**MassWateR Script for Beta Testing**

## #Install the MassWateR package - only necessary for updates

# Enable massbays-tech universe

options(repos = c(

massbaystech = 'https://massbays-tech.r-universe.dev',

CRAN = 'https://cloud.r-project.org'))

install.packages('MassWateR')

## #Activate libraries every time

library(MassWateR)

library(dplyr) #Needed for %>% in outlier review

## #Load files

respth <- "C:/Documents/…/BetaResults\_9-2-22.xlsx"

dqoaccpth <- "C:/Documents/…/BetaDQOAccuracy\_9-2-22.xlsx"

dqofrecompth <- "C:/Documents/…/BetaDQOFreqComp\_9-2-22.xlsx"

sitespth <- "C:/Documents/…/BetaSites\_9-2-22.xlsx"

resdat <- readMWRresults(respth)

dqoaccdat <- readMWRacc(dqoaccpth)

dqofrecomdat <- readMWRfrecom(dqofrecompth)

sitedat <- readMWRsites(sitespth)

## #Review files

str(resdat)

head(resdat)

View(resdat)

View(dqoaccdat)

View(paramsMWR)

View(thresholdMWR)

## #QC Review - full report

qcMWRreview(res=resdat,acc=dqoaccdat,frecom=dqofrecomdat,

output\_dir="C:/Documents/",

output\_file = "QCReport", rawdata = FALSE)

## #QC Review - individual reports

tabMWRfre(res=resdat,frecom=dqofrecomdat,type = "summary")

tabMWRfre(res=resdat,frecom=dqofrecomdat,type = "percent")

tabMWRacc(res=resdat,acc=dqoaccdat,accchk = "Field Duplicates",type = "individual")

tabMWRacc(res=resdat,acc=dqoaccdat,type = "summary",frecom = dqofrecomdat)

tabMWRacc(res=resdat,acc=dqoaccdat,type = "percent",frecom = dqofrecomdat)

tabMWRcom(res=resdat,frecom=dqofrecomdat)

## #Analyze Outliers

anlzMWRoutlier(res=resdat,param="E.coli",acc=dqoaccdat,type="box",

group="month")# labsize = 2)

#dtrng = c("2021-06-01","2021-07-31"))

anlzMWRoutlier(res=resdat,param="Ammonia",acc=dqoaccdat,group="month",

outliers = TRUE)# %>%

#print(width=Inf)

anlzMWRoutlierall(res=resdat, acc=dqoaccdat, group = "month", format="word",

output\_dir = "D:/Documents", output\_file = "my\_outliers")

#fig\_height = 3)

## #Seasonal Analysis

anlzMWRseason(res=resdat,param="TP",acc=dqoaccdat,group="month",

type="box", thresh="fresh")

anlzMWRseason(res=resdat,param="TP",acc=dqoaccdat,group="month",

type="jitterbar", thresh="fresh")# site="ABT-077",

#sit=sitedat, locgroup = "Sudbury")

#resultatt = "Low")

#dtrng = c("2021-06-01","2021-07-01"))

anlzMWRseason(res=resdat,param="TP",acc=dqoaccdat,group="month",

type="box", thresh="fresh") +

labs(x="Month", y="Total Phosphorus (mg/L)",

title="Total Phosphorus 2022") +

geom\_hline(yintercept = 0.15, color = "green", show.legend = TRUE)

#theme\_gray()

#coord\_cartesian(ylim = c(0.1,0.2))

#facet\_wrap(~`Monitoring Location ID`)

#coord\_flip()

## #Time-series Analysis

anlzMWRdate(res=resdat, param="pH", acc=dqoaccdat, thresh="fresh",

sit = sitedat, group="site", locgroup = "Sudbury")

anlzMWRdate(res=resdat, param="pH", acc=dqoaccdat, thresh="fresh",

site=c("ABT-077","ABT-144","CND-009"))

#repel=TRUE, colleg = TRUE, threshcol="red")

#sit = sitedat, group="locgroup")

#locgroup = c("Assabet","Sudbury"))# confint=TRUE)

## #By-site Analysis

anlzMWRsite(res=resdat,param="DO",acc=dqoaccdat,type="box",thresh="fresh",

sit=sitedat, locgroup = "Sudbury")

anlzMWRsite(res=resdat,param="E.coli",acc=dqoaccdat,type="jitterbar",

thresh="fresh", site=c("ABT-077","ABT-162","CND-009"),

fill="pink")

#resultatt = "Wet")

#byresultatt = TRUE)

## #Map Analysis

anlzMWRmap(res=resdat, param="DO", acc=dqoaccdat, sit=sitedat)

anlzMWRmap(res=resdat, param="DO", acc=dqoaccdat, sit=sitedat,

maptype = NULL, addwater = "nhd", dLevel = "high",

palcol = "Spectral", ptsize = 2, labsize = 2, latlon = FALSE,

site = c("HBS-016","HBS-098"))

#northloc = "tr", scaleloc = "tl")

#locgroup = c("Assabet"))

#dtrng = c("2021-05-01","2021-07-31"))

anlzMWRmap(res=resdat, param="DO", acc=dqoaccdat, sit=sitedat,

palcol = "YlOrRd", buffdist = 0.2,

locgroup = c("Assabet"), ptsize = 2.5, labsize = 2.5,

maptype = "terrain-lines", addwater = "nhd", dLevel = "low")

#maptype = "terrain-background", addwater = NULL)