SASP slopes

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Set working environment; load packages and data

```
# Clear and set working directory
rm(list = ls())

library("dplyr")
library("tidyr")
library("broom") #to extract stat results as table
# setwd("~/GitHub/ssp_phage/data")
# d <- read.csv("~/GitHub/ssp_phage/data/HeatDecaySlopes.csv", header = TRUE)
library(here)
d <- read.csv(here("data/HeatDecaySlopes.csv"), header = TRUE)
```

Does deletion of sspAB diminish slope?

Bacillus culture was split into three phage treatments: (SPO1, Goe2, noPhage). The "group" column refers
to spores that were assayed on same day. The "colony" column reflects pairing to be accounted for in analysis.

```
# subset slopes by colony origin
cfu.1 <- filter(d, assay == "CFU" & phage == "noPhage") %>%
  dplyr::select(host, assay, colony, slope)

# extract slopes from wildtype
x.wt <-  cfu.1 %>%
  filter(host == "wt") %>%
  pull(slope)

# extract slopes from mutant
y.mut <-  cfu.1 %>%
  filter(host == "dsspAB") %>%
  pull(slope)

# conduct one-sided, paired t-test
cfu.1.test <- t.test(x.wt, y.mut, alternative = "greater")

# Answer: deletion of sspAB reduces heat tolerance
# two-sided: P = 0.005858 (alternative = "two.sided")
# one-sided: P = 0.002929 (alternative = "greater")
```

Does infection with phage ameliorate effects of sspAB deletion?

```r
# subset slopes by host, phage, and group
cfu.2 <- filter(d, assay == "CFU", host == "dsspAB") %>%
  dplyr::select(host, phage, assay, colony, slope)

# convert to wide
cfu.2 <- cfu.2 %>%
  # spread(phage, slope)
  tidyr::pivot_wider(names_from = phage, values_from = slope)

# calculate difference in slopes between no-phage and plus-phage treatments
cfu.2 <- mutate(cfu.2, dif.goe2 = cfu.2$noPhage-cfu.2$Goe2,
              dif.spo1 = cfu.2$noPhage - cfu.2$SPO1)

# Tests

# 1) Goe2: one-sided, paired t-test
cfu.Goe2.test <- t.test(cfu.2$dif.goe2, mu = 0, alternative = "less")
# one-sided: P = 0.1314 (alternative = "less" -> does phage ameliorate?)
# answer = no

# 2) SPO1: one-sided, paired t-test
cfu.SPO1.test <- t.test(cfu.2$dif.spo1, mu = 0, alternative = "less")
# one-sided: P = 0.06147
# answer = maybe

# 3) Phage (Goe2 and SPO1), paired t-test: does "phage" ameliorate
cfu.both.test <- t.test(c(cfu.2$dif.goe2, cfu.2$dif.spo1), mu = 0, alternative = "less")
# one-sided: P = 0.01357
# answer = yes

# 4) Difference in Goe2 vs SPO1 slopes, paired
cfu.GvsS.test <- t.test(x=cfu.2$Goe2, y=cfu.2$SPO1, mu = 0, alternative = "two.sided")
# two-sided: P = 0.6836
# answer = no

cfu.table <- dplyr::bind_rows(
  broom::glance(cfu.Goe2.test),
  broom::glance(cfu.SPO1.test),
  broom::glance(cfu.both.test),
  broom::glance(cfu.GvsS.test)
)
```

Does infection with phage ameliorate effects of sspAB deletion in virospores?

Compare slopes of viral spores to slopes of colony-forming spores in the WT. There are no viral spores in non-infected cultures.

```r
# subset slopes by deletion host, phage treatment, and group
pfu <- filter(d,  host == "dsspAB") %>%
  # select CFU for noPhage and PFU for infected cultures
  filter((phage == "noPhage" &  assay == "CFU") | (assay == "PFU")) %>%
  dplyr::select(host, phage,  colony, slope)

# convert to wide
pfu <- pfu %>%
  # spread(phage, slope)
  tidyr::pivot_wider(names_from = phage, values_from = slope)

# calculate differences in slopes between no-phage and plus-phage treatments
pfu <- mutate(pfu, dif.goe2 = pfu$noPhage-pfu$Goe2,
                   dif.spo1 = pfu$noPhage - pfu$SPO1)

# Tests

# 1) Goe2: one-sided, paired t-test
pfu.Goe2.test <- t.test(pfu$dif.goe2, mu = 0, alternative = "less")
# one-sided: P = 0.3231
# answer: no

# 2) SPO1: one-sided, paired t-test
pfu.SPO1.test <- t.test(pfu$dif.spo1, mu = 0, alternative = "less")
# one-sided: P = 0.4109
# answer: no

# 3) Phage (Goe2 and SPO1)
pfu.both.test <- t.test(c(pfu$dif.goe2, pfu$dif.spo1), mu = 0,
                        alternative = "less")
# one-sided: P = 0.2765
# answer: no

# 4) Difference in Goe2 vs SPO1
pfu.GvsS.test <- t.test(x=pfu$Goe2, y=pfu$SPO1, mu = 0, alternative = "two.sided")
# two-sided: 0.8138
# answer: no

pfu.table <-dplyr::bind_rows(
  broom::glance(pfu.Goe2.test),
  broom::glance(pfu.SPO1.test),
  broom::glance(pfu.both.test),
  broom::glance(pfu.GvsS.test)
)
```

Do colony-forming spores and viral spores differ from each other when infecting the mutant host?

One-sided hypothesis: viral spores are more resistant. That is, they have a greater slope value: slope.PFU-slopePFU > 0

```r
# subset slopes by deletion host, assay type (CFU vs. PFU), and colony
cfu.pfu <- filter(d,  host == "dsspAB", phage != "noPhage") %>%
    dplyr::select(host, phage, assay , colony, slope)

# convert to wide
cfu.pfu  <- cfu.pfu  %>%
  # spread(phage, slope)
  tidyr::pivot_wider(names_from = assay, values_from = slope)

# calculate differences in slopes between CFU and PFU
cfu.pfu  <- mutate(cfu.pfu , dif = PFU-CFU)

cfu.pfu.Goe2.test <-
  cfu.pfu %>%
  filter(phage  =="Goe2") %>%
  pull(dif) %>%
  t.test(., mu = 0, alternative = "greater")
# one-sided: P = 0.3425

cfu.pfu.SPO1.test <-
  cfu.pfu %>%
  filter(phage == "SPO1") %>%
  pull(dif) %>%
  t.test(., mu = 0, alternative = "greater")
# one-sided: P = 0.9197
# answer: no

cfu.pfu.phage.test <-
  cfu.pfu %>%
  t.test(dif~phage, mu = 0, alternative = "two.sided", data =.)
# one-sided: P = 0.4173
# answer: no

cfu.pfu.table <- dplyr::bind_rows(
  broom::glance(cfu.pfu.Goe2.test),
  broom::glance(cfu.pfu.SPO1.test),
  broom::glance(cfu.pfu.phage.test)
)
```

Does infection with phage compromise resistance of WT spores?

If spores from infected cultures are more resistant, than slope(noPhage)-slope(phage)>0.

```r
cfu.3 <- filter(d, assay == "CFU", host == "wt") %>%
  dplyr::select(host, phage, assay, colony, slope)

# convert to wide
cfu.3 <- cfu.3 %>%
  # spread(phage, slope)
  tidyr::pivot_wider(names_from=phage, values_from=slope)

# calculate difference and test
```

```
cfu.3 <- mutate(cfu.3, dif.goe2 = cfu.3$noPhage-cfu.3$Goe2,
                dif.spo1 = cfu.3$noPhage - cfu.3$SPO1)

cfu.3.Goe2.test <- t.test(cfu.3$dif.goe2, mu = 0, alternative = "greater")
# one-sided: P = 0.09148

cfu.3.SPO1.test <- t.test(cfu.3$dif.spo1, mu = 0, alternative = "greater")
# one-sided: P = 0.2998

cfu.3.both.test <- t.test(c(cfu.3$dif.goe2, cfu.3$dif.spo1), mu = 0,
                          alternative = "greater")
# one-sided: P = 0.06574

cfu.3.GvsS.test <- t.test(x=cfu.3$dif.goe2, y= cfu.3$dif.spo1, mu = 0,
                          alternative = "two.sided")
# one-sided: P = 0.2114

cfu.wt.table <- dplyr::bind_rows(
  broom::glance(cfu.3.Goe2.test),
  broom::glance(cfu.3.SPO1.test),
  broom::glance(cfu.3.both.test),
  broom::glance(cfu.3.GvsS.test)
)
```