

Seahorse statistical analysis

Glycolysis Stress OCR - Jurkat EB1 clones

```
library(lattice)
library(AICcmodavg)
library(emmeans)
library(lme4)
```

```
## Loading required package: Matrix
```

```
##
```

```
## Attaching package: 'lme4'
```

```
## The following object is masked from 'package:AICcmodavg':
```

```
##
```

```
##      checkConv
```

```
library(lmerTest)
```

```
##
```

```
## Attaching package: 'lmerTest'
```

```
## The following object is masked from 'package:lme4':
```

```
##
```

```
##      lmer
```

```
## The following object is masked from 'package:stats':
```

```
##
```

```
##      step
```

```
library(lmtest)
```

```
## Loading required package: zoo
```

```
##
```

```
## Attaching package: 'zoo'
```

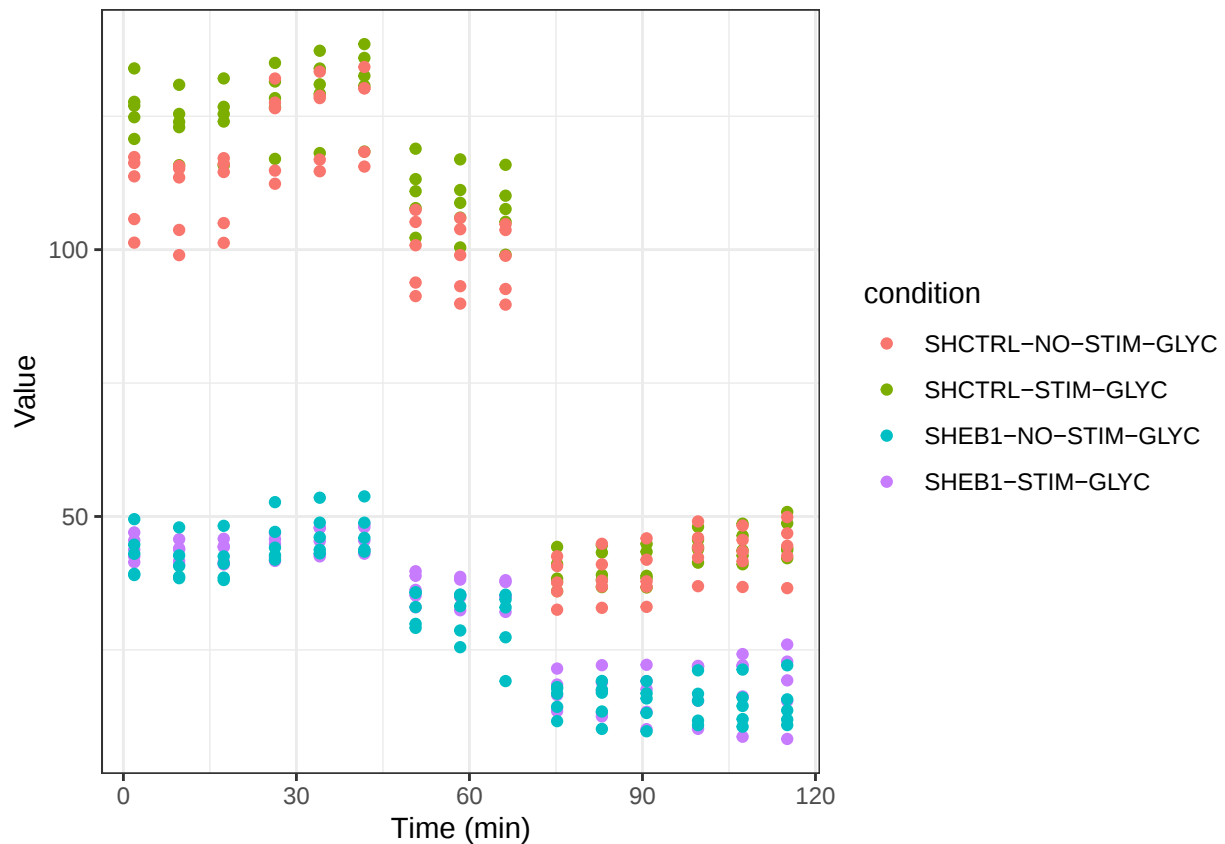
```
## The following objects are masked from 'package:base':
```

```
##
```

```
##      as.Date, as.Date.numeric
```

```
library(ggplot2)
```

```
ggplot(seahorse1, aes(time, value, colour=condition))+
  geom_point()+
  theme_bw()+
  xlab("Time (min)") +
  ylab('Value')
```



```
m1<-lm(value ~ treatment*condition, data=seahorse1)
summary(m1)
```

```
##
## Call:
## lm(formula = value ~ treatment * condition, data = seahorse1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -12.6045  -2.9476   0.2799   3.3369   9.9649
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    110.3693     1.2281  89.873  < 2e-16 ***
## treatmentb      13.9046     1.7367   8.006 3.18e-14 ***
## treatmentc     -11.6995     1.7367  -6.737 9.20e-11 ***
```

```
## treatmentd -71.7978 1.7367 -41.341 < 2e-16 ***
## treatmente -66.7226 1.7367 -38.418 < 2e-16 ***
## conditionSHCTRL-STIM-GLYC 14.7876 1.7367 8.515 1.04e-15 ***
## conditionSHEB1-NO-STIM-GLYC -68.1907 1.7367 -39.264 < 2e-16 ***
## conditionSHEB1-STIM-GLYC -66.8059 1.7367 -38.466 < 2e-16 ***
## treatmentb:conditionSHCTRL-STIM-GLYC -9.4439 2.4561 -3.845 0.000149 ***
## treatmentc:conditionSHCTRL-STIM-GLYC -4.5030 2.4561 -1.833 0.067809 .
## treatmentd:conditionSHCTRL-STIM-GLYC -13.2418 2.4561 -5.391 1.49e-07 ***
## treatmente:conditionSHCTRL-STIM-GLYC -13.4276 2.4561 -5.467 1.01e-07 ***
## treatmentb:conditionSHEB1-NO-STIM-GLYC -9.4319 2.4561 -3.840 0.000152 ***
## treatmentc:conditionSHEB1-NO-STIM-GLYC 0.9006 2.4561 0.367 0.714143
## treatmentd:conditionSHEB1-NO-STIM-GLYC 45.0052 2.4561 18.324 < 2e-16 ***
## treatmente:conditionSHEB1-NO-STIM-GLYC 39.5433 2.4561 16.100 < 2e-16 ***
## treatmentb:conditionSHEB1-STIM-GLYC -12.3366 2.4561 -5.023 9.08e-07 ***
## treatmentc:conditionSHEB1-STIM-GLYC 4.1682 2.4561 1.697 0.090793 .
## treatmentd:conditionSHEB1-STIM-GLYC 44.9594 2.4561 18.305 < 2e-16 ***
## treatmente:conditionSHEB1-STIM-GLYC 41.5973 2.4561 16.936 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.756 on 280 degrees of freedom
## Multiple R-squared: 0.9865, Adjusted R-squared: 0.9856
## F-statistic: 1081 on 19 and 280 DF, p-value: < 2.2e-16
```

```
summary(emmeans(m1, pairwise ~ condition|treatment, infer=T))
```

```
## $emmeans
## treatment = a:
## condition emmean SE df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM-GLYC 110.4 1.23 280 108.0 112.8 89.873 <.0001
## SHCTRL-STIM-GLYC 125.2 1.23 280 122.7 127.6 101.915 <.0001
## SHEB1-NO-STIM-GLYC 42.2 1.23 280 39.8 44.6 34.346 <.0001
## SHEB1-STIM-GLYC 43.6 1.23 280 41.1 46.0 35.474 <.0001
##
## treatment = b:
## condition emmean SE df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM-GLYC 124.3 1.23 280 121.9 126.7 101.196 <.0001
## SHCTRL-STIM-GLYC 129.6 1.23 280 127.2 132.0 105.547 <.0001
## SHEB1-NO-STIM-GLYC 46.7 1.23 280 44.2 49.1 37.988 <.0001
## SHEB1-STIM-GLYC 45.1 1.23 280 42.7 47.5 36.750 <.0001
##
## treatment = c:
## condition emmean SE df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM-GLYC 98.7 1.23 280 96.3 101.1 80.346 <.0001
## SHCTRL-STIM-GLYC 109.0 1.23 280 106.5 111.4 88.721 <.0001
## SHEB1-NO-STIM-GLYC 31.4 1.23 280 29.0 33.8 25.552 <.0001
## SHEB1-STIM-GLYC 36.0 1.23 280 33.6 38.4 29.341 <.0001
##
## treatment = d:
## condition emmean SE df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM-GLYC 38.6 1.23 280 36.2 41.0 31.409 <.0001
## SHCTRL-STIM-GLYC 40.1 1.23 280 37.7 42.5 32.667 <.0001
## SHEB1-NO-STIM-GLYC 15.4 1.23 280 13.0 17.8 12.529 <.0001
## SHEB1-STIM-GLYC 16.7 1.23 280 14.3 19.1 13.619 <.0001
```

```

##
## treatment = e:
##      condition      emmean    SE    df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM-GLYC    43.6  1.23  280     41.2     46.1  35.541 <.0001
## SHCTRL-STIM-GLYC      45.0  1.23  280     42.6     47.4  36.649 <.0001
## SHEB1-NO-STIM-GLYC    15.0  1.23  280     12.6     17.4  12.214 <.0001
## SHEB1-STIM-GLYC      18.4  1.23  280     16.0     20.9  15.014 <.0001
##
## Confidence level used: 0.95
##
## $contrasts
## treatment = a:
##      contrast      estimate    SE    df lower.CL
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC)    -14.79  1.74  280    -19.28
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)    68.19  1.74  280     63.70
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)    66.81  1.74  280     62.32
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)    82.98  1.74  280     78.49
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC)    81.59  1.74  280     77.10
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)    -1.38  1.74  280     -5.87
##      upper.CL t.ratio p.value
##      -10.299  -8.515 <.0001
##       72.679  39.264 <.0001
##       71.295  38.466 <.0001
##       87.467  47.778 <.0001
##       86.082  46.981 <.0001
##        3.104  -0.797  0.8556
##
## treatment = b:
##      contrast      estimate    SE    df lower.CL
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC)    -5.34  1.74  280    -9.83
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)    77.62  1.74  280     73.13
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)    79.14  1.74  280     74.65
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)    82.97  1.74  280     78.48
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC)    84.49  1.74  280     80.00
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)     1.52  1.74  280     -2.97
##      upper.CL t.ratio p.value
##      -0.855  -3.077  0.0122
##      82.111  44.695 <.0001
##      83.631  45.570 <.0001
##      87.455  47.772 <.0001
##      88.975  48.647 <.0001
##       6.008   0.875  0.8177
##
## treatment = c:
##      contrast      estimate    SE    df lower.CL
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC)   -10.28  1.74  280   -14.77
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)    67.29  1.74  280     62.80
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)    62.64  1.74  280     58.15
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)    77.57  1.74  280     73.09
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC)    72.92  1.74  280     68.43
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)    -4.65  1.74  280     -9.14
##      upper.CL t.ratio p.value
##      -5.796  -5.922 <.0001
##      71.779  38.745 <.0001

```

```

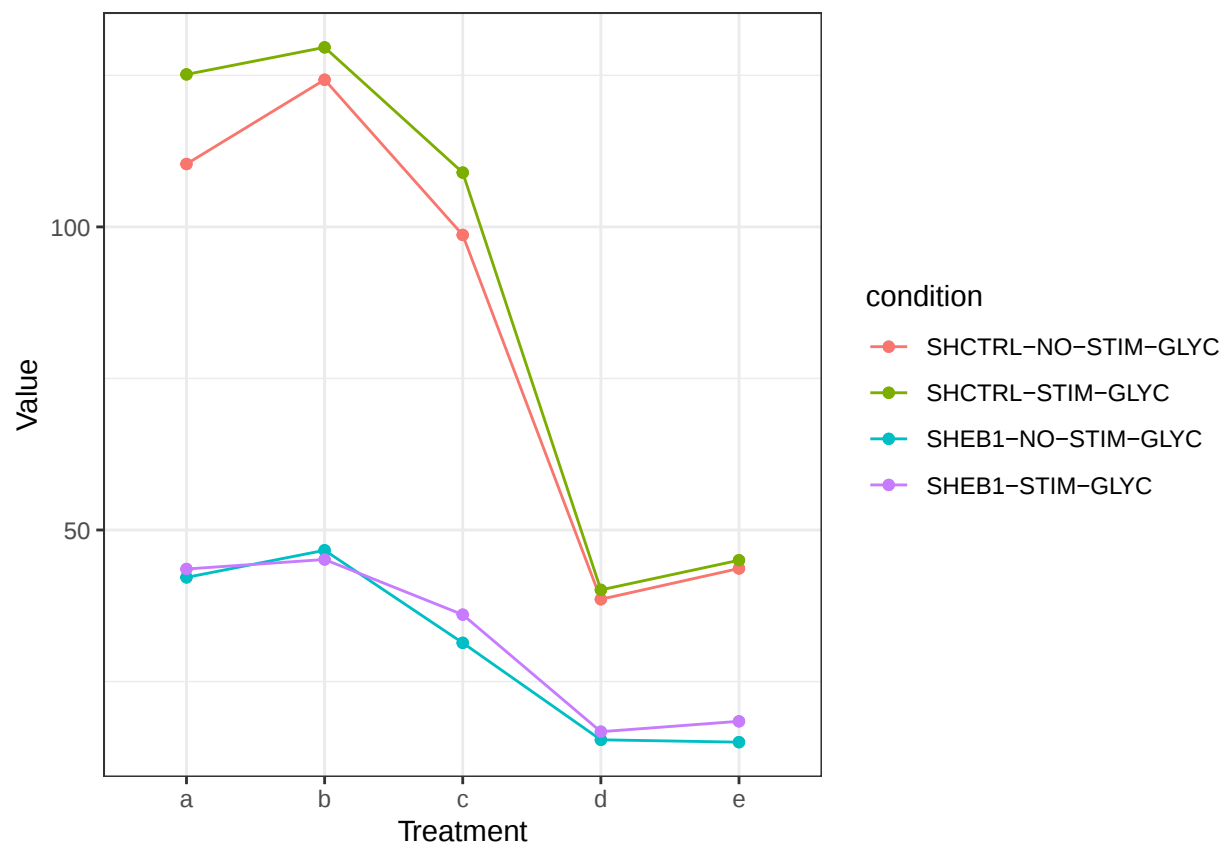
##      67.126  36.066  <.0001
##      82.063  44.667  <.0001
##      77.411  41.988  <.0001
##      -0.164  -2.679  0.0389
##
## treatment = d:
## contrast                estimate    SE  df lower.CL
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC)    -1.55  1.74  280    -6.03
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)   23.19  1.74  280    18.70
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)     21.85  1.74  280    17.36
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)     24.73  1.74  280    20.24
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC)        23.39  1.74  280    18.90
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)     -1.34  1.74  280    -5.83
## upper.CL t.ratio p.value
##      2.943  -0.890  0.8100
##      27.674  13.350  <.0001
##      26.335  12.579  <.0001
##      29.220  14.240  <.0001
##      27.881  13.469  <.0001
##      3.150  -0.771  0.8675
##
## treatment = e:
## contrast                estimate    SE  df lower.CL
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC)    -1.36  1.74  280    -5.85
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)   28.65  1.74  280    24.16
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)     25.21  1.74  280    20.72
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)     30.01  1.74  280    25.52
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC)        26.57  1.74  280    22.08
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)     -3.44  1.74  280    -7.93
## upper.CL t.ratio p.value
##      3.129  -0.783  0.8621
##      33.136  16.495  <.0001
##      29.697  14.515  <.0001
##      34.496  17.278  <.0001
##      31.057  15.298  <.0001
##      1.050  -1.980  0.1980
##
## Confidence level used: 0.95
## Conf-level adjustment: tukey method for comparing a family of 4 estimates
## P value adjustment: tukey method for comparing a family of 4 estimates

```

```

emmip(m1, condition ~ treatment) +
  theme_bw() +
  xlab('Treatment') +
  ylab('Value')

```



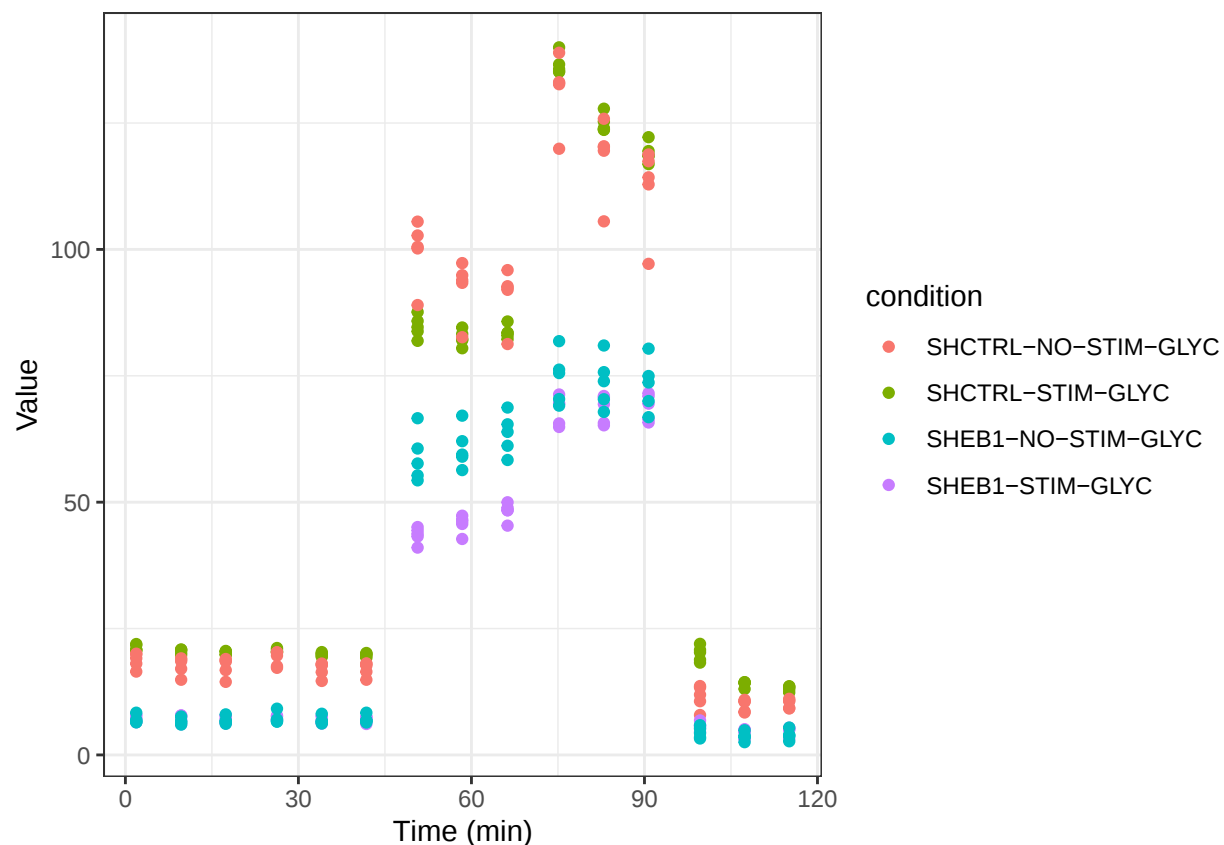
```
summary(pairs(emmeans(m1, "condition", by = "treatment", level = 0.95, infer = TRUE)))
```

```
## treatment = a:
## contrast                estimate    SE  df t.ratio p.value
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC)    -14.79  1.74  280   -8.515  <.0001
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)    68.19  1.74  280   39.264  <.0001
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)     66.81  1.74  280   38.466  <.0001
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)     82.98  1.74  280   47.778  <.0001
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC)      81.59  1.74  280   46.981  <.0001
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)      -1.38  1.74  280    -0.797  0.8556
##
## treatment = b:
## contrast                estimate    SE  df t.ratio p.value
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC)     -5.34  1.74  280    -3.077  0.0122
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)    77.62  1.74  280   44.695  <.0001
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)     79.14  1.74  280   45.570  <.0001
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)     82.97  1.74  280   47.772  <.0001
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC)      84.49  1.74  280   48.647  <.0001
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)       1.52  1.74  280     0.875  0.8177
##
## treatment = c:
## contrast                estimate    SE  df t.ratio p.value
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC)    -10.28  1.74  280    -5.922  <.0001
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)    67.29  1.74  280   38.745  <.0001
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)     62.64  1.74  280   36.066  <.0001
```

```
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)      77.57 1.74 280  44.667 <.0001
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC)         72.92 1.74 280  41.988 <.0001
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)       -4.65 1.74 280   -2.679 0.0389
##
## treatment = d:
## contrast      estimate    SE  df t.ratio p.value
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC)     -1.55 1.74 280   -0.890 0.8100
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)    23.19 1.74 280   13.350 <.0001
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)       21.85 1.74 280   12.579 <.0001
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)       24.73 1.74 280   14.240 <.0001
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC)          23.39 1.74 280   13.469 <.0001
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)       -1.34 1.74 280   -0.771 0.8675
##
## treatment = e:
## contrast      estimate    SE  df t.ratio p.value
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC)     -1.36 1.74 280   -0.783 0.8621
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)    28.65 1.74 280   16.495 <.0001
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)       25.21 1.74 280   14.515 <.0001
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)       30.01 1.74 280   17.278 <.0001
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC)          26.57 1.74 280   15.298 <.0001
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)       -3.44 1.74 280   -1.980 0.1980
##
## P value adjustment: tukey method for comparing a family of 4 estimates
```

Glycolysis Stress ECAR - Jurkat EB1 clones

```
ggplot(seahorse2, aes(time, value, colour=condition))+
  geom_point()+
  theme_bw()+
  xlab("Time (min)") +
  ylab('Value')
```



```
m2<-lm(value ~ treatment*condition, data=seahorse2)
summary(m2)
```

```
##
## Call:
## lm(formula = value ~ treatment * condition, data = seahorse2)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-23.4930	-1.1957	-0.0878	0.9518	18.2661

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	17.9608	1.0141	17.712	< 2e-16 ***
treatmentb	-0.3064	1.4341	-0.214	0.8310
treatmentc	76.3316	1.4341	53.226	< 2e-16 ***
treatmentd	102.6775	1.4341	71.597	< 2e-16 ***
treatmente	-7.4720	1.4341	-5.210	3.66e-07 ***
conditionSHCTRL-STIM-GLYC	2.6646	1.4341	1.858	0.0642 .
conditionSHEB1-NO-STIM-GLYC	-11.1531	1.4341	-7.777	1.43e-13 ***
conditionSHEB1-STIM-GLYC	-10.7562	1.4341	-7.500	8.46e-13 ***
treatmentb:conditionSHCTRL-STIM-GLYC	-0.2191	2.0281	-0.108	0.9140
treatmentc:conditionSHCTRL-STIM-GLYC	-13.3361	2.0281	-6.576	2.37e-10 ***
treatmentd:conditionSHCTRL-STIM-GLYC	3.5458	2.0281	1.748	0.0815 .
treatmente:conditionSHCTRL-STIM-GLYC	2.5908	2.0281	1.277	0.2025

```
## treatmentb:conditionSHEB1-NO-STIM-GLYC    0.5263    2.0281    0.259    0.7955
## treatmentc:conditionSHEB1-NO-STIM-GLYC -22.0758    2.0281   -10.885 < 2e-16 ***
## treatmentd:conditionSHEB1-NO-STIM-GLYC -35.6315    2.0281   -17.569 < 2e-16 ***
## treatmente:conditionSHEB1-NO-STIM-GLYC    4.6693    2.0281    2.302    0.0221 *
## treatmentb:conditionSHEB1-STIM-GLYC      0.2260    2.0281    0.111    0.9113
## treatmentc:conditionSHEB1-STIM-GLYC   -37.7384    2.0281   -18.608 < 2e-16 ***
## treatmentd:conditionSHEB1-STIM-GLYC   -41.4123    2.0281   -20.419 < 2e-16 ***
## treatmente:conditionSHEB1-STIM-GLYC     5.2335    2.0281    2.580    0.0104 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.927 on 280 degrees of freedom
## Multiple R-squared:  0.9909, Adjusted R-squared:  0.9903
## F-statistic: 1607 on 19 and 280 DF,  p-value: < 2.2e-16
```

```
summary(emmeans(m2, pairwise ~ condition|treatment, infer=T))
```

```
## $emmeans
## treatment = a:
## condition      emmean    SE  df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM-GLYC  17.96 1.01 280    15.96    19.96  17.712 <.0001
## SHCTRL-STIM-GLYC    20.63 1.01 280    18.63    22.62  20.339 <.0001
## SHEB1-NO-STIM-GLYC   6.81 1.01 280     4.81     8.80   6.713 <.0001
## SHEB1-STIM-GLYC      7.20 1.01 280     5.21     9.20   7.105 <.0001
##
## treatment = b:
## condition      emmean    SE  df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM-GLYC  17.65 1.01 280    15.66    19.65  17.410 <.0001
## SHCTRL-STIM-GLYC    20.10 1.01 280    18.10    22.10  19.821 <.0001
## SHEB1-NO-STIM-GLYC   7.03 1.01 280     5.03     9.02   6.930 <.0001
## SHEB1-STIM-GLYC      7.12 1.01 280     5.13     9.12   7.025 <.0001
##
## treatment = c:
## condition      emmean    SE  df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM-GLYC  94.29 1.01 280    92.30    96.29  92.985 <.0001
## SHCTRL-STIM-GLYC    83.62 1.01 280    81.62    85.62  82.461 <.0001
## SHEB1-NO-STIM-GLYC  61.06 1.01 280    59.07    63.06  60.217 <.0001
## SHEB1-STIM-GLYC     45.80 1.01 280    43.80    47.79  45.163 <.0001
##
## treatment = d:
## condition      emmean    SE  df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM-GLYC 120.64 1.01 280   118.64   122.63 118.965 <.0001
## SHCTRL-STIM-GLYC   126.85 1.01 280   124.85   128.84 125.090 <.0001
## SHEB1-NO-STIM-GLYC  73.85 1.01 280    71.86    75.85  72.830 <.0001
## SHEB1-STIM-GLYC     68.47 1.01 280    66.47    70.47  67.520 <.0001
##
## treatment = e:
## condition      emmean    SE  df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM-GLYC  10.49 1.01 280     8.49    12.48  10.343 <.0001
## SHCTRL-STIM-GLYC    15.74 1.01 280    13.75    17.74  15.526 <.0001
## SHEB1-NO-STIM-GLYC   4.01 1.01 280     2.01     6.00   3.950 0.0001
## SHEB1-STIM-GLYC      4.97 1.01 280     2.97     6.96   4.897 <.0001
##
## Confidence level used: 0.95
```

```

##
## $contrasts
## treatment = a:
## contrast estimate SE df lower.CL
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC) -2.6646 1.43 280 -6.37
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC) 11.1531 1.43 280 7.45
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC) 10.7562 1.43 280 7.05
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC) 13.8177 1.43 280 10.11
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC) 13.4208 1.43 280 9.71
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC) -0.3968 1.43 280 -4.10
## upper.CL t.ratio p.value
## 1.04 -1.858 0.2487
## 14.86 7.777 <.0001
## 14.46 7.500 <.0001
## 17.52 9.635 <.0001
## 17.13 9.358 <.0001
## 3.31 -0.277 0.9926
##
## treatment = b:
## contrast estimate SE df lower.CL
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC) -2.4455 1.43 280 -6.15
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC) 10.6268 1.43 280 6.92
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC) 10.5302 1.43 280 6.82
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC) 13.0723 1.43 280 9.37
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC) 12.9757 1.43 280 9.27
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC) -0.0966 1.43 280 -3.80
## upper.CL t.ratio p.value
## 1.26 -1.705 0.3229
## 14.33 7.410 <.0001
## 14.24 7.343 <.0001
## 16.78 9.115 <.0001
## 16.68 9.048 <.0001
## 3.61 -0.067 0.9999
##
## treatment = c:
## contrast estimate SE df lower.CL
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC) 10.6716 1.43 280 6.97
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC) 33.2289 1.43 280 29.52
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC) 48.4947 1.43 280 44.79
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC) 22.5573 1.43 280 18.85
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC) 37.8231 1.43 280 34.12
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC) 15.2658 1.43 280 11.56
## upper.CL t.ratio p.value
## 14.38 7.441 <.0001
## 36.94 23.171 <.0001
## 52.20 33.815 <.0001
## 26.26 15.729 <.0001
## 41.53 26.374 <.0001
## 18.97 10.645 <.0001
##
## treatment = d:
## contrast estimate SE df lower.CL
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC) -6.2104 1.43 280 -9.92
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC) 46.7846 1.43 280 43.08

```

```

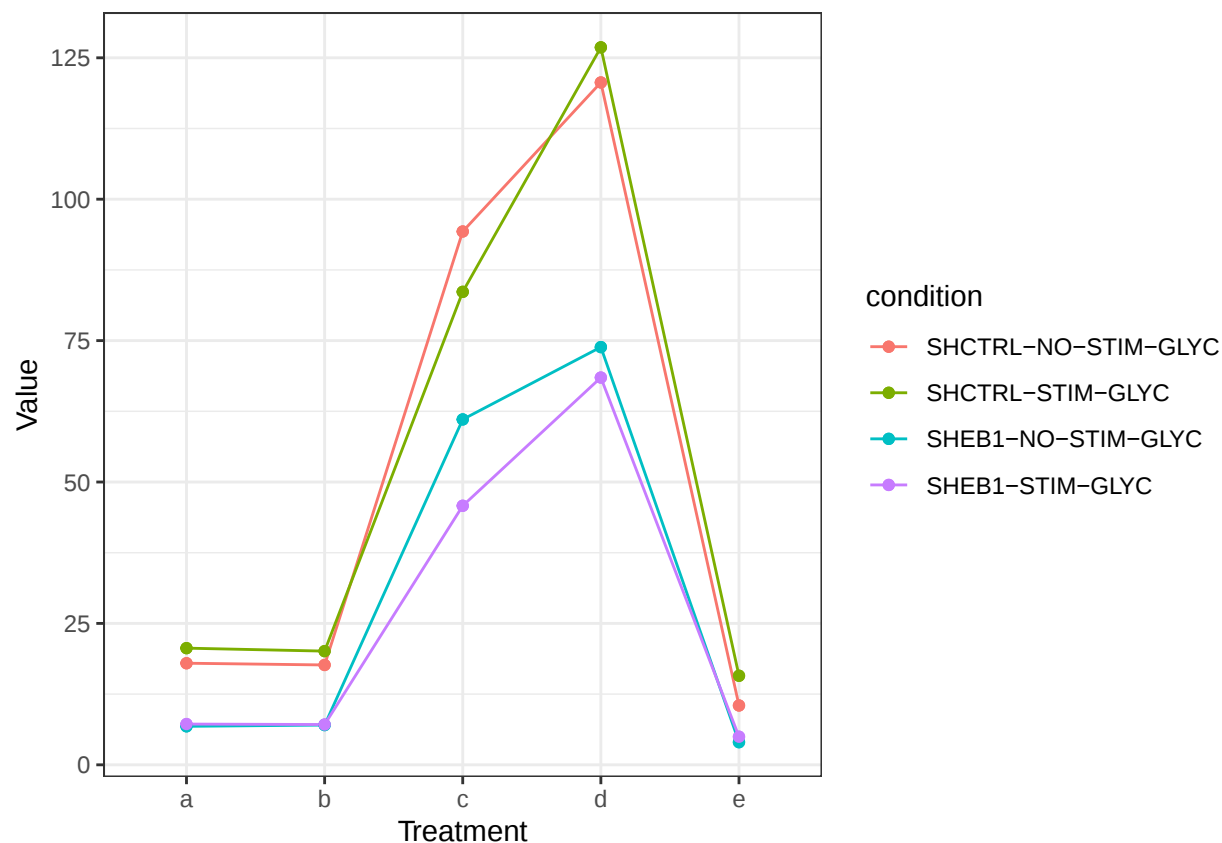
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)      52.1686 1.43 280      48.46
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)      52.9950 1.43 280      49.29
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC)         58.3789 1.43 280      54.67
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)        5.3840 1.43 280       1.68
## upper.CL t.ratio p.value
##      -2.50  -4.330  0.0001
##      50.49  32.623  <.0001
##      55.88  36.377  <.0001
##      56.70  36.953  <.0001
##      62.09  40.708  <.0001
##       9.09   3.754  0.0012
##
## treatment = e:
## contrast                estimate    SE  df lower.CL
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC)    -5.2554 1.43 280     -8.96
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)    6.4838 1.43 280      2.78
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)     5.5227 1.43 280      1.82
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)     11.7391 1.43 280      8.03
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC)        10.7781 1.43 280      7.07
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)     -0.9610 1.43 280     -4.67
## upper.CL t.ratio p.value
##      -1.55  -3.665  0.0017
##      10.19   4.521  0.0001
##       9.23   3.851  0.0008
##      15.45   8.186  <.0001
##      14.48   7.516  <.0001
##       2.75  -0.670  0.9083
##
## Confidence level used: 0.95
## Conf-level adjustment: tukey method for comparing a family of 4 estimates
## P value adjustment: tukey method for comparing a family of 4 estimates

```

```

emmip(m2, condition ~ treatment) +
  theme_bw()+
  xlab('Treatment') +
  ylab('Value')

```



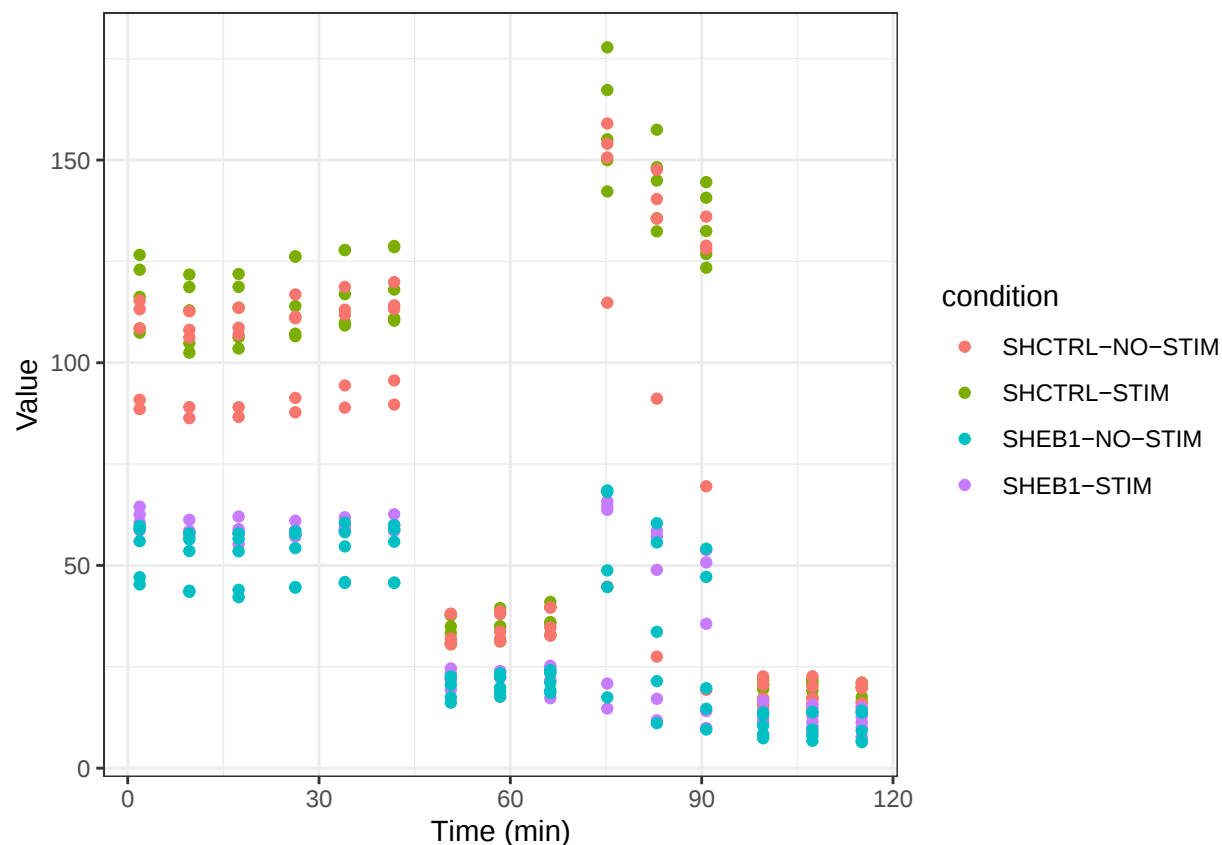
```
summary(pairs(emmeans(m2, "condition", by = "treatment", level = 0.95, infer = TRUE)))
```

```
## treatment = a:
## contrast
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC) estimate SE df t.ratio p.value
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC) 11.1531 1.43 280 7.777 <.0001
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC) 10.7562 1.43 280 7.500 <.0001
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC) 13.8177 1.43 280 9.635 <.0001
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC) 13.4208 1.43 280 9.358 <.0001
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC) -0.3968 1.43 280 -0.277 0.9926
##
## treatment = b:
## contrast
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC) estimate SE df t.ratio p.value
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC) 10.6268 1.43 280 7.410 <.0001
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC) 10.5302 1.43 280 7.343 <.0001
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC) 13.0723 1.43 280 9.115 <.0001
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC) 12.9757 1.43 280 9.048 <.0001
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC) -0.0966 1.43 280 -0.067 0.9999
##
## treatment = c:
## contrast
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC) estimate SE df t.ratio p.value
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC) 33.2289 1.43 280 23.171 <.0001
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC) 48.4947 1.43 280 33.815 <.0001
```

```
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)      22.5573 1.43 280 15.729 <.0001
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC)         37.8231 1.43 280 26.374 <.0001
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)       15.2658 1.43 280 10.645 <.0001
##
## treatment = d:
## contrast                estimate    SE  df t.ratio p.value
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC)     -6.2104 1.43 280 -4.330 0.0001
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)   46.7846 1.43 280 32.623 <.0001
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)      52.1686 1.43 280 36.377 <.0001
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)      52.9950 1.43 280 36.953 <.0001
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC)         58.3789 1.43 280 40.708 <.0001
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)        5.3840 1.43 280 3.754 0.0012
##
## treatment = e:
## contrast                estimate    SE  df t.ratio p.value
## (SHCTRL-NO-STIM-GLYC) - (SHCTRL-STIM-GLYC)     -5.2554 1.43 280 -3.665 0.0017
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)    6.4838 1.43 280 4.521 0.0001
## (SHCTRL-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)       5.5227 1.43 280 3.851 0.0008
## (SHCTRL-STIM-GLYC) - (SHEB1-NO-STIM-GLYC)      11.7391 1.43 280 8.186 <.0001
## (SHCTRL-STIM-GLYC) - (SHEB1-STIM-GLYC)         10.7781 1.43 280 7.516 <.0001
## (SHEB1-NO-STIM-GLYC) - (SHEB1-STIM-GLYC)       -0.9610 1.43 280 -0.670 0.9083
##
## P value adjustment: tukey method for comparing a family of 4 estimates
```

MitoStress OCR - Jurkat EB1 clones

```
ggplot(seahorse3, aes(time, value, colour=condition))+
  geom_point()+
  theme_bw()+
  xlab("Time (min)") +
  ylab('Value')
```



```
m3<-lm(value ~ treatment*condition, data=seahorse3)
summary(m3)
```

```
##
## Call:
## lm(formula = value ~ treatment * condition, data = seahorse3)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -90.488  -3.547   0.045   4.774  49.203
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    101.5747     3.6451  27.866 < 2e-16 ***
## treatmentb         3.6173     5.1549   0.702 0.483441
## treatmentc    -66.7329     5.1549 -12.946 < 2e-16 ***
## treatmentd      8.2474     5.1549   1.600 0.110743
## treatmente   -83.7212     5.1549 -16.241 < 2e-16 ***
## conditionSHCTRL-STIM    12.1857     5.1549   2.364 0.018766 *
## conditionSHEB1-NO-STIM -49.8175     5.1549  -9.664 < 2e-16 ***
## conditionSHEB1-STIM   -42.2007     5.1549  -8.187 9.58e-15 ***
## treatmentb:conditionSHCTRL-STIM    0.5207     7.2901   0.071 0.943114
## treatmentc:conditionSHCTRL-STIM  -11.1125     7.2901  -1.524 0.128558
## treatmentd:conditionSHCTRL-STIM   23.2685     7.2901   3.192 0.001575 **
## treatmente:conditionSHCTRL-STIM  -10.3432     7.2901  -1.419 0.157071
```

```
## treatmentb:conditionSHEB1-NO-STIM -2.6578 7.2901 -0.365 0.715708
## treatmentc:conditionSHEB1-NO-STIM 35.5139 7.2901 4.872 1.86e-06 ***
## treatmentd:conditionSHEB1-NO-STIM -21.6730 7.2901 -2.973 0.003206 **
## treatmente:conditionSHEB1-NO-STIM 42.3114 7.2901 5.804 1.75e-08 ***
## treatmentb:conditionSHEB1-STIM -3.7531 7.2901 -0.515 0.607085
## treatmentc:conditionSHEB1-STIM 29.6049 7.2901 4.061 6.35e-05 ***
## treatmentd:conditionSHEB1-STIM -28.4745 7.2901 -3.906 0.000118 ***
## treatmente:conditionSHEB1-STIM 36.1790 7.2901 4.963 1.21e-06 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 14.12 on 280 degrees of freedom
## Multiple R-squared: 0.899, Adjusted R-squared: 0.8922
## F-statistic: 131.2 on 19 and 280 DF, p-value: < 2.2e-16
```

```
summary(emmeans(m3, pairwise ~ condition|treatment, infer=T))
```

```
## $emmeans
## treatment = a:
## condition emmean SE df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM 101.6 3.65 280 94.40 108.7 27.866 <.0001
## SHCTRL-STIM 113.8 3.65 280 106.59 120.9 31.209 <.0001
## SHEB1-NO-STIM 51.8 3.65 280 44.58 58.9 14.199 <.0001
## SHEB1-STIM 59.4 3.65 280 52.20 66.5 16.289 <.0001
##
## treatment = b:
## condition emmean SE df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM 105.2 3.65 280 98.02 112.4 28.859 <.0001
## SHCTRL-STIM 117.9 3.65 280 110.72 125.1 32.345 <.0001
## SHEB1-NO-STIM 52.7 3.65 280 45.54 59.9 14.463 <.0001
## SHEB1-STIM 59.2 3.65 280 52.06 66.4 16.252 <.0001
##
## treatment = c:
## condition emmean SE df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM 34.8 3.65 280 27.67 42.0 9.559 <.0001
## SHCTRL-STIM 35.9 3.65 280 28.74 43.1 9.853 <.0001
## SHEB1-NO-STIM 20.5 3.65 280 13.36 27.7 5.635 <.0001
## SHEB1-STIM 22.2 3.65 280 15.07 29.4 6.103 <.0001
##
## treatment = d:
## condition emmean SE df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM 109.8 3.65 280 102.65 117.0 30.129 <.0001
## SHCTRL-STIM 145.3 3.65 280 138.10 152.5 39.856 <.0001
## SHEB1-NO-STIM 38.3 3.65 280 31.16 45.5 10.516 <.0001
## SHEB1-STIM 39.1 3.65 280 31.97 46.3 10.740 <.0001
##
## treatment = e:
## condition emmean SE df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM 17.9 3.65 280 10.68 25.0 4.898 <.0001
## SHCTRL-STIM 19.7 3.65 280 12.52 26.9 5.403 <.0001
## SHEB1-NO-STIM 10.3 3.65 280 3.17 17.5 2.839 0.0049
## SHEB1-STIM 11.8 3.65 280 4.66 19.0 3.246 0.0013
##
## Confidence level used: 0.95
```

```

##
## $contrasts
## treatment = a:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)   -12.186  5.15  280  -25.509    1.137  -2.364
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)   49.817  5.15  280   36.495   63.140   9.664
## (SHCTRL-NO-STIM) - (SHEB1-STIM)    42.201  5.15  280   28.878   55.524   8.187
## (SHCTRL-STIM) - (SHEB1-NO-STIM)    62.003  5.15  280   48.680   75.326  12.028
## (SHCTRL-STIM) - (SHEB1-STIM)    54.386  5.15  280   41.063   67.709  10.550
## (SHEB1-NO-STIM) - (SHEB1-STIM)    -7.617  5.15  280  -20.940    5.706  -1.478
## p.value
## 0.0866
## <.0001
## <.0001
## <.0001
## <.0001
## 0.4524
##
## treatment = b:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)   -12.706  5.15  280  -26.029    0.617  -2.465
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)   52.475  5.15  280   39.152   65.798  10.180
## (SHCTRL-NO-STIM) - (SHEB1-STIM)    45.954  5.15  280   32.631   59.277   8.915
## (SHCTRL-STIM) - (SHEB1-NO-STIM)    65.182  5.15  280   51.859   78.505  12.645
## (SHCTRL-STIM) - (SHEB1-STIM)    58.660  5.15  280   45.337   71.983  11.379
## (SHEB1-NO-STIM) - (SHEB1-STIM)    -6.521  5.15  280  -19.844    6.802  -1.265
## p.value
## 0.0678
## <.0001
## <.0001
## <.0001
## <.0001
## 0.5859
##
## treatment = c:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)   -1.073  5.15  280  -14.396   12.250  -0.208
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)   14.304  5.15  280    0.981   27.627   2.775
## (SHCTRL-NO-STIM) - (SHEB1-STIM)    12.596  5.15  280   -0.727   25.919   2.443
## (SHCTRL-STIM) - (SHEB1-NO-STIM)    15.377  5.15  280    2.054   28.700   2.983
## (SHCTRL-STIM) - (SHEB1-STIM)    13.669  5.15  280    0.346   26.992   2.652
## (SHEB1-NO-STIM) - (SHEB1-STIM)    -1.708  5.15  280  -15.031   11.615  -0.331
## p.value
## 0.9968
## 0.0299
## 0.0714
## 0.0163
## 0.0419
## 0.9874
##
## treatment = d:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)  -35.454  5.15  280  -48.777  -22.131  -6.878
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)   71.490  5.15  280   58.167   84.813  13.868

```

```

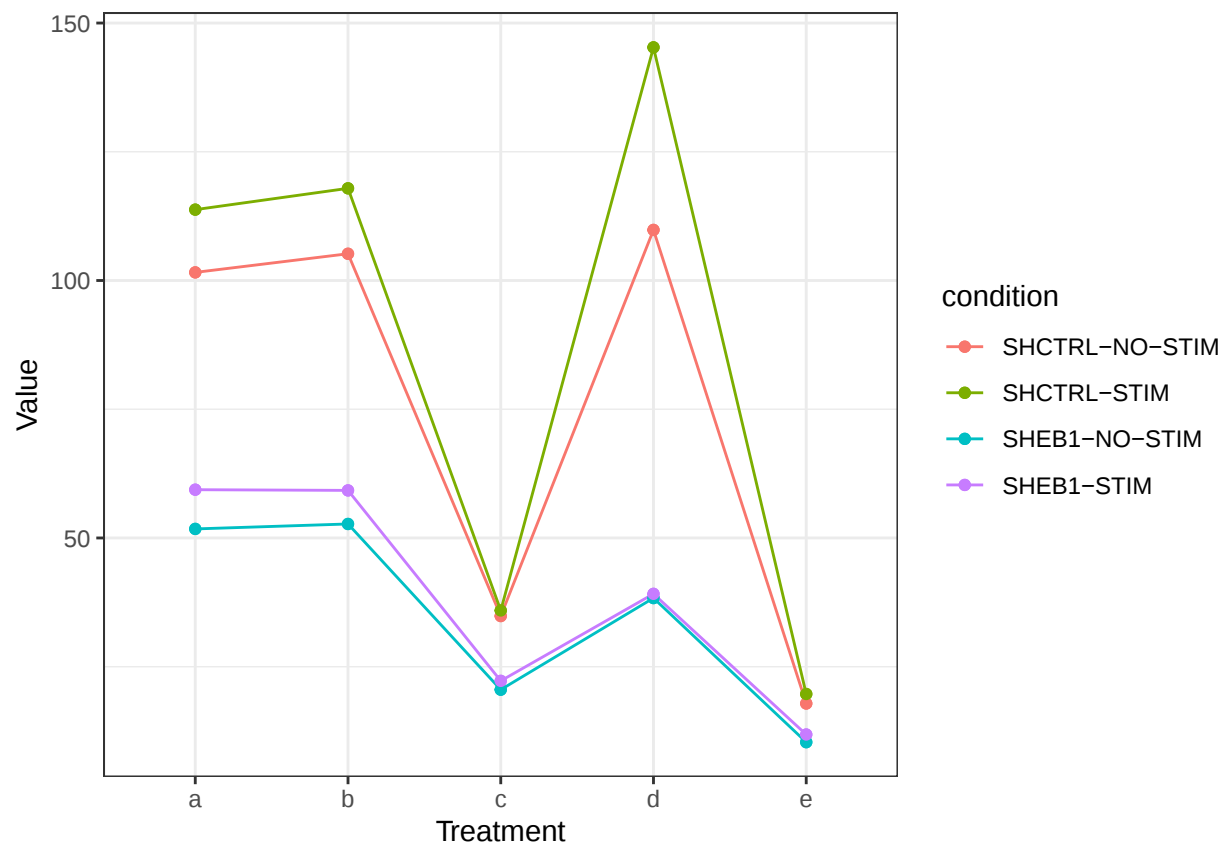
## (SHCTRL-NO-STIM) - (SHEB1-STIM)      70.675 5.15 280    57.352    83.998 13.710
## (SHCTRL-STIM) - (SHEB1-NO-STIM)      106.945 5.15 280    93.622   120.268 20.746
## (SHCTRL-STIM) - (SHEB1-STIM)         106.129 5.15 280    92.806   119.452 20.588
## (SHEB1-NO-STIM) - (SHEB1-STIM)        -0.815 5.15 280   -14.138    12.508 -0.158
## p.value
## <.0001
## <.0001
## <.0001
## <.0001
## <.0001
## 0.9986
##
## treatment = e:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)    -1.843 5.15 280   -15.165    11.480  -0.357
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)    7.506 5.15 280    -5.817    20.829   1.456
## (SHCTRL-NO-STIM) - (SHEB1-STIM)      6.022 5.15 280    -7.301    19.345   1.168
## (SHCTRL-STIM) - (SHEB1-NO-STIM)      9.349 5.15 280    -3.974    22.672   1.814
## (SHCTRL-STIM) - (SHEB1-STIM)        7.864 5.15 280    -5.459    21.187   1.526
## (SHEB1-NO-STIM) - (SHEB1-STIM)     -1.484 5.15 280   -14.807    11.839  -0.288
## p.value
## 0.9843
## 0.4656
## 0.6475
## 0.2691
## 0.4236
## 0.9917
##
## Confidence level used: 0.95
## Conf-level adjustment: tukey method for comparing a family of 4 estimates
## P value adjustment: tukey method for comparing a family of 4 estimates

```

```

emmip(m3, condition ~ treatment) +
  theme_bw()+
  xlab('Treatment') +
  ylab('Value')

```



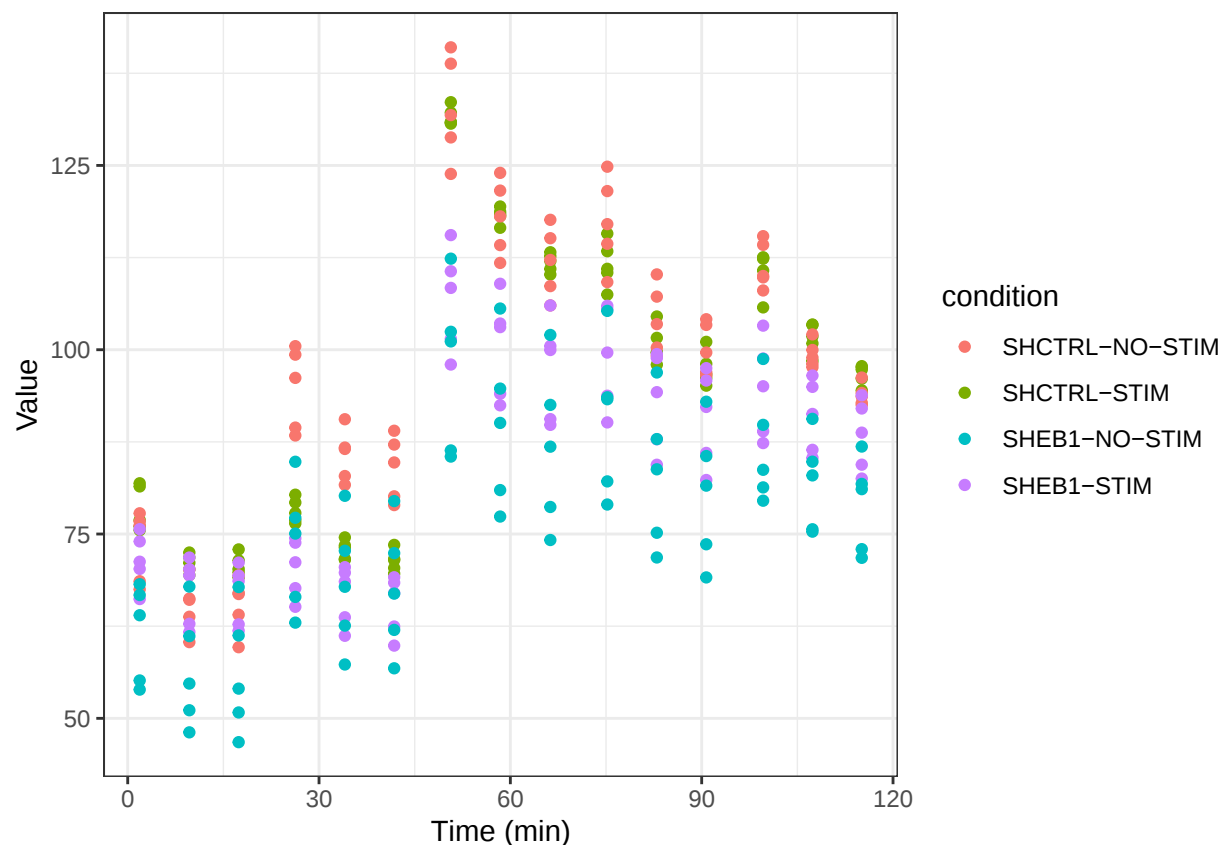
```
summary(pairs(emmeans(m3, "condition", by = "treatment", level = 0.95, infer = TRUE)))
```

```
## treatment = a:
## contrast      estimate    SE  df t.ratio p.value
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)   -12.186  5.15  280  -2.364  0.0866
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)   49.817  5.15  280   9.664 <.0001
## (SHCTRL-NO-STIM) - (SHEB1-STIM)     42.201  5.15  280   8.187 <.0001
## (SHCTRL-STIM) - (SHEB1-NO-STIM)     62.003  5.15  280  12.028 <.0001
## (SHCTRL-STIM) - (SHEB1-STIM)       54.386  5.15  280  10.550 <.0001
## (SHEB1-NO-STIM) - (SHEB1-STIM)     -7.617  5.15  280  -1.478  0.4524
##
## treatment = b:
## contrast      estimate    SE  df t.ratio p.value
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)   -12.706  5.15  280  -2.465  0.0678
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)   52.475  5.15  280  10.180 <.0001
## (SHCTRL-NO-STIM) - (SHEB1-STIM)     45.954  5.15  280   8.915 <.0001
## (SHCTRL-STIM) - (SHEB1-NO-STIM)     65.182  5.15  280  12.645 <.0001
## (SHCTRL-STIM) - (SHEB1-STIM)       58.660  5.15  280  11.379 <.0001
## (SHEB1-NO-STIM) - (SHEB1-STIM)     -6.521  5.15  280  -1.265  0.5859
##
## treatment = c:
## contrast      estimate    SE  df t.ratio p.value
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)    -1.073  5.15  280  -0.208  0.9968
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)   14.304  5.15  280   2.775  0.0299
## (SHCTRL-NO-STIM) - (SHEB1-STIM)     12.596  5.15  280   2.443  0.0714
```

```
## (SHCTRL-STIM) - (SHEB1-NO-STIM)      15.377 5.15 280    2.983 0.0163
## (SHCTRL-STIM) - (SHEB1-STIM)         13.669 5.15 280    2.652 0.0419
## (SHEB1-NO-STIM) - (SHEB1-STIM)       -1.708 5.15 280   -0.331 0.9874
##
## treatment = d:
## contrast                estimate    SE  df t.ratio p.value
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)   -35.454 5.15 280   -6.878 <.0001
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)   71.490 5.15 280   13.868 <.0001
## (SHCTRL-NO-STIM) - (SHEB1-STIM)      70.675 5.15 280   13.710 <.0001
## (SHCTRL-STIM) - (SHEB1-NO-STIM)     106.945 5.15 280   20.746 <.0001
## (SHCTRL-STIM) - (SHEB1-STIM)        106.129 5.15 280   20.588 <.0001
## (SHEB1-NO-STIM) - (SHEB1-STIM)       -0.815 5.15 280   -0.158 0.9986
##
## treatment = e:
## contrast                estimate    SE  df t.ratio p.value
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)    -1.843 5.15 280   -0.357 0.9843
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)    7.506 5.15 280    1.456 0.4656
## (SHCTRL-NO-STIM) - (SHEB1-STIM)       6.022 5.15 280    1.168 0.6475
## (SHCTRL-STIM) - (SHEB1-NO-STIM)      9.349 5.15 280    1.814 0.2691
## (SHCTRL-STIM) - (SHEB1-STIM)         7.864 5.15 280    1.526 0.4236
## (SHEB1-NO-STIM) - (SHEB1-STIM)      -1.484 5.15 280   -0.288 0.9917
##
## P value adjustment: tukey method for comparing a family of 4 estimates
```

MitoStress ECAR - Jurkat EB1 clones

```
ggplot(seahorse4, aes(time, value, colour=condition))+
  geom_point()+
  theme_bw()+
  xlab("Time (min)") +
  ylab('Value')
```



```
m4<-lm(value ~ treatment*condition, data=seahorse4)
summary(m4)
```

```
##
## Call:
## lm(formula = value ~ treatment * condition, data = seahorse4)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -17.1919  -5.2366  -0.9988   4.5113  20.9710
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      68.024     1.927   35.296 < 2e-16 ***
## treatmentb       20.115     2.725    7.380 1.81e-12 ***
## treatmentc       52.875     2.725   19.400 < 2e-16 ***
## treatmentd       39.171     2.725   14.372 < 2e-16 ***
## treatmente       33.541     2.725   12.306 < 2e-16 ***
## conditionSHCTRL-STIM      5.335     2.725    1.957 0.051286 .
## conditionSHEB1-NO-STIM    -9.923     2.725   -3.641 0.000324 ***
## conditionSHEB1-STIM      0.446     2.725    0.164 0.870139
## treatmentb:conditionSHCTRL-STIM -19.362     3.854   -5.023 9.07e-07 ***
## treatmentc:conditionSHCTRL-STIM  -5.671     3.854   -1.471 0.142345
## treatmentd:conditionSHCTRL-STIM  -9.297     3.854   -2.412 0.016508 *
## treatmente:conditionSHCTRL-STIM  -3.900     3.854   -1.012 0.312460
```

```
## treatmentb:conditionSHEB1-NO-STIM    -8.567      3.854   -2.223 0.027044 *
## treatmentc:conditionSHEB1-NO-STIM    -19.596      3.854   -5.084 6.77e-07 ***
## treatmentd:conditionSHEB1-NO-STIM     -12.497      3.854   -3.242 0.001329 **
## treatmente:conditionSHEB1-NO-STIM     -9.180      3.854   -2.382 0.017908 *
## treatmentb:conditionSHEB1-STIM        -21.067      3.854   -5.466 1.02e-07 ***
## treatmentc:conditionSHEB1-STIM        -19.815      3.854   -5.141 5.14e-07 ***
## treatmentd:conditionSHEB1-STIM        -13.397      3.854   -3.476 0.000590 ***
## treatmente:conditionSHEB1-STIM        -10.716      3.854   -2.780 0.005801 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.464 on 280 degrees of freedom
## Multiple R-squared:  0.8578, Adjusted R-squared:  0.8481
## F-statistic: 88.86 on 19 and 280 DF,  p-value: < 2.2e-16
```

```
summary(emmeans(m4, pairwise ~ condition|treatment, infer=T))
```

```
## $emmeans
## treatment = a:
##   condition    emmean    SE  df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM    68.0  1.93 280     64.2     71.8  35.296 <.0001
## SHCTRL-STIM       73.4  1.93 280     69.6     77.2  38.065 <.0001
## SHEB1-NO-STIM     58.1  1.93 280     54.3     61.9  30.147 <.0001
## SHEB1-STIM        68.5  1.93 280     64.7     72.3  35.528 <.0001
##
## treatment = b:
##   condition    emmean    SE  df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM    88.1  1.93 280     84.3     91.9  45.733 <.0001
## SHCTRL-STIM       74.1  1.93 280     70.3     77.9  38.455 <.0001
## SHEB1-NO-STIM     69.6  1.93 280     65.9     73.4  36.139 <.0001
## SHEB1-STIM        67.5  1.93 280     63.7     71.3  35.034 <.0001
##
## treatment = c:
##   condition    emmean    SE  df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM   120.9  1.93 280    117.1    124.7  62.732 <.0001
## SHCTRL-STIM      120.6  1.93 280    116.8    124.4  62.558 <.0001
## SHEB1-NO-STIM    91.4  1.93 280     87.6     95.2  47.415 <.0001
## SHEB1-STIM      101.5  1.93 280     97.7    105.3  52.682 <.0001
##
## treatment = d:
##   condition    emmean    SE  df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM   107.2  1.93 280    103.4    111.0  55.621 <.0001
## SHCTRL-STIM      103.2  1.93 280     99.4    107.0  53.565 <.0001
## SHEB1-NO-STIM    84.8  1.93 280     81.0     88.6  43.988 <.0001
## SHEB1-STIM       94.2  1.93 280     90.5     98.0  48.901 <.0001
##
## treatment = e:
##   condition    emmean    SE  df lower.CL upper.CL t.ratio p.value
## SHCTRL-NO-STIM   101.6  1.93 280     97.8    105.4  52.700 <.0001
## SHCTRL-STIM      103.0  1.93 280     99.2    106.8  53.445 <.0001
## SHEB1-NO-STIM    82.5  1.93 280     78.7     86.3  42.788 <.0001
## SHEB1-STIM       91.3  1.93 280     87.5     95.1  47.371 <.0001
##
## Confidence level used: 0.95
```

```

##
## $contrasts
## treatment = a:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)    -5.335  2.73  280    -12.38     1.71   -1.957
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)    9.923  2.73  280     2.88    16.97    3.641
## (SHCTRL-NO-STIM) - (SHEB1-STIM)    -0.446  2.73  280    -7.49     6.60   -0.164
## (SHCTRL-STIM) - (SHEB1-NO-STIM)    15.258  2.73  280     8.21    22.30    5.598
## (SHCTRL-STIM) - (SHEB1-STIM)     4.889  2.73  280    -2.16    11.93    1.794
## (SHEB1-NO-STIM) - (SHEB1-STIM)   -10.369  2.73  280   -17.41    -3.33   -3.805
## p.value
## 0.2068
## 0.0018
## 0.9984
## <.0001
## 0.2784
## 0.0010
##
## treatment = b:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)    14.027  2.73  280     6.98    21.07    5.146
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)   18.490  2.73  280    11.45    25.53    6.784
## (SHCTRL-NO-STIM) - (SHEB1-STIM)    20.621  2.73  280    13.58    27.67    7.566
## (SHCTRL-STIM) - (SHEB1-NO-STIM)     4.463  2.73  280    -2.58    11.51    1.638
## (SHCTRL-STIM) - (SHEB1-STIM)     6.594  2.73  280    -0.45    13.64    2.419
## (SHEB1-NO-STIM) - (SHEB1-STIM)     2.131  2.73  280    -4.91     9.17    0.782
## p.value
## <.0001
## <.0001
## <.0001
## 0.3592
## 0.0758
## 0.8627
##
## treatment = c:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)     0.336  2.73  280    -6.71     7.38    0.123
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)   29.520  2.73  280    22.48    36.56   10.831
## (SHCTRL-NO-STIM) - (SHEB1-STIM)    19.369  2.73  280    12.33    26.41    7.107
## (SHCTRL-STIM) - (SHEB1-NO-STIM)    29.184  2.73  280    22.14    36.23   10.708
## (SHCTRL-STIM) - (SHEB1-STIM)    19.033  2.73  280    11.99    26.08    6.983
## (SHEB1-NO-STIM) - (SHEB1-STIM)   -10.150  2.73  280   -17.19    -3.11   -3.724
## p.value
## 0.9993
## <.0001
## <.0001
## <.0001
## <.0001
## 0.0013
##
## treatment = d:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)     3.962  2.73  280    -3.08    11.01    1.454
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)   22.420  2.73  280    15.38    29.46    8.226

```

```

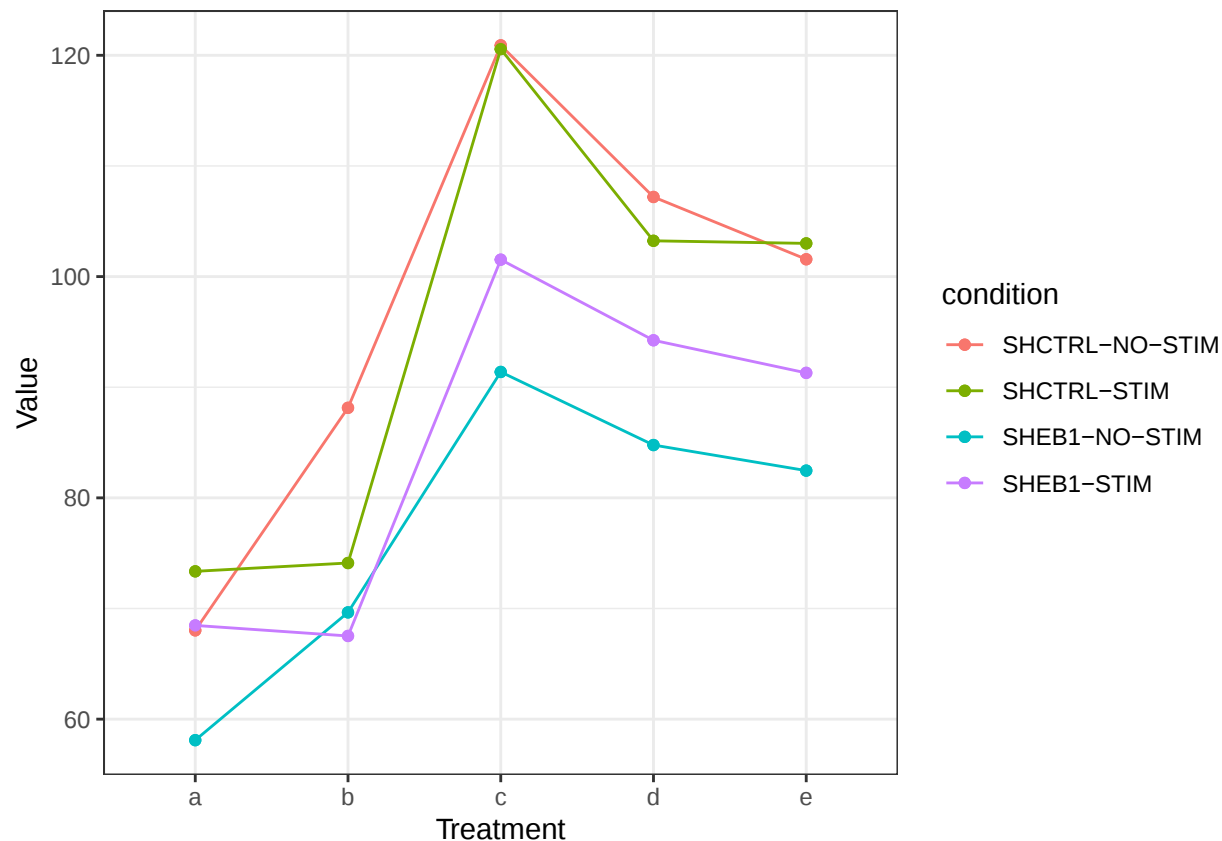
## (SHCTRL-NO-STIM) - (SHEB1-STIM)      12.951 2.73 280      5.91    20.00   4.752
## (SHCTRL-STIM) - (SHEB1-NO-STIM)      18.459 2.73 280     11.41    25.50   6.772
## (SHCTRL-STIM) - (SHEB1-STIM)         8.989 2.73 280      1.94    16.03   3.298
## (SHEB1-NO-STIM) - (SHEB1-STIM)      -9.470 2.73 280    -16.51    -2.43  -3.474
## p.value
## 0.4671
## <.0001
## <.0001
## <.0001
## 0.0060
## 0.0033
##
## treatment = e:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)    -1.435 2.73 280     -8.48     5.61  -0.526
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)   19.103 2.73 280     12.06    26.15   7.009
## (SHCTRL-NO-STIM) - (SHEB1-STIM)     10.270 2.73 280      3.23    17.31   3.768
## (SHCTRL-STIM) - (SHEB1-NO-STIM)     20.538 2.73 280     13.49    27.58   7.535
## (SHCTRL-STIM) - (SHEB1-STIM)        11.705 2.73 280      4.66    18.75   4.295
## (SHEB1-NO-STIM) - (SHEB1-STIM)     -8.833 2.73 280    -15.88    -1.79  -3.241
## p.value
## 0.9526
## <.0001
## 0.0011
## <.0001
## 0.0001
## 0.0073
##
## Confidence level used: 0.95
## Conf-level adjustment: tukey method for comparing a family of 4 estimates
## P value adjustment: tukey method for comparing a family of 4 estimates

```

```

emmip(m4, condition ~ treatment) +
  theme_bw()+
  xlab('Treatment') +
  ylab('Value')

```



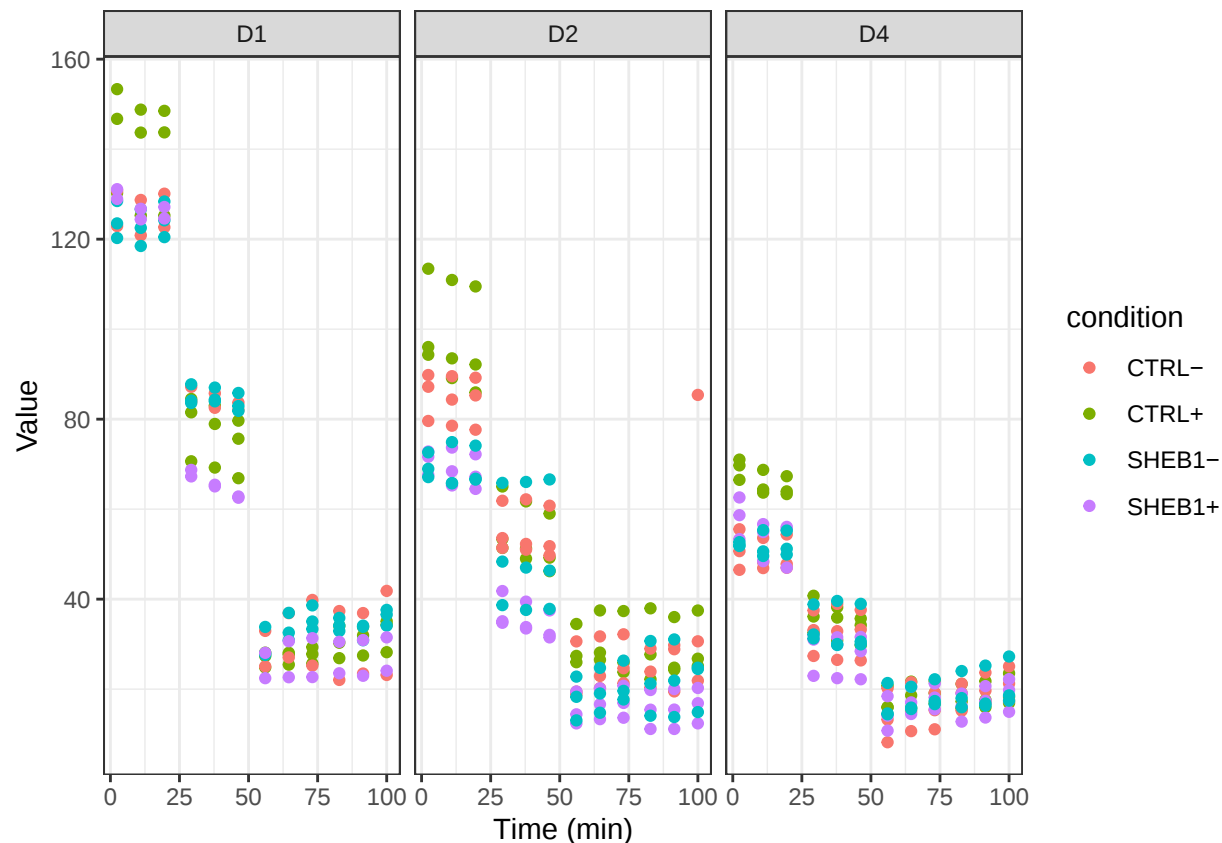
```
summary(pairs(emmeans(m4, "condition", by = "treatment", level = 0.95, infer = TRUE)))
```

```
## treatment = a:
## contrast                estimate    SE  df t.ratio p.value
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)   -5.335  2.73  280  -1.957  0.2068
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)   9.923  2.73  280   3.641  0.0018
## (SHCTRL-NO-STIM) - (SHEB1-STIM)    -0.446  2.73  280  -0.164  0.9984
## (SHCTRL-STIM) - (SHEB1-NO-STIM)   15.258  2.73  280   5.598 <.0001
## (SHCTRL-STIM) - (SHEB1-STIM)     4.889  2.73  280   1.794  0.2784
## (SHEB1-NO-STIM) - (SHEB1-STIM)   -10.369  2.73  280  -3.805  0.0010
##
## treatment = b:
## contrast                estimate    SE  df t.ratio p.value
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)   14.027  2.73  280   5.146 <.0001
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)  18.490  2.73  280   6.784 <.0001
## (SHCTRL-NO-STIM) - (SHEB1-STIM)   20.621  2.73  280   7.566 <.0001
## (SHCTRL-STIM) - (SHEB1-NO-STIM)    4.463  2.73  280   1.638  0.3592
## (SHCTRL-STIM) - (SHEB1-STIM)     6.594  2.73  280   2.419  0.0758
## (SHEB1-NO-STIM) - (SHEB1-STIM)    2.131  2.73  280   0.782  0.8627
##
## treatment = c:
## contrast                estimate    SE  df t.ratio p.value
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)    0.336  2.73  280   0.123  0.9993
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)  29.520  2.73  280  10.831 <.0001
## (SHCTRL-NO-STIM) - (SHEB1-STIM)   19.369  2.73  280   7.107 <.0001
```

```
## (SHCTRL-STIM) - (SHEB1-NO-STIM)      29.184 2.73 280 10.708 <.0001
## (SHCTRL-STIM) - (SHEB1-STIM)         19.033 2.73 280  6.983 <.0001
## (SHEB1-NO-STIM) - (SHEB1-STIM)      -10.150 2.73 280 -3.724 0.0013
##
## treatment = d:
## contrast      estimate    SE  df t.ratio p.value
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)      3.962 2.73 280  1.454 0.4671
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)    22.420 2.73 280  8.226 <.0001
## (SHCTRL-NO-STIM) - (SHEB1-STIM)      12.951 2.73 280  4.752 <.0001
## (SHCTRL-STIM) - (SHEB1-NO-STIM)      18.459 2.73 280  6.772 <.0001
## (SHCTRL-STIM) - (SHEB1-STIM)         8.989 2.73 280  3.298 0.0060
## (SHEB1-NO-STIM) - (SHEB1-STIM)      -9.470 2.73 280 -3.474 0.0033
##
## treatment = e:
## contrast      estimate    SE  df t.ratio p.value
## (SHCTRL-NO-STIM) - (SHCTRL-STIM)     -1.435 2.73 280 -0.526 0.9526
## (SHCTRL-NO-STIM) - (SHEB1-NO-STIM)    19.103 2.73 280  7.009 <.0001
## (SHCTRL-NO-STIM) - (SHEB1-STIM)      10.270 2.73 280  3.768 0.0011
## (SHCTRL-STIM) - (SHEB1-NO-STIM)      20.538 2.73 280  7.535 <.0001
## (SHCTRL-STIM) - (SHEB1-STIM)         11.705 2.73 280  4.295 0.0001
## (SHEB1-NO-STIM) - (SHEB1-STIM)      -8.833 2.73 280 -3.241 0.0073
##
## P value adjustment: tukey method for comparing a family of 4 estimates
```

Glycolysis Stress OCR - Lymphoblasts

```
ggplot(seahorse5, aes(time, value, colour=condition))+
  geom_point()+
  theme_bw()+
  xlab("Time (min)") +
  ylab('Value')+
  facet_wrap(~ind)
```



```
m5<-lmer(value ~ treatment*condition + (1|ind), data=seahorse5)
summary(m5)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: value ~ treatment * condition + (1 | ind)
## Data: seahorse5
##
## REML criterion at convergence: 3151
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.1796 -0.7549 -0.0583  0.6661  4.7421
##
## Random effects:
## Groups Name Variance Std.Dev.
## ind (Intercept) 327.7 18.10
## Residual 154.4 12.43
## Number of obs: 408, groups: ind, 3
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  84.42625   10.75470    2.22658   7.850 0.011537 *
## treatmentb  -28.10904    3.58690  389.99931  -7.837 4.45e-14 ***
## treatmentc  -59.35218    3.58690  389.99931 -16.547 < 2e-16 ***
```

```
## treatmentd          -54.75655    3.58690 389.99931 -15.266 < 2e-16 ***
## conditionCTRL+      17.39578    3.48767 390.00236  4.988 9.21e-07 ***
## conditionSHEB1-     -2.80067    3.48767 390.00236 -0.803 0.422451
## conditionSHEB1+     -3.68045    3.58690 389.99931 -1.026 0.305489
## treatmentb:conditionCTRL+ -18.51707  4.92973 389.99931 -3.756 0.000199 ***
## treatmentc:conditionCTRL+ -17.36122  4.92973 389.99931 -3.522 0.000479 ***
## treatmentd:conditionCTRL+ -20.66765  4.92973 389.99931 -4.192 3.42e-05 ***
## treatmentb:conditionSHEB1-  2.66090  4.92973 389.99931  0.540 0.589666
## treatmentc:conditionSHEB1-  1.12210  4.92973 389.99931  0.228 0.820062
## treatmentd:conditionSHEB1- -1.44113  4.92973 389.99931 -0.292 0.770186
## treatmentb:conditionSHEB1+ -10.06586  5.07265 389.99931 -1.984 0.047918 *
## treatmentc:conditionSHEB1+  0.03046  5.07265 389.99931  0.006 0.995212
## treatmentd:conditionSHEB1+ -4.27251  5.07265 389.99931 -0.842 0.400157
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation matrix not shown by default, as p = 16 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)          if you need it
```

```
summary(emmeans(m5, pairwise ~ condition|treatment, infer=T))
```

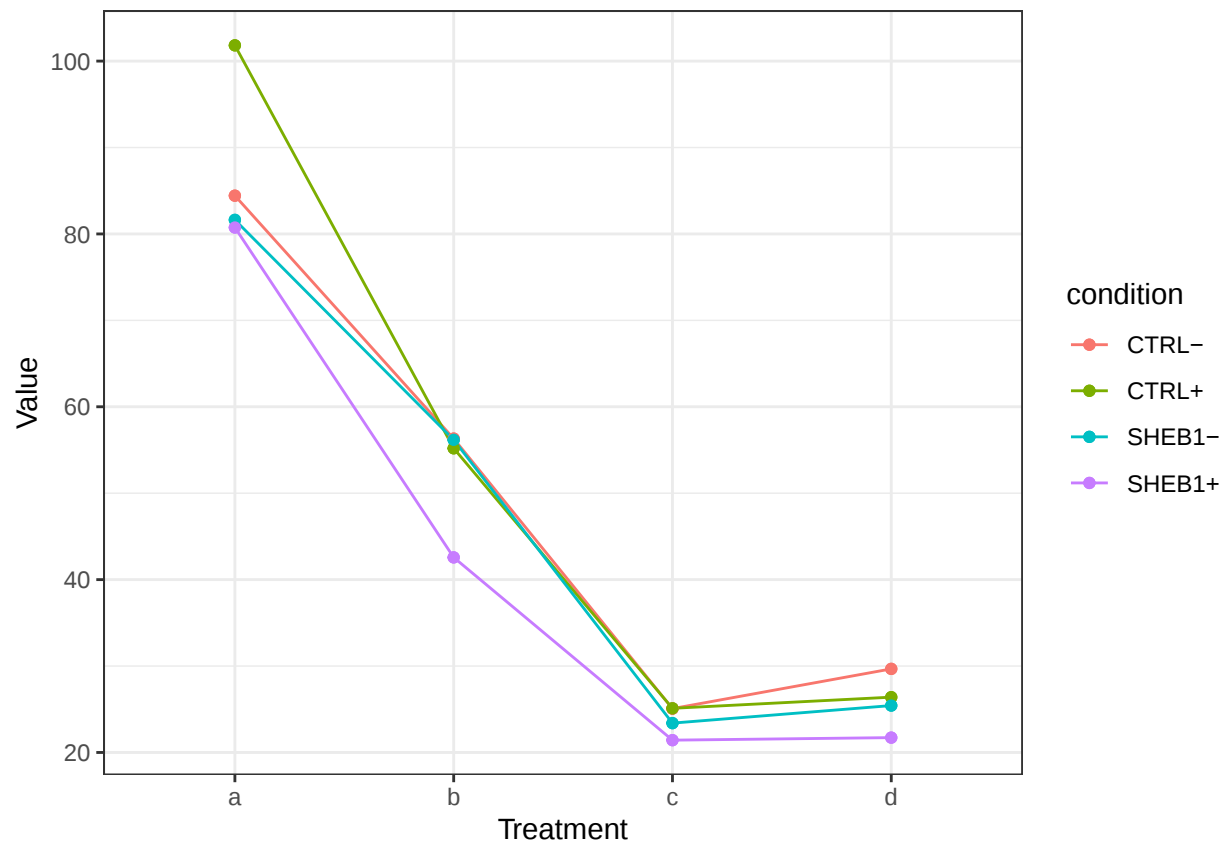
```
## Cannot use mode = "kenward-roger" because *pbkrtest* package is not installed
```

```
## $emmeans
## treatment = a:
##   condition emmean    SE    df lower.CL upper.CL t.ratio p.value
## CTRL-      84.4 10.8 2.23   42.385   126.5    7.850 0.0115
## CTRL+     101.8 10.7 2.20   59.467   144.2    9.498 0.0080
## SHEB1-     81.6 10.7 2.20   39.270   124.0    7.614 0.0128
## SHEB1+     80.7 10.8 2.23   38.704   122.8    7.508 0.0127
##
## treatment = b:
##   condition emmean    SE    df lower.CL upper.CL t.ratio p.value
## CTRL-      56.3 10.8 2.23   14.276    98.4    5.237 0.0274
## CTRL+      55.2 10.7 2.20   12.841    97.6    5.148 0.0292
## SHEB1-     56.2 10.7 2.20   13.822    98.5    5.240 0.0281
## SHEB1+     42.6 10.8 2.23    0.529    84.6    3.958 0.0488
##
## treatment = c:
##   condition emmean    SE    df lower.CL upper.CL t.ratio p.value
## CTRL-      25.1 10.8 2.23  -16.968    67.1    2.331 0.1321
## CTRL+      25.1 10.7 2.20  -17.247    67.5    2.342 0.1325
## SHEB1-     23.4 10.7 2.20  -18.960    65.8    2.182 0.1492
## SHEB1+     21.4 10.8 2.23  -20.618    63.5    1.992 0.1715
##
## treatment = d:
##   condition emmean    SE    df lower.CL upper.CL t.ratio p.value
## CTRL-      29.7 10.8 2.23  -12.372    71.7    2.759 0.0979
## CTRL+      26.4 10.7 2.20  -15.957    68.8    2.462 0.1215
## SHEB1-     25.4 10.7 2.20  -16.927    67.8    2.372 0.1297
## SHEB1+     21.7 10.8 2.23  -20.325    63.8    2.019 0.1678
```

```
##
## Degrees-of-freedom method: satterthwaite
## Confidence level used: 0.95
##
## $contrasts
## treatment = a:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio p.value
## (CTRL-) - (CTRL+) -17.3958 3.49 390 -26.39 -8.40 -4.988 <.0001
## (CTRL-) - (SHEB1-)  2.8007 3.49 390 -6.20 11.80 0.803 0.8530
## (CTRL-) - (SHEB1+)  3.6805 3.59 390 -5.57 12.94 1.026 0.7343
## (CTRL+) - (SHEB1-) 20.1965 3.38 390 11.47 28.92 5.972 <.0001
## (CTRL+) - (SHEB1+) 21.0762 3.49 390 12.08 30.07 6.043 <.0001
## (SHEB1-) - (SHEB1+) 0.8798 3.49 390 -8.12 9.88 0.252 0.9944
##
## treatment = b:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio p.value
## (CTRL-) - (CTRL+)  1.1213 3.49 390 -7.88 10.12 0.322 0.9885
## (CTRL-) - (SHEB1-) 0.1398 3.49 390 -8.86 9.14 0.040 1.0000
## (CTRL-) - (SHEB1+) 13.7463 3.59 390 4.49 23.00 3.832 0.0008
## (CTRL+) - (SHEB1-) -0.9815 3.38 390 -9.71 7.74 -0.290 0.9915
## (CTRL+) - (SHEB1+) 12.6250 3.49 390 3.63 21.62 3.620 0.0019
## (SHEB1-) - (SHEB1+) 13.6065 3.49 390 4.61 22.61 3.901 0.0006
##
## treatment = c:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio p.value
## (CTRL-) - (CTRL+) -0.0346 3.49 390 -9.03 8.96 -0.010 1.0000
## (CTRL-) - (SHEB1-) 1.6786 3.49 390 -7.32 10.68 0.481 0.9632
## (CTRL-) - (SHEB1+) 3.6500 3.59 390 -5.60 12.90 1.018 0.7392
## (CTRL+) - (SHEB1-) 1.7131 3.38 390 -7.01 10.44 0.507 0.9575
## (CTRL+) - (SHEB1+) 3.6846 3.49 390 -5.31 12.68 1.056 0.7162
## (SHEB1-) - (SHEB1+) 1.9714 3.49 390 -7.03 10.97 0.565 0.9423
##
## treatment = d:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio p.value
## (CTRL-) - (CTRL+)  3.2719 3.49 390 -5.73 12.27 0.938 0.7843
## (CTRL-) - (SHEB1-) 4.2418 3.49 390 -4.76 13.24 1.216 0.6169
## (CTRL-) - (SHEB1+) 7.9530 3.59 390 -1.30 17.21 2.217 0.1204
## (CTRL+) - (SHEB1-) 0.9699 3.38 390 -7.76 9.70 0.287 0.9918
## (CTRL+) - (SHEB1+) 4.6811 3.49 390 -4.32 13.68 1.342 0.5366
## (SHEB1-) - (SHEB1+) 3.7112 3.49 390 -5.29 12.71 1.064 0.7116
##
## Degrees-of-freedom method: satterthwaite
## Confidence level used: 0.95
## Conf-level adjustment: tukey method for comparing a family of 4 estimates
## P value adjustment: tukey method for comparing a family of 4 estimates
```

```
emmip(m5, condition ~ treatment) +
  theme_bw() +
  xlab('Treatment') +
  ylab('Value')
```

```
## Cannot use mode = "kenward-roger" because *pbkrtest* package is not installed
```



```
summary(pairs(emmeans(m5, "condition", by = "treatment", level = 0.95, infer = TRUE)))
```

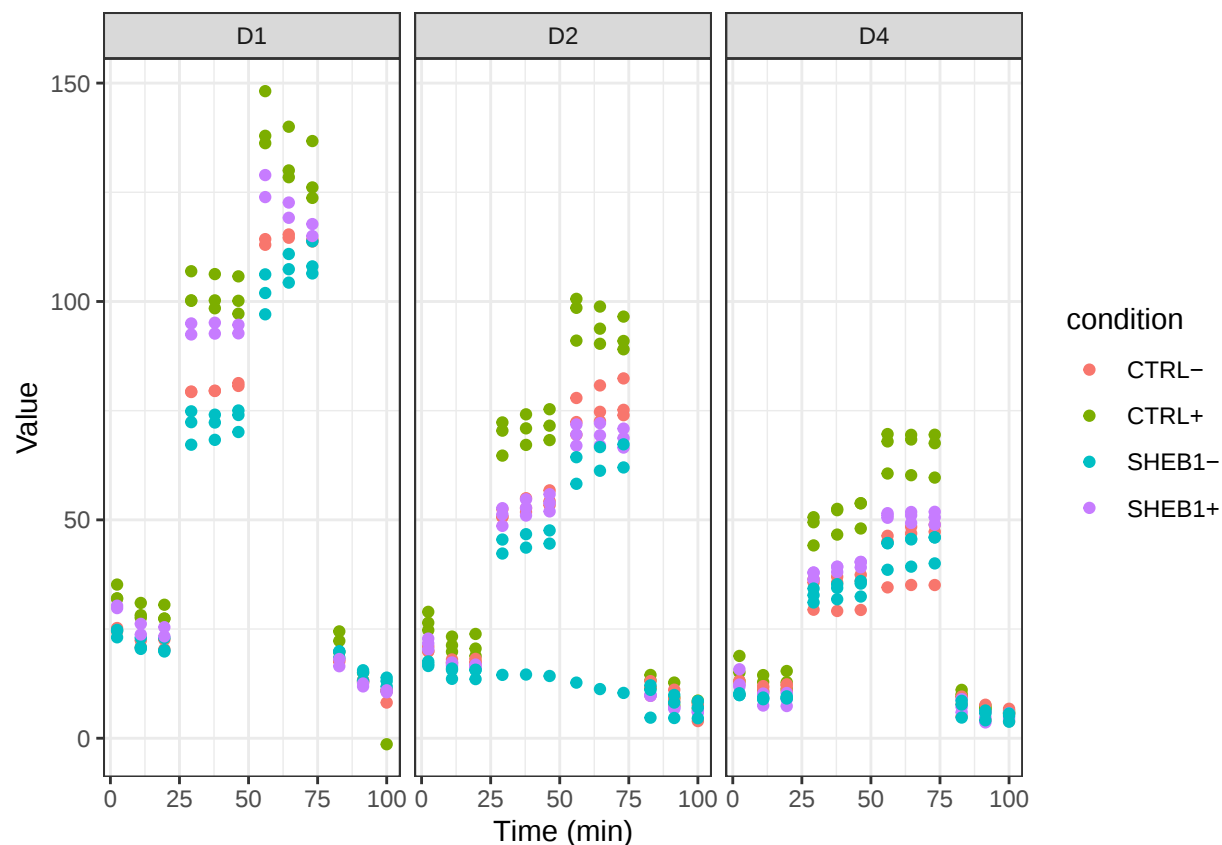
```
## Cannot use mode = "kenward-roger" because *pbkrtest* package is not installed
```

```
## treatment = a:
## contrast      estimate    SE  df t.ratio p.value
## (CTRL-) - (CTRL+) -17.3958 3.49 390  -4.988 <.0001
## (CTRL-) - (SHEB1-)  2.8007 3.49 390   0.803 0.8530
## (CTRL-) - (SHEB1+)  3.6805 3.59 390   1.026 0.7343
## (CTRL+) - (SHEB1-) 20.1965 3.38 390   5.972 <.0001
## (CTRL+) - (SHEB1+) 21.0762 3.49 390   6.043 <.0001
## (SHEB1-) - (SHEB1+)  0.8798 3.49 390   0.252 0.9944
##
## treatment = b:
## contrast      estimate    SE  df t.ratio p.value
## (CTRL-) - (CTRL+)  1.1213 3.49 390   0.322 0.9885
## (CTRL-) - (SHEB1-)  0.1398 3.49 390   0.040 1.0000
## (CTRL-) - (SHEB1+) 13.7463 3.59 390   3.832 0.0008
## (CTRL+) - (SHEB1-) -0.9815 3.38 390  -0.290 0.9915
## (CTRL+) - (SHEB1+) 12.6250 3.49 390   3.620 0.0019
## (SHEB1-) - (SHEB1+) 13.6065 3.49 390   3.901 0.0006
##
## treatment = c:
## contrast      estimate    SE  df t.ratio p.value
## (CTRL-) - (CTRL+) -0.0346 3.49 390  -0.010 1.0000
```

```
## (CTRL-) - (SHEB1-)      1.6786 3.49 390    0.481  0.9632
## (CTRL-) - (SHEB1+)      3.6500 3.59 390    1.018  0.7392
## (CTRL+) - (SHEB1-)      1.7131 3.38 390    0.507  0.9575
## (CTRL+) - (SHEB1+)      3.6846 3.49 390    1.056  0.7162
## (SHEB1-) - (SHEB1+)    1.9714 3.49 390    0.565  0.9423
##
## treatment = d:
## contrast      estimate    SE  df t.ratio p.value
## (CTRL-) - (CTRL+)    3.2719 3.49 390    0.938  0.7843
## (CTRL-) - (SHEB1-)    4.2418 3.49 390    1.216  0.6169
## (CTRL-) - (SHEB1+)    7.9530 3.59 390    2.217  0.1204
## (CTRL+) - (SHEB1-)    0.9699 3.38 390    0.287  0.9918
## (CTRL+) - (SHEB1+)    4.6811 3.49 390    1.342  0.5366
## (SHEB1-) - (SHEB1+)    3.7112 3.49 390    1.064  0.7116
##
## Degrees-of-freedom method: satterthwaite
## P value adjustment: tukey method for comparing a family of 4 estimates
```

Glycolysis Stress ECAR - Lymphoblasts

```
ggplot(seahorse6, aes(time, value, colour=condition))+
  geom_point()+
  theme_bw()+
  xlab("Time (min)") +
  ylab('Value')+
  facet_wrap(~ind)
```



```
m6<-lmer(value ~ treatment*condition + (1|ind), data=seahorse6)
summary(m6)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: value ~ treatment * condition + (1 | ind)
## Data: seahorse6
##
## REML criterion at convergence: 3127.5
##
## Scaled residuals:
## Min      1Q  Median      3Q      Max
## -4.2059 -0.6507  0.1572  0.6069  2.6581
##
## Random effects:
## Groups Name Variance Std.Dev.
## ind (Intercept) 307.6 17.54
## Residual 145.4 12.06
## Number of obs: 408, groups: ind, 3
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 19.3651 10.4207 2.2273 1.858 0.191121
## treatmentb 35.6755 3.4810 389.9992 10.249 < 2e-16 ***
## treatmentc 56.0404 3.4810 389.9992 16.099 < 2e-16 ***
```

```
## treatmentd          -7.8007      3.4810 389.9992 -2.241 0.025593 *
## conditionCTRL+       2.9938      3.3847 390.0023  0.885 0.376966
## conditionSHEB1-     -3.5795      3.3847 390.0023 -1.058 0.290910
## conditionSHEB1+       0.4347      3.4810 389.9992  0.125 0.900695
## treatmentb:conditionCTRL+ 16.0927    4.7842 389.9992  3.364 0.000845 ***
## treatmentc:conditionCTRL+ 19.7494    4.7842 389.9992  4.128 4.48e-05 ***
## treatmentd:conditionCTRL+ -3.8167    4.7842 389.9992 -0.798 0.425486
## treatmentb:conditionSHEB1- -4.5962    4.7842 389.9992 -0.961 0.337292
## treatmentc:conditionSHEB1- -6.6210    4.7842 389.9992 -1.384 0.167171
## treatmentd:conditionSHEB1-  1.7648    4.7842 389.9992  0.369 0.712413
## treatmentb:conditionSHEB1+  4.5828    4.9229 389.9992  0.931 0.352473
## treatmentc:conditionSHEB1+  1.8496    4.9229 389.9992  0.376 0.707335
## treatmentd:conditionSHEB1+ -1.2337    4.9229 389.9992 -0.251 0.802253
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation matrix not shown by default, as p = 16 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)          if you need it
```

```
summary(emmeans(m6, pairwise ~ condition|treatment, infer=T))
```

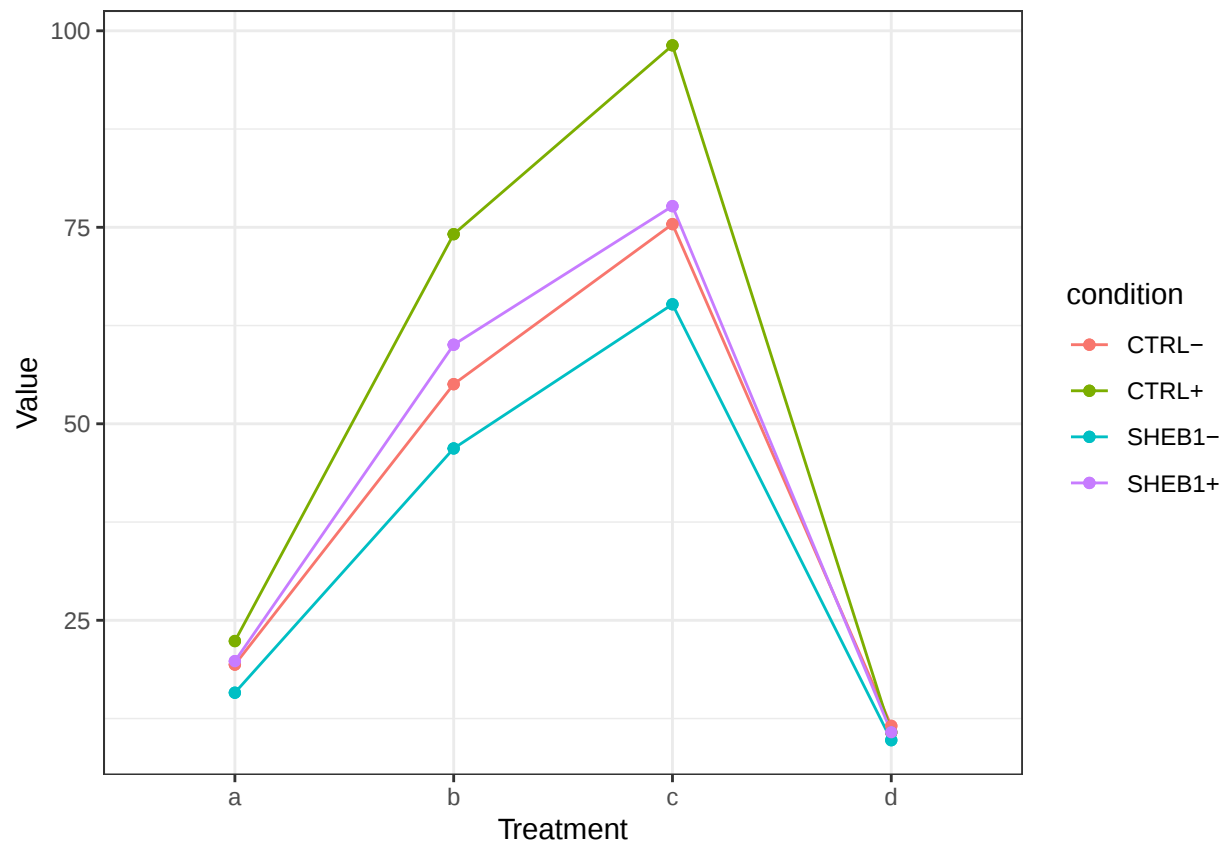
```
## Cannot use mode = "kenward-roger" because *pbkrtest* package is not installed
```

```
## $emmeans
## treatment = a:
##   condition emmean    SE    df lower.CL upper.CL t.ratio p.value
## CTRL-      19.37 10.4 2.23   -21.36    60.1    1.858 0.1911
## CTRL+      22.36 10.4 2.20   -18.67    63.4    2.152 0.1526
## SHEB1-     15.79 10.4 2.20   -25.24    56.8    1.520 0.2570
## SHEB1+     19.80 10.4 2.23   -20.93    60.5    1.900 0.1847
##
## treatment = b:
##   condition emmean    SE    df lower.CL upper.CL t.ratio p.value
## CTRL-      55.04 10.4 2.23    14.32    95.8    5.282 0.0269
## CTRL+      74.13 10.4 2.20    33.10   115.2    7.136 0.0147
## SHEB1-     46.86 10.4 2.20     5.84    87.9    4.512 0.0383
## SHEB1+     60.06 10.4 2.23    19.33   100.8    5.763 0.0224
##
## treatment = c:
##   condition emmean    SE    df lower.CL upper.CL t.ratio p.value
## CTRL-      75.41 10.4 2.23    34.68   116.1    7.236 0.0137
## CTRL+      98.15 10.4 2.20    57.12   139.2    9.448 0.0080
## SHEB1-     65.21 10.4 2.20    24.18   106.2    6.277 0.0193
## SHEB1+     77.69 10.4 2.23    36.96   118.4    7.455 0.0129
##
## treatment = d:
##   condition emmean    SE    df lower.CL upper.CL t.ratio p.value
## CTRL-      11.56 10.4 2.23   -29.16    52.3    1.110 0.3725
## CTRL+      10.74 10.4 2.20   -30.29    51.8    1.034 0.4012
## SHEB1-       9.75 10.4 2.20   -31.28    50.8    0.939 0.4392
## SHEB1+      10.77 10.4 2.23   -29.96    51.5    1.033 0.4005
```

```
##
## Degrees-of-freedom method: satterthwaite
## Confidence level used: 0.95
##
## $contrasts
## treatment = a:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio p.value
## (CTRL-) - (CTRL+)   -2.9938 3.38 390  -11.727    5.74  -0.885  0.8129
## (CTRL-) - (SHEB1-)   3.5795 3.38 390   -5.153   12.31   1.058  0.7155
## (CTRL-) - (SHEB1+)  -0.4346 3.48 390   -9.416    8.55  -0.125  0.9993
## (CTRL+) - (SHEB1-)   6.5733 3.28 390   -1.894   15.04   2.003  0.1886
## (CTRL+) - (SHEB1+)   2.5591 3.38 390   -6.174   11.29   0.756  0.8740
## (SHEB1-) - (SHEB1+) -4.0142 3.38 390  -12.747    4.72  -1.186  0.6361
##
## treatment = b:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio p.value
## (CTRL-) - (CTRL+)  -19.0865 3.38 390  -27.820  -10.35  -5.639 <.0001
## (CTRL-) - (SHEB1-)   8.1757 3.38 390   -0.557   16.91   2.416  0.0758
## (CTRL-) - (SHEB1+)  -5.0174 3.48 390  -13.999    3.96  -1.441  0.4743
## (CTRL+) - (SHEB1-)  27.2623 3.28 390   18.794   35.73   8.307 <.0001
## (CTRL+) - (SHEB1+)  14.0691 3.38 390    5.336   22.80   4.157  0.0002
## (SHEB1-) - (SHEB1+) -13.1932 3.38 390  -21.926   -4.46  -3.898  0.0007
##
## treatment = c:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio p.value
## (CTRL-) - (CTRL+)  -22.7432 3.38 390  -31.476  -14.01  -6.719 <.0001
## (CTRL-) - (SHEB1-)  10.2005 3.38 390    1.467   18.93   3.014  0.0146
## (CTRL-) - (SHEB1+)  -2.2842 3.48 390  -11.266    6.70  -0.656  0.9133
## (CTRL+) - (SHEB1-)  32.9437 3.28 390   24.476   41.41  10.038 <.0001
## (CTRL+) - (SHEB1+)  20.4590 3.38 390   11.726   29.19   6.045 <.0001
## (SHEB1-) - (SHEB1+) -12.4847 3.38 390  -21.218   -3.75  -3.689  0.0015
##
## treatment = d:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio p.value
## (CTRL-) - (CTRL+)   0.8229 3.38 390   -7.910    9.56   0.243  0.9949
## (CTRL-) - (SHEB1-)   1.8147 3.38 390   -6.918   10.55   0.536  0.9502
## (CTRL-) - (SHEB1+)   0.7990 3.48 390   -8.182    9.78   0.230  0.9957
## (CTRL+) - (SHEB1-)   0.9918 3.28 390   -7.476    9.46   0.302  0.9904
## (CTRL+) - (SHEB1+)  -0.0239 3.38 390   -8.757    8.71  -0.007  1.0000
## (SHEB1-) - (SHEB1+) -1.0157 3.38 390   -9.749    7.72  -0.300  0.9906
##
## Degrees-of-freedom method: satterthwaite
## Confidence level used: 0.95
## Conf-level adjustment: tukey method for comparing a family of 4 estimates
## P value adjustment: tukey method for comparing a family of 4 estimates
```

```
emmip(m6, condition ~ treatment) +
  theme_bw() +
  xlab('Treatment') +
  ylab('Value')
```

```
## Cannot use mode = "kenward-roger" because *pbkrtest* package is not installed
```



```
summary(pairs(emmeans(m6, "condition", by = "treatment", level = 0.95, infer = TRUE)))
```

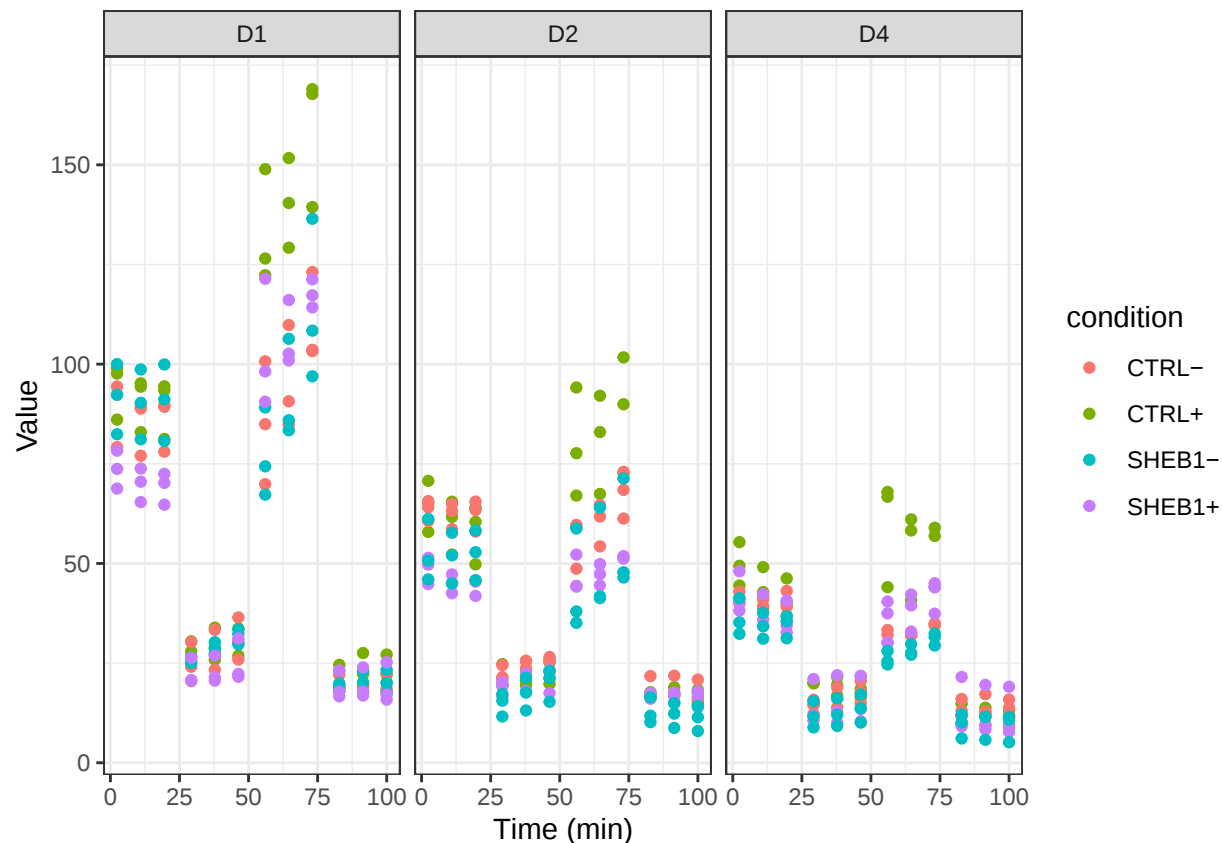
```
## Cannot use mode = "kenward-roger" because *pbkrtest* package is not installed
```

```
## treatment = a:
## contrast      estimate    SE  df t.ratio p.value
## (CTRL-) - (CTRL+)   -2.9938  3.38 390  -0.885  0.8129
## (CTRL-) - (SHEB1-)   3.5795  3.38 390   1.058  0.7155
## (CTRL-) - (SHEB1+)  -0.4346  3.48 390  -0.125  0.9993
## (CTRL+) - (SHEB1-)   6.5733  3.28 390   2.003  0.1886
## (CTRL+) - (SHEB1+)   2.5591  3.38 390   0.756  0.8740
## (SHEB1-) - (SHEB1+) -4.0142  3.38 390  -1.186  0.6361
##
## treatment = b:
## contrast      estimate    SE  df t.ratio p.value
## (CTRL-) - (CTRL+)  -19.0865  3.38 390  -5.639 <.0001
## (CTRL-) - (SHEB1-)   8.1757  3.38 390   2.416  0.0758
## (CTRL-) - (SHEB1+)  -5.0174  3.48 390  -1.441  0.4743
## (CTRL+) - (SHEB1-)  27.2623  3.28 390   8.307 <.0001
## (CTRL+) - (SHEB1+)  14.0691  3.38 390   4.157  0.0002
## (SHEB1-) - (SHEB1+) -13.1932  3.38 390  -3.898  0.0007
##
## treatment = c:
## contrast      estimate    SE  df t.ratio p.value
## (CTRL-) - (CTRL+)  -22.7432  3.38 390  -6.719 <.0001
```

```
## (CTRL-) - (SHEB1-)    10.2005 3.38 390    3.014 0.0146
## (CTRL-) - (SHEB1+)   -2.2842 3.48 390   -0.656 0.9133
## (CTRL+) - (SHEB1-)   32.9437 3.28 390   10.038 <.0001
## (CTRL+) - (SHEB1+)   20.4590 3.38 390    6.045 <.0001
## (SHEB1-) - (SHEB1+) -12.4847 3.38 390   -3.689 0.0015
##
## treatment = d:
## contrast            estimate    SE  df t.ratio p.value
## (CTRL-) - (CTRL+)      0.8229 3.38 390    0.243 0.9949
## (CTRL-) - (SHEB1-)     1.8147 3.38 390    0.536 0.9502
## (CTRL-) - (SHEB1+)     0.7990 3.48 390    0.230 0.9957
## (CTRL+) - (SHEB1-)     0.9918 3.28 390    0.302 0.9904
## (CTRL+) - (SHEB1+)    -0.0239 3.38 390   -0.007 1.0000
## (SHEB1-) - (SHEB1+)   -1.0157 3.38 390   -0.300 0.9906
##
## Degrees-of-freedom method: satterthwaite
## P value adjustment: tukey method for comparing a family of 4 estimates
```

MitoStress OCR - Lymphoblasts

```
ggplot(seahorse7, aes(time, value, colour=condition))+
  geom_point()+
  theme_bw()+
  xlab("Time (min)") +
  ylab('Value')+
  facet_wrap(~ind)
```



```
m7<-lmer(value ~ treatment*condition + (1|ind), data=seahorse7)
summary(m7)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: value ~ treatment * condition + (1 | ind)
## Data: seahorse7
##
## REML criterion at convergence: 3405.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.8339 -0.7952  0.1120  0.5584  4.4758
##
## Random effects:
## Groups Name Variance Std.Dev.
## ind (Intercept) 305.6 17.48
## Residual 180.3 13.43
## Number of obs: 432, groups: ind, 3
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept)    63.3326    10.4182  2.2523   6.079  0.01942 *
## treatmentb   -40.6075     3.6543 414.0000 -11.112 < 2e-16 ***
## treatmentc     0.3034     3.6543 414.0000  0.083  0.93386
```

```
## treatmentd          -45.8667      3.6543 414.0000 -12.551 < 2e-16 ***
## conditionCTRL+       2.4137      3.6543 414.0000  0.661 0.50930
## conditionSHEB1-      -4.0229      3.6543 414.0000 -1.101 0.27160
## conditionSHEB1+     -11.5162      3.6543 414.0000 -3.151 0.00174 **
## treatmentb:conditionCTRL+ -1.8503      5.1680 414.0000 -0.358 0.72051
## treatmentc:conditionCTRL+ 28.0084      5.1680 414.0000  5.420 1.02e-07 ***
## treatmentd:conditionCTRL+ -2.6378      5.1680 414.0000 -0.510 0.61003
## treatmentb:conditionSHEB1-  0.8923      5.1680 414.0000  0.173 0.86301
## treatmentc:conditionSHEB1- -2.2532      5.1680 414.0000 -0.436 0.66308
## treatmentd:conditionSHEB1-  0.3109      5.1680 414.0000  0.060 0.95205
## treatmentb:conditionSHEB1+  8.3169      5.1680 414.0000  1.609 0.10831
## treatmentc:conditionSHEB1+ 13.2487      5.1680 414.0000  2.564 0.01071 *
## treatmentd:conditionSHEB1+ 10.2159      5.1680 414.0000  1.977 0.04873 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation matrix not shown by default, as p = 16 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)      if you need it
```

```
summary(emmeans(m7, pairwise ~ condition|treatment, infer=T))
```

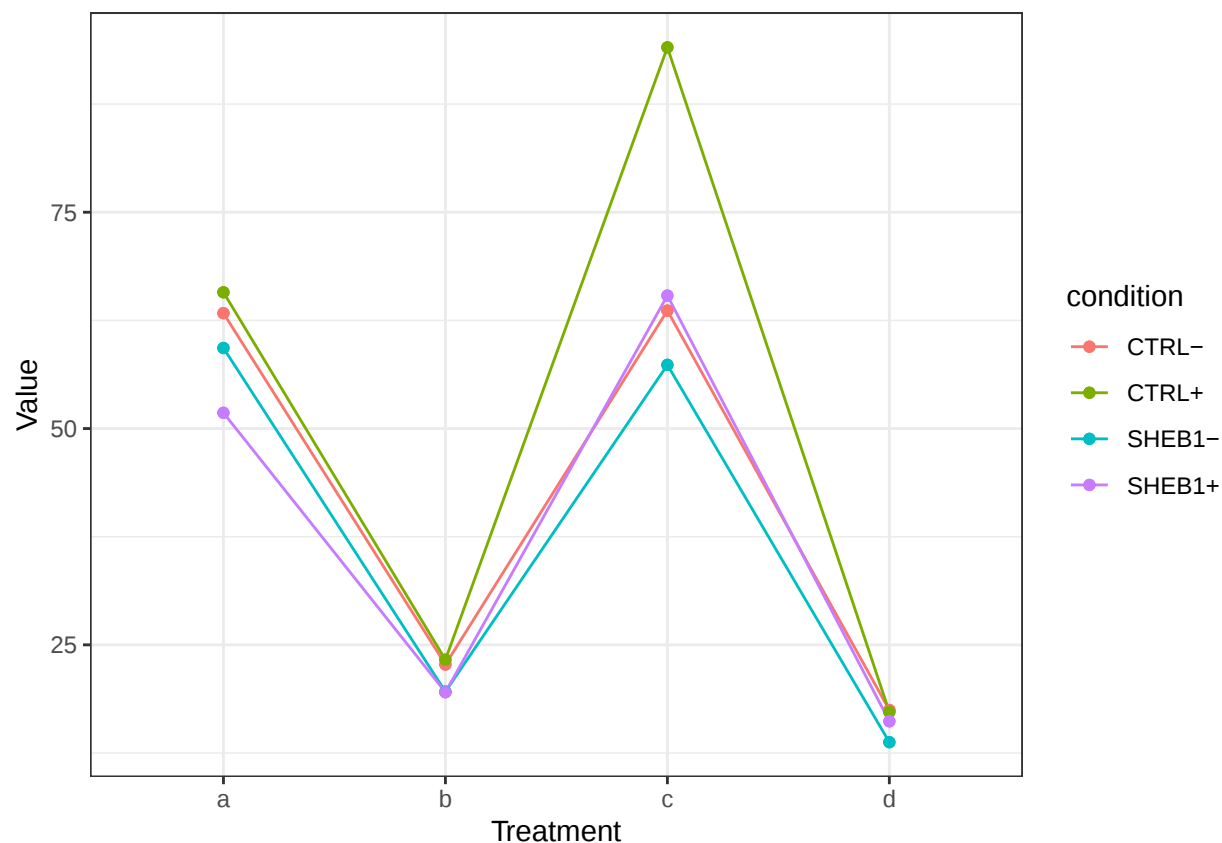
```
## Cannot use mode = "kenward-roger" because *pbkrtest* package is not installed
```

```
## $emmeans
## treatment = a:
##   condition emmean    SE    df lower.CL upper.CL t.ratio p.value
## CTRL-      63.3  10.4  2.25    23.0    103.7   6.079 0.0194
## CTRL+      65.7  10.4  2.25    25.4    106.1   6.311 0.0179
## SHEB1-     59.3  10.4  2.25    19.0     99.7   5.693 0.0224
## SHEB1+     51.8  10.4  2.25    11.5     92.2   4.974 0.0298
##
## treatment = b:
##   condition emmean    SE    df lower.CL upper.CL t.ratio p.value
## CTRL-      22.7  10.4  2.25   -17.6     63.1   2.181 0.1465
## CTRL+      23.3  10.4  2.25   -17.1     63.6   2.235 0.1406
## SHEB1-     19.6  10.4  2.25   -20.7     59.9   1.881 0.1863
## SHEB1+     19.5  10.4  2.25   -20.8     59.9   1.874 0.1873
##
## treatment = c:
##   condition emmean    SE    df lower.CL upper.CL t.ratio p.value
## CTRL-      63.6  10.4  2.25    23.3    104.0   6.108 0.0192
## CTRL+      94.1  10.4  2.25    53.7    134.4   9.028 0.0082
## SHEB1-     57.4  10.4  2.25    17.0     97.7   5.506 0.0240
## SHEB1+     65.4  10.4  2.25    25.0    105.7   6.274 0.0181
##
## treatment = d:
##   condition emmean    SE    df lower.CL upper.CL t.ratio p.value
## CTRL-      17.5  10.4  2.25   -22.9     57.8   1.676 0.2215
## CTRL+      17.2  10.4  2.25   -23.1     57.6   1.655 0.2257
## SHEB1-     13.8  10.4  2.25   -26.6     54.1   1.320 0.3049
## SHEB1+     16.2  10.4  2.25   -24.2     56.5   1.552 0.2472
```

```
##
## Degrees-of-freedom method: satterthwaite
## Confidence level used: 0.95
##
## $contrasts
## treatment = a:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio p.value
## (CTRL-) - (CTRL+)   -2.4137 3.65 414   -11.84    7.01  -0.661  0.9118
## (CTRL-) - (SHEB1-)   4.0229 3.65 414    -5.40   13.45   1.101  0.6892
## (CTRL-) - (SHEB1+)  11.5162 3.65 414     2.09   20.94   3.151  0.0094
## (CTRL+) - (SHEB1-)   6.4366 3.65 414    -2.99   15.86   1.761  0.2936
## (CTRL+) - (SHEB1+)  13.9299 3.65 414     4.50   23.36   3.812  0.0009
## (SHEB1-) - (SHEB1+)  7.4932 3.65 414    -1.93   16.92   2.051  0.1714
##
## treatment = b:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio p.value
## (CTRL-) - (CTRL+)   -0.5635 3.65 414    -9.99    8.86  -0.154  0.9987
## (CTRL-) - (SHEB1-)   3.1307 3.65 414    -6.30   12.56   0.857  0.8271
## (CTRL-) - (SHEB1+)   3.1992 3.65 414    -6.23   12.63   0.875  0.8176
## (CTRL+) - (SHEB1-)   3.6941 3.65 414    -5.73   13.12   1.011  0.7432
## (CTRL+) - (SHEB1+)   3.7627 3.65 414    -5.66   13.19   1.030  0.7321
## (SHEB1-) - (SHEB1+)  0.0686 3.65 414    -9.36    9.49   0.019  1.0000
##
## treatment = c:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio p.value
## (CTRL-) - (CTRL+)  -30.4221 3.65 414   -39.85  -21.00  -8.325 <.0001
## (CTRL-) - (SHEB1-)   6.2761 3.65 414    -3.15   15.70   1.717  0.3159
## (CTRL-) - (SHEB1+)  -1.7325 3.65 414   -11.16    7.69  -0.474  0.9648
## (CTRL+) - (SHEB1-)  36.6981 3.65 414   27.27   46.12  10.042 <.0001
## (CTRL+) - (SHEB1+)  28.6896 3.65 414   19.26   38.12   7.851 <.0001
## (SHEB1-) - (SHEB1+) -8.0086 3.65 414   -17.43    1.42  -2.192  0.1273
##
## treatment = d:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio p.value
## (CTRL-) - (CTRL+)   0.2241 3.65 414    -9.20    9.65   0.061  0.9999
## (CTRL-) - (SHEB1-)   3.7120 3.65 414    -5.71   13.14   1.016  0.7403
## (CTRL-) - (SHEB1+)   1.3002 3.65 414    -8.13   10.73   0.356  0.9845
## (CTRL+) - (SHEB1-)   3.4878 3.65 414    -5.94   12.91   0.954  0.7753
## (CTRL+) - (SHEB1+)   1.0761 3.65 414    -8.35   10.50   0.294  0.9911
## (SHEB1-) - (SHEB1+) -2.4117 3.65 414   -11.84    7.01  -0.660  0.9120
##
## Degrees-of-freedom method: satterthwaite
## Confidence level used: 0.95
## Conf-level adjustment: tukey method for comparing a family of 4 estimates
## P value adjustment: tukey method for comparing a family of 4 estimates
```

```
emmip(m7, condition ~ treatment) +
  theme_bw() +
  xlab('Treatment') +
  ylab('Value')
```

```
## Cannot use mode = "kenward-roger" because *pbkrtest* package is not installed
```



```
summary(pairs(emmeans(m7, "condition", by = "treatment", level = 0.95, infer = TRUE)))
```

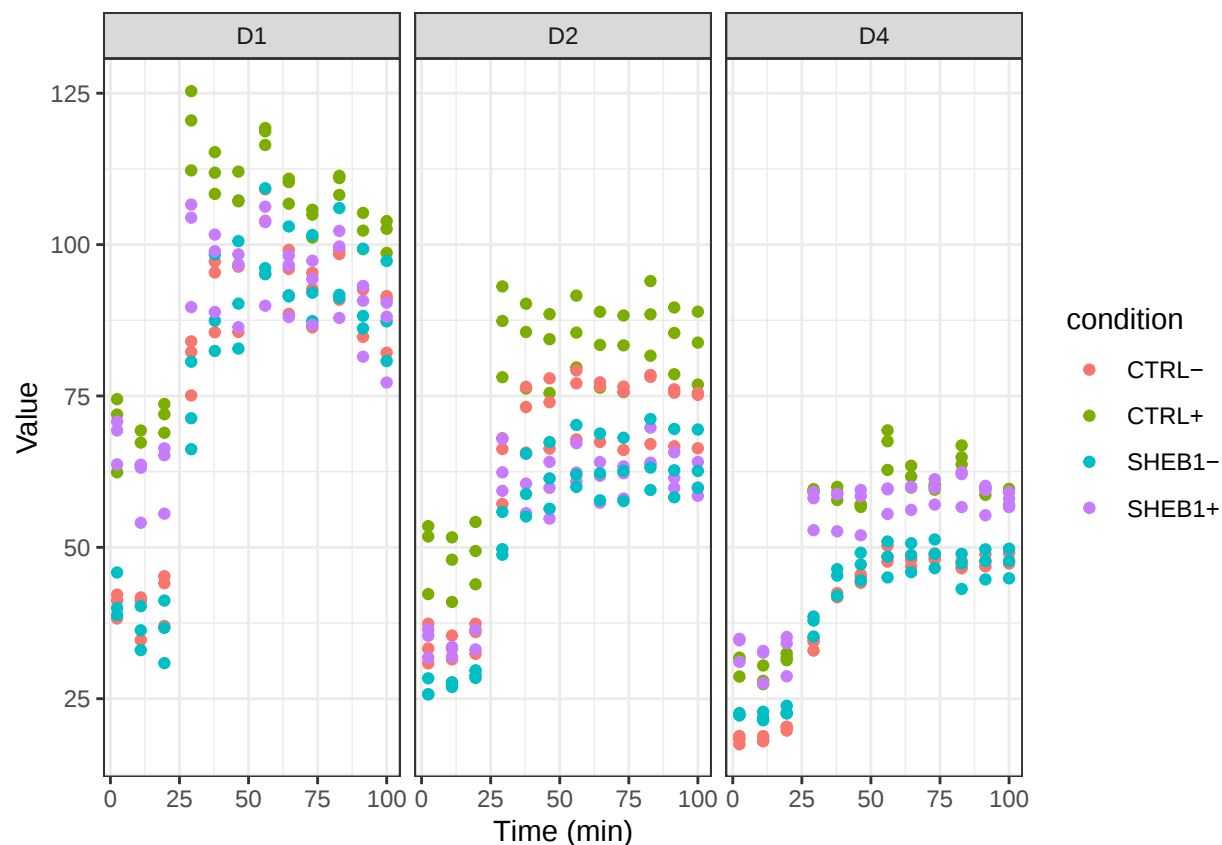
```
## Cannot use mode = "kenward-roger" because *pbkrtest* package is not installed
```

```
## treatment = a:
## contrast      estimate    SE  df t.ratio p.value
## (CTRL-) - (CTRL+)   -2.4137 3.65 414  -0.661  0.9118
## (CTRL-) - (SHEB1-)   4.0229 3.65 414   1.101  0.6892
## (CTRL-) - (SHEB1+)  11.5162 3.65 414   3.151  0.0094
## (CTRL+) - (SHEB1-)   6.4366 3.65 414   1.761  0.2936
## (CTRL+) - (SHEB1+)  13.9299 3.65 414   3.812  0.0009
## (SHEB1-) - (SHEB1+)  7.4932 3.65 414   2.051  0.1714
##
## treatment = b:
## contrast      estimate    SE  df t.ratio p.value
## (CTRL-) - (CTRL+)   -0.5635 3.65 414  -0.154  0.9987
## (CTRL-) - (SHEB1-)   3.1307 3.65 414   0.857  0.8271
## (CTRL-) - (SHEB1+)   3.1992 3.65 414   0.875  0.8176
## (CTRL+) - (SHEB1-)   3.6941 3.65 414   1.011  0.7432
## (CTRL+) - (SHEB1+)   3.7627 3.65 414   1.030  0.7321
## (SHEB1-) - (SHEB1+)  0.0686 3.65 414   0.019  1.0000
##
## treatment = c:
## contrast      estimate    SE  df t.ratio p.value
## (CTRL-) - (CTRL+)  -30.4221 3.65 414  -8.325  <.0001
```

```
## (CTRL-) - (SHEB1-)      6.2761 3.65 414    1.717  0.3159
## (CTRL-) - (SHEB1+)     -1.7325 3.65 414   -0.474  0.9648
## (CTRL+) - (SHEB1-)     36.6981 3.65 414   10.042 <.0001
## (CTRL+) - (SHEB1+)     28.6896 3.65 414    7.851 <.0001
## (SHEB1-) - (SHEB1+)    -8.0086 3.65 414   -2.192  0.1273
##
## treatment = d:
## contrast      estimate    SE  df t.ratio p.value
## (CTRL-) - (CTRL+)    0.2241 3.65 414    0.061  0.9999
## (CTRL-) - (SHEB1-)    3.7120 3.65 414    1.016  0.7403
## (CTRL-) - (SHEB1+)    1.3002 3.65 414    0.356  0.9845
## (CTRL+) - (SHEB1-)    3.4878 3.65 414    0.954  0.7753
## (CTRL+) - (SHEB1+)    1.0761 3.65 414    0.294  0.9911
## (SHEB1-) - (SHEB1+)  -2.4117 3.65 414   -0.660  0.9120
##
## Degrees-of-freedom method: satterthwaite
## P value adjustment: tukey method for comparing a family of 4 estimates
```

MitoStress ECAR - Lymphoblasts

```
ggplot(seahorse8, aes(time, value, colour=condition))+
  geom_point()+
  theme_bw()+
  xlab("Time (min)") +
  ylab('Value')+
  facet_wrap(~ind)
```



```
m8<-lmer(value ~ treatment*condition + (1|ind), data=seahorse8)
summary(m8)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: value ~ treatment * condition + (1 | ind)
## Data: seahorse8
##
## REML criterion at convergence: 2892.2
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.75001 -0.75368 -0.04085  0.76579  2.58247
##
## Random effects:
## Groups Name Variance Std.Dev.
## ind (Intercept) 401.94 20.048
## Residual 52.15 7.221
## Number of obs: 432, groups: ind, 3
##
## Fixed effects:
##
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 31.226 11.658 2.054 2.678 0.1125
## treatmentb 34.931 1.965 414.000 17.773 < 2e-16 ***
## treatmentc 41.544 1.965 414.000 21.138 < 2e-16 ***
```

```
## treatmentd      39.551      1.965 414.000  20.124 < 2e-16 ***
## conditionCTRL+  18.134      1.965 414.000   9.227 < 2e-16 ***
## conditionSHEB1- -1.823      1.965 414.000  -0.928  0.3541
## conditionSHEB1+ 11.716      1.965 414.000   5.961 5.37e-09 ***
## treatmentb:conditionCTRL+  1.068      2.779 414.000   0.384  0.7010
## treatmentc:conditionCTRL+ -5.290      2.779 414.000  -1.903  0.0577 .
## treatmentd:conditionCTRL+ -5.330      2.779 414.000  -1.918  0.0558 .
## treatmentb:conditionSHEB1- -2.659      2.779 414.000  -0.957  0.3393
## treatmentc:conditionSHEB1- -1.555      2.779 414.000  -0.560  0.5761
## treatmentd:conditionSHEB1- -1.240      2.779 414.000  -0.446  0.6557
## treatmentb:conditionSHEB1+ -6.328      2.779 414.000  -2.277  0.0233 *
## treatmentc:conditionSHEB1+ -12.352      2.779 414.000  -4.444 1.14e-05 ***
## treatmentd:conditionSHEB1+ -11.836      2.779 414.000  -4.258 2.55e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Correlation matrix not shown by default, as p = 16 > 12.
## Use print(x, correlation=TRUE) or
##      vcov(x)      if you need it
```

```
summary(emmeans(m8, pairwise ~ condition|treatment, infer=T))
```

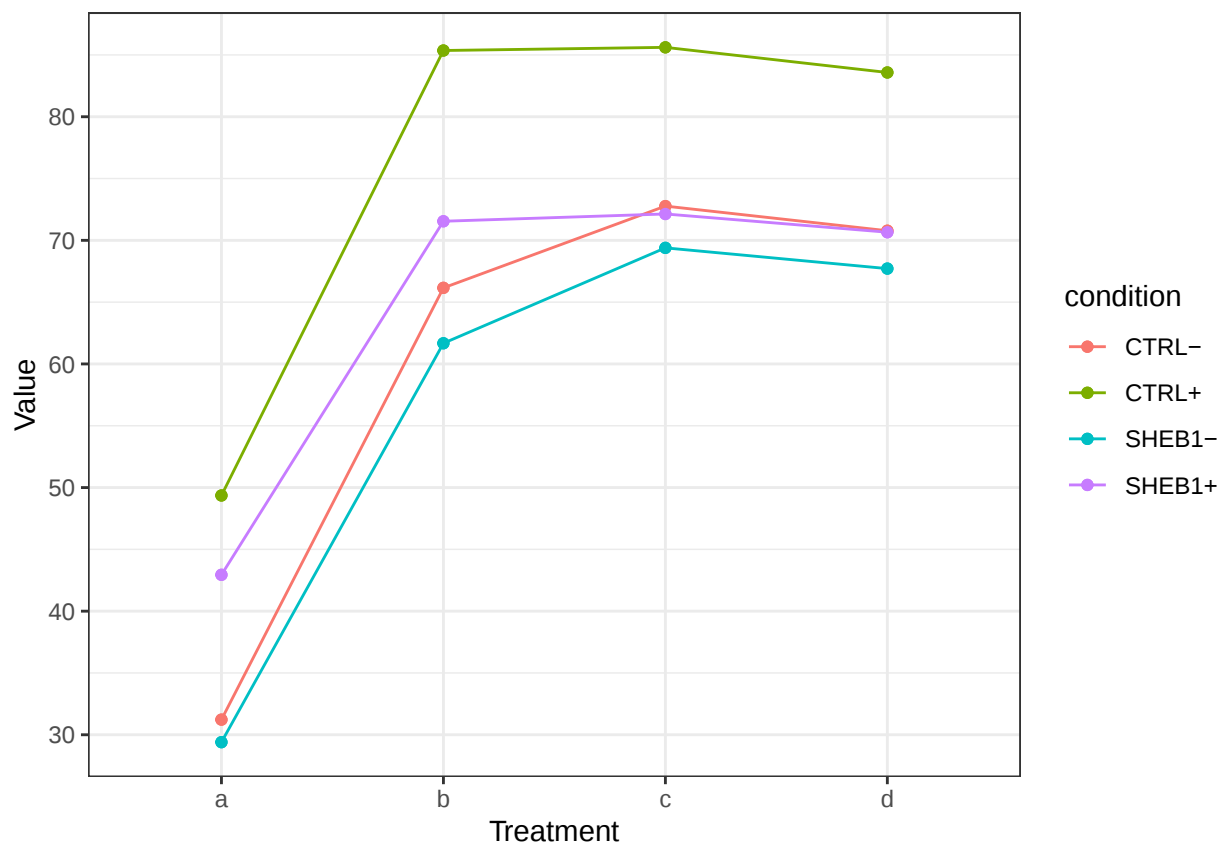
```
## Cannot use mode = "kenward-roger" because *pbkrtest* package is not installed
```

```
## $emmeans
## treatment = a:
##   condition emmean    SE    df lower.CL upper.CL t.ratio p.value
## CTRL-      31.2 11.7 2.05   -17.68    80.1    2.678 0.1125
## CTRL+      49.4 11.7 2.05    0.45    98.3    4.234 0.0491
## SHEB1-     29.4 11.7 2.05   -19.51    78.3    2.522 0.1245
## SHEB1+     42.9 11.7 2.05    -5.97    91.9    3.683 0.0638
##
## treatment = b:
##   condition emmean    SE    df lower.CL upper.CL t.ratio p.value
## CTRL-      66.2 11.7 2.05    17.25   115.1    5.675 0.0279
## CTRL+      85.4 11.7 2.05    36.45   134.3    7.322 0.0169
## SHEB1-     61.7 11.7 2.05    12.76   110.6    5.290 0.0320
## SHEB1+     71.5 11.7 2.05    22.63   120.5    6.137 0.0239
##
## treatment = c:
##   condition emmean    SE    df lower.CL upper.CL t.ratio p.value
## CTRL-      72.8 11.7 2.05    23.86   121.7    6.242 0.0231
## CTRL+      85.6 11.7 2.05    36.70   134.5    7.344 0.0168
## SHEB1-     69.4 11.7 2.05    20.48   118.3    5.952 0.0254
## SHEB1+     72.1 11.7 2.05    23.22   121.0    6.187 0.0235
##
## treatment = d:
##   condition emmean    SE    df lower.CL upper.CL t.ratio p.value
## CTRL-      70.8 11.7 2.05    21.87   119.7    6.071 0.0244
## CTRL+      83.6 11.7 2.05    34.67   132.5    7.169 0.0176
## SHEB1-     67.7 11.7 2.05    18.80   116.6    5.808 0.0267
## SHEB1+     70.7 11.7 2.05    21.75   119.6    6.061 0.0245
```

```
##
## Degrees-of-freedom method: satterthwaite
## Confidence level used: 0.95
##
## $contrasts
## treatment = a:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio p.value
## (CTRL-) - (CTRL+)   -18.134 1.97 414  -23.204  -13.064  -9.227  <.0001
## (CTRL-) - (SHEB1-)    1.823 1.97 414   -3.246   6.893   0.928  0.7900
## (CTRL-) - (SHEB1+)  -11.716 1.97 414  -16.786  -6.646  -5.961  <.0001
## (CTRL+) - (SHEB1-)   19.957 1.97 414   14.888   25.027  10.154  <.0001
## (CTRL+) - (SHEB1+)    6.418 1.97 414    1.348   11.488   3.266  0.0065
## (SHEB1-) - (SHEB1+) -13.539 1.97 414  -18.609  -8.470  -6.889  <.0001
##
## treatment = b:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio p.value
## (CTRL-) - (CTRL+)  -19.202 1.97 414  -24.272  -14.132  -9.770  <.0001
## (CTRL-) - (SHEB1-)   4.482 1.97 414   -0.587   9.552   2.281  0.1042
## (CTRL-) - (SHEB1+)  -5.388 1.97 414  -10.458  -0.318  -2.741  0.0323
## (CTRL+) - (SHEB1-)   23.684 1.97 414   18.615   28.754  12.051  <.0001
## (CTRL+) - (SHEB1+)   13.814 1.97 414    8.744   18.884   7.029  <.0001
## (SHEB1-) - (SHEB1+) -9.870 1.97 414  -14.940  -4.801  -5.022  <.0001
##
## treatment = c:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio p.value
## (CTRL-) - (CTRL+)  -12.844 1.97 414  -17.914  -7.775  -6.535  <.0001
## (CTRL-) - (SHEB1-)   3.378 1.97 414   -1.691   8.448   1.719  0.3151
## (CTRL-) - (SHEB1+)   0.636 1.97 414   -4.434   5.705   0.323  0.9883
## (CTRL+) - (SHEB1-)   16.223 1.97 414   11.153   21.292   8.254  <.0001
## (CTRL+) - (SHEB1+)   13.480 1.97 414    8.410   18.550   6.859  <.0001
## (SHEB1-) - (SHEB1+) -2.743 1.97 414   -7.812   2.327  -1.396  0.5029
##
## treatment = d:
## contrast      estimate    SE  df lower.CL upper.CL t.ratio p.value
## (CTRL-) - (CTRL+)  -12.804 1.97 414  -17.873  -7.734  -6.515  <.0001
## (CTRL-) - (SHEB1-)   3.063 1.97 414   -2.006   8.133   1.559  0.4036
## (CTRL-) - (SHEB1+)   0.120 1.97 414   -4.950   5.189   0.061  0.9999
## (CTRL+) - (SHEB1-)   15.867 1.97 414   10.797   20.937   8.073  <.0001
## (CTRL+) - (SHEB1+)   12.923 1.97 414    7.854   17.993   6.576  <.0001
## (SHEB1-) - (SHEB1+) -2.944 1.97 414   -8.013   2.126  -1.498  0.4398
##
## Degrees-of-freedom method: satterthwaite
## Confidence level used: 0.95
## Conf-level adjustment: tukey method for comparing a family of 4 estimates
## P value adjustment: tukey method for comparing a family of 4 estimates
```

```
emmip(m8, condition ~ treatment) +
  theme_bw() +
  xlab('Treatment') +
  ylab('Value')
```

```
## Cannot use mode = "kenward-roger" because *pbkrtest* package is not installed
```



```
summary(pairs(emmeans(m8, "condition", by = "treatment", level = 0.95, infer = TRUE)))
```

```
## Cannot use mode = "kenward-roger" because *pbkrtest* package is not installed
```

```
## treatment = a:
## contrast      estimate    SE  df t.ratio p.value
## (CTRL-) - (CTRL+)   -18.134  1.97 414  -9.227 <.0001
## (CTRL-) - (SHEB1-)    1.823  1.97 414   0.928  0.7900
## (CTRL-) - (SHEB1+)  -11.716  1.97 414  -5.961 <.0001
## (CTRL+) - (SHEB1-)   19.957  1.97 414  10.154 <.0001
## (CTRL+) - (SHEB1+)    6.418  1.97 414   3.266  0.0065
## (SHEB1-) - (SHEB1+) -13.539  1.97 414  -6.889 <.0001
##
## treatment = b:
## contrast      estimate    SE  df t.ratio p.value
## (CTRL-) - (CTRL+)   -19.202  1.97 414  -9.770 <.0001
## (CTRL-) - (SHEB1-)    4.482  1.97 414   2.281  0.1042
## (CTRL-) - (SHEB1+)   -5.388  1.97 414  -2.741  0.0323
## (CTRL+) - (SHEB1-)   23.684  1.97 414  12.051 <.0001
## (CTRL+) - (SHEB1+)   13.814  1.97 414   7.029 <.0001
## (SHEB1-) - (SHEB1+)  -9.870  1.97 414  -5.022 <.0001
##
## treatment = c:
## contrast      estimate    SE  df t.ratio p.value
## (CTRL-) - (CTRL+)   -12.844  1.97 414  -6.535 <.0001
```

```

## (CTRL-) - (SHEB1-)      3.378 1.97 414    1.719 0.3151
## (CTRL-) - (SHEB1+)      0.636 1.97 414    0.323 0.9883
## (CTRL+) - (SHEB1-)     16.223 1.97 414    8.254 <.0001
## (CTRL+) - (SHEB1+)     13.480 1.97 414    6.859 <.0001
## (SHEB1-) - (SHEB1+)    -2.743 1.97 414   -1.396 0.5029
##
## treatment = d:
## contrast      estimate    SE  df t.ratio p.value
## (CTRL-) - (CTRL+)   -12.804 1.97 414   -6.515 <.0001
## (CTRL-) - (SHEB1-)    3.063 1.97 414    1.559 0.4036
## (CTRL-) - (SHEB1+)    0.120 1.97 414    0.061 0.9999
## (CTRL+) - (SHEB1-)   15.867 1.97 414    8.073 <.0001
## (CTRL+) - (SHEB1+)   12.923 1.97 414    6.576 <.0001
## (SHEB1-) - (SHEB1+)  -2.944 1.97 414   -1.498 0.4398
##
## Degrees-of-freedom method: satterthwaite
## P value adjustment: tukey method for comparing a family of 4 estimates

```