#Joint-Analysis of Variance#

> library(metan)

> j\_an <- anova\_joint(data, env = ENV, gen = GEN, rep = REP, resp = Disease Score)

#Generation of Heat Maps#

> ge\_plot(data, ENV, GEN, Disease Score)

# Estimating the WAASB and WAASBY indices#

>WAASB = data %>% waasb(ENV, GEN, BLOCK, Disease Score, random = "all", wresp = 65, mresp='l')

> indices = WAASB$Disease Score$model

> gmd(WAASB, "lrt")

#BLUP for genotypes#

> blup = WAASB$Disease Score$blupGEN

#Plotting the BLUP for genotypes#

> plot = plot\_blup(WAASB$Disease Score)

#Biplot: Disease Score × WAASB#

> plot = plot\_scores(WAASB$Disease Score, type = 3)

#Plotting WAASBY Indices#

> plot = plot\_waasby(WAASB$Disease Score)

# Calculating Climatic parameters #

> library(tidyverse)

> library(metan)

> library(EnvRtype)

> ENV <- c("MDZ17", "PLM17", "DWD17", "JBL17", "IND17", "MDZ18", "PLM18", "DWD18", "JBL18", "IND18", "MDZ19", "PLM19", "DWD19", "JBL19", "IND19")

>

> LAT <- c(25.753717, 32.100048, 15.498779, 23.215343, 22.679201, 25.753717, 32.100048, 15.498779, 23.215343, 22.679201, 25.753717, 32.100048, 15.498779, 23.215343, 22.679201 )

>

> LON <- c(93.857852, 76.546847, 74.985373, 79.945885, 75.873164, 93.857852, 76.546847, 74.985373, 79.945885, 75.873164, 93.857852, 76.546847, 74.985373, 79.945885, 75.873164 )

> ALT <- c(449.07, 1270, 678, 390.4, 550, 449.07, 1270, 678, 390.4, 550, 449.07, 1270, 678, 390.4, 550 )

> ALT <- data.frame(env = ENV, alt = ALT)

> start<-c("2017-06-01", "2017-06-01", "2017-06-01", "2017-06-01", "2017-06-01", "2018-06-01", "2018-06-01", "2018-06-01", "2018-06-01", "2018-06-01", "2019-06-01", "2019-06-01", "2019-06-01", "2019-06-01", "2019-06-01")

> end<-c("2017-10-31", "2017-10-31", "2017-10-31", "2017-10-31", "2017-10-31", "2018-10-31", "2018-10-31", "2018-10-31", "2018-10-31", "2018-10-31", "2019-10-31", "2019-10-31", "2019-10-31", "2019-10-31", "2019-10-31")

> df <- get\_weather(env.id = ENV, lat = LAT, lon = LON, start, end, save = TRUE)

> df2 <- df %>% left\_join(ALT) %>% relocate(alt, .after = LAT)

> env.data <- df2 %>% as.data.frame() %>% param\_temperature(Tbase1 = 8, Tbase2 = 45, merge = TRUE) %>% param\_atmospheric(merge = TRUE) %>% param\_radiation(merge = TRUE) %>% remove\_cols(PRECTOT, PETP, daysFromStart)

> df\_long <- env.data %>% # filter(!ENV %in% envs) %>% select(-YYYYMMDD) %>% pivot\_longer(-c(env:DOY))

> pca <- df\_long %>% group\_by(env, YEAR, name) %>% summarise(across(value, list(min = min, mean = mean, max = max, q25 = ~quantile(., prob = 0.25), q75 = ~quantile(., prob = 0.75), n = ~n()))) %>% mutate(range = value\_max - value\_min)

> pca\_mean <- env.data %>% means\_by(env, YEAR)%>% remove\_cols(DOY, MM, DD, N, RH2M, T2MDEW, YEAR, n)

# Binding the calculated parameters with the climatic variables recoded at individual locations, Mean disease score at each environment and WAASB Index of each environment #

> finalpca<-bind\_cols(pca\_mean, pcaa)

# Principal Component Analysis#

> pca\_model <- prcomp(finalpca, scale = TRUE)

> library(factoextra)

> fviz\_contrib(pca\_model, "var", axes = 1:2)

> fviz\_pca\_biplot(pca\_model)