> intcoxfam <- lmer(cox~bodymass+pop\*acc+(1|fam), data=Intercostals\_Enzyme\_Summary)

> intcoxsex <- lmer(cox~bodymass+pop\*acc+(1|sex), data=Intercostals\_Enzyme\_Summary)

boundary (singular) fit: see ?isSingular

> anova(intcoxfamsex,intcoxfam)

refitting model(s) with ML (instead of REML)

Data: Intercostals\_Enzyme\_Summary

Models:

intcoxfam: cox ~ bodymass + pop \* acc + (1 | fam)

intcoxfamsex: cox ~ bodymass + pop \* acc + (1 | fam) + (1 | sex)

npar AIC BIC logLik deviance Chisq Df Pr(>Chisq)

intcoxfam 7 184.19 192.44 -85.097 170.19

intcoxfamsex 8 186.19 195.62 -85.097 170.19 0 1 1

> anova(intcoxfamsex,intcoxsex)

refitting model(s) with ML (instead of REML)

Data: Intercostals\_Enzyme\_Summary

Models:

intcoxsex: cox ~ bodymass + pop \* acc + (1 | sex)

intcoxfamsex: cox ~ bodymass + pop \* acc + (1 | fam) + (1 | sex)

npar AIC BIC logLik deviance Chisq Df Pr(>Chisq)

intcoxsex 7 193.26 201.51 -89.632 179.26

intcoxfamsex 8 186.19 195.62 -85.097 170.19 9.0686 1 0.0026 \*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> intcoxfamsex <- lmer(cox~bodymass+pop\*acc+(1|fam)+(1|sex)+(1|id), data=Intercostals\_Enzyme\_Summary)

Error: number of levels of each grouping factor must be < number of observations (problems: id)

> Intercostals\_Enzyme\_Summary <- read.csv("C:/Users/Emily/OneDrive - McMaster University/MSc documents/MSc R stuff/Team-Deer-Mouse/Intercostals\_Enzyme\_Summary.csv")

> View(Intercostals\_Enzyme\_Summary)

> intercoxfamsex <- lmer(cox~bodymass+pop\*acc + (1|fam)+(1|sex)+(1|id), data=Intercostals\_Enzyme\_Summary)

Error: number of levels of each grouping factor must be < number of observations (problems: id)

> Intercostals\_Enzyme\_Summary <- read.csv("C:/Users/Emily/OneDrive - McMaster University/MSc documents/MSc R stuff/Team-Deer-Mouse/Intercostals\_Enzyme\_Summary.csv")

> View(Intercostals\_Enzyme\_Summary)

> intercoxfamsex <- lmer(cox~bodymass+pop\*acc + (1|fam)+(1|sex)+(1|id), data=Intercostals\_Enzyme\_Summary)

Error: number of levels of each grouping factor must be < number of observations (problems: id)

> intercoxfamsex <- lmer(cox~bodymass+pop\*acc + (1|fam)+(1|sex)+(1|id), data=Intercostals\_Enzyme\_Summary)

Error: number of levels of each grouping factor must be < number of observations (problems: id)

> intercoxfamsex <- lmer(cox~bodymass+pop\*acc\*id + (1|fam)+(1|sex), data=Intercostals\_Enzyme\_Summary)

fixed-effect model matrix is rank deficient so dropping 73 columns / coefficients

Error in is.nloptr(ret) : objective in x0 returns NA

> intercoxfamsex <- lmer(cox~bodymass+pop\*acc + (1|fam)+(1|sex), data=Intercostals\_Enzyme\_Summary)

boundary (singular) fit: see ?isSingular

> Intercostals\_Enzyme\_Summary <- read.csv("C:/Users/Emily/OneDrive - McMaster University/MSc documents/MSc R stuff/Team-Deer-Mouse/Intercostals\_Enzyme\_Summary.csv")

> View(Intercostals\_Enzyme\_Summary)

> intercoxfamsex <- lmer(cox~bodymass+pop\*acc + (1|fam)+(1|sex)+(1|id), data=Intercostals\_Enzyme\_Summary)

Error: number of levels of each grouping factor must be < number of observations (problems: id)

> intcoxsexfam <- lme(cox~bodymass+pop\*acc, random=~1|fam + random=~1|sex, data=Intercostals\_Enzyme\_Summary)

Error: unexpected '=' in "intcoxsexfam <- lme(cox~bodymass+pop\*acc, random=~1|fam + random="

> intcoxfamsex <- lmer(cox~bodymass+pop\*acc+(1|fam)+(1|sex), data=Intercostals\_Enzyme\_Summary)

boundary (singular) fit: see ?isSingular

> intcoxfam <- lmer(cox~bodymass+pop\*acc+(1|fam), data=Intercostals\_Enzyme\_Summary)

> intcoxsex <- lmer(cox~bodymass+pop\*acc+(1|sex), data=Intercostals\_Enzyme\_Summary)

boundary (singular) fit: see ?isSingular

> anova(intcoxfamsex,intcoxfam)

refitting model(s) with ML (instead of REML)

Data: Intercostals\_Enzyme\_Summary

Models:

intcoxfam: cox ~ bodymass + pop \* acc + (1 | fam)

intcoxfamsex: cox ~ bodymass + pop \* acc + (1 | fam) + (1 | sex)

npar AIC BIC logLik deviance Chisq Df Pr(>Chisq)

intcoxfam 7 184.12 192.36 -85.058 170.12

intcoxfamsex 8 186.12 195.54 -85.058 170.12 0 1 1

> anova(intcoxfamsex,intcoxsex)

refitting model(s) with ML (instead of REML)

Data: Intercostals\_Enzyme\_Summary

Models:

intcoxsex: cox ~ bodymass + pop \* acc + (1 | sex)

intcoxfamsex: cox ~ bodymass + pop \* acc + (1 | fam) + (1 | sex)

npar AIC BIC logLik deviance Chisq Df Pr(>Chisq)

intcoxsex 7 193.26 201.51 -89.632 179.26

intcoxfamsex 8 186.12 195.54 -85.058 170.12 9.1475 1 0.002491 \*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> summary(intcoxfam)

Linear mixed model fit by REML. t-tests use Satterthwaite's method [lmerModLmerTest]

Formula: cox ~ bodymass + pop \* acc + (1 | fam)

Data: Intercostals\_Enzyme\_Summary

REML criterion at convergence: 150

Scaled residuals:

Min 1Q Median 3Q Max

-1.7992 -0.6319 0.1327 0.5926 1.3198

Random effects:

Groups Name Variance Std.Dev.

fam (Intercept) 79.13 8.896

Residual 52.31 7.233

Number of obs: 24, groups: fam, 8

Fixed effects:

Estimate Std. Error df t value Pr(>|t|)

(Intercept) 38.5158 11.6752 18.9186 3.299 0.00379 \*\*

bodymass -0.3192 0.5864 16.8373 -0.544 0.59340

popme 11.7098 7.8761 8.4737 1.487 0.17331

accnx 10.3904 5.4615 18.1637 1.902 0.07309 .

popme:accnx 1.0283 6.9887 16.9569 0.147 0.88476

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:

(Intr) bdymss popme accnx

bodymass -0.884

popme -0.084 -0.271

accnx 0.177 -0.371 0.323

popme:accnx -0.136 0.287 -0.377 -0.781

> lsmeans(intcoxfam, pairwise~pop\*acc, adjust=tukey)

Error in .zap.args(object = object, ..., omit = "submodel") :

object 'tukey' not found

> lsmeans(intcoxfam, pairwise~pop\*acc, adjust= tukey)

Error in .zap.args(object = object, ..., omit = "submodel") :

object 'tukey' not found

> lsmeans(intcoxfam, pairwise~pop\*acc, adjust= "tukey")

$lsmeans

pop acc lsmean SE df lower.CL upper.CL

ln hx 32.2 5.74 7.20 18.7 45.7

me hx 43.9 5.34 6.56 31.1 56.7

ln nx 42.6 6.22 9.40 28.6 56.5

me nx 55.3 5.90 8.39 41.8 68.8

Degrees-of-freedom method: kenward-roger

Confidence level used: 0.95

$contrasts

contrast estimate SE df t.ratio p.value

ln hx - me hx -11.71 8.00 7.25 -1.464 0.5021

ln hx - ln nx -10.39 5.84 17.92 -1.779 0.3153

ln hx - me nx -23.13 8.39 8.12 -2.756 0.0929

me hx - ln nx 1.32 8.11 7.91 0.163 0.9983

me hx - me nx -11.42 4.42 13.81 -2.586 0.0896

ln nx - me nx -12.74 8.49 8.81 -1.501 0.4761

Degrees-of-freedom method: kenward-roger

P value adjustment: tukey method for comparing a family of 4 estimates

> intcox <- aov(cox~pop\*acc, data=Intercostals\_Enzyme\_Summary)

> summary(intcox)

Df Sum Sq Mean Sq F value Pr(>F)

pop 1 855.8 855.8 6.707 0.0175 \*

acc 1 653.7 653.7 5.123 0.0349 \*

pop:acc 1 2.6 2.6 0.020 0.8889

Residuals 20 2551.9 127.6

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> intcoxmass <- aov(cox~bodymass+pop\*acc, data=Intercostals\_Enzyme\_Summary)

> summary(intcoxmass)

Df Sum Sq Mean Sq F value Pr(>F)

bodymass 1 26.3 26.3 0.202 0.658

pop 1 869.6 869.6 6.706 0.018 \*

acc 1 704.1 704.1 5.430 0.031 \*

pop:acc 1 0.0 0.0 0.000 0.987

Residuals 19 2463.8 129.7

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> inthoadmass <- aov(hoad~bodymass+pop\*acc, data=Intercostals\_Enzyme\_Summary)

> summary(inthoadmass)

Df Sum Sq Mean Sq F value Pr(>F)

bodymass 1 523.4 523.4 6.107 0.02310 \*

pop 1 760.4 760.4 8.873 0.00772 \*\*

acc 1 6.3 6.3 0.074 0.78906

pop:acc 1 163.6 163.6 1.908 0.18317

Residuals 19 1628.4 85.7

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1