standardized parameters were obtained by fitting the model on a standardized
## version of the dataset. 95% Confidence Intervals (CIs) and p-values were
## computed using a Wald t-distribution approximation.
```

```
#Represent data predicted by the model vs real data
Uptake.na$Predicted <- exp(predict(fit_best_C, re.form = NA))
```





```
#Pairwise comparison
emmeans (fit_best_C, pairwise ~ Fe + Mn + Light + Size, adjust = "tukey")
```

```
## $emmeans
##  Fe    Mn    Light Size      emmean    SE   df lower.CL upper.CL
##  FALSE FALSE HL    0.2-2 μm -1.3886 0.109 47.1  -1.6087  -1.1685
##   TRUE FALSE HL    0.2-2 μm -0.0426 0.109 46.8  -0.2624   0.1772
##  FALSE  TRUE HL    0.2-2 μm -1.0859 0.109 46.9  -1.3057  -0.8661
##   TRUE  TRUE HL    0.2-2 μm  0.2601 0.109 46.9   0.0400   0.4802
##  FALSE FALSE LL    0.2-2 μm -3.5952 0.109 46.9  -3.8150  -3.3754
##   TRUE FALSE LL    0.2-2 μm -3.5545 0.109 47.1  -3.7746  -3.3344
##  FALSE  TRUE LL    0.2-2 μm -3.2925 0.109 47.1  -3.5126  -3.0724
##   TRUE  TRUE LL    0.2-2 μm -3.2518 0.109 46.9  -3.4716  -3.0320
##  FALSE FALSE HL    2-20 μm  -1.5590 0.109 47.1  -1.7790  -1.3389
##   TRUE FALSE HL    2-20 μm  -0.1651 0.109 46.8  -0.3848   0.0547
##  FALSE  TRUE HL    2-20 μm  -1.2563 0.109 46.9  -1.4760  -1.0365
##   TRUE  TRUE HL    2-20 μm   0.1377 0.109 46.9  -0.0825   0.3578
##  FALSE FALSE LL    2-20 μm  -4.0390 0.109 46.9  -4.2588  -3.8192
##   TRUE FALSE LL    2-20 μm  -3.9505 0.109 47.1  -4.1705  -3.7304
##  FALSE  TRUE LL    2-20 μm  -3.7363 0.109 47.1  -3.9564  -3.5162
##   TRUE  TRUE LL    2-20 μm  -3.6478 0.109 46.9  -3.8675  -3.4280
##  FALSE FALSE HL    >20 μm   -0.1307 0.109 47.0  -0.3505   0.0892
##   TRUE FALSE HL    >20 μm    1.8346 0.112 51.0   1.6088   2.0604
##  FALSE  TRUE HL    >20 μm    0.1720 0.110 47.4  -0.0484   0.3925
##   TRUE  TRUE HL    >20 μm    2.1373 0.114 52.8   1.9086   2.3660
##  FALSE FALSE LL    >20 μm   -3.0936 0.110 47.4  -3.3141  -2.8732
```

```
##   TRUE FALSE LL    >20 µm   -2.4337 0.109 47.0  -2.6536  -2.2139
##  FALSE  TRUE LL    >20 µm   -2.7909 0.109 47.0  -3.0108  -2.5711
##   TRUE  TRUE LL    >20 µm   -2.1310 0.110 47.4  -2.3515  -1.9106
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $contrasts
##  contrast                                              estimate     SE   df
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE FALSE HL 0.2-2 µm)   -1.3460 0.1360 44.2
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE TRUE HL 0.2-2 µm)   -0.3027 0.0877 30.3
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE TRUE HL 0.2-2 µm)    -1.6488 0.1620 39.7
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE FALSE LL 0.2-2 µm)   2.2066 0.1360 44.3
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE FALSE LL 0.2-2 µm)    2.1659 0.1471 57.3
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE TRUE LL 0.2-2 µm)    1.9039 0.1620 39.8
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)     1.8632 0.1712 48.8
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)    0.1703 0.0844 53.9
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)    -1.2236 0.1445 54.2
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)    -0.1324 0.1217 78.1
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)     -1.5263 0.1692 46.7
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)    2.6504 0.1445 54.3
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)     2.5618 0.1388 47.6
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)     2.3477 0.1692 46.8
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)      2.2591 0.1641 41.9
##  (FALSE FALSE HL 0.2-2 µm) - FALSE FALSE HL >20 µm      -1.2579 0.0849 54.0
##  (FALSE FALSE HL 0.2-2 µm) - TRUE FALSE HL >20 µm       -3.2232 0.1480 57.6
##  (FALSE FALSE HL 0.2-2 µm) - FALSE TRUE HL >20 µm       -1.5607 0.1224 78.5
##  (FALSE FALSE HL 0.2-2 µm) - TRUE TRUE HL >20 µm        -3.5259 0.1731 50.0
##  (FALSE FALSE HL 0.2-2 µm) - FALSE FALSE LL >20 µm       1.7050 0.1444 54.2
##  (FALSE FALSE HL 0.2-2 µm) - TRUE FALSE LL >20 µm        1.0451 0.1390 47.9
##  (FALSE FALSE HL 0.2-2 µm) - FALSE TRUE LL >20 µm        1.4023 0.1688 46.5
##  (FALSE FALSE HL 0.2-2 µm) - TRUE TRUE LL >20 µm         0.7424 0.1647 42.4
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE TRUE HL 0.2-2 µm)     1.0433 0.1616 39.5
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE TRUE HL 0.2-2 µm)     -0.3027 0.0877 30.3
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE FALSE LL 0.2-2 µm)    3.5526 0.1471 57.2
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE FALSE LL 0.2-2 µm)     3.5119 0.1360 44.2
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE TRUE LL 0.2-2 µm)     3.2499 0.1712 48.8
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)      3.2092 0.1616 39.5
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)     1.5164 0.1445 54.2
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)      0.1225 0.0844 53.9
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)      1.2137 0.1688 46.5
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)      -0.1802 0.1217 78.1
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)     3.9964 0.1388 47.5
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)      3.9079 0.1445 54.2
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)      3.6937 0.1641 41.9
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)       3.6052 0.1688 46.5
##  (TRUE FALSE HL 0.2-2 µm) - FALSE FALSE HL >20 µm        0.0881 0.1444 54.1
##  (TRUE FALSE HL 0.2-2 µm) - TRUE FALSE HL >20 µm        -1.8772 0.0885 54.8
##  (TRUE FALSE HL 0.2-2 µm) - FALSE TRUE HL >20 µm        -0.2146 0.1690 46.6
##  (TRUE FALSE HL 0.2-2 µm) - TRUE TRUE HL >20 µm         -2.1799 0.1259 80.2
##  (TRUE FALSE HL 0.2-2 µm) - FALSE FALSE LL >20 µm        3.0511 0.1390 47.8
##  (TRUE FALSE HL 0.2-2 µm) - TRUE FALSE LL >20 µm         2.3911 0.1444 54.1
##  (TRUE FALSE HL 0.2-2 µm) - FALSE TRUE LL >20 µm         2.7483 0.1640 41.8
##  (TRUE FALSE HL 0.2-2 µm) - TRUE TRUE LL >20 µm          2.0884 0.1690 46.6
```

```
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE TRUE HL 0.2-2 µm)     -1.3460 0.1360 44.2
##  (FALSE TRUE HL 0.2-2 µm) - (FALSE FALSE LL 0.2-2 µm)    2.5093 0.1616 39.5
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE FALSE LL 0.2-2 µm)     2.4686 0.1712 48.8
##  (FALSE TRUE HL 0.2-2 µm) - (FALSE TRUE LL 0.2-2 µm)     2.2066 0.1360 44.3
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)      2.1659 0.1471 57.3
##  (FALSE TRUE HL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)     0.4731 0.1217 78.1
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)     -0.9209 0.1688 46.5
##  (FALSE TRUE HL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)      0.1703 0.0844 53.9
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)      -1.2236 0.1445 54.2
##  (FALSE TRUE HL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)     2.9531 0.1688 46.5
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)      2.8646 0.1641 41.9
##  (FALSE TRUE HL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)      2.6504 0.1445 54.3
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)       2.5618 0.1388 47.6
##  (FALSE TRUE HL 0.2-2 µm) - FALSE FALSE HL >20 µm       -0.9552 0.1216 78.0
##  (FALSE TRUE HL 0.2-2 µm) - TRUE FALSE HL >20 µm        -2.9205 0.1709 48.2
##  (FALSE TRUE HL 0.2-2 µm) - FALSE TRUE HL >20 µm        -1.2579 0.0849 54.0
##  (FALSE TRUE HL 0.2-2 µm) - TRUE TRUE HL >20 µm         -3.2232 0.1480 57.6
##  (FALSE TRUE HL 0.2-2 µm) - FALSE FALSE LL >20 µm        2.0077 0.1690 46.6
##  (FALSE TRUE HL 0.2-2 µm) - TRUE FALSE LL >20 µm         1.3478 0.1640 41.8
##  (FALSE TRUE HL 0.2-2 µm) - FALSE TRUE LL >20 µm         1.7050 0.1444 54.2
##  (FALSE TRUE HL 0.2-2 µm) - TRUE TRUE LL >20 µm          1.0451 0.1390 47.9
##  (TRUE TRUE HL 0.2-2 µm) - (FALSE FALSE LL 0.2-2 µm)     3.8553 0.1712 48.6
##  (TRUE TRUE HL 0.2-2 µm) - (TRUE FALSE LL 0.2-2 µm)      3.8146 0.1620 39.7
##  (TRUE TRUE HL 0.2-2 µm) - (FALSE TRUE LL 0.2-2 µm)      3.5526 0.1471 57.2
##  (TRUE TRUE HL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)       3.5119 0.1360 44.2
##  (TRUE TRUE HL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)      1.8191 0.1692 46.7
##  (TRUE TRUE HL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)       0.4252 0.1217 78.1
##  (TRUE TRUE HL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)       1.5164 0.1445 54.2
##  (TRUE TRUE HL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)        0.1225 0.0844 53.9
##  (TRUE TRUE HL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)      4.2992 0.1641 41.8
##  (TRUE TRUE HL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)       4.2106 0.1692 46.7
##  (TRUE TRUE HL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)       3.9964 0.1388 47.5
##  (TRUE TRUE HL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)        3.9079 0.1445 54.2
##  (TRUE TRUE HL 0.2-2 µm) - FALSE FALSE HL >20 µm         0.3908 0.1688 46.3
##  (TRUE TRUE HL 0.2-2 µm) - TRUE FALSE HL >20 µm         -1.5745 0.1233 78.9
##  (TRUE TRUE HL 0.2-2 µm) - FALSE TRUE HL >20 µm          0.0881 0.1444 54.1
##  (TRUE TRUE HL 0.2-2 µm) - TRUE TRUE HL >20 µm          -1.8772 0.0885 54.8
##  (TRUE TRUE HL 0.2-2 µm) - FALSE FALSE LL >20 µm         3.3538 0.1647 42.2
##  (TRUE TRUE HL 0.2-2 µm) - TRUE FALSE LL >20 µm          2.6938 0.1688 46.3
##  (TRUE TRUE HL 0.2-2 µm) - FALSE TRUE LL >20 µm          3.0511 0.1390 47.8
##  (TRUE TRUE HL 0.2-2 µm) - TRUE TRUE LL >20 µm           2.3911 0.1444 54.1
##  (FALSE FALSE LL 0.2-2 µm) - (TRUE FALSE LL 0.2-2 µm)   -0.0407 0.1360 44.3
##  (FALSE FALSE LL 0.2-2 µm) - (FALSE TRUE LL 0.2-2 µm)   -0.3027 0.0877 30.3
##  (FALSE FALSE LL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)    -0.3434 0.1616 39.5
##  (FALSE FALSE LL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)   -2.0362 0.1445 54.3
##  (FALSE FALSE LL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)    -3.4301 0.1388 47.5
##  (FALSE FALSE LL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)    -2.3389 0.1688 46.5
##  (FALSE FALSE LL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)     -3.7328 0.1641 41.8
##  (FALSE FALSE LL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)    0.4438 0.0844 53.9
##  (FALSE FALSE LL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)     0.3553 0.1445 54.3
##  (FALSE FALSE LL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)     0.1411 0.1217 78.1
##  (FALSE FALSE LL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)      0.0526 0.1688 46.5
##  (FALSE FALSE LL 0.2-2 µm) - FALSE FALSE HL >20 µm      -3.4645 0.1444 54.2
##  (FALSE FALSE LL 0.2-2 µm) - TRUE FALSE HL >20 µm       -5.4298 0.1413 50.1
```

```
##  (FALSE FALSE LL 0.2-2 µm) - FALSE TRUE HL >20 µm      -3.7672 0.1690 46.6
##  (FALSE FALSE LL 0.2-2 µm) - TRUE TRUE HL >20 µm       -5.7325 0.1672 44.4
##  (FALSE FALSE LL 0.2-2 µm) - FALSE FALSE LL >20 µm     -0.5016 0.0849 54.0
##  (FALSE FALSE LL 0.2-2 µm) - TRUE FALSE LL >20 µm      -1.1615 0.1444 54.2
##  (FALSE FALSE LL 0.2-2 µm) - FALSE TRUE LL >20 µm      -0.8043 0.1216 78.0
##  (FALSE FALSE LL 0.2-2 µm) - TRUE TRUE LL >20 µm       -1.4642 0.1690 46.6
##  (TRUE FALSE LL 0.2-2 µm) - (FALSE TRUE LL 0.2-2 µm)   -0.2620 0.1620 39.8
##  (TRUE FALSE LL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)    -0.3027 0.0877 30.3
##  (TRUE FALSE LL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)   -1.9955 0.1388 47.6
##  (TRUE FALSE LL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)    -3.3894 0.1445 54.2
##  (TRUE FALSE LL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)    -2.2982 0.1641 41.9
##  (TRUE FALSE LL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)     -3.6921 0.1692 46.7
##  (TRUE FALSE LL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)    0.4845 0.1445 54.3
##  (TRUE FALSE LL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)     0.3960 0.0844 53.9
##  (TRUE FALSE LL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)     0.1818 0.1692 46.8
##  (TRUE FALSE LL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)      0.0933 0.1217 78.1
##  (TRUE FALSE LL 0.2-2 µm) - FALSE FALSE HL >20 µm      -3.4238 0.1390 47.9
##  (TRUE FALSE LL 0.2-2 µm) - TRUE FALSE HL >20 µm       -5.3891 0.1480 57.6
##  (TRUE FALSE LL 0.2-2 µm) - FALSE TRUE HL >20 µm       -3.7265 0.1647 42.4
##  (TRUE FALSE LL 0.2-2 µm) - TRUE TRUE HL >20 µm        -5.6918 0.1731 50.0
##  (TRUE FALSE LL 0.2-2 µm) - FALSE FALSE LL >20 µm      -0.4609 0.1444 54.2
##  (TRUE FALSE LL 0.2-2 µm) - TRUE FALSE LL >20 µm       -1.1208 0.0849 54.0
##  (TRUE FALSE LL 0.2-2 µm) - FALSE TRUE LL >20 µm       -0.7636 0.1688 46.5
##  (TRUE FALSE LL 0.2-2 µm) - TRUE TRUE LL >20 µm        -1.4235 0.1224 78.5
##  (FALSE TRUE LL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)    -0.0407 0.1360 44.3
##  (FALSE TRUE LL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)   -1.7335 0.1692 46.8
##  (FALSE TRUE LL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)    -3.1274 0.1641 41.9
##  (FALSE TRUE LL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)    -2.0362 0.1445 54.3
##  (FALSE TRUE LL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)     -3.4301 0.1388 47.5
##  (FALSE TRUE LL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)    0.7465 0.1217 78.1
##  (FALSE TRUE LL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)     0.6580 0.1692 46.8
##  (FALSE TRUE LL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)     0.4438 0.0844 53.9
##  (FALSE TRUE LL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)      0.3553 0.1445 54.3
##  (FALSE TRUE LL 0.2-2 µm) - FALSE FALSE HL >20 µm      -3.1618 0.1688 46.5
##  (FALSE TRUE LL 0.2-2 µm) - TRUE FALSE HL >20 µm       -5.1271 0.1653 42.9
##  (FALSE TRUE LL 0.2-2 µm) - FALSE TRUE HL >20 µm       -3.4645 0.1444 54.2
##  (FALSE TRUE LL 0.2-2 µm) - TRUE TRUE HL >20 µm        -5.4298 0.1413 50.1
##  (FALSE TRUE LL 0.2-2 µm) - FALSE FALSE LL >20 µm      -0.1988 0.1224 78.5
##  (FALSE TRUE LL 0.2-2 µm) - TRUE FALSE LL >20 µm       -0.8588 0.1688 46.5
##  (FALSE TRUE LL 0.2-2 µm) - FALSE TRUE LL >20 µm       -0.5016 0.0849 54.0
##  (FALSE TRUE LL 0.2-2 µm) - TRUE TRUE LL >20 µm        -1.1615 0.1444 54.2
##  (TRUE TRUE LL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)    -1.6928 0.1641 41.9
##  (TRUE TRUE LL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)     -3.0867 0.1688 46.5
##  (TRUE TRUE LL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)     -1.9955 0.1388 47.6
##  (TRUE TRUE LL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)      -3.3894 0.1445 54.2
##  (TRUE TRUE LL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)     0.7872 0.1688 46.5
##  (TRUE TRUE LL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)      0.6987 0.1217 78.1
##  (TRUE TRUE LL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)      0.4845 0.1445 54.3
##  (TRUE TRUE LL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)       0.3960 0.0844 53.9
##  (TRUE TRUE LL 0.2-2 µm) - FALSE FALSE HL >20 µm       -3.1211 0.1640 41.8
##  (TRUE TRUE LL 0.2-2 µm) - TRUE FALSE HL >20 µm        -5.0864 0.1709 48.2
##  (TRUE TRUE LL 0.2-2 µm) - FALSE TRUE HL >20 µm        -3.4238 0.1390 47.9
##  (TRUE TRUE LL 0.2-2 µm) - TRUE TRUE HL >20 µm         -5.3891 0.1480 57.6
##  (TRUE TRUE LL 0.2-2 µm) - FALSE FALSE LL >20 µm       -0.1581 0.1690 46.6
```

```
##  (TRUE TRUE LL 0.2-2 µm) - TRUE FALSE LL >20 µm         -0.8181 0.1216 78.0
##  (TRUE TRUE LL 0.2-2 µm) - FALSE TRUE LL >20 µm         -0.4609 0.1444 54.2
##  (TRUE TRUE LL 0.2-2 µm) - TRUE TRUE LL >20 µm          -1.1208 0.0849 54.0
##  (FALSE FALSE HL 2-20 µm) - (TRUE FALSE HL 2-20 µm)     -1.3939 0.1360 44.2
##  (FALSE FALSE HL 2-20 µm) - (FALSE TRUE HL 2-20 µm)     -0.3027 0.0877 30.3
##  (FALSE FALSE HL 2-20 µm) - (TRUE TRUE HL 2-20 µm)      -1.6966 0.1620 39.7
##  (FALSE FALSE HL 2-20 µm) - (FALSE FALSE LL 2-20 µm)     2.4801 0.1360 44.3
##  (FALSE FALSE HL 2-20 µm) - (TRUE FALSE LL 2-20 µm)      2.3915 0.1471 57.3
##  (FALSE FALSE HL 2-20 µm) - (FALSE TRUE LL 2-20 µm)      2.1774 0.1620 39.8
##  (FALSE FALSE HL 2-20 µm) - (TRUE TRUE LL 2-20 µm)       2.0888 0.1712 48.8
##  (FALSE FALSE HL 2-20 µm) - FALSE FALSE HL >20 µm       -1.4283 0.0849 54.0
##  (FALSE FALSE HL 2-20 µm) - TRUE FALSE HL >20 µm        -3.3936 0.1480 57.6
##  (FALSE FALSE HL 2-20 µm) - FALSE TRUE HL >20 µm        -1.7310 0.1224 78.5
##  (FALSE FALSE HL 2-20 µm) - TRUE TRUE HL >20 µm         -3.6963 0.1731 50.0
##  (FALSE FALSE HL 2-20 µm) - FALSE FALSE LL >20 µm        1.5347 0.1444 54.2
##  (FALSE FALSE HL 2-20 µm) - TRUE FALSE LL >20 µm         0.8747 0.1390 47.9
##  (FALSE FALSE HL 2-20 µm) - FALSE TRUE LL >20 µm         1.2320 0.1688 46.5
##  (FALSE FALSE HL 2-20 µm) - TRUE TRUE LL >20 µm          0.5720 0.1647 42.4
##  (TRUE FALSE HL 2-20 µm) - (FALSE TRUE HL 2-20 µm)       1.0912 0.1616 39.5
##  (TRUE FALSE HL 2-20 µm) - (TRUE TRUE HL 2-20 µm)       -0.3027 0.0877 30.3
##  (TRUE FALSE HL 2-20 µm) - (FALSE FALSE LL 2-20 µm)      3.8740 0.1471 57.2
##  (TRUE FALSE HL 2-20 µm) - (TRUE FALSE LL 2-20 µm)       3.7854 0.1360 44.2
##  (TRUE FALSE HL 2-20 µm) - (FALSE TRUE LL 2-20 µm)       3.5713 0.1712 48.8
##  (TRUE FALSE HL 2-20 µm) - (TRUE TRUE LL 2-20 µm)        3.4827 0.1616 39.5
##  (TRUE FALSE HL 2-20 µm) - FALSE FALSE HL >20 µm        -0.0344 0.1444 54.1
##  (TRUE FALSE HL 2-20 µm) - TRUE FALSE HL >20 µm         -1.9997 0.0885 54.8
##  (TRUE FALSE HL 2-20 µm) - FALSE TRUE HL >20 µm         -0.3371 0.1690 46.6
##  (TRUE FALSE HL 2-20 µm) - TRUE TRUE HL >20 µm          -2.3024 0.1259 80.2
##  (TRUE FALSE HL 2-20 µm) - FALSE FALSE LL >20 µm         2.9286 0.1390 47.8
##  (TRUE FALSE HL 2-20 µm) - TRUE FALSE LL >20 µm          2.2687 0.1444 54.1
##  (TRUE FALSE HL 2-20 µm) - FALSE TRUE LL >20 µm          2.6259 0.1640 41.8
##  (TRUE FALSE HL 2-20 µm) - TRUE TRUE LL >20 µm           1.9659 0.1690 46.6
##  (FALSE TRUE HL 2-20 µm) - (TRUE TRUE HL 2-20 µm)       -1.3939 0.1360 44.2
##  (FALSE TRUE HL 2-20 µm) - (FALSE FALSE LL 2-20 µm)      2.7828 0.1616 39.5
##  (FALSE TRUE HL 2-20 µm) - (TRUE FALSE LL 2-20 µm)       2.6942 0.1712 48.8
##  (FALSE TRUE HL 2-20 µm) - (FALSE TRUE LL 2-20 µm)       2.4801 0.1360 44.3
##  (FALSE TRUE HL 2-20 µm) - (TRUE TRUE LL 2-20 µm)        2.3915 0.1471 57.3
##  (FALSE TRUE HL 2-20 µm) - FALSE FALSE HL >20 µm        -1.1256 0.1216 78.0
##  (FALSE TRUE HL 2-20 µm) - TRUE FALSE HL >20 µm         -3.0909 0.1709 48.2
##  (FALSE TRUE HL 2-20 µm) - FALSE TRUE HL >20 µm         -1.4283 0.0849 54.0
##  (FALSE TRUE HL 2-20 µm) - TRUE TRUE HL >20 µm          -3.3936 0.1480 57.6
##  (FALSE TRUE HL 2-20 µm) - FALSE FALSE LL >20 µm         1.8374 0.1690 46.6
##  (FALSE TRUE HL 2-20 µm) - TRUE FALSE LL >20 µm          1.1775 0.1640 41.8
##  (FALSE TRUE HL 2-20 µm) - FALSE TRUE LL >20 µm          1.5347 0.1444 54.2
##  (FALSE TRUE HL 2-20 µm) - TRUE TRUE LL >20 µm           0.8747 0.1390 47.9
##  (TRUE TRUE HL 2-20 µm) - (FALSE FALSE LL 2-20 µm)       4.1767 0.1712 48.6
##  (TRUE TRUE HL 2-20 µm) - (TRUE FALSE LL 2-20 µm)        4.0881 0.1620 39.7
##  (TRUE TRUE HL 2-20 µm) - (FALSE TRUE LL 2-20 µm)        3.8740 0.1471 57.2
##  (TRUE TRUE HL 2-20 µm) - (TRUE TRUE LL 2-20 µm)         3.7854 0.1360 44.2
##  (TRUE TRUE HL 2-20 µm) - FALSE FALSE HL >20 µm          0.2683 0.1688 46.3
##  (TRUE TRUE HL 2-20 µm) - TRUE FALSE HL >20 µm          -1.6969 0.1233 78.9
##  (TRUE TRUE HL 2-20 µm) - FALSE TRUE HL >20 µm          -0.0344 0.1444 54.1
##  (TRUE TRUE HL 2-20 µm) - TRUE TRUE HL >20 µm           -1.9997 0.0885 54.8
##  (TRUE TRUE HL 2-20 µm) - FALSE FALSE LL >20 µm          3.2313 0.1647 42.2
```

```
##  (TRUE TRUE HL 2-20 µm) - TRUE FALSE LL >20 µm           2.5714 0.1688 46.3
##  (TRUE TRUE HL 2-20 µm) - FALSE TRUE LL >20 µm           2.9286 0.1390 47.8
##  (TRUE TRUE HL 2-20 µm) - TRUE TRUE LL >20 µm            2.2687 0.1444 54.1
##  (FALSE FALSE LL 2-20 µm) - (TRUE FALSE LL 2-20 µm)     -0.0886 0.1360 44.3
##  (FALSE FALSE LL 2-20 µm) - (FALSE TRUE LL 2-20 µm)     -0.3027 0.0877 30.3
##  (FALSE FALSE LL 2-20 µm) - (TRUE TRUE LL 2-20 µm)      -0.3913 0.1616 39.5
##  (FALSE FALSE LL 2-20 µm) - FALSE FALSE HL >20 µm       -3.9083 0.1444 54.2
##  (FALSE FALSE LL 2-20 µm) - TRUE FALSE HL >20 µm        -5.8736 0.1413 50.1
##  (FALSE FALSE LL 2-20 µm) - FALSE TRUE HL >20 µm        -4.2111 0.1690 46.6
##  (FALSE FALSE LL 2-20 µm) - TRUE TRUE HL >20 µm         -6.1763 0.1672 44.4
##  (FALSE FALSE LL 2-20 µm) - FALSE FALSE LL >20 µm       -0.9454 0.0849 54.0
##  (FALSE FALSE LL 2-20 µm) - TRUE FALSE LL >20 µm        -1.6053 0.1444 54.2
##  (FALSE FALSE LL 2-20 µm) - FALSE TRUE LL >20 µm        -1.2481 0.1216 78.0
##  (FALSE FALSE LL 2-20 µm) - TRUE TRUE LL >20 µm         -1.9080 0.1690 46.6
##  (TRUE FALSE LL 2-20 µm) - (FALSE TRUE LL 2-20 µm)      -0.2142 0.1620 39.8
##  (TRUE FALSE LL 2-20 µm) - (TRUE TRUE LL 2-20 µm)       -0.3027 0.0877 30.3
##  (TRUE FALSE LL 2-20 µm) - FALSE FALSE HL >20 µm        -3.8198 0.1390 47.9
##  (TRUE FALSE LL 2-20 µm) - TRUE FALSE HL >20 µm         -5.7851 0.1480 57.6
##  (TRUE FALSE LL 2-20 µm) - FALSE TRUE HL >20 µm         -4.1225 0.1647 42.4
##  (TRUE FALSE LL 2-20 µm) - TRUE TRUE HL >20 µm          -6.0878 0.1731 50.0
##  (TRUE FALSE LL 2-20 µm) - FALSE FALSE LL >20 µm        -0.8568 0.1444 54.2
##  (TRUE FALSE LL 2-20 µm) - TRUE FALSE LL >20 µm         -1.5168 0.0849 54.0
##  (TRUE FALSE LL 2-20 µm) - FALSE TRUE LL >20 µm         -1.1595 0.1688 46.5
##  (TRUE FALSE LL 2-20 µm) - TRUE TRUE LL >20 µm          -1.8195 0.1224 78.5
##  (FALSE TRUE LL 2-20 µm) - (TRUE TRUE LL 2-20 µm)       -0.0886 0.1360 44.3
##  (FALSE TRUE LL 2-20 µm) - FALSE FALSE HL >20 µm        -3.6056 0.1688 46.5
##  (FALSE TRUE LL 2-20 µm) - TRUE FALSE HL >20 µm         -5.5709 0.1653 42.9
##  (FALSE TRUE LL 2-20 µm) - FALSE TRUE HL >20 µm         -3.9083 0.1444 54.2
##  (FALSE TRUE LL 2-20 µm) - TRUE TRUE HL >20 µm          -5.8736 0.1413 50.1
##  (FALSE TRUE LL 2-20 µm) - FALSE FALSE LL >20 µm        -0.6427 0.1224 78.5
##  (FALSE TRUE LL 2-20 µm) - TRUE FALSE LL >20 µm         -1.3026 0.1688 46.5
##  (FALSE TRUE LL 2-20 µm) - FALSE TRUE LL >20 µm         -0.9454 0.0849 54.0
##  (FALSE TRUE LL 2-20 µm) - TRUE TRUE LL >20 µm          -1.6053 0.1444 54.2
##  (TRUE TRUE LL 2-20 µm) - FALSE FALSE HL >20 µm         -3.5171 0.1640 41.8
##  (TRUE TRUE LL 2-20 µm) - TRUE FALSE HL >20 µm          -5.4824 0.1709 48.2
##  (TRUE TRUE LL 2-20 µm) - FALSE TRUE HL >20 µm          -3.8198 0.1390 47.9
##  (TRUE TRUE LL 2-20 µm) - TRUE TRUE HL >20 µm           -5.7851 0.1480 57.6
##  (TRUE TRUE LL 2-20 µm) - FALSE FALSE LL >20 µm         -0.5541 0.1690 46.6
##  (TRUE TRUE LL 2-20 µm) - TRUE FALSE LL >20 µm          -1.2140 0.1216 78.0
##  (TRUE TRUE LL 2-20 µm) - FALSE TRUE LL >20 µm          -0.8568 0.1444 54.2
##  (TRUE TRUE LL 2-20 µm) - TRUE TRUE LL >20 µm           -1.5168 0.0849 54.0
##  FALSE FALSE HL >20 µm - TRUE FALSE HL >20 µm           -1.9653 0.1379 46.2
##  FALSE FALSE HL >20 µm - FALSE TRUE HL >20 µm           -0.3027 0.0877 30.3
##  FALSE FALSE HL >20 µm - TRUE TRUE HL >20 µm            -2.2680 0.1643 41.6
##  FALSE FALSE HL >20 µm - FALSE FALSE LL >20 µm           2.9630 0.1364 44.7
##  FALSE FALSE HL >20 µm - TRUE FALSE LL >20 µm            2.3030 0.1471 57.3
##  FALSE FALSE HL >20 µm - FALSE TRUE LL >20 µm            2.6602 0.1617 39.5
##  FALSE FALSE HL >20 µm - TRUE TRUE LL >20 µm             2.0003 0.1712 48.8
##  TRUE FALSE HL >20 µm - FALSE TRUE HL >20 µm             1.6626 0.1626 40.3
##  TRUE FALSE HL >20 µm - TRUE TRUE HL >20 µm             -0.3027 0.0877 30.3
##  TRUE FALSE HL >20 µm - FALSE FALSE LL >20 µm            4.9282 0.1513 61.1
##  TRUE FALSE HL >20 µm - TRUE FALSE LL >20 µm             4.2683 0.1379 46.2
##  TRUE FALSE HL >20 µm - FALSE TRUE LL >20 µm             4.6255 0.1737 50.8
##  TRUE FALSE HL >20 µm - TRUE TRUE LL >20 µm              3.9656 0.1626 40.3
```

```
##  FALSE TRUE HL >20 µm - TRUE TRUE HL >20 µm            -1.9653 0.1379 46.2
##  FALSE TRUE HL >20 µm - FALSE FALSE LL >20 µm           3.2657 0.1626 40.3
##  FALSE TRUE HL >20 µm - TRUE FALSE LL >20 µm            2.6057 0.1712 48.8
##  FALSE TRUE HL >20 µm - FALSE TRUE LL >20 µm            2.9630 0.1364 44.7
##  FALSE TRUE HL >20 µm - TRUE TRUE LL >20 µm             2.3030 0.1471 57.3
##  TRUE TRUE HL >20 µm - FALSE FALSE LL >20 µm            5.2309 0.1761 52.7
##  TRUE TRUE HL >20 µm - TRUE FALSE LL >20 µm             4.5710 0.1643 41.6
##  TRUE TRUE HL >20 µm - FALSE TRUE LL >20 µm             4.9282 0.1513 61.1
##  TRUE TRUE HL >20 µm - TRUE TRUE LL >20 µm              4.2683 0.1379 46.2
##  FALSE FALSE LL >20 µm - TRUE FALSE LL >20 µm          -0.6599 0.1364 44.7
##  FALSE FALSE LL >20 µm - FALSE TRUE LL >20 µm          -0.3027 0.0877 30.3
##  FALSE FALSE LL >20 µm - TRUE TRUE LL >20 µm           -0.9626 0.1626 40.3
##  TRUE FALSE LL >20 µm - FALSE TRUE LL >20 µm            0.3572 0.1617 39.5
##  TRUE FALSE LL >20 µm - TRUE TRUE LL >20 µm            -0.3027 0.0877 30.3
##  FALSE TRUE LL >20 µm - TRUE TRUE LL >20 µm            -0.6599 0.1364 44.7
##  t.ratio p.value
##   -9.897  <.0001
##   -3.453  0.1569
##  -10.176  <.0001
##   16.224  <.0001
##   14.728  <.0001
##   11.751  <.0001
##   10.883  <.0001
##    2.018  0.9264
##   -8.470  <.0001
##   -1.088  1.0000
##   -9.021  <.0001
##   18.346  <.0001
##   18.463  <.0001
##   13.876  <.0001
##   13.765  <.0001
##  -14.823  <.0001
##  -21.779  <.0001
##  -12.746  <.0001
##  -20.366  <.0001
##   11.810  <.0001
##    7.516  <.0001
##    8.308  <.0001
##    4.508  0.0091
##    6.457  <.0001
##   -3.453  0.1569
##   24.157  <.0001
##   25.823  <.0001
##   18.983  <.0001
##   19.861  <.0001
##   10.496  <.0001
##    1.451  0.9983
##    7.191  <.0001
##   -1.481  0.9981
##   28.802  <.0001
##   27.050  <.0001
##   22.506  <.0001
##   21.362  <.0001
##    0.610  1.0000
```

```
##  -21.204  <.0001
##   -1.270  0.9997
##  -17.321  <.0001
##   21.944  <.0001
##   16.562  <.0001
##   16.754  <.0001
##   12.357  <.0001
##   -9.897  <.0001
##   15.529  <.0001
##   14.419  <.0001
##   16.224  <.0001
##   14.728  <.0001
##    3.888  0.0355
##   -5.456  0.0004
##    2.018  0.9264
##   -8.470  <.0001
##   17.498  <.0001
##   17.454  <.0001
##   18.346  <.0001
##   18.463  <.0001
##   -7.857  <.0001
##  -17.092  <.0001
##  -14.823  <.0001
##  -21.779  <.0001
##   11.880  <.0001
##    8.216  <.0001
##   11.810  <.0001
##    7.516  <.0001
##   22.519  <.0001
##   23.544  <.0001
##   24.157  <.0001
##   25.823  <.0001
##   10.752  <.0001
##    3.494  0.1059
##   10.496  <.0001
##    1.451  0.9983
##   26.195  <.0001
##   24.887  <.0001
##   28.802  <.0001
##   27.050  <.0001
##    2.315  0.7882
##  -12.769  <.0001
##    0.610  1.0000
##  -21.204  <.0001
##   20.365  <.0001
##   15.959  <.0001
##   21.944  <.0001
##   16.562  <.0001
##   -0.299  1.0000
##   -3.453  0.1569
##   -2.125  0.8812
##  -14.095  <.0001
##  -24.721  <.0001
##  -13.859  <.0001
```

```
##   -22.744  <.0001
##     5.259  0.0006
##     2.459  0.6989
##     1.160  1.0000
##     0.312  1.0000
##   -23.996  <.0001
##   -38.426  <.0001
##   -22.291  <.0001
##   -34.278  <.0001
##    -5.910  0.0001
##    -8.045  <.0001
##    -6.616  <.0001
##    -8.664  <.0001
##    -1.617  0.9917
##    -3.453  0.1569
##   -14.382  <.0001
##   -23.462  <.0001
##   -14.003  <.0001
##   -21.823  <.0001
##     3.354  0.1620
##     4.692  0.0038
##     1.075  1.0000
##     0.767  1.0000
##   -24.625  <.0001
##   -36.413  <.0001
##   -22.628  <.0001
##   -32.875  <.0001
##    -3.192  0.2289
##   -13.206  <.0001
##    -4.524  0.0077
##   -11.626  <.0001
##    -0.299  1.0000
##   -10.246  <.0001
##   -19.056  <.0001
##   -14.095  <.0001
##   -24.721  <.0001
##     6.135  <.0001
##     3.889  0.0463
##     5.259  0.0006
##     2.459  0.6989
##   -18.731  <.0001
##   -31.012  <.0001
##   -23.996  <.0001
##   -38.426  <.0001
##    -1.624  0.9936
##    -5.088  0.0013
##    -5.910  0.0001
##    -8.045  <.0001
##   -10.314  <.0001
##   -18.290  <.0001
##   -14.382  <.0001
##   -23.462  <.0001
##     4.665  0.0051
##     5.742  <.0001
```

```
##    3.354  0.1620
##    4.692  0.0038
##  -19.026  <.0001
##  -29.767  <.0001
##  -24.625  <.0001
##  -36.413  <.0001
##   -0.936  1.0000
##   -6.729  <.0001
##   -3.192  0.2289
##  -13.206  <.0001
##  -10.249  <.0001
##   -3.453  0.1569
##  -10.472  <.0001
##   18.235  <.0001
##   16.262  <.0001
##   13.439  <.0001
##   12.201  <.0001
##  -16.830  <.0001
##  -22.930  <.0001
##  -14.138  <.0001
##  -21.349  <.0001
##   10.630  <.0001
##    6.291  <.0001
##    7.299  <.0001
##    3.474  0.1333
##    6.753  <.0001
##   -3.453  0.1569
##   26.343  <.0001
##   27.834  <.0001
##   20.860  <.0001
##   21.554  <.0001
##   -0.238  1.0000
##  -22.587  <.0001
##   -1.995  0.9316
##  -18.294  <.0001
##   21.063  <.0001
##   15.714  <.0001
##   16.007  <.0001
##   11.632  <.0001
##  -10.249  <.0001
##   17.222  <.0001
##   15.737  <.0001
##   18.235  <.0001
##   16.262  <.0001
##   -9.259  <.0001
##  -18.088  <.0001
##  -16.830  <.0001
##  -22.930  <.0001
##   10.872  <.0001
##    7.178  <.0001
##   10.630  <.0001
##    6.291  <.0001
##   24.396  <.0001
##   25.232  <.0001
```

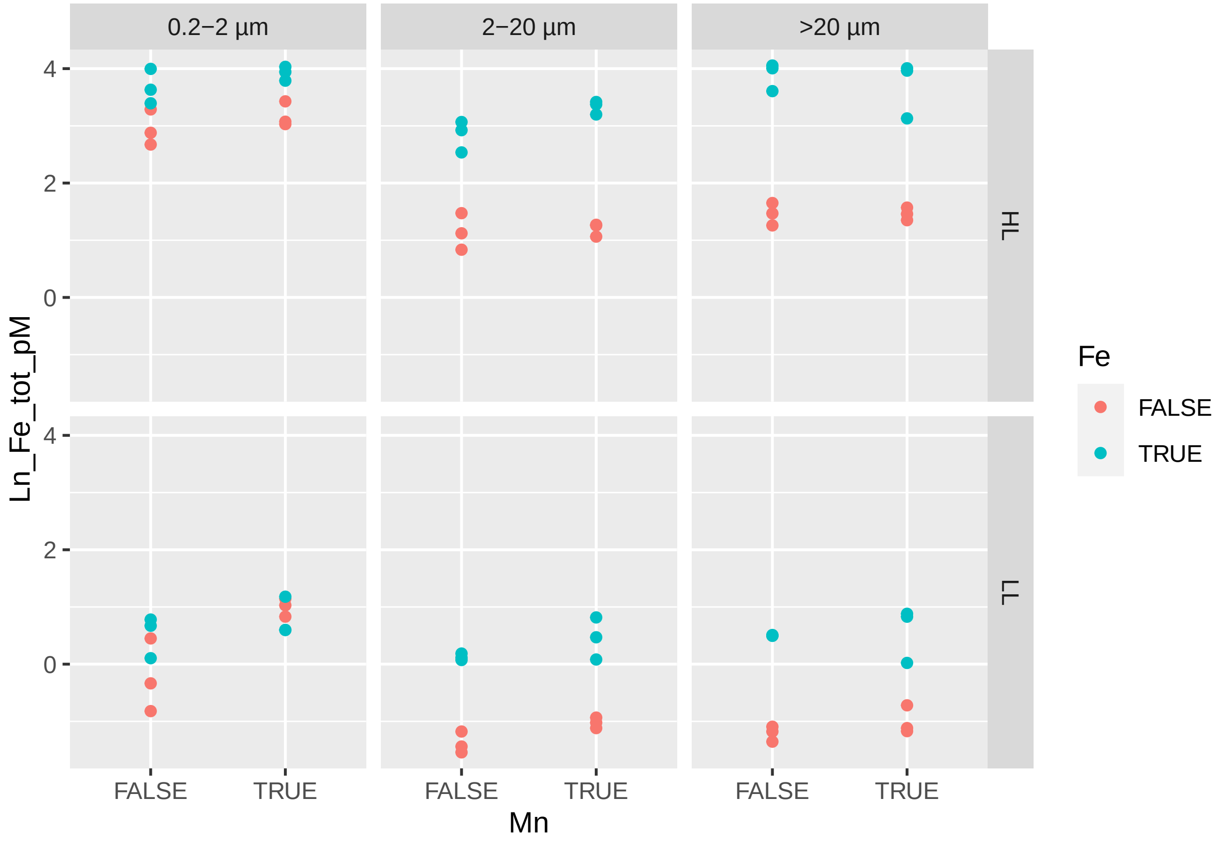
```
##   26.343  <.0001
##   27.834  <.0001
##    1.590  0.9938
##  -13.763  <.0001
##   -0.238  1.0000
##  -22.587  <.0001
##   19.621  <.0001
##   15.234  <.0001
##   21.063  <.0001
##   15.714  <.0001
##   -0.651  1.0000
##   -3.453  0.1569
##   -2.421  0.7210
##  -27.071  <.0001
##  -41.567  <.0001
##  -24.917  <.0001
##  -36.932  <.0001
##  -11.140  <.0001
##  -11.119  <.0001
##  -10.266  <.0001
##  -11.290  <.0001
##   -1.322  0.9994
##   -3.453  0.1569
##  -27.473  <.0001
##  -39.089  <.0001
##  -25.033  <.0001
##  -35.163  <.0001
##   -5.935  0.0001
##  -17.872  <.0001
##   -6.869  <.0001
##  -14.860  <.0001
##   -0.651  1.0000
##  -21.361  <.0001
##  -33.696  <.0001
##  -27.071  <.0001
##  -41.567  <.0001
##   -5.249  0.0003
##   -7.717  <.0001
##  -11.140  <.0001
##  -11.119  <.0001
##  -21.440  <.0001
##  -32.084  <.0001
##  -27.473  <.0001
##  -39.089  <.0001
##   -3.279  0.1972
##   -9.986  <.0001
##   -5.935  0.0001
##  -17.872  <.0001
##  -14.248  <.0001
##   -3.453  0.1569
##  -13.805  <.0001
##   21.724  <.0001
##   15.660  <.0001
##   16.453  <.0001
```

```
##   11.684  <.0001
##   10.227  <.0001
##   -3.453  0.1569
##   32.568  <.0001
##   30.944  <.0001
##   26.636  <.0001
##   24.394  <.0001
##  -14.248  <.0001
##   20.089  <.0001
##   15.220  <.0001
##   21.724  <.0001
##   15.660  <.0001
##   29.708  <.0001
##   27.823  <.0001
##   32.568  <.0001
##   30.944  <.0001
##   -4.838  0.0031
##   -3.453  0.1569
##   -5.922  0.0001
##    2.209  0.8427
##   -3.453  0.1569
##   -4.838  0.0031
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 24 estimates
```

6.2 Iron uptake

```
Uptake$Ln_Fe_tot_pM <- log(Uptake$Fe_tot_pM)   #data log-transformed
```

```
#Plot using ggplot2
ggplot(Uptake) +
  geom_point(aes(x = Mn, y = Ln_Fe_tot_pM, col = Fe)) +
  facet_grid(Light ~ Size)
```



```
#model fit with all factors (Mn, Fe, Light and Size)
fit_Fe <- lmer(Ln_Fe_tot_pM ~ Mn + Fe + Light + Size +
               Mn:Fe + Mn:Light + Fe:Light + Mn:Size + Fe:Size +
                 Light:Size + (1|Bottle),
             data = Uptake, na.action=na.fail, REML = FALSE)

summary(fit_Fe)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: Ln_Fe_tot_pM ~ Mn + Fe + Light + Size + Mn:Fe + Mn:Light + Fe:Light +
##     Mn:Size + Fe:Size + Light:Size + (1 | Bottle)
##    Data: Uptake
##
##      AIC      BIC   logLik deviance df.resid
##     44.1     82.8     -5.0     10.1       55
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.15060 -0.66124 -0.01608  0.66146  1.56202
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.01131  0.1063
##  Residual             0.05773  0.2403
## Number of obs: 72, groups:  Bottle, 24
```

```
##
## Fixed effects:
##                       Estimate Std. Error t value
## (Intercept)          2.8307419  0.1237993  22.866
## MnTRUE               0.4312104  0.1472807   2.928
## FeTRUE               0.8381154  0.1472807   5.691
## LightLL             -2.7857621  0.1472807 -18.915
## Size2-20 µm         -1.8082377  0.1387242 -13.035
## Size>20 µm          -1.3083691  0.1387242  -9.431
## MnTRUE:FeTRUE       -0.1436772  0.1427202  -1.007
## MnTRUE:LightLL       0.2755992  0.1427202   1.931
## FeTRUE:LightLL      -0.5248625  0.1427202  -3.678
## MnTRUE:Size2-20 µm  -0.1879686  0.1387242  -1.355
## MnTRUE:Size>20 µm   -0.4736506  0.1387242  -3.414
## FeTRUE:Size2-20 µm   1.2021081  0.1387242   8.665
## FeTRUE:Size>20 µm    1.4861547  0.1387242  10.713
## LightLL:Size2-20 µm  0.3244418  0.1387242   2.339
## LightLL:Size>20 µm  -0.0002235  0.1387242  -0.002
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_Fe, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## Ln_Fe_tot_pM ~ Mn + Fe + Light + Size + Mn:Fe + Mn:Light + Fe:Light +
##     Mn:Size + Fe:Size + Light:Size + (1 | Bottle)
##            npar     AIC    LRT    Pr(Chi)
## <none>           44.083
## Mn:Fe         1  43.076  0.993  0.319097
## Mn:Light      1  45.549  3.466  0.062637 .
## Fe:Light      1  52.810 10.727  0.001056 **
## Mn:Size       2  50.652 10.569  0.005069 **
## Fe:Size       2 107.912 67.829 1.867e-15 ***
## Light:Size    2  46.877  6.794  0.033478 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#it shows that Fe:Light, Fe:Size, Mn:Size and Light:Size
#interactions are significant
#all other interactions are removed from the model

#second model fit
fit_Fe2 <- lmer(Ln_Fe_tot_pM ~ Fe + Mn + Light + Size + Fe:Light
                + Fe:Size + Mn:Size + Light:Size + (1|Bottle),
                  data = Uptake, na.action=na.fail, REML = FALSE)
summary(fit_Fe2)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: Ln_Fe_tot_pM ~ Fe + Mn + Light + Size + Fe:Light + Fe:Size +
##     Mn:Size + Light:Size + (1 | Bottle)
##    Data: Uptake
##
```

```
##      AIC      BIC   logLik deviance df.resid
##     44.4     78.6     -7.2     14.4       57
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.2527 -0.4728 -0.0745  0.5690  1.7696
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.01735  0.1317
##  Residual             0.05773  0.2403
## Number of obs: 72, groups:  Bottle, 24
##
## Fixed effects:
##                        Estimate Std. Error t value
## (Intercept)           2.7977614  0.1184817  23.613
## FeTRUE                0.7662768  0.1364251   5.617
## MnTRUE                0.4971714  0.1118629   4.444
## LightLL              -2.6479625  0.1364251 -19.410
## Size2-20 µm          -1.8082377  0.1387242 -13.035
## Size>20 µm           -1.3083691  0.1387242  -9.431
## FeTRUE:LightLL       -0.5248625  0.1561857  -3.361
## FeTRUE:Size2-20 µm    1.2021081  0.1387242   8.665
## FeTRUE:Size>20 µm     1.4861547  0.1387242  10.713
## MnTRUE:Size2-20 µm   -0.1879686  0.1387242  -1.355
## MnTRUE:Size>20 µm    -0.4736506  0.1387242  -3.414
## LightLL:Size2-20 µm   0.3244418  0.1387242   2.339
## LightLL:Size>20 µm   -0.0002235  0.1387242  -0.002
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_Fe2, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## Ln_Fe_tot_pM ~ Fe + Mn + Light + Size + Fe:Light + Fe:Size +
##     Mn:Size + Light:Size + (1 | Bottle)
##            npar     AIC    LRT   Pr(Chi)
## <none>           44.411
## Fe:Light      1  51.666  9.255  0.002348 **
## Fe:Size       2 106.385 65.975 4.718e-15 ***
## Mn:Size       2  50.980 10.569  0.005069 **
## Light:Size    2  47.204  6.794  0.033478 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#best model identified by drop
fit_best_Fe <- lmer(Ln_Fe_tot_pM ~Fe + Mn + Light + Size + Fe:Light + Mn:Size +
                      Fe:Size + Light:Size + (1|Bottle),
                  data = Uptake, na.action=na.fail, REML = FALSE)
summary(fit_best_Fe)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
```

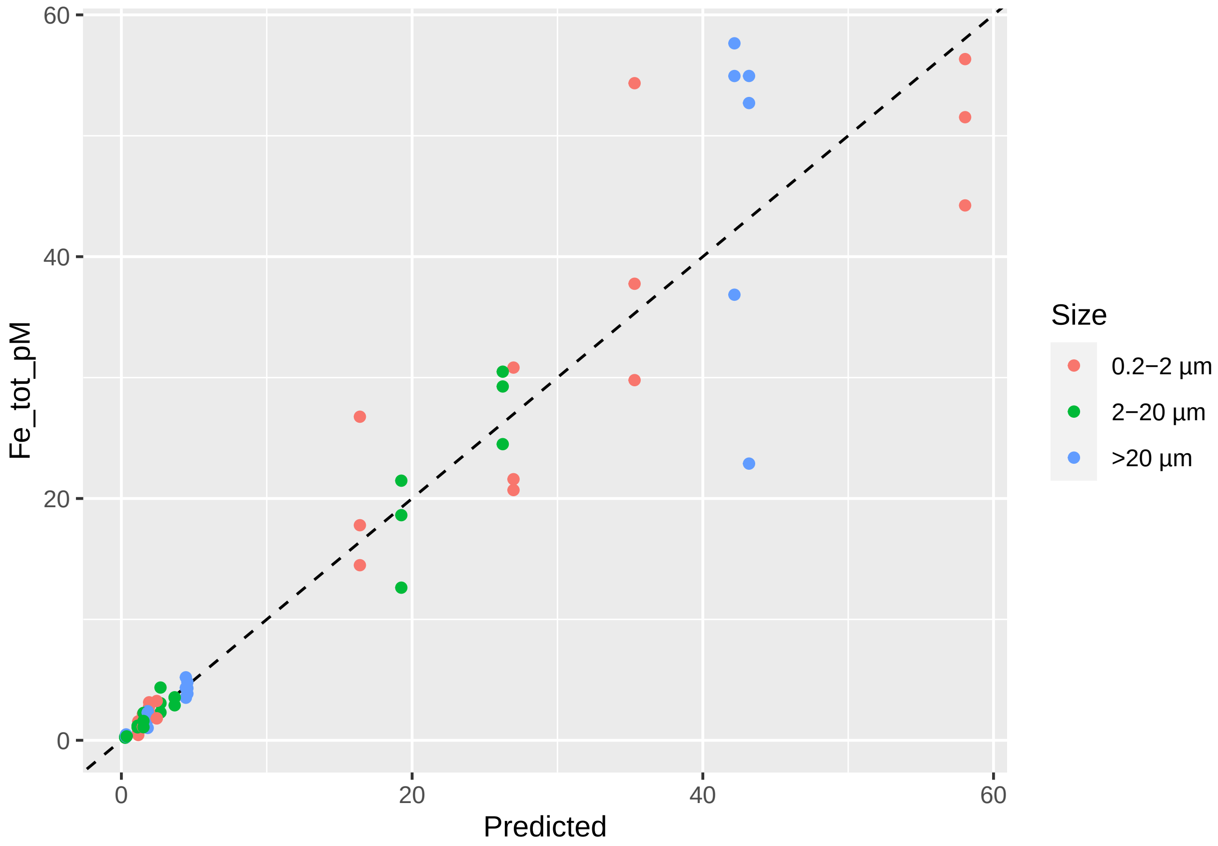
```
## Formula: Ln_Fe_tot_pM ~ Fe + Mn + Light + Size + Fe:Light + Mn:Size +
##     Fe:Size + Light:Size + (1 | Bottle)
##    Data: Uptake
##
##      AIC      BIC   logLik deviance df.resid
##     44.4     78.6     -7.2     14.4       57
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.2527 -0.4728 -0.0745  0.5690  1.7696
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.01735  0.1317
##  Residual             0.05773  0.2403
## Number of obs: 72, groups:  Bottle, 24
##
## Fixed effects:
##                       Estimate Std. Error t value
## (Intercept)          2.7977614  0.1184817  23.613
## FeTRUE               0.7662768  0.1364251   5.617
## MnTRUE               0.4971714  0.1118629   4.444
## LightLL             -2.6479625  0.1364251 -19.410
## Size2-20 µm         -1.8082377  0.1387242 -13.035
## Size>20 µm          -1.3083691  0.1387242  -9.431
## FeTRUE:LightLL      -0.5248625  0.1561857  -3.361
## MnTRUE:Size2-20 µm  -0.1879686  0.1387242  -1.355
## MnTRUE:Size>20 µm   -0.4736506  0.1387242  -3.414
## FeTRUE:Size2-20 µm   1.2021081  0.1387242   8.665
## FeTRUE:Size>20 µm    1.4861547  0.1387242  10.713
## LightLL:Size2-20 µm  0.3244418  0.1387242   2.339
## LightLL:Size>20 µm  -0.0002235  0.1387242  -0.002
```

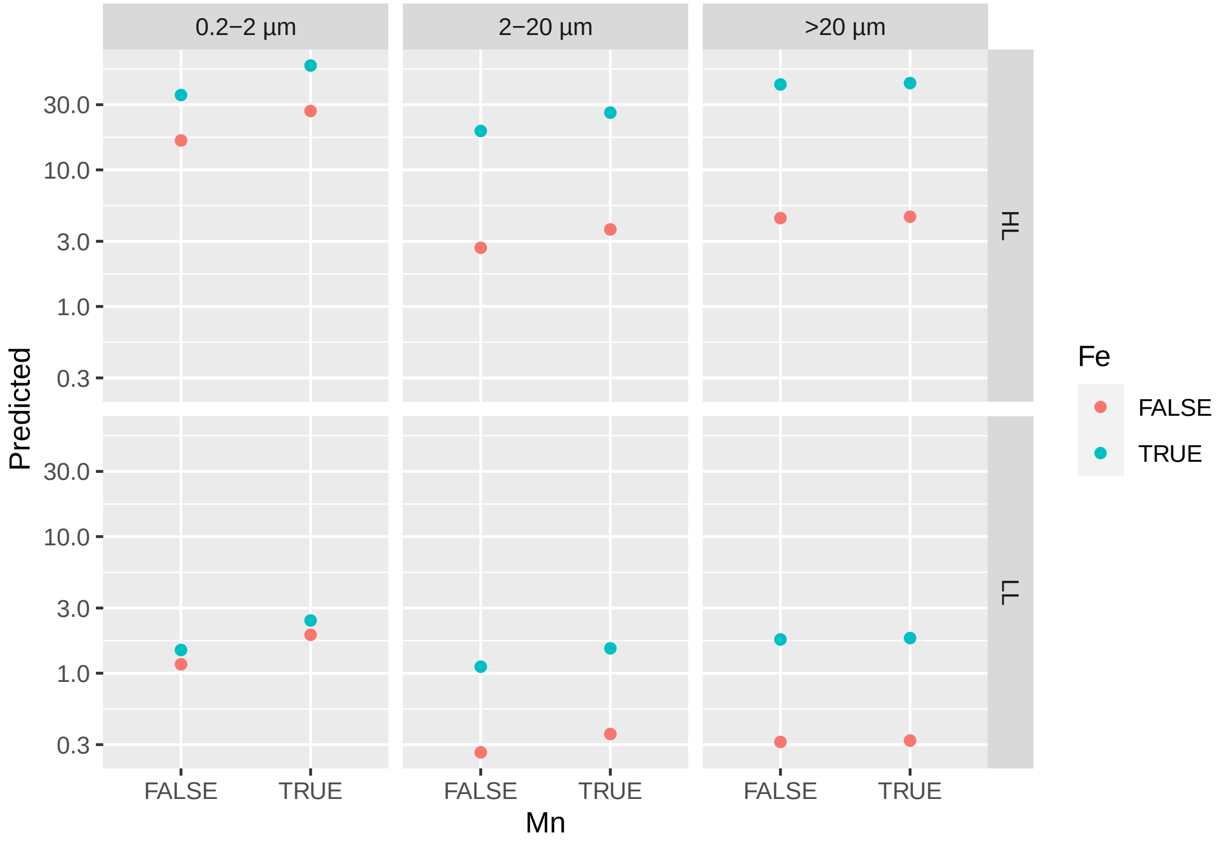
```
#Report results
report(fit_best_Fe)
```

```
## We fitted a linear mixed model (estimated using ML and nloptwrap optimizer) to
## predict Ln_Fe_tot_pM with Fe, Mn, Light and Size (formula: Ln_Fe_tot_pM ~ Fe +
## Mn + Light + Size + Fe:Light + Mn:Size + Fe:Size + Light:Size). The model
## included Bottle as random effect (formula: ~1 | Bottle). The model's total
## explanatory power is substantial (conditional R2 = 0.98) and the part related
## to the fixed effects alone (marginal R2) is of 0.97. The model's intercept,
## corresponding to Fe = [?], Mn = [?], Light = HL and Size = 0.2-2 µm, is at 2.80
## (95% CI [2.56, 3.04], t(57) = 23.61, p < .001). Within this model:
##
##   - The effect of FeTRUE is statistically significant and positive (beta = 0.77,
## 95% CI [0.49, 1.04], t(57) = 5.62, p < .001; Std. beta = 0.45, 95% CI [0.29,
## 0.60])
##   - The effect of MnTRUE is statistically significant and positive (beta = 0.50,
## 95% CI [0.27, 0.72], t(57) = 4.44, p < .001; Std. beta = 0.29, 95% CI [0.16,
## 0.42])
##   - The effect of Light [LL] is statistically significant and negative (beta =
## -2.65, 95% CI [-2.92, -2.37], t(57) = -19.41, p < .001; Std. beta = -1.54, 95%
## CI [-1.70, -1.38])
```

```
##   - The effect of Size [2-20 µm] is statistically significant and negative (beta
## = -1.81, 95% CI [-2.09, -1.53], t(57) = -13.03, p < .001; Std. beta = -1.05,
## 95% CI [-1.21, -0.89])
##   - The effect of Size [>20 µm] is statistically significant and negative (beta =
## -1.31, 95% CI [-1.59, -1.03], t(57) = -9.43, p < .001; Std. beta = -0.76, 95%
## CI [-0.92, -0.60])
##   - The effect of FeTRUE × Light [LL] is statistically significant and negative
## (beta = -0.52, 95% CI [-0.84, -0.21], t(57) = -3.36, p = 0.001; Std. beta =
## -0.31, 95% CI [-0.49, -0.12])
##   - The effect of MnTRUE × Size [2-20 µm] is statistically non-significant and
## negative (beta = -0.19, 95% CI [-0.47, 0.09], t(57) = -1.35, p = 0.181; Std.
## beta = -0.11, 95% CI [-0.27, 0.05])
##   - The effect of MnTRUE × Size [>20 µm] is statistically significant and
## negative (beta = -0.47, 95% CI [-0.75, -0.20], t(57) = -3.41, p = 0.001; Std.
## beta = -0.28, 95% CI [-0.44, -0.11])
##   - The effect of FeTRUE × Size [2-20 µm] is statistically significant and
## positive (beta = 1.20, 95% CI [0.92, 1.48], t(57) = 8.67, p < .001; Std. beta =
## 0.70, 95% CI [0.54, 0.86])
##   - The effect of FeTRUE × Size [>20 µm] is statistically significant and
## positive (beta = 1.49, 95% CI [1.21, 1.76], t(57) = 10.71, p < .001; Std. beta
## = 0.86, 95% CI [0.70, 1.03])
##   - The effect of Light [LL] × Size [2-20 µm] is statistically significant and
## positive (beta = 0.32, 95% CI [0.05, 0.60], t(57) = 2.34, p = 0.023; Std. beta
## = 0.19, 95% CI [0.03, 0.35])
##   - The effect of Light [LL] × Size [>20 µm] is statistically non-significant and
## negative (beta = -2.23e-04, 95% CI [-0.28, 0.28], t(57) = -1.61e-03, p = 0.999;
## Std. beta = -1.30e-04, 95% CI [-0.16, 0.16])
##
## Standardized parameters were obtained by fitting the model on a standardized
## version of the dataset. 95% Confidence Intervals (CIs) and p-values were
## computed using a Wald t-distribution approximation.
```

```r
#Represent data predicted by the model vs real data
Uptake$Predicted <- exp(predict(fit_best_Fe, re.form = NA))
```


Fe_tot_pM
60
40
20
0
0
20
40
60
Predicted
Size
0.2−2 µm
2−20 µm
>20 µm



```r
#Pairwise comparison
emmeans (fit_best_Fe, pairwise ~ Fe + Mn + Light + Size, adjust = "tukey")
```

```
## $emmeans
##  Fe    Mn    Light Size     emmean    SE   df lower.CL upper.CL
##  FALSE FALSE HL    0.2-2 µm  2.798 0.132 74.9    2.536    3.060
##   TRUE FALSE HL    0.2-2 µm  3.564 0.132 74.9    3.302    3.826
##  FALSE  TRUE HL    0.2-2 µm  3.295 0.132 74.9    3.033    3.557
##   TRUE  TRUE HL    0.2-2 µm  4.061 0.132 74.9    3.799    4.323
##  FALSE FALSE LL    0.2-2 µm  0.150 0.132 74.9   -0.112    0.412
##   TRUE FALSE LL    0.2-2 µm  0.391 0.132 74.9    0.129    0.653
##  FALSE  TRUE LL    0.2-2 µm  0.647 0.132 74.9    0.385    0.909
##   TRUE  TRUE LL    0.2-2 µm  0.888 0.132 74.9    0.626    1.151
##  FALSE FALSE HL    2-20 µm   0.990 0.132 74.9    0.727    1.252
##   TRUE FALSE HL    2-20 µm   2.958 0.132 74.9    2.696    3.220
##  FALSE  TRUE HL    2-20 µm   1.299 0.132 74.9    1.036    1.561
##   TRUE  TRUE HL    2-20 µm   3.267 0.132 74.9    3.005    3.529
##  FALSE FALSE LL    2-20 µm  -1.334 0.132 74.9   -1.596   -1.072
##   TRUE FALSE LL    2-20 µm   0.110 0.132 74.9   -0.153    0.372
##  FALSE  TRUE LL    2-20 µm  -1.025 0.132 74.9   -1.287   -0.763
##   TRUE  TRUE LL    2-20 µm   0.419 0.132 74.9    0.156    0.681
##  FALSE FALSE HL    >20 µm    1.489 0.132 74.9    1.227    1.752
##   TRUE FALSE HL    >20 µm    3.742 0.132 74.9    3.480    4.004
##  FALSE  TRUE HL    >20 µm    1.513 0.132 74.9    1.251    1.775
##   TRUE  TRUE HL    >20 µm    3.765 0.132 74.9    3.503    4.028
##  FALSE FALSE LL    >20 µm   -1.159 0.132 74.9   -1.421   -0.897
```

```
##   TRUE FALSE LL    >20 µm    0.569 0.132 74.9    0.307    0.831
##  FALSE  TRUE LL    >20 µm   -1.135 0.132 74.9   -1.398   -0.873
##   TRUE  TRUE LL    >20 µm    0.592 0.132 74.9    0.330    0.855
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $contrasts
##  contrast                                              estimate    SE   df
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE FALSE HL 0.2-2 µm)   -0.7663 0.152 61.6
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE TRUE HL 0.2-2 µm)   -0.4972 0.124 80.7
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE TRUE HL 0.2-2 µm)    -1.2634 0.196 69.7
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE FALSE LL 0.2-2 µm)   2.6480 0.152 61.6
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE FALSE LL 0.2-2 µm)    2.4065 0.176 80.7
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE TRUE LL 0.2-2 µm)    2.1508 0.196 69.7
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)     1.9094 0.215 80.7
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)    1.8082 0.152 57.6
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)    -0.1601 0.186 85.1
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)     1.4990 0.164 86.1
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)     -0.4693 0.196 69.7
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)    4.1318 0.186 85.1
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)     2.6882 0.176 80.7
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)     3.8226 0.196 69.7
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)      2.3790 0.186 61.6
##  (FALSE FALSE HL 0.2-2 µm) - FALSE FALSE HL >20 µm       1.3084 0.152 57.6
##  (FALSE FALSE HL 0.2-2 µm) - TRUE FALSE HL >20 µm       -0.9441 0.186 85.1
##  (FALSE FALSE HL 0.2-2 µm) - FALSE TRUE HL >20 µm        1.2848 0.164 86.1
##  (FALSE FALSE HL 0.2-2 µm) - TRUE TRUE HL >20 µm        -0.9676 0.196 69.7
##  (FALSE FALSE HL 0.2-2 µm) - FALSE FALSE LL >20 µm       3.9566 0.186 85.1
##  (FALSE FALSE HL 0.2-2 µm) - TRUE FALSE LL >20 µm        2.2290 0.176 80.7
##  (FALSE FALSE HL 0.2-2 µm) - FALSE TRUE LL >20 µm        3.9330 0.196 69.7
##  (FALSE FALSE HL 0.2-2 µm) - TRUE TRUE LL >20 µm         2.2055 0.186 61.6
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE TRUE HL 0.2-2 µm)     0.2691 0.196 69.7
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE TRUE HL 0.2-2 µm)     -0.4972 0.124 80.7
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE FALSE LL 0.2-2 µm)    3.4142 0.176 80.7
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE FALSE LL 0.2-2 µm)     3.1728 0.152 61.6
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE TRUE LL 0.2-2 µm)     2.9171 0.215 80.7
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)      2.6757 0.196 69.7
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)     2.5745 0.186 85.1
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)      0.6061 0.152 57.6
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)      2.2653 0.196 69.7
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)       0.2969 0.164 86.1
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)     4.8980 0.176 80.7
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)      3.4545 0.186 85.1
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)      4.5888 0.186 61.6
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)       3.1453 0.196 69.7
##  (TRUE FALSE HL 0.2-2 µm) - FALSE FALSE HL >20 µm        2.0746 0.186 85.1
##  (TRUE FALSE HL 0.2-2 µm) - TRUE FALSE HL >20 µm        -0.1778 0.152 57.6
##  (TRUE FALSE HL 0.2-2 µm) - FALSE TRUE HL >20 µm         2.0511 0.196 69.7
##  (TRUE FALSE HL 0.2-2 µm) - TRUE TRUE HL >20 µm         -0.2013 0.164 86.1
##  (TRUE FALSE HL 0.2-2 µm) - FALSE FALSE LL >20 µm        4.7228 0.176 80.7
##  (TRUE FALSE HL 0.2-2 µm) - TRUE FALSE LL >20 µm         2.9953 0.186 85.1
##  (TRUE FALSE HL 0.2-2 µm) - FALSE TRUE LL >20 µm         4.6993 0.186 61.6
##  (TRUE FALSE HL 0.2-2 µm) - TRUE TRUE LL >20 µm          2.9717 0.196 69.7
```

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##  (FALSE TRUE HL 0.2-2 µm) - (TRUE TRUE HL 0.2-2 µm)     -0.7663 0.152 61.6
##  (FALSE TRUE HL 0.2-2 µm) - (FALSE FALSE LL 0.2-2 µm)    3.1451 0.196 69.7
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE FALSE LL 0.2-2 µm)     2.9037 0.215 80.7
##  (FALSE TRUE HL 0.2-2 µm) - (FALSE TRUE LL 0.2-2 µm)     2.6480 0.152 61.6
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)      2.4065 0.176 80.7
##  (FALSE TRUE HL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)     2.3054 0.164 86.1
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)      0.3370 0.196 69.7
##  (FALSE TRUE HL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)      1.9962 0.152 57.6
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)       0.0278 0.186 85.1
##  (FALSE TRUE HL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)     4.6289 0.196 69.7
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)      3.1854 0.186 61.6
##  (FALSE TRUE HL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)      4.3197 0.186 85.1
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)       2.8762 0.176 80.7
##  (FALSE TRUE HL 0.2-2 µm) - FALSE FALSE HL >20 µm        1.8055 0.164 86.1
##  (FALSE TRUE HL 0.2-2 µm) - TRUE FALSE HL >20 µm        -0.4469 0.196 69.7
##  (FALSE TRUE HL 0.2-2 µm) - FALSE TRUE HL >20 µm         1.7820 0.152 57.6
##  (FALSE TRUE HL 0.2-2 µm) - TRUE TRUE HL >20 µm         -0.4704 0.186 85.1
##  (FALSE TRUE HL 0.2-2 µm) - FALSE FALSE LL >20 µm        4.4537 0.196 69.7
##  (FALSE TRUE HL 0.2-2 µm) - TRUE FALSE LL >20 µm         2.7262 0.186 61.6
##  (FALSE TRUE HL 0.2-2 µm) - FALSE TRUE LL >20 µm         4.4302 0.186 85.1
##  (FALSE TRUE HL 0.2-2 µm) - TRUE TRUE LL >20 µm          2.7026 0.176 80.7
##  (TRUE TRUE HL 0.2-2 µm) - (FALSE FALSE LL 0.2-2 µm)     3.9114 0.215 80.7
##  (TRUE TRUE HL 0.2-2 µm) - (TRUE FALSE LL 0.2-2 µm)      3.6700 0.196 69.7
##  (TRUE TRUE HL 0.2-2 µm) - (FALSE TRUE LL 0.2-2 µm)      3.4142 0.176 80.7
##  (TRUE TRUE HL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)       3.1728 0.152 61.6
##  (TRUE TRUE HL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)      3.0717 0.196 69.7
##  (TRUE TRUE HL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)       1.1033 0.164 86.1
##  (TRUE TRUE HL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)       2.7625 0.186 85.1
##  (TRUE TRUE HL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)        0.7941 0.152 57.6
##  (TRUE TRUE HL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)      5.3952 0.186 61.6
##  (TRUE TRUE HL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)       3.9517 0.196 69.7
##  (TRUE TRUE HL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)       5.0860 0.176 80.7
##  (TRUE TRUE HL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)        3.6425 0.186 85.1
##  (TRUE TRUE HL 0.2-2 µm) - FALSE FALSE HL >20 µm         2.5718 0.196 69.7
##  (TRUE TRUE HL 0.2-2 µm) - TRUE FALSE HL >20 µm          0.3194 0.164 86.1
##  (TRUE TRUE HL 0.2-2 µm) - FALSE TRUE HL >20 µm          2.5483 0.186 85.1
##  (TRUE TRUE HL 0.2-2 µm) - TRUE TRUE HL >20 µm           0.2959 0.152 57.6
##  (TRUE TRUE HL 0.2-2 µm) - FALSE FALSE LL >20 µm         5.2200 0.186 61.6
##  (TRUE TRUE HL 0.2-2 µm) - TRUE FALSE LL >20 µm          3.4924 0.196 69.7
##  (TRUE TRUE HL 0.2-2 µm) - FALSE TRUE LL >20 µm          5.1965 0.176 80.7
##  (TRUE TRUE HL 0.2-2 µm) - TRUE TRUE LL >20 µm           3.4689 0.186 85.1
##  (FALSE FALSE LL 0.2-2 µm) - (TRUE FALSE LL 0.2-2 µm)   -0.2414 0.152 61.6
##  (FALSE FALSE LL 0.2-2 µm) - (FALSE TRUE LL 0.2-2 µm)   -0.4972 0.124 80.7
##  (FALSE FALSE LL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)    -0.7386 0.196 69.7
##  (FALSE FALSE LL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)   -0.8397 0.186 85.1
##  (FALSE FALSE LL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)    -2.8081 0.176 80.7
##  (FALSE FALSE LL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)    -1.1489 0.196 69.7
##  (FALSE FALSE LL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)     -3.1173 0.186 61.6
##  (FALSE FALSE LL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)    1.4838 0.152 57.6
##  (FALSE FALSE LL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)     0.0403 0.186 85.1
##  (FALSE FALSE LL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)     1.1746 0.164 86.1
##  (FALSE FALSE LL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)     -0.2689 0.196 69.7
##  (FALSE FALSE LL 0.2-2 µm) - FALSE FALSE HL >20 µm      -1.3396 0.186 85.1
##  (FALSE FALSE LL 0.2-2 µm) - TRUE FALSE HL >20 µm       -3.5920 0.176 80.7
```

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##  (FALSE FALSE LL 0.2-2 µm) - FALSE TRUE HL >20 µm      -1.3631 0.196 69.7
##  (FALSE FALSE LL 0.2-2 µm) - TRUE TRUE HL >20 µm       -3.6155 0.186 61.6
##  (FALSE FALSE LL 0.2-2 µm) - FALSE FALSE LL >20 µm      1.3086 0.152 57.6
##  (FALSE FALSE LL 0.2-2 µm) - TRUE FALSE LL >20 µm      -0.4190 0.186 85.1
##  (FALSE FALSE LL 0.2-2 µm) - FALSE TRUE LL >20 µm       1.2851 0.164 86.1
##  (FALSE FALSE LL 0.2-2 µm) - TRUE TRUE LL >20 µm       -0.4425 0.196 69.7
##  (TRUE FALSE LL 0.2-2 µm) - (FALSE TRUE LL 0.2-2 µm)   -0.2558 0.196 69.7
##  (TRUE FALSE LL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)    -0.4972 0.124 80.7
##  (TRUE FALSE LL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)   -0.5983 0.176 80.7
##  (TRUE FALSE LL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)    -2.5667 0.186 85.1
##  (TRUE FALSE LL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)    -0.9075 0.186 61.6
##  (TRUE FALSE LL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)     -2.8759 0.196 69.7
##  (TRUE FALSE LL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)    1.7252 0.186 85.1
##  (TRUE FALSE LL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)     0.2817 0.152 57.6
##  (TRUE FALSE LL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)     1.4160 0.196 69.7
##  (TRUE FALSE LL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)     -0.0275 0.164 86.1
##  (TRUE FALSE LL 0.2-2 µm) - FALSE FALSE HL >20 µm      -1.0982 0.176 80.7
##  (TRUE FALSE LL 0.2-2 µm) - TRUE FALSE HL >20 µm       -3.3506 0.186 85.1
##  (TRUE FALSE LL 0.2-2 µm) - FALSE TRUE HL >20 µm       -1.1217 0.186 61.6
##  (TRUE FALSE LL 0.2-2 µm) - TRUE TRUE HL >20 µm        -3.3741 0.196 69.7
##  (TRUE FALSE LL 0.2-2 µm) - FALSE FALSE LL >20 µm       1.5500 0.186 85.1
##  (TRUE FALSE LL 0.2-2 µm) - TRUE FALSE LL >20 µm       -0.1776 0.152 57.6
##  (TRUE FALSE LL 0.2-2 µm) - FALSE TRUE LL >20 µm        1.5265 0.196 69.7
##  (TRUE FALSE LL 0.2-2 µm) - TRUE TRUE LL >20 µm        -0.2011 0.164 86.1
##  (FALSE TRUE LL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)    -0.2414 0.152 61.6
##  (FALSE TRUE LL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)   -0.3426 0.196 69.7
##  (FALSE TRUE LL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)    -2.3109 0.186 61.6
##  (FALSE TRUE LL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)    -0.6518 0.186 85.1
##  (FALSE TRUE LL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)     -2.6201 0.176 80.7
##  (FALSE TRUE LL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)    1.9810 0.164 86.1
##  (FALSE TRUE LL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)     0.5374 0.196 69.7
##  (FALSE TRUE LL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)     1.6718 0.152 57.6
##  (FALSE TRUE LL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)      0.2282 0.186 85.1
##  (FALSE TRUE LL 0.2-2 µm) - FALSE FALSE HL >20 µm      -0.8424 0.196 69.7
##  (FALSE TRUE LL 0.2-2 µm) - TRUE FALSE HL >20 µm       -3.0949 0.186 61.6
##  (FALSE TRUE LL 0.2-2 µm) - FALSE TRUE HL >20 µm       -0.8659 0.186 85.1
##  (FALSE TRUE LL 0.2-2 µm) - TRUE TRUE HL >20 µm        -3.1184 0.176 80.7
##  (FALSE TRUE LL 0.2-2 µm) - FALSE FALSE LL >20 µm       1.8058 0.164 86.1
##  (FALSE TRUE LL 0.2-2 µm) - TRUE FALSE LL >20 µm        0.0782 0.196 69.7
##  (FALSE TRUE LL 0.2-2 µm) - FALSE TRUE LL >20 µm        1.7822 0.152 57.6
##  (FALSE TRUE LL 0.2-2 µm) - TRUE TRUE LL >20 µm         0.0547 0.186 85.1
##  (TRUE TRUE LL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)    -0.1011 0.186 61.6
##  (TRUE TRUE LL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)     -2.0695 0.196 69.7
##  (TRUE TRUE LL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)     -0.4103 0.176 80.7
##  (TRUE TRUE LL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)      -2.3787 0.186 85.1
##  (TRUE TRUE LL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)     2.2224 0.196 69.7
##  (TRUE TRUE LL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)      0.7789 0.164 86.1
##  (TRUE TRUE LL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)      1.9132 0.186 85.1
##  (TRUE TRUE LL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)       0.4697 0.152 57.6
##  (TRUE TRUE LL 0.2-2 µm) - FALSE FALSE HL >20 µm       -0.6010 0.186 61.6
##  (TRUE TRUE LL 0.2-2 µm) - TRUE FALSE HL >20 µm        -2.8534 0.196 69.7
##  (TRUE TRUE LL 0.2-2 µm) - FALSE TRUE HL >20 µm        -0.6245 0.176 80.7
##  (TRUE TRUE LL 0.2-2 µm) - TRUE TRUE HL >20 µm         -2.8770 0.186 85.1
##  (TRUE TRUE LL 0.2-2 µm) - FALSE FALSE LL >20 µm        2.0472 0.196 69.7
```

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##  (TRUE TRUE LL 0.2-2 µm) - TRUE FALSE LL >20 µm          0.3196 0.164 86.1
##  (TRUE TRUE LL 0.2-2 µm) - FALSE TRUE LL >20 µm          2.0237 0.186 85.1
##  (TRUE TRUE LL 0.2-2 µm) - TRUE TRUE LL >20 µm           0.2961 0.152 57.6
##  (FALSE FALSE HL 2-20 µm) - (TRUE FALSE HL 2-20 µm)     -1.9684 0.152 61.6
##  (FALSE FALSE HL 2-20 µm) - (FALSE TRUE HL 2-20 µm)     -0.3092 0.124 80.7
##  (FALSE FALSE HL 2-20 µm) - (TRUE TRUE HL 2-20 µm)      -2.2776 0.196 69.7
##  (FALSE FALSE HL 2-20 µm) - (FALSE FALSE LL 2-20 µm)     2.3235 0.152 61.6
##  (FALSE FALSE HL 2-20 µm) - (TRUE FALSE LL 2-20 µm)      0.8800 0.176 80.7
##  (FALSE FALSE HL 2-20 µm) - (FALSE TRUE LL 2-20 µm)      2.0143 0.196 69.7
##  (FALSE FALSE HL 2-20 µm) - (TRUE TRUE LL 2-20 µm)       0.5708 0.215 80.7
##  (FALSE FALSE HL 2-20 µm) - FALSE FALSE HL >20 µm       -0.4999 0.152 57.6
##  (FALSE FALSE HL 2-20 µm) - TRUE FALSE HL >20 µm        -2.7523 0.186 85.1
##  (FALSE FALSE HL 2-20 µm) - FALSE TRUE HL >20 µm        -0.5234 0.164 86.1
##  (FALSE FALSE HL 2-20 µm) - TRUE TRUE HL >20 µm         -2.7758 0.196 69.7
##  (FALSE FALSE HL 2-20 µm) - FALSE FALSE LL >20 µm        2.1483 0.186 85.1
##  (FALSE FALSE HL 2-20 µm) - TRUE FALSE LL >20 µm         0.4207 0.176 80.7
##  (FALSE FALSE HL 2-20 µm) - FALSE TRUE LL >20 µm         2.1248 0.196 69.7
##  (FALSE FALSE HL 2-20 µm) - TRUE TRUE LL >20 µm          0.3972 0.186 61.6
##  (TRUE FALSE HL 2-20 µm) - (FALSE TRUE HL 2-20 µm)       1.6592 0.196 69.7
##  (TRUE FALSE HL 2-20 µm) - (TRUE TRUE HL 2-20 µm)       -0.3092 0.124 80.7
##  (TRUE FALSE HL 2-20 µm) - (FALSE FALSE LL 2-20 µm)      4.2919 0.176 80.7
##  (TRUE FALSE HL 2-20 µm) - (TRUE FALSE LL 2-20 µm)       2.8484 0.152 61.6
##  (TRUE FALSE HL 2-20 µm) - (FALSE TRUE LL 2-20 µm)       3.9827 0.215 80.7
##  (TRUE FALSE HL 2-20 µm) - (TRUE TRUE LL 2-20 µm)        2.5392 0.196 69.7
##  (TRUE FALSE HL 2-20 µm) - FALSE FALSE HL >20 µm         1.4685 0.186 85.1
##  (TRUE FALSE HL 2-20 µm) - TRUE FALSE HL >20 µm         -0.7839 0.152 57.6
##  (TRUE FALSE HL 2-20 µm) - FALSE TRUE HL >20 µm          1.4450 0.196 69.7
##  (TRUE FALSE HL 2-20 µm) - TRUE TRUE HL >20 µm          -0.8074 0.164 86.1
##  (TRUE FALSE HL 2-20 µm) - FALSE FALSE LL >20 µm         4.1167 0.176 80.7
##  (TRUE FALSE HL 2-20 µm) - TRUE FALSE LL >20 µm          2.3891 0.186 85.1
##  (TRUE FALSE HL 2-20 µm) - FALSE TRUE LL >20 µm          4.0932 0.186 61.6
##  (TRUE FALSE HL 2-20 µm) - TRUE TRUE LL >20 µm           2.3656 0.196 69.7
##  (FALSE TRUE HL 2-20 µm) - (TRUE TRUE HL 2-20 µm)       -1.9684 0.152 61.6
##  (FALSE TRUE HL 2-20 µm) - (FALSE FALSE LL 2-20 µm)      2.6327 0.196 69.7
##  (FALSE TRUE HL 2-20 µm) - (TRUE FALSE LL 2-20 µm)       1.1892 0.215 80.7
##  (FALSE TRUE HL 2-20 µm) - (FALSE TRUE LL 2-20 µm)       2.3235 0.152 61.6
##  (FALSE TRUE HL 2-20 µm) - (TRUE TRUE LL 2-20 µm)        0.8800 0.176 80.7
##  (FALSE TRUE HL 2-20 µm) - FALSE FALSE HL >20 µm        -0.1907 0.164 86.1
##  (FALSE TRUE HL 2-20 µm) - TRUE FALSE HL >20 µm         -2.4431 0.196 69.7
##  (FALSE TRUE HL 2-20 µm) - FALSE TRUE HL >20 µm         -0.2142 0.152 57.6
##  (FALSE TRUE HL 2-20 µm) - TRUE TRUE HL >20 µm          -2.4666 0.186 85.1
##  (FALSE TRUE HL 2-20 µm) - FALSE FALSE LL >20 µm         2.4575 0.196 69.7
##  (FALSE TRUE HL 2-20 µm) - TRUE FALSE LL >20 µm          0.7300 0.186 61.6
##  (FALSE TRUE HL 2-20 µm) - FALSE TRUE LL >20 µm          2.4340 0.186 85.1
##  (FALSE TRUE HL 2-20 µm) - TRUE TRUE LL >20 µm           0.7064 0.176 80.7
##  (TRUE TRUE HL 2-20 µm) - (FALSE FALSE LL 2-20 µm)       4.6011 0.215 80.7
##  (TRUE TRUE HL 2-20 µm) - (TRUE FALSE LL 2-20 µm)        3.1576 0.196 69.7
##  (TRUE TRUE HL 2-20 µm) - (FALSE TRUE LL 2-20 µm)        4.2919 0.176 80.7
##  (TRUE TRUE HL 2-20 µm) - (TRUE TRUE LL 2-20 µm)         2.8484 0.152 61.6
##  (TRUE TRUE HL 2-20 µm) - FALSE FALSE HL >20 µm          1.7777 0.196 69.7
##  (TRUE TRUE HL 2-20 µm) - TRUE FALSE HL >20 µm          -0.4747 0.164 86.1
##  (TRUE TRUE HL 2-20 µm) - FALSE TRUE HL >20 µm           1.7542 0.186 85.1
##  (TRUE TRUE HL 2-20 µm) - TRUE TRUE HL >20 µm           -0.4982 0.152 57.6
##  (TRUE TRUE HL 2-20 µm) - FALSE FALSE LL >20 µm          4.4259 0.186 61.6
```

```
##  (TRUE TRUE HL 2-20 µm) - TRUE FALSE LL >20 µm           2.6983 0.196 69.7
##  (TRUE TRUE HL 2-20 µm) - FALSE TRUE LL >20 µm           4.4024 0.176 80.7
##  (TRUE TRUE HL 2-20 µm) - TRUE TRUE LL >20 µm            2.6748 0.186 85.1
##  (FALSE FALSE LL 2-20 µm) - (TRUE FALSE LL 2-20 µm)     -1.4435 0.152 61.6
##  (FALSE FALSE LL 2-20 µm) - (FALSE TRUE LL 2-20 µm)     -0.3092 0.124 80.7
##  (FALSE FALSE LL 2-20 µm) - (TRUE TRUE LL 2-20 µm)      -1.7527 0.196 69.7
##  (FALSE FALSE LL 2-20 µm) - FALSE FALSE HL >20 µm       -2.8234 0.186 85.1
##  (FALSE FALSE LL 2-20 µm) - TRUE FALSE HL >20 µm        -5.0758 0.176 80.7
##  (FALSE FALSE LL 2-20 µm) - FALSE TRUE HL >20 µm        -2.8469 0.196 69.7
##  (FALSE FALSE LL 2-20 µm) - TRUE TRUE HL >20 µm         -5.0993 0.186 61.6
##  (FALSE FALSE LL 2-20 µm) - FALSE FALSE LL >20 µm       -0.1752 0.152 57.6
##  (FALSE FALSE LL 2-20 µm) - TRUE FALSE LL >20 µm        -1.9028 0.186 85.1
##  (FALSE FALSE LL 2-20 µm) - FALSE TRUE LL >20 µm        -0.1987 0.164 86.1
##  (FALSE FALSE LL 2-20 µm) - TRUE TRUE LL >20 µm         -1.9263 0.196 69.7
##  (TRUE FALSE LL 2-20 µm) - (FALSE TRUE LL 2-20 µm)       1.1343 0.196 69.7
##  (TRUE FALSE LL 2-20 µm) - (TRUE TRUE LL 2-20 µm)       -0.3092 0.124 80.7
##  (TRUE FALSE LL 2-20 µm) - FALSE FALSE HL >20 µm        -1.3799 0.176 80.7
##  (TRUE FALSE LL 2-20 µm) - TRUE FALSE HL >20 µm         -3.6323 0.186 85.1
##  (TRUE FALSE LL 2-20 µm) - FALSE TRUE HL >20 µm         -1.4034 0.186 61.6
##  (TRUE FALSE LL 2-20 µm) - TRUE TRUE HL >20 µm          -3.6558 0.196 69.7
##  (TRUE FALSE LL 2-20 µm) - FALSE FALSE LL >20 µm         1.2683 0.186 85.1
##  (TRUE FALSE LL 2-20 µm) - TRUE FALSE LL >20 µm         -0.4592 0.152 57.6
##  (TRUE FALSE LL 2-20 µm) - FALSE TRUE LL >20 µm          1.2448 0.196 69.7
##  (TRUE FALSE LL 2-20 µm) - TRUE TRUE LL >20 µm          -0.4828 0.164 86.1
##  (FALSE TRUE LL 2-20 µm) - (TRUE TRUE LL 2-20 µm)       -1.4435 0.152 61.6
##  (FALSE TRUE LL 2-20 µm) - FALSE FALSE HL >20 µm        -2.5142 0.196 69.7
##  (FALSE TRUE LL 2-20 µm) - TRUE FALSE HL >20 µm         -4.7666 0.186 61.6
##  (FALSE TRUE LL 2-20 µm) - FALSE TRUE HL >20 µm         -2.5377 0.186 85.1
##  (FALSE TRUE LL 2-20 µm) - TRUE TRUE HL >20 µm          -4.7901 0.176 80.7
##  (FALSE TRUE LL 2-20 µm) - FALSE FALSE LL >20 µm         0.1340 0.164 86.1
##  (FALSE TRUE LL 2-20 µm) - TRUE FALSE LL >20 µm         -1.5936 0.196 69.7
##  (FALSE TRUE LL 2-20 µm) - FALSE TRUE LL >20 µm          0.1105 0.152 57.6
##  (FALSE TRUE LL 2-20 µm) - TRUE TRUE LL >20 µm          -1.6171 0.186 85.1
##  (TRUE TRUE LL 2-20 µm) - FALSE FALSE HL >20 µm         -1.0707 0.186 61.6
##  (TRUE TRUE LL 2-20 µm) - TRUE FALSE HL >20 µm          -3.3231 0.196 69.7
##  (TRUE TRUE LL 2-20 µm) - FALSE TRUE HL >20 µm          -1.0942 0.176 80.7
##  (TRUE TRUE LL 2-20 µm) - TRUE TRUE HL >20 µm           -3.3466 0.186 85.1
##  (TRUE TRUE LL 2-20 µm) - FALSE FALSE LL >20 µm          1.5775 0.196 69.7
##  (TRUE TRUE LL 2-20 µm) - TRUE FALSE LL >20 µm          -0.1500 0.164 86.1
##  (TRUE TRUE LL 2-20 µm) - FALSE TRUE LL >20 µm           1.5540 0.186 85.1
##  (TRUE TRUE LL 2-20 µm) - TRUE TRUE LL >20 µm           -0.1736 0.152 57.6
##  FALSE FALSE HL >20 µm - TRUE FALSE HL >20 µm           -2.2524 0.152 61.6
##  FALSE FALSE HL >20 µm - FALSE TRUE HL >20 µm           -0.0235 0.124 80.7
##  FALSE FALSE HL >20 µm - TRUE TRUE HL >20 µm            -2.2760 0.196 69.7
##  FALSE FALSE HL >20 µm - FALSE FALSE LL >20 µm           2.6482 0.152 61.6
##  FALSE FALSE HL >20 µm - TRUE FALSE LL >20 µm            0.9206 0.176 80.7
##  FALSE FALSE HL >20 µm - FALSE TRUE LL >20 µm            2.6247 0.196 69.7
##  FALSE FALSE HL >20 µm - TRUE TRUE LL >20 µm             0.8971 0.215 80.7
##  TRUE FALSE HL >20 µm - FALSE TRUE HL >20 µm             2.2289 0.196 69.7
##  TRUE FALSE HL >20 µm - TRUE TRUE HL >20 µm             -0.0235 0.124 80.7
##  TRUE FALSE HL >20 µm - FALSE FALSE LL >20 µm            4.9006 0.176 80.7
##  TRUE FALSE HL >20 µm - TRUE FALSE LL >20 µm             3.1730 0.152 61.6
##  TRUE FALSE HL >20 µm - FALSE TRUE LL >20 µm             4.8771 0.215 80.7
##  TRUE FALSE HL >20 µm - TRUE TRUE LL >20 µm              3.1495 0.196 69.7
```

```
##  FALSE TRUE HL >20 µm - TRUE TRUE HL >20 µm             -2.2524 0.152 61.6
##  FALSE TRUE HL >20 µm - FALSE FALSE LL >20 µm            2.6717 0.196 69.7
##  FALSE TRUE HL >20 µm - TRUE FALSE LL >20 µm             0.9441 0.215 80.7
##  FALSE TRUE HL >20 µm - FALSE TRUE LL >20 µm             2.6482 0.152 61.6
##  FALSE TRUE HL >20 µm - TRUE TRUE LL >20 µm              0.9206 0.176 80.7
##  TRUE TRUE HL >20 µm - FALSE FALSE LL >20 µm             4.9241 0.215 80.7
##  TRUE TRUE HL >20 µm - TRUE FALSE LL >20 µm              3.1966 0.196 69.7
##  TRUE TRUE HL >20 µm - FALSE TRUE LL >20 µm              4.9006 0.176 80.7
##  TRUE TRUE HL >20 µm - TRUE TRUE LL >20 µm               3.1730 0.152 61.6
##  FALSE FALSE LL >20 µm - TRUE FALSE LL >20 µm           -1.7276 0.152 61.6
##  FALSE FALSE LL >20 µm - FALSE TRUE LL >20 µm           -0.0235 0.124 80.7
##  FALSE FALSE LL >20 µm - TRUE TRUE LL >20 µm            -1.7511 0.196 69.7
##  TRUE FALSE LL >20 µm - FALSE TRUE LL >20 µm             1.7040 0.196 69.7
##  TRUE FALSE LL >20 µm - TRUE TRUE LL >20 µm             -0.0235 0.124 80.7
##  FALSE TRUE LL >20 µm - TRUE TRUE LL >20 µm             -1.7276 0.152 61.6
##  t.ratio p.value
##   -5.041  0.0010
##   -4.006  0.0243
##   -6.439  <.0001
##   17.421  <.0001
##   13.712  <.0001
##   10.961  <.0001
##    8.883  <.0001
##   11.899  <.0001
##   -0.860  1.0000
##    9.132  <.0001
##   -2.392  0.7457
##   22.196  <.0001
##   15.317  <.0001
##   19.480  <.0001
##   12.779  <.0001
##    8.610  <.0001
##   -5.072  0.0005
##    7.827  <.0001
##   -4.931  0.0012
##   21.255  <.0001
##   12.700  <.0001
##   20.043  <.0001
##   11.847  <.0001
##    1.371  0.9993
##   -4.006  0.0243
##   19.454  <.0001
##   20.874  <.0001
##   13.571  <.0001
##   13.635  <.0001
##   13.830  <.0001
##    3.989  0.0310
##   11.544  <.0001
##    1.809  0.9776
##   27.908  <.0001
##   18.558  <.0001
##   24.650  <.0001
##   16.029  <.0001
##   11.145  <.0001
```

```
##   -1.170  0.9999
##   10.453  <.0001
##   -1.226  0.9999
##   26.910  <.0001
##   16.091  <.0001
##   25.243  <.0001
##   15.144  <.0001
##   -5.041  0.0010
##   16.028  <.0001
##   13.509  <.0001
##   17.421  <.0001
##   13.712  <.0001
##   14.044  <.0001
##    1.718  0.9868
##   13.136  <.0001
##    0.149  1.0000
##   23.589  <.0001
##   17.111  <.0001
##   23.206  <.0001
##   16.388  <.0001
##   10.999  <.0001
##   -2.277  0.8155
##   11.727  <.0001
##   -2.527  0.6531
##   22.697  <.0001
##   14.644  <.0001
##   23.799  <.0001
##   15.399  <.0001
##   18.197  <.0001
##   18.703  <.0001
##   19.454  <.0001
##   20.874  <.0001
##   15.654  <.0001
##    6.721  <.0001
##   14.840  <.0001
##    5.226  0.0006
##   28.981  <.0001
##   20.138  <.0001
##   28.979  <.0001
##   19.568  <.0001
##   13.106  <.0001
##    1.946  0.9520
##   13.690  <.0001
##    1.947  0.9477
##   28.040  <.0001
##   17.798  <.0001
##   29.609  <.0001
##   18.635  <.0001
##   -1.588  0.9947
##   -4.006  0.0243
##   -3.764  0.0533
##   -4.511  0.0044
##  -16.000  <.0001
##   -5.855  <.0001
```

```
##   -16.745  <.0001
##     9.764  <.0001
##     0.216  1.0000
##     7.155  <.0001
##    -1.370  0.9993
##    -7.196  <.0001
##   -20.467  <.0001
##    -6.947  <.0001
##   -19.421  <.0001
##     8.611  <.0001
##    -2.251  0.8325
##     7.828  <.0001
##    -2.255  0.8279
##    -1.303  0.9997
##    -4.006  0.0243
##    -3.409  0.1303
##   -13.788  <.0001
##    -4.875  0.0017
##   -14.656  <.0001
##     9.268  <.0001
##     1.854  0.9677
##     7.216  <.0001
##    -0.168  1.0000
##    -6.257  <.0001
##   -18.000  <.0001
##    -6.025  <.0001
##   -17.195  <.0001
##     8.327  <.0001
##    -1.168  0.9999
##     7.779  <.0001
##    -1.225  0.9999
##    -1.588  0.9947
##    -1.746  0.9841
##   -12.414  <.0001
##    -3.501  0.1019
##   -14.929  <.0001
##    12.067  <.0001
##     2.739  0.4984
##    11.001  <.0001
##     1.226  0.9999
##    -4.293  0.0107
##   -16.624  <.0001
##    -4.652  0.0026
##   -17.768  <.0001
##    11.000  <.0001
##     0.398  1.0000
##    11.728  <.0001
##     0.294  1.0000
##    -0.543  1.0000
##   -10.547  <.0001
##    -2.338  0.7812
##   -12.779  <.0001
##    11.325  <.0001
##     4.745  0.0018
```

```
##   10.278  <.0001
##    3.091  0.2776
##   -3.228  0.2078
##  -14.541  <.0001
##   -3.558  0.0888
##  -15.455  <.0001
##   10.433  <.0001
##    1.947  0.9516
##   10.871  <.0001
##    1.948  0.9473
##  -12.950  <.0001
##   -2.492  0.6785
##  -11.607  <.0001
##   15.286  <.0001
##    5.014  0.0007
##   10.265  <.0001
##    2.655  0.5583
##   -3.289  0.1844
##  -14.786  <.0001
##   -3.188  0.2161
##  -14.146  <.0001
##   11.541  <.0001
##    2.397  0.7433
##   10.828  <.0001
##    2.134  0.8852
##    8.455  <.0001
##   -2.492  0.6785
##   24.455  <.0001
##   18.739  <.0001
##   18.529  <.0001
##   12.940  <.0001
##    7.889  <.0001
##   -5.159  0.0007
##    7.364  <.0001
##   -4.919  0.0010
##   23.456  <.0001
##   12.835  <.0001
##   21.987  <.0001
##   12.055  <.0001
##  -12.950  <.0001
##   13.417  <.0001
##    5.532  0.0001
##   15.286  <.0001
##    5.014  0.0007
##   -1.161  1.0000
##  -12.450  <.0001
##   -1.409  0.9989
##  -13.251  <.0001
##   12.524  <.0001
##    3.921  0.0362
##   13.076  <.0001
##    4.025  0.0229
##   21.406  <.0001
##   16.091  <.0001
```

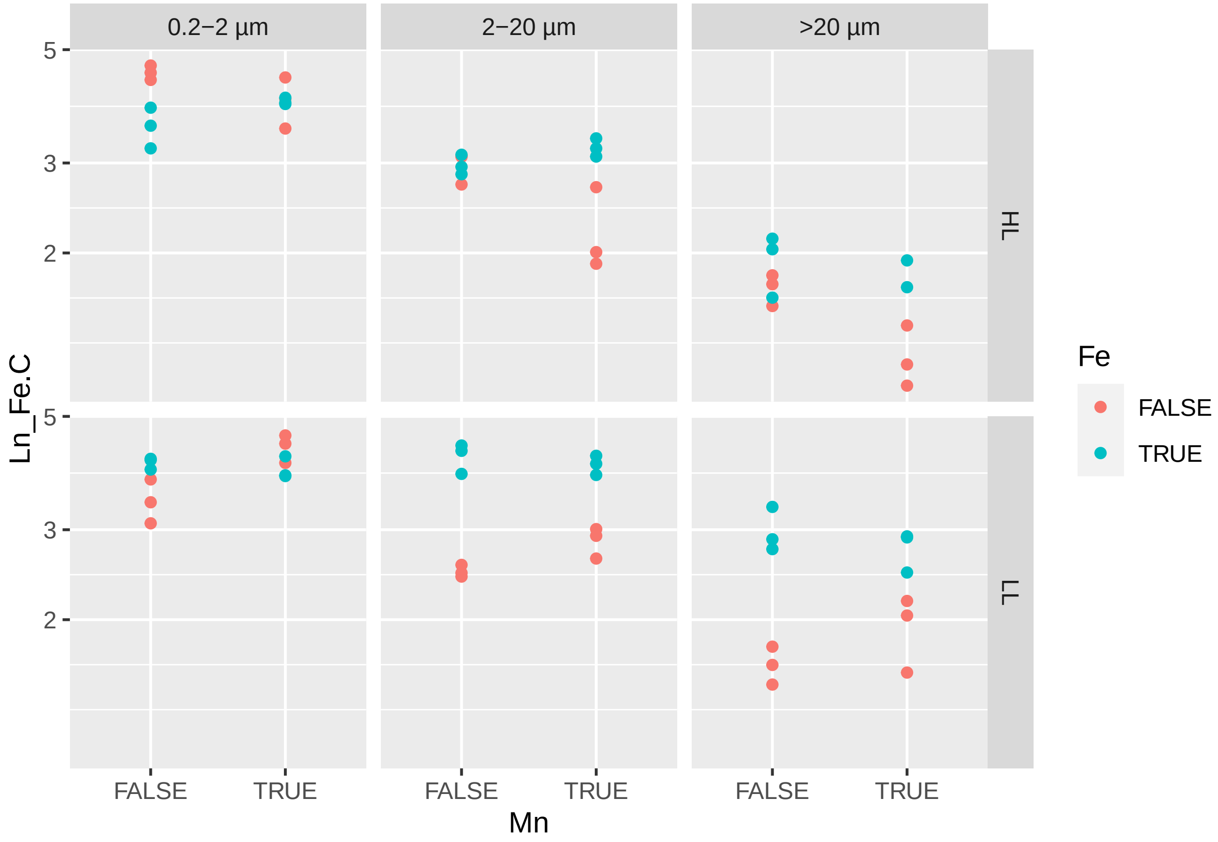
```
##   24.455  <.0001
##   18.739  <.0001
##    9.059  <.0001
##   -2.892  0.3878
##    9.424  <.0001
##   -3.279  0.1888
##   23.774  <.0001
##   13.751  <.0001
##   25.084  <.0001
##   14.369  <.0001
##   -9.497  <.0001
##   -2.492  0.6785
##   -8.932  <.0001
##  -15.167  <.0001
##  -28.921  <.0001
##  -14.508  <.0001
##  -27.392  <.0001
##   -1.153  1.0000
##  -10.222  <.0001
##   -1.211  0.9999
##   -9.817  <.0001
##    5.781  <.0001
##   -2.492  0.6785
##   -7.862  <.0001
##  -19.513  <.0001
##   -7.538  <.0001
##  -18.630  <.0001
##    6.813  <.0001
##   -3.022  0.3157
##    6.344  <.0001
##   -2.941  0.3554
##   -9.497  <.0001
##  -12.813  <.0001
##  -25.605  <.0001
##  -13.633  <.0001
##  -27.293  <.0001
##    0.816  1.0000
##   -8.121  <.0001
##    0.727  1.0000
##   -8.687  <.0001
##   -5.751  0.0001
##  -16.935  <.0001
##   -6.234  <.0001
##  -17.978  <.0001
##    8.039  <.0001
##   -0.914  1.0000
##    8.348  <.0001
##   -1.142  1.0000
##  -14.818  <.0001
##   -0.190  1.0000
##  -11.598  <.0001
##   17.422  <.0001
##    5.246  0.0003
##   13.376  <.0001
```

```
##    4.174  0.0143
##   11.359  <.0001
##   -0.190  1.0000
##   27.923  <.0001
##   20.875  <.0001
##   22.689  <.0001
##   16.050  <.0001
##  -14.818  <.0001
##   13.615  <.0001
##    4.392  0.0069
##   17.422  <.0001
##    5.246  0.0003
##   22.908  <.0001
##   16.290  <.0001
##   27.923  <.0001
##   20.875  <.0001
##  -11.365  <.0001
##   -0.190  1.0000
##   -8.924  <.0001
##    8.684  <.0001
##   -0.190  1.0000
##  -11.365  <.0001
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 24 estimates
```

6.3 Fe:C ratios

```
Uptake.na$Ln_Fe.C <- log(Uptake.na$Fe.C_umol.mol)   #data log-transformed
```

```
#Plot using ggplot2
ggplot(Uptake.na) +
  geom_point(aes(x = Mn, y = Ln_Fe.C, col = Fe)) +
  facet_grid(Light ~ Size) +
  scale_y_log10()
```



```
#model fit with all factors (Mn, Fe, Light and Size)
fit_Fe.C <- lmer(Ln_Fe.C ~ Fe + Mn + Light + Size +
               Mn:Fe + Mn:Light + Fe:Light + Mn:Size + Fe:Size + Light:Size + (1|Bottle),
             data = Uptake.na, na.action=na.fail, REML = FALSE)

summary(fit_Fe.C)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: Ln_Fe.C ~ Fe + Mn + Light + Size + Mn:Fe + Mn:Light + Fe:Light +
##     Mn:Size + Fe:Size + Light:Size + (1 | Bottle)
##    Data: Uptake.na
##
##      AIC      BIC   logLik deviance df.resid
##     38.3     76.8     -2.2      4.3       54
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.37479 -0.62823 -0.04078  0.70267  2.03135
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.04083  0.2021
##  Residual             0.03854  0.1963
## Number of obs: 71, groups:  Bottle, 24
##
```

```
## Fixed effects:
##                      Estimate Std. Error t value
## (Intercept)           4.28876    0.14125  30.363
## FeTRUE               -0.57835    0.17642  -3.278
## MnTRUE               -0.03200    0.17642  -0.181
## LightLL              -0.60980    0.17697  -3.446
## Size2-20 µm          -1.60570    0.11335 -14.166
## Size>20 µm           -2.63189    0.11335 -23.219
## FeTRUE:MnTRUE         0.04097    0.18969   0.216
## MnTRUE:LightLL        0.38165    0.18969   2.012
## FeTRUE:LightLL        0.73588    0.18969   3.879
## MnTRUE:Size2-20 µm   -0.25668    0.11335  -2.265
## MnTRUE:Size>20 µm    -0.29501    0.11526  -2.559
## FeTRUE:Size2-20 µm    1.15815    0.11335  10.218
## FeTRUE:Size>20 µm     0.94204    0.11526   8.173
## LightLL:Size2-20 µm   0.59619    0.11335   5.260
## LightLL:Size>20 µm    0.69185    0.11526   6.002
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_Fe.C, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## Ln_Fe.C ~ Fe + Mn + Light + Size + Mn:Fe + Mn:Light + Fe:Light +
##     Mn:Size + Fe:Size + Light:Size + (1 | Bottle)
##            npar    AIC    LRT   Pr(Chi)
## <none>          38.340
## Fe:Mn         1 36.387  0.047 0.8290628
## Mn:Light      1 40.068  3.728 0.0535131 .
## Fe:Light      1 47.974 11.634 0.0006477 ***
## Mn:Size       2 41.664  7.323 0.0256880 *
## Fe:Size       2 92.929 58.589 1.895e-13 ***
## Light:Size    2 65.172 30.832 2.018e-07 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
```

```
#it shows that Fe:Light, Fe:Size, Mn:Size and Light:Size
#interactions are significant
#all other interactions are removed from the model

#second model fit
fit_Fe.C2 <- lmer(Ln_Fe.C ~ Fe + Mn + Light + Size + Fe:Light
                + Fe:Size + Mn:Size + Light:Size + (1|Bottle),
                  data = Uptake.na, na.action=na.fail, REML = FALSE)
summary(fit_Fe.C2)
```

```
## Linear mixed model fit by maximum likelihood  [’lmerMod’]
## Formula: Ln_Fe.C ~ Fe + Mn + Light + Size + Fe:Light + Fe:Size + Mn:Size +
##     Light:Size + (1 | Bottle)
##    Data: Uptake.na
##
##      AIC      BIC   logLik deviance df.resid
```

```
##     38.1     72.1     -4.1      8.1       56
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.41209 -0.60923 -0.07203  0.65000  1.97993
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.05023  0.2241
##  Residual             0.03848  0.1962
## Number of obs: 71, groups:  Bottle, 24
##
## Fixed effects:
##                       Estimate Std. Error t value
## (Intercept)             4.1825     0.1320  31.685
## FeTRUE                 -0.5567     0.1592  -3.497
## MnTRUE                  0.1793     0.1216   1.475
## LightLL                -0.4178     0.1592  -2.625
## Size2-20 µm            -1.6057     0.1133 -14.177
## Size>20 µm             -2.6319     0.1133 -23.238
## FeTRUE:LightLL          0.7336     0.2055   3.570
## FeTRUE:Size2-20 µm      1.1582     0.1133  10.226
## FeTRUE:Size>20 µm       0.9455     0.1152   8.209
## MnTRUE:Size2-20 µm     -0.2567     0.1133  -2.266
## MnTRUE:Size>20 µm      -0.2916     0.1152  -2.531
## LightLL:Size2-20 µm     0.5962     0.1133   5.264
## LightLL:Size>20 µm      0.6884     0.1152   5.977
```

```
#drop function perform valid likelihood ratio tests
drop1(fit_Fe.C2, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## Ln_Fe.C ~ Fe + Mn + Light + Size + Fe:Light + Fe:Size + Mn:Size +
##     Light:Size + (1 | Bottle)
##            npar    AIC    LRT   Pr(Chi)
## <none>          38.113
## Fe:Light      1 46.319 10.206    0.0014 **
## Fe:Size       2 93.053 58.940 1.590e-13 ***
## Mn:Size       2 41.337  7.224    0.0270 *
## Light:Size    2 64.755 30.643 2.218e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#best model identified by drop
fit_best_Fe.C <- lmer(Ln_Fe.C ~ Fe + Mn + Light + Size + Fe:Light
                + Fe:Size + Mn:Size + Light:Size + (1|Bottle),
                 data = Uptake.na, na.action=na.fail, REML = FALSE)
summary(fit_best_Fe.C)
```

```
## Linear mixed model fit by maximum likelihood  ['lmerMod']
## Formula: Ln_Fe.C ~ Fe + Mn + Light + Size + Fe:Light + Fe:Size + Mn:Size +
```

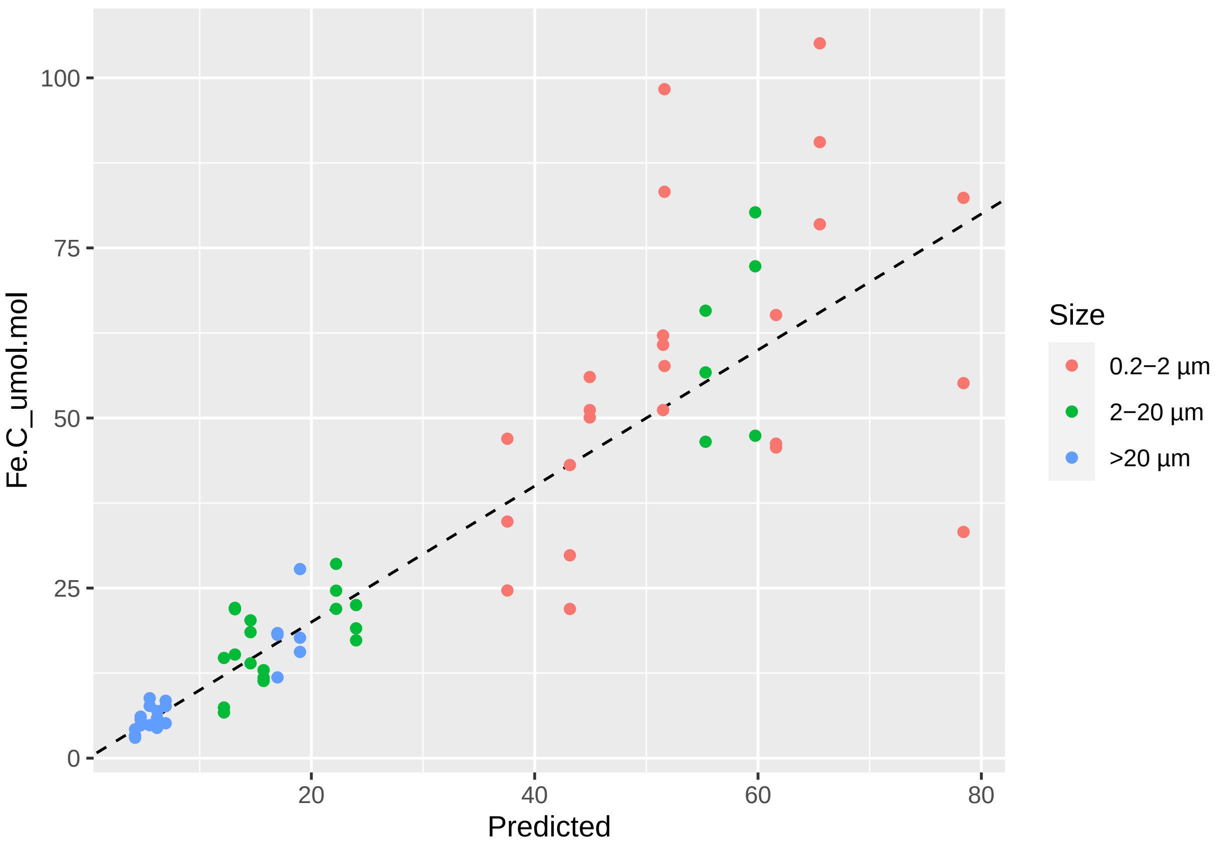
```
##     Light:Size + (1 | Bottle)
##    Data: Uptake.na
##
##      AIC      BIC   logLik deviance df.resid
##     38.1     72.1     -4.1      8.1       56
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.41209 -0.60923 -0.07203  0.65000  1.97993
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Bottle   (Intercept) 0.05023  0.2241
##  Residual             0.03848  0.1962
## Number of obs: 71, groups:  Bottle, 24
##
## Fixed effects:
##                     Estimate Std. Error t value
## (Intercept)           4.1825     0.1320  31.685
## FeTRUE               -0.5567     0.1592  -3.497
## MnTRUE                0.1793     0.1216   1.475
## LightLL              -0.4178     0.1592  -2.625
## Size2-20 µm          -1.6057     0.1133 -14.177
## Size>20 µm           -2.6319     0.1133 -23.238
## FeTRUE:LightLL        0.7336     0.2055   3.570
## FeTRUE:Size2-20 µm    1.1582     0.1133  10.226
## FeTRUE:Size>20 µm     0.9455     0.1152   8.209
## MnTRUE:Size2-20 µm   -0.2567     0.1133  -2.266
## MnTRUE:Size>20 µm    -0.2916     0.1152  -2.531
## LightLL:Size2-20 µm   0.5962     0.1133   5.264
## LightLL:Size>20 µm    0.6884     0.1152   5.977
```

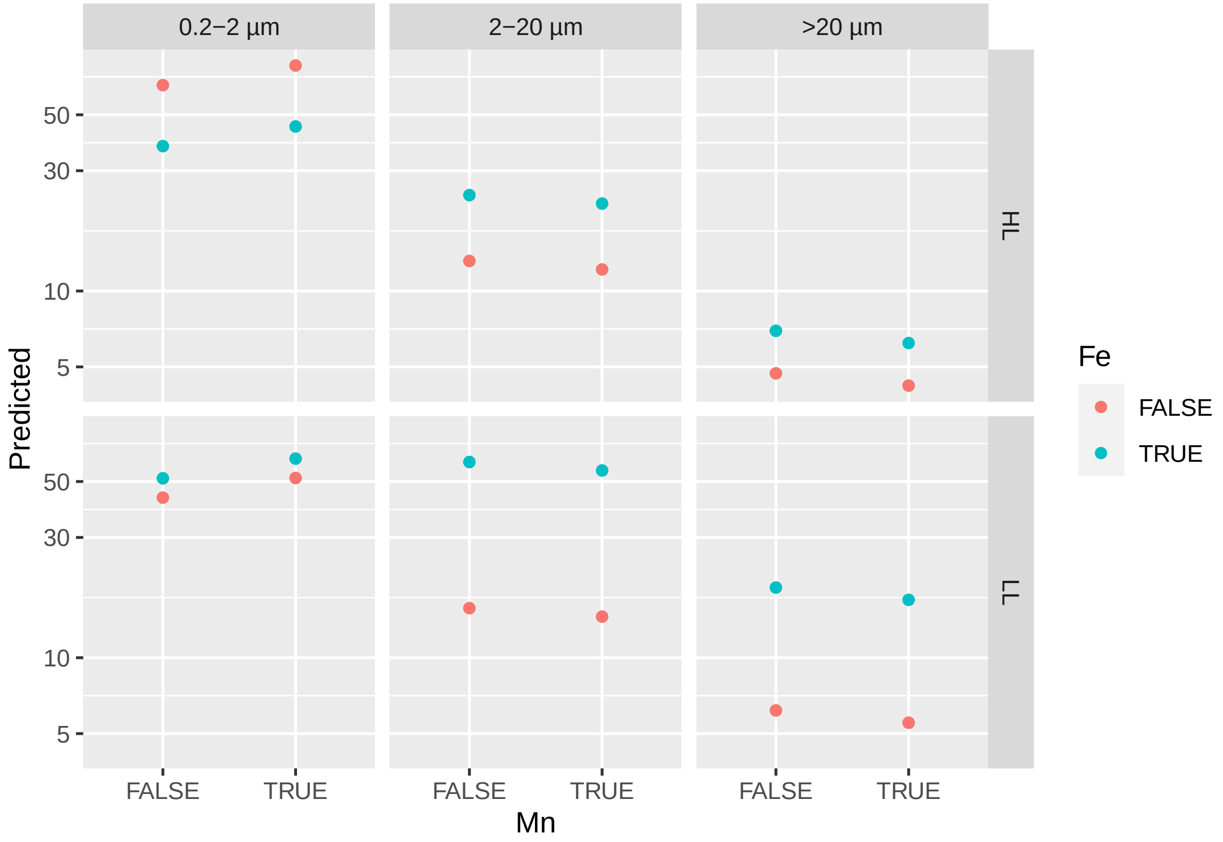
```
#Report results
report(fit_best_Fe.C)
```

```
## We fitted a linear mixed model (estimated using ML and nloptwrap optimizer) to
## predict Ln_Fe.C with Fe, Mn, Light and Size (formula: Ln_Fe.C ~ Fe + Mn + Light
## + Size + Fe:Light + Fe:Size + Mn:Size + Light:Size). The model included Bottle
## as random effect (formula: ~1 | Bottle). The model's total explanatory power is
## substantial (conditional R2 = 0.96) and the part related to the fixed effects
## alone (marginal R2) is of 0.91. The model's intercept, corresponding to Fe =
## [?], Mn = [?], Light = HL and Size = 0.2-2 µm, is at 4.18 (95% CI [3.92, 4.45],
## t(56) = 31.69, p < .001). Within this model:
##
##   - The effect of FeTRUE is statistically significant and negative (beta = -0.56,
## 95% CI [-0.88, -0.24], t(56) = -3.50, p < .001; Std. beta = -0.57, 95% CI
## [-0.89, -0.24])
##   - The effect of MnTRUE is statistically non-significant and positive (beta =
## 0.18, 95% CI [-0.06, 0.42], t(56) = 1.47, p = 0.146; Std. beta = 0.18, 95% CI
## [-0.07, 0.43])
##   - The effect of Light [LL] is statistically significant and negative (beta =
## -0.42, 95% CI [-0.74, -0.10], t(56) = -2.62, p = 0.011; Std. beta = -0.42, 95%
## CI [-0.75, -0.10])
##   - The effect of Size [2-20 µm] is statistically significant and negative (beta
```

```
## = -1.61, 95% CI [-1.83, -1.38], t(56) = -14.18, p < .001; Std. beta = -1.63,
## 95% CI [-1.86, -1.40])
##   - The effect of Size [>20 µm] is statistically significant and negative (beta =
## -2.63, 95% CI [-2.86, -2.41], t(56) = -23.24, p < .001; Std. beta = -2.68, 95%
## CI [-2.91, -2.44])
##   - The effect of FeTRUE × Light [LL] is statistically significant and positive
## (beta = 0.73, 95% CI [0.32, 1.15], t(56) = 3.57, p < .001; Std. beta = 0.75,
## 95% CI [0.33, 1.16])
##   - The effect of FeTRUE × Size [2-20 µm] is statistically significant and
## positive (beta = 1.16, 95% CI [0.93, 1.39], t(56) = 10.23, p < .001; Std. beta
## = 1.18, 95% CI [0.95, 1.41])
##   - The effect of FeTRUE × Size [>20 µm] is statistically significant and
## positive (beta = 0.95, 95% CI [0.71, 1.18], t(56) = 8.21, p < .001; Std. beta =
## 0.96, 95% CI [0.73, 1.20])
##   - The effect of MnTRUE × Size [2-20 µm] is statistically significant and
## negative (beta = -0.26, 95% CI [-0.48, -0.03], t(56) = -2.27, p = 0.027; Std.
## beta = -0.26, 95% CI [-0.49, -0.03])
##   - The effect of MnTRUE × Size [>20 µm] is statistically significant and
## negative (beta = -0.29, 95% CI [-0.52, -0.06], t(56) = -2.53, p = 0.014; Std.
## beta = -0.30, 95% CI [-0.53, -0.06])
##   - The effect of Light [LL] × Size [2-20 µm] is statistically significant and
## positive (beta = 0.60, 95% CI [0.37, 0.82], t(56) = 5.26, p < .001; Std. beta =
## 0.61, 95% CI [0.38, 0.84])
##   - The effect of Light [LL] × Size [>20 µm] is statistically significant and
## positive (beta = 0.69, 95% CI [0.46, 0.92], t(56) = 5.98, p < .001; Std. beta =
## 0.70, 95% CI [0.47, 0.93])
##
## Standardized parameters were obtained by fitting the model on a standardized
## version of the dataset. 95% Confidence Intervals (CIs) and p-values were
## computed using a Wald t-distribution approximation.
```

```r
#Represent data predicted by the model vs real data
Uptake.na$Predicted <- exp(predict(fit_best_Fe.C, re.form = NA))
```


Fe.C_umol.mol
0
25
50
75
100
20
40
60
80
Predicted
Size
0.2−2 µm
2−20 µm
>20 µm



```
#Pairwise comparison
emmeans (fit_best_Fe.C, pairwise ~ Fe + Mn + Light + Size, adjust = "tukey")
```

```
## $emmeans
##  Fe    Mn    Light Size     emmean    SE   df lower.CL upper.CL
##  FALSE FALSE HL    0.2-2 µm   4.18 0.148 50.2     3.89     4.48
##   TRUE FALSE HL    0.2-2 µm   3.63 0.148 50.1     3.33     3.92
##  FALSE  TRUE HL    0.2-2 µm   4.36 0.148 50.2     4.07     4.66
##   TRUE  TRUE HL    0.2-2 µm   3.81 0.148 50.0     3.51     4.10
##  FALSE FALSE LL    0.2-2 µm   3.76 0.148 50.2     3.47     4.06
##   TRUE FALSE LL    0.2-2 µm   3.94 0.148 50.2     3.65     4.24
##  FALSE  TRUE LL    0.2-2 µm   3.94 0.148 50.2     3.65     4.24
##   TRUE  TRUE LL    0.2-2 µm   4.12 0.148 50.2     3.82     4.42
##  FALSE FALSE HL    2-20 µm    2.58 0.148 50.2     2.28     2.87
##   TRUE FALSE HL    2-20 µm    3.18 0.148 50.1     2.88     3.47
##  FALSE  TRUE HL    2-20 µm    2.50 0.148 50.2     2.20     2.80
##   TRUE  TRUE HL    2-20 µm    3.10 0.148 50.0     2.80     3.40
##  FALSE FALSE LL    2-20 µm    2.76 0.148 50.2     2.46     3.05
##   TRUE FALSE LL    2-20 µm    4.09 0.148 50.2     3.79     4.39
##  FALSE  TRUE LL    2-20 µm    2.68 0.148 50.2     2.38     2.97
##   TRUE  TRUE LL    2-20 µm    4.01 0.148 50.2     3.72     4.31
##  FALSE FALSE HL    >20 µm     1.55 0.148 50.2     1.25     1.85
##   TRUE FALSE HL    >20 µm     1.94 0.150 52.5     1.64     2.24
##  FALSE  TRUE HL    >20 µm     1.44 0.149 51.3     1.14     1.74
##   TRUE  TRUE HL    >20 µm     1.83 0.156 57.8     1.52     2.14
##  FALSE FALSE LL    >20 µm     1.82 0.149 51.3     1.52     2.12
```

```
##   TRUE FALSE LL    >20 µm      2.94 0.148 50.2     2.65     3.24
##  FALSE  TRUE LL    >20 µm      1.71 0.148 50.2     1.41     2.01
##   TRUE  TRUE LL    >20 µm      2.83 0.149 51.3     2.53     3.13
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $contrasts
##  contrast                                              estimate    SE   df
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE FALSE HL 0.2-2 µm)   0.55671 0.178 42.8
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE TRUE HL 0.2-2 µm)  -0.17931 0.136 54.8
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE TRUE HL 0.2-2 µm)    0.37740 0.224 46.9
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE FALSE LL 0.2-2 µm)  0.41782 0.178 42.8
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE FALSE LL 0.2-2 µm)   0.24096 0.192 54.9
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE TRUE LL 0.2-2 µm)   0.23851 0.224 46.9
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)    0.06165 0.235 54.8
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)   1.60570 0.124 56.6
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)    1.00426 0.199 60.4
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)    1.68307 0.162 79.2
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)     1.08163 0.224 46.9
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)   1.42734 0.199 60.4
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)    0.09232 0.192 54.9
##  (FALSE FALSE HL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)    1.50471 0.224 46.9
##  (FALSE FALSE HL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)     0.16969 0.218 42.7
##  (FALSE FALSE HL 0.2-2 µm) - FALSE FALSE HL >20 µm      2.63189 0.124 56.6
##  (FALSE FALSE HL 0.2-2 µm) - TRUE FALSE HL >20 µm       2.24310 0.201 61.9
##  (FALSE FALSE HL 0.2-2 µm) - FALSE TRUE HL >20 µm       2.74413 0.163 80.0
##  (FALSE FALSE HL 0.2-2 µm) - TRUE TRUE HL >20 µm        2.35534 0.230 50.8
##  (FALSE FALSE HL 0.2-2 µm) - FALSE FALSE LL >20 µm      2.36132 0.199 60.8
##  (FALSE FALSE HL 0.2-2 µm) - TRUE FALSE LL >20 µm       1.23895 0.192 54.9
##  (FALSE FALSE HL 0.2-2 µm) - FALSE TRUE LL >20 µm       2.47356 0.224 46.9
##  (FALSE FALSE HL 0.2-2 µm) - TRUE TRUE LL >20 µm        1.35119 0.219 43.5
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE TRUE HL 0.2-2 µm)   -0.73602 0.224 46.9
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE TRUE HL 0.2-2 µm)    -0.17931 0.136 54.8
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE FALSE LL 0.2-2 µm)  -0.13889 0.192 54.8
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE FALSE LL 0.2-2 µm)   -0.31575 0.178 42.8
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE TRUE LL 0.2-2 µm)   -0.31820 0.235 54.8
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)    -0.49506 0.224 46.9
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)    1.04899 0.199 60.4
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)     0.44755 0.124 56.6
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)     1.12636 0.224 46.9
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)      0.52492 0.162 79.2
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)    0.87062 0.192 54.8
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)    -0.46440 0.199 60.4
##  (TRUE FALSE HL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)     0.94800 0.218 42.7
##  (TRUE FALSE HL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)     -0.38702 0.224 46.9
##  (TRUE FALSE HL 0.2-2 µm) - FALSE FALSE HL >20 µm       2.07518 0.199 60.4
##  (TRUE FALSE HL 0.2-2 µm) - TRUE FALSE HL >20 µm        1.68639 0.126 57.0
##  (TRUE FALSE HL 0.2-2 µm) - FALSE TRUE HL >20 µm        2.18742 0.224 47.2
##  (TRUE FALSE HL 0.2-2 µm) - TRUE TRUE HL >20 µm         1.79863 0.168 82.0
##  (TRUE FALSE HL 0.2-2 µm) - FALSE FALSE LL >20 µm       1.80460 0.193 55.8
##  (TRUE FALSE HL 0.2-2 µm) - TRUE FALSE LL >20 µm        0.68224 0.199 60.4
##  (TRUE FALSE HL 0.2-2 µm) - FALSE TRUE LL >20 µm        1.91685 0.218 42.7
##  (TRUE FALSE HL 0.2-2 µm) - TRUE TRUE LL >20 µm         0.79448 0.224 47.2
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##  (FALSE TRUE HL 0.2-2 µm) - (TRUE TRUE HL 0.2-2 µm)     0.55671 0.178 42.8
##  (FALSE TRUE HL 0.2-2 µm) - (FALSE FALSE LL 0.2-2 µm)   0.59713 0.224 46.9
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE FALSE LL 0.2-2 µm)    0.42027 0.235 54.8
##  (FALSE TRUE HL 0.2-2 µm) - (FALSE TRUE LL 0.2-2 µm)    0.41782 0.178 42.8
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)     0.24096 0.192 54.9
##  (FALSE TRUE HL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)    1.78501 0.162 79.2
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)     1.18357 0.224 46.9
##  (FALSE TRUE HL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)     1.86238 0.124 56.6
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)      1.26094 0.199 60.4
##  (FALSE TRUE HL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)    1.60665 0.224 46.9
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)     0.27163 0.218 42.7
##  (FALSE TRUE HL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)     1.68402 0.199 60.4
##  (FALSE TRUE HL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)      0.34900 0.192 54.9
##  (FALSE TRUE HL 0.2-2 µm) - FALSE FALSE HL >20 µm       2.81120 0.162 79.2
##  (FALSE TRUE HL 0.2-2 µm) - TRUE FALSE HL >20 µm        2.42241 0.226 48.2
##  (FALSE TRUE HL 0.2-2 µm) - FALSE TRUE HL >20 µm        2.92344 0.126 57.0
##  (FALSE TRUE HL 0.2-2 µm) - TRUE TRUE HL >20 µm         2.53465 0.206 65.1
##  (FALSE TRUE HL 0.2-2 µm) - FALSE FALSE LL >20 µm       2.54063 0.224 47.2
##  (FALSE TRUE HL 0.2-2 µm) - TRUE FALSE LL >20 µm        1.41826 0.218 42.7
##  (FALSE TRUE HL 0.2-2 µm) - FALSE TRUE LL >20 µm        2.65287 0.199 60.4
##  (FALSE TRUE HL 0.2-2 µm) - TRUE TRUE LL >20 µm         1.53050 0.193 55.9
##  (TRUE TRUE HL 0.2-2 µm) - (FALSE FALSE LL 0.2-2 µm)    0.04042 0.235 54.8
##  (TRUE TRUE HL 0.2-2 µm) - (TRUE FALSE LL 0.2-2 µm)    -0.13644 0.224 46.9
##  (TRUE TRUE HL 0.2-2 µm) - (FALSE TRUE LL 0.2-2 µm)    -0.13889 0.192 54.8
##  (TRUE TRUE HL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)     -0.31575 0.178 42.8
##  (TRUE TRUE HL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)     1.22830 0.224 46.9
##  (TRUE TRUE HL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)      0.62686 0.162 79.2
##  (TRUE TRUE HL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)      1.30567 0.199 60.4
##  (TRUE TRUE HL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)       0.70423 0.124 56.6
##  (TRUE TRUE HL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)     1.04993 0.218 42.6
##  (TRUE TRUE HL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)     -0.28509 0.224 46.9
##  (TRUE TRUE HL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)      1.12731 0.192 54.8
##  (TRUE TRUE HL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)      -0.20771 0.199 60.4
##  (TRUE TRUE HL 0.2-2 µm) - FALSE FALSE HL >20 µm        2.25449 0.224 46.9
##  (TRUE TRUE HL 0.2-2 µm) - TRUE FALSE HL >20 µm         1.86570 0.163 80.0
##  (TRUE TRUE HL 0.2-2 µm) - FALSE TRUE HL >20 µm         2.36673 0.199 60.7
##  (TRUE TRUE HL 0.2-2 µm) - TRUE TRUE HL >20 µm          1.97794 0.133 57.8
##  (TRUE TRUE HL 0.2-2 µm) - FALSE FALSE LL >20 µm        1.98391 0.219 43.4
##  (TRUE TRUE HL 0.2-2 µm) - TRUE FALSE LL >20 µm         0.86155 0.224 46.9
##  (TRUE TRUE HL 0.2-2 µm) - FALSE TRUE LL >20 µm         2.09616 0.192 54.8
##  (TRUE TRUE HL 0.2-2 µm) - TRUE TRUE LL >20 µm          0.97379 0.199 60.7
##  (FALSE FALSE LL 0.2-2 µm) - (TRUE FALSE LL 0.2-2 µm)  -0.17687 0.178 42.8
##  (FALSE FALSE LL 0.2-2 µm) - (FALSE TRUE LL 0.2-2 µm)  -0.17931 0.136 54.8
##  (FALSE FALSE LL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)   -0.35618 0.224 46.9
##  (FALSE FALSE LL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)   1.18787 0.199 60.4
##  (FALSE FALSE LL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)    0.58643 0.192 54.8
##  (FALSE FALSE LL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)    1.26525 0.224 46.9
##  (FALSE FALSE LL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)     0.66381 0.218 42.6
##  (FALSE FALSE LL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)   1.00951 0.124 56.6
##  (FALSE FALSE LL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)   -0.32551 0.199 60.4
##  (FALSE FALSE LL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)    1.08688 0.162 79.2
##  (FALSE FALSE LL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)    -0.24814 0.224 46.9
##  (FALSE FALSE LL 0.2-2 µm) - FALSE FALSE HL >20 µm      2.21407 0.199 60.4
##  (FALSE FALSE LL 0.2-2 µm) - TRUE FALSE HL >20 µm       1.82528 0.193 55.8
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##  (FALSE FALSE LL 0.2-2 µm) - FALSE TRUE HL >20 µm       2.32631 0.224 47.2
##  (FALSE FALSE LL 0.2-2 µm) - TRUE TRUE HL >20 µm        1.93752 0.223 45.7
##  (FALSE FALSE LL 0.2-2 µm) - FALSE FALSE LL >20 µm      1.94349 0.126 57.0
##  (FALSE FALSE LL 0.2-2 µm) - TRUE FALSE LL >20 µm       0.82113 0.199 60.4
##  (FALSE FALSE LL 0.2-2 µm) - FALSE TRUE LL >20 µm       2.05573 0.162 79.2
##  (FALSE FALSE LL 0.2-2 µm) - TRUE TRUE LL >20 µm        0.93337 0.224 47.2
##  (TRUE FALSE LL 0.2-2 µm) - (FALSE TRUE LL 0.2-2 µm)   -0.00244 0.224 46.9
##  (TRUE FALSE LL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)    -0.17931 0.136 54.8
##  (TRUE FALSE LL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)    1.36474 0.192 54.9
##  (TRUE FALSE LL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)     0.76330 0.199 60.4
##  (TRUE FALSE LL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)     1.44211 0.218 42.7
##  (TRUE FALSE LL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)      0.84067 0.224 46.9
##  (TRUE FALSE LL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)    1.18638 0.199 60.4
##  (TRUE FALSE LL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)    -0.14864 0.124 56.6
##  (TRUE FALSE LL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)     1.26375 0.224 46.9
##  (TRUE FALSE LL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)     -0.07127 0.162 79.2
##  (TRUE FALSE LL 0.2-2 µm) - FALSE FALSE HL >20 µm       2.39093 0.192 54.9
##  (TRUE FALSE LL 0.2-2 µm) - TRUE FALSE HL >20 µm        2.00215 0.201 61.9
##  (TRUE FALSE LL 0.2-2 µm) - FALSE TRUE HL >20 µm        2.50317 0.219 43.5
##  (TRUE FALSE LL 0.2-2 µm) - TRUE TRUE HL >20 µm         2.11439 0.230 50.8
##  (TRUE FALSE LL 0.2-2 µm) - FALSE FALSE LL >20 µm       2.12036 0.199 60.8
##  (TRUE FALSE LL 0.2-2 µm) - TRUE FALSE LL >20 µm        0.99799 0.124 56.6
##  (TRUE FALSE LL 0.2-2 µm) - FALSE TRUE LL >20 µm        2.23260 0.224 46.9
##  (TRUE FALSE LL 0.2-2 µm) - TRUE TRUE LL >20 µm         1.11023 0.163 80.0
##  (FALSE TRUE LL 0.2-2 µm) - (TRUE TRUE LL 0.2-2 µm)    -0.17687 0.178 42.8
##  (FALSE TRUE LL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)    1.36718 0.224 46.9
##  (FALSE TRUE LL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)     0.76574 0.218 42.7
##  (FALSE TRUE LL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)     1.44456 0.199 60.4
##  (FALSE TRUE LL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)      0.84312 0.192 54.8
##  (FALSE TRUE LL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)    1.18882 0.162 79.2
##  (FALSE TRUE LL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)    -0.14620 0.224 46.9
##  (FALSE TRUE LL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)     1.26619 0.124 56.6
##  (FALSE TRUE LL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)     -0.06883 0.199 60.4
##  (FALSE TRUE LL 0.2-2 µm) - FALSE FALSE HL >20 µm       2.39338 0.224 46.9
##  (FALSE TRUE LL 0.2-2 µm) - TRUE FALSE HL >20 µm        2.00459 0.219 43.5
##  (FALSE TRUE LL 0.2-2 µm) - FALSE TRUE HL >20 µm        2.50562 0.199 60.8
##  (FALSE TRUE LL 0.2-2 µm) - TRUE TRUE HL >20 µm         2.11683 0.198 58.8
##  (FALSE TRUE LL 0.2-2 µm) - FALSE FALSE LL >20 µm       2.12280 0.163 80.0
##  (FALSE TRUE LL 0.2-2 µm) - TRUE FALSE LL >20 µm        1.00044 0.224 46.9
##  (FALSE TRUE LL 0.2-2 µm) - FALSE TRUE LL >20 µm        2.23504 0.124 56.6
##  (FALSE TRUE LL 0.2-2 µm) - TRUE TRUE LL >20 µm         1.11268 0.199 60.8
##  (TRUE TRUE LL 0.2-2 µm) - (FALSE FALSE HL 2-20 µm)     1.54405 0.218 42.7
##  (TRUE TRUE LL 0.2-2 µm) - (TRUE FALSE HL 2-20 µm)      0.94261 0.224 46.9
##  (TRUE TRUE LL 0.2-2 µm) - (FALSE TRUE HL 2-20 µm)      1.62142 0.192 54.9
##  (TRUE TRUE LL 0.2-2 µm) - (TRUE TRUE HL 2-20 µm)       1.01998 0.199 60.4
##  (TRUE TRUE LL 0.2-2 µm) - (FALSE FALSE LL 2-20 µm)     1.36569 0.224 46.9
##  (TRUE TRUE LL 0.2-2 µm) - (TRUE FALSE LL 2-20 µm)      0.03067 0.162 79.2
##  (TRUE TRUE LL 0.2-2 µm) - (FALSE TRUE LL 2-20 µm)      1.44306 0.199 60.4
##  (TRUE TRUE LL 0.2-2 µm) - (TRUE TRUE LL 2-20 µm)       0.10804 0.124 56.6
##  (TRUE TRUE LL 0.2-2 µm) - FALSE FALSE HL >20 µm        2.57024 0.218 42.7
##  (TRUE TRUE LL 0.2-2 µm) - TRUE FALSE HL >20 µm         2.18146 0.226 48.2
##  (TRUE TRUE LL 0.2-2 µm) - FALSE TRUE HL >20 µm         2.68248 0.193 55.9
##  (TRUE TRUE LL 0.2-2 µm) - TRUE TRUE HL >20 µm          2.29370 0.206 65.1
##  (TRUE TRUE LL 0.2-2 µm) - FALSE FALSE LL >20 µm        2.29967 0.224 47.2
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##  (TRUE TRUE LL 0.2-2 µm) - TRUE FALSE LL >20 µm         1.17730 0.162 79.2
##  (TRUE TRUE LL 0.2-2 µm) - FALSE TRUE LL >20 µm         2.41191 0.199 60.4
##  (TRUE TRUE LL 0.2-2 µm) - TRUE TRUE LL >20 µm          1.28954 0.126 57.0
##  (FALSE FALSE HL 2-20 µm) - (TRUE FALSE HL 2-20 µm)    -0.60144 0.178 42.8
##  (FALSE FALSE HL 2-20 µm) - (FALSE TRUE HL 2-20 µm)     0.07737 0.136 54.8
##  (FALSE FALSE HL 2-20 µm) - (TRUE TRUE HL 2-20 µm)     -0.52407 0.224 46.9
##  (FALSE FALSE HL 2-20 µm) - (FALSE FALSE LL 2-20 µm)   -0.17836 0.178 42.8
##  (FALSE FALSE HL 2-20 µm) - (TRUE FALSE LL 2-20 µm)    -1.51338 0.192 54.9
##  (FALSE FALSE HL 2-20 µm) - (FALSE TRUE LL 2-20 µm)    -0.10099 0.224 46.9
##  (FALSE FALSE HL 2-20 µm) - (TRUE TRUE LL 2-20 µm)     -1.43601 0.235 54.8
##  (FALSE FALSE HL 2-20 µm) - FALSE FALSE HL >20 µm       1.02619 0.124 56.6
##  (FALSE FALSE HL 2-20 µm) - TRUE FALSE HL >20 µm        0.63740 0.201 61.9
##  (FALSE FALSE HL 2-20 µm) - FALSE TRUE HL >20 µm        1.13843 0.163 80.0
##  (FALSE FALSE HL 2-20 µm) - TRUE TRUE HL >20 µm         0.74965 0.230 50.8
##  (FALSE FALSE HL 2-20 µm) - FALSE FALSE LL >20 µm       0.75562 0.199 60.8
##  (FALSE FALSE HL 2-20 µm) - TRUE FALSE LL >20 µm       -0.36675 0.192 54.9
##  (FALSE FALSE HL 2-20 µm) - FALSE TRUE LL >20 µm        0.86786 0.224 46.9
##  (FALSE FALSE HL 2-20 µm) - TRUE TRUE LL >20 µm        -0.25451 0.219 43.5
##  (TRUE FALSE HL 2-20 µm) - (FALSE TRUE HL 2-20 µm)      0.67881 0.224 46.9
##  (TRUE FALSE HL 2-20 µm) - (TRUE TRUE HL 2-20 µm)       0.07737 0.136 54.8
##  (TRUE FALSE HL 2-20 µm) - (FALSE FALSE LL 2-20 µm)     0.42308 0.192 54.8
##  (TRUE FALSE HL 2-20 µm) - (TRUE FALSE LL 2-20 µm)     -0.91194 0.178 42.8
##  (TRUE FALSE HL 2-20 µm) - (FALSE TRUE LL 2-20 µm)      0.50045 0.235 54.8
##  (TRUE FALSE HL 2-20 µm) - (TRUE TRUE LL 2-20 µm)      -0.83457 0.224 46.9
##  (TRUE FALSE HL 2-20 µm) - FALSE FALSE HL >20 µm        1.62763 0.199 60.4
##  (TRUE FALSE HL 2-20 µm) - TRUE FALSE HL >20 µm         1.23885 0.126 57.0
##  (TRUE FALSE HL 2-20 µm) - FALSE TRUE HL >20 µm         1.73988 0.224 47.2
##  (TRUE FALSE HL 2-20 µm) - TRUE TRUE HL >20 µm          1.35109 0.168 82.0
##  (TRUE FALSE HL 2-20 µm) - FALSE FALSE LL >20 µm        1.35706 0.193 55.8
##  (TRUE FALSE HL 2-20 µm) - TRUE FALSE LL >20 µm         0.23469 0.199 60.4
##  (TRUE FALSE HL 2-20 µm) - FALSE TRUE LL >20 µm         1.46930 0.218 42.7
##  (TRUE FALSE HL 2-20 µm) - TRUE TRUE LL >20 µm          0.34693 0.224 47.2
##  (FALSE TRUE HL 2-20 µm) - (TRUE TRUE HL 2-20 µm)      -0.60144 0.178 42.8
##  (FALSE TRUE HL 2-20 µm) - (FALSE FALSE LL 2-20 µm)    -0.25574 0.224 46.9
##  (FALSE TRUE HL 2-20 µm) - (TRUE FALSE LL 2-20 µm)     -1.59076 0.235 54.8
##  (FALSE TRUE HL 2-20 µm) - (FALSE TRUE LL 2-20 µm)     -0.17836 0.178 42.8
##  (FALSE TRUE HL 2-20 µm) - (TRUE TRUE LL 2-20 µm)      -1.51338 0.192 54.9
##  (FALSE TRUE HL 2-20 µm) - FALSE FALSE HL >20 µm        0.94882 0.162 79.2
##  (FALSE TRUE HL 2-20 µm) - TRUE FALSE HL >20 µm         0.56003 0.226 48.2
##  (FALSE TRUE HL 2-20 µm) - FALSE TRUE HL >20 µm         1.06106 0.126 57.0
##  (FALSE TRUE HL 2-20 µm) - TRUE TRUE HL >20 µm          0.67227 0.206 65.1
##  (FALSE TRUE HL 2-20 µm) - FALSE FALSE LL >20 µm        0.67824 0.224 47.2
##  (FALSE TRUE HL 2-20 µm) - TRUE FALSE LL >20 µm        -0.44412 0.218 42.7
##  (FALSE TRUE HL 2-20 µm) - FALSE TRUE LL >20 µm         0.79049 0.199 60.4
##  (FALSE TRUE HL 2-20 µm) - TRUE TRUE LL >20 µm         -0.33188 0.193 55.9
##  (TRUE TRUE HL 2-20 µm) - (FALSE FALSE LL 2-20 µm)      0.34571 0.235 54.8
##  (TRUE TRUE HL 2-20 µm) - (TRUE FALSE LL 2-20 µm)      -0.98931 0.224 46.9
##  (TRUE TRUE HL 2-20 µm) - (FALSE TRUE LL 2-20 µm)       0.42308 0.192 54.8
##  (TRUE TRUE HL 2-20 µm) - (TRUE TRUE LL 2-20 µm)       -0.91194 0.178 42.8
##  (TRUE TRUE HL 2-20 µm) - FALSE FALSE HL >20 µm         1.55026 0.224 46.9
##  (TRUE TRUE HL 2-20 µm) - TRUE FALSE HL >20 µm          1.16147 0.163 80.0
##  (TRUE TRUE HL 2-20 µm) - FALSE TRUE HL >20 µm          1.66250 0.199 60.7
##  (TRUE TRUE HL 2-20 µm) - TRUE TRUE HL >20 µm           1.27371 0.133 57.8
##  (TRUE TRUE HL 2-20 µm) - FALSE FALSE LL >20 µm         1.27969 0.219 43.4
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##  (TRUE TRUE HL 2-20 μm) - TRUE FALSE LL >20 μm          0.15732 0.224 46.9
##  (TRUE TRUE HL 2-20 μm) - FALSE TRUE LL >20 μm          1.39193 0.192 54.8
##  (TRUE TRUE HL 2-20 μm) - TRUE TRUE LL >20 μm           0.26956 0.199 60.7
##  (FALSE FALSE LL 2-20 μm) - (TRUE FALSE LL 2-20 μm)    -1.33502 0.178 42.8
##  (FALSE FALSE LL 2-20 μm) - (FALSE TRUE LL 2-20 μm)     0.07737 0.136 54.8
##  (FALSE FALSE LL 2-20 μm) - (TRUE TRUE LL 2-20 μm)     -1.25765 0.224 46.9
##  (FALSE FALSE LL 2-20 μm) - FALSE FALSE HL >20 μm       1.20456 0.199 60.4
##  (FALSE FALSE LL 2-20 μm) - TRUE FALSE HL >20 μm        0.81577 0.193 55.8
##  (FALSE FALSE LL 2-20 μm) - FALSE TRUE HL >20 μm        1.31680 0.224 47.2
##  (FALSE FALSE LL 2-20 μm) - TRUE TRUE HL >20 μm         0.92801 0.223 45.7
##  (FALSE FALSE LL 2-20 μm) - FALSE FALSE LL >20 μm       0.93398 0.126 57.0
##  (FALSE FALSE LL 2-20 μm) - TRUE FALSE LL >20 μm       -0.18839 0.199 60.4
##  (FALSE FALSE LL 2-20 μm) - FALSE TRUE LL >20 μm        1.04622 0.162 79.2
##  (FALSE FALSE LL 2-20 μm) - TRUE TRUE LL >20 μm        -0.07614 0.224 47.2
##  (TRUE FALSE LL 2-20 μm) - (FALSE TRUE LL 2-20 μm)      1.41239 0.224 46.9
##  (TRUE FALSE LL 2-20 μm) - (TRUE TRUE LL 2-20 μm)       0.07737 0.136 54.8
##  (TRUE FALSE LL 2-20 μm) - FALSE FALSE HL >20 μm        2.53958 0.192 54.9
##  (TRUE FALSE LL 2-20 μm) - TRUE FALSE HL >20 μm         2.15079 0.201 61.9
##  (TRUE FALSE LL 2-20 μm) - FALSE TRUE HL >20 μm         2.65182 0.219 43.5
##  (TRUE FALSE LL 2-20 μm) - TRUE TRUE HL >20 μm          2.26303 0.230 50.8
##  (TRUE FALSE LL 2-20 μm) - FALSE FALSE LL >20 μm        2.26900 0.199 60.8
##  (TRUE FALSE LL 2-20 μm) - TRUE FALSE LL >20 μm         1.14663 0.124 56.6
##  (TRUE FALSE LL 2-20 μm) - FALSE TRUE LL >20 μm         2.38124 0.224 46.9
##  (TRUE FALSE LL 2-20 μm) - TRUE TRUE LL >20 μm          1.25888 0.163 80.0
##  (FALSE TRUE LL 2-20 μm) - (TRUE TRUE LL 2-20 μm)      -1.33502 0.178 42.8
##  (FALSE TRUE LL 2-20 μm) - FALSE FALSE HL >20 μm        1.12718 0.224 46.9
##  (FALSE TRUE LL 2-20 μm) - TRUE FALSE HL >20 μm         0.73840 0.219 43.5
##  (FALSE TRUE LL 2-20 μm) - FALSE TRUE HL >20 μm         1.23942 0.199 60.8
##  (FALSE TRUE LL 2-20 μm) - TRUE TRUE HL >20 μm          0.85064 0.198 58.8
##  (FALSE TRUE LL 2-20 μm) - FALSE FALSE LL >20 μm        0.85661 0.163 80.0
##  (FALSE TRUE LL 2-20 μm) - TRUE FALSE LL >20 μm        -0.26576 0.224 46.9
##  (FALSE TRUE LL 2-20 μm) - FALSE TRUE LL >20 μm         0.96885 0.124 56.6
##  (FALSE TRUE LL 2-20 μm) - TRUE TRUE LL >20 μm         -0.15352 0.199 60.8
##  (TRUE TRUE LL 2-20 μm) - FALSE FALSE HL >20 μm         2.46220 0.218 42.7
##  (TRUE TRUE LL 2-20 μm) - TRUE FALSE HL >20 μm          2.07341 0.226 48.2
##  (TRUE TRUE LL 2-20 μm) - FALSE TRUE HL >20 μm          2.57444 0.193 55.9
##  (TRUE TRUE LL 2-20 μm) - TRUE TRUE HL >20 μm           2.18566 0.206 65.1
##  (TRUE TRUE LL 2-20 μm) - FALSE FALSE LL >20 μm         2.19163 0.224 47.2
##  (TRUE TRUE LL 2-20 μm) - TRUE FALSE LL >20 μm          1.06926 0.162 79.2
##  (TRUE TRUE LL 2-20 μm) - FALSE TRUE LL >20 μm          2.30387 0.199 60.4
##  (TRUE TRUE LL 2-20 μm) - TRUE TRUE LL >20 μm           1.18150 0.126 57.0
##  FALSE FALSE HL >20 μm - TRUE FALSE HL >20 μm          -0.38879 0.181 44.7
##  FALSE FALSE HL >20 μm - FALSE TRUE HL >20 μm           0.11224 0.138 56.9
##  FALSE FALSE HL >20 μm - TRUE TRUE HL >20 μm           -0.27655 0.230 50.8
##  FALSE FALSE HL >20 μm - FALSE FALSE LL >20 μm         -0.27058 0.179 43.2
##  FALSE FALSE HL >20 μm - TRUE FALSE LL >20 μm          -1.39294 0.192 54.9
##  FALSE FALSE HL >20 μm - FALSE TRUE LL >20 μm          -0.15833 0.224 46.9
##  FALSE FALSE HL >20 μm - TRUE TRUE LL >20 μm           -1.28070 0.236 55.5
##  TRUE FALSE HL >20 μm - FALSE TRUE HL >20 μm            0.50103 0.224 46.9
##  TRUE FALSE HL >20 μm - TRUE TRUE HL >20 μm             0.11224 0.138 56.9
##  TRUE FALSE HL >20 μm - FALSE FALSE LL >20 μm           0.11821 0.198 58.8
##  TRUE FALSE HL >20 μm - TRUE FALSE LL >20 μm           -1.00415 0.181 44.7
##  TRUE FALSE HL >20 μm - FALSE TRUE LL >20 μm            0.23045 0.236 55.5
##  TRUE FALSE HL >20 μm - TRUE TRUE LL >20 μm            -0.89191 0.224 46.9
```

```
##  FALSE TRUE HL >20 µm - TRUE TRUE HL >20 µm           -0.38879 0.181 44.7
##  FALSE TRUE HL >20 µm - FALSE FALSE LL >20 µm         -0.38282 0.227 48.9
##  FALSE TRUE HL >20 µm - TRUE FALSE LL >20 µm          -1.50518 0.236 55.5
##  FALSE TRUE HL >20 µm - FALSE TRUE LL >20 µm          -0.27058 0.179 43.2
##  FALSE TRUE HL >20 µm - TRUE TRUE LL >20 µm           -1.39294 0.192 54.9
##  TRUE TRUE HL >20 µm - FALSE FALSE LL >20 µm           0.00597 0.245 60.6
##  TRUE TRUE HL >20 µm - TRUE FALSE LL >20 µm           -1.11639 0.230 50.8
##  TRUE TRUE HL >20 µm - FALSE TRUE LL >20 µm            0.11821 0.198 58.8
##  TRUE TRUE HL >20 µm - TRUE TRUE LL >20 µm            -1.00415 0.181 44.7
##  FALSE FALSE LL >20 µm - TRUE FALSE LL >20 µm         -1.12237 0.179 43.2
##  FALSE FALSE LL >20 µm - FALSE TRUE LL >20 µm          0.11224 0.138 56.9
##  FALSE FALSE LL >20 µm - TRUE TRUE LL >20 µm          -1.01012 0.227 48.9
##  TRUE FALSE LL >20 µm - FALSE TRUE LL >20 µm           1.23461 0.224 46.9
##  TRUE FALSE LL >20 µm - TRUE TRUE LL >20 µm            0.11224 0.138 56.9
##  FALSE TRUE LL >20 µm - TRUE TRUE LL >20 µm           -1.12237 0.179 43.2
##  t.ratio p.value
##    3.123  0.2722
##   -1.321  0.9996
##    1.684  0.9877
##    2.344  0.7702
##    1.255  0.9998
##    1.064  1.0000
##    0.262  1.0000
##   12.916  <.0001
##    5.052  0.0010
##   10.405  <.0001
##    4.827  0.0030
##    7.181  <.0001
##    0.481  1.0000
##    6.715  <.0001
##    0.778  1.0000
##   21.171  <.0001
##   11.158  <.0001
##   16.792  <.0001
##   10.220  <.0001
##   11.853  <.0001
##    6.452  <.0001
##   11.038  <.0001
##    6.159  <.0001
##   -3.284  0.1946
##   -1.321  0.9996
##   -0.723  1.0000
##   -1.771  0.9778
##   -1.353  0.9994
##   -2.209  0.8459
##    5.277  0.0004
##    3.600  0.0892
##    5.026  0.0016
##    3.245  0.1925
##    4.534  0.0062
##   -2.336  0.7792
##    4.346  0.0143
##   -1.727  0.9837
##   10.440  <.0001
```

```
##   13.333  <.0001
##    9.744  <.0001
##   10.685  <.0001
##    9.329  <.0001
##    3.432  0.1317
##    8.788  <.0001
##    3.539  0.1105
##    3.123  0.2722
##    2.665  0.5556
##    1.787  0.9777
##    2.344  0.7702
##    1.255  0.9998
##   11.036  <.0001
##    5.282  0.0007
##   14.981  <.0001
##    6.344  <.0001
##    7.170  <.0001
##    1.245  0.9998
##    8.472  <.0001
##    1.817  0.9733
##   17.380  <.0001
##   10.714  <.0001
##   23.113  <.0001
##   12.308  <.0001
##   11.317  <.0001
##    6.502  <.0001
##   13.347  <.0001
##    7.912  <.0001
##    0.172  1.0000
##   -0.609  1.0000
##   -0.723  1.0000
##   -1.771  0.9778
##    5.481  0.0004
##    3.875  0.0366
##    6.569  <.0001
##    5.665  0.0001
##    4.813  0.0036
##   -1.272  0.9997
##    5.871  0.0001
##   -1.045  1.0000
##   10.061  <.0001
##   11.416  <.0001
##   11.880  <.0001
##   14.897  <.0001
##    9.044  <.0001
##    3.845  0.0520
##   10.916  <.0001
##    4.888  0.0017
##   -0.992  1.0000
##   -1.321  0.9996
##   -1.589  0.9938
##    5.976  <.0001
##    3.054  0.2992
##    5.646  0.0002
```

```
##    3.043  0.3144
##    8.120  <.0001
##   -1.638  0.9921
##    6.719  <.0001
##   -1.107  1.0000
##   11.139  <.0001
##    9.436  <.0001
##   10.362  <.0001
##    8.686  <.0001
##   15.365  <.0001
##    4.131  0.0198
##   12.709  <.0001
##    4.158  0.0221
##   -0.011  1.0000
##   -1.321  0.9996
##    7.107  <.0001
##    3.840  0.0459
##    6.611  <.0001
##    3.751  0.0660
##    5.969  <.0001
##   -1.196  0.9999
##    5.639  0.0002
##   -0.441  1.0000
##   12.451  <.0001
##    9.959  <.0001
##   11.411  <.0001
##    9.174  <.0001
##   10.643  <.0001
##    8.028  <.0001
##    9.963  <.0001
##    6.794  <.0001
##   -0.992  1.0000
##    6.101  <.0001
##    3.510  0.1224
##    7.268  <.0001
##    4.391  0.0097
##    7.350  <.0001
##   -0.652  1.0000
##   10.185  <.0001
##   -0.346  1.0000
##   10.680  <.0001
##    9.138  <.0001
##   12.577  <.0001
##   10.713  <.0001
##   12.990  <.0001
##    4.464  0.0091
##   17.979  <.0001
##    5.585  0.0001
##    7.079  <.0001
##    4.206  0.0194
##    8.444  <.0001
##    5.132  0.0007
##    6.094  <.0001
##    0.190  1.0000
```

```
##    7.260  <.0001
##    0.869  1.0000
##   11.783  <.0001
##    9.648  <.0001
##   13.868  <.0001
##   11.138  <.0001
##   10.244  <.0001
##    7.278  <.0001
##   12.134  <.0001
##   10.195  <.0001
##   -3.374  0.1651
##    0.570  1.0000
##   -2.339  0.7745
##   -1.001  1.0000
##   -7.881  <.0001
##   -0.451  1.0000
##   -6.106  <.0001
##    8.255  <.0001
##    3.171  0.2343
##    6.966  <.0001
##    3.253  0.2044
##    3.793  0.0522
##   -1.910  0.9559
##    3.873  0.0483
##   -1.160  0.9999
##    3.029  0.3186
##    0.570  1.0000
##    2.203  0.8513
##   -5.115  0.0014
##    2.128  0.8859
##   -3.724  0.0707
##    8.189  <.0001
##    9.794  <.0001
##    7.750  <.0001
##    8.026  <.0001
##    7.016  <.0001
##    1.181  0.9999
##    6.736  <.0001
##    1.545  0.9957
##   -3.374  0.1651
##   -1.141  1.0000
##   -6.764  <.0001
##   -1.001  1.0000
##   -7.881  <.0001
##    5.866  <.0001
##    2.477  0.6863
##    8.389  <.0001
##    3.265  0.1903
##    3.021  0.3229
##   -2.036  0.9168
##    3.977  0.0312
##   -1.716  0.9859
##    1.470  0.9980
##   -4.415  0.0106
```

```
##    2.203  0.8513
##   -5.115  0.0014
##    6.918  <.0001
##    7.107  <.0001
##    8.345  <.0001
##    9.593  <.0001
##    5.833  0.0001
##    0.702  1.0000
##    7.249  <.0001
##    1.353  0.9994
##   -7.489  <.0001
##    0.570  1.0000
##   -5.612  0.0002
##    6.060  <.0001
##    4.217  0.0162
##    5.866  0.0001
##    4.160  0.0226
##    7.384  <.0001
##   -0.948  1.0000
##    6.468  <.0001
##   -0.339  1.0000
##    6.303  <.0001
##    0.570  1.0000
##   13.225  <.0001
##   10.699  <.0001
##   12.088  <.0001
##    9.819  <.0001
##   11.389  <.0001
##    9.223  <.0001
##   10.626  <.0001
##    7.703  <.0001
##   -7.489  <.0001
##    5.030  0.0016
##    3.366  0.1671
##    6.221  <.0001
##    4.305  0.0119
##    5.242  0.0003
##   -1.186  0.9999
##    7.793  <.0001
##   -0.771  1.0000
##   11.288  <.0001
##    9.170  <.0001
##   13.309  <.0001
##   10.614  <.0001
##    9.762  <.0001
##    6.611  <.0001
##   11.591  <.0001
##    9.341  <.0001
##   -2.150  0.8727
##    0.815  1.0000
##   -1.200  0.9999
##   -1.513  0.9965
##   -7.254  <.0001
##   -0.707  1.0000
```

```
##   -5.419  0.0003
##    2.236  0.8323
##    0.815  1.0000
##    0.598  1.0000
##   -5.554  0.0003
##    0.975  1.0000
##   -3.980  0.0363
##   -2.150  0.8727
##   -1.684  0.9880
##   -6.369  <.0001
##   -1.513  0.9965
##   -7.254  <.0001
##    0.024  1.0000
##   -4.844  0.0025
##    0.598  1.0000
##   -5.554  0.0003
##   -6.278  <.0001
##    0.815  1.0000
##   -4.444  0.0093
##    5.509  0.0003
##    0.815  1.0000
##   -6.278  <.0001
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 24 estimates
```