R-code for the analysis II.) Estimation of how often and how accurately the replicate experiments predict the overall effect

Please note that in the following code variables referring to the ‘conventional standardised design’ contain the labels ‘s’ or ‘S’ and variables referring to the ‘mini-experiment design’ contain the labels ‘h’ or ‘H’.

library**(**metafor**)**

library**(**lme4**)**

#library(car)

library**(**lsmeans**)**

setwd**(**"//nwz.wwu.de/dfs/Home/V/v\_vonk01/Vanessa\_I/PhD/Batchprojekt/Daten"**)**

data**<-**read.csv2**(**"Rawdata\_mini-experiment.csv"**)**

data**<-**data**[**,**-**c**(**22**:**36**)]**

### be sure outcome measures in data are numeric

**for** **(**k **in** 6**:**21**){**

data**[**,k**]<-**as.numeric**(**as.character**(**data**[**,k**]))**

**}**

### data table organisation ####

############################

###### data split in replicate and strain ################

#split in replicate

s1**<-**data**[**data**$**Replicate.experiment**==**'Con 1',**]**

s2**<-**data**[**data**$**Replicate.experiment**==**'Con 2',**]**

s3**<-**data**[**data**$**Replicate.experiment**==**'Con 3',**]**

s4**<-**data**[**data**$**Replicate.experiment**==**'Con 4',**]**

h1**<-**data**[**data**$**Replicate.experiment**==**'Mini 1',**]**

h2**<-**data**[**data**$**Replicate.experiment**==**'Mini 2',**]**

h3**<-**data**[**data**$**Replicate.experiment**==**'Mini 3',**]**

h4**<-**data**[**data**$**Replicate.experiment**==**'Mini 4',**]**

#split in strain

sDBA1**<-**s1**[**s1**$**Strain**==**'DBA/2',**]**

sDBA2**<-**s2**[**s2**$**Strain**==**'DBA/2',**]**

sDBA3**<-**s3**[**s3**$**Strain**==**'DBA/2',**]**

sDBA4**<-**s4**[**s4**$**Strain**==**'DBA/2',**]**

hDBA1**<-**h1**[**h1**$**Strain**==**'DBA/2',**]**

hDBA2**<-**h2**[**h2**$**Strain**==**'DBA/2',**]**

hDBA3**<-**h3**[**h3**$**Strain**==**'DBA/2',**]**

hDBA4**<-**h4**[**h4**$**Strain**==**'DBA/2',**]**

sBL1**<-**s1**[**s1**$**Strain**==**'C57BL/6',**]**

sBL2**<-**s2**[**s2**$**Strain**==**'C57BL/6',**]**

sBL3**<-**s3**[**s3**$**Strain**==**'C57BL/6',**]**

sBL4**<-**s4**[**s4**$**Strain**==**'C57BL/6',**]**

hBL1**<-**h1**[**h1**$**Strain**==**'C57BL/6',**]**

hBL2**<-**h2**[**h2**$**Strain**==**'C57BL/6',**]**

hBL3**<-**h3**[**h3**$**Strain**==**'C57BL/6',**]**

hBL4**<-**h4**[**h4**$**Strain**==**'C57BL/6',**]**

sBALB1**<-**s1**[**s1**$**Strain**==**'Balb/c',**]**

sBALB2**<-**s2**[**s2**$**Strain**==**'Balb/c',**]**

sBALB3**<-**s3**[**s3**$**Strain**==**'Balb/c',**]**

sBALB4**<-**s4**[**s4**$**Strain**==**'Balb/c',**]**

hBALB1**<-**h1**[**h1**$**Strain**==**'Balb/c',**]**

hBALB2**<-**h2**[**h2**$**Strain**==**'Balb/c',**]**

hBALB3**<-**h3**[**h3**$**Strain**==**'Balb/c',**]**

hBALB4**<-**h4**[**h4**$**Strain**==**'Balb/c',**]**

sBDF1**<-**s1**[**s1**$**Strain**==**'B6D2F1',**]**

sBDF2**<-**s2**[**s2**$**Strain**==**'B6D2F1',**]**

sBDF3**<-**s3**[**s3**$**Strain**==**'B6D2F1',**]**

sBDF4**<-**s4**[**s4**$**Strain**==**'B6D2F1',**]**

hBDF1**<-**h1**[**h1**$**Strain**==**'B6D2F1',**]**

hBDF2**<-**h2**[**h2**$**Strain**==**'B6D2F1',**]**

hBDF3**<-**h3**[**h3**$**Strain**==**'B6D2F1',**]**

hBDF4**<-**h4**[**h4**$**Strain**==**'B6D2F1',**]**

###### random effect meta-analysis for each strain comparison ##########

######################################################################

############### 1. BL6 - DBA ###############

#########################################

##### bind data tables in strain effects

##### strain and block as factor

s1\_BL6\_DBA**<-**rbind**(**sBL1,sDBA1**)**

s2\_BL6\_DBA**<-**rbind**(**sBL2,sDBA2**)**

s3\_BL6\_DBA**<-**rbind**(**sBL3,sDBA3**)**

s4\_BL6\_DBA**<-**rbind**(**sBL4,sDBA4**)**

s1\_BL6\_DBA**$**Strain**<-**as.factor**(**s1\_BL6\_DBA**$**Strain**)**

s1\_BL6\_DBA**$**block**<-**as.factor**(**s1\_BL6\_DBA**$**Block**)**

s2\_BL6\_DBA**$**Strain**<-**as.factor**(**s2\_BL6\_DBA**$**Strain**)**

s2\_BL6\_DBA**$**block**<-**as.factor**(**s2\_BL6\_DBA**$**Block**)**

s3\_BL6\_DBA**$**Strain**<-**as.factor**(**s3\_BL6\_DBA**$**Strain**)**

s3\_BL6\_DBA**$**block**<-**as.factor**(**s3\_BL6\_DBA**$**Block**)**

s4\_BL6\_DBA**$**Strain**<-**as.factor**(**s4\_BL6\_DBA**$**Strain**)**

s4\_BL6\_DBA**$**block**<-**as.factor**(**s4\_BL6\_DBA**$**Block**)**

h1\_BL6\_DBA**<-**rbind**(**hBL1,hDBA1**)**

h2\_BL6\_DBA**<-**rbind**(**hBL2,hDBA2**)**

h3\_BL6\_DBA**<-**rbind**(**hBL3,hDBA3**)**

h4\_BL6\_DBA**<-**rbind**(**hBL4,hDBA4**)**

h1\_BL6\_DBA**$**Strain**<-**as.factor**(**h1\_BL6\_DBA**$**Strain**)**

h1\_BL6\_DBA**$**block**<-**as.factor**(**h1\_BL6\_DBA**$**Block**)**

h2\_BL6\_DBA**$**Strain**<-**as.factor**(**h2\_BL6\_DBA**$**Strain**)**

h2\_BL6\_DBA**$**block**<-**as.factor**(**h2\_BL6\_DBA**$**Block**)**

h3\_BL6\_DBA**$**Strain**<-**as.factor**(**h3\_BL6\_DBA**$**Strain**)**

h3\_BL6\_DBA**$**block**<-**as.factor**(**h3\_BL6\_DBA**$**Block**)**

h4\_BL6\_DBA**$**Strain**<-**as.factor**(**h4\_BL6\_DBA**$**Strain**)**

h4\_BL6\_DBA**$**block**<-**as.factor**(**h4\_BL6\_DBA**$**Block**)**

#### Step 1 estimate effect size and SE for each replicate Con1 - Con4 and Mini1 - Mini4 ##############

############################################

### model includes block to account for structure, here Bl6 vs DBA -> effect size estimate + SE

#overview and test run for loop

model**<-**lmer**(**s1\_BL6\_DBA**$**HCB.percentage.active**~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_BL6\_DBA**)**

sum**<-**summary**(**model**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

#### loop for all outcome measures #####

BL6\_DBA**=**matrix**(NA**,nrow **=** 16,ncol **=** 16**)** #create empty matrix to fill in the ES and SE, NA to detect errors when something is missing

rownames**(**BL6\_DBA**)=**c**(**'ES\_s1', 'ES\_s2','ES\_s3','ES\_s4','ES\_h1','ES\_h2','ES\_h3','ES\_h4','SE\_s1', 'SE\_s2','SE\_s3','SE\_s4','SE\_h1','SE\_h2','SE\_h3','SE\_h4'**)**

colnames**(**BL6\_DBA**)<-**names**(**data**)[-**c**(**1**:**5**)]**

####### conventional design replicates #####

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s1\_BL6\_DBA**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_BL6\_DBA**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_DBA**[**1,k**-**5**]<-**ES

BL6\_DBA**[**9,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s2\_BL6\_DBA**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s2\_BL6\_DBA**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_DBA**[**2,k**-**5**]<-**ES

BL6\_DBA**[**10,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s3\_BL6\_DBA**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s3\_BL6\_DBA**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_DBA**[**3,k**-**5**]<-**ES

BL6\_DBA**[**11,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s4\_BL6\_DBA**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s4\_BL6\_DBA**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_DBA**[**4,k**-**5**]<-**ES

BL6\_DBA**[**12,k**-**5**]<-**SE

**}**

##### mini-experiment design replicates #################

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h1\_BL6\_DBA**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h1\_BL6\_DBA**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_DBA**[**5,k**-**5**]<-**ES

BL6\_DBA**[**13,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h2\_BL6\_DBA**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h2\_BL6\_DBA**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_DBA**[**6,k**-**5**]<-**ES

BL6\_DBA**[**14,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h3\_BL6\_DBA**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h3\_BL6\_DBA**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_DBA**[**7,k**-**5**]<-**ES

BL6\_DBA**[**15,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h4\_BL6\_DBA**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h4\_BL6\_DBA**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_DBA**[**8,k**-**5**]<-**ES

BL6\_DBA**[**16,k**-**5**]<-**SE

**}**

#save matrix as csv

write.csv**(**BL6\_DBA, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)\\ESandSE\_BL6\_DBA.csv", row.names **=** **TRUE)**

### Step 2. overall pooled effect (across all replicates, regardless of the design) ######

########## BL6 - DBA ##############

##### Overview and test run ###

yi**<--(**BL6\_DBA**[**c**(**1**:**8**)**,1**])** # ES stored in vector

sei**<-**BL6\_DBA**[**c**(**9**:**16**)**,1**]** # SE stored in vector

# random meta analysis based on ES and SE of all replicate experiments

R\_MA\_model **<-** rma**(**yi, sei**)**

#help(rma)

R\_MA\_model

#overall Effect size and confidence interval

CI\_lb**<-**R\_MA\_model**$**ci.lb

CI\_ub**<-**R\_MA\_model**$**ci.ub

ES**<-**R\_MA\_model**$**beta**[**1,1**]**

###### loop overall effect (ES + CI) for all outcome measures 'BL6- DBA' ########

true\_BL6\_DBA**=**matrix**(NA**,nrow **=** 3,ncol **=** 16**)** #create empty matrix to fill in values, NA to detect errors when something is missing !!! anpassen nrows

rownames**(**true\_BL6\_DBA**)=**c**(**'true ES', 'CI\_lb','CI\_ub'**)**

colnames**(**true\_BL6\_DBA**)<-**names**(**data**)[-**c**(**1**:**5**)]**

**for** **(**k **in** 1**:**16**)** **{**

yi**<--(**BL6\_DBA**[**c**(**1**:**8**)**,k**])**

sei**<-**BL6\_DBA**[**c**(**9**:**16**)**,k**]**

R\_MA\_model **<-** rma**(**yi, sei**)**

R\_MA\_model

CI\_lb**<-**R\_MA\_model**$**ci.lb

CI\_ub**<-**R\_MA\_model**$**ci.ub

ES**<-**R\_MA\_model**$**beta**[**1,1**]**

true\_BL6\_DBA**[**1,k**]<-**ES

true\_BL6\_DBA**[**2,k**]<-**CI\_lb

true\_BL6\_DBA**[**3,k**]<-**CI\_ub

**}**

#save overall effect as csv file

write.csv**(**true\_BL6\_DBA, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)\\overall\_ES\_CI\_BL6\_DBA.csv", row.names **=** **TRUE)**

##########################################################################################

#### Step 3: calculate individual mean strain differences + CI for all replicates to create forest plots (Pc and Pa) afterwards ####

#overview and test run for loop

model**<-**lmer**(**s1\_BL6\_DBA**$**HCB.percentage.active**~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_BL6\_DBA**)**

sum**<-**summary**(**model**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

emmeans**(**model,'Strain'**)**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

CI\_lb**<-**R\_ES**-**CI

CI\_ub**<-**R\_ES**+**CI

######## loop for all outcome measures and all replicates ################

#######################

ES\_BL6\_DBA**=**matrix**(NA**,nrow **=** 8,ncol **=** 18**)** #create empty matrix to fill in values, NA to detect errors when something is missing

colnames**(**ES\_BL6\_DBA**)<-**c**(**names**(**data**)[**c**(**6**:**21**)]**,'Design','Replicate'**)**

rownames**(**ES\_BL6\_DBA**)=**c**(**'Rep S1', 'Rep S2', 'Rep S3','Rep S4','Rep H1', 'Rep H2', 'Rep H3','Rep H4'**)**

CI\_BL6\_DBA**=**matrix**(NA**,nrow **=** 8,ncol **=** 18**)**

colnames**(**CI\_BL6\_DBA**)<-**c**(**names**(**data**)[**c**(**6**:**21**)]**,'Design','Replicate'**)**

rownames**(**CI\_BL6\_DBA**)=**c**(**'Rep S1', 'Rep S2', 'Rep S3','Rep S4','Rep H1', 'Rep H2', 'Rep H3','Rep H4'**)**

#label replicates and design in empty matrix

ES\_BL6\_DBA**[**,18**]<-**c**(**'1','2','3','4','1','2','3','4'**)**

ES\_BL6\_DBA**[**,17**]<-**c**(**'Con','Con','Con','Con','Mini','Mini','Mini','Mini'**)**

CI\_BL6\_DBA**[**,18**]<-**c**(**'1','2','3','4','1','2','3','4'**)**

CI\_BL6\_DBA**[**,17**]<-**c**(**'Con','Con','Con','Con','Mini','Mini','Mini','Mini'**)**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s1\_BL6\_DBA**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_BL6\_DBA**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_DBA**[**1,k**-**5**]<-**R\_ES

CI\_BL6\_DBA**[**1,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s2\_BL6\_DBA**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s2\_BL6\_DBA**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_DBA**[**2,k**-**5**]<-**R\_ES

CI\_BL6\_DBA**[**2,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s3\_BL6\_DBA**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s3\_BL6\_DBA**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_DBA**[**3,k**-**5**]<-**R\_ES

CI\_BL6\_DBA**[**3,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s4\_BL6\_DBA**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s4\_BL6\_DBA**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_DBA**[**4,k**-**5**]<-**R\_ES

CI\_BL6\_DBA**[**4,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h1\_BL6\_DBA**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h1\_BL6\_DBA**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_DBA**[**5,k**-**5**]<-**R\_ES

CI\_BL6\_DBA**[**5,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h2\_BL6\_DBA**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h2\_BL6\_DBA**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_DBA**[**6,k**-**5**]<-**R\_ES

CI\_BL6\_DBA**[**6,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h3\_BL6\_DBA**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h3\_BL6\_DBA**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_DBA**[**7,k**-**5**]<-**R\_ES

CI\_BL6\_DBA**[**7,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h4\_BL6\_DBA**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h4\_BL6\_DBA**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_DBA**[**8,k**-**5**]<-**R\_ES

CI\_BL6\_DBA**[**8,k**-**5**]<-**CI

**}**

write.csv**(**ES\_BL6\_DBA, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)/BL6\_DBA\\ES\_BL6\_DBA.csv", row.names **=** **TRUE)**

write.csv**(**CI\_BL6\_DBA, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)/BL6\_DBA\\CI\_BL6\_DBA.csv", row.names **=** **TRUE)**

############### 2. BL6 - BALB ###############

#########################################

##### bind data tables in strain effects

##### strain and block as factor

s1\_BL6\_BALB**<-**rbind**(**sBL1,sBALB1**)**

s2\_BL6\_BALB**<-**rbind**(**sBL2,sBALB2**)**

s3\_BL6\_BALB**<-**rbind**(**sBL3,sBALB3**)**

s4\_BL6\_BALB**<-**rbind**(**sBL4,sBALB4**)**

s1\_BL6\_BALB**$**Strain**<-**as.factor**(**s1\_BL6\_BALB**$**Strain**)**

s1\_BL6\_BALB**$**block**<-**as.factor**(**s1\_BL6\_BALB**$**Block**)**

s2\_BL6\_BALB**$**Strain**<-**as.factor**(**s2\_BL6\_BALB**$**Strain**)**

s2\_BL6\_BALB**$**block**<-**as.factor**(**s2\_BL6\_BALB**$**Block**)**

s3\_BL6\_BALB**$**Strain**<-**as.factor**(**s3\_BL6\_BALB**$**Strain**)**

s3\_BL6\_BALB**$**block**<-**as.factor**(**s3\_BL6\_BALB**$**Block**)**

s4\_BL6\_BALB**$**Strain**<-**as.factor**(**s4\_BL6\_BALB**$**Strain**)**

s4\_BL6\_BALB**$**block**<-**as.factor**(**s4\_BL6\_BALB**$**Block**)**

h1\_BL6\_BALB**<-**rbind**(**hBL1,hBALB1**)**

h2\_BL6\_BALB**<-**rbind**(**hBL2,hBALB2**)**

h3\_BL6\_BALB**<-**rbind**(**hBL3,hBALB3**)**

h4\_BL6\_BALB**<-**rbind**(**hBL4,hBALB4**)**

h1\_BL6\_BALB**$**Strain**<-**as.factor**(**h1\_BL6\_BALB**$**Strain**)**

h1\_BL6\_BALB**$**block**<-**as.factor**(**h1\_BL6\_BALB**$**Block**)**

h2\_BL6\_BALB**$**Strain**<-**as.factor**(**h2\_BL6\_BALB**$**Strain**)**

h2\_BL6\_BALB**$**block**<-**as.factor**(**h2\_BL6\_BALB**$**Block**)**

h3\_BL6\_BALB**$**Strain**<-**as.factor**(**h3\_BL6\_BALB**$**Strain**)**

h3\_BL6\_BALB**$**block**<-**as.factor**(**h3\_BL6\_BALB**$**Block**)**

h4\_BL6\_BALB**$**Strain**<-**as.factor**(**h4\_BL6\_BALB**$**Strain**)**

h4\_BL6\_BALB**$**block**<-**as.factor**(**h4\_BL6\_BALB**$**Block**)**

#### Step 1 estimate effect size and SE for each replicate Con1 - Con4 and Mini1 - Mini4 ##############

############################################

### model includes block to account for structure, here Bl6 vs BALB -> effect size estimate + SE

#overview and test run for loop

model**<-**lmer**(**s1\_BL6\_BALB**$**HCB.percentage.active**~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_BL6\_BALB**)**

sum**<-**summary**(**model**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

#### loop for all outcome measures #####

BL6\_BALB**=**matrix**(NA**,nrow **=** 16,ncol **=** 16**)** #create empty matrix to fill in the ES and SE, NA to detect errors when something is missing

rownames**(**BL6\_BALB**)=**c**(**'ES\_s1', 'ES\_s2','ES\_s3','ES\_s4','ES\_h1','ES\_h2','ES\_h3','ES\_h4','SE\_s1', 'SE\_s2','SE\_s3','SE\_s4','SE\_h1','SE\_h2','SE\_h3','SE\_h4'**)**

colnames**(**BL6\_BALB**)<-**names**(**data**)[-**c**(**1**:**5**)]**

####### conventional design replicates #####

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s1\_BL6\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_BL6\_BALB**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_BALB**[**1,k**-**5**]<-**ES

BL6\_BALB**[**9,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s2\_BL6\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s2\_BL6\_BALB**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_BALB**[**2,k**-**5**]<-**ES

BL6\_BALB**[**10,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s3\_BL6\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s3\_BL6\_BALB**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_BALB**[**3,k**-**5**]<-**ES

BL6\_BALB**[**11,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s4\_BL6\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s4\_BL6\_BALB**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_BALB**[**4,k**-**5**]<-**ES

BL6\_BALB**[**12,k**-**5**]<-**SE

**}**

##### mini-experiment design replicates #################

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h1\_BL6\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h1\_BL6\_BALB**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_BALB**[**5,k**-**5**]<-**ES

BL6\_BALB**[**13,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h2\_BL6\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h2\_BL6\_BALB**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_BALB**[**6,k**-**5**]<-**ES

BL6\_BALB**[**14,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h3\_BL6\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h3\_BL6\_BALB**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_BALB**[**7,k**-**5**]<-**ES

BL6\_BALB**[**15,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h4\_BL6\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h4\_BL6\_BALB**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_BALB**[**8,k**-**5**]<-**ES

BL6\_BALB**[**16,k**-**5**]<-**SE

**}**

#save matrix as csv

write.csv**(**BL6\_BALB, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)\\ESandSE\_BL6\_BALB.csv", row.names **=** **TRUE)**

### Step 2. overall pooled effect (across all replicates, regardless of the design) ######

########## BL6 - BALB ##############

##### Overview and test run ###

yi**<--(**BL6\_BALB**[**c**(**1**:**8**)**,1**])** # ES stored in vector

sei**<-**BL6\_BALB**[**c**(**9**:**16**)**,1**]** # SE stored in vector

# random meta analysis based on ES and SE of all replicate experiments

R\_MA\_model **<-** rma**(**yi, sei**)**

#help(rma)

R\_MA\_model

#overall Effect size and confidence interval

CI\_lb**<-**R\_MA\_model**$**ci.lb

CI\_ub**<-**R\_MA\_model**$**ci.ub

ES**<-**R\_MA\_model**$**beta**[**1,1**]**

###### loop overall effect (ES + CI) for all outcome measures 'BL6- BALB' ########

true\_BL6\_BALB**=**matrix**(NA**,nrow **=** 3,ncol **=** 16**)** #create empty matrix to fill in values, NA to detect errors when something is missing !!! anpassen nrows

rownames**(**true\_BL6\_BALB**)=**c**(**'true ES', 'CI\_lb','CI\_ub'**)**

colnames**(**true\_BL6\_BALB**)<-**names**(**data**)[-**c**(**1**:**5**)]**

**for** **(**k **in** 1**:**16**)** **{**

yi**<--(**BL6\_BALB**[**c**(**1**:**8**)**,k**])**

sei**<-**BL6\_BALB**[**c**(**9**:**16**)**,k**]**

R\_MA\_model **<-** rma**(**yi, sei**)**

R\_MA\_model

CI\_lb**<-**R\_MA\_model**$**ci.lb

CI\_ub**<-**R\_MA\_model**$**ci.ub

ES**<-**R\_MA\_model**$**beta**[**1,1**]**

true\_BL6\_BALB**[**1,k**]<-**ES

true\_BL6\_BALB**[**2,k**]<-**CI\_lb

true\_BL6\_BALB**[**3,k**]<-**CI\_ub

**}**

#save overall effect as csv file

write.csv**(**true\_BL6\_BALB, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)\\overall\_ES\_CI\_BL6\_BALB.csv", row.names **=** **TRUE)**

##########################################################################################

#### Step 3: calculate individual mean strain differences + CI for all replicates to create forest plots (Pc and Pa) afterwards ####

#overview and test run for loop

model**<-**lmer**(**s1\_BL6\_BALB**$**HCB.percentage.active**~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_BL6\_BALB**)**

sum**<-**summary**(**model**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

emmeans**(**model,'Strain'**)**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

CI\_lb**<-**R\_ES**-**CI

CI\_ub**<-**R\_ES**+**CI

######## loop for all outcome measures and all replicates ################

#######################

ES\_BL6\_BALB**=**matrix**(NA**,nrow **=** 8,ncol **=** 18**)** #create empty matrix to fill in values, NA to detect errors when something is missing

colnames**(**ES\_BL6\_BALB**)<-**c**(**names**(**data**)[**c**(**6**:**21**)]**,'Design','Replicate'**)**

rownames**(**ES\_BL6\_BALB**)=**c**(**'Rep S1', 'Rep S2', 'Rep S3','Rep S4','Rep H1', 'Rep H2', 'Rep H3','Rep H4'**)**

CI\_BL6\_BALB**=**matrix**(NA**,nrow **=** 8,ncol **=** 18**)**

colnames**(**CI\_BL6\_BALB**)<-**c**(**names**(**data**)[**c**(**6**:**21**)]**,'Design','Replicate'**)**

rownames**(**CI\_BL6\_BALB**)=**c**(**'Rep S1', 'Rep S2', 'Rep S3','Rep S4','Rep H1', 'Rep H2', 'Rep H3','Rep H4'**)**

#label replicates and design in empty matrix

ES\_BL6\_BALB**[**,18**]<-**c**(**'1','2','3','4','1','2','3','4'**)**

ES\_BL6\_BALB**[**,17**]<-**c**(**'Con','Con','Con','Con','Mini','Mini','Mini','Mini'**)**

CI\_BL6\_BALB**[**,18**]<-**c**(**'1','2','3','4','1','2','3','4'**)**

CI\_BL6\_BALB**[**,17**]<-**c**(**'Con','Con','Con','Con','Mini','Mini','Mini','Mini'**)**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s1\_BL6\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_BL6\_BALB**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_BALB**[**1,k**-**5**]<-**R\_ES

CI\_BL6\_BALB**[**1,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s2\_BL6\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s2\_BL6\_BALB**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_BALB**[**2,k**-**5**]<-**R\_ES

CI\_BL6\_BALB**[**2,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s3\_BL6\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s3\_BL6\_BALB**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_BALB**[**3,k**-**5**]<-**R\_ES

CI\_BL6\_BALB**[**3,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s4\_BL6\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s4\_BL6\_BALB**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_BALB**[**4,k**-**5**]<-**R\_ES

CI\_BL6\_BALB**[**4,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h1\_BL6\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h1\_BL6\_BALB**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_BALB**[**5,k**-**5**]<-**R\_ES

CI\_BL6\_BALB**[**5,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h2\_BL6\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h2\_BL6\_BALB**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_BALB**[**6,k**-**5**]<-**R\_ES

CI\_BL6\_BALB**[**6,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h3\_BL6\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h3\_BL6\_BALB**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_BALB**[**7,k**-**5**]<-**R\_ES

CI\_BL6\_BALB**[**7,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h4\_BL6\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h4\_BL6\_BALB**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_BALB**[**8,k**-**5**]<-**R\_ES

CI\_BL6\_BALB**[**8,k**-**5**]<-**CI

**}**

write.csv**(**ES\_BL6\_BALB, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)/BL6\_BALB\\ES\_BL6\_BALB.csv", row.names **=** **TRUE)**

write.csv**(**CI\_BL6\_BALB, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)/BL6\_BALB\\CI\_BL6\_BALB.csv", row.names **=** **TRUE)**

############### 3. BL6 - BDF ###############

#########################################

##### bind data tables in strain effects

##### strain and block as factor

s1\_BL6\_BDF**<-**rbind**(**sBL1,sBDF1**)**

s2\_BL6\_BDF**<-**rbind**(**sBL2,sBDF2**)**

s3\_BL6\_BDF**<-**rbind**(**sBL3,sBDF3**)**

s4\_BL6\_BDF**<-**rbind**(**sBL4,sBDF4**)**

s1\_BL6\_BDF**$**Strain**<-**as.factor**(**s1\_BL6\_BDF**$**Strain**)**

s1\_BL6\_BDF**$**block**<-**as.factor**(**s1\_BL6\_BDF**$**Block**)**

s2\_BL6\_BDF**$**Strain**<-**as.factor**(**s2\_BL6\_BDF**$**Strain**)**

s2\_BL6\_BDF**$**block**<-**as.factor**(**s2\_BL6\_BDF**$**Block**)**

s3\_BL6\_BDF**$**Strain**<-**as.factor**(**s3\_BL6\_BDF**$**Strain**)**

s3\_BL6\_BDF**$**block**<-**as.factor**(**s3\_BL6\_BDF**$**Block**)**

s4\_BL6\_BDF**$**Strain**<-**as.factor**(**s4\_BL6\_BDF**$**Strain**)**

s4\_BL6\_BDF**$**block**<-**as.factor**(**s4\_BL6\_BDF**$**Block**)**

h1\_BL6\_BDF**<-**rbind**(**hBL1,hBDF1**)**

h2\_BL6\_BDF**<-**rbind**(**hBL2,hBDF2**)**

h3\_BL6\_BDF**<-**rbind**(**hBL3,hBDF3**)**

h4\_BL6\_BDF**<-**rbind**(**hBL4,hBDF4**)**

h1\_BL6\_BDF**$**Strain**<-**as.factor**(**h1\_BL6\_BDF**$**Strain**)**

h1\_BL6\_BDF**$**block**<-**as.factor**(**h1\_BL6\_BDF**$**Block**)**

h2\_BL6\_BDF**$**Strain**<-**as.factor**(**h2\_BL6\_BDF**$**Strain**)**

h2\_BL6\_BDF**$**block**<-**as.factor**(**h2\_BL6\_BDF**$**Block**)**

h3\_BL6\_BDF**$**Strain**<-**as.factor**(**h3\_BL6\_BDF**$**Strain**)**

h3\_BL6\_BDF**$**block**<-**as.factor**(**h3\_BL6\_BDF**$**Block**)**

h4\_BL6\_BDF**$**Strain**<-**as.factor**(**h4\_BL6\_BDF**$**Strain**)**

h4\_BL6\_BDF**$**block**<-**as.factor**(**h4\_BL6\_BDF**$**Block**)**

#### Step 1 estimate effect size and SE for each replicate Con1 - Con4 and Mini1 - Mini4 ##############

############################################

### model includes block to account for structure, here Bl6 vs BDF -> effect size estimate + SE

#overview and test run for loop

model**<-**lmer**(**s1\_BL6\_BDF**$**HCB.percentage.active**~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_BL6\_BDF**)**

sum**<-**summary**(**model**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

#### loop for all outcome measures #####

BL6\_BDF**=**matrix**(NA**,nrow **=** 16,ncol **=** 16**)** #create empty matrix to fill in the ES and SE, NA to detect errors when something is missing

rownames**(**BL6\_BDF**)=**c**(**'ES\_s1', 'ES\_s2','ES\_s3','ES\_s4','ES\_h1','ES\_h2','ES\_h3','ES\_h4','SE\_s1', 'SE\_s2','SE\_s3','SE\_s4','SE\_h1','SE\_h2','SE\_h3','SE\_h4'**)**

colnames**(**BL6\_BDF**)<-**names**(**data**)[-**c**(**1**:**5**)]**

####### conventional design replicates #####

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s1\_BL6\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_BL6\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_BDF**[**1,k**-**5**]<-**ES

BL6\_BDF**[**9,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s2\_BL6\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s2\_BL6\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_BDF**[**2,k**-**5**]<-**ES

BL6\_BDF**[**10,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s3\_BL6\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s3\_BL6\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_BDF**[**3,k**-**5**]<-**ES

BL6\_BDF**[**11,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s4\_BL6\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s4\_BL6\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_BDF**[**4,k**-**5**]<-**ES

BL6\_BDF**[**12,k**-**5**]<-**SE

**}**

##### mini-experiment design replicates #################

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h1\_BL6\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h1\_BL6\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_BDF**[**5,k**-**5**]<-**ES

BL6\_BDF**[**13,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h2\_BL6\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h2\_BL6\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_BDF**[**6,k**-**5**]<-**ES

BL6\_BDF**[**14,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h3\_BL6\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h3\_BL6\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_BDF**[**7,k**-**5**]<-**ES

BL6\_BDF**[**15,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h4\_BL6\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h4\_BL6\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BL6\_BDF**[**8,k**-**5**]<-**ES

BL6\_BDF**[**16,k**-**5**]<-**SE

**}**

#save matrix as csv

write.csv**(**BL6\_BDF, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)\\ESandSE\_BL6\_BDF.csv", row.names **=** **TRUE)**

### Step 2. overall pooled effect (across all replicates, regardless of the design) ######

########## BL6 - BDF ##############

##### Overview and test run ###

yi**<--(**BL6\_BDF**[**c**(**1**:**8**)**,1**])** # ES stored in vector

sei**<-**BL6\_BDF**[**c**(**9**:**16**)**,1**]** # SE stored in vector

# random meta analysis based on ES and SE of all replicate experiments

R\_MA\_model **<-** rma**(**yi, sei**)**

#help(rma)

R\_MA\_model

#overall Effect size and confidence interval

CI\_lb**<-**R\_MA\_model**$**ci.lb

CI\_ub**<-**R\_MA\_model**$**ci.ub

ES**<-**R\_MA\_model**$**beta**[**1,1**]**

###### loop overall effect (ES + CI) for all outcome measures 'BL6- BDF' ########

true\_BL6\_BDF**=**matrix**(NA**,nrow **=** 3,ncol **=** 16**)** #create empty matrix to fill in values, NA to detect errors when something is missing !!! anpassen nrows

rownames**(**true\_BL6\_BDF**)=**c**(**'true ES', 'CI\_lb','CI\_ub'**)**

colnames**(**true\_BL6\_BDF**)<-**names**(**data**)[-**c**(**1**:**5**)]**

**for** **(**k **in** 1**:**16**)** **{**

yi**<--(**BL6\_BDF**[**c**(**1**:**8**)**,k**])**

sei**<-**BL6\_BDF**[**c**(**9**:**16**)**,k**]**

R\_MA\_model **<-** rma**(**yi, sei**)**

R\_MA\_model

CI\_lb**<-**R\_MA\_model**$**ci.lb

CI\_ub**<-**R\_MA\_model**$**ci.ub

ES**<-**R\_MA\_model**$**beta**[**1,1**]**

true\_BL6\_BDF**[**1,k**]<-**ES

true\_BL6\_BDF**[**2,k**]<-**CI\_lb

true\_BL6\_BDF**[**3,k**]<-**CI\_ub

**}**

#save overall effect as csv file

write.csv**(**true\_BL6\_BDF, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)\\overall\_ES\_CI\_BL6\_BDF.csv", row.names **=** **TRUE)**

##########################################################################################

#### Step 3: calculate individual mean strain differences + CI for all replicates to create forest plots (Pc and Pa) afterwards ####

#overview and test run for loop

model**<-**lmer**(**s1\_BL6\_BDF**$**HCB.percentage.active**~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_BL6\_BDF**)**

sum**<-**summary**(**model**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

emmeans**(**model,'Strain'**)**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

CI\_lb**<-**R\_ES**-**CI

CI\_ub**<-**R\_ES**+**CI

######## loop for all outcome measures and all replicates ################

#######################

ES\_BL6\_BDF**=**matrix**(NA**,nrow **=** 8,ncol **=** 18**)** #create empty matrix to fill in values, NA to detect errors when something is missing

colnames**(**ES\_BL6\_BDF**)<-**c**(**names**(**data**)[**c**(**6**:**21**)]**,'Design','Replicate'**)**

rownames**(**ES\_BL6\_BDF**)=**c**(**'Rep S1', 'Rep S2', 'Rep S3','Rep S4','Rep H1', 'Rep H2', 'Rep H3','Rep H4'**)**

CI\_BL6\_BDF**=**matrix**(NA**,nrow **=** 8,ncol **=** 18**)**

colnames**(**CI\_BL6\_BDF**)<-**c**(**names**(**data**)[**c**(**6**:**21**)]**,'Design','Replicate'**)**

rownames**(**CI\_BL6\_BDF**)=**c**(**'Rep S1', 'Rep S2', 'Rep S3','Rep S4','Rep H1', 'Rep H2', 'Rep H3','Rep H4'**)**

#label replicates and design in empty matrix

ES\_BL6\_BDF**[**,18**]<-**c**(**'1','2','3','4','1','2','3','4'**)**

ES\_BL6\_BDF**[**,17**]<-**c**(**'Con','Con','Con','Con','Mini','Mini','Mini','Mini'**)**

CI\_BL6\_BDF**[**,18**]<-**c**(**'1','2','3','4','1','2','3','4'**)**

CI\_BL6\_BDF**[**,17**]<-**c**(**'Con','Con','Con','Con','Mini','Mini','Mini','Mini'**)**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s1\_BL6\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_BL6\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_BDF**[**1,k**-**5**]<-**R\_ES

CI\_BL6\_BDF**[**1,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s2\_BL6\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s2\_BL6\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_BDF**[**2,k**-**5**]<-**R\_ES

CI\_BL6\_BDF**[**2,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s3\_BL6\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s3\_BL6\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_BDF**[**3,k**-**5**]<-**R\_ES

CI\_BL6\_BDF**[**3,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s4\_BL6\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s4\_BL6\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_BDF**[**4,k**-**5**]<-**R\_ES

CI\_BL6\_BDF**[**4,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h1\_BL6\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h1\_BL6\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_BDF**[**5,k**-**5**]<-**R\_ES

CI\_BL6\_BDF**[**5,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h2\_BL6\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h2\_BL6\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_BDF**[**6,k**-**5**]<-**R\_ES

CI\_BL6\_BDF**[**6,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h3\_BL6\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h3\_BL6\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_BDF**[**7,k**-**5**]<-**R\_ES

CI\_BL6\_BDF**[**7,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h4\_BL6\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h4\_BL6\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BL6\_BDF**[**8,k**-**5**]<-**R\_ES

CI\_BL6\_BDF**[**8,k**-**5**]<-**CI

**}**

write.csv**(**ES\_BL6\_BDF, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)/BL6\_BDF\\ES\_BL6\_BDF.csv", row.names **=** **TRUE)**

write.csv**(**CI\_BL6\_BDF, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)/BL6\_BDF\\CI\_BL6\_BDF.csv", row.names **=** **TRUE)**

############### 4. DBA - BALB ###############

#########################################

##### bind data tables in strain effects

##### strain and block as factor

s1\_DBA\_BALB**<-**rbind**(**sDBA1,sBALB1**)**

s2\_DBA\_BALB**<-**rbind**(**sDBA2,sBALB2**)**

s3\_DBA\_BALB**<-**rbind**(**sDBA3,sBALB3**)**

s4\_DBA\_BALB**<-**rbind**(**sDBA4,sBALB4**)**

s1\_DBA\_BALB**$**Strain**<-**as.factor**(**s1\_DBA\_BALB**$**Strain**)**

s1\_DBA\_BALB**$**block**<-**as.factor**(**s1\_DBA\_BALB**$**Block**)**

s2\_DBA\_BALB**$**Strain**<-**as.factor**(**s2\_DBA\_BALB**$**Strain**)**

s2\_DBA\_BALB**$**block**<-**as.factor**(**s2\_DBA\_BALB**$**Block**)**

s3\_DBA\_BALB**$**Strain**<-**as.factor**(**s3\_DBA\_BALB**$**Strain**)**

s3\_DBA\_BALB**$**block**<-**as.factor**(**s3\_DBA\_BALB**$**Block**)**

s4\_DBA\_BALB**$**Strain**<-**as.factor**(**s4\_DBA\_BALB**$**Strain**)**

s4\_DBA\_BALB**$**block**<-**as.factor**(**s4\_DBA\_BALB**$**Block**)**

h1\_DBA\_BALB**<-**rbind**(**hDBA1,hBALB1**)**

h2\_DBA\_BALB**<-**rbind**(**hDBA2,hBALB2**)**

h3\_DBA\_BALB**<-**rbind**(**hDBA3,hBALB3**)**

h4\_DBA\_BALB**<-**rbind**(**hDBA4,hBALB4**)**

h1\_DBA\_BALB**$**Strain**<-**as.factor**(**h1\_DBA\_BALB**$**Strain**)**

h1\_DBA\_BALB**$**block**<-**as.factor**(**h1\_DBA\_BALB**$**Block**)**

h2\_DBA\_BALB**$**Strain**<-**as.factor**(**h2\_DBA\_BALB**$**Strain**)**

h2\_DBA\_BALB**$**block**<-**as.factor**(**h2\_DBA\_BALB**$**Block**)**

h3\_DBA\_BALB**$**Strain**<-**as.factor**(**h3\_DBA\_BALB**$**Strain**)**

h3\_DBA\_BALB**$**block**<-**as.factor**(**h3\_DBA\_BALB**$**Block**)**

h4\_DBA\_BALB**$**Strain**<-**as.factor**(**h4\_DBA\_BALB**$**Strain**)**

h4\_DBA\_BALB**$**block**<-**as.factor**(**h4\_DBA\_BALB**$**Block**)**

#### Step 1 estimate effect size and SE for each replicate Con1 - Con4 and Mini1 - Mini4 ##############

############################################

### model includes block to account for structure, here DBA vs BALB -> effect size estimate + SE

#overview and test run for loop

model**<-**lmer**(**s1\_DBA\_BALB**$**HCB.percentage.active**~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_DBA\_BALB**)**

sum**<-**summary**(**model**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

#### loop for all outcome measures #####

DBA\_BALB**=**matrix**(NA**,nrow **=** 16,ncol **=** 16**)** #create empty matrix to fill in the ES and SE, NA to detect errors when something is missing

rownames**(**DBA\_BALB**)=**c**(**'ES\_s1', 'ES\_s2','ES\_s3','ES\_s4','ES\_h1','ES\_h2','ES\_h3','ES\_h4','SE\_s1', 'SE\_s2','SE\_s3','SE\_s4','SE\_h1','SE\_h2','SE\_h3','SE\_h4'**)**

colnames**(**DBA\_BALB**)<-**names**(**data**)[-**c**(**1**:**5**)]**

####### conventional design replicates #####

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s1\_DBA\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_DBA\_BALB**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

DBA\_BALB**[**1,k**-**5**]<-**ES

DBA\_BALB**[**9,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s2\_DBA\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s2\_DBA\_BALB**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

DBA\_BALB**[**2,k**-**5**]<-**ES

DBA\_BALB**[**10,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s3\_DBA\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s3\_DBA\_BALB**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

DBA\_BALB**[**3,k**-**5**]<-**ES

DBA\_BALB**[**11,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s4\_DBA\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s4\_DBA\_BALB**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

DBA\_BALB**[**4,k**-**5**]<-**ES

DBA\_BALB**[**12,k**-**5**]<-**SE

**}**

##### mini-experiment design replicates #################

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h1\_DBA\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h1\_DBA\_BALB**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

DBA\_BALB**[**5,k**-**5**]<-**ES

DBA\_BALB**[**13,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h2\_DBA\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h2\_DBA\_BALB**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

DBA\_BALB**[**6,k**-**5**]<-**ES

DBA\_BALB**[**14,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h3\_DBA\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h3\_DBA\_BALB**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

DBA\_BALB**[**7,k**-**5**]<-**ES

DBA\_BALB**[**15,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h4\_DBA\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h4\_DBA\_BALB**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

DBA\_BALB**[**8,k**-**5**]<-**ES

DBA\_BALB**[**16,k**-**5**]<-**SE

**}**

#save matrix as csv

write.csv**(**DBA\_BALB, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)\\ESandSE\_DBA\_BALB.csv", row.names **=** **TRUE)**

### Step 2. overall pooled effect (across all replicates, regardless of the design) ######

########## DBA - BALB ##############

##### Overview and test run ###

yi**<--(**DBA\_BALB**[**c**(**1**:**8**)**,1**])** # ES stored in vector

sei**<-**DBA\_BALB**[**c**(**9**:**16**)**,1**]** # SE stored in vector

# random meta analysis based on ES and SE of all replicate experiments

R\_MA\_model **<-** rma**(**yi, sei**)**

#help(rma)

R\_MA\_model

#overall Effect size and confidence interval

CI\_lb**<-**R\_MA\_model**$**ci.lb

CI\_ub**<-**R\_MA\_model**$**ci.ub

ES**<-**R\_MA\_model**$**beta**[**1,1**]**

###### loop overall effect (ES + CI) for all outcome measures 'DBA- BALB' ########

true\_DBA\_BALB**=**matrix**(NA**,nrow **=** 3,ncol **=** 16**)** #create empty matrix to fill in values, NA to detect errors when something is missing !!! anpassen nrows

rownames**(**true\_DBA\_BALB**)=**c**(**'true ES', 'CI\_lb','CI\_ub'**)**

colnames**(**true\_DBA\_BALB**)<-**names**(**data**)[-**c**(**1**:**5**)]**

**for** **(**k **in** 1**:**16**)** **{**

yi**<--(**DBA\_BALB**[**c**(**1**:**8**)**,k**])**

sei**<-**DBA\_BALB**[**c**(**9**:**16**)**,k**]**

R\_MA\_model **<-** rma**(**yi, sei**)**

R\_MA\_model

CI\_lb**<-**R\_MA\_model**$**ci.lb

CI\_ub**<-**R\_MA\_model**$**ci.ub

ES**<-**R\_MA\_model**$**beta**[**1,1**]**

true\_DBA\_BALB**[**1,k**]<-**ES

true\_DBA\_BALB**[**2,k**]<-**CI\_lb

true\_DBA\_BALB**[**3,k**]<-**CI\_ub

**}**

#save overall effect as csv file

write.csv**(**true\_DBA\_BALB, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)\\overall\_ES\_CI\_DBA\_BALB.csv", row.names **=** **TRUE)**

##########################################################################################

#### Step 3: calculate individual mean strain differences + CI for all replicates to create forest plots (Pc and Pa) afterwards ####

#overview and test run for loop

model**<-**lmer**(**s1\_DBA\_BALB**$**HCB.percentage.active**~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_DBA\_BALB**)**

sum**<-**summary**(**model**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

emmeans**(**model,'Strain'**)**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

CI\_lb**<-**R\_ES**-**CI

CI\_ub**<-**R\_ES**+**CI

######## loop for all outcome measures and all replicates ################

#######################

ES\_DBA\_BALB**=**matrix**(NA**,nrow **=** 8,ncol **=** 18**)** #create empty matrix to fill in values, NA to detect errors when something is missing

colnames**(**ES\_DBA\_BALB**)<-**c**(**names**(**data**)[**c**(**6**:**21**)]**,'Design','Replicate'**)**

rownames**(**ES\_DBA\_BALB**)=**c**(**'Rep S1', 'Rep S2', 'Rep S3','Rep S4','Rep H1', 'Rep H2', 'Rep H3','Rep H4'**)**

CI\_DBA\_BALB**=**matrix**(NA**,nrow **=** 8,ncol **=** 18**)**

colnames**(**CI\_DBA\_BALB**)<-**c**(**names**(**data**)[**c**(**6**:**21**)]**,'Design','Replicate'**)**

rownames**(**CI\_DBA\_BALB**)=**c**(**'Rep S1', 'Rep S2', 'Rep S3','Rep S4','Rep H1', 'Rep H2', 'Rep H3','Rep H4'**)**

#label replicates and design in empty matrix

ES\_DBA\_BALB**[**,18**]<-**c**(**'1','2','3','4','1','2','3','4'**)**

ES\_DBA\_BALB**[**,17**]<-**c**(**'Con','Con','Con','Con','Mini','Mini','Mini','Mini'**)**

CI\_DBA\_BALB**[**,18**]<-**c**(**'1','2','3','4','1','2','3','4'**)**

CI\_DBA\_BALB**[**,17**]<-**c**(**'Con','Con','Con','Con','Mini','Mini','Mini','Mini'**)**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s1\_DBA\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_DBA\_BALB**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_DBA\_BALB**[**1,k**-**5**]<-**R\_ES

CI\_DBA\_BALB**[**1,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s2\_DBA\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s2\_DBA\_BALB**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_DBA\_BALB**[**2,k**-**5**]<-**R\_ES

CI\_DBA\_BALB**[**2,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s3\_DBA\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s3\_DBA\_BALB**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_DBA\_BALB**[**3,k**-**5**]<-**R\_ES

CI\_DBA\_BALB**[**3,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s4\_DBA\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s4\_DBA\_BALB**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_DBA\_BALB**[**4,k**-**5**]<-**R\_ES

CI\_DBA\_BALB**[**4,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h1\_DBA\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h1\_DBA\_BALB**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_DBA\_BALB**[**5,k**-**5**]<-**R\_ES

CI\_DBA\_BALB**[**5,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h2\_DBA\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h2\_DBA\_BALB**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_DBA\_BALB**[**6,k**-**5**]<-**R\_ES

CI\_DBA\_BALB**[**6,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h3\_DBA\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h3\_DBA\_BALB**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_DBA\_BALB**[**7,k**-**5**]<-**R\_ES

CI\_DBA\_BALB**[**7,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h4\_DBA\_BALB**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h4\_DBA\_BALB**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_DBA\_BALB**[**8,k**-**5**]<-**R\_ES

CI\_DBA\_BALB**[**8,k**-**5**]<-**CI

**}**

write.csv**(**ES\_DBA\_BALB, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)/DBA\_BALB\\ES\_DBA\_BALB.csv", row.names **=** **TRUE)**

write.csv**(**CI\_DBA\_BALB, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)/DBA\_BALB\\CI\_DBA\_BALB.csv", row.names **=** **TRUE)**

############### 5. DBA - BDF ###############

#########################################

##### bind data tables in strain effects

##### strain and block as factor

s1\_DBA\_BDF**<-**rbind**(**sDBA1,sBDF1**)**

s2\_DBA\_BDF**<-**rbind**(**sDBA2,sBDF2**)**

s3\_DBA\_BDF**<-**rbind**(**sDBA3,sBDF3**)**

s4\_DBA\_BDF**<-**rbind**(**sDBA4,sBDF4**)**

s1\_DBA\_BDF**$**Strain**<-**as.factor**(**s1\_DBA\_BDF**$**Strain**)**

s1\_DBA\_BDF**$**block**<-**as.factor**(**s1\_DBA\_BDF**$**Block**)**

s2\_DBA\_BDF**$**Strain**<-**as.factor**(**s2\_DBA\_BDF**$**Strain**)**

s2\_DBA\_BDF**$**block**<-**as.factor**(**s2\_DBA\_BDF**$**Block**)**

s3\_DBA\_BDF**$**Strain**<-**as.factor**(**s3\_DBA\_BDF**$**Strain**)**

s3\_DBA\_BDF**$**block**<-**as.factor**(**s3\_DBA\_BDF**$**Block**)**

s4\_DBA\_BDF**$**Strain**<-**as.factor**(**s4\_DBA\_BDF**$**Strain**)**

s4\_DBA\_BDF**$**block**<-**as.factor**(**s4\_DBA\_BDF**$**Block**)**

h1\_DBA\_BDF**<-**rbind**(**hDBA1,hBDF1**)**

h2\_DBA\_BDF**<-**rbind**(**hDBA2,hBDF2**)**

h3\_DBA\_BDF**<-**rbind**(**hDBA3,hBDF3**)**

h4\_DBA\_BDF**<-**rbind**(**hDBA4,hBDF4**)**

h1\_DBA\_BDF**$**Strain**<-**as.factor**(**h1\_DBA\_BDF**$**Strain**)**

h1\_DBA\_BDF**$**block**<-**as.factor**(**h1\_DBA\_BDF**$**Block**)**

h2\_DBA\_BDF**$**Strain**<-**as.factor**(**h2\_DBA\_BDF**$**Strain**)**

h2\_DBA\_BDF**$**block**<-**as.factor**(**h2\_DBA\_BDF**$**Block**)**

h3\_DBA\_BDF**$**Strain**<-**as.factor**(**h3\_DBA\_BDF**$**Strain**)**

h3\_DBA\_BDF**$**block**<-**as.factor**(**h3\_DBA\_BDF**$**Block**)**

h4\_DBA\_BDF**$**Strain**<-**as.factor**(**h4\_DBA\_BDF**$**Strain**)**

h4\_DBA\_BDF**$**block**<-**as.factor**(**h4\_DBA\_BDF**$**Block**)**

#### Step 1 estimate effect size and SE for each replicate Con1 - Con4 and Mini1 - Mini4 ##############

############################################

### model includes block to account for structure, here DBA vs BDF -> effect size estimate + SE

#overview and test run for loop

model**<-**lmer**(**s1\_DBA\_BDF**$**HCB.percentage.active**~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_DBA\_BDF**)**

sum**<-**summary**(**model**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

#### loop for all outcome measures #####

DBA\_BDF**=**matrix**(NA**,nrow **=** 16,ncol **=** 16**)** #create empty matrix to fill in the ES and SE, NA to detect errors when something is missing

rownames**(**DBA\_BDF**)=**c**(**'ES\_s1', 'ES\_s2','ES\_s3','ES\_s4','ES\_h1','ES\_h2','ES\_h3','ES\_h4','SE\_s1', 'SE\_s2','SE\_s3','SE\_s4','SE\_h1','SE\_h2','SE\_h3','SE\_h4'**)**

colnames**(**DBA\_BDF**)<-**names**(**data**)[-**c**(**1**:**5**)]**

####### conventional design replicates #####

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s1\_DBA\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_DBA\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

DBA\_BDF**[**1,k**-**5**]<-**ES

DBA\_BDF**[**9,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s2\_DBA\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s2\_DBA\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

DBA\_BDF**[**2,k**-**5**]<-**ES

DBA\_BDF**[**10,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s3\_DBA\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s3\_DBA\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

DBA\_BDF**[**3,k**-**5**]<-**ES

DBA\_BDF**[**11,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s4\_DBA\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s4\_DBA\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

DBA\_BDF**[**4,k**-**5**]<-**ES

DBA\_BDF**[**12,k**-**5**]<-**SE

**}**

##### mini-experiment design replicates #################

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h1\_DBA\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h1\_DBA\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

DBA\_BDF**[**5,k**-**5**]<-**ES

DBA\_BDF**[**13,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h2\_DBA\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h2\_DBA\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

DBA\_BDF**[**6,k**-**5**]<-**ES

DBA\_BDF**[**14,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h3\_DBA\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h3\_DBA\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

DBA\_BDF**[**7,k**-**5**]<-**ES

DBA\_BDF**[**15,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h4\_DBA\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h4\_DBA\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

DBA\_BDF**[**8,k**-**5**]<-**ES

DBA\_BDF**[**16,k**-**5**]<-**SE

**}**

#save matrix as csv

write.csv**(**DBA\_BDF, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)\\ESandSE\_DBA\_BDF.csv", row.names **=** **TRUE)**

### Step 2. overall pooled effect (across all replicates, regardless of the design) ######

########## DBA - BDF ##############

##### Overview and test run ###

yi**<--(**DBA\_BDF**[**c**(**1**:**8**)**,1**])** # ES stored in vector

sei**<-**DBA\_BDF**[**c**(**9**:**16**)**,1**]** # SE stored in vector

# random meta analysis based on ES and SE of all replicate experiments

R\_MA\_model **<-** rma**(**yi, sei**)**

#help(rma)

R\_MA\_model

#overall Effect size and confidence interval

CI\_lb**<-**R\_MA\_model**$**ci.lb

CI\_ub**<-**R\_MA\_model**$**ci.ub

ES**<-**R\_MA\_model**$**beta**[**1,1**]**

###### loop overall effect (ES + CI) for all outcome measures 'DBA- BDF' ########

true\_DBA\_BDF**=**matrix**(NA**,nrow **=** 3,ncol **=** 16**)** #create empty matrix to fill in values, NA to detect errors when something is missing !!! anpassen nrows

rownames**(**true\_DBA\_BDF**)=**c**(**'true ES', 'CI\_lb','CI\_ub'**)**

colnames**(**true\_DBA\_BDF**)<-**names**(**data**)[-**c**(**1**:**5**)]**

**for** **(**k **in** 1**:**16**)** **{**

yi**<--(**DBA\_BDF**[**c**(**1**:**8**)**,k**])**

sei**<-**DBA\_BDF**[**c**(**9**:**16**)**,k**]**

R\_MA\_model **<-** rma**(**yi, sei**)**

R\_MA\_model

CI\_lb**<-**R\_MA\_model**$**ci.lb

CI\_ub**<-**R\_MA\_model**$**ci.ub

ES**<-**R\_MA\_model**$**beta**[**1,1**]**

true\_DBA\_BDF**[**1,k**]<-**ES

true\_DBA\_BDF**[**2,k**]<-**CI\_lb

true\_DBA\_BDF**[**3,k**]<-**CI\_ub

**}**

#save overall effect as csv file

write.csv**(**true\_DBA\_BDF, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)\\overall\_ES\_CI\_DBA\_BDF.csv", row.names **=** **TRUE)**

##########################################################################################

#### Step 3: calculate individual mean strain differences + CI for all replicates to create forest plots (Pc and Pa) afterwards ####

#overview and test run for loop

model**<-**lmer**(**s1\_DBA\_BDF**$**HCB.percentage.active**~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_DBA\_BDF**)**

sum**<-**summary**(**model**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

emmeans**(**model,'Strain'**)**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

CI\_lb**<-**R\_ES**-**CI

CI\_ub**<-**R\_ES**+**CI

######## loop for all outcome measures and all replicates ################

#######################

ES\_DBA\_BDF**=**matrix**(NA**,nrow **=** 8,ncol **=** 18**)** #create empty matrix to fill in values, NA to detect errors when something is missing

colnames**(**ES\_DBA\_BDF**)<-**c**(**names**(**data**)[**c**(**6**:**21**)]**,'Design','Replicate'**)**

rownames**(**ES\_DBA\_BDF**)=**c**(**'Rep S1', 'Rep S2', 'Rep S3','Rep S4','Rep H1', 'Rep H2', 'Rep H3','Rep H4'**)**

CI\_DBA\_BDF**=**matrix**(NA**,nrow **=** 8,ncol **=** 18**)**

colnames**(**CI\_DBA\_BDF**)<-**c**(**names**(**data**)[**c**(**6**:**21**)]**,'Design','Replicate'**)**

rownames**(**CI\_DBA\_BDF**)=**c**(**'Rep S1', 'Rep S2', 'Rep S3','Rep S4','Rep H1', 'Rep H2', 'Rep H3','Rep H4'**)**

#label replicates and design in empty matrix

ES\_DBA\_BDF**[**,18**]<-**c**(**'1','2','3','4','1','2','3','4'**)**

ES\_DBA\_BDF**[**,17**]<-**c**(**'Con','Con','Con','Con','Mini','Mini','Mini','Mini'**)**

CI\_DBA\_BDF**[**,18**]<-**c**(**'1','2','3','4','1','2','3','4'**)**

CI\_DBA\_BDF**[**,17**]<-**c**(**'Con','Con','Con','Con','Mini','Mini','Mini','Mini'**)**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s1\_DBA\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_DBA\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_DBA\_BDF**[**1,k**-**5**]<-**R\_ES

CI\_DBA\_BDF**[**1,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s2\_DBA\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s2\_DBA\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_DBA\_BDF**[**2,k**-**5**]<-**R\_ES

CI\_DBA\_BDF**[**2,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s3\_DBA\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s3\_DBA\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_DBA\_BDF**[**3,k**-**5**]<-**R\_ES

CI\_DBA\_BDF**[**3,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s4\_DBA\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s4\_DBA\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_DBA\_BDF**[**4,k**-**5**]<-**R\_ES

CI\_DBA\_BDF**[**4,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h1\_DBA\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h1\_DBA\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_DBA\_BDF**[**5,k**-**5**]<-**R\_ES

CI\_DBA\_BDF**[**5,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h2\_DBA\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h2\_DBA\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_DBA\_BDF**[**6,k**-**5**]<-**R\_ES

CI\_DBA\_BDF**[**6,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h3\_DBA\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h3\_DBA\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_DBA\_BDF**[**7,k**-**5**]<-**R\_ES

CI\_DBA\_BDF**[**7,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h4\_DBA\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h4\_DBA\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_DBA\_BDF**[**8,k**-**5**]<-**R\_ES

CI\_DBA\_BDF**[**8,k**-**5**]<-**CI

**}**

write.csv**(**ES\_DBA\_BDF, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)/DBA\_BDF\\ES\_DBA\_BDF.csv", row.names **=** **TRUE)**

write.csv**(**CI\_DBA\_BDF, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)/DBA\_BDF\\CI\_DBA\_BDF.csv", row.names **=** **TRUE)**

############### 6. BALB - BDF ###############

#########################################

##### bind data tables in strain effects

##### strain and block as factor

s1\_BALB\_BDF**<-**rbind**(**sBALB1,sBDF1**)**

s2\_BALB\_BDF**<-**rbind**(**sBALB2,sBDF2**)**

s3\_BALB\_BDF**<-**rbind**(**sBALB3,sBDF3**)**

s4\_BALB\_BDF**<-**rbind**(**sBALB4,sBDF4**)**

s1\_BALB\_BDF**$**Strain**<-**as.factor**(**s1\_BALB\_BDF**$**Strain**)**

s1\_BALB\_BDF**$**block**<-**as.factor**(**s1\_BALB\_BDF**$**Block**)**

s2\_BALB\_BDF**$**Strain**<-**as.factor**(**s2\_BALB\_BDF**$**Strain**)**

s2\_BALB\_BDF**$**block**<-**as.factor**(**s2\_BALB\_BDF**$**Block**)**

s3\_BALB\_BDF**$**Strain**<-**as.factor**(**s3\_BALB\_BDF**$**Strain**)**

s3\_BALB\_BDF**$**block**<-**as.factor**(**s3\_BALB\_BDF**$**Block**)**

s4\_BALB\_BDF**$**Strain**<-**as.factor**(**s4\_BALB\_BDF**$**Strain**)**

s4\_BALB\_BDF**$**block**<-**as.factor**(**s4\_BALB\_BDF**$**Block**)**

h1\_BALB\_BDF**<-**rbind**(**hBALB1,hBDF1**)**

h2\_BALB\_BDF**<-**rbind**(**hBALB2,hBDF2**)**

h3\_BALB\_BDF**<-**rbind**(**hBALB3,hBDF3**)**

h4\_BALB\_BDF**<-**rbind**(**hBALB4,hBDF4**)**

h1\_BALB\_BDF**$**Strain**<-**as.factor**(**h1\_BALB\_BDF**$**Strain**)**

h1\_BALB\_BDF**$**block**<-**as.factor**(**h1\_BALB\_BDF**$**Block**)**

h2\_BALB\_BDF**$**Strain**<-**as.factor**(**h2\_BALB\_BDF**$**Strain**)**

h2\_BALB\_BDF**$**block**<-**as.factor**(**h2\_BALB\_BDF**$**Block**)**

h3\_BALB\_BDF**$**Strain**<-**as.factor**(**h3\_BALB\_BDF**$**Strain**)**

h3\_BALB\_BDF**$**block**<-**as.factor**(**h3\_BALB\_BDF**$**Block**)**

h4\_BALB\_BDF**$**Strain**<-**as.factor**(**h4\_BALB\_BDF**$**Strain**)**

h4\_BALB\_BDF**$**block**<-**as.factor**(**h4\_BALB\_BDF**$**Block**)**

#### Step 1 estimate effect size and SE for each replicate Con1 - Con4 and Mini1 - Mini4 ##############

############################################

### model includes block to account for structure, here BALB vs BDF -> effect size estimate + SE

#overview and test run for loop

model**<-**lmer**(**s1\_BALB\_BDF**$**HCB.percentage.active**~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_BALB\_BDF**)**

sum**<-**summary**(**model**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

#### loop for all outcome measures #####

BALB\_BDF**=**matrix**(NA**,nrow **=** 16,ncol **=** 16**)** #create empty matrix to fill in the ES and SE, NA to detect errors when something is missing

rownames**(**BALB\_BDF**)=**c**(**'ES\_s1', 'ES\_s2','ES\_s3','ES\_s4','ES\_h1','ES\_h2','ES\_h3','ES\_h4','SE\_s1', 'SE\_s2','SE\_s3','SE\_s4','SE\_h1','SE\_h2','SE\_h3','SE\_h4'**)**

colnames**(**BALB\_BDF**)<-**names**(**data**)[-**c**(**1**:**5**)]**

####### conventional design replicates #####

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s1\_BALB\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_BALB\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BALB\_BDF**[**1,k**-**5**]<-**ES

BALB\_BDF**[**9,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s2\_BALB\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s2\_BALB\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BALB\_BDF**[**2,k**-**5**]<-**ES

BALB\_BDF**[**10,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s3\_BALB\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s3\_BALB\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BALB\_BDF**[**3,k**-**5**]<-**ES

BALB\_BDF**[**11,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**s4\_BALB\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s4\_BALB\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BALB\_BDF**[**4,k**-**5**]<-**ES

BALB\_BDF**[**12,k**-**5**]<-**SE

**}**

##### mini-experiment design replicates #################

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h1\_BALB\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h1\_BALB\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BALB\_BDF**[**5,k**-**5**]<-**ES

BALB\_BDF**[**13,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h2\_BALB\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h2\_BALB\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BALB\_BDF**[**6,k**-**5**]<-**ES

BALB\_BDF**[**14,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h3\_BALB\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h3\_BALB\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BALB\_BDF**[**7,k**-**5**]<-**ES

BALB\_BDF**[**15,k**-**5**]<-**SE

**}**

**for** **(**k **in** 6**:**21**){**

LMM**<-**lmer**(**h4\_BALB\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h4\_BALB\_BDF**)**

sum**<-**summary**(**LMM**)**

ES**<-**sum**$**coefficients**[**2,1**]**

SE**<-**sum**$**coefficients**[**2,2**]**

BALB\_BDF**[**8,k**-**5**]<-**ES

BALB\_BDF**[**16,k**-**5**]<-**SE

**}**

#save matrix as csv

write.csv**(**BALB\_BDF, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)\\ESandSE\_BALB\_BDF.csv", row.names **=** **TRUE)**

### Step 2. overall pooled effect (across all replicates, regardless of the design) ######

########## BALB - BDF ##############

##### Overview and test run ###

yi**<--(**BALB\_BDF**[**c**(**1**:**8**)**,1**])** # ES stored in vector

sei**<-**BALB\_BDF**[**c**(**9**:**16**)**,1**]** # SE stored in vector

# random meta analysis based on ES and SE of all replicate experiments

R\_MA\_model **<-** rma**(**yi, sei**)**

#help(rma)

R\_MA\_model

#overall Effect size and confidence interval

CI\_lb**<-**R\_MA\_model**$**ci.lb

CI\_ub**<-**R\_MA\_model**$**ci.ub

ES**<-**R\_MA\_model**$**beta**[**1,1**]**

###### loop overall effect (ES + CI) for all outcome measures 'BALB- BDF' ########

true\_BALB\_BDF**=**matrix**(NA**,nrow **=** 3,ncol **=** 16**)** #create empty matrix to fill in values, NA to detect errors when something is missing !!! anpassen nrows

rownames**(**true\_BALB\_BDF**)=**c**(**'true ES', 'CI\_lb','CI\_ub'**)**

colnames**(**true\_BALB\_BDF**)<-**names**(**data**)[-**c**(**1**:**5**)]**

**for** **(**k **in** 1**:**16**)** **{**

yi**<--(**BALB\_BDF**[**c**(**1**:**8**)**,k**])**

sei**<-**BALB\_BDF**[**c**(**9**:**16**)**,k**]**

R\_MA\_model **<-** rma**(**yi, sei**)**

R\_MA\_model

CI\_lb**<-**R\_MA\_model**$**ci.lb

CI\_ub**<-**R\_MA\_model**$**ci.ub

ES**<-**R\_MA\_model**$**beta**[**1,1**]**

true\_BALB\_BDF**[**1,k**]<-**ES

true\_BALB\_BDF**[**2,k**]<-**CI\_lb

true\_BALB\_BDF**[**3,k**]<-**CI\_ub

**}**

#save overall effect as csv file

write.csv**(**true\_BALB\_BDF, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)\\overall\_ES\_CI\_BALB\_BDF.csv", row.names **=** **TRUE)**

##########################################################################################

#### Step 3: calculate individual mean strain differences + CI for all replicates to create forest plots (Pc and Pa) afterwards ####

#overview and test run for loop

model**<-**lmer**(**s1\_BALB\_BDF**$**HCB.percentage.active**~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_BALB\_BDF**)**

sum**<-**summary**(**model**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

emmeans**(**model,'Strain'**)**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

CI\_lb**<-**R\_ES**-**CI

CI\_ub**<-**R\_ES**+**CI

######## loop for all outcome measures and all replicates ################

#######################

ES\_BALB\_BDF**=**matrix**(NA**,nrow **=** 8,ncol **=** 18**)** #create empty matrix to fill in values, NA to detect errors when something is missing

colnames**(**ES\_BALB\_BDF**)<-**c**(**names**(**data**)[**c**(**6**:**21**)]**,'Design','Replicate'**)**

rownames**(**ES\_BALB\_BDF**)=**c**(**'Rep S1', 'Rep S2', 'Rep S3','Rep S4','Rep H1', 'Rep H2', 'Rep H3','Rep H4'**)**

CI\_BALB\_BDF**=**matrix**(NA**,nrow **=** 8,ncol **=** 18**)**

colnames**(**CI\_BALB\_BDF**)<-**c**(**names**(**data**)[**c**(**6**:**21**)]**,'Design','Replicate'**)**

rownames**(**CI\_BALB\_BDF**)=**c**(**'Rep S1', 'Rep S2', 'Rep S3','Rep S4','Rep H1', 'Rep H2', 'Rep H3','Rep H4'**)**

#label replicates and design in empty matrix

ES\_BALB\_BDF**[**,18**]<-**c**(**'1','2','3','4','1','2','3','4'**)**

ES\_BALB\_BDF**[**,17**]<-**c**(**'Con','Con','Con','Con','Mini','Mini','Mini','Mini'**)**

CI\_BALB\_BDF**[**,18**]<-**c**(**'1','2','3','4','1','2','3','4'**)**

CI\_BALB\_BDF**[**,17**]<-**c**(**'Con','Con','Con','Con','Mini','Mini','Mini','Mini'**)**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s1\_BALB\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s1\_BALB\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BALB\_BDF**[**1,k**-**5**]<-**R\_ES

CI\_BALB\_BDF**[**1,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s2\_BALB\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s2\_BALB\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BALB\_BDF**[**2,k**-**5**]<-**R\_ES

CI\_BALB\_BDF**[**2,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s3\_BALB\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s3\_BALB\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BALB\_BDF**[**3,k**-**5**]<-**R\_ES

CI\_BALB\_BDF**[**3,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**s4\_BALB\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**s4\_BALB\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BALB\_BDF**[**4,k**-**5**]<-**R\_ES

CI\_BALB\_BDF**[**4,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h1\_BALB\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h1\_BALB\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BALB\_BDF**[**5,k**-**5**]<-**R\_ES

CI\_BALB\_BDF**[**5,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h2\_BALB\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h2\_BALB\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BALB\_BDF**[**6,k**-**5**]<-**R\_ES

CI\_BALB\_BDF**[**6,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h3\_BALB\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h3\_BALB\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BALB\_BDF**[**7,k**-**5**]<-**R\_ES

CI\_BALB\_BDF**[**7,k**-**5**]<-**CI

**}**

**for** **(**k **in** 6**:**21**){**

model**<-**lmer**(**h4\_BALB\_BDF**[**,k**]~**Strain**+(**1**|**block**)+(**1**|**block**:**Strain**)**,data**=**h4\_BALB\_BDF**)**

pair\_ES**<-**pairs**(**emmeans**(**model, **~** Strain, adjust**=**"none"**))**

pair\_ES**<-**as.data.frame**(**pair\_ES**)**

R\_ES**<-**pair\_ES**$**estimate

R\_SE**<-**pair\_ES**$**SE

CI**<-**1.96**\***R\_SE

ES\_BALB\_BDF**[**8,k**-**5**]<-**R\_ES

CI\_BALB\_BDF**[**8,k**-**5**]<-**CI

**}**

write.csv**(**ES\_BALB\_BDF, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)/BALB\_BDF\\ES\_BALB\_BDF.csv", row.names **=** **TRUE)**

write.csv**(**CI\_BALB\_BDF, "I:/Vanessa\_I/PhD/Batchprojekt/Daten/Auswertung/Analyse PC and PA (Voelkl)/BALB\_BDF\\CI\_BALB\_BDF.csv", row.names **=** **TRUE)**