```r
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----------------------- tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.4.4     v tibble    3.2.1
## v lubridate 1.9.3     v tidyr     1.3.1
## v purrr     1.0.2
## -- Conflicts ------------------------------------------- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```r
mouse = readxl::read_excel(file.choose(),
                           sheet = "mouse",
                           skip = 2,
                           na="") %>%
  mutate(diet = as.factor(diet)) %>%
  mutate(sex = as.factor(sex))

rat = readxl::read_excel(file.choose(),
                         sheet = "rat",
                         skip = 2,
                         na="") %>%
  mutate(diet = as.factor(diet)) %>%
  mutate(sex = as.factor(sex))
```

Mouse Model Filtered & Individually Ran

```r
mouse.p2 = mouse %>% filter(relax_var == 'p2')
mouse.p3 = mouse %>% filter(relax_var == 'p3')
mouse.t2 = mouse %>% filter(relax_var == 't2')
mouse.t3 = mouse %>% filter(relax_var == 't3')

mouse.p2.mdl = lmerTest::lmer(relax_var_num ~ diet*sex + (1|mouse_id), mouse.p2)
mouse.p3.mdl = lmerTest::lmer(relax_var_num ~ diet*sex + (1|mouse_id), mouse.p3)
mouse.t2.mdl = lmerTest::lmer(relax_var_num ~ diet*sex + (1|mouse_id), mouse.t2)
mouse.t3.mdl = lmerTest::lmer(relax_var_num ~ diet*sex + (1|mouse_id), mouse.t3)

anova(mouse.p2.mdl)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq    Mean Sq NumDF   DenDF F value Pr(>F)
## diet    0.0056925 0.0056925     1  39.652  0.9559 0.3341
## sex     0.0093610 0.0093610     1 131.501  1.5719 0.2121
## diet:sex 0.0015283 0.0015283    1  34.400  0.2566 0.6157
```

```r
anova(mouse.p3.mdl)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##          Sum Sq   Mean Sq NumDF   DenDF F value Pr(>F)
## diet    0.0056925 0.0056925     1  39.652  0.9559 0.3341
## sex     0.0093610 0.0093610     1 131.501  1.5719 0.2121
## diet:sex 0.0015283 0.0015283    1  34.400  0.2566 0.6157
```

```
anova(mouse.t2.mdl)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##         Sum Sq Mean Sq NumDF   DenDF F value   Pr(>F)
## diet      5.01    5.01     1  42.209  0.0575 0.81160
## sex     333.69  333.69     1 130.750  3.8307 0.05245 .
## diet:sex 24.96   24.96     1  35.943  0.2866 0.59572
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(mouse.t3.mdl)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##          Sum Sq Mean Sq NumDF   DenDF F value  Pr(>F)
## diet     11833.5 11833.5     1  41.419  3.5035 0.06831 .
## sex      18396.2 18396.2     1 123.999  5.4465 0.02122 *
## diet:sex  4407.1  4407.1     1  32.019  1.3048 0.26181
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(multcomp::glht(mouse.t2.mdl, linfct = multcomp::mcp(sex = "Tukey")))
```

```
## Warning in mcp2matrix(model, linfct = linfct): covariate interactions found --
## default contrast might be inappropriate
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lmerTest::lmer(formula = relax_var_num ~ diet * sex + (1 | mouse_id),
##     data = mouse.t2)
##
## Linear Hypotheses:
##            Estimate Std. Error z value Pr(>|z|)
## 1 - 0 == 0   -2.295      2.544  -0.902    0.367
## (Adjusted p values reported -- single-step method)
```

```
summary(multcomp::glht(mouse.t3.mdl, linfct = multcomp::mcp(diet = "Tukey")))
```

```
## Warning in mcp2matrix(model, linfct = linfct): covariate interactions found --
## default contrast might be inappropriate
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lmerTest::lmer(formula = relax_var_num ~ diet * sex + (1 | mouse_id),
##     data = mouse.t3)
##
## Linear Hypotheses:
##            Estimate Std. Error z value Pr(>|z|)
## 1 - 0 == 0    35.00      17.48   2.002   0.0452 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
summary(multcomp::glht(mouse.t3.mdl, linfct = multcomp::mcp(sex = "Tukey")))
```

```
## Warning in mcp2matrix(model, linfct = linfct): covariate interactions found --
## default contrast might be inappropriate
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lmerTest::lmer(formula = relax_var_num ~ diet * sex + (1 | mouse_id),
##     data = mouse.t3)
##
## Linear Hypotheses:
##            Estimate Std. Error z value Pr(>|z|)
## 1 - 0 == 0    38.31      16.48   2.325   0.0201 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

Rat Model Filtered & Individually Ran

```
rat.p2 = rat %>% filter(relax_var == 'p2')
rat.p3 = rat %>% filter(relax_var == 'p3')
rat.t2 = rat %>% filter(relax_var == 't2')
rat.t3 = rat %>% filter(relax_var == 't3')


rat.p2.mdl = lmerTest::lmer(relax_var_num ~ diet*sex + (1|rat_id), rat.p2)
rat.p3.mdl = lmerTest::lmer(relax_var_num ~ diet*sex + (1|rat_id), rat.p3)
rat.t2.mdl = lmerTest::lmer(relax_var_num ~ diet*sex + (1|rat_id), rat.t2)
rat.t3.mdl = lmerTest::lmer(relax_var_num ~ diet*sex + (1|rat_id), rat.t3)
```

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

```
anova(rat.p2.mdl)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##            Sum Sq  Mean Sq NumDF   DenDF F value  Pr(>F)
## diet     0.013785 0.013785     1  60.620  1.6587 0.20268
## sex      0.030493 0.030493     1 100.388  3.6691 0.05828 .
## diet:sex 0.038391 0.038391     1  45.674  4.6193 0.03695 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(rat.p3.mdl)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##            Sum Sq  Mean Sq NumDF  DenDF F value  Pr(>F)
## diet     0.023216 0.023216     1 57.090  3.0479 0.08622 .
## sex      0.043026 0.043026     1 97.848  5.6487 0.01941 *
## diet:sex 0.043384 0.043384     1 44.108  5.6957 0.02136 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(rat.t2.mdl)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## diet      187.12  187.12     1 39.016  1.9250   0.17318
## sex      1742.40 1742.40     1 86.384 17.9249 5.713e-05 ***
## diet:sex  585.69  585.69     1 30.682  6.0253   0.01998 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(rat.t3.mdl)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF DenDF F value  Pr(>F)
## diet       289.6   289.6     1   114  0.0568 0.81206
## sex      23209.9 23209.9     1   114  4.5519 0.03503 *
## diet:sex    77.6    77.6     1   114  0.0152 0.90203
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(multcomp::glht(rat.p2.mdl, linfct = multcomp::mcp(diet = "Tukey")))
```

```
## Warning in mcp2matrix(model, linfct = linfct): covariate interactions found --
## default contrast might be inappropriate
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
```

```
## 
## Fit: lmerTest::lmer(formula = relax_var_num ~ diet * sex + (1 | rat_id),
##     data = rat.p2)
## 
## Linear Hypotheses:
##            Estimate Std. Error z value Pr(>|z|)
## 1 - 0 == 0 -0.02190    0.03463  -0.632    0.527
## (Adjusted p values reported -- single-step method)
```

```r
summary(multcomp::glht(rat.p3.mdl, linfct = multcomp::mcp(sex = "Tukey")))
```

```
## Warning in mcp2matrix(model, linfct = linfct): covariate interactions found --
## default contrast might be inappropriate
```

```
## 
##   Simultaneous Tests for General Linear Hypotheses
## 
## Multiple Comparisons of Means: Tukey Contrasts
## 
## 
## Fit: lmerTest::lmer(formula = relax_var_num ~ diet * sex + (1 | rat_id),
##     data = rat.p3)
## 
## Linear Hypotheses:
##            Estimate Std. Error z value Pr(>|z|)
## 1 - 0 == 0 0.008944   0.030125   0.297    0.767
## (Adjusted p values reported -- single-step method)
```

```r
summary(multcomp::glht(rat.t2.mdl, linfct = multcomp::mcp(sex = "Tukey")))
```

```
## Warning in mcp2matrix(model, linfct = linfct): covariate interactions found --
## default contrast might be inappropriate
```

```
## 
##   Simultaneous Tests for General Linear Hypotheses
## 
## Multiple Comparisons of Means: Tukey Contrasts
## 
## 
## Fit: lmerTest::lmer(formula = relax_var_num ~ diet * sex + (1 | rat_id),
##     data = rat.t2)
## 
## Linear Hypotheses:
##            Estimate Std. Error z value Pr(>|z|)
## 1 - 0 == 0   13.386      3.052   4.386 1.15e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```r
summary(multcomp::glht(rat.t3.mdl, linfct = multcomp::mcp(sex = "Tukey")))
```

```
## Warning in mcp2matrix(model, linfct = linfct): covariate interactions found --
## default contrast might be inappropriate
```

```
##
##    Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lmerTest::lmer(formula = relax_var_num ~ diet * sex + (1 | rat_id),
##     data = rat.t3)
##
## Linear Hypotheses:
##            Estimate Std. Error z value Pr(>|z|)
## 1 - 0 == 0    27.07      20.48   1.322    0.186
## (Adjusted p values reported -- single-step method)
```

The code below is me messing around. It spits out a ton of information, most of it being not useful. However this was just an attempt to try and run the lmer over all the dependent variables without having to filter four times (p2,p3,t2,t3). Thought I would include if you're interested. I have not compared to see if the p-values below are similar to above.

Mouse Model Shortened

```
mouse.mdl = lmerTest::lmer(relax_var_num ~ relax_var + diet*sex + (1|mouse_id), data = mouse)
anova(mouse.mdl)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##            Sum Sq Mean Sq NumDF  DenDF  F value  Pr(>F)
## relax_var 2237286  745762     3 514.31 854.7448 < 2e-16 ***
## diet         3813    3813     1  64.09   4.3706 0.04053 *
## sex          2824    2824     1 437.67   3.2369 0.07269 .
## diet:sex     1603    1603     1  45.88   1.8370 0.18194
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
emmeans::emmeans(mouse.mdl, list(pairwise ~ relax_var + diet*sex), adjust = "tukey")
```

```
## $`emmeans of relax_var, diet, sex`
##  relax_var diet sex emmean   SE   df lower.CL upper.CL
##  p2           0   0  -7.27 4.34 82.0   -15.90    1.353
##  p3           0   0  -7.85 4.34 82.0   -16.48    0.771
##  t2           0   0  18.61 4.34 82.1     9.98   27.239
##  t3           0   0 150.67 4.38 88.3   141.98  159.369
##  p2           1   0   3.31 3.80 64.8    -4.29   10.911
##  p3           1   0   2.73 3.80 64.8    -4.87   10.329
##  t2           1   0  29.19 3.82 65.8    21.57   36.818
##  t3           1   0 161.26 3.90 68.0   153.48  169.035
```

```
##  p2         0    1      1.77 3.76 62.9     -5.74     9.279
##  p3         0    1      1.19 3.76 62.9     -6.32     8.697
##  t2         0    1     27.65 3.76 63.3     20.13    35.163
##  t3         0    1    159.71 3.78 65.5    152.17   167.257
##  p2         1    1      3.93 3.81 64.5     -3.67    11.536
##  p3         1    1      3.35 3.81 64.5     -4.25    10.954
##  t2         1    1     29.81 3.81 64.4     22.20    37.427
##  t3         1    1    161.88 3.87 66.9    154.16   169.599
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of relax_var, diet, sex`
##  1                             estimate   SE    df t.ratio p.value
##  p2 diet0 sex0 - p3 diet0 sex0    0.5820 3.58 517.6   0.162  1.0000
##  p2 diet0 sex0 - t2 diet0 sex0  -25.8800 3.59 517.6  -7.211  <.0001
##  p2 diet0 sex0 - t3 diet0 sex0 -157.9467 3.64 518.2 -43.398  <.0001
##  p2 diet0 sex0 - p2 diet1 sex0  -10.5841 4.78  89.5  -2.213  0.6858
##  p2 diet0 sex0 - p3 diet1 sex0  -10.0021 5.98 193.4  -1.674  0.9512
##  p2 diet0 sex0 - t2 diet1 sex0  -36.4641 5.99 194.8  -6.091  <.0001
##  p2 diet0 sex0 - t3 diet1 sex0 -168.5308 6.04 189.3 -27.900  <.0001
##  p2 diet0 sex0 - p2 diet0 sex1   -9.0401 4.38 170.2  -2.063  0.7852
##  p2 diet0 sex0 - p3 diet0 sex1   -8.4581 5.66 325.0  -1.495  0.9825
##  p2 diet0 sex0 - t2 diet0 sex1  -34.9201 5.66 326.4  -6.167  <.0001
##  p2 diet0 sex0 - t3 diet0 sex1 -166.9868 5.68 321.3 -29.412  <.0001
##  p2 diet0 sex0 - p2 diet1 sex1  -11.2032 4.47 158.7  -2.505  0.4736
##  p2 diet0 sex0 - p3 diet1 sex1  -10.6212 5.73 306.6  -1.854  0.8943
##  p2 diet0 sex0 - t2 diet1 sex1  -37.0832 5.74 306.2  -6.465  <.0001
##  p2 diet0 sex0 - t3 diet1 sex1 -169.1499 5.78 297.7 -29.280  <.0001
##  p3 diet0 sex0 - t2 diet0 sex0  -26.4620 3.59 517.6  -7.374  <.0001
##  p3 diet0 sex0 - t3 diet0 sex0 -158.5287 3.64 518.2 -43.558  <.0001
##  p3 diet0 sex0 - p2 diet1 sex0  -11.1661 5.98 193.4  -1.869  0.8867
##  p3 diet0 sex0 - p3 diet1 sex0  -10.5841 4.78  89.5  -2.213  0.6858
##  p3 diet0 sex0 - t2 diet1 sex0  -37.0461 5.99 194.8  -6.188  <.0001
##  p3 diet0 sex0 - t3 diet1 sex0 -169.1128 6.04 189.3 -27.996  <.0001
##  p3 diet0 sex0 - p2 diet0 sex1   -9.6220 5.66 325.0  -1.700  0.9456
##  p3 diet0 sex0 - p3 diet0 sex1   -9.0401 4.38 170.2  -2.063  0.7852
##  p3 diet0 sex0 - t2 diet0 sex1  -35.5021 5.66 326.4  -6.270  <.0001
##  p3 diet0 sex0 - t3 diet0 sex1 -167.5688 5.68 321.3 -29.515  <.0001
##  p3 diet0 sex0 - p2 diet1 sex1  -11.7852 5.73 306.6  -2.057  0.7908
##  p3 diet0 sex0 - p3 diet1 sex1  -11.2032 4.47 158.7  -2.505  0.4736
##  p3 diet0 sex0 - t2 diet1 sex1  -37.6652 5.74 306.2  -6.567  <.0001
##  p3 diet0 sex0 - t3 diet1 sex1 -169.7319 5.78 297.7 -29.381  <.0001
##  t2 diet0 sex0 - t3 diet0 sex0 -132.0667 3.65 518.0 -36.227  <.0001
##  t2 diet0 sex0 - p2 diet1 sex0   15.2959 5.97 192.8   2.561  0.4322
##  t2 diet0 sex0 - p3 diet1 sex0   15.8779 5.97 192.8   2.658  0.3654
##  t2 diet0 sex0 - t2 diet1 sex0  -10.5841 4.78  89.5  -2.213  0.6858
##  t2 diet0 sex0 - t3 diet1 sex0 -142.6508 6.04 188.8 -23.629  <.0001
##  t2 diet0 sex0 - p2 diet0 sex1   16.8400 5.66 324.5   2.973  0.1865
##  t2 diet0 sex0 - p3 diet0 sex1   17.4219 5.66 324.5   3.076  0.1449
##  t2 diet0 sex0 - t2 diet0 sex1   -9.0401 4.38 170.2  -2.063  0.7852
##  t2 diet0 sex0 - t3 diet0 sex1 -141.1068 5.68 320.9 -24.833  <.0001
##  t2 diet0 sex0 - p2 diet1 sex1   14.6768 5.73 307.8   2.560  0.4308
##  t2 diet0 sex0 - p3 diet1 sex1   15.2588 5.73 307.8   2.661  0.3606
```

```
##  t2 diet0 sex0 - t2 diet1 sex1  -11.2032 4.47 158.7  -2.505  0.4736
##  t2 diet0 sex0 - t3 diet1 sex1 -143.2699 5.78 299.0 -24.789  <.0001
##  t3 diet0 sex0 - p2 diet1 sex0  147.3626 5.98 204.0  24.643  <.0001
##  t3 diet0 sex0 - p3 diet1 sex0  147.9446 5.98 204.0  24.741  <.0001
##  t3 diet0 sex0 - t2 diet1 sex0  121.4826 5.99 205.5  20.279  <.0001
##  t3 diet0 sex0 - t3 diet1 sex0  -10.5841 4.78  89.5  -2.213  0.6858
##  t3 diet0 sex0 - p2 diet0 sex1  148.9067 5.71 335.4  26.062  <.0001
##  t3 diet0 sex0 - p3 diet0 sex1  149.4887 5.71 335.4  26.164  <.0001
##  t3 diet0 sex0 - t2 diet0 sex1  123.0266 5.72 336.9  21.521  <.0001
##  t3 diet0 sex0 - t3 diet0 sex1   -9.0401 4.38 170.2  -2.063  0.7852
##  t3 diet0 sex0 - p2 diet1 sex1  146.7435 5.76 322.6  25.495  <.0001
##  t3 diet0 sex0 - p3 diet1 sex1  147.3255 5.76 322.6  25.596  <.0001
##  t3 diet0 sex0 - t2 diet1 sex1  120.8635 5.76 322.2  20.980  <.0001
##  t3 diet0 sex0 - t3 diet1 sex1  -11.2032 4.47 158.7  -2.505  0.4736
##  p2 diet1 sex0 - p3 diet1 sex0    0.5820 3.58 517.6   0.162  1.0000
##  p2 diet1 sex0 - t2 diet1 sex0  -25.8800 3.59 517.6  -7.211  <.0001
##  p2 diet1 sex0 - t3 diet1 sex0 -157.9467 3.64 518.2 -43.398  <.0001
##  p2 diet1 sex0 - p2 diet0 sex1    1.5440 3.88 179.1   0.398  1.0000
##  p2 diet1 sex0 - p3 diet0 sex1    2.1260 5.28 366.0   0.402  1.0000
##  p2 diet1 sex0 - t2 diet0 sex1  -24.3360 5.28 366.1  -4.611  0.0006
##  p2 diet1 sex0 - t3 diet0 sex1 -156.4027 5.27 380.0 -29.691  <.0001
##  p2 diet1 sex0 - p2 diet1 sex1   -0.6191 4.09  96.3  -0.152  1.0000
##  p2 diet1 sex0 - p3 diet1 sex1   -0.0371 5.43 239.7  -0.007  1.0000
##  p2 diet1 sex0 - t2 diet1 sex1  -26.4991 5.43 238.1  -4.878  0.0002
##  p2 diet1 sex0 - t3 diet1 sex1 -158.5658 5.45 244.2 -29.095  <.0001
##  p3 diet1 sex0 - t2 diet1 sex0  -26.4620 3.59 517.6  -7.374  <.0001
##  p3 diet1 sex0 - t3 diet1 sex0 -158.5287 3.64 518.2 -43.558  <.0001
##  p3 diet1 sex0 - p2 diet0 sex1    0.9620 5.28 366.0   0.182  1.0000
##  p3 diet1 sex0 - p3 diet0 sex1    1.5440 3.88 179.1   0.398  1.0000
##  p3 diet1 sex0 - t2 diet0 sex1  -24.9180 5.28 366.1  -4.721  0.0004
##  p3 diet1 sex0 - t3 diet0 sex1 -156.9847 5.27 380.0 -29.802  <.0001
##  p3 diet1 sex0 - p2 diet1 sex1   -1.2011 5.43 239.7  -0.221  1.0000
##  p3 diet1 sex0 - p3 diet1 sex1   -0.6191 4.09  96.3  -0.152  1.0000
##  p3 diet1 sex0 - t2 diet1 sex1  -27.0811 5.43 238.1  -4.985  0.0001
##  p3 diet1 sex0 - t3 diet1 sex1 -159.1478 5.45 244.2 -29.202  <.0001
##  t2 diet1 sex0 - t3 diet1 sex0 -132.0667 3.65 518.0 -36.227  <.0001
##  t2 diet1 sex0 - p2 diet0 sex1   27.4241 5.30 366.8   5.178  <.0001
##  t2 diet1 sex0 - p3 diet0 sex1   28.0060 5.30 366.8   5.288  <.0001
##  t2 diet1 sex0 - t2 diet0 sex1    1.5440 3.88 179.1   0.398  1.0000
##  t2 diet1 sex0 - t3 diet0 sex1 -130.5227 5.28 380.8 -24.716  <.0001
##  t2 diet1 sex0 - p2 diet1 sex1   25.2609 5.45 242.2   4.639  0.0006
##  t2 diet1 sex0 - p3 diet1 sex1   25.8429 5.45 242.2   4.746  0.0004
##  t2 diet1 sex0 - t2 diet1 sex1   -0.6191 4.09  96.3  -0.152  1.0000
##  t2 diet1 sex0 - t3 diet1 sex1 -132.6858 5.46 246.8 -24.299  <.0001
##  t3 diet1 sex0 - p2 diet0 sex1  159.4908 5.38 359.4  29.673  <.0001
##  t3 diet1 sex0 - p3 diet0 sex1  160.0727 5.38 359.4  29.781  <.0001
##  t3 diet1 sex0 - t2 diet0 sex1  133.6107 5.37 359.6  24.880  <.0001
##  t3 diet1 sex0 - t3 diet0 sex1    1.5440 3.88 179.1   0.398  1.0000
##  t3 diet1 sex0 - p2 diet1 sex1  157.3276 5.49 242.7  28.634  <.0001
##  t3 diet1 sex0 - p3 diet1 sex1  157.9096 5.49 242.7  28.740  <.0001
##  t3 diet1 sex0 - t2 diet1 sex1  131.4476 5.49 241.3  23.935  <.0001
##  t3 diet1 sex0 - t3 diet1 sex1   -0.6191 4.09  96.3  -0.152  1.0000
##  p2 diet0 sex1 - p3 diet0 sex1    0.5820 3.58 517.6   0.162  1.0000
##  p2 diet0 sex1 - t2 diet0 sex1  -25.8800 3.59 517.6  -7.211  <.0001
```

```
## p2 diet0 sex1 - t3 diet0 sex1 -157.9467 3.64 518.2 -43.398  <.0001
## p2 diet0 sex1 - p2 diet1 sex1   -2.1631 4.32  54.2  -0.501  1.0000
## p2 diet0 sex1 - p3 diet1 sex1   -1.5812 5.61 144.7  -0.282  1.0000
## p2 diet0 sex1 - t2 diet1 sex1  -28.0432 5.62 144.4  -4.992  0.0002
## p2 diet0 sex1 - t3 diet1 sex1 -160.1099 5.68 146.0 -28.205  <.0001
## p3 diet0 sex1 - t2 diet0 sex1  -26.4620 3.59 517.6  -7.374  <.0001
## p3 diet0 sex1 - t3 diet0 sex1 -158.5287 3.64 518.2 -43.558  <.0001
## p3 diet0 sex1 - p2 diet1 sex1   -2.7451 5.61 144.7  -0.489  1.0000
## p3 diet0 sex1 - p3 diet1 sex1   -2.1631 4.32  54.2  -0.501  1.0000
## p3 diet0 sex1 - t2 diet1 sex1  -28.6252 5.62 144.4  -5.096  0.0001
## p3 diet0 sex1 - t3 diet1 sex1 -160.6918 5.68 146.0 -28.308  <.0001
## t2 diet0 sex1 - t3 diet0 sex1 -132.0667 3.65 518.0 -36.227  <.0001
## t2 diet0 sex1 - p2 diet1 sex1   23.7169 5.61 145.8   4.225  0.0041
## t2 diet0 sex1 - p3 diet1 sex1   24.2989 5.61 145.8   4.329  0.0028
## t2 diet0 sex1 - t2 diet1 sex1   -2.1631 4.32  54.2  -0.501  1.0000
## t2 diet0 sex1 - t3 diet1 sex1 -134.2298 5.68 147.1 -23.639  <.0001
## t3 diet0 sex1 - p2 diet1 sex1  155.7836 5.62 149.3  27.727  <.0001
## t3 diet0 sex1 - p3 diet1 sex1  156.3656 5.62 149.3  27.830  <.0001
## t3 diet0 sex1 - t2 diet1 sex1  129.9035 5.62 149.0  23.095  <.0001
## t3 diet0 sex1 - t3 diet1 sex1   -2.1631 4.32  54.2  -0.501  1.0000
## p2 diet1 sex1 - p3 diet1 sex1    0.5820 3.58 517.6   0.162  1.0000
## p2 diet1 sex1 - t2 diet1 sex1  -25.8800 3.59 517.6  -7.211  <.0001
## p2 diet1 sex1 - t3 diet1 sex1 -157.9467 3.64 518.2 -43.398  <.0001
## p3 diet1 sex1 - t2 diet1 sex1  -26.4620 3.59 517.6  -7.374  <.0001
## p3 diet1 sex1 - t3 diet1 sex1 -158.5287 3.64 518.2 -43.558  <.0001
## t2 diet1 sex1 - t3 diet1 sex1 -132.0667 3.65 518.0 -36.227  <.0001
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 16 estimates
```

Rat Model Shortened

```r
rat.mdl = lmerTest::lmer(relax_var_num ~ relax_var + diet*sex + (1|rat_id), data = rat)
```

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

```r
anova(rat.mdl)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##            Sum Sq Mean Sq NumDF DenDF  F value    Pr(>F)
## relax_var 2400496  800165     3   472 618.7399 < 2.2e-16 ***
## diet            1       1     1   472   0.0009  0.976453
## sex          9716    9716     1   472   7.5132  0.006357 **
## diet:sex       52      52     1   472   0.0399  0.841726
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
emmeans::emmeans(rat.mdl, list(pairwise ~ relax_var + diet*sex), adjust = "tukey")
```

```
## $`emmeans of relax_var, diet, sex`
##  relax_var diet sex emmean   SE   df lower.CL upper.CL
##  p2         0    0    -4.98 5.12 67.7   -15.18     5.23
##  p3         0    0    -5.43 5.12 68.7   -15.64     4.79
##  t2         0    0    24.72 5.20 74.3    14.35    35.09
##  t3         0    0   166.45 5.17 68.0   156.14   176.76
##  p2         1    0    -4.20 4.36 94.7   -12.87     4.46
##  p3         1    0    -4.65 4.37 94.7   -13.33     4.02
##  t2         1    0    25.49 4.39 95.8    16.79    34.20
##  t3         1    0   167.22 4.38 97.2   158.53   175.92
##  p2         0    1     4.94 4.34 47.2    -3.79    13.66
##  p3         0    1     4.49 4.34 47.4    -4.25    13.22
##  t2         0    1    34.63 4.35 50.2    25.90    43.37
##  t3         0    1   176.36 4.42 49.4   167.48   185.25
##  p2         1    1     4.36 4.17 87.6    -3.93    12.65
##  p3         1    1     3.91 4.19 88.6    -4.42    12.25
##  t2         1    1    34.06 4.21 90.0    25.69    42.43
##  t3         1    1   175.79 4.19 91.0   167.47   184.11
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
##
## $`pairwise differences of relax_var, diet, sex`
##  1                            estimate   SE    df t.ratio p.value
##  p2 diet0 sex0 - p3 diet0 sex0    0.450 4.61 458.9   0.098  1.0000
##  p2 diet0 sex0 - t2 diet0 sex0  -29.697 4.64 459.1  -6.394  <.0001
##  p2 diet0 sex0 - t3 diet0 sex0 -171.427 4.64 459.1 -36.913  <.0001
##  p2 diet0 sex0 - p2 diet1 sex0   -0.773 5.49  32.5  -0.141  1.0000
##  p2 diet0 sex0 - p3 diet1 sex0   -0.323 7.17  96.2  -0.045  1.0000
##  p2 diet0 sex0 - t2 diet1 sex0  -30.470 7.14  93.8  -4.268  0.0045
##  p2 diet0 sex0 - t3 diet1 sex0 -172.200 7.16  99.0 -24.039  <.0001
##  p2 diet0 sex0 - p2 diet0 sex1   -9.912 5.31  61.0  -1.868  0.8798
##  p2 diet0 sex0 - p3 diet0 sex1   -9.462 7.03 166.3  -1.346  0.9935
##  p2 diet0 sex0 - t2 diet0 sex1  -39.609 6.99 166.6  -5.663  <.0001
##  p2 diet0 sex0 - t3 diet0 sex1 -181.339 7.07 170.8 -25.662  <.0001
##  p2 diet0 sex0 - p2 diet1 sex1   -9.338 5.27  64.2  -1.771  0.9176
##  p2 diet0 sex0 - p3 diet1 sex1   -8.888 7.02 175.7  -1.266  0.9966
##  p2 diet0 sex0 - t2 diet1 sex1  -39.035 6.99 171.8  -5.587  <.0001
##  p2 diet0 sex0 - t3 diet1 sex1 -180.765 7.00 182.4 -25.822  <.0001
##  p3 diet0 sex0 - t2 diet0 sex0  -30.147 4.65 459.3  -6.478  <.0001
##  p3 diet0 sex0 - t3 diet0 sex0 -171.877 4.65 459.3 -36.932  <.0001
##  p3 diet0 sex0 - p2 diet1 sex0   -1.223 7.17  97.7  -0.171  1.0000
##  p3 diet0 sex0 - p3 diet1 sex0   -0.773 5.49  32.5  -0.141  1.0000
##  p3 diet0 sex0 - t2 diet1 sex0  -30.920 7.15  94.7  -4.327  0.0036
##  p3 diet0 sex0 - t3 diet1 sex0 -172.650 7.17 100.0 -24.082  <.0001
##  p3 diet0 sex0 - p2 diet0 sex1  -10.362 7.03 168.9  -1.474  0.9840
##  p3 diet0 sex0 - p3 diet0 sex1   -9.912 5.31  61.0  -1.868  0.8798
##  p3 diet0 sex0 - t2 diet0 sex1  -40.059 7.00 168.2  -5.722  <.0001
##  p3 diet0 sex0 - t3 diet0 sex1 -181.789 7.07 172.5 -25.704  <.0001
##  p3 diet0 sex0 - p2 diet1 sex1   -9.788 7.00 178.2  -1.399  0.9904
##  p3 diet0 sex0 - p3 diet1 sex1   -9.338 5.27  64.2  -1.771  0.9176
##  p3 diet0 sex0 - t2 diet1 sex1  -39.485 6.98 173.3  -5.655  <.0001
##  p3 diet0 sex0 - t3 diet1 sex1 -181.215 7.00 184.1 -25.904  <.0001
##  t2 diet0 sex0 - t3 diet0 sex0 -141.730 4.68 459.7 -30.258  <.0001
```

```
##  t2 diet0 sex0 - p2 diet1 sex0    28.924 7.24 102.0    3.996  0.0110
##  t2 diet0 sex0 - p3 diet1 sex0    29.374 7.24 101.5    4.055  0.0091
##  t2 diet0 sex0 - t2 diet1 sex0    -0.773 5.49  32.5   -0.141  1.0000
##  t2 diet0 sex0 - t3 diet1 sex0  -142.503 7.24 104.4  -19.687  <.0001
##  t2 diet0 sex0 - p2 diet0 sex1    19.786 7.11 171.2    2.784  0.2886
##  t2 diet0 sex0 - p3 diet0 sex1    20.235 7.11 170.2    2.844  0.2549
##  t2 diet0 sex0 - t2 diet0 sex1    -9.912 5.31  61.0   -1.868  0.8798
##  t2 diet0 sex0 - t3 diet0 sex1  -151.642 7.15 174.7  -21.213  <.0001
##  t2 diet0 sex0 - p2 diet1 sex1    20.359 7.07 185.0    2.881  0.2349
##  t2 diet0 sex0 - p3 diet1 sex1    20.809 7.08 184.0    2.937  0.2074
##  t2 diet0 sex0 - t2 diet1 sex1    -9.338 5.27  64.2   -1.771  0.9176
##  t2 diet0 sex0 - t3 diet1 sex1  -151.068 7.07 190.9  -21.377  <.0001
##  t3 diet0 sex0 - p2 diet1 sex0   170.654 7.21  96.7   23.658  <.0001
##  t3 diet0 sex0 - p3 diet1 sex0   171.104 7.22  96.2   23.698  <.0001
##  t3 diet0 sex0 - t2 diet1 sex0   140.957 7.19  93.8   19.604  <.0001
##  t3 diet0 sex0 - t3 diet1 sex0    -0.773 5.49  32.5   -0.141  1.0000
##  t3 diet0 sex0 - p2 diet0 sex1   161.516 7.04 166.9   22.956  <.0001
##  t3 diet0 sex0 - p3 diet0 sex1   161.966 7.04 166.0   22.998  <.0001
##  t3 diet0 sex0 - t2 diet0 sex1   131.818 7.01 166.2   18.815  <.0001
##  t3 diet0 sex0 - t3 diet0 sex1    -9.912 5.31  61.0   -1.868  0.8798
##  t3 diet0 sex0 - p2 diet1 sex1   162.089 7.05 174.3   22.980  <.0001
##  t3 diet0 sex0 - p3 diet1 sex1   162.539 7.07 173.5   22.986  <.0001
##  t3 diet0 sex0 - t2 diet1 sex1   132.392 7.04 169.6   18.805  <.0001
##  t3 diet0 sex0 - t3 diet1 sex1    -9.338 5.27  64.2   -1.771  0.9176
##  p2 diet1 sex0 - p3 diet1 sex0     0.450 4.61 458.9    0.098  1.0000
##  p2 diet1 sex0 - t2 diet1 sex0   -29.697 4.64 459.1   -6.394  <.0001
##  p2 diet1 sex0 - t3 diet1 sex0  -171.427 4.64 459.1  -36.913  <.0001
##  p2 diet1 sex0 - p2 diet0 sex1    -9.139 4.65  37.8   -1.965  0.8286
##  p2 diet1 sex0 - p3 diet0 sex1    -8.689 6.55 137.6   -1.326  0.9942
##  p2 diet1 sex0 - t2 diet0 sex1   -38.836 6.57 142.8   -5.915  <.0001
##  p2 diet1 sex0 - t3 diet0 sex1  -180.566 6.62 138.1  -27.293  <.0001
##  p2 diet1 sex0 - p2 diet1 sex1    -8.565 4.53  38.6   -1.889  0.8653
##  p2 diet1 sex0 - p3 diet1 sex1    -8.115 6.48 143.6   -1.252  0.9969
##  p2 diet1 sex0 - t2 diet1 sex1   -38.262 6.50 145.2   -5.884  <.0001
##  p2 diet1 sex0 - t3 diet1 sex1  -179.992 6.49 145.2  -27.734  <.0001
##  p3 diet1 sex0 - t2 diet1 sex0   -30.147 4.65 459.3   -6.478  <.0001
##  p3 diet1 sex0 - t3 diet1 sex0  -171.877 4.65 459.3  -36.932  <.0001
##  p3 diet1 sex0 - p2 diet0 sex1    -9.589 6.55 137.1   -1.464  0.9847
##  p3 diet1 sex0 - p3 diet0 sex1    -9.139 4.65  37.8   -1.965  0.8286
##  p3 diet1 sex0 - t2 diet0 sex1   -39.286 6.57 142.9   -5.977  <.0001
##  p3 diet1 sex0 - t3 diet0 sex1  -181.016 6.62 138.3  -27.333  <.0001
##  p3 diet1 sex0 - p2 diet1 sex1    -9.015 6.46 142.6   -1.396  0.9904
##  p3 diet1 sex0 - p3 diet1 sex1    -8.565 4.53  38.6   -1.889  0.8653
##  p3 diet1 sex0 - t2 diet1 sex1   -38.712 6.50 145.0   -5.958  <.0001
##  p3 diet1 sex0 - t3 diet1 sex1  -180.442 6.48 145.1  -27.825  <.0001
##  t2 diet1 sex0 - t3 diet1 sex0  -141.730 4.68 459.7  -30.258  <.0001
##  t2 diet1 sex0 - p2 diet0 sex1    20.558 6.58 134.8    3.125  0.1359
##  t2 diet1 sex0 - p3 diet0 sex1    21.008 6.59 135.4    3.190  0.1152
##  t2 diet1 sex0 - t2 diet0 sex1    -9.139 4.65  37.8   -1.965  0.8286
##  t2 diet1 sex0 - t3 diet0 sex1  -150.869 6.65 135.9  -22.686  <.0001
##  t2 diet1 sex0 - p2 diet1 sex1    21.132 6.48 143.9    3.262  0.0948
##  t2 diet1 sex0 - p3 diet1 sex1    21.582 6.50 144.7    3.321  0.0805
##  t2 diet1 sex0 - t2 diet1 sex1    -8.565 4.53  38.6   -1.889  0.8653
##  t2 diet1 sex0 - t3 diet1 sex1  -150.295 6.51 146.2  -23.097  <.0001
```

```
##  t3 diet1 sex0 - p2 diet0 sex1  162.289 6.53 139.3  24.859  <.0001
##  t3 diet1 sex0 - p3 diet0 sex1  162.738 6.54 139.9  24.901  <.0001
##  t3 diet1 sex0 - t2 diet0 sex1  132.591 6.55 145.1  20.242  <.0001
##  t3 diet1 sex0 - t3 diet0 sex1   -9.139 4.65  37.8  -1.965  0.8286
##  t3 diet1 sex0 - p2 diet1 sex1  162.862 6.49 143.8  25.088  <.0001
##  t3 diet1 sex0 - p3 diet1 sex1  163.312 6.51 144.7  25.085  <.0001
##  t3 diet1 sex0 - t2 diet1 sex1  133.165 6.53 146.2  20.387  <.0001
##  t3 diet1 sex0 - t3 diet1 sex1   -8.565 4.53  38.6  -1.889  0.8653
##  p2 diet0 sex1 - p3 diet0 sex1    0.450 4.61 458.9   0.098  1.0000
##  p2 diet0 sex1 - t2 diet0 sex1  -29.697 4.64 459.1  -6.394  <.0001
##  p2 diet0 sex1 - t3 diet0 sex1 -171.427 4.64 459.1 -36.913  <.0001
##  p2 diet0 sex1 - p2 diet1 sex1    0.574 4.57  19.4   0.126  1.0000
##  p2 diet0 sex1 - p3 diet1 sex1    1.024 6.51  82.4   0.157  1.0000
##  p2 diet0 sex1 - t2 diet1 sex1  -29.123 6.53  81.5  -4.457  0.0026
##  p2 diet0 sex1 - t3 diet1 sex1 -170.853 6.47  83.2 -26.402  <.0001
##  p3 diet0 sex1 - t2 diet0 sex1  -30.147 4.65 459.3  -6.478  <.0001
##  p3 diet0 sex1 - t3 diet0 sex1 -171.877 4.65 459.3 -36.932  <.0001
##  p3 diet0 sex1 - p2 diet1 sex1    0.124 6.48  81.9   0.019  1.0000
##  p3 diet0 sex1 - p3 diet1 sex1    0.574 4.57  19.4   0.126  1.0000
##  p3 diet0 sex1 - t2 diet1 sex1  -29.573 6.53  81.5  -4.529  0.0020
##  p3 diet0 sex1 - t3 diet1 sex1 -171.303 6.47  83.2 -26.492  <.0001
##  t2 diet0 sex1 - t3 diet0 sex1 -141.730 4.68 459.7 -30.258  <.0001
##  t2 diet0 sex1 - p2 diet1 sex1   30.271 6.50  84.7   4.658  0.0012
##  t2 diet0 sex1 - p3 diet1 sex1   30.721 6.52  85.3   4.714  0.0010
##  t2 diet0 sex1 - t2 diet1 sex1    0.574 4.57  19.4   0.126  1.0000
##  t2 diet0 sex1 - t3 diet1 sex1 -141.156 6.48  86.1 -21.777  <.0001
##  t3 diet0 sex1 - p2 diet1 sex1  172.001 6.56  82.9  26.215  <.0001
##  t3 diet0 sex1 - p3 diet1 sex1  172.451 6.58  83.5  26.209  <.0001
##  t3 diet0 sex1 - t2 diet1 sex1  142.304 6.61  82.6  21.537  <.0001
##  t3 diet0 sex1 - t3 diet1 sex1    0.574 4.57  19.4   0.126  1.0000
##  p2 diet1 sex1 - p3 diet1 sex1    0.450 4.61 458.9   0.098  1.0000
##  p2 diet1 sex1 - t2 diet1 sex1  -29.697 4.64 459.1  -6.394  <.0001
##  p2 diet1 sex1 - t3 diet1 sex1 -171.427 4.64 459.1 -36.913  <.0001
##  p3 diet1 sex1 - t2 diet1 sex1  -30.147 4.65 459.3  -6.478  <.0001
##  p3 diet1 sex1 - t3 diet1 sex1 -171.877 4.65 459.3 -36.932  <.0001
##  t2 diet1 sex1 - t3 diet1 sex1 -141.730 4.68 459.7 -30.258  <.0001
##
## Degrees-of-freedom method: kenward-roger
## P value adjustment: tukey method for comparing a family of 16 estimates
```