Supplement Material Description
(For publication)
RGxE: An R Program for Genotype x Environment Interaction Analysis

Description

The supplemental material provides RGxE program, instructions for user enetered field needed in RGxE program, independent module of ANOVA model case 2 to 5 (Table 1), interpretation of univariate stability statistics, example input data and output from example input data generated from RGxE program.

1. **The RGxE program.**

RGxE program

```
#############################################################################
#Program Name: RGxE
#Version: 1.1
#Purpose: It computes various stability analysis statistics for Genotype x
#         Environment Interaction data
#         Overall ANOVA with different combination of random and fixed
effects;
#         Regression coefficients - slope and Deviation from regression;
#         Shukla Sigma; Shukla SSquare; Wricke's Ecovalence; Kang's YS;
#         Location statistics: Genotype F ratio across location and
environment;
#         correlation of individual location with average location;
#         Descriptive statistics on genotype, location, environment, year and
#         replication;
#         Cluster analysis of location
#libraries and packages used: dplyr, tidyr, sqldf, broom, agricolae
#                            (stability.par), cluster, lme4, afex
#Developers: Mahendra Dia,Todd C. Wehner and Consuelo Arellano
#            NC State University, NC, USA
#Last Modified: March 11, 2016
#############################################################################

#Install packages

install.packages("tidyr")
install.packages("dplyr")
install.packages ("sqldf")
install.packages("lme4")
install.packages("afex")
install.packages("broom")
install.packages("agricolae")


#call libraries

library (tidyr)
library (dplyr)
library (sqldf)
library(lme4)
library(afex)
library(broom)
library(agricolae)
library(cluster)
library(grDevices)

#list current objects
```

```
ls()

#to remove list of all objects from workspace

rm(list=ls())

#to identify current directory

getwd()

#set current directory
###user NEED to replace input data file path###

setwd("E:/PhD Research Work/PhD Articles
/BLUE_BLUP_Prediction_Interval_SAS_R")

#check current directory

getwd()

#########################################################################
####################        For Windows user         ####################
#########################################################################

#######################################
##########  Option 1  #################
#######################################

#import input data
###user NEED to replace input data file name###

tempa <-read.csv("RGxEInputData2_2016_02_15.csv", header = TRUE)

#######################################
##########  Option 2  #################
#######################################

#opens pop up window to select file
#file.name <- file.choose()

#read csv file
#tempa <-read.csv(file.name)

#########################################################################
####################          For Mac user           ####################
#########################################################################

#file.name <- file.choose()
#file.name

#copy path from console and paste here
#file.name <- "/Users/toddwehner/Desktop/RCodeCurrent/GxeR14Data4.csv"

#create object path for where the data will go at the end
# I append the file name with "_out" so I know its data coming out of R
#out.file <- "/Users/toddwehner/Desktop/RCodeCurrent/GxeR14Out4.csv"
#tempa <-read.csv(file.name)

#########################################################################
######           Define trait that need to be analyzed           #######
#########################################################################

#user need to define trait name for analysis
```

```r
#example: MKMGHA = Marketable mega-gram per hectare

tempa <- tempa %>% rename(Trait = Trait) %>%
  select(YR, LC, RP, CLT, Trait)

#view top 6 rows of input data

head(tempa)

#view bottom 6 rows of input data

tail(tempa)

#Get dimension of data

dim(tempa)

#Get data type

class(tempa)

#Get structure of data (character vs. numeric vs. matrix vs. vector vs.
factor)
#make sure: numeric value should be numeric

str(tempa)

#validate the variable types

tempa$YR <- as.factor(tempa$YR)
tempa$RP <- as.factor(tempa$RP)
tempa$LC <- as.factor(tempa$LC)
tempa$CLT <- as.factor(tempa$CLT)
tempa$Trait <- as.numeric(tempa$Trait)


##########################################################################
##                ANOVA: Compute analysis of variance                   ##
##########################################################################

#Generate unique id for replication for anova

tempa$RPid<-as.factor(paste(tempa$YR, tempa$LC, tempa$RP, sep="."))

##########################################################################
###         ANOVA Case 1: CLT, YR, LC and RP - All Random              ###
##########################################################################

#full model

fit.f1<-lmer(Trait~ 1 + (1|YR)  + (1|LC) + (1|CLT) + (1|YR:LC) + (1|YR:CLT) +
               (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)


#model summary

summary1 <- summary(fit.f1)

#variance of random factors

variance <- as.data.frame(summary1$varcor)

#drop rownames
```

```
rownames(variance) <- NULL
variance1 <- variance %>% select (-var1, -var2) %>%
  rename(sov=grp, Variance=vcov, stddev=sdcor)

#Type 3  test of hypothesis
#Type III Wald chisquare tests

anova(fit.f1, type="III")

#Type 2  test of hypothesis

anova(fit.f1, type="marginal", test="F")

#model fitness

anovacase1 <- plot(fit.f1,
                   main="Model fitness Case 1: CLT, YR, LC and RP - All
Random",
                   xlab="Predicated Value", ylab="Residual")

#LRT - likelihood ratio test for computing significance of random effect

#create function for Likelihood ratio test
#a=outputdatasetname; example-anova1r
#b=full model name; example-fit.f1
#c=reduced model name; example-fit.f1r
#d=effect name; example- "RPid", NOTE: call it in quotation

anova_lrt <- function (a,b,c,d){
  #level of significance
  a <-anova(b,c)
  #convert anova into data frame
  a <- data.frame(a)
  #convert rownames into column
  a$name <- rownames(a)
  # drop rownames
  rownames(a) <- NULL
  a <- a %>% filter(name=="b") %>%
    mutate(sov=d) %>% select(sov, Pr_Chisq = starts_with("Pr..Chisq."))
  # return the result
  return(a)
}

#null model for YR

fit.f1y<-lmer(Trait~ 1 + (1|LC) + (1|CLT) + (1|YR:LC) + (1|YR:CLT) +
                (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova1y <- anova_lrt(anova1y,fit.f1,fit.f1y,"YR")

#null model for LC

fit.f1l<-lmer(Trait~ 1 + (1|YR)  + (1|CLT) + (1|YR:LC) + (1|YR:CLT) +
                (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova1l <- anova_lrt(anova1l,fit.f1,fit.f1l,"LC")

#null model for CLT
```

```
fit.f1c<-lmer(Trait~ 1 + (1|YR)  + (1|LC) + (1|YR:LC) + (1|YR:CLT) +
                (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova1c <- anova_lrt(anova1c,fit.f1,fit.f1c,"CLT")

#null model for YR:LC
fit.f1yl<-lmer(Trait~ 1 + (1|YR)  + (1|LC) + (1|CLT) + (1|YR:CLT) +
                 (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova1yl <- anova_lrt(anova1yl,fit.f1,fit.f1yl,"YR:LC")

#null model for YR:CLT

fit.f1yc<-lmer(Trait~ 1 + (1|YR)  + (1|LC) + (1|CLT) + (1|YR:LC) +
                 (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova1yc <- anova_lrt(anova1yc,fit.f1,fit.f1yc,"YR:CLT")

#null model for LC:CLT

fit.f1lc<-lmer(Trait~ 1 + (1|YR)  + (1|LC) + (1|CLT) + (1|YR:LC) +
                 (1|YR:CLT) +
                 (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova1lc <- anova_lrt(anova1lc,fit.f1,fit.f1lc,"LC:CLT")

#null model for YR:LC:CLT

fit.f1ylc<-lmer(Trait~ 1 + (1|YR)  + (1|LC) + (1|CLT) + (1|YR:LC) +
                  (1|YR:CLT) +
                  (1|LC:CLT) +   (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova1ylc <- anova_lrt(anova1ylc,fit.f1,fit.f1ylc,"YR:LC:CLT")

#null model for RP

fit.f1r<-lmer(Trait~ 1 + (1|YR)  + (1|LC) + (1|CLT) + (1|YR:LC) +
                (1|YR:CLT) +
                (1|LC:CLT) + (1|YR:LC:CLT) , data=tempa)

#level of significance
#call function anova_lrt

anova1r <- anova_lrt(anova1ylr,fit.f1,fit.f1r,"RPid")

#Merge anova and level of significance

anova1 <- bind_rows(anova1y, anova1l)%>% bind_rows(anova1c)%>%
```

```
  bind_rows(anova1yl)%>% bind_rows(anova1yc)%>%
  bind_rows(anova1r)%>% bind_rows(anova1lc)%>%bind_rows(anova1ylc)
anova1 <- as.data.frame(anova1)

#Merge final output

anova_randall <- variance1%>% left_join(anova1 , by ="sov")
anova_randall$Pr_Chisq[anova_randall$stddev == 0] <- NA

#Compute BLUP for CLT
#BLUP - Best linear unbiased predictor

randeffect1 <- ranef(fit.f1)

#BLUP for clt

BLUP_CLT <- as.data.frame(randeffect1$CLT)

#convert rownames into column

BLUP_CLT$genotype <- rownames(BLUP_CLT)

#drop rownames

rownames(BLUP_CLT) <- NULL

#rename variable name

BLUP_CLT <- BLUP_CLT %>% select(genotype,Blup = starts_with("(Intercept)"))

#return estimate of fixed effect from full model summary to compute BLUP

fixestimate1 <- as.data.frame(summary1$coefficients)

#compute BLUP value

BLUP_CLT1 <- BLUP_CLT %>%
             mutate(Blup = Blup + fixestimate1$Estimate)

#final output for BLUP for cultivars

BLUP_CLT1 <- as.data.frame(BLUP_CLT1)

#########################################################################
##          ANOVA Case 2: CLT, YR and LC - Fixed; RP - Random          ##
#########################################################################

#full model

fit.f2<-lmer(Trait~ YR*LC*CLT + (1|RPid), data=tempa)

#model summary

summary2 <- summary(fit.f2)

##variance of random factors

variance2 <- as.data.frame(summary2$varcor)

#drop rownames

rownames(variance2) <- NULL
variance2 <- variance2 %>% select (-var1, -var2) %>%
  rename(sov=grp, Mean_Sq=vcov, stddev=sdcor)
```

```r
#Type 3  test of hypothesis

anova.f2t3 <- as.data.frame(anova(fit.f2, type="III"))

#convert rownames into column

anova.f2t3$name <- rownames(anova.f2t3)

#drop rownames

rownames(anova.f2t3) <- NULL

#Type 2  test of hypothesis

anova.f2t2 <- anova(fit.f2, type="marginal", test="F")

#model fitness

anovacase2 <- plot(fit.f2,
                   main="Model fitness Case 2: CLT, YR and LC - Fixed; RP -
Random",
                   xlab="Predicated Value", ylab="Residual")

#level of significance: "KR" is implemented corresponding to
#the Kenward-Rogers approximation for degrees of freedom

anova_f2t3 <- mixed(Trait~ YR*LC*CLT + (1|RPid), data=tempa)

anova_f2t3 <- as.data.frame(anova_f2t3$anova_table)

#convert rownames into column

anova_f2t3$name <- rownames(anova_f2t3)

#drop rownames

rownames(anova_f2t3) <- NULL

anova_f2t3 <- anova_f2t3 %>% select(name, Prob_F = starts_with("Pr(>F)"))

#final output for case 2: CLT, YR and LC - Fixed

anova_f2 <- anova.f2t3 %>% left_join(anova_f2t3, by = "name")%>%
  rename(sov = name)%>%
  select(sov, Df,Sum_Sq=starts_with("Sum Sq"),
         Mean_Sq = starts_with("Mean Sq"),
         F_value=starts_with("F value"), Prob_F)

anova_f2 <- anova_f2 %>% bind_rows(variance2)
anova_f2a <- as.data.frame(anova_f2) # print for output

#########################################################################
##          ANOVA CASE 3: CLT - Fixed; YR, LC and RP - Random          ##
#########################################################################

fit.f3<-lmer(Trait~ 1 + (1|YR)  + (1|LC) + CLT + (1|YR:LC) +
               (1|YR:CLT) +
               (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#model summary

summary3 <- summary(fit.f3)
```

```r
##variance of random factors

variance3 <- as.data.frame(summary3$varcor)

#drop rownames

rownames(variance3) <- NULL
variance3 <- variance3 %>% select (-var1, -var2) %>%
  rename(sov=grp, Mean_Sq=vcov, stddev=sdcor)

#Type 3 test of hypothesis

anova.f3t3 <- as.data.frame(anova(fit.f3, type="III"))

#convert rownames into column

anova.f3t3$name <- rownames(anova.f3t3)

#drop rownames

rownames(anova.f3t3) <- NULL

#Type 2  test of hypothesis

anova.f3t2 <- anova(fit.f3, type="marginal", test="F")

#model fitness

anovacase3 <- plot(fit.f3,
                   main="Model fitness Case 3: CLT - Fixed; YR, LC and RP -
Random",
                   xlab="Predicated Value", ylab="Residual")

#p value for fixed effects

anova_f3t3 <- mixed(Trait~ 1 + (1|YR)  + (1|LC) + CLT + (1|YR:LC) +
                      (1|YR:CLT) + (1|LC:CLT) + (1|YR:LC:CLT) +
                      (1|RPid), data=tempa)

anova_f3t3 <- as.data.frame(anova_f3t3$anova_table)

#convert rownames into column

anova_f3t3$name <- rownames(anova_f3t3)

#drop rownames

rownames(anova_f3t3) <- NULL

anova_f3t3 <- anova_f3t3 %>% select(name, Prob_F = starts_with("Pr(>F)"))

#final output of case 3 for fixed effect - CLT

anova_f3 <- anova.f3t3 %>% left_join(anova_f3t3, by = "name")%>%
  rename(sov = name)%>%
  select(sov, Df,Sum_Sq=starts_with("Sum Sq"),
         Mean_Sq = starts_with("Mean Sq"),
         F_value=starts_with("F value"), Prob_F)

#level of significance for random effects
#null model for CLT

fit.f3c <- lmer(Trait~ 1 + (1|YR) + (1|LC) + (1|YR:LC) + (1|YR:LC) +
                  (1|YR:CLT) + (1|LC:CLT) + (1|YR:LC:CLT) +
```

```
                  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova3c <- anova_lrt(anova3c,fit.f3,fit.f3c,"CLT")

#null model for LC

fit.f3l <- lmer(Trait~ 1 + CLT + (1|YR) + (1|YR:LC) + (1|YR:CLT) +
                  (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt
anova3l <- anova_lrt(anova3l,fit.f3,fit.f3l,"LC")

#null model for YR

fit.f3y <- lmer(Trait~ 1 + CLT + (1|LC) + (1|YR:LC) + (1|YR:CLT) +
                  (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova3y <- anova_lrt(anova3y,fit.f3,fit.f3y,"YR")

#null model for YR:LC

fit.f3yl <- lmer(Trait~ 1 + CLT + (1|LC) + (1|YR) + (1|YR:CLT) +
                   (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova3yl <- anova_lrt(anova3yl,fit.f3,fit.f3yl,"YR:LC")

#null model for YR:CLT

fit.f3yc <- lmer(Trait~ 1 + CLT + (1|LC) + (1|YR) + (1|YR:LC) +
                   (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova3yc <- anova_lrt(anova3yc,fit.f3,fit.f3yc,"YR:CLT")

#null model for LC:CLT

fit.f3lc <- lmer(Trait~ 1 + CLT + (1|LC) + (1|YR) + (1|YR:LC) +
                   (1|YR:CLT) +
                   (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova3lc <- anova_lrt(anova3lc,fit.f3,fit.f3lc,"LC:CLT")

#null model for YR:LC:CLT

fit.f3ylc <- lmer(Trait~ 1 + CLT + (1|LC) + (1|YR) + (1|YR:LC) +
                    (1|YR:CLT) +
                    (1|LC:CLT) + (1|RPid), data=tempa)

#level of significance
```

```r
#call function anova_lrt

anova3ylc <- anova_lrt(anova3ylc,fit.f3,fit.f3ylc,"YR:LC:CLT")

#null model for RPid or replication

fit.f3r <- lmer(Trait~ 1 + CLT + (1|LC) + (1|YR) + (1|YR:LC) +
                  (1|YR:CLT) +
                  (1|LC:CLT) + (1|YR:LC:CLT), data=tempa)

#level of significance
#call function anova_lrt

anova3r <- anova_lrt(anova3r,fit.f3,fit.f3r,"RPid")

#Merge anova and level of significance

anova3 <- bind_rows(anova3y, anova3l)%>% bind_rows(anova3yl)%>%
  bind_rows(anova3yc)%>% bind_rows(anova3r)%>%
  bind_rows(anova3lc)%>%bind_rows(anova3ylc)
anova3 <- as.data.frame(anova3)

#Merge final output

anova_cfix <- variance3%>% left_join(anova3 , by ="sov")
anova_cfix$Pr_Chisq[anova_cfix$stddev == 0] <- NA

##########################################################################
##          ANOVA Case 4: LC - Fixed; YR, CLT and RP - Random           ##
##########################################################################

fit.f4 <- lmer(Trait~ 1 +  LC + (1|YR) + (1|CLT) + (1|YR:LC) +
                 (1|YR:CLT) +
                 (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#model summary

summary4 <- summary(fit.f4)

##variance of random factors

variance4 <- as.data.frame(summary4$varcor)

# drop rownames

rownames(variance4) <- NULL
variance4 <- variance4 %>% select (-var1, -var2) %>%
  rename(sov=grp, Mean_Sq=vcov, stddev=sdcor)

#Type 3 test of hypothesis

anova.f4t3 <- as.data.frame(anova(fit.f4, type="III"))

#convert rownames into column

anova.f4t3$name <- rownames(anova.f4t3)

#drop rownames

rownames(anova.f4t3) <- NULL

#Type 2 test of hypothesis

anova.f4t2 <- anova(fit.f3, type="marginal", test="F")
```

```r
#model fitness

anovacase4 <- plot(fit.f4,
                   main="Model fitness Case 4: LC - Fixed; YR, CLT and RP -
Random",
                   xlab="Predicated Value", ylab="Residual")

#level of significance for fixed effects

anova_f4t3 <- mixed(Trait~ 1 + LC + (1|YR)  + (1|CLT) + (1|YR:LC) +
                      (1|YR:CLT) +
                      (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

anova_f4t3 <- as.data.frame(anova_f4t3$anova_table)

#convert rownames into column

anova_f4t3$name <- rownames(anova_f4t3)

#drop rownames

rownames(anova_f4t3) <- NULL

anova_f4t3 <- anova_f4t3 %>% select(name, Prob_F = starts_with("Pr(>F)"))

#final output of case 4 for fixed effect - LC

anova_f4 <- anova.f4t3 %>% left_join(anova_f4t3, by = "name")%>%
  rename(sov = name)%>%
  select(sov, Df,Sum_Sq=starts_with("Sum Sq"),
         Mean_Sq = starts_with("Mean Sq"),
         F_value=starts_with("F value"), Prob_F)

#level of significance of random effect
#null model for CLT

fit.f4c <- lmer(Trait~ 1 + LC + (1|YR) +  (1|YR:LC) + (1|YR:LC) +
                  (1|YR:CLT)+
                  (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova4c <- anova_lrt(anova4c,fit.f4,fit.f4c,"CLT")

#null model for LC

fit.f4l <- lmer(Trait~ 1 + (1|CLT) + (1|YR) + (1|YR:LC) + (1|YR:CLT) +
                  (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova4l <- anova_lrt(anova4l,fit.f4,fit.f4l,"LC")

#null model for YR

fit.f4y <- lmer(Trait~ 1 + LC + (1|CLT) + (1|YR:LC) + (1|YR:CLT) +
                  (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt
```

```
anova4y <- anova_lrt(anova4y,fit.f4,fit.f4y,"YR")

#null model for YR:LC

fit.f4yl <- lmer(Trait~ 1 + LC + (1|CLT) + (1|YR) + (1|YR:CLT) +
                   (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova4yl <- anova_lrt(anova4yl,fit.f4,fit.f4yl,"YR:LC")

#null model for YR:CLT

fit.f4yc <- lmer(Trait~ 1 + LC + (1|CLT) + (1|YR) + (1|YR:LC) +
                   (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova4yc <- anova_lrt(anova4yc,fit.f4,fit.f4yc,"YR:CLT")

#null model for LC:CLT

fit.f4lc <- lmer(Trait~ 1 + LC + (1|CLT) + (1|YR) + (1|YR:LC) +
                   (1|YR:CLT) +
                   (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova4lc <- anova_lrt(anova4lc,fit.f4,fit.f4lc,"LC:CLT")

#null model for YR:LC:CLT

fit.f4ylc <- lmer(Trait~ 1 + LC + (1|CLT) + (1|YR) + (1|YR:LC) +
                    (1|YR:CLT) +
                    (1|LC:CLT) + (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova4ylc <- anova_lrt(anova4ylc,fit.f4,fit.f4ylc,"YR:LC:CLT")

#null model for RPid or replication

fit.f4r <- lmer(Trait~ 1 + LC + (1|CLT) + (1|YR) + (1|YR:LC) +
                  (1|YR:CLT) +
                  (1|LC:CLT) + (1|YR:LC:CLT), data=tempa)

#level of significance
#call function anova_lrt

anova4r <- anova_lrt(anova4r,fit.f4,fit.f4r,"RPid")

#Merge anova and level of significance

anova4 <- bind_rows(anova4c, anova4y)%>% bind_rows(anova4yl)%>%
  bind_rows(anova4yc)%>% bind_rows(anova4r)%>%
  bind_rows(anova4lc)%>%bind_rows(anova4ylc)
anova4 <- as.data.frame(anova4)

#Merge final output
```

```r
anova_lfix <- variance4%>% left_join(anova4 , by ="sov")
anova_lfix$Pr_Chisq[anova_lfix$stddev == 0] <- NA

#########################################################################
##      ANOVA Case 5: CLT and LC - Fixed; YR, and RP - Random          ##
#########################################################################

fit.f5 <- lmer(Trait~ 1 +  CLT + LC + LC:CLT + (1|YR) + (1|YR:LC) +
                 (1|YR:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#model summary

summary5 <- summary(fit.f5)

##variance of random factors

variance5 <- as.data.frame(summary5$varcor)

#drop rownames

rownames(variance5) <- NULL
variance5 <- variance5 %>% select (-var1, -var2) %>%
  rename(sov=grp, Mean_Sq=vcov, stddev=sdcor)

#Type 3 test of hypothesis

anova.f5t3 <- as.data.frame(anova(fit.f5, type="III"))

#convert rownames into column

anova.f5t3$name <- rownames(anova.f5t3)

#drop rownames

rownames(anova.f5t3) <- NULL

#Type 2 test of hypothesis

anova.f5t2 <- anova(fit.f3, type="marginal", test="F")

#model fitness

anovacase5 <- plot(fit.f5,
                   main="Model fitness Case 5: CLT and LC - Fixed; YR and RP
- Random",
                   xlab="Predicated Value", ylab="Residual")

#level of significance for fixed effects

anova_f5t3 <- mixed(Trait~ 1 +  CLT + LC + LC:CLT + (1|YR) +
                      (1|YR:LC) + (1|YR:CLT) + (1|YR:LC:CLT) +
                      (1|RPid), data=tempa)

anova_f5t3 <- as.data.frame(anova_f5t3$anova_table)

#convert rownames into column

anova_f5t3$name <- rownames(anova_f5t3)

#drop rownames

rownames(anova_f5t3) <- NULL

anova_f5t3 <- anova_f5t3 %>% select(name, Prob_F = starts_with("Pr(>F)"))
```

```r
#final output of case 5 for fixed effect - CLT and LC

anova_f5 <- anova.f5t3 %>% left_join(anova_f5t3, by = "name")%>%
  rename(sov = name)%>%
  select(sov, Df,Sum_Sq=starts_with("Sum Sq"),
         Mean_Sq = starts_with("Mean Sq"),
         F_value=starts_with("F value"), Prob_F)

#level of significance for random effects
#null model for CLT

fit.f5c <- lmer(Trait~ 1 +  LC + LC:CLT + (1|YR) + (1|YR:LC) +
                  (1|YR:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova5c <- anova_lrt(anova5c,fit.f5,fit.f5c,"CLT")

#null model for LC

fit.f5l <- lmer(Trait~ 1 +  CLT + LC:CLT + (1|YR) + (1|YR:LC) +
                  (1|YR:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova5l <- anova_lrt(anova5l,fit.f5,fit.f5l,"LC")

#null model for YR

fit.f5y <- lmer(Trait~ 1 +  CLT + LC + LC:CLT + (1|YR:LC) +
                  (1|YR:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova5y <- anova_lrt(anova5y,fit.f5,fit.f5y,"YR")

#null model for YR:LC

fit.f5yl <- lmer(Trait~ 1 +  CLT + LC + LC:CLT + (1|YR) +
                   (1|YR:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova5yl <- anova_lrt(anova5yl,fit.f5,fit.f5yl,"YR:LC")

#null model for YR:CLT

fit.f5yc <- lmer(Trait~ 1 +  CLT + LC + LC:CLT + (1|YR) + (1|YR:LC) +
                   (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova5yc <- anova_lrt(anova5yc,fit.f5,fit.f5yc,"YR:CLT")

#null model for LC:CLT

fit.f5lc <- lmer(Trait~ 1 +  CLT + LC + (1|YR) + (1|YR:LC) +
                   (1|YR:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)
```

```r
#level of significance
#call function anova_lrt

anova5lc <- anova_lrt(anova5lc,fit.f5,fit.f5lc,"LC:CLT")

#null model for YR:LC:CLT

fit.f5ylc <- lmer(Trait~ 1 +  CLT + LC + LC:CLT + (1|YR) + (1|YR:LC) +
                    (1|YR:CLT) + (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova5ylc <- anova_lrt(anova5ylc,fit.f5,fit.f5ylc,"YR:LC:CLT")

#null model for RPid or replication

fit.f5r <- lmer(Trait~ 1 +  CLT + LC + LC:CLT + (1|YR) + (1|YR:LC) +
                  (1|YR:CLT) + (1|YR:LC:CLT) , data=tempa)

#level of significance
#call function anova_lrt

anova5r <- anova_lrt(anova5r,fit.f5,fit.f5r,"RPid")

#Merge anova and level of significance

anova5 <- bind_rows(anova5y, anova5yl)%>%
  bind_rows(anova5yc)%>% bind_rows(anova5r)%>%
  bind_rows(anova5ylc)
anova5 <- as.data.frame(anova5)

#Merge final output

anova_clfix <- variance5%>% left_join(anova5 , by ="sov")
anova_clfix$Pr_Chisq[anova_clfix$stddev == 0] <- NA

#############################################################################
#   Compute Mean and CV of genotype, location, year, rep, environment  #
#############################################################################

#Compute environment -  Location by year combination

tempa2 <- tempa %>%
  mutate (ENV = paste(LC,YR, sep='-')) %>%
  #remove missing records
  na.omit()

head(tempa2)

#validate data

tempa2$YR <- as.factor(tempa2$YR)
tempa2$RP <- as.factor(tempa2$RP)
tempa2$LC <- as.factor(tempa2$LC)
tempa2$CLT <- as.factor(tempa2$CLT)
tempa2$ENV <- as.factor(tempa2$ENV)
tempa2$Trait <- as.numeric(tempa2$Trait)

#compute descritptive statistics
#trait mean over genotype and environment

mean_ge <- tempa2 %>%
```

```
  group_by (CLT, ENV) %>%
  summarize (Trait = mean(Trait,na.rm=FALSE))

mean_ge1 <- mean_ge %>%
  spread (ENV, Trait) #transpose using library tidyr

mean_ge2 <- as.data.frame(mean_ge1)

#trait mean over genotype and year

mean_gy <- tempa2 %>%
  group_by (CLT, YR) %>%
  summarize (Trait = mean(Trait,na.rm=FALSE))

mean_gy1 <- mean_gy %>%
  spread (YR, Trait) #transpose using library tidyr

mean_gy2 <- as.data.frame(mean_gy1)

#trait sum over genotype and year

sum_gy <- tempa2 %>%
  group_by (CLT, YR) %>%
  summarize (Trait = sum(Trait,na.rm=FALSE))

sum_gy1 <- sum_gy %>%
  spread (YR, Trait) #transpose using library tidyr

sum_gy2 <- as.data.frame(sum_gy1)

#trait standard deviation (sd) over genotype and year

sd_gy <- tempa2 %>%
  group_by (CLT, YR) %>%
  summarize (Trait = sd(Trait,na.rm=FALSE))

sd_gy1 <- sd_gy %>%
  spread (YR, Trait) #transpose using library tidyr

sd_gy2 <- as.data.frame(sd_gy1)

#trait mean over genotype and location

mean_gl <- tempa2 %>%
  group_by (CLT, LC) %>%
  summarize (Trait = mean(Trait,na.rm=FALSE))

mean_gl1 <- mean_gl %>%
  spread (LC, Trait) #transpose using library tidyr

mean_gl2 <- as.data.frame(mean_gl1)

#trait sum over genotype and location

sum_gl <- tempa2 %>%
  group_by (CLT, LC) %>%
  summarize (Trait = sum(Trait,na.rm=FALSE))

sum_gl1 <- sum_gl %>%
  spread (LC, Trait) #transpose using library tidyr

sum_gl2 <- as.data.frame(sum_gl1)

#trait standard deviation (sd) over genotype and location
```

```r
sd_gl <- tempa2 %>%
  group_by (CLT, LC) %>%
  summarize (Trait = sd(Trait,na.rm=FALSE))

sd_gl1 <- sd_gl %>%
  spread (LC, Trait) #transpose using library tidyr

sd_gl2 <- as.data.frame(sd_gl1)

#trait mean over genotype, location and year

mean_gly <- tempa2 %>%
  group_by (CLT, LC, YR) %>%
  summarize (Trait = mean(Trait,na.rm=FALSE))

mean_gly1 <- mean_gly %>%
  spread (LC, Trait) #transpose using library tidyr

mean_gly2 <- as.data.frame(mean_gly1)

#trait sum over genotype, location and year

sum_gly <- tempa2 %>%
  group_by (CLT, LC, YR) %>%
  summarize (Trait = sum(Trait,na.rm=FALSE))

sum_gly1 <- sum_gly %>%
  spread (LC, Trait) #transpose using library tidyr

sum_gly2 <- as.data.frame(sum_gly1)

#trait standard deviation (sd) over genotype, location and year

sd_gly <- tempa2 %>%
  group_by (CLT, LC, YR) %>%
  summarize (Trait = sd(Trait,na.rm=FALSE))

sd_gly1 <- sd_gly %>%
  spread (LC, Trait) #transpose using library tidyr

sd_gly2 <- as.data.frame(sd_gly1)

#trait mean over genotype, location and rep

mean_glr <- tempa2 %>%
  group_by (CLT, LC, RP) %>%
  summarize (Trait = mean(Trait,na.rm=FALSE))

mean_glr1 <- mean_glr %>%
  spread (LC, Trait) #transpose using library tidyr

mean_glr2 <- as.data.frame(mean_glr1)

#trait mean over location and year

mean_ly <- tempa2 %>%
  group_by (LC, YR) %>%
  summarize (Trait = mean(Trait,na.rm=FALSE))

mean_ly1 <- mean_ly %>%
  spread (YR, Trait) #transpose using library tidyr

mean_ly2 <- as.data.frame(mean_ly1)
```

```
#trait mean over location and replication

mean_lr <- tempa2 %>%
  group_by (LC, RP) %>%
  summarize (Trait = mean(Trait,na.rm=FALSE))

mean_lr1 <- mean_lr %>%
  spread (RP, Trait) #transpose using library tidyr

mean_lr2 <- as.data.frame(mean_lr1)

#trait count, min, max, mean, sum, median, var, sd over location

mean_l <- tempa2 %>%
  group_by (LC ) %>%
  summarize (count = n(),
             min = min(Trait,na.rm=FALSE),
             max = max(Trait,na.rm=FALSE),
             mean = mean(Trait,na.rm=FALSE),
             sum = sum(Trait,na.rm=FALSE),
             median = median(Trait,na.rm=FALSE),
             var = var(Trait,na.rm=FALSE),
             sd = sd(Trait,na.rm=FALSE))

stat_l1 <- as.data.frame(mean_l)

#trait count, min, max, mean, sum, median, var, sd over year

mean_y <- tempa2 %>%
  group_by (YR ) %>%
  summarize (count = n(),
             min = min(Trait,na.rm=FALSE),
             max = max(Trait,na.rm=FALSE),
             mean = mean(Trait,na.rm=FALSE),
             sum = sum(Trait,na.rm=FALSE),
             median = median(Trait,na.rm=FALSE),
             var = var(Trait,na.rm=FALSE),
             sd = sd(Trait,na.rm=FALSE))

stat_y1 <- as.data.frame(mean_y)

#trait count, min, max, mean, sum, median, var, sd over genotype

mean_g <- tempa2 %>%
  group_by (CLT ) %>%
  summarize (count = n(),
             min = min(Trait,na.rm=FALSE),
             max = max(Trait,na.rm=FALSE),
             mean = mean(Trait,na.rm=FALSE),
             sum = sum(Trait,na.rm=FALSE),
             median = median(Trait,na.rm=FALSE),
             var = var(Trait,na.rm=FALSE),
             sd = sd(Trait,na.rm=FALSE))

stat_g1 <- as.data.frame(mean_g)

#trait count, min, max, mean, sum, median, var, sd over environment

mean_e <- tempa2 %>%
  group_by (ENV) %>%
  summarize (count = n(),
             min = min(Trait,na.rm=FALSE),
             max = max(Trait,na.rm=FALSE),
```

```
              mean = mean(Trait,na.rm=FALSE),
              sum = sum(Trait,na.rm=FALSE),
              median = median(Trait,na.rm=FALSE),
              var = var(Trait,na.rm=FALSE),
              sd = sd(Trait,na.rm=FALSE))

stat_e1 <- as.data.frame(mean_e)

#trait CV over genotype and location
#CV = (standard deviation /mean) *100

cv_gl <- tempa2 %>%
  group_by (CLT, LC) %>%
  summarise (Trait_m = mean(Trait,na.rm=FALSE) ,
             Trait_s = sd(Trait,na.rm=FALSE)) %>%
  mutate (Trait = (Trait_s/Trait_m)*100) %>% # CV
  select (-Trait_m, -Trait_s)

cv_gl1 <- cv_gl %>%
  spread (LC, Trait) #transpose using library tidyr

cv_gl2 <- as.data.frame(cv_gl1)

#########################################################################
##    Compute univariate stability statistics - regression analysis   ##
#########################################################################

#Compute regression (slope) and deviation from regression
#compute environmental index

dsterm <- tempa2 %>%
  group_by (ENV, RP, YR, LC) %>%
  summarize (ENVTrait = mean(Trait,na.rm=FALSE))

dst02 <- tempa2 %>%
  left_join(dsterm, by=c("ENV", "RP")) %>% #Left join on multiple columns
  arrange (CLT) %>%
  rename (YR= YR.x, LC = LC.x )

#fit model

fit_model <- dst02 %>%
  group_by(CLT) %>% #group regression analysis by cultivar
  do (model=lm(Trait~ENVTrait + ENV + RP, data=.))

#parameter estimates

paramlm <- as.data.frame(fit_model %>% tidy(model))
glancelm <- as.data.frame(fit_model %>% glance(model))
augmentlm <- as.data.frame(fit_model %>% augment(model))

outmsed <- lapply(fit_model$model, anova) #anova output
outmsed2 <- as.data.frame(do.call(rbind, outmsed)) #convert list into
data.frame

#convert rownames into column

outmsed2$SOV <- rownames(outmsed2)

# drop rownames

rownames(outmsed2) <- NULL

#remove numeric values from string of rownames using function gsub
```

```
outmsed2 <- outmsed2 %>% mutate(SOV = gsub("\\d+","",SOV))

#extract unique cultivar name and merge to outmsed2 dataset

genotypes <- dst02 %>% select(CLT) %>% distinct (CLT) %>% arrange(CLT)

#Stack 4 times to match number of rows with outmsed2 dataset

genotypes1 <- genotypes %>% bind_rows(genotypes) %>%
  bind_rows(genotypes) %>% bind_rows(genotypes) %>% arrange(CLT)

#attach list of cultivars to outmsed2

outmsed3 <- as.data.frame(outmsed2 %>% bind_cols(genotypes1))

#transpose outmsed3

outmsed4 <- outmsed3 %>%
  select (CLT, SOV, MS = starts_with("Mean")) %>%  #rename variables
  filter (SOV != "RP")

#transpose MS values

MSDS <- outmsed4 %>%
  spread (SOV, MS) %>% #transpose using library tidyr
  arrange (CLT)

#Transpose degress of freedoms for F-test

FDS3 <- outmsed3 %>%
  filter (SOV != "RP")%>%
  select (CLT, SOV, Df) %>%
  spread (SOV, Df) %>% #transpose using library tidyr
  rename (DF_ENVTrait = ENVTrait, DF_Residuals = Residuals,
          DF_ENV = ENV)

#Subset parameters - paramlm dataset

REGCOEFGS <- paramlm %>%
  filter (term == "ENVTrait") %>%
  select (-statistic, -p.value)

#Test and level of significance of regression and deviation from regression
#Merge MSDS, FDS3, REGCOEFGS

slope <- MSDS %>% inner_join (REGCOEFGS, by = "CLT") %>%
  inner_join (FDS3, by = "CLT") %>%
  rename (MSE = Residuals, LREGMS=ENVTrait, DEVLMS = ENV,
          BI= estimate, STDERR = std.error)

#test significance levels

slope1 <- slope %>%
  mutate (T_H01 = (BI-1)/STDERR , #Null Hypothesis for slope = 1
          PT_H01 = 2*pt(-abs(T_H01), DF_Residuals),
          F_DEVREG=DEVLMS/MSE, #NULL HYPOTHESIS: PREDICTED-ACTUAL = 0
          PF_H00= 1-pf(F_DEVREG, DF_ENV, DF_Residuals))

#add legend for level of significance

slope2 <- slope1 %>%
  mutate (SIG_SLOPE = ifelse(PT_H01 <= 0.001, "***",
                             ifelse(PT_H01 <= 0.01, "**",
```

```
                                        ifelse(PT_H01 <= 0.05, "*",""))) %>%
  mutate (SIG_DEVREG = ifelse(PF_HO0 <= 0.001, "***",
                              ifelse(PF_HO0 <= 0.01, "**",
                                     ifelse(PF_HO0 <= 0.05, "*",""))))

#final regression output

options(digits=5)
univariate2 <- slope2 %>%
  mutate (SLOPE = paste(BI,SIG_SLOPE, sep=""),
          DEVREG = paste(DEVLMS,SIG_DEVREG, sep="") ) %>%
  select (CLT,SLOPE, DEVREG )

#########################################################################
#   Compute univariate stability statistics - shukla, ecovalence, YS   #
#########################################################################

#Compute Shukla, Wricke Ecovalense, Kangs YS

repno <- tempa2 %>%
  summarise (total_rep = n_distinct(RP)) #count total number of rep

dstgl <- tempa2 %>%
  group_by (CLT, LC) %>%
  #Summarize genotype performance across locations
  summarize (Trait = mean(Trait,na.rm=FALSE))

dstgl1 <- dstgl %>%
  spread (LC, Trait) #transpose values

#convert into data frame so that row containing structure information is
deleted

dstgl2 <- as.data.frame(dstgl1)

#create rownames

rownames(dstgl2) <- dstgl2[ ,1]
shukla <- dstgl2[,-1]

#compute MS error term

tempa3 <- glm(Trait ~ LC + YR + LC:YR + RP %in% (LC:YR) + CLT + CLT:LC +
                CLT:YR + CLT:LC:YR, family = gaussian , data= tempa2 )

#model summary

summary1 <- summary.glm(tempa3)

#Error SS

error_ss <- as.data.frame(summary1$deviance)
error_ss1 <- error_ss %>%
  #rename variable
  select (Deviance = starts_with("summary"), everything())

#Error DF

error_df <- as.data.frame(summary1$df.residual)
error_df1 <- error_df %>%
  #rename variable
  select (Df = starts_with("summary"), everything())

#MS of error
```

```r
mse1 <- as.data.frame(error_ss1/error_df1)
mse <- mse1 %>%
  #rename variable
  rename (MS = Deviance)

# MSError is used populated from ANOVA

univariate1a <- stability.par(shukla, rep= repno$total_rep , MSerror=mse$MS,
                              alpha=0.1, main="Genotype")

#pool results into individual columns

univariate1b <- univariate1a$statistics

#create column genotype from rownames

univariate1b$genotype <- rownames(univariate1b)
rownames(univariate1b) = NULL #remove rownames
names(univariate1b)[3] <- "significane_sigma"    # rename duplicate name dot
names(univariate1b)[5] <- "significane_s2"    # rename duplicate name dot
names(univariate1b)[2] <- "sigma"    # rename
names(univariate1b)[4] <- "ssquare"    # rename

univariate1c <- univariate1a$stability

#create column genotype from rownames

univariate1c$genotype <- rownames(univariate1c)
rownames(univariate1c) = NULL #remove rownames
names(univariate1c)[8] <- "legend"    # rename variable ... to legend

#Merge

univariate1d <- univariate1b %>%
  inner_join (univariate1c , by = "genotype") %>%
  # deselect all columns between Yield and Stab.rating
  select (-Yield: -Stab.rating) %>%
  # arrange the column order for final output
  select (CLT=genotype, Mean, sigma,
          significane_sigma, ssquare,
          significane_s2, Ecovalence,YSi, legend)


#Final stability statistics
#Merge Univariate2 and Univariate1d

univariate <- univariate2 %>%
  inner_join(univariate1d, by = "CLT") %>%
  mutate (SIGMA=paste(sigma,significane_sigma, ""),
          SIGMA_SQUARE=paste(ssquare,significane_s2, ""),
          YS_Kang =paste(YSi,legend, "")) %>%
  select (Genotype = CLT, Mean, SLOPE, DEVREG, SIGMA,
          SIGMA_SQUARE,Ecovalence, YS_Kang)

#########################################################################
##        Compute location statistics - genotype F ratio across        ##
##        location and environment; location correlation               ##
#########################################################################

#Location values
#F-value of genotype across location
#fit model
```

```
fit_modellc <- tempa2 %>%
  group_by(LC) %>% #group regression analysis by location
  do (model1=lm(Trait~CLT + YR + CLT:YR + RP%in%YR , data=.))

#parameter estimates

paramlmlc <- as.data.frame(fit_modellc %>% tidy(model1))
glancelmlc <- as.data.frame(fit_modellc %>% glance(model1))
augmentlmlc <- as.data.frame(fit_modellc %>% augment(model1))

outmsedlc <- lapply(fit_modellc$model1, anova) #anova output

#convert list into data.frame

outmsedlc2 <- as.data.frame(do.call(rbind, outmsedlc))

#convert rownames into column

outmsedlc2$SOV <- rownames(outmsedlc2)

#drop rownames

rownames(outmsedlc2) <- NULL

#remove numeric values from string of rownames using function gsub

outmsedlc2 <- outmsedlc2 %>% mutate(SOV = gsub("\\d+","",SOV))

#extract unique location name and merge to outmsedlc2 dataset

location <- dst02 %>% select(LC) %>% distinct (LC) %>% arrange(LC)

#Extract gentype F value for each location

locvalue <- outmsedlc2 %>%
  filter(SOV == "CLT") %>%
  select (FRatioGenotype = starts_with("F value")) %>%
  bind_cols (location) %>% select (LC, FRatioGenotype)

locvalue <- as.data.frame (locvalue)

#Correlation between location and average location for each genotype
#compute genotype mean at each location

glcmean1 <- tempa2 %>%
  group_by (CLT, LC) %>%
  summarize (glcmean = mean(Trait,na.rm=FALSE)) %>%
  as.data.frame(select (CLT, LC, glcmean))


#compute genotype mean across all location -average location

gmean1 <- tempa2 %>%
  group_by (CLT ) %>%
  summarize (gmean = mean(Trait,na.rm=FALSE)) %>%
  as.data.frame(select (CLT, gmean))

#merge location mean with average location for each genotype

lgmean <- glcmean1 %>%
  left_join(gmean1, by="CLT") %>%
  arrange(LC) %>% select (-CLT)

#compute correlation with level of significance
```

```
lcgcorr <- lgmean %>%
  group_by(LC) %>%
  do(tidy(cor.test(.$glcmean, .$gmean, method = c("pearson"))))

lcgcorr1 <- lcgcorr %>%
  select (LC, Corr_Value = starts_with ("estimate"),
          Pvalue = starts_with("p.value"))

#post process correlation value

lcgcorr2 <- lcgcorr1 %>%
  mutate (SIG_CORR = ifelse(Pvalue <= 0.001, "***",
                            ifelse(Pvalue <= 0.01, "**",
                                   ifelse(Pvalue <= 0.05, "*",""))))

#concatenate p value symbol with correlation value

lcgcorr3 <- lcgcorr2 %>%
  mutate (LocCorrelation=paste(Corr_Value,SIG_CORR, sep="")) %>%
  select (LC, LocCorrelation)

lcgcorr3 <- as.data.frame(lcgcorr3)

#Final location value table for output
#compute location mean

Locmean <- tempa2 %>%
  group_by (LC ) %>%
  summarize (Trait = mean(Trait,na.rm=FALSE))%>%
  select (LC, Mean = starts_with("Trait"))

Locmean <- as.data.frame(Locmean)

#merge all location value outputs for print

LocationValue <- Locmean %>%
  inner_join (locvalue, by = "LC") %>%
  inner_join(lcgcorr3, by = "LC") %>%
  rename (Location = LC)

#########################################################################
###               F-value of genotype across environmen                ##
#########################################################################

#fit model

fit_modelen <- tempa2 %>%
  group_by(ENV) %>% #group regression analysis by location
  do (model2=lm(Trait~CLT + RP , data=.))

#parameter estimates

paramlmen <- as.data.frame(fit_modelen %>% tidy(model2))
glancelmen <- as.data.frame(fit_modelen %>% glance(model2))
augmentlmen <- as.data.frame(fit_modelen %>% augment(model2))

outmseden <- lapply(fit_modelen$model2, anova) #anova output

#convert list into data.frame

outmseden2 <- as.data.frame(do.call(rbind, outmseden))

#convert rownames into column
```

```
outmseden2$SOV <- rownames(outmseden2)

# drop rownames

rownames(outmseden2) <- NULL

#remove numeric values from string of rownames using function gsub

outmseden2 <- outmseden2 %>% mutate(SOV = gsub("\\d+","",SOV))

#extract unique environment name and merge to outmseden2 dataset

environment <- dst02 %>% select(ENV) %>% distinct (ENV) %>% arrange(ENV)

#Extract gentype F value for each location

locvalue2 <- outmseden2 %>%
  filter(SOV == "CLT") %>%
  select (FRatioGenotype = starts_with("F value")) %>%
  bind_cols (environment) %>% select (ENV, FRatioGenotype)

locvalue2 <- as.data.frame (locvalue2)

#########################################################################
###                Compute cluster analysis of location               ###
#########################################################################

#location cluster analysis
#Euclidean distance
#Ward Hierarchical Clustering

#trait mean over location

mean_l <- tempa2 %>%
  group_by (LC ) %>%
  summarize (Trait = mean(Trait,na.rm=FALSE))
mean_l1 <- as.data.frame(mean_l)

clusterdata <- mean_l1 %>% select (Trait)
clusterdata <- na.omit(clusterdata)
distance <- dist(clusterdata, method = "euclidean") # distance matrix
hcluster <- hclust(d=distance, method="ward.D")
locationcluster <- plot(hcluster, labels=mean_l1$LC) # display dendogram



#########################################################################
####                          Clear console                          ####
#########################################################################

#clear console
cat("\014")

#########################################################################
###                  Export output in .CSV or .TXT                    ###
###                  Print final output in console                    ###
#########################################################################

#user can turn on and off .csv or .txt file by commenting/uncommenting
#codes in below 2 lines

#sink(file="RGxEOutput.csv", append=FALSE, split=TRUE)
sink(file="RGxEOutput.txt", append=FALSE, split=TRUE)
```

```
""
""
"#############      Print date and time     #################"
""
print(Sys.time())
""
"##########################################################################"
"###           Section 1: Identify level of significance of             ###"
"###              different effects, variances and BLUP                 ###"
"##########################################################################"
""
""
"##########################################################################"
"###                 ANOVA - ANALYSIS OF VARIANCE                       ####"
"##########################################################################"
""
"##########################################################################"
"##             ANOVA Case 1: CLT, YR, LC and RP - All Random            ##"
"##########################################################################"
""
"##Print ANOVA"
"#Note: P values are generated using LRT-Likelihood Ratio Test via "
"#model comparison and anova"
""
print(anova_randall, row.names = FALSE)
""
"##Print BLUP-Best linear unbiased predictor value for random genotypes"
""
print(BLUP_CLT1, row.names = FALSE)
""
"##########################################################################"
"##          ANOVA Case 2: CLT, YR and LC - Fixed; RP - Random            ##"
"##########################################################################"
""
"##Print ANOVA"
"#Note: P values are computed for F ratio using KR method "
"#Kenward-Rogers approximation for degrees of freedom"
""
print(anova_f2a, row.names = FALSE)
""
"##########################################################################"
"##           ANOVA Case 3: CLT - Fixed; YR, LC and RP - Random           ##"
"##########################################################################"
""
"##Print ANOVA"
"#Note: For fixed effects P values are computed for F ratio using "
"#KR method Kenward-Rogers approximation for degrees of freedom"
""
print(anova_f3, row.names = FALSE)
""
"#For random effect P values are generated using LRT-Likelihood Ratio Test "
"#via model comparison and anova"
""
print(anova_cfix, row.names = FALSE)
""
"##########################################################################"
"##          ANOVA Case 4: LC - Fixed; YR, CLT and RP - Random            ##"
"##########################################################################"
""
"##Print ANOVA"
"#Note: For fixed effects P values are computed for F ratio using"
"#KR method Kenward-Rogers approximation for degrees of freedom"
""
print(anova_f4, row.names = FALSE)
```

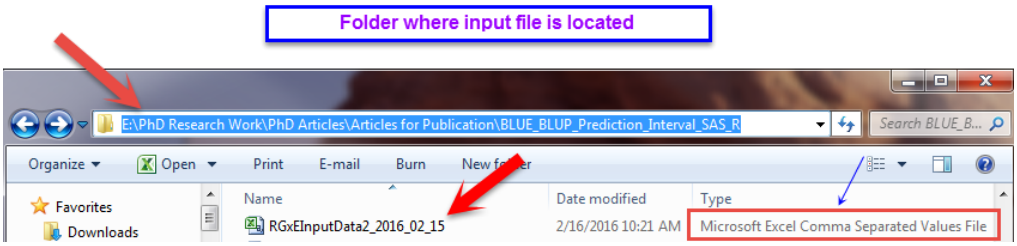
```
""
"#For random effect P values are generated using LRT-Likelihood Ratio Test"
"#via model comparison and anova"
""
print(anova_lfix, row.names = FALSE)
""
"##########################################################################"
"##        ANOVA Case 5: CLT and LC - Fixed; YR, and RP - Random         ##"
"##########################################################################"
""
"##Print ANOVA"
"#Note: For fixed effects P values are computed for F ratio using "
"#KR method Kenward-Rogers approximation for degrees of freedom"
""
print(anova_f5, row.names = FALSE)
""
"#For random effect P values are generated using LRT-Likelihood Ratio Test"
"#via model comparison and anova"
""
print(anova_clfix, row.names = FALSE)
""
""
"##########################################################################"
"###       Section 2: Identify general statistcs (mean and CV) of       ###"
"###       genotype, location, year, replication and environment        ###"
"##########################################################################"
""
""
"##########################################################################"
"###                        Descriptive Statistics                      ###"
"##########################################################################"
""
"#Descriptive Statistics - Means and CV"
""
"#trait mean across genotype and environment(location x year combination)"
""
print(mean_ge2, row.names = FALSE)
""
"#trait mean across genotype and years"
""
print(mean_gy2, row.names = FALSE)
""
"#trait mean across genotype and location"
""
print(mean_gl2, row.names = FALSE)
""
"#trait mean across genotype, location and year"
""
print(mean_gly2, row.names = FALSE)
""
"#trait mean across genotype, location and replication"
""
print(mean_glr2, row.names = FALSE)
""
"#trait mean across location and year"
""
print(mean_ly2, row.names = FALSE)
""
"#trait mean across location and replication"
""
print(mean_lr2, row.names = FALSE)
""
"#trait count, min, max, mean, sum, median, var, sd over location"
""
```

```
print(stat_l1, row.names = FALSE)
""
"#trait count, min, max, mean, sum, median, var, sd over year"
""
print(stat_y1, row.names = FALSE)
""
"#trait count, min, max, mean, sum, median, var, sd over genotype"
""
print(stat_g1, row.names = FALSE)
""
"#trait count, min, max, mean, sum, median, var, sd over environment"
""
print(stat_e1, row.names = FALSE)
""
"#trait coefficient of variation (cv) across gentoype and location"
""
print(cv_gl2, row.names = FALSE)
""
"trait sum across genotype and location"
""
print(sum_gl2, row.names = FALSE)
""
"trait sum across genotype, location and year"
""
print(sum_gly2, row.names = FALSE)
""
"trait sum across genotype and year"
""
print(sum_gy2, row.names = FALSE)
""
"trait standard deviation (sd) across genotype and location"
""
print(sd_gl2, row.names = FALSE)
""
"trait standard deviation (sd) across genotype, location and year"
""
print(sd_gly2, row.names = FALSE)
""
"trait standard deviation (sd) across genotype and year"
""
print(sd_gy2, row.names = FALSE)
""
""
""
"#########################################################################"
"###              Section 3: Choose stable and best genotype           ###"
"#########################################################################"
""
""
"#########################################################################"
"###                        Stability Statistics                       ###"
"#########################################################################"
""
"#Univariate statistics - mean, slope, deviation from regression,"
"#Shukla,Ecovalence, Kang"
""
print(univariate, row.names = FALSE)
""
""
"#########################################################################"
"##    Section 4: Choose discriminative and representative location    ##"
"#########################################################################"
""
""
```

```
"#########################################################################"
"###       location statistics - genotype F ratio across location      ###"
"###                  and environment; location correlation            ###"
"#########################################################################"
""
"#location value"
"# location mean, genotype F ratio across location,"
"#correlation of location with average location performace"
""
print(LocationValue, row.names = FALSE)
""
"#location value-genotype F ratio across location,"
""
print(locvalue2, row.names = FALSE)
sink()

#########################################################################
###              ANOVA model fitness plots : Case 1 to 5              ###
#########################################################################

#Print model fitness of Case I to Case V
#pdf file is sent to same folder where input file is located

#Model fitness Case 1: CLT, YR, LC and RP - All Random
#Model fitness Case 2: CLT, YR and LC - Fixed; RP - Random
#Model fitness Case 3: CLT - Fixed; YR, LC and RP - Random
#Model fitness Case 4: LC - Fixed; YR, CLT and RP - Random
#Model fitness Case 5: CLT and LC - Fixed; YR and RP - Random

pdf("modelfitness.pdf")
anovacase1
anovacase2
anovacase3
anovacase4
anovacase5
dev.off()

#########################################################################
###             Cluster analysis of location performance              ###
#########################################################################

#print dendogram for location
#pdf file is sent to same folder where input file is located
dev.print(pdf, 'locationcluster.pdf')
dev.off()

#End
```

2. Instructions for user entered field

A. Define input file information.



```
#set current directory
###user NEED to replace input data file path###

setwd("E:/PhD Research Work/PhD Articles/Articles for Publication/BLUE_BLUP_Prediction_Interval_SAS_R")

```

a. For Windows user

I. Option 1

```
#########################################################################
###################        For Windows user          ####################
#########################################################################

#####################################
#########  Option 1  ################
#####################################

#import input data
###user NEED to replace input data file name###

tempa <-read.csv("RGxEInputData2_2016_02_15.csv", header = TRUE)
```

name of input file

II. Option 2

```
#####################################
#########  Option 2  ################
#####################################

#opens pop up window to select file
file.name <- file.choose()

#read csv file
tempa <-read.csv(file.name)
```

It will pop up folder where current directory is set.

User can choose .csv file

b. For Ois or Mac user

This function open folder through which user can navigate to folder of interest where input data is placed

```
#########################################################################
###################             For Mac user          ###################
#########################################################################

file.name <- file.choose()
file.name

#copy path from console and paste here
file.name <- "/Users/toddwehner/Desktop/RCodeCurrent/GxeR14Data4.csv"

#create object path for where the data will go at the end
# I append the file name with "_out" so I know its data coming out of R
out.file <- "/Users/toddwehner/Desktop/RCodeCurrent/GxeR14Out4.csv"
tempa <-read.csv(file.name)
```

B. Define trait name that needs to be analyzed.

```
102 ##########################################################################
103 ######           Define trait that need to be analyzed           #######
104 ##########################################################################
105
106 #user need to define trait name for analysis
107 #example: MKMGHA = Marketable mega-gram per hectare
108
109 tempa <- tempa %>% rename(Trait = MKMGHA) %>%
110           select(YR, LC, RP, CLT, Trait)
```

	A	B	C	D	E
1	YR	LC	RP	CLT	MKMGHA
2	2009	KN	1	Early Canada	56.236
3	2009	KN	1	Calhoun Gray	74.167
4	2009	KN	1	Starbrite F1	32.601
5	2009	KN	1	Crimson Sweet	74.167
6	2009	KN	1	Georgia Rattlesnake	64.794
7	2009	KN	1	Fiesta F1	70.907
8	2009	KN	1	Mickylee	57.051
9	2009	KN	1	Sugar Baby	28.118

Snapshot of input file

C. Define output file information.

```
1655 ##########################################################################
1656 ###                  Export output in .CSV or .TXT                     ###
1657 ###                  Print final output in console                     ###
1658 ##########################################################################
1659
1660 #user can turn on and off .csv or .txt file by commenting/uncommenting
1661 #codes in below 2 lines
1662
1663 #sink(file="RGxEOutput.csv", append=FALSE, split=TRUE)
1664 sink(file="RGxEOutput.txt", append=FALSE, split=TRUE)
1665 ""
```

.csv

.txt

Output file name and type

User can uncomment or comment out code according to required output

3. Independent module of ANOVA model cases 2 to 5

Alike ANOVA model case 1, user can independently compute ANOVA case 2, ANOVA case 3, ANOVA case 4 and ANOVA case 5 from below code. The user defined function `anova_lrt()`, which stored in ANOVA model Case I code, is used for likelihood ratio test for computing significance of random effects.

```
##########################################################################
##          ANOVA Case 2: CLT, YR and LC - Fixed; RP - Random           ##
##########################################################################

#full model

fit.f2<-lmer(Trait~ YR*LC*CLT + (1|RPid), data=tempa)

#model summary

summary2 <- summary(fit.f2)
```

```
##variance of random factors

variance2 <- as.data.frame(summary2$varcor)

#drop rownames

rownames(variance2) <- NULL
variance2 <- variance2 %>% select (-var1, -var2) %>%
  rename(sov=grp, Mean_Sq=vcov, stddev=sdcor)

#Type 3  test of hypothesis

anova.f2t3 <- as.data.frame(anova(fit.f2, type="III"))

#convert rownames into column

anova.f2t3$name <- rownames(anova.f2t3)

#drop rownames

rownames(anova.f2t3) <- NULL

#Type 2  test of hypothesis

anova.f2t2 <- anova(fit.f2, type="marginal", test="F")

#model fitness

anovacase2 <- plot(fit.f2,
            main="Model fitness Case 2: CLT, YR and LC - Fixed; RP - Random",
            xlab="Predicated Value", ylab="Residual")

#level of significance: "KR" is implemented corresponding to
#the Kenward-Rogers approximation for degrees of freedom

anova_f2t3 <- mixed(Trait~ YR*LC*CLT + (1|RPid), data=tempa)

anova_f2t3 <- as.data.frame(anova_f2t3$anova_table)

#convert rownames into column

anova_f2t3$name <- rownames(anova_f2t3)

#drop rownames

rownames(anova_f2t3) <- NULL

anova_f2t3 <- anova_f2t3 %>% select(name, Prob_F = starts_with("Pr(>F)"))

#final output for case 2: CLT, YR and LC - Fixed

anova_f2 <- anova.f2t3 %>% left_join(anova_f2t3, by = "name")%>%
  rename(sov = name)%>%
  select(sov, Df,Sum_Sq=starts_with("Sum Sq"),
         Mean_Sq = starts_with("Mean Sq"),
         F_value=starts_with("F value"), Prob_F)

anova_f2 <- anova_f2 %>% bind_rows(variance2)
anova_f2a <- as.data.frame(anova_f2) # print for output
```

The output of ANOVA model Case 2 can be viewed using `print(anova_f2a)` command and is presented below.

```
"#Note: P values are computed for F ratio using KR method "
```

```
"#Kenward-Rogers approximation for degrees of freedom"
```

sov	Df	Sum_Sq	Mean_Sq	F_value	Prob_F	stddev
YR	1	120.4704	120.47042	0.367819	5.487578e-01	NA
LC	4	73133.5245	18283.38113	55.822625	1.801102e-13	NA
CLT	9	44948.8523	4994.31692	15.248595	4.888724e-20	NA
YR:LC	4	5372.9402	1343.23505	4.101151	9.076711e-03	NA
YR:CLT	9	4564.9326	507.21473	1.548623	1.309478e-01	NA
LC:CLT	36	15018.7208	417.18669	1.273750	1.455183e-01	NA
YR:LC:CLT	36	23058.4845	640.51346	1.955609	1.516985e-03	NA
RPid	NA	NA	73.91369	NA	NA	8.597307
Residual	NA	NA	327.52636	NA	NA	18.097689

Where `sov` = source of variance, `Sum_Sq` = sum of square, `Mean_Sq` = Mean square, `F_value` = *F* ratio, `Prob_F` = probability for *F* test, `stddev` = standard deviation,

```
#########################################################################
##          ANOVA CASE 3: CLT - Fixed; YR, LC and RP - Random          ##
#########################################################################

fit.f3<-lmer(Trait~ 1 + (1|YR)  + (1|LC) + CLT + (1|YR:LC) +
               (1|YR:CLT) +
               (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#model summary

summary3 <- summary(fit.f3)

##variance of random factors

variance3 <- as.data.frame(summary3$varcor)

#drop rownames

rownames(variance3) <- NULL
variance3 <- variance3 %>% select (-var1, -var2) %>%
  rename(sov=grp, Mean_Sq=vcov, stddev=sdcor)

#Type 3 test of hypothesis

anova.f3t3 <- as.data.frame(anova(fit.f3, type="III"))

#convert rownames into column

anova.f3t3$name <- rownames(anova.f3t3)

#drop rownames

rownames(anova.f3t3) <- NULL

#Type 2  test of hypothesis

anova.f3t2 <- anova(fit.f3, type="marginal", test="F")

#model fitness

anovacase3 <- plot(fit.f3,
            main="Model fitness Case 3: CLT - Fixed; YR, LC and RP - Random",
                   xlab="Predicated Value", ylab="Residual")

#p value for fixed effects
```

```
anova_f3t3 <- mixed(Trait~ 1 + (1|YR)  + (1|LC) + CLT + (1|YR:LC) +
                      (1|YR:CLT) + (1|LC:CLT) + (1|YR:LC:CLT) +
                      (1|RPid), data=tempa)

anova_f3t3 <- as.data.frame(anova_f3t3$anova_table)

#convert rownames into column

anova_f3t3$name <- rownames(anova_f3t3)

#drop rownames

rownames(anova_f3t3) <- NULL

anova_f3t3 <- anova_f3t3 %>% select(name, Prob_F = starts_with("Pr(>F)"))

#final output of case 3 for fixed effect - CLT

anova_f3 <- anova.f3t3 %>% left_join(anova_f3t3, by = "name")%>%
  rename(sov = name)%>%
  select(sov, Df,Sum_Sq=starts_with("Sum Sq"),
         Mean_Sq = starts_with("Mean Sq"),
         F_value=starts_with("F value"), Prob_F)

#level of significance for random effects
#null model for CLT

fit.f3c <- lmer(Trait~ 1 + (1|YR) + (1|LC) + (1|YR:LC) + (1|YR:LC) +
                  (1|YR:CLT) + (1|LC:CLT) + (1|YR:LC:CLT) +
                  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova3c <- anova_lrt(anova3c,fit.f3,fit.f3c,"CLT")

#null model for LC

fit.f3l <- lmer(Trait~ 1 + CLT + (1|YR) + (1|YR:LC) + (1|YR:CLT) +
                  (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt
anova3l <- anova_lrt(anova3l,fit.f3,fit.f3l,"LC")

#null model for YR

fit.f3y <- lmer(Trait~ 1 + CLT + (1|LC) + (1|YR:LC) + (1|YR:CLT) +
                  (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova3y <- anova_lrt(anova3y,fit.f3,fit.f3y,"YR")

#null model for YR:LC

fit.f3yl <- lmer(Trait~ 1 + CLT + (1|LC) + (1|YR) + (1|YR:CLT) +
                   (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova3yl <- anova_lrt(anova3yl,fit.f3,fit.f3yl,"YR:LC")
```

```
#null model for YR:CLT

fit.f3yc <- lmer(Trait~ 1 + CLT + (1|LC) + (1|YR) + (1|YR:LC) +
                   (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova3yc <- anova_lrt(anova3yc,fit.f3,fit.f3yc,"YR:CLT")

#null model for LC:CLT

fit.f3lc <- lmer(Trait~ 1 + CLT + (1|LC) + (1|YR) + (1|YR:LC) +
                   (1|YR:CLT) +
                   (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova3lc <- anova_lrt(anova3lc,fit.f3,fit.f3lc,"LC:CLT")

#null model for YR:LC:CLT

fit.f3ylc <- lmer(Trait~ 1 + CLT + (1|LC) + (1|YR) + (1|YR:LC) +
                    (1|YR:CLT) +
                    (1|LC:CLT) + (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova3ylc <- anova_lrt(anova3ylc,fit.f3,fit.f3ylc,"YR:LC:CLT")

#null model for RPid or replication

fit.f3r <- lmer(Trait~ 1 + CLT + (1|LC) + (1|YR) + (1|YR:LC) +
                  (1|YR:CLT) +
                  (1|LC:CLT) + (1|YR:LC:CLT), data=tempa)

#level of significance
#call function anova_lrt

anova3r <- anova_lrt(anova3r,fit.f3,fit.f3r,"RPid")

#Merge anova and level of significance

anova3 <- bind_rows(anova3y, anova3l)%>% bind_rows(anova3yl)%>%
  bind_rows(anova3yc)%>% bind_rows(anova3r)%>%
  bind_rows(anova3lc)%>%bind_rows(anova3ylc)

anova3 <- as.data.frame(anova3)

#Merge final output

anova_cfix <- variance3%>% left_join(anova3 , by ="sov")
anova_cfix$Pr_Chisq[anova_cfix$stddev == 0] <- NA
```

The output of ANOVA model Case 3 can be viewed using `print(anova_f3)` and `print(anova_cfix)` commands; and is presented below.

```
"#Note: P values are computed for F ratio using KR method "
"#Kenward-Rogers approximation for degrees of freedom"

sov Df   Sum_Sq  Mean_Sq  F_value      Prob_F
```

```
CLT  9 27964.75 3107.195 9.486854 0.006364982
```

Where `sov` = source of variance, `Sum_Sq` = sum of square, `Mean_Sq` = Mean square, `F_value` = *F* ratio, `Prob_F` = probability for *F* test

```
"#For random effect P values are generated using LRT-Likelihood Ratio Test"
"#via model comparison and anova"
```

sov	Mean_Sq	stddev	Pr_Chisq
YR:LC:CLT	49.72992	7.051945	2.724821e-02
LC:CLT	0.00000	0.000000	NA
RPid	73.91370	8.597308	4.145811e-07
YR:CLT	0.00000	0.000000	NA
YR:LC	57.81306	7.603490	6.776546e-02
LC	699.57346	26.449451	9.446027e-03
YR	0.00000	0.000000	NA
Residual	327.52637	18.097690	NA

Where `sov` = source of variance, `Mean_Sq` = Mean square, `stddev` = standard deviation, `Pr_Chisq` = Chi-Square probability

```
#########################################################################
##          ANOVA Case 4: LC - Fixed; YR, CLT and RP - Random          ##
#########################################################################

fit.f4 <- lmer(Trait~ 1 +  LC + (1|YR) + (1|CLT) + (1|YR:LC) +
                 (1|YR:CLT) + (1|LC:CLT) + (1|YR:LC:CLT) +
                  (1|RPid), data=tempa)

#model summary

summary4 <- summary(fit.f4)

##variance of random factors

variance4 <- as.data.frame(summary4$varcor)

# drop rownames

rownames(variance4) <- NULL
variance4 <- variance4 %>% select (-var1, -var2) %>%
  rename(sov=grp, Mean_Sq=vcov, stddev=sdcor)

#Type 3 test of hypothesis

anova.f4t3 <- as.data.frame(anova(fit.f4, type="III"))

#convert rownames into column

anova.f4t3$name <- rownames(anova.f4t3)

#drop rownames

rownames(anova.f4t3) <- NULL

#Type 2 test of hypothesis

anova.f4t2 <- anova(fit.f3, type="marginal", test="F")

#model fitness

anovacase4 <- plot(fit.f4,
            main="Model fitness Case 4: LC - Fixed; YR, CLT and RP - Random",
```

```
                  xlab="Predicated Value", ylab="Residual")

#level of significance for fixed effects

anova_f4t3 <- mixed(Trait~ 1 + LC + (1|YR)  + (1|CLT) + (1|YR:LC) +
                      (1|YR:CLT) +
                      (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

anova_f4t3 <- as.data.frame(anova_f4t3$anova_table)

#convert rownames into column

anova_f4t3$name <- rownames(anova_f4t3)

#drop rownames

rownames(anova_f4t3) <- NULL

anova_f4t3 <- anova_f4t3 %>% select(name, Prob_F = starts_with("Pr(>F)"))

#final output of case 4 for fixed effect - LC

anova_f4 <- anova.f4t3 %>% left_join(anova_f4t3, by = "name")%>%
  rename(sov = name)%>%
  select(sov, Df,Sum_Sq=starts_with("Sum Sq"),
         Mean_Sq = starts_with("Mean Sq"),
         F_value=starts_with("F value"), Prob_F)

#level of significance of random effect
#null model for CLT

fit.f4c <- lmer(Trait~ 1 + LC + (1|YR) +  (1|YR:LC) + (1|YR:LC) +
                  (1|YR:CLT)+
                  (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova4c <- anova_lrt(anova4c,fit.f4,fit.f4c,"CLT")

#null model for LC

fit.f4l <- lmer(Trait~ 1 + (1|CLT) + (1|YR) + (1|YR:LC) + (1|YR:CLT) +
                  (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova4l <- anova_lrt(anova4l,fit.f4,fit.f4l,"LC")

#null model for YR

fit.f4y <- lmer(Trait~ 1 + LC + (1|CLT) + (1|YR:LC) + (1|YR:CLT) +
                  (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova4y <- anova_lrt(anova4y,fit.f4,fit.f4y,"YR")

#null model for YR:LC

fit.f4yl <- lmer(Trait~ 1 + LC + (1|CLT) + (1|YR) + (1|YR:CLT) +
                   (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)
```

```
#level of significance
#call function anova_lrt

anova4yl <- anova_lrt(anova4yl,fit.f4,fit.f4yl,"YR:LC")

#null model for YR:CLT

fit.f4yc <- lmer(Trait~ 1 + LC + (1|CLT) + (1|YR) + (1|YR:LC) +
                   (1|LC:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova4yc <- anova_lrt(anova4yc,fit.f4,fit.f4yc,"YR:CLT")

#null model for LC:CLT

fit.f4lc <- lmer(Trait~ 1 + LC + (1|CLT) + (1|YR) + (1|YR:LC) +
                   (1|YR:CLT) +
                   (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova4lc <- anova_lrt(anova4lc,fit.f4,fit.f4lc,"LC:CLT")

#null model for YR:LC:CLT

fit.f4ylc <- lmer(Trait~ 1 + LC + (1|CLT) + (1|YR) + (1|YR:LC) +
                    (1|YR:CLT) +
                    (1|LC:CLT) + (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova4ylc <- anova_lrt(anova4ylc,fit.f4,fit.f4ylc,"YR:LC:CLT")

#null model for RPid or replication

fit.f4r <- lmer(Trait~ 1 + LC + (1|CLT) + (1|YR) + (1|YR:LC) +
                  (1|YR:CLT) +
                  (1|LC:CLT) + (1|YR:LC:CLT), data=tempa)

#level of significance
#call function anova_lrt

anova4r <- anova_lrt(anova4r,fit.f4,fit.f4r,"RPid")

#Merge anova and level of significance

anova4 <- bind_rows(anova4c, anova4y)%>% bind_rows(anova4yl)%>%
  bind_rows(anova4yc)%>% bind_rows(anova4r)%>%
  bind_rows(anova4lc)%>%bind_rows(anova4ylc)
anova4 <- as.data.frame(anova4)

#Merge final output

anova_lfix <- variance4%>% left_join(anova4 , by ="sov")
anova_lfix$Pr_Chisq[anova_lfix$stddev == 0] <- NA
```

The output of ANOVA model Case 4 can be viewed using `print(anova_f4)` and `print(anova_lfix)` commands; and is presented below.

```
"#Note: P values are computed for F ratio using KR method "
"#Kenward-Rogers approximation for degrees of freedom"

sov Df   Sum_Sq  Mean_Sq F_value      Prob_F
 LC  4 21801.73 5450.432 16.6412 0.009420459
```

Where `sov` = source of variance, `Sum_Sq` = sum of square, `Mean_Sq` = Mean square, `F_value` = *F* ratio, `Prob_F` = probability for *F* test

```
"#For random effect P values are generated using LRT-Likelihood Ratio Test"
"#via model comparison and anova"

       sov   Mean_Sq    stddev     Pr_Chisq
 YR:LC:CLT  49.72997  7.051948 8.212358e-03
    LC:CLT   0.00000  0.000000           NA
      RPid  73.91371  8.597308 4.145811e-07
    YR:CLT   0.00000  0.000000           NA
     YR:LC  57.81300  7.603486 3.980432e-01
       CLT 111.69670 10.568666           NA
        YR   0.00000  0.000000           NA
  Residual 327.52635 18.097689           NA
```

Where `sov` = source of variance, `Mean_Sq` = Mean square, `stddev` = standard deviation, `Pr_Chisq` = Chi-Square probability

```
##########################################################################
##      ANOVA Case 5: CLT and LC - Fixed; YR, and RP - Random           ##
##########################################################################

fit.f5 <- lmer(Trait~ 1 +  CLT + LC + LC:CLT + (1|YR) + (1|YR:LC) +
                 (1|YR:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#model summary

summary5 <- summary(fit.f5)

##variance of random factors

variance5 <- as.data.frame(summary5$varcor)

#drop rownames

rownames(variance5) <- NULL
variance5 <- variance5 %>% select (-var1, -var2) %>%
  rename(sov=grp, Mean_Sq=vcov, stddev=sdcor)

#Type 3 test of hypothesis

anova.f5t3 <- as.data.frame(anova(fit.f5, type="III"))

#convert rownames into column

anova.f5t3$name <- rownames(anova.f5t3)

#drop rownames

rownames(anova.f5t3) <- NULL

#Type 2 test of hypothesis

anova.f5t2 <- anova(fit.f3, type="marginal", test="F")

#model fitness
```

```
anovacase5 <- plot(fit.f5,
                   main="Model fitness Case 5: CLT and LC - Fixed; YR and RP
- Random",
                   xlab="Predicated Value", ylab="Residual")

#level of significance for fixed effects

anova_f5t3 <- mixed(Trait~ 1 +  CLT + LC + LC:CLT + (1|YR) +
                      (1|YR:LC) + (1|YR:CLT) + (1|YR:LC:CLT) +
                      (1|RPid), data=tempa)

anova_f5t3 <- as.data.frame(anova_f5t3$anova_table)

#convert rownames into column

anova_f5t3$name <- rownames(anova_f5t3)

#drop rownames

rownames(anova_f5t3) <- NULL

anova_f5t3 <- anova_f5t3 %>% select(name, Prob_F = starts_with("Pr(>F)"))

#final output of case 5 for fixed effect - CLT and LC

anova_f5 <- anova.f5t3 %>% left_join(anova_f5t3, by = "name")%>%
  rename(sov = name)%>%
  select(sov, Df,Sum_Sq=starts_with("Sum Sq"),
         Mean_Sq = starts_with("Mean Sq"),
         F_value=starts_with("F value"), Prob_F)

#level of significance for random effects
#null model for CLT

fit.f5c <- lmer(Trait~ 1 +  LC + LC:CLT + (1|YR) + (1|YR:LC) +
                  (1|YR:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova5c <- anova_lrt(anova5c,fit.f5,fit.f5c,"CLT")

#null model for LC

fit.f5l <- lmer(Trait~ 1 +  CLT + LC:CLT + (1|YR) + (1|YR:LC) +
                  (1|YR:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova5l <- anova_lrt(anova5l,fit.f5,fit.f5l,"LC")

#null model for YR

fit.f5y <- lmer(Trait~ 1 +  CLT + LC + LC:CLT + (1|YR:LC) +
                  (1|YR:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova5y <- anova_lrt(anova5y,fit.f5,fit.f5y,"YR")

#null model for YR:LC
```

```
fit.f5yl <- lmer(Trait~ 1 +  CLT + LC + LC:CLT + (1|YR) +
                   (1|YR:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova5yl <- anova_lrt(anova5yl,fit.f5,fit.f5yl,"YR:LC")

#null model for YR:CLT

fit.f5yc <- lmer(Trait~ 1 +  CLT + LC + LC:CLT + (1|YR) + (1|YR:LC) +
                   (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova5yc <- anova_lrt(anova5yc,fit.f5,fit.f5yc,"YR:CLT")

#null model for LC:CLT

fit.f5lc <- lmer(Trait~ 1 +  CLT + LC + (1|YR) + (1|YR:LC) +
                   (1|YR:CLT) + (1|YR:LC:CLT) +  (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova5lc <- anova_lrt(anova5lc,fit.f5,fit.f5lc,"LC:CLT")

#null model for YR:LC:CLT

fit.f5ylc <- lmer(Trait~ 1 +  CLT + LC + LC:CLT + (1|YR) + (1|YR:LC) +
                    (1|YR:CLT) + (1|RPid), data=tempa)

#level of significance
#call function anova_lrt

anova5ylc <- anova_lrt(anova5ylc,fit.f5,fit.f5ylc,"YR:LC:CLT")

#null model for RPid or replication

fit.f5r <- lmer(Trait~ 1 +  CLT + LC + LC:CLT + (1|YR) + (1|YR:LC) +
                  (1|YR:CLT) + (1|YR:LC:CLT) , data=tempa)

#level of significance
#call function anova_lrt

anova5r <- anova_lrt(anova5r,fit.f5,fit.f5r,"RPid")

#Merge anova and level of significance

anova5 <- bind_rows(anova5y, anova5yl)%>%
  bind_rows(anova5yc)%>% bind_rows(anova5r)%>%
  bind_rows(anova5ylc)
anova5 <- as.data.frame(anova5)

#Merge final output

anova_clfix <- variance5%>% left_join(anova5 , by ="sov")
anova_clfix$Pr_Chisq[anova_clfix$stddev == 0] <- NA
```

The output of ANOVA model Case 5 can be viewed using `print(anova_f5)` and `print(anova_clfix)`commands; and is presented below.

```
"#Note: P values are computed for F ratio using KR method "
"#Kenward-Rogers approximation for degrees of freedom"

    sov Df    Sum_Sq   Mean_Sq   F_value      Prob_F
    CLT  9 23982.801 2664.7557  8.136004 0.002267970
     LC  4 21801.728 5450.4320 16.641201 0.009275436
 CLT:LC 36  8013.352  222.5931  0.679619 0.874336050
```

Where `sov` = source of variance, `Sum_Sq` = sum of square, `Mean_Sq` = Mean square, `F_value` = *F* ratio, `Prob_F` = probability for *F* test

```
"#For random effect P values are generated using LRT-Likelihood Ratio Test"
"#via model comparison and anova"

       sov   Mean_Sq    stddev     Pr_Chisq
 YR:LC:CLT  71.58186  8.460607 1.000000e+00
      RPid  73.91368  8.597307 1.305383e-07
    YR:CLT   0.00000  0.000000           NA
     YR:LC  55.62783  7.458407 2.975676e-01
        YR   0.00000  0.000000           NA
  Residual 327.52636 18.097689           NA
```

Where `sov` = source of variance, `Mean_Sq` = Mean square, `stddev` = standard deviation, `Pr_Chisq` = Chi-Square probability

Fitness of ANOVA model case 2, case 3, case 4 and case 5 can be plotted using command `print(anovacase2)`, `print(anovacase3)`, `print(anovacase4)` and `print(anovacase1)`, respectively.

4. Interpretation of univariate stability statistics

4.1 Linear regression coefficient (b_i)

Regression coefficient (b_i) of genotypes approximating unity (P<0.01) along with high trait mean is considered to stable across wide range of environment. When this is associated with low trait mean performance, genotypes are poorly adapted to all environments. A b_i greater than unity describes genotypes with higher sensitivity to environmental change (below average stability), and greater specificity of adaptability to high yielding environments.

4.2 Deviation from regression (S^2_d)

Genotype is considered to be stable when deviation from regression (S^2_d) is not significantly different from zero.

4.3 Shukla stability variance (σ_i^2), ssquare, and Wricke's ecovalence (W_i^2)

Genotype with low σ_i^2, ssquare and W_i^2 is regarded as stable.

4.4 Kang stability statistic (YS_i)

According to this method, genotypes with YS_i greater than the mean YS_i are considered stable. Stable genotypes are marked with symbol '+'.

5. Output (.txt) from sample data

```
[1] "#############      Print date and time     #################"
[1] ""
```

```
[1] "2016-03-12 15:13:22 EST"
[1] ""
"##############################################################################"
[1] "###      Section 1: Identify level of significance of           ###"
[1] "###         different effects, variances and BLUP               ###"
"##############################################################################"
[1] ""
[1] ""
[1]
"##############################################################################"
[1] "###          ANOVA - ANALYSIS OF VARIANCE                      ####"
[1]
"##############################################################################"
[1] ""
[1]
"##############################################################################"
[1] "##      ANOVA Case 1: CLT, YR, LC and RP - All Random           ##"
[1]
"##############################################################################"
[1] ""
[1] "##Print ANOVA"
[1] "#Note: P values are generated using LRT-Likelihood Ratio Test via "
[1] "#model comparison and anova"
[1] ""
       sov Variance  stddev   Pr_Chisq
 YR:LC:CLT   49.730  7.0519 8.8942e-03
    LC:CLT    0.000  0.0000         NA
      RPid   73.914  8.5973 4.1458e-07
    YR:CLT    0.000  0.0000         NA
     YR:LC   57.813  7.6035 7.8725e-02
       CLT  111.697 10.5687 1.3867e-03
        LC  699.569 26.4494 9.0836e-03
        YR    0.000  0.0000         NA
  Residual  327.526 18.0977         NA
[1] ""
[1] "##Print BLUP-Best linear unbiased predictor value for random
genotypes"
[1] ""
          genotype   Blup
       CalhounGray 76.255
      CrimsonSweet 62.535
       EarlyCanada 59.840
          FiestaF1 77.283
 GeorgiaRattlesnake 70.710
            Legacy 68.417
          Mickylee 61.300
          Quetzali 58.744
       StarbriteF1 83.422
         SugarBaby 51.169
[1] ""
"##############################################################################"
[1] "##    ANOVA Case 2: CLT, YR and LC - Fixed; RP - Random          ##"
"##############################################################################"
[1] ""
```

```
[1] "##Print ANOVA"
[1] "#Note: P values are computed for F ratio using KR method "
[1] "#Kenward-Rogers approximation for degrees of freedom"
[1] ""
       sov Df   Sum_Sq   Mean_Sq  F_value     Prob_F  stddev
        YR  1   120.47   120.470  0.36782 5.4876e-01      NA
        LC  4 73133.52 18283.381 55.82263 1.8011e-13      NA
       CLT  9 44948.85  4994.317 15.24860 4.8887e-20      NA
     YR:LC  4  5372.94  1343.235  4.10115 9.0767e-03      NA
    YR:CLT  9  4564.93   507.215  1.54862 1.3095e-01      NA
    LC:CLT 36 15018.72   417.187  1.27375 1.4552e-01      NA
 YR:LC:CLT 36 23058.48   640.513  1.95561 1.5170e-03      NA
      RPid NA       NA    73.914       NA         NA  8.5973
  Residual NA       NA   327.526       NA         NA 18.0977
[1] ""
[1]
"##############################################################################"
[1] "##    ANOVA Case 3: CLT - Fixed; YR, LC and RP - Random         ##"
"##############################################################################"
[1] ""
[1] "##Print ANOVA"
[1] "#Note: For fixed effects P values are computed for F ratio using "
[1] "#KR method Kenward-Rogers approximation for degrees of freedom"
[1] ""
 sov Df Sum_Sq Mean_Sq F_value   Prob_F
 CLT  9  27965  3107.2  9.4869 0.006365
[1] ""
[1] "#For random effect P values are generated using LRT-Likelihood Ratio
Test "
[1] "#via model comparison and anova"
[1] ""
       sov Mean_Sq  stddev   Pr_Chisq
 YR:LC:CLT  49.730  7.0519 2.7248e-02
    LC:CLT   0.000  0.0000         NA
      RPid  73.914  8.5973 4.1458e-07
    YR:CLT   0.000  0.0000         NA
     YR:LC  57.813  7.6035 6.7765e-02
        LC 699.573 26.4495 9.4460e-03
        YR   0.000  0.0000         NA
  Residual 327.526 18.0977         NA
[1] ""
[1]
"##############################################################################"
[1] "##    ANOVA Case 4: LC - Fixed; YR, CLT and RP - Random          ##"
"##############################################################################"
[1] ""
[1] "##Print ANOVA"
[1] "#Note: For fixed effects P values are computed for F ratio using"
[1] "#KR method Kenward-Rogers approximation for degrees of freedom"
[1] ""
 sov Df Sum_Sq Mean_Sq F_value    Prob_F
  LC  4  21802  5450.4  16.641 0.0094205
[1] ""
```

```
[1] "#For random effect P values are generated using LRT-Likelihood Ratio
Test"
[1] "#via model comparison and anova"
[1] ""
       sov Mean_Sq  stddev   Pr_Chisq
 YR:LC:CLT  49.730  7.0519 8.2124e-03
    LC:CLT   0.000  0.0000         NA
      RPid  73.914  8.5973 4.1458e-07
    YR:CLT   0.000  0.0000         NA
     YR:LC  57.813  7.6035 3.9804e-01
       CLT 111.697 10.5687         NA
        YR   0.000  0.0000         NA
  Residual 327.526 18.0977         NA
[1] ""
[1]
"##############################################################################"
[1] "##   ANOVA Case 5: CLT and LC - Fixed; YR, and RP - Random       ##"
"##############################################################################"
 [1] "##Print ANOVA"
[1] "#Note: For fixed effects P values are computed for F ratio using "
[1] "#KR method Kenward-Rogers approximation for degrees of freedom"
[1] ""
    sov Df  Sum_Sq Mean_Sq  F_value    Prob_F
    CLT  9 23982.8 2664.76  8.13600 0.0022680
     LC  4 21801.7 5450.43 16.64120 0.0092754
 CLT:LC 36  8013.4  222.59  0.67962 0.8743361
[1] ""
[1] "#For random effect P values are generated using LRT-Likelihood Ratio
Test"
[1] "#via model comparison and anova"
[1] ""
       sov Mean_Sq  stddev   Pr_Chisq
 YR:LC:CLT  71.582  8.4606 1.0000e+00
      RPid  73.914  8.5973 1.3054e-07
    YR:CLT   0.000  0.0000         NA
     YR:LC  55.628  7.4584 2.9757e-01
        YR   0.000  0.0000         NA
  Residual 327.526 18.0977         NA
[1] ""
[1] ""
"##############################################################################"
[1] "###  Section 2: Identify general statistcs (mean and CV) of     ###"
[1] "###  genotype, location, year, replication and environment      ###"
"##############################################################################"
[1] ""
"##############################################################################"
[1] "###                 Descriptive Statistics                         ###"
"##############################################################################"
[1] "#Descriptive Statistics - Means and CV"
[1] ""
[1] "#trait mean across genotype and environment(location x year
combination)"
[1] ""
             CLT CI-2009 CI-2010 FL-2009 FL-2010 KN-2009 KN-2010 SC-2009 SC-2010 TX-2009 TX-2010
CalhounGray  64.590  81.502 106.663 121.151  68.767  70.805 104.374  89.694  48.932 17.0135
```

```
      CrimsonSweet  25.775  73.046 110.511  65.791  62.960  57.561  74.870 112.900  21.176 15.5362
       EarlyCanada  50.939  55.320  90.613 116.482  57.051  55.421  55.767  74.885  21.744 11.7770
          FiestaF1  69.379  81.298 109.561  99.026  80.178  67.647  89.577 123.786  42.324 22.2093
 GeorgiaRattlesnake  52.671  72.843 102.128 109.443  69.990  62.960  87.217  79.128  62.326 12.8060
            Legacy  52.467  66.323 105.471  89.036  81.298  72.435  88.606  63.556  50.802 15.8825
          Mickylee  49.410  59.089  78.977 113.275  70.194  51.448  82.658  48.035  40.334 12.8977
          Quetzali  40.751  62.757  79.424  87.583  61.432  48.697  79.719  77.865  29.735  9.7903
       StarbriteF1  77.936  84.457 125.971 120.292  70.601  79.974 112.504 102.433  57.339 22.0972
         SugarBaby  42.381  57.866  80.657  91.010  37.491  48.799  53.531  52.595  18.116 10.6258
[1] ""
[1] "#trait mean across genotype and years"
[1] ""
                CLT   2009   2010
       CalhounGray 78.665 76.033
      CrimsonSweet 59.059 64.967
       EarlyCanada 55.223 62.777
          FiestaF1 78.204 78.793
GeorgiaRattlesnake 74.866 67.436
            Legacy 75.729 61.447
          Mickylee 64.314 56.949
          Quetzali 58.212 57.338
       StarbriteF1 88.870 81.850
         SugarBaby 46.435 52.179
[1] ""
[1] "#trait mean across genotype and location"
[1] ""
                CLT     CI      FL     KN      SC     TX
       CalhounGray 73.046 113.907 69.786  97.034 32.973
      CrimsonSweet 49.411  88.151 60.261  93.885 18.356
       EarlyCanada 53.129 103.548 56.236  65.326 16.761
          FiestaF1 75.338 104.294 73.912 106.682 32.266
GeorgiaRattlesnake 62.757 105.786 66.475  83.173 37.566
            Legacy 59.395  97.253 76.867  76.081 33.342
          Mickylee 54.250  96.126 60.821  65.347 26.616
          Quetzali 51.754  83.503 55.065  78.792 19.763
       StarbriteF1 81.196 123.132 75.288 107.468 39.718
         SugarBaby 50.124  85.834 43.145  53.063 14.371
[1] ""
[1] "#trait mean across genotype, location and year"
[1] ""
                CLT   YR     CI      FL     KN      SC      TX
       CalhounGray 2009 64.590 106.663 68.767 104.374 48.9320
       CalhounGray 2010 81.502 121.151 70.805  89.694 17.0135
      CrimsonSweet 2009 25.775 110.511 62.960  74.870 21.1758
      CrimsonSweet 2010 73.046  65.791 57.561 112.900 15.5362
       EarlyCanada 2009 50.939  90.613 57.051  55.767 21.7445
       EarlyCanada 2010 55.320 116.482 55.421  74.885 11.7770
          FiestaF1 2009 69.379 109.561 80.178  89.577 42.3235
          FiestaF1 2010 81.298  99.026 67.647 123.786 22.2093
GeorgiaRattlesnake 2009 52.671 102.128 69.990  87.217 62.3257
GeorgiaRattlesnake 2010 72.843 109.443 62.960  79.128 12.8060
            Legacy 2009 52.467 105.471 81.298  88.606 50.8020
            Legacy 2010 66.323  89.036 72.435  63.556 15.8825
          Mickylee 2009 49.410  78.977 70.194  82.658 40.3335
          Mickylee 2010 59.089 113.275 51.448  48.035 12.8977
          Quetzali 2009 40.751  79.424 61.432  79.719 29.7353
          Quetzali 2010 62.757  87.583 48.697  77.865  9.7903
```

```
        StarbriteF1 2009 77.936 125.971 70.601 112.504 57.3388
        StarbriteF1 2010 84.457 120.292 79.974 102.433 22.0972
          SugarBaby 2009 42.381  80.657 37.491  53.531 18.1155
          SugarBaby 2010 57.866  91.010 48.799  52.595 10.6258
[1] ""
[1] "#trait mean across genotype, location and replication"
[1] ""
                CLT RP     CI      FL      KN      SC      TX
        CalhounGray  1 98.413  95.809  62.349  89.448 54.4325
        CalhounGray  2 69.684 136.038  55.625 103.293 25.3965
        CalhounGray  3 59.292 118.781  70.296  87.128 15.2330
        CalhounGray  4 64.794 105.000  90.875 108.266 36.8290
       CrimsonSweet  1 37.491  39.581  62.349  79.465 31.2560
       CrimsonSweet  2 59.293 130.710  58.885  94.685 13.5540
       CrimsonSweet  3 63.979  93.970  55.218 109.528 19.0985
       CrimsonSweet  4 36.880  88.343  64.591  91.863  9.5155
        EarlyCanada  1 64.386 104.058  51.346  72.465 10.1675
        EarlyCanada  2 45.233 107.547  52.772  59.435 15.2815
        EarlyCanada  3 61.331 104.386  48.901  59.649 27.9405
        EarlyCanada  4 41.566  98.200  71.925  69.755 13.6535
           FiestaF1  1 78.650  67.163  70.703 111.038 51.4160
           FiestaF1  2 70.499 145.651  72.944 117.007 31.7220
           FiestaF1  3 63.164  97.226  82.114  98.525 18.9710
           FiestaF1  4 89.041 107.133  69.888 100.156 26.9565
 GeorgiaRattlesnake  1 70.499  95.776  61.941  84.538 49.4325
 GeorgiaRattlesnake  2 60.923 106.091  61.738  78.721 58.1390
 GeorgiaRattlesnake  3 58.274 105.629  74.167  69.766 13.2595
 GeorgiaRattlesnake  4 61.331 115.646  68.054  99.667 29.4325
            Legacy  1 64.794  80.311  66.424  84.233 48.1675
            Legacy  2 41.159 104.211  71.315  82.887 37.6610
            Legacy  3 55.829  97.647  87.614  68.635 29.0530
            Legacy  4 75.797 106.844  82.113  68.570 18.4875
          Mickylee  1 51.550  95.789  54.810  72.913 53.3065
          Mickylee  2 60.923 107.262  72.333  59.385 21.7000
          Mickylee  3 36.880  95.143  59.700  63.388 19.0495
          Mickylee  4 67.647  86.310  56.440  65.701 12.4065
          Quetzali  1 64.590  73.935  53.587  94.370 27.9930
          Quetzali  2 53.791 101.604  50.328  75.674 22.7275
          Quetzali  3 50.939  79.901  47.883  62.777 18.2570
          Quetzali  4 37.694  78.573  68.462  82.347 10.0735
        StarbriteF1  1 71.722  76.359  54.199  80.066 40.4225
        StarbriteF1  2 86.189 124.965  70.296 110.171 61.3850
        StarbriteF1  3 90.875 126.852  70.296 103.640 31.6680
        StarbriteF1  4 76.001 164.350 106.361 135.996 25.3965
          SugarBaby  1 60.923  71.728  35.861  59.690 12.6045
          SugarBaby  2 58.070  94.041  30.563  52.498 15.8565
          SugarBaby  3 36.472  85.855  50.735  53.883 13.8400
          SugarBaby  4 45.029  91.711  55.421  46.181 15.1815
[1] ""
[1] "#trait mean across location and year"
[1] ""
 LC   2009    2010
 CI 52.630  69.450
 FL 98.998 101.309
```

```
 KN 65.996  61.575
 SC 82.882  82.488
 TX 39.283  15.064
[1] ""
[1] "#trait mean across location and replication"
[1] ""
 LC      1       2       3       4
 CI 66.302  60.576  57.703  59.578
 FL 80.051 115.812 100.539 104.211
 KN 57.357  59.680  64.692  73.413
 SC 82.823  83.376  77.692  86.850
 TX 37.920  30.342  20.637  19.793
[1] ""
[1] "#trait count, min, max, mean, sum, median, var, sd over location"
[1] ""
 LC count    min    max    mean    sum median    var     sd
 CI    80  0.000 108.81  61.040 4883.2 59.904 422.13 20.546
 FL    80  0.000 180.91 100.153 8012.3 99.492 886.48 29.774
 KN    80 19.153 109.21  63.786 5102.8 63.776 305.04 17.465
 SC    80 30.522 144.67  82.685 6614.8 81.462 740.18 27.206
 TX    80  0.000 102.63  27.173 2173.8 20.388 505.83 22.491
[1] ""
[1] "#trait count, min, max, mean, sum, median, var, sd over year"
[1] ""
   YR count min    max   mean   sum median    var     sd
 2009   200   0 172.06 67.958 13592 68.735 1005.8 31.714
 2010   200   0 180.91 65.977 13195 65.405 1324.4 36.392
[1] ""
[1] "#trait count, min, max, mean, sum, median, var, sd over genotype"
[1] ""
               CLT count    min    max   mean    sum median     var     sd
       CalhounGray    40  9.454 152.04 77.349 3094.0 81.777 1275.65 35.716
      CrimsonSweet    40  0.000 147.98 62.013 2480.5 61.738 1468.58 38.322
       EarlyCanada    40  7.213 119.75 59.000 2360.0 56.644 1009.08 31.766
          FiestaF1    40  4.034 180.91 78.498 3139.9 79.792 1334.98 36.537
 GeorgiaRattlesnake    40  4.157 144.54 71.151 2846.0 69.277 1055.36 32.486
            Legacy    40  5.990 120.69 68.588 2743.5 68.808  835.44 28.904
          Mickylee    40 10.229 128.39 60.632 2425.3 59.395  892.20 29.870
          Quetzali    40  5.909 110.52 57.775 2311.0 60.433  759.80 27.564
       StarbriteF1    40  7.417 172.06 85.360 3414.4 83.540 1462.50 38.243
         SugarBaby    40  8.884 106.33 49.307 1972.3 51.245  653.62 25.566
[1] ""
[1] "#trait count, min, max, mean, sum, median, var, sd over environment"
[1] ""
     ENV count    min     max    mean     sum  median     var      sd
 CI-2009    40  0.000 108.805  52.630 2105.19  54.199  489.72 22.1297
 CI-2010    40 42.789  97.395  69.450 2778.00  67.851  220.28 14.8417
 FL-2009    40 56.717 172.065  98.998 3959.91  95.171  553.49 23.5265
 FL-2010    40  0.000 180.906 101.309 4052.36 107.077 1239.46 35.2060
 KN-2009    40 19.153 109.213  65.996 2639.85  66.424  419.76 20.4881
 KN-2010    40 35.861 105.138  61.575 2462.99  60.922  188.12 13.7157
 SC-2009    40 30.522 144.666  82.882 3315.30  82.864  705.88 26.5683
 SC-2010    40 40.853 141.956  82.488 3299.51  76.512  793.38 28.1671
 TX-2009    40  0.000 102.626  39.283 1571.31  32.904  658.22 25.6559
 TX-2010    40  4.034  34.231  15.064  602.54  13.143   65.60  8.0994
```

```
[1] ""
[1] "#trait coefficient of variation (cv) across gentoype and location"
[1] ""
                CLT     CI     FL     KN     SC     TX
        CalhounGray 31.949 23.999 32.158 16.135 83.562
       CrimsonSweet 62.295 49.664 13.229 30.140 66.446
        EarlyCanada 21.952 15.884 29.933 30.311 70.379
           FiestaF1 21.779 43.048 13.199 22.666 56.006
 GeorgiaRattlesnake 19.610 20.215 10.081 38.647 94.577
             Legacy 29.606 27.040 15.967 24.143 71.471
           Mickylee 29.351 21.866 25.915 33.958 99.438
           Quetzali 31.077 21.406 21.994 22.743 75.846
        StarbriteF1 21.454 30.106 31.218 21.508 65.571
          SugarBaby 28.754 13.669 30.860 20.260 33.650
[1] ""
[1] "trait sum across genotype and location"
[1] ""
                CLT     CI     FL     KN     SC     TX
        CalhounGray 584.37 911.26 558.29 776.27 263.78
       CrimsonSweet 395.29 705.21 482.08 751.08 146.85
        EarlyCanada 425.03 828.38 449.89 522.61 134.09
           FiestaF1 602.71 834.35 591.30 853.45 258.13
 GeorgiaRattlesnake 502.05 846.28 531.80 665.38 300.53
             Legacy 475.16 778.03 614.93 608.65 266.74
           Mickylee 434.00 769.01 486.57 522.77 212.93
           Quetzali 414.03 668.03 440.52 630.34 158.10
        StarbriteF1 649.57 985.05 602.30 859.74 317.74
          SugarBaby 400.99 686.67 345.16 424.50 114.97
[1] ""
[1] "trait sum across genotype, location and year"
[1] ""
                CLT   YR     CI     FL     KN     SC      TX
        CalhounGray 2009 258.36 426.65 275.07 417.50 195.728
        CalhounGray 2010 326.01 484.60 283.22 358.78  68.054
       CrimsonSweet 2009 103.10 442.05 251.84 299.48  84.703
       CrimsonSweet 2010 292.19 263.16 230.24 451.60  62.145
        EarlyCanada 2009 203.75 362.45 228.20 223.07  86.978
        EarlyCanada 2010 221.28 465.93 221.69 299.54  47.108
           FiestaF1 2009 277.51 438.25 320.71 358.31 169.294
           FiestaF1 2010 325.19 396.10 270.59 495.14  88.837
 GeorgiaRattlesnake 2009 210.68 408.51 279.96 348.87 249.303
 GeorgiaRattlesnake 2010 291.37 437.77 251.84 316.51  51.224
             Legacy 2009 209.87 421.88 325.19 354.42 203.208
             Legacy 2010 265.29 356.14 289.74 254.23  63.530
           Mickylee 2009 197.64 315.91 280.77 330.63 161.334
           Mickylee 2010 236.36 453.10 205.79 192.14  51.591
           Quetzali 2009 163.00 317.69 245.73 318.88 118.941
           Quetzali 2010 251.03 350.33 194.79 311.46  39.161
        StarbriteF1 2009 311.75 503.89 282.40 450.01 229.355
        StarbriteF1 2010 337.83 481.17 319.90 409.73  88.389
          SugarBaby 2009 169.52 322.63 149.96 214.12  72.462
          SugarBaby 2010 231.46 364.04 195.20 210.38  42.503
[1] ""
[1] "trait sum across genotype and year"
```

```
[1] ""
                CLT   2009   2010
        CalhounGray 1573.3 1520.7
       CrimsonSweet 1181.2 1299.3
        EarlyCanada 1104.5 1255.5
           FiestaF1 1564.1 1575.9
 GeorgiaRattlesnake 1497.3 1348.7
             Legacy 1514.6 1228.9
           Mickylee 1286.3 1139.0
           Quetzali 1164.2 1146.8
        StarbriteF1 1777.4 1637.0
          SugarBaby  928.7 1043.6
[1] ""
[1] "trait standard deviation (sd) across genotype and location"
[1] ""
                CLT     CI     FL      KN     SC      TX
        CalhounGray 23.337 27.336 22.4419 15.657 27.5527
       CrimsonSweet 30.780 43.780  7.9720 28.297 12.1968
        EarlyCanada 11.663 16.447 16.8332 19.801 11.7961
           FiestaF1 16.408 44.896  9.7560 24.180 18.0711
 GeorgiaRattlesnake 12.306 21.384  6.7012 32.143 35.5286
             Legacy 17.584 26.297 12.2736 18.368 23.8302
           Mickylee 15.923 21.019 15.7614 22.191 26.4661
           Quetzali 16.084 17.875 12.1110 17.919 14.9893
        StarbriteF1 17.420 37.069 23.5036 23.114 26.0434
          SugarBaby 14.413 11.732 13.3147 10.750  4.8357
[1] ""
[1] "trait standard deviation (sd) across genotype, location and year"
[1] ""
                CLT   YR      CI      FL      KN      SC      TX
        CalhounGray 2009 32.0192 32.1452 30.7113 11.6864 32.5363
        CalhounGray 2010  7.4101 23.8823 15.1397 17.0801  5.7921
       CrimsonSweet 2009 19.1151 28.5590  7.8283 23.4217 15.1403
       CrimsonSweet 2010 18.8557 48.2005  8.2203 18.8560  9.8325
        EarlyCanada 2009 13.8353 12.3116 23.6429 23.2914 15.9525
        EarlyCanada 2010 10.6391  5.7846 10.0205 11.3460  1.9904
           FiestaF1 2009 19.4961  6.6594  7.4503 10.2947 17.5309
           FiestaF1 2010 12.3851 67.7116  7.8670 21.8657 13.5988
 GeorgiaRattlesnake 2009  5.7280 17.4036  6.9186 41.5767 35.6340
 GeorgiaRattlesnake 2010  7.0215 26.9899  4.8959 25.2695  6.3833
             Legacy 2009 12.1090 19.9329 15.5727 16.8878 19.9047
             Legacy 2010 21.1391 32.1907  7.5245  9.1512 10.7674
           Mickylee 2009 21.8298  5.4043 18.3739 16.7378 33.4959
           Mickylee 2010  7.2519 14.7424  2.7913  8.3460  3.2569
           Quetzali 2009 11.7591 15.8267 10.3753 20.2266 15.1437
           Quetzali 2010 11.9366 21.2281 11.2465 18.3803  5.4514
        StarbriteF1 2009 24.6272 32.8501 30.6391 27.8233 25.5900
        StarbriteF1 2010  8.5569 45.8879 17.0780 20.1214  9.9889
          SugarBaby 2009 16.6566  7.8131 16.4254 14.9464  3.3705
          SugarBaby 2010  6.8838 13.7355  7.6551  6.7591  2.4096
[1] ""
[1] "trait standard deviation (sd) across genotype and year"
[1] ""
                CLT   2009   2010
```

```
        CalhounGray 34.861 37.410
       CrimsonSweet 38.308 39.097
        EarlyCanada 27.794 35.619
           FiestaF1 25.759 45.569
 GeorgiaRattlesnake 29.401 35.676
             Legacy 26.536 30.055
           Mickylee 25.412 34.015
           Quetzali 24.665 30.835
         StarbriteF1 36.771 40.298
           SugarBaby 24.071 27.292
[1] ""
[1] ""
"#############################################################################"
[1] "###       Section 3: Choose stable and best genotype            ###"
"#############################################################################"
[1] ""
"#############################################################################"
[1] "###                  Stability Statistics                             ###"
"#############################################################################"
[1] ""
[1] "#Univariate statistics - mean, slope, deviation from regression,"
[1] "#Shukla,Ecovalence, Kang"
[1] ""
        Genotype   Mean             SLOPE             DEVREG          SIGMA   SIGMA_SQUARE Ecovalence YS_Kang
      CalhounGray 77.349   1.31693830164876    124.670028621208  61.346841 ns   15.761172 ns      279.75   10 +
     CrimsonSweet 62.013   1.36454332357129 1450.03510073339*** 439.124582 ns  567.987945 ns     1488.64     4
      EarlyCanada 59.000 0.320939654616631*   686.251275445017* 253.229481 ns  285.369649 ns      893.77     2
         FiestaF1 78.498   1.58347941482123    657.873266033708 300.285026 ns  385.996807 ns     1044.35   11 +
GeorgiaRattlesnake 71.151  0.917198392144549    220.063304045718  52.212609 ns   44.863403 ns      250.52    8 +
           Legacy 68.588   1.13392930476125    428.070344903385 287.393522 ns   262.48765 ns     1003.10    7 +
         Mickylee 60.632  0.593584749858975   705.480966435745* 188.105058 ns  195.125992 ns      685.37     3
         Quetzali 57.775  0.971528006198702    96.5321084597175  82.808549 ns   86.103189 ns      348.42     1
       StarbriteF1 85.360   1.29338936247089    221.136796113672 157.240582 ns   78.371337 ns      586.61   12 +
         SugarBaby 49.307 0.504469489907715*   332.181769968082* 264.187195 ns  308.429643 ns      928.84    -1
[1] ""
[1] ""
"#############################################################################"
[1] "## Section 4: Choose discriminative and representative location  ##"
"#############################################################################"
 [1] ""
"#############################################################################"
[1] "###  location statistics - genotype F ratio across location     ###"
[1] "###           and environment; location correlation             ###"
"#############################################################################"
[1] ""
[1] "#location value"
[1] "# location mean, genotype F ratio across location,"
[1] "#correlation of location with average location performace"
[1] ""
 Location    Mean FRatioGenotype       LocCorrelation
       CI  61.040         4.1804 0.949049766419943***
       FL 100.153         2.2579  0.864975641187942**
       KN  63.786         4.6964 0.896401033871258***
       SC  82.685         6.8813  0.87603982110229***
       TX  27.173         2.9966  0.89062492518194***
[1] ""
[1] "#location value-genotype F ratio across location,"
[1] ""
```

```
    ENV FRatioGenotype
CI-2009         2.4015
CI-2010         3.3665
FL-2009         2.6914
FL-2010         1.7231
KN-2009         1.9999
KN-2010         6.3971
SC-2009         2.8729
SC-2010         8.0454
TX-2009         2.5003
TX-2010         1.4619
```

6. Sample data

YR	LC	RP	CLT	Trait
2009	KN	1	Early Canada	56.236
2009	KN	1	Calhoun Gray	74.167
2009	KN	1	Starbrite F1	32.601
2009	KN	1	Crimson Sweet	74.167
2009	KN	1	Georgia Rattlesnake	64.794
2009	KN	1	Fiesta F1	70.907
2009	KN	1	Mickylee	57.051
2009	KN	1	Sugar Baby	28.118
2009	KN	1	Legacy	68.054
2009	KN	1	Quetzali	57.866
2009	KN	2	Early Canada	56.236
2009	KN	2	Georgia Rattlesnake	64.387
2009	KN	2	Quetzali	64.794
2009	KN	2	Mickylee	96.580
2009	KN	2	Calhoun Gray	38.306
2009	KN	2	Fiesta F1	85.577
2009	KN	2	Starbrite F1	69.684
2009	KN	2	Sugar Baby	19.153
2009	KN	2	Crimson Sweet	56.236
2009	KN	2	Legacy	72.537
2009	KN	3	Fiesta F1	86.800
2009	KN	3	Quetzali	49.309
2009	KN	3	Crimson Sweet	59.496
2009	KN	3	Sugar Baby	50.531
2009	KN	3	Early Canada	28.933
2009	KN	3	Legacy	103.100
2009	KN	3	Starbrite F1	72.537
2009	KN	3	Georgia Rattlesnake	79.057
2009	KN	3	Mickylee	68.869
2009	KN	3	Calhoun Gray	53.384

2009	KN	4	Crimson Sweet	61.942
2009	KN	4	Early Canada	86.800
2009	KN	4	Starbrite F1	107.583
2009	KN	4	Mickylee	58.274
2009	KN	4	Quetzali	73.759
2009	KN	4	Sugar Baby	52.161
2009	KN	4	Fiesta F1	77.427
2009	KN	4	Calhoun Gray	109.213
2009	KN	4	Georgia Rattlesnake	71.722
2009	KN	4	Legacy	81.502
2009	CI	1	Mickylee	37.898
2009	CI	1	Crimson Sweet	0.000
2009	CI	1	Fiesta F1	59.904
2009	CI	1	Calhoun Gray	108.805
2009	CI	1	Georgia Rattlesnake	59.904
2009	CI	1	Legacy	66.832
2009	CI	1	Starbrite F1	47.679
2009	CI	1	Quetzali	56.236
2009	CI	1	Early Canada	68.054
2009	CI	1	Sugar Baby	55.014
2009	CI	2	Calhoun Gray	59.496
2009	CI	2	Georgia Rattlesnake	46.049
2009	CI	2	Legacy	39.528
2009	CI	2	Early Canada	44.826
2009	CI	2	Crimson Sweet	45.234
2009	CI	2	Quetzali	43.196
2009	CI	2	Sugar Baby	56.644
2009	CI	2	Mickylee	62.757
2009	CI	2	Fiesta F1	59.904
2009	CI	2	Starbrite F1	97.395
2009	CI	3	Starbrite F1	98.617
2009	CI	3	Quetzali	33.823
2009	CI	3	Crimson Sweet	33.008
2009	CI	3	Calhoun Gray	32.193
2009	CI	3	Mickylee	24.858
2009	CI	3	Early Canada	55.014
2009	CI	3	Sugar Baby	21.598
2009	CI	3	Fiesta F1	59.089
2009	CI	3	Legacy	46.049
2009	CI	3	Georgia Rattlesnake	51.346
2009	CI	4	Sugar Baby	36.268
2009	CI	4	Calhoun Gray	57.866
2009	CI	4	Georgia Rattlesnake	53.384

2009	CI	4	Crimson Sweet	24.858
2009	CI	4	Fiesta F1	98.617
2009	CI	4	Legacy	57.459
2009	CI	4	Quetzali	29.748
2009	CI	4	Early Canada	35.861
2009	CI	4	Starbrite F1	68.054
2009	CI	4	Mickylee	72.129
2009	SC	1	Georgia Rattlesnake	86.331
2009	SC	1	Legacy	109.967
2009	SC	1	Calhoun Gray	95.215
2009	SC	1	Mickylee	102.407
2009	SC	1	Starbrite F1	80.830
2009	SC	1	Quetzali	84.355
2009	SC	1	Fiesta F1	80.121
2009	SC	1	Sugar Baby	74.228
2009	SC	1	Early Canada	72.374
2009	SC	1	Crimson Sweet	42.198
2009	SC	2	Georgia Rattlesnake	44.357
2009	SC	2	Starbrite F1	124.189
2009	SC	2	Calhoun Gray	121.397
2009	SC	2	Fiesta F1	94.237
2009	SC	2	Sugar Baby	53.852
2009	SC	2	Mickylee	70.601
2009	SC	2	Early Canada	30.522
2009	SC	2	Crimson Sweet	97.578
2009	SC	2	Legacy	91.567
2009	SC	2	Quetzali	88.348
2009	SC	3	Calhoun Gray	98.842
2009	SC	3	Early Canada	41.688
2009	SC	3	Starbrite F1	100.329
2009	SC	3	Mickylee	67.076
2009	SC	3	Quetzali	50.246
2009	SC	3	Crimson Sweet	82.399
2009	SC	3	Georgia Rattlesnake	74.513
2009	SC	3	Legacy	69.562
2009	SC	3	Sugar Baby	46.252
2009	SC	3	Fiesta F1	101.857
2009	SC	4	Calhoun Gray	102.041
2009	SC	4	Legacy	83.328
2009	SC	4	Sugar Baby	39.793
2009	SC	4	Crimson Sweet	77.305
2009	SC	4	Starbrite F1	144.666
2009	SC	4	Early Canada	78.486

2009	SC	4	Quetzali	95.928
2009	SC	4	Georgia Rattlesnake	143.668
2009	SC	4	Fiesta F1	82.093
2009	SC	4	Mickylee	90.549
2009	FL	1	Calhoun Gray	103.316
2009	FL	1	Starbrite F1	98.132
2009	FL	1	Crimson Sweet	79.163
2009	FL	1	Legacy	115.950
2009	FL	1	Sugar Baby	70.393
2009	FL	1	Early Canada	88.616
2009	FL	1	Georgia Rattlesnake	98.554
2009	FL	1	Fiesta F1	118.457
2009	FL	1	Quetzali	81.374
2009	FL	1	Mickylee	76.863
2009	FL	2	Calhoun Gray	152.036
2009	FL	2	Legacy	120.695
2009	FL	2	Crimson Sweet	147.984
2009	FL	2	Sugar Baby	81.751
2009	FL	2	Quetzali	92.686
2009	FL	2	Starbrite F1	126.095
2009	FL	2	Georgia Rattlesnake	96.119
2009	FL	2	Mickylee	86.136
2009	FL	2	Early Canada	107.270
2009	FL	2	Fiesta F1	110.397
2009	FL	3	Calhoun Gray	94.223
2009	FL	3	Quetzali	86.918
2009	FL	3	Fiesta F1	102.984
2009	FL	3	Crimson Sweet	102.912
2009	FL	3	Starbrite F1	107.594
2009	FL	3	Mickylee	73.358
2009	FL	3	Legacy	76.494
2009	FL	3	Sugar Baby	81.086
2009	FL	3	Early Canada	89.020
2009	FL	3	Georgia Rattlesnake	127.092
2009	FL	4	Starbrite F1	172.065
2009	FL	4	Crimson Sweet	111.987
2009	FL	4	Mickylee	79.549
2009	FL	4	Legacy	108.744
2009	FL	4	Georgia Rattlesnake	86.747
2009	FL	4	Fiesta F1	106.407
2009	FL	4	Sugar Baby	89.398
2009	FL	4	Early Canada	77.546
2009	FL	4	Calhoun Gray	77.078

2009	FL	4	Quetzali	56.717
2009	TX	1	Quetzali	50.077
2009	TX	1	Starbrite F1	56.476
2009	TX	1	Early Canada	7.213
2009	TX	1	Sugar Baby	15.266
2009	TX	1	Fiesta F1	68.601
2009	TX	1	Georgia Rattlesnake	79.305
2009	TX	1	Crimson Sweet	34.842
2009	TX	1	Legacy	78.364
2009	TX	1	Mickylee	88.968
2009	TX	1	Calhoun Gray	92.646
2009	TX	2	Sugar Baby	22.829
2009	TX	2	Legacy	45.166
2009	TX	2	Crimson Sweet	21.444
2009	TX	2	Starbrite F1	93.552
2009	TX	2	Fiesta F1	32.636
2009	TX	2	Early Canada	21.639
2009	TX	2	Quetzali	27.688
2009	TX	2	Mickylee	33.171
2009	TX	2	Georgia Rattlesnake	102.626
2009	TX	2	Calhoun Gray	27.606
2009	TX	3	Mickylee	26.281
2009	TX	3	Crimson Sweet	28.417
2009	TX	3	Sugar Baby	18.185
2009	TX	3	Early Canada	43.982
2009	TX	3	Legacy	48.693
2009	TX	3	Quetzali	27.753
2009	TX	3	Starbrite F1	35.951
2009	TX	3	Georgia Rattlesnake	22.362
2009	TX	3	Fiesta F1	33.908
2009	TX	3	Calhoun Gray	21.012
2009	TX	4	Sugar Baby	16.182
2009	TX	4	Calhoun Gray	54.464
2009	TX	4	Quetzali	13.423
2009	TX	4	Early Canada	14.144
2009	TX	4	Fiesta F1	34.149
2009	TX	4	Starbrite F1	43.376
2009	TX	4	Crimson Sweet	0.000
2009	TX	4	Georgia Rattlesnake	45.010
2009	TX	4	Legacy	30.985
2009	TX	4	Mickylee	12.914
2010	KN	1	Calhoun Gray	50.531
2010	KN	1	Fiesta F1	70.499

2010	KN	1	Georgia Rattlesnake	59.089
2010	KN	1	Legacy	64.794
2010	KN	1	Crimson Sweet	50.531
2010	KN	1	Starbrite F1	75.797
2010	KN	1	Quetzali	49.309
2010	KN	1	Mickylee	52.569
2010	KN	1	Early Canada	46.456
2010	KN	1	Sugar Baby	43.604
2010	KN	2	Sugar Baby	41.974
2010	KN	2	Legacy	70.092
2010	KN	2	Calhoun Gray	72.944
2010	KN	2	Starbrite F1	70.907
2010	KN	2	Early Canada	49.309
2010	KN	2	Quetzali	35.861
2010	KN	2	Mickylee	48.086
2010	KN	2	Georgia Rattlesnake	59.089
2010	KN	2	Crimson Sweet	61.534
2010	KN	2	Fiesta F1	60.311
2010	KN	3	Quetzali	46.456
2010	KN	3	Sugar Baby	50.939
2010	KN	3	Mickylee	50.531
2010	KN	3	Fiesta F1	77.427
2010	KN	3	Georgia Rattlesnake	69.277
2010	KN	3	Crimson Sweet	50.939
2010	KN	3	Early Canada	68.869
2010	KN	3	Starbrite F1	68.054
2010	KN	3	Calhoun Gray	87.207
2010	KN	3	Legacy	72.129
2010	KN	4	Quetzali	63.164
2010	KN	4	Starbrite F1	105.138
2010	KN	4	Sugar Baby	58.681
2010	KN	4	Legacy	82.725
2010	KN	4	Georgia Rattlesnake	64.387
2010	KN	4	Fiesta F1	62.349
2010	KN	4	Calhoun Gray	72.537
2010	KN	4	Mickylee	54.606
2010	KN	4	Early Canada	57.051
2010	KN	4	Crimson Sweet	67.239
2010	CI	1	Quetzali	72.944
2010	CI	1	Crimson Sweet	74.982
2010	CI	1	Fiesta F1	97.395
2010	CI	1	Early Canada	60.719
2010	CI	1	Mickylee	65.202

2010	CI	1	Georgia Rattlesnake	81.094
2010	CI	1	Sugar Baby	66.832
2010	CI	1	Calhoun Gray	88.022
2010	CI	1	Starbrite F1	95.765
2010	CI	1	Legacy	62.757
2010	CI	2	Mickylee	59.089
2010	CI	2	Legacy	42.789
2010	CI	2	Georgia Rattlesnake	75.797
2010	CI	2	Crimson Sweet	73.352
2010	CI	2	Calhoun Gray	79.872
2010	CI	2	Sugar Baby	59.496
2010	CI	2	Starbrite F1	74.982
2010	CI	2	Fiesta F1	81.094
2010	CI	2	Early Canada	45.641
2010	CI	2	Quetzali	64.387
2010	CI	3	Fiesta F1	67.239
2010	CI	3	Sugar Baby	51.346
2010	CI	3	Early Canada	67.647
2010	CI	3	Quetzali	68.054
2010	CI	3	Legacy	65.609
2010	CI	3	Crimson Sweet	94.950
2010	CI	3	Calhoun Gray	86.392
2010	CI	3	Georgia Rattlesnake	65.202
2010	CI	3	Mickylee	48.901
2010	CI	3	Starbrite F1	83.132
2010	CI	4	Calhoun Gray	71.722
2010	CI	4	Sugar Baby	53.791
2010	CI	4	Crimson Sweet	48.901
2010	CI	4	Early Canada	47.271
2010	CI	4	Mickylee	63.164
2010	CI	4	Legacy	94.135
2010	CI	4	Georgia Rattlesnake	69.277
2010	CI	4	Fiesta F1	79.464
2010	CI	4	Quetzali	45.641
2010	CI	4	Starbrite F1	83.947
2010	SC	1	Quetzali	104.384
2010	SC	1	Starbrite F1	79.301
2010	SC	1	Georgia Rattlesnake	82.745
2010	SC	1	Crimson Sweet	116.731
2010	SC	1	Legacy	58.498
2010	SC	1	Mickylee	43.420
2010	SC	1	Fiesta F1	141.956
2010	SC	1	Calhoun Gray	83.682

2010	SC	1	Sugar Baby	45.152
2010	SC	1	Early Canada	72.557
2010	SC	2	Sugar Baby	51.143
2010	SC	2	Calhoun Gray	85.190
2010	SC	2	Legacy	74.208
2010	SC	2	Quetzali	63.001
2010	SC	2	Early Canada	88.348
2010	SC	2	Starbrite F1	96.152
2010	SC	2	Mickylee	48.168
2010	SC	2	Fiesta F1	139.776
2010	SC	2	Crimson Sweet	91.792
2010	SC	2	Georgia Rattlesnake	113.084
2010	SC	3	Quetzali	75.308
2010	SC	3	Crimson Sweet	136.658
2010	SC	3	Mickylee	59.700
2010	SC	3	Legacy	67.708
2010	SC	3	Fiesta F1	95.194
2010	SC	3	Early Canada	77.610
2010	SC	3	Starbrite F1	106.951
2010	SC	3	Georgia Rattlesnake	65.018
2010	SC	3	Sugar Baby	61.514
2010	SC	3	Calhoun Gray	75.414
2010	SC	4	Early Canada	61.025
2010	SC	4	Georgia Rattlesnake	55.666
2010	SC	4	Calhoun Gray	114.490
2010	SC	4	Legacy	53.812
2010	SC	4	Mickylee	40.853
2010	SC	4	Quetzali	68.767
2010	SC	4	Fiesta F1	118.219
2010	SC	4	Crimson Sweet	106.421
2010	SC	4	Starbrite F1	127.326
2010	SC	4	Sugar Baby	52.569
2010	FL	1	Crimson Sweet	0.000
2010	FL	1	Legacy	44.673
2010	FL	1	Quetzali	66.497
2010	FL	1	Fiesta F1	15.869
2010	FL	1	Sugar Baby	73.064
2010	FL	1	Starbrite F1	54.587
2010	FL	1	Calhoun Gray	88.303
2010	FL	1	Early Canada	119.500
2010	FL	1	Mickylee	114.715
2010	FL	1	Georgia Rattlesnake	92.999
2010	FL	2	Crimson Sweet	113.437

2010	FL	2	Fiesta F1	180.906
2010	FL	2	Starbrite F1	123.836
2010	FL	2	Sugar Baby	106.330
2010	FL	2	Legacy	87.727
2010	FL	2	Early Canada	107.824
2010	FL	2	Quetzali	110.522
2010	FL	2	Georgia Rattlesnake	116.064
2010	FL	2	Calhoun Gray	120.040
2010	FL	2	Mickylee	128.388
2010	FL	3	Mickylee	116.927
2010	FL	3	Sugar Baby	90.624
2010	FL	3	Fiesta F1	91.469
2010	FL	3	Starbrite F1	146.110
2010	FL	3	Calhoun Gray	143.339
2010	FL	3	Crimson Sweet	85.028
2010	FL	3	Legacy	118.799
2010	FL	3	Quetzali	72.884
2010	FL	3	Georgia Rattlesnake	84.165
2010	FL	3	Early Canada	119.752
2010	FL	4	Legacy	104.945
2010	FL	4	Fiesta F1	107.860
2010	FL	4	Mickylee	93.071
2010	FL	4	Georgia Rattlesnake	144.545
2010	FL	4	Crimson Sweet	64.698
2010	FL	4	Sugar Baby	94.024
2010	FL	4	Quetzali	100.429
2010	FL	4	Calhoun Gray	132.922
2010	FL	4	Early Canada	118.853
2010	FL	4	Starbrite F1	156.635
2010	TX	1	Sugar Baby	9.943
2010	TX	1	Legacy	17.971
2010	TX	1	Starbrite F1	24.369
2010	TX	1	Crimson Sweet	27.670
2010	TX	1	Fiesta F1	34.231
2010	TX	1	Mickylee	17.645
2010	TX	1	Georgia Rattlesnake	19.560
2010	TX	1	Early Canada	13.122
2010	TX	1	Calhoun Gray	16.219
2010	TX	1	Quetzali	5.909
2010	TX	2	Quetzali	17.767
2010	TX	2	Legacy	30.156
2010	TX	2	Sugar Baby	8.884
2010	TX	2	Mickylee	10.229

2010	TX	2	Crimson Sweet	5.664
2010	TX	2	Georgia Rattlesnake	13.652
2010	TX	2	Early Canada	8.924
2010	TX	2	Starbrite F1	29.218
2010	TX	2	Fiesta F1	30.808
2010	TX	2	Calhoun Gray	23.187
2010	TX	3	Quetzali	8.761
2010	TX	3	Legacy	9.413
2010	TX	3	Fiesta F1	4.034
2010	TX	3	Georgia Rattlesnake	4.157
2010	TX	3	Crimson Sweet	9.780
2010	TX	3	Starbrite F1	27.385
2010	TX	3	Mickylee	11.818
2010	TX	3	Early Canada	11.899
2010	TX	3	Sugar Baby	9.495
2010	TX	3	Calhoun Gray	9.454
2010	TX	4	Fiesta F1	19.764
2010	TX	4	Calhoun Gray	19.194
2010	TX	4	Sugar Baby	14.181
2010	TX	4	Legacy	5.990
2010	TX	4	Crimson Sweet	19.031
2010	TX	4	Mickylee	11.899
2010	TX	4	Georgia Rattlesnake	13.855
2010	TX	4	Early Canada	13.163
2010	TX	4	Quetzali	6.724
2010	TX	4	Starbrite F1	7.417