Top5mVersusBottom1m

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# Initial stuff, including loading packages and importing data

##loading packages

library(here)  
library(rstatix)  
library(ggplot2)  
library(tidyverse)  
library(dplyr)

## loading files

# Tell R where files are stored  
here::i\_am("scripts/Top5mVersusBottom1m.Rmd")  
  
# Load Files  
a <- readr::read\_csv(here("data/SporeConcentrationsByDepthAll.csv"))

### Walsh Ordospora 6 meters

wo6 = a %>%  
 filter(Parasite== "Ordospora",  
 Lake=="Walsh",  
 Depth =="6")  
wo6.spores <- wo6$Concentration  
  
wo = a %>%  
 filter(Parasite== "Ordospora",  
 Lake=="Walsh",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
wo.spores<- wo$Concentration  
  
walsh.ordo <- data.frame(   
 group = c(rep("6",7), rep("other",66)),  
 spores = c(wo6.spores, wo.spores)  
 )  
  
res.wo <- wilcox.test(wo6.spores, wo.spores)  
res.wo

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: wo6.spores and wo.spores  
## W = 371.5, p-value = 0.00833  
## alternative hypothesis: true location shift is not equal to 0

### significantly different, W = 371.5, p = 0.0083

### Walsh Metschnikowia 6 meters

wm6 = a %>%  
 filter(Parasite== "Metschnikowia",  
 Lake=="Walsh",  
 Depth =="6")  
wm6.spores <- wm6$Concentration  
  
wm = a %>%  
 filter(Parasite== "Metschnikowia",  
 Lake=="Walsh",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
wm.spores<- wm$Concentration  
  
walsh.metsch <- data.frame(   
 group = c(rep("6",7), rep("other",66)),  
 spores = c(wm6.spores, wm.spores)  
 )  
  
res.wm <- wilcox.test(wm6.spores, wm.spores)  
res.wm

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: wm6.spores and wm.spores  
## W = 413, p-value = 0.0005576  
## alternative hypothesis: true location shift is not equal to 0

### significantly different, W = 413, p = 0.0005

### Walsh Blastulidium 6 meters

wb6 = a %>%  
 filter(Parasite== "Blastulidium",  
 Lake=="Walsh",  
 Depth =="6")  
wb6.spores <- wb6$Concentration  
  
wb = a %>%  
 filter(Parasite== "Blastulidium",  
 Lake=="Walsh",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
wb.spores<- wb$Concentration  
  
walsh.brood <- data.frame(   
 group = c(rep("6",7), rep("other",66)),  
 spores = c(wb6.spores, wb.spores)  
 )  
  
res.wb <- wilcox.test(wb6.spores, wb.spores)  
res.wb

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: wb6.spores and wb.spores  
## W = 299.5, p-value = 0.2018  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 299.5, p = 0.20

### Walsh Pasteuria 6 meters

wp6 = a %>%  
 filter(Parasite== "Pasteuria",  
 Lake=="Walsh",  
 Depth =="6")  
wp6.spores <- wp6$Concentration  
  
wp = a %>%  
 filter(Parasite== "Pasteuria",  
 Lake=="Walsh",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
wp.spores<- wp$Concentration  
  
walsh.past <- data.frame(   
 group = c(rep("6",7), rep("other",66)),  
 spores = c(wp6.spores, wp.spores)  
 )  
  
res.wp <- wilcox.test(wp6.spores, wp.spores)  
res.wp

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: wp6.spores and wp.spores  
## W = 393.5, p-value = 0.001553  
## alternative hypothesis: true location shift is not equal to 0

### significantly different, W = 393.5, p = 0.0015

## Walsh Spirobacillus 6 meters

ws6 = a %>%  
 filter(Parasite== "Spirobacillus",  
 Lake=="Walsh",  
 Depth =="6")  
ws6.spores <- ws6$Concentration  
  
ws = a %>%  
 filter(Parasite== "Spirobacillus",  
 Lake=="Walsh",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
ws.spores<- ws$Concentration  
  
walsh.spiro <- data.frame(   
 group = c(rep("6",7), rep("other",66)),  
 spores = c(ws6.spores, ws.spores)  
 )  
  
res.ws <- wilcox.test(ws6.spores, ws.spores)  
res.ws

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: ws6.spores and ws.spores  
## W = 326, p-value = 0.07665  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 326, p = 0.07

### Mill Ordospora 6 meters

mo6 = a %>%  
 filter(Parasite== "Ordospora",  
 Lake=="Mill",  
 Depth =="6")  
mo6.spores <- mo6$Concentration  
  
mo = a %>%  
 filter(Parasite== "Ordospora",  
 Lake=="Mill",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
mo.spores<- mo$Concentration  
  
mill.ordo <- data.frame(   
 group = c(rep("6",6), rep("other",65)),  
 spores = c(mo6.spores, mo.spores)  
 )  
  
res.mo <- wilcox.test(mo6.spores, mo.spores)  
res.mo

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: mo6.spores and mo.spores  
## W = 218.5, p-value = 0.6288  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 218.5, p = 0.63

### Mill Metschnikowia 6 meters

mm6 = a %>%  
 filter(Parasite== "Metschnikowia",  
 Lake=="Mill",  
 Depth =="6")  
mm6.spores <- mm6$Concentration  
  
mm = a %>%  
 filter(Parasite== "Metschnikowia",  
 Lake=="Mill",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
mm.spores<- mm$Concentration  
  
mill.metsch <- data.frame(   
 group = c(rep("6",6), rep("other",65)),  
 spores = c(mm6.spores, mm.spores)  
 )  
  
res.mm <- wilcox.test(mm6.spores, mm.spores)  
res.mm

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: mm6.spores and mm.spores  
## W = 228, p-value = 0.457  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 228, p = 0.457

### Mill Blastulidium 6 meters

mb6 = a %>%  
 filter(Parasite== "Blastulidium",  
 Lake=="Mill",  
 Depth =="6")  
mb6.spores <- mb6$Concentration  
  
mb = a %>%  
 filter(Parasite== "Blastulidium",  
 Lake=="Mill",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
mb.spores<- mb$Concentration  
  
res.mb <- wilcox.test(mb6.spores, mb.spores)  
res.mb

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: mb6.spores and mb.spores  
## W = 300.5, p-value = 0.0274  
## alternative hypothesis: true location shift is not equal to 0

### significantly different, W = 300.5, p = 0.027

### Mill Pasteuria 6 meters

mp6 = a %>%  
 filter(Parasite== "Pasteuria",  
 Lake=="Mill",  
 Depth =="6")  
mp6.spores <- mp6$Concentration  
  
mp = a %>%  
 filter(Parasite== "Pasteuria",  
 Lake=="Mill",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
mp.spores<- mp$Concentration  
  
res.mp <- wilcox.test(mp6.spores, mp.spores)  
res.mp

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: mp6.spores and mp.spores  
## W = 273, p-value = 0.02798  
## alternative hypothesis: true location shift is not equal to 0

### significantly different, W = 273, p = 0.027

## Mill Spirobacillus 6 meters

ms6 = a %>%  
 filter(Parasite== "Spirobacillus",  
 Lake=="Mill",  
 Depth =="6")  
ms6.spores <- ms6$Concentration  
  
ms = a %>%  
 filter(Parasite== "Spirobacillus",  
 Lake=="Mill",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
ms.spores<- ms$Concentration  
  
res.ms <- wilcox.test(ms6.spores, ms.spores)  
res.ms

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: ms6.spores and ms.spores  
## W = 154, p-value = 0.4021  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 326, p = 0.4

### Cedar Ordospora top 5 meters v. 1 meter

co6 = a %>%  
 filter(Parasite== "Ordospora",  
 Lake=="Cedar",  
 Depth =="7")  
co6.spores <- co6$Concentration  
  
co = a %>%  
 filter(Parasite== "Ordospora",  
 Lake=="Cedar",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
co.spores<- co$Concentration  
  
res.co <- wilcox.test(co6.spores, co.spores)  
res.co

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: co6.spores and co.spores  
## W = 461, p-value = 0.1274  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 461, p = 0.13

### Cedar Metschnikowia top 5 meters v. 1 meter

cm6 = a %>%  
 filter(Parasite== "Metschnikowia",  
 Lake=="Cedar",  
 Depth =="7")  
cm6.spores <- cm6$Concentration  
  
cm = a %>%  
 filter(Parasite== "Metschnikowia",  
 Lake=="Cedar",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
cm.spores<- cm$Concentration  
  
res.cm <- wilcox.test(cm6.spores, cm.spores)  
res.cm

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: cm6.spores and cm.spores  
## W = 434.5, p-value = 0.1635  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 434, p = 0.16

### Cedar Blastulidium top 5 meters v. 1 meter

cb6 = a %>%  
 filter(Parasite== "Blastulidium",  
 Lake=="Cedar",  
 Depth =="7")  
cb6.spores <- cb6$Concentration  
  
cb = a %>%  
 filter(Parasite== "Blastulidium",  
 Lake=="Cedar",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
cb.spores<- cb$Concentration  
  
res.cb <- wilcox.test(cb6.spores, cb.spores)  
res.cb

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: cb6.spores and cb.spores  
## W = 415, p-value = 0.4  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 415, p = 0.4

### Cedar Pasteuria top 5 meters v. 1 meter

cp6 = a %>%  
 filter(Parasite== "Pasteuria",  
 Lake=="Cedar",  
 Depth =="7")  
cp6.spores <- cp6$Concentration  
  
cp = a %>%  
 filter(Parasite== "Pasteuria",  
 Lake=="Cedar",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
cp.spores<- cp$Concentration  
  
res.cp <- wilcox.test(cp6.spores, cp.spores)  
res.cp

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: cp6.spores and cp.spores  
## W = 563.5, p-value = 0.0003214  
## alternative hypothesis: true location shift is not equal to 0

### significantly different, W = 563, p = 0.0003

## Cedar Spirobacillus top 5 meters v. 1 meter

cs6 = a %>%  
 filter(Parasite== "Spirobacillus",  
 Lake=="Cedar",  
 Depth =="7")  
cs6.spores <- cs6$Concentration  
  
cs = a %>%  
 filter(Parasite== "Spirobacillus",  
 Lake=="Cedar",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
cs.spores<- cs$Concentration  
  
res.cs <- wilcox.test(cs6.spores, cs.spores)  
res.cs

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: cs6.spores and cs.spores  
## W = 477, p-value = 0.07894  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 477, p = 0.07

### Crooked W Ordospora 6 meters

cwo6 = a %>%  
 filter(Parasite== "Ordospora",  
 Lake=="CrookedW",  
 Depth =="6")  
cwo6.spores <- cwo6$Concentration  
  
cwo = a %>%  
 filter(Parasite== "Ordospora",  
 Lake=="CrookedW",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
cwo.spores<- cwo$Concentration  
  
res.cwo <- wilcox.test(cwo6.spores, cwo.spores)  
res.cwo

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: cwo6.spores and cwo.spores  
## W = 537, p-value = 0.007174  
## alternative hypothesis: true location shift is not equal to 0

### significantly different, W = 537, p = 0.007

### Crooked W Metschnikowia 6 meters

cwm6 = a %>%  
 filter(Parasite== "Metschnikowia",  
 Lake=="CrookedW",  
 Depth =="6")  
cwm6.spores <- cwm6$Concentration  
  
cwm = a %>%  
 filter(Parasite== "Metschnikowia",  
 Lake=="CrookedW",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
cwm.spores<- cwm$Concentration  
  
res.cwm <- wilcox.test(cwm6.spores, cwm.spores)  
res.cwm

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: cwm6.spores and cwm.spores  
## W = 288.5, p-value = 0.2841  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 288.5, p = 0.28

### Crooked W Blastulidium 6 meters

cwb6 = a %>%  
 filter(Parasite== "Blastulidium",  
 Lake=="CrookedW",  
 Depth =="6")  
cwb6.spores <- cwb6$Concentration  
  
cwb = a %>%  
 filter(Parasite== "Blastulidium",  
 Lake=="CrookedW",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
cwb.spores<- cwb$Concentration  
  
res.cwb <- wilcox.test(cwb6.spores, cwb.spores)  
res.cwb

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: cwb6.spores and cwb.spores  
## W = 559, p-value = 0.0009387  
## alternative hypothesis: true location shift is not equal to 0

### significantly different, W = 559, p = 0.0009

### Crooked W Pasteuria 6 meters

cwp6 = a %>%  
 filter(Parasite== "Pasteuria",  
 Lake=="CrookedW",  
 Depth =="6")  
cwp6.spores <- cwp6$Concentration  
  
cwp = a %>%  
 filter(Parasite== "Pasteuria",  
 Lake=="CrookedW",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
cwp.spores<- cwp$Concentration  
  
res.cwp <- wilcox.test(cwp6.spores, cwp.spores)  
res.cwp

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: cwp6.spores and cwp.spores  
## W = 477.5, p-value = 0.04192  
## alternative hypothesis: true location shift is not equal to 0

### significantly different, W = 477.5, p = 0.04

## Crooked W Spirobacillus 6 meters

cws6 = a %>%  
 filter(Parasite== "Spirobacillus",  
 Lake=="CrookedW",  
 Depth =="6")  
cws6.spores <- cws6$Concentration  
  
cws = a %>%  
 filter(Parasite== "Spirobacillus",  
 Lake=="CrookedW",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
cws.spores<- cws$Concentration  
  
res.cws <- wilcox.test(cws6.spores, cws.spores)  
res.cws

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: cws6.spores and cws.spores  
## W = 466, p-value = 0.1108  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 466, p = 0.11

### LilAp Ordospora 6 meters

lo6 = a %>%  
 filter(Parasite== "Ordospora",  
 Lake=="LilAp",  
 Depth =="6")  
lo6.spores <- lo6$Concentration  
  
lo = a %>%  
 filter(Parasite== "Ordospora",  
 Lake=="LilAp",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
lo.spores<- lo$Concentration  
  
res.lo <- wilcox.test(lo6.spores, lo.spores)  
res.lo

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: lo6.spores and lo.spores  
## W = 394, p-value = 0.9582  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 394, p = 0.95

### LilAp Metschnikowia 6 meters

lm6 = a %>%  
 filter(Parasite== "Metschnikowia",  
 Lake=="LilAp",  
 Depth =="6")  
lm6.spores <- lm6$Concentration  
  
lm = a %>%  
 filter(Parasite== "Metschnikowia",  
 Lake=="LilAp",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
lm.spores<- lm$Concentration  
  
res.lm <- wilcox.test(lm6.spores, lm.spores)  
res.lm

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: lm6.spores and lm.spores  
## W = 379.5, p-value = 0.8803  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 379.5, p = 0.88

### LilAp Blastulidium 6 meters

lb6 = a %>%  
 filter(Parasite== "Blastulidium",  
 Lake=="LilAp",  
 Depth =="6")  
lb6.spores <- lb6$Concentration  
  
lb = a %>%  
 filter(Parasite== "Blastulidium",  
 Lake=="LilAp",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
lb.spores<- lb$Concentration  
  
res.lb <- wilcox.test(lb6.spores, lb.spores)  
res.lb

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: lb6.spores and lb.spores  
## W = 349, p-value = 0.4742  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 349, p = 0.47

### LilAp Pasteuria 6 meters

lp6 = a %>%  
 filter(Parasite== "Pasteuria",  
 Lake=="LilAp",  
 Depth =="6")  
lp6.spores <- lp6$Concentration  
  
lp = a %>%  
 filter(Parasite== "Pasteuria",  
 Lake=="LilAp",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
lp.spores<- lp$Concentration  
  
res.lp <- wilcox.test(lp6.spores, lp.spores)  
res.lp

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: lp6.spores and lp.spores  
## W = 471, p-value = 0.2297  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 471, p = 0.22

## LilAp Spirobacillus 6 meters

ls6 = a %>%  
 filter(Parasite== "Spirobacillus",  
 Lake=="LilAp",  
 Depth =="6")  
ls6.spores <- ls6$Concentration  
  
ls = a %>%  
 filter(Parasite== "Spirobacillus",  
 Lake=="LilAp",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")   
  
ls.spores<- ls$Concentration  
  
res.ls <- wilcox.test(ls6.spores, ls.spores)  
res.ls

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: ls6.spores and ls.spores  
## W = 637.5, p-value = 0.0005196  
## alternative hypothesis: true location shift is not equal to 0

### significantly different, W = 637.5, p = 0.0005

### Bishop Ordospora top 5 v bottom 1 meter

bot = a %>%  
 filter(Parasite== "Ordospora",  
 Lake=="Bishop",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")  
bot.spores <- bot$Concentration  
  
bob = a %>%  
 filter(Parasite== "Ordospora",  
 Lake=="Bishop",  
 Depth == "16")   
  
bob.spores<- bob$Concentration  
  
res.bo <- wilcox.test(bot.spores, bob.spores)  
res.bo

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: bot.spores and bob.spores  
## W = 434.5, p-value = 0.08481  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 434.5, p = .0848

### Bishop Blastulidium top 5 v bottom 1 meter

bbt = a %>%  
 filter(Parasite== "Blastulidium",  
 Lake=="Bishop",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")  
bbt.spores <- bbt$Concentration  
  
bbb = a %>%  
 filter(Parasite== "Blastulidium",  
 Lake=="Bishop",  
 Depth == "16")   
  
bbb.spores<- bbb$Concentration  
  
res.bb <- wilcox.test(bbt.spores, bbb.spores)  
res.bb

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: bbt.spores and bbb.spores  
## W = 404, p-value = 0.05906  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 404, p = 0.0591

### Bishop Metschnikowia top 5 v bottom 1 meter

bmt = a %>%  
 filter(Parasite== "Metschnikowia",  
 Lake=="Bishop",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")  
bmt.spores <- bmt$Concentration  
  
bmb = a %>%  
 filter(Parasite== "Metschnikowia",  
 Lake=="Bishop",  
 Depth == "16")   
  
bmb.spores<- bmb$Concentration  
  
res.bm <- wilcox.test(bmt.spores, bmb.spores)  
res.bm

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: bmt.spores and bmb.spores  
## W = 229, p-value = 0.05513  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 229, p = 0.0551

### Bishop Pasteuria top 5 v bottom 1 meter

bpt = a %>%  
 filter(Parasite== "Pasteuria",  
 Lake=="Bishop",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")  
bpt.spores <- bpt$Concentration  
  
bpb = a %>%  
 filter(Parasite== "Pasteuria",  
 Lake=="Bishop",  
 Depth == "16")   
  
bpb.spores<- bpb$Concentration  
  
res.bp <- wilcox.test(bpt.spores, bpb.spores)  
res.bp

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: bpt.spores and bpb.spores  
## W = 342.5, p-value = 0.7812  
## alternative hypothesis: true location shift is not equal to 0

### not significantly different, W = 342.5, p = 0.781

### Bishop Spirobacillus top 5 v bottom 1 meter

bst = a %>%  
 filter(Parasite== "Spirobacillus",  
 Lake=="Bishop",  
 Depth =="0" | Depth == "1" | Depth =="2"| Depth == "3"|Depth == "4"|Depth == "5")  
bst.spores <- bst$Concentration  
  
bsb = a %>%  
 filter(Parasite== "Spirobacillus",  
 Lake=="Bishop",  
 Depth == "16")   
  
bsb.spores<- bsb$Concentration  
  
res.bs <- wilcox.test(bst.spores, bsb.spores)  
res.bs

##   
## Wilcoxon rank sum test with continuity correction  
##   
## data: bst.spores and bsb.spores  
## W = 110, p-value = 0.0008282  
## alternative hypothesis: true location shift is not equal to 0

### significantly different, W = 110, p = 0.0008