############################# metan ##########################################

install.packages("metan")

library(metan)

install.packages("ggplot2")

library(ggplot2)

options(max.print = 10000)

############################### set wd ######################################

getwd()

############################## importing data ###############################

library(readxl)

MMET <- read\_excel("MMET.xlsx")

View(MMET)

class(MMET)

str(MMET)

############################# factors with unique levels ####################

MMET$ENV <- factor(MMET$ENV, levels=unique(MMET$ENV))

MMET$GEN <- factor(MMET$GEN, levels=unique(MMET$GEN))

MMET$REP <- factor(MMET$REP, levels=unique(MMET$REP))

str(MMET)

###################### data inspection and manipulation #####################

inspect(MMET, plot=TRUE)

##################### check for outliers ###################################

find\_outliers(MMET, var=HT, plots=TRUE)

find\_outliers(MMET, var=YLD, plots=TRUE)

##################### extra clean functions ###############################

##################### remove NA ###########################################

remove\_rows\_na(MMET)

####################### replace zero #####################################

replace\_zero(MMET)

###################### find text in numbers ##############################

find\_text\_in\_num(MMET$HT)

find\_text\_in\_num(MMET$YLD)

######################### data analysis ##################################

###################### descriptive stats ################################

desc\_stat(MMET)

desc\_stat(MMET, stats="all")

ds <- desc\_stat(MMET, stats="all")

ds

View(ds)

class(ds)

######################### importing a table ############################

install.packages("writexl")

library(writexl)

write\_xlsx(ds, "ds.xlsx")

######################## mean performance ##############################

####################### mean of genotypes #############################

mg <- means\_by(MMET, GEN)

mg

View(mg)8

######################### mean of environments #######################

me <- means\_by(MMET, ENV)

me

View(me)

########### mean performance of genotypes across environments ###########

mge <- MMET %>%

group\_by(ENV, GEN) %>%

desc\_stat(HT, YLD, stats="mean")

mge

View(mge)

############### plotting performace across environments ################

## HT

pht <- ge\_plot(MMET, ENV, GEN, HT)

pht

pht2 <- ge\_plot(MMET, ENV, GEN, HT, type=2)

pht2

## YLD

pyd <- ge\_plot(MMET, ENV, GEN, YLD)

pyd

pyd2 <- ge\_plot(MMET, ENV, GEN, YLD, type=2)

pyd2

######################## winners within each env ###########################

win <- ge\_winners(MMET, ENV, GEN, resp = everything())

View(win)

####################### ranks of genotypes #################################

ranks <- ge\_winners(MMET, ENV, GEN, resp = everything(), type = "ranks")

View(ranks)

##### more details on performance

ge\_details(MMET, ENV, GEN, resp = everything())

########################## fixed effect models #############################

########################### ind anova ####################################

indav <- anova\_ind(MMET, ENV, GEN, REP, resp = c(HT, YLD))

# anova for height

indav$HT$individual

iaht <- indav$HT$individual

View(iaht)

?anova\_ind

## Bartlett test

bartlett.test(MMET$HT~MMET$ENV, data = MMET)

# anova for yield

indav$YLD$individual

iayd <- indav$YLD$individual

View(iayd)

write\_xlsx(iayd, "yieldanv.xlsx")

######################## pooled anova #####################################

# pooled anova for height

panv1 <- anova\_joint(MMET, ENV, GEN, REP, HT)

pavt1 <- panv1$HT$anova

View(pavt1)

# pooled anova for yield

panv2 <- anova\_joint(MMET, ENV, GEN, REP, YLD)

pavt2 <- panv2$YLD$anova

View(pavt2)

######################## stability analysis ###########################

######################## anova based stability #######################

# Annichiarico env index

ann1 <- Annicchiarico(MMET, ENV, GEN, REP, HT)

print(ann1)

View(ann1$HT$environments)

ann2 <- Annicchiarico(MMET, ENV, GEN, REP, YLD)

print(ann2)

View(ann2$YLD$environments)

# ecovalence

eco1 <- ecovalence(MMET, ENV, GEN, REP, HT)

eco1

View(eco1$HT)

eco2 <- ecovalence(MMET, ENV, GEN, REP, YLD)

eco2

print(eco2)

# Shukla

shu1 <- Shukla(MMET, ENV, GEN, REP, HT)

shu1

shu2 <- Shukla(MMET, ENV, GEN, REP, YLD)

shu2

## Reg based

reg1 <- ge\_reg(MMET, ENV, GEN, REP, HT)

print(reg1)

reg1anv <- reg1$HT$anova

View(reg1anv)

write\_xlsx(reg1anv, "reganv1.xlsx")

plot(reg1)

reg2 <- ge\_reg(MMET, ENV, GEN, REP, YLD)

print(reg2)

reg2anv <- reg2$YLD$anova

View(reg2anv)

plot(reg2)

################################ non parametric ###########################

## superiority by Lin and Binns

super1 <- superiority(MMET, ENV, GEN, HT)

print(super1)

?superiority

View(super1$HT$index)

View(super1$HT$environments)

super2 <- superiority(MMET, ENV, GEN, YLD)

View(super2$YLD$index)

View(super2$YLD$environments)

## fox top third cirteria

?Fox

fox1 <- Fox(MMET, ENV, GEN, HT)

View(fox1$HT)

fox2 <- Fox(MMET, ENV, GEN, YLD)

View(fox2$YLD)

############################ factor based #################################

fact1 <- ge\_factanal(MMET, ENV, GEN, REP, HT)

print(fact1)

fact2 <- ge\_factanal(MMET, ENV, GEN, REP, YLD)

print(fact2)

plot(fact2)

View(fact2$YLD$PCA)

?ge\_factanal

########################## wrap stab parameters ############################

stabp1 <- ge\_stats(MMET, ENV, GEN, REP, HT)

data1 <- get\_model\_data(stabp1)

View(data1)

View(stabp1$HT)

ranksp1 <- get\_model\_data(stabp1, "ranks")

View(ranksp1)

stabp2 <- ge\_stats(MMET, ENV, GEN, REP, YLD)

View(stabp2$YLD)

data2 <- get\_model\_data(stabp2)

View(data2)

ranks2 <- get\_model\_data(stabp2, "ranks")

View(ranks2)

?ge\_stats

####################### correlation b/w stab index #######################

csi1 <- corr\_stab\_ind(stabp1)

csi1

View(csi1$corr)

View(csi1$pval)

csi2 <- corr\_stab\_ind(stabp2, stats = "ammi")

?corr\_stab\_ind

View(csi2$corr)

###################### ammi models #####################################

## HT

amod1 <- performs\_ammi(MMET, ENV, GEN, REP, HT)

print(amod1)

plot(amod1)

View(amod1$HT$ANOVA)

write\_xlsx(amod1$HT$ANOVA, "ammianova1.xlsx")

## YLD

amod2 <- performs\_ammi(MMET, ENV, GEN, REP, YLD)

print(amod2)

View(amod2$YLD$ANOVA)

#### Significance of ipca

get\_model\_data(amod1, "ipca\_pval")

get\_model\_data(amod2, "ipca\_pval")

########################## ammi biplots ###################################

### HT

a1 <- plot\_scores(amod1)

a1

a1 <- plot\_scores(amod1, x.lab = "Height")

a1

b1 <- plot\_scores(amod1, type = 2)

b1

b1 <- plot\_scores(amod1, type = 2, polygon = TRUE)

b1

b1 <- plot\_scores(amod1,

type = 2,

col.env = "blue",

col.gen = transparent\_color(),

col.segm.env = "orange",

highlight = c("G1", "G2"),

col.highlight = "darkcyan",

axis.expand = 1.5)

b1

# export

c1 <- plot\_scores(amod1, type = 4)

c1

?plot\_scores

c1 <- plot\_scores(amod1, type=4, repulsion = 2)

c1

c1 <- plot\_scores(amod1, type = 4,

size.tex.gen = 2,

x.lab = "PC1 of E",

y.lab = "Nominal Height",

title=FALSE,

col.alpha.gen = 0)

c1

arrange\_ggplot(a1, b1, c1, tag\_levels = "a", nrow = 1)

## Yield

a2 <- plot\_scores(amod2)

a2

a2 <- plot\_scores(amod2, x.lab = "Yield")

a2

b2 <- plot\_scores(amod2, type = 2, polygon = TRUE)

b2

c2 <- plot\_scores(amod2, type = 4, size.tex.gen = 2,

x.lab = "PC1 of E",

y.lab = "Nominal Yield")

c2

######################### ammi based stability statistics ##################

abs1 <- AMMI\_indexes(amod1)

print(abs1)

View(abs1$HT)

abs2 <- AMMI\_indexes(amod2)

print(abs2)

View(abs2$YLD)

################ ammi based on waas #################################

## Height

waas1 <- waas(MMET, ENV, GEN, REP, HT)

View(waas1$HT$anova)

print(waas1)

wp1\_3 <- plot\_scores(waas1, type = 3)

wp1\_3

wp1\_2 <- plot\_scores(waas1, type = 2, polygon = TRUE)

wp1\_2

## Yield

waas2 <- waas(MMET, ENV, GEN, REP, YLD)

View(waas2$YLD$anova)

wp2\_3 <- plot\_scores(waas2, type = 3)

wp2\_3

################### waas based stats ################################

wabs1 <- AMMI\_indexes(waas1)

View(wabs1$HT)

print(wabs1)

wabs2 <- AMMI\_indexes(waas2)

View(wabs2$YLD)

################### cross verification #############################

###################### GGE Model ###############################

# svp = environment # by default

## Height

gge\_model1 <- gge(MMET, ENV, GEN, HT)

predict(gge\_model1)

pgge1 <- predict(gge\_model1)

View(pgge1$HT)

## yield

gge\_model2 <- gge(MMET, ENV, GEN, YLD)

pgge2 <- predict(gge\_model2)

View(pgge2$YLD)

# 1 Basic biplot

# HT

bbp1 <- plot(gge\_model1)

bbp1

bbp1 <- plot(gge\_model1, col.gen = "red")

bbp1

# YLD

bbp2 <- plot(gge\_model2)

bbp2

# 2 Discriminativeness vs representativeness

# HT

dvr1 <- plot(gge\_model1, type = 4)

dvr1

# YLD

dvr2 <- plot(gge\_model1, type = 4)

dvr2

dvr2 <- plot(gge\_model1, type = 4, plot\_theme = theme\_gray())

dvr2

?theme

# 3 Ranking environments

## HT

re1 <- plot(gge\_model1, type = 6)

re1

## YLD

re2 <- plot(gge\_model2, type = 6)

re2

# 4 relation among environments

## HT

rae1 <- plot(gge\_model1, type = 10)

rae1

## YLD

rae2 <- plot(gge\_model2, type = 10)

rae2

############################# svp = genotype ############################

# Height

gpg1 <- gge(MMET, ENV, GEN, HT, svp="genotype")

pgpg1 <- predict(gpg1)

View(pgpg1$HT)

# Yield

gpg2 <- gge(MMET, ENV, GEN, YLD, svp="genotype")

pgpg2 <- predict(gpg2)

View(pgpg2$YLD)

# 5 Mean performance vs stability

## HT

mvs1 <- plot(gpg1, type=2)

mvs1

## YLD

mvs2 <- plot(gpg2, type=2)

mvs2

# 6 Examine a genotype

eg6ht <- plot(gpg1, type = 7, sel\_gen = "G6")

eg6ht

eg1yd <- plot(gpg2, type = 7, sel\_gen = "G1")

eg1yd

# 7 Ranking of genotype

# HT

rg1 <- plot(gpg1, type = 8)

rg1

# YLD

rg2 <- plot(gpg2,type=8)

rg2

######################### svp = symmetrical ################################

## Height

gps1 <- gge(MMET, ENV, GEN, HT, svp = "symmetrical")

pgps1 <- predict(gps1)

View(pgps1$HT)

## Yield

gps2 <- gge(MMET, ENV, GEN, YLD, svp = "symmetrical")

pgps2 <- predict(gps2)

View(pgps2$YLD)

# 8 Which won where

## HT

www1 <- plot(gps1, type = 3)

www1

## YLD

www2 <- plot(gps2, type = 3)

www2

# 9 Examine a environment

e1ht <- plot(gps1, type = 5, sel\_env = "E1")

e1ht

e2yd <- plot(gps2, type = 5, sel\_env = "E2")

e2yd

# 10 comparison between two genotypes

ht2and3 <- plot(gps1, type = 9, sel\_gen1 = "G2", sel\_gen2 = "G3")

ht2and3

yd1and6 <- plot(gps2, type = 9, sel\_gen1 = "G1", sel\_gen2 = "G6")

yd1and6

####################### correlation and covariance #########################

de1 <- subset(MMET, ENV=="E1")

View(de1)

cr\_cv <- covcor\_design(de1, GEN, REP, resp = c(HT, YLD), design = "RCBD")

cr\_cv

View(cr\_cv$geno\_cor)