> bbcox <- lm(cox~bodymass+pop\*acc, data=bbrachiienzyme)

> summary(bbcox)

Call:

lm(formula = cox ~ bodymass + pop \* acc, data = bbrachiienzyme)

Residuals:

Min 1Q Median 3Q Max

-13.9988 -1.9147 0.1502 1.6064 12.4388

Coefficients:

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

(Intercept) 33.2453 8.0631 4.123 0.000578 \*\*\*

bodymass -0.1970 0.4311 -0.457 0.652798

popme -2.4160 3.7079 -0.652 0.522462

accnx -1.7316 3.8079 -0.455 0.654454

popme:accnx 12.4784 5.3507 2.332 0.030849 \*

---

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

Residual standard error: 6.347 on 19 degrees of freedom

Multiple R-squared: 0.3403, Adjusted R-squared: 0.2014

F-statistic: 2.45 on 4 and 19 DF, p-value: 0.08138

> bbhoad <- lm(hoad~bodymass+pop\*acc, data=bbrachiienzyme)

> summary(bbhoad)

Call:

lm(formula = hoad ~ bodymass + pop \* acc, data = bbrachiienzyme)

Residuals:

Min 1Q Median 3Q Max

-28.455 -5.820 1.867 7.027 14.314

Coefficients:

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

(Intercept) 42.5020 13.2433 3.209 0.00462 \*\*

bodymass -0.1150 0.7080 -0.162 0.87268

popme 0.9191 6.0900 0.151 0.88163

accnx -0.2197 6.2543 -0.035 0.97235

popme:accnx 13.8831 8.7884 1.580 0.13068

---

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

Residual standard error: 10.42 on 19 degrees of freedom

Multiple R-squared: 0.2789, Adjusted R-squared: 0.1271

F-statistic: 1.837 on 4 and 19 DF, p-value: 0.1633

bbcsfamsex <- lmer(cs~bodymass+pop\*acc+(1|fam)+(1|sex), data=bbrachiienzyme)

boundary (singular) fit: see ?isSingular

> summary(bbcsfamsex)

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

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

Data: bbrachiienzyme

REML criterion at convergence: 158.9

Scaled residuals:

Min 1Q Median 3Q Max

-1.5340 -0.7175 0.1074 0.6644 2.0166

Random effects:

Groups Name Variance Std.Dev.

fam (Intercept) 0.0 0.0

sex (Intercept) 0.0 0.0

Residual 129.9 11.4

Number of obs: 24, groups: fam, 7; sex, 2

Fixed effects:

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

(Intercept) 37.7660 14.4796 19.0000 2.608 0.0173 \*

bodymass 0.9763 0.7741 19.0000 1.261 0.2225

popme -12.3999 6.6586 19.0000 -1.862 0.0781 .

accnx -6.1688 6.8381 19.0000 -0.902 0.3783

popme:accnx 23.0042 9.6088 19.0000 2.394 0.0271 \*

---

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

Correlation of Fixed Effects:

(Intr) bdymss popme accnx

bodymass -0.955

popme 0.193 -0.404

accnx 0.021 -0.218 0.496

popme:accnx -0.046 0.188 -0.656 -0.719

optimizer (nloptwrap) convergence code: 0 (OK)

boundary (singular) fit: see ?isSingular

> bbldhfamsex <- lmer(ldh~bodymass+pop\*acc+(1|fam)+(1|sex), data=bbrachiienzyme)

boundary (singular) fit: see ?isSingular

> summary(bbldhfamsex)

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

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

Data: bbrachiienzyme

REML criterion at convergence: 234.4

Scaled residuals:

Min 1Q Median 3Q Max

-1.8583 -0.5180 -0.0509 0.5018 1.8333

Random effects:

Groups Name Variance Std.Dev.

fam (Intercept) 0.0 0.00

sex (Intercept) 238.6 15.45

Residual 6813.2 82.54

Number of obs: 24, groups: fam, 7; sex, 2

Fixed effects:

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

(Intercept) 706.731 108.431 12.951 6.518 1.98e-05 \*\*\*

bodymass -14.730 5.765 15.240 -2.555 0.0218 \*

popme -68.094 48.261 18.172 -1.411 0.1752

accnx -1.209 49.527 18.019 -0.024 0.9808

popme:accnx 36.292 69.669 18.239 0.521 0.6087

---

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

Correlation of Fixed Effects:

(Intr) bdymss popme accnx

bodymass -0.952

popme 0.196 -0.402

accnx 0.017 -0.209 0.495

popme:accnx -0.033 0.171 -0.653 -0.718

optimizer (nloptwrap) convergence code: 0 (OK)

boundary (singular) fit: see ?isSingular

> bbhkfam <- lmer(hk~bodymass+pop\*acc+(1|fam), data=bbrachiienzyme)

boundary (singular) fit: see ?isSingular

> summary(bbhkfam)

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

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

Data: bbrachiienzyme

REML criterion at convergence: 76.8

Scaled residuals:

Min 1Q Median 3Q Max

-2.64164 -0.39405 -0.05136 0.42539 1.84826

Random effects:

Groups Name Variance Std.Dev.

fam (Intercept) 0.000 0.000

Residual 1.725 1.313

Number of obs: 24, groups: fam, 7

Fixed effects:

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

(Intercept) 5.153e+00 1.668e+00 1.900e+01 3.089 0.00604 \*\*

bodymass 5.051e-04 8.919e-02 1.900e+01 0.006 0.99554

popme 4.144e-01 7.672e-01 1.900e+01 0.540 0.59539

accnx 4.714e-01 7.879e-01 1.900e+01 0.598 0.55672

popme:accnx 6.914e-01 1.107e+00 1.900e+01 0.625 0.53972

---

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

Correlation of Fixed Effects:

(Intr) bdymss popme accnx

bodymass -0.955

popme 0.193 -0.404

accnx 0.021 -0.218 0.496

popme:accnx -0.046 0.188 -0.656 -0.719

optimizer (nloptwrap) convergence code: 0 (OK)

boundary (singular) fit: see ?isSingula

> bfcox <- lm(cox~bodymass+pop\*acc, data=bfemorisenzyme)

> summary(bfcox)

Call:

lm(formula = cox ~ bodymass + pop \* acc, data = bfemorisenzyme)

Residuals:

Min 1Q Median 3Q Max

-12.999 -3.901 1.508 4.911 11.508

Coefficients:

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

(Intercept) -4.5638 9.3068 -0.490 0.62949

bodymass 1.5905 0.4975 3.197 0.00475 \*\*

popme -5.8541 4.2798 -1.368 0.18732

accnx -9.5760 4.3952 -2.179 0.04215 \*

popme:accnx 16.0025 6.1761 2.591 0.01792 \*

---

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

Residual standard error: 7.326 on 19 degrees of freedom

Multiple R-squared: 0.4709, Adjusted R-squared: 0.3595

F-statistic: 4.227 on 4 and 19 DF, p-value: 0.01294

> bfhoadfamsex <- lmer(hoad~bodymass+pop\*acc+(1|fam)+(1|sex), data=bfemorisenzyme)

boundary (singular) fit: see ?isSingular

> summary(bfhoadfamsex)

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

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

Data: bfemorisenzyme

REML criterion at convergence: 159.2

Scaled residuals:

Min 1Q Median 3Q Max

-1.5064 -0.7228 0.1774 0.3940 2.8264

Random effects:

Groups Name Variance Std.Dev.

fam (Intercept) 0.0 0.00

sex (Intercept) 0.0 0.00

Residual 132.4 11.51

Number of obs: 24, groups: fam, 7; sex, 2

Fixed effects:

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

(Intercept) 44.58818 14.61814 19.00000 3.050 0.00659 \*\*

bodymass 0.08424 0.78148 19.00000 0.108 0.91529

popme 8.39500 6.72226 19.00000 1.249 0.22689

accnx 4.93243 6.90355 19.00000 0.714 0.48362

popme:accnx -11.45020 9.70071 19.00000 -1.180 0.25243

---

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

Correlation of Fixed Effects:

(Intr) bdymss popme accnx

bodymass -0.955

popme 0.193 -0.404

accnx 0.021 -0.218 0.496

popme:accnx -0.046 0.188 -0.656 -0.719

optimizer (nloptwrap) convergence code: 0 (OK)

boundary (singular) fit: see ?isSingular

> bfcsfam <- lmer(cs~bodymass+pop\*acc+(1|fam), data=bfemorisenzyme)

> summary(bfcsfam)

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

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

Data: bfemorisenzyme

REML criterion at convergence: 158.1

Scaled residuals:

Min 1Q Median 3Q Max

-1.4488 -0.4672 -0.1990 0.4606 1.8585

Random effects:

Groups Name Variance Std.Dev.

fam (Intercept) 47.72 6.908

Residual 103.35 10.166

Number of obs: 24, groups: fam, 7

Fixed effects:

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

(Intercept) -6.3696 15.1259 18.1062 -0.421 0.67864

bodymass 2.6122 0.7794 18.9008 3.351 0.00337 \*\*

popme -4.1538 8.0311 6.0342 -0.517 0.62341

accnx -5.9720 7.1938 18.9379 -0.830 0.41679

popme:accnx 6.2905 9.4240 18.2402 0.667 0.51282

---

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

Correlation of Fixed Effects:

(Intr) bdymss popme accnx

bodymass -0.930

popme 0.037 -0.314

accnx 0.187 -0.330 0.328

popme:accnx -0.149 0.258 -0.439 -0.765

> bfldhfamsex <- lmer(ldh~bodymass+pop\*acc+(1|fam)+(1|sex), data=bfemorisenzyme)

boundary (singular) fit: see ?isSingular

> summary(bfldhfamsex)

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

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

Data: bfemorisenzyme

REML criterion at convergence: 229

Scaled residuals:

Min 1Q Median 3Q Max

-1.69941 -0.43315 0.03052 0.72144 1.34477

Random effects:

Groups Name Variance Std.Dev.

fam (Intercept) 5.959e-12 2.441e-06

sex (Intercept) 7.621e-15 8.730e-08

Residual 5.207e+03 7.216e+01

Number of obs: 24, groups: fam, 7; sex, 2

Fixed effects:

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

(Intercept) 792.705 91.670 19.000 8.647 5.18e-08 \*\*\*

bodymass -5.955 4.901 19.000 -1.215 0.239

popme -54.603 42.155 19.000 -1.295 0.211

accnx 49.778 43.292 19.000 1.150 0.264

popme:accnx -6.979 60.833 19.000 -0.115 0.910

---

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

Correlation of Fixed Effects:

(Intr) bdymss popme accnx

bodymass -0.955

popme 0.193 -0.404

accnx 0.021 -0.218 0.496

popme:accnx -0.046 0.188 -0.656 -0.719

optimizer (nloptwrap) convergence code: 0 (OK)

boundary (singular) fit: see ?isSingular

> bfhkfamsex <- lmer(hk~bodymass+pop\*acc+(1|fam)+(1|sex), data=bfemorisenzyme)

boundary (singular) fit: see ?isSingular

> summary(bfhkfamsex)

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

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

Data: bfemorisenzyme

REML criterion at convergence: 69.5

Scaled residuals:

Min 1Q Median 3Q Max

-1.41910 -0.65401 -0.05476 0.43281 1.67656

Random effects:

Groups Name Variance Std.Dev.

fam (Intercept) 0.000 0.000

sex (Intercept) 0.000 0.000

Residual 1.174 1.084

Number of obs: 24, groups: fam, 7; sex, 2

Fixed effects:

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

(Intercept) 3.44400 1.37670 19.00000 2.502 0.0217 \*

bodymass 0.09262 0.07360 19.00000 1.259 0.2235

popme 0.98846 0.63308 19.00000 1.561 0.1349

accnx -0.81188 0.65016 19.00000 -1.249 0.2269

popme:accnx 0.30176 0.91359 19.00000 0.330 0.7448

---

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

Correlation of Fixed Effects:

(Intr) bdymss popme accnx

bodymass -0.955

popme 0.193 -0.404

accnx 0.021 -0.218 0.496

popme:accnx -0.046 0.188 -0.656 -0.719

optimizer (nloptwrap) convergence code: 0 (OK)

boundary (singular) fit: see ?isSingular

> dpcox1 <- lm(cox~pop\*acc, data=diapenzyme)

> summary(dpcox1)

Call:

lm(formula = cox ~ pop \* acc, data = diapenzyme)

Residuals:

Min 1Q Median 3Q Max

-23.08 -10.68 -1.07 8.56 28.30

Coefficients:

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

(Intercept) 61.130 5.455 11.206 4.51e-10 \*\*\*

popme 15.191 7.714 1.969 0.0629 .

accnx -2.577 8.451 -0.305 0.7635

popme:accnx 9.965 11.951 0.834 0.4142

---

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

Residual standard error: 14.43 on 20 degrees of freedom

Multiple R-squared: 0.3678, Adjusted R-squared: 0.2729

F-statistic: 3.878 on 3 and 20 DF, p-value: 0.02457

> dphk <- lm(hk~bodymass+pop\*acc, data=diapenzyme)

> summary(dphk)

Call:

lm(formula = hk ~ bodymass + pop \* acc, data = diapenzyme)

Residuals:

Min 1Q Median 3Q Max

-3.0671 -0.7587 0.1112 0.7863 3.6063

Coefficients:

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

(Intercept) 11.91937 2.18515 5.455 2.91e-05 \*\*\*

bodymass 0.01601 0.11682 0.137 0.8924

popme 2.23756 1.00486 2.227 0.0383 \*

accnx -0.96079 1.03196 -0.931 0.3635

popme:accnx 0.59677 1.45008 0.412 0.6853

---

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

Residual standard error: 1.72 on 19 degrees of freedom

Multiple R-squared: 0.4234, Adjusted R-squared: 0.302

F-statistic: 3.487 on 4 and 19 DF, p-value: 0.02688