9/29/2023

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> ###

> # create table that fits the organization of the Linear Mixed-Effects Example.R function

> # and then call it to analyze the data statistically

> ###

> print('')

[1] ""

> print('')

[1] ""

> print('')

[1] ""

> degree=3

>

> # WT and alpha9 gain vs pupilsize

> dTab<-rename(v2,id=experiment, cohort=pupilSize,gain=gain1)

> dTab<-filter(dTab,condition==conditions[1])

> dTab<-filter(dTab,protocol==protocols[1])

> dTable<-filter(dTab,genotype==genotypes[1])

> dTable<-subset(dTable, select = -c(condition,protocol,genotype,gain2))

> dTable<-filter(dTable,freq>8)

> filename='AriWT gain vs pupilsize.pdf'

> fit<-lmer(gain ~ cohort \* stats::poly(freq,degree) + (1|id), data=dTable)

> fit\_anova<-anova(fit)

> #print(fit\_anova)

> print(sprintf('p-value: %5.5f',last(fit\_anova$`Pr(>F)`)))

[1] "p-value: 0.88185"

> if (last(fit\_anova$`Pr(>F)`)<0.05) {

+ dT=select(dTable,select=c(cohort,freq,gain))

+ p=TRUE

+ checkTtests(dT,p)

+ }

>

> dTable<-filter(dTab,genotype==genotypes[2])

> dTable<-subset(dTable, select = -c(condition,protocol,genotype,gain2))

> dTable<-filter(dTable,freq>8)

> filename='AriAlpha9 gain vs pupilsize.pdf'

> fit<-lmer(gain ~ cohort \* stats::poly(freq,degree) + (1|id), data=dTable)

> fit\_anova<-anova(fit)

> #print(fit\_anova)

> print(sprintf('p-value: %5.5f',last(fit\_anova$`Pr(>F)`)))

[1] "p-value: 0.92760"

> if (last(fit\_anova$`Pr(>F)`)<0.05) {

+ dT=select(dTable,select=c(cohort,freq,gain))

+ p=TRUE

+ checkTtests(dT,p)

+ }

>

> # WT and alpha9 BF and Q10dB vs pupilsize

> dTab<-rename(v3,id=experiment, cohort=pupilSize)

> dTab<-filter(dTab,condition==conditions[1])

> dTab<-filter(dTab,protocol==protocols[1])

> dTable<-filter(dTab,genotype==genotypes[1])

> dTable<-subset(dTable, select = -c(condition,protocol,genotype))

> dTable<-filter(dTable,level>15)

> filename='AriWT BF vs pupilsize.pdf'

> fit<-lmer(bf ~ cohort \* stats::poly(level,degree) + (1|id), data=dTable)

> fit\_anova<-anova(fit)

> #print(fit\_anova)

> print(sprintf('p-value: %5.5f',last(fit\_anova$`Pr(>F)`)))

[1] "p-value: 0.91817"

> if (last(fit\_anova$`Pr(>F)`)<0.05) {

+ dT=select(dTable,select=c(cohort,level,bf))

+ p=TRUE

+ checkTtests(dT,p)

+ }

>

> filename='AriWT Q10dB vs pupilsize.pdf'

> fit<-lmer(q ~ cohort \* stats::poly(level,degree) + (1|id), data=dTable)

> fit\_anova<-anova(fit)

> #print(fit\_anova)

> print(sprintf('p-value: %5.5f',last(fit\_anova$`Pr(>F)`)))

[1] "p-value: 0.81894"

> if (last(fit\_anova$`Pr(>F)`)<0.05) {

+ dT=select(dTable,select=c(cohort,level,q))

+ p=TRUE

+ checkTtests(dT,p)

+ }

>

> dTable<-filter(dTab,genotype==genotypes[2])

> dTable<-subset(dTable, select = -c(condition,protocol,genotype))

> dTable<-filter(dTable,level>15)

> filename='AriAlpha9 BF vs pupilsize.pdf'

> fit<-lmer(bf ~ cohort \* stats::poly(level,degree) + (1|id), data=dTable)

> fit\_anova<-anova(fit)

> #print(fit\_anova)

> print(sprintf('p-value: %5.5f',last(fit\_anova$`Pr(>F)`)))

[1] "p-value: 0.99151"

> if (last(fit\_anova$`Pr(>F)`)<0.05) {

+ dT=select(dTable,select=c(cohort,level,bf))

+ p=TRUE

+ checkTtests(dT,p)

+ }

>

> filename='AriAlpha9 Q10dB vs pupilsize.pdf'

> fit<-lmer(q ~ cohort \* stats::poly(level,degree) + (1|id), data=dTable)

> fit\_anova<-anova(fit)

> #print(fit\_anova)

> print(sprintf('p-value: %5.5f',last(fit\_anova$`Pr(>F)`)))

[1] "p-value: 0.97926"

> if (last(fit\_anova$`Pr(>F)`)<0.05) {

+ dT=select(dTable,select=c(cohort,level,q))

+ p=TRUE

+ checkTtests(dT,p)

+ }

>

>

> # WT and alpha9 gain vs AA

> dTab<-rename(v2AA,id=experiment, cohort=condition,gain=gain1)

> dTable<-filter(dTab,genotype==genotypes[1])

> dTable<-subset(dTable, select = -c(protocol,pupilSize,genotype,gain2))

> dTable<-filter(dTable,freq>8)

> filename='AriWT gain vs AA'

> fit<-lmer(gain ~ cohort \* stats::poly(freq,degree) + (1|id), data=dTable)

> fit\_anova<-anova(fit)

> #print(fit\_anova)

> print(sprintf('p-value: %5.5f',last(fit\_anova$`Pr(>F)`)))

[1] "p-value: 0.66857"

> if (last(fit\_anova$`Pr(>F)`)<0.05) {

+ dT=select(dTable,select=c(cohort,freq,gain))

+ p=TRUE

+ checkTtests(dT,p)

+ }

>

> dTable<-filter(dTab,genotype==genotypes[2])

> dTable<-subset(dTable, select = -c(protocol,pupilSize,genotype,gain2))

> dTable<-filter(dTable,freq>8)

> filename='AriAlpha9 gain vs AA.pdf'

> fit<-lmer(gain ~ cohort \* stats::poly(freq,degree) + (1|id), data=dTable)

> fit\_anova<-anova(fit)

> #print(fit\_anova)

> print(sprintf('p-value: %5.5f',last(fit\_anova$`Pr(>F)`)))

[1] "p-value: 0.00008"

> if (last(fit\_anova$`Pr(>F)`)<0.05) {

+ dT=select(dTable,select=c(cohort,freq,gain))

+ p=TRUE

+ checkTtests(dT,p)

+ }

[1] "x axis with a significant p-value: 8.3"

Pairwise comparisons using paired t tests

data: dTsub$select3 and dTsub$select1

Awake

Anesth 0.036

P value adjustment method: bonferroni

[1] "x axis with a significant p-value: 9.9"

Pairwise comparisons using paired t tests

data: dTsub$select3 and dTsub$select1

Awake

Anesth 0.022

P value adjustment method: bonferroni

[1] "x axis with a significant p-value: 12.7"

Pairwise comparisons using paired t tests

data: dTsub$select3 and dTsub$select1

Awake

Anesth 0.014

P value adjustment method: bonferroni

[1] "Number of x axis steps with a significant p-value: 3"

>

>

> # WT and alpha9 BF and Q10dB vs AA

> dTab<-rename(v3AA,id=experiment, cohort=condition)

> dTable<-filter(dTab,genotype==genotypes[1])

> dTable<-subset(dTable, select = -c(pupilSize,protocol,genotype))

> dTable<-filter(dTable,level<80)

> filename='AriWT BF vs AA.pdf'

> fit<-lmer(bf ~ cohort \* stats::poly(level,degree) + (1|id), data=dTable)

> fit\_anova<-anova(fit)

> #print(fit\_anova)

> print(sprintf('p-value: %5.5f',last(fit\_anova$`Pr(>F)`)))

[1] "p-value: 0.46878"

> if (last(fit\_anova$`Pr(>F)`)<0.05) {

+ dT=select(dTable,select=c(cohort,level,bf))

+ p=TRUE

+ checkTtests(dT,p)

+ }

>

> filename='AriWT Q10dB vs AA.pdf'

> fit<-lmer(q ~ cohort \* stats::poly(level,degree) + (1|id), data=dTable)

> fit\_anova<-anova(fit)

> #print(fit\_anova)

> print(sprintf('p-value: %5.5f',last(fit\_anova$`Pr(>F)`)))

[1] "p-value: 0.48510"

> if (last(fit\_anova$`Pr(>F)`)<0.05) {

+ dT=select(dTable,select=c(cohort,level,q))

+ p=TRUE

+ checkTtests(dT,p)

+ }

>

> dTable<-filter(dTab,genotype==genotypes[2])

> dTable<-subset(dTable, select = -c(pupilSize,protocol,genotype))

> dTable<-filter(dTable,level<80)

> filename='AriAlpha9 BF vs AA.pdf'

> fit<-lmer(bf ~ cohort \* stats::poly(level,degree) + (1|id), data=dTable)

> fit\_anova<-anova(fit)

> #print(fit\_anova)

> print(sprintf('p-value: %5.5f',last(fit\_anova$`Pr(>F)`)))

[1] "p-value: 0.10195"

> if (last(fit\_anova$`Pr(>F)`)<0.05) {

+ dT=select(dTable,select=c(cohort,level,bf))

+ p=TRUE

+ checkTtests(dT,p)

+ }

>

> filename='AriAlpha9 Q10dB vs AA.pdf'

> fit<-lmer(q ~ cohort \* stats::poly(level,degree) + (1|id), data=dTable)

> fit\_anova<-anova(fit)

> #print(fit\_anova)

> print(sprintf('p-value: %5.5f',last(fit\_anova$`Pr(>F)`)))

[1] "p-value: 0.03933"

> if (last(fit\_anova$`Pr(>F)`)<0.05) {

+ dT=select(dTable,select=c(cohort,level,q))

+ p=TRUE

+ checkTtests(dT,p)

+ }

[1] "x axis with a significant p-value: 20.0"

Pairwise comparisons using paired t tests

data: dTsub$select3 and dTsub$select1

Awake

Anesth 0.015

P value adjustment method: bonferroni

[1] "x axis with a significant p-value: 30.0"

Pairwise comparisons using paired t tests

data: dTsub$select3 and dTsub$select1

Awake

Anesth 0.035

P value adjustment method: bonferroni

[1] "Number of x axis steps with a significant p-value: 2"

>

>

> # analyze binned pupil data

> degree=3

> dTab<-rename(vBin,id=experiment)

> dTable<-dTab

> filename='Ari\_bin gain.pdf'

> fit<-lmer(gain ~ genotype \* stats::poly(pupilBin,degree) + (1|id), data=dTable)

> fit\_anova<-anova(fit)

> print(fit\_anova)

Type III Analysis of Variance Table with Satterthwaite's method

Sum Sq Mean Sq NumDF DenDF F value Pr(>F)

genotype 0.4956 0.49564 1 10.498 0.7053 0.4197

stats::poly(pupilBin, degree) 3.8351 1.27837 3 27.174 1.8192 0.1673

genotype:stats::poly(pupilBin, degree) 1.4408 0.48026 3 27.174 0.6835 0.5699

> #print(sprintf('p-value: %5.5f',last(fit\_anova$`Pr(>F)`)))

> filename='Ari\_bin CF.pdf'

> fit<-lmer(cf ~ genotype \* stats::poly(pupilBin,degree) + (1|id), data=dTable)

> fit\_anova<-anova(fit)

> print(fit\_anova)

Type III Analysis of Variance Table with Satterthwaite's method

Sum Sq Mean Sq NumDF DenDF F value Pr(>F)

genotype 38867 38867 1 9.6957 3.2842 0.1010

stats::poly(pupilBin, degree) 2345 782 3 27.0787 0.0660 0.9774

genotype:stats::poly(pupilBin, degree) 22792 7597 3 27.0787 0.6420 0.5947

> #print(sprintf('p-value: %5.5f',last(fit\_anova$`Pr(>F)`)))

> filename='Ari\_bin Q10dB.pdf'

> fit<-lmer(q ~ genotype \* stats::poly(pupilBin,degree) + (1|id), data=dTable)

> fit\_anova<-anova(fit)

> print(fit\_anova)

Type III Analysis of Variance Table with Satterthwaite's method

Sum Sq Mean Sq NumDF DenDF F value Pr(>F)

genotype 0.039675 0.039675 1 9.6099 1.4877 0.2517

stats::poly(pupilBin, degree) 0.045826 0.015275 3 5.9297 0.5728 0.6537

genotype:stats::poly(pupilBin, degree) 0.105683 0.035228 3 5.9297 1.3209 0.3528

> #print(sprintf('p-value: %5.5f',last(fit\_anova$`Pr(>F)`)))

> filename='Ari\_bin magBF.pdf'

> fit<-lmer(mag ~ genotype \* stats::poly(pupilBin,degree) + (1|id), data=dTable)

> fit\_anova<-anova(fit)

> print(fit\_anova)

Type III Analysis of Variance Table with Satterthwaite's method

Sum Sq Mean Sq NumDF DenDF F value Pr(>F)

genotype 0.001477 0.001477 1 13.720 0.0345 0.8553

stats::poly(pupilBin, degree) 0.141921 0.047307 3 27.427 1.1066 0.3633

genotype:stats::poly(pupilBin, degree) 0.268978 0.089659 3 27.427 2.0973 0.1237

> #print(sprintf('p-value: %5.5f',last(fit\_anova$`Pr(>F)`)))

> filename='Ari\_bin maghalfBF.pdf'

> fit<-lmer(maglow ~ genotype \* stats::poly(pupilBin,degree) + (1|id), data=dTable)

> fit\_anova<-anova(fit)

> print(fit\_anova)

Type III Analysis of Variance Table with Satterthwaite's method

Sum Sq Mean Sq NumDF DenDF F value Pr(>F)

genotype 0.007846 0.0078461 1 10.660 0.3690 0.5563

stats::poly(pupilBin, degree) 0.050863 0.0169544 3 28.186 0.7974 0.5057

genotype:stats::poly(pupilBin, degree) 0.024798 0.0082661 3 28.186 0.3888 0.7620

> #print(sprintf('p-value: %5.5f',last(fit\_anova$`Pr(>F)`)))

> filename='Ari\_bin phaseCF.pdf'

> fit<-lmer(phase ~ genotype \* stats::poly(pupilBin,degree) + (1|id), data=dTable)

> fit\_anova<-anova(fit)

> print(fit\_anova)

Type III Analysis of Variance Table with Satterthwaite's method

Sum Sq Mean Sq NumDF DenDF F value Pr(>F)

genotype 0.039445 0.039445 1 10.207 4.5067 0.05919 .

stats::poly(pupilBin, degree) 0.069280 0.023093 3 27.120 2.6385 0.06975 .

genotype:stats::poly(pupilBin, degree) 0.047098 0.015699 3 27.120 1.7937 0.17205

---

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

> #print(sprintf('p-value: %5.5f',last(fit\_anova$`Pr(>F)`)))

>

>

> # WT and alpha9 tuning curves vs pupilsize

> dTab<-rename(v1,id=experiment, cohort=pupilSize,phase=phi)

> dTab<-filter(dTab,condition==conditions[1])

> dTab<-filter(dTab,protocol==protocols[1])

> dTable<-filter(dTab,genotype==genotypes[1])

> dTable<-subset(dTable, select = -c(condition,protocol,genotype))

> filename='AriWT TC vs pupilsize.pdf'

> compareTuningCurves(dTable,filename,degree)

[1] "Mag:Number of frequencies with a significant p-value: 1"

[1] "Phase:Number of frequencies with a significant p-value: 0"

[1] "Magnitude data cohort comparison p-value: 0.50521"

[1] "Phase data cohort comparison p-value: 0.10718"

[1] ""

Warning messages:

1: Some predictor variables are on very different scales: consider rescaling

2: Some predictor variables are on very different scales: consider rescaling

3: Removed 9 rows containing missing values (`geom\_point()`).

4: Removed 38 rows containing missing values (`geom\_line()`).

5: Removed 168 rows containing missing values (`geom\_point()`).

6: Some predictor variables are on very different scales: consider rescaling

7: Some predictor variables are on very different scales: consider rescaling

8: Removed 5 rows containing missing values (`geom\_point()`).

>

> dTable<-filter(dTab,genotype==genotypes[2])

> dTable<-subset(dTable, select = -c(condition,protocol,genotype))

> dTable<-filter(dTable,freq<13)

> filename='AriAlpha9 TC vs pupilsize.pdf'

> compareTuningCurves(dTable,filename,degree)

[1] "Mag:Number of frequencies with a significant p-value: 0"

[1] "Phase:Number of frequencies with a significant p-value: 0"

[1] "Magnitude data cohort comparison p-value: 0.84162"

[1] "Phase data cohort comparison p-value: 0.73062"

[1] ""

Warning messages:

1: Some predictor variables are on very different scales: consider rescaling

2: Some predictor variables are on very different scales: consider rescaling

3: Removed 6 rows containing missing values (`geom\_point()`).

4: Removed 26 rows containing missing values (`geom\_line()`).

5: Removed 173 rows containing missing values (`geom\_point()`).

6: Some predictor variables are on very different scales: consider rescaling

7: Some predictor variables are on very different scales: consider rescaling

>

> # WT and alpha9 tuning curves awake vs anesthetized

> dTab<-rename(v1AA,id=experiment, cohort=condition,phase=phi)

> dTable<-filter(dTab,genotype==genotypes[1])

> dTable<-subset(dTable, select = -c(pupilSize,protocol,genotype))

> filename='AriWT TC vs AA.pdf'

> compareTuningCurves(dTable,filename,degree)

[1] "Mag:Number of frequencies with a significant p-value: 3"

[1] "Phase:Number of frequencies with a significant p-value: 2"

[1] "Magnitude data cohort comparison p-value: 0.36317"

[1] "Phase data cohort comparison p-value: 0.64881"

[1] ""

Warning messages:

1: Some predictor variables are on very different scales: consider rescaling

2: Some predictor variables are on very different scales: consider rescaling

3: Removed 11 rows containing missing values (`geom\_point()`).

4: Removed 40 rows containing missing values (`geom\_line()`).

5: Removed 163 rows containing missing values (`geom\_point()`).

6: Some predictor variables are on very different scales: consider rescaling

7: Some predictor variables are on very different scales: consider rescaling

8: Removed 8 rows containing missing values (`geom\_point()`).

>

> dTable<-filter(dTab,genotype==genotypes[2])

> dTable<-subset(dTable, select = -c(pupilSize,protocol,genotype))

> dTable<-filter(dTable,freq<13)

> filename='AriAlpha9 TC vs AA.pdf'

> compareTuningCurves(dTable,filename,degree)

[1] "Mag:Number of frequencies with a significant p-value: 1"

[1] "Phase:Number of frequencies with a significant p-value: 2"

[1] "Magnitude data cohort comparison p-value: 0.20695"

[1] "Phase data cohort comparison p-value: 0.61478"

[1] ""

Warning messages:

1: Some predictor variables are on very different scales: consider rescaling

2: Some predictor variables are on very different scales: consider rescaling

3: Removed 27 rows containing missing values (`geom\_point()`).

4: Removed 26 rows containing missing values (`geom\_line()`).

5: Removed 166 rows containing missing values (`geom\_point()`).

6: Some predictor variables are on very different scales: consider rescaling

7: Some predictor variables are on very different scales: consider rescaling