

Linear Mixed Effects Model

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Analysis of sample data

```
## Do not touch
```

```
# run model
```

```
colnames(df)
```

```
## [1] "Condition"          "Field of view ID" "Nucleus ID"        "NPC pore ID"  
## [5] "Radius (nm)"
```

```
df$Condition <- as.factor(df$Condition)
```

```
m1 <- lmer(`Radius (nm)` ~ Condition + (1 | `Field of view ID`/`Nucleus ID`), data=df)
```

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

```
summary(m1)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [  
## lmerModLmerTest]  
## Formula: 'Radius (nm)' ~ Condition + (1 | 'Field of view ID'/'Nucleus ID')  
## Data: df  
##  
## REML criterion at convergence: 15823.8  
##  
## Scaled residuals:  
##      Min       1Q   Median       3Q      Max   
## -5.8425 -0.5823  0.0041  0.6184  4.8275   
##  
## Random effects:  
## Groups                                Name      Variance Std.Dev.  
## 'Nucleus ID': 'Field of view ID' (Intercept) 0.0000   0.000  
## Field of view ID                    (Intercept) 0.1043   0.323  
## Residual                            8.4559   2.908  
## Number of obs: 3179, groups:  
## 'Nucleus ID': 'Field of view ID', 19; Field of view ID, 9  
##  
## Fixed effects:  
##              Estimate Std. Error      df t value Pr(>|t|)
```

```
## (Intercept)          52.4219      0.2057  5.1636 254.845 8.71e-12 ***
## Condition(+)Gluc     0.8535      0.2917  5.2157   2.925  0.0312 *
## ConditionNaN3        0.4582      0.2994  5.6689   1.530  0.1797
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Cn(+)G
## Cndtn(+)Glc -0.705
## ConditinNN3 -0.687  0.484
## optimizer (nlptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
means <- lsmeansLT(m1, test.effs="Condition")
means$rn <- row.names(means)
print(means)
```

```
## Least Squares Means table:
##
##              Estimate Std. Error  df t value    lower    upper  Pr(>|t|)
## Condition(-)Gluc  52.42192    0.20570  5.2  254.84  51.89814  52.94569  8.7133e-12
## Condition(+)Gluc  53.27537    0.20689  5.3  257.50  52.75157  53.79917  5.2651e-12
## ConditionNaN3     52.88007    0.21755  6.2  243.08  52.35161  53.40853  1.5066e-13
##              rn
## Condition(-)Gluc  1
## Condition(+)Gluc  2
## ConditionNaN3     3
##
## Confidence level: 95%
## Degrees of freedom method: Satterthwaite
```

```
pw_means <- emmeans(m1, "Condition")
```

```
## Note: D.f. calculations have been disabled because the number of observations exceeds 3000.
## To enable adjustments, add the argument 'pbkrtest.limit = 3179' (or larger)
## [or, globally, 'set emm_options(pbkrtest.limit = 3179)' or larger];
## but be warned that this may result in large computation time and memory use.
```

```
## Note: D.f. calculations have been disabled because the number of observations exceeds 3000.
## To enable adjustments, add the argument 'lmerTest.limit = 3179' (or larger)
## [or, globally, 'set emm_options(lmerTest.limit = 3179)' or larger];
## but be warned that this may result in large computation time and memory use.
```

```
pairs(pw_means) # This line can take a few extra seconds. Totally normal.
```

```
## contrast          estimate    SE df z.ratio p.value
## ((-)Gluc) - ((+)Gluc)  -0.853 0.292 Inf  -2.925  0.0096
## ((-)Gluc) - NaN3      -0.458 0.299 Inf  -1.530  0.2767
## ((+)Gluc) - NaN3       0.395 0.300 Inf   1.317  0.3858
##
## Degrees-of-freedom method: asymptotic
## P value adjustment: tukey method for comparing a family of 3 estimates
```

```
## The conditions in df are: (+)Gluc, (-)Gluc, NaN3
```

```
## The conditions in df_alt are: (+)Gluc, (-)Gluc, (-)ATP NaN3
```

```
## The number of nuclei is: 3
```

```
## The min and max of Radius (nm) are: 36.2 and 67.3
```

