Pseudomonas Epiphytic Growth and Virulence Analysis

2024 Summer

Contents

Load Libraries

```
pacman::p_load(ggplot2, readxl, RColorBrewer, paletteer, viridis, wesanderson, ggbeeswarm,
    dplyr, tidyverse, devtools, emmeans, cowplot, knitr, survival, here, tibble,
    survminer, lubridate, formatR, gridExtra, ggsurvfit, gtsummary, tidycmprsk, install = FALSE)
```

Load Data

```r
# Define the desired order of the treatments
strains_order <- c("194", "200", "204", "205", "215", "216", "220", "221", "227",
    "228", "B728a", "Cit7", "pisi", "Control")

strains_df <- read_excel("data/strains_R.xlsx")

epi_growth_data <- read_excel("data/pseud_epi_growth_2024summer_R.xlsx")

# Convert the strain variable to a factor with the specified order
epi_growth_data$strain <- factor(epi_growth_data$strain, levels = strains_order)

aphid_virulence_data <- read_csv("data/virulence_new_all.csv")
```

```
## Rows: 4973 Columns: 6
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (3): date, treatment, replicate
## dbl (3): individual, censored, time
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```r
# Convert the treatment variable to a factor with the specified order
aphid_virulence_data$treatment <- factor(aphid_virulence_data$treatment, levels = strains_order)

# Join the strains dataframe to virulence
aphid_virulence_data <- left_join(aphid_virulence_data, strains_df, by = "treatment")

aphid_virulence_data <- aphid_virulence_data %>%
    mutate(species = replace_na(species, "Control"))
```

Load colors

```r
# Extract the default ggplot colors
default_colors <- (scales::hue_pal())(length(strains_order) - 1)

# Create a named vector for strain colors, ensuring 'Control' is black
strain_colors <- setNames(c(default_colors, "black"), strains_order)

# Load species colors
species_colors <- c(`P. fluorescens` = "dodgerblue2", `P. syringae` = "springgreen3",
    `P. paralactis` = "sienna4", Control = "black")

species_colors_manual <- c(`194` = "sienna4", `200` = "dodgerblue2", `204` = "dodgerblue2",
    `205` = "dodgerblue2", `215` = "springgreen3", `216` = "dodgerblue2", `220` = "sienna4",
    `221` = "dodgerblue2", `227` = "dodgerblue2", `228` = "dodgerblue2", B728a = "springgreen3",
    Cit7 = "springgreen3", pisi = "springgreen3", Control = "black")
```

Goals

- Create Kaplan-Meier curve for Pseud. virulence data
- Use stats (Wilcox?) to determine statistical significance of each strain
- Compare virulence data with epiphitic growth ability

Virulence Analysis

Note: *In order to help me with this analysis, I am using the following sites - Survival Analysis in R and Hazard Ratio: Interpretation & Definition.*

Caclulcate survival probabilities for each strain and create dataframe

Survival model

```
# Fit the survival model
km_fit <- survfit(Surv(time, censored) ~ treatment, data = aphid_virulence_data)
```

Extract survival probability

```
# Fit the survival model
km_fit <- survfit(Surv(time, censored) ~ treatment, data = aphid_virulence_data)

# Extract survival probabilities at specific time points
time_points <- c(72)
km_summary <- summary(km_fit, times = time_points)

# Calculate standard error (assuming fit includes the necessary information)
std_error <- summary(km_fit, times = time_points)$std.err

# Initialize empty lists to store the results
times_list <- list()
treatment_list <- list()
surv_prob_list <- list()
std_error_list <- list()

# Loop over each treatment group and extract survival probabilities at
# specified time points
for (i in 1:length(km_fit$strata)) {
    treatment_name <- names(km_fit$strata)[i]
    for (t in time_points) {
        idx <- which(km_summary$time == t & km_summary$strata == treatment_name)
        if (length(idx) > 0) {
            times_list <- c(times_list, t)
            treatment_list <- c(treatment_list, treatment_name)
            surv_prob_list <- c(surv_prob_list, km_summary$surv[idx])
            std_error_list <- c(std_error_list, km_summary$std.err[idx])
        } else {
```

```r
            times_list <- c(times_list, t)
            treatment_list <- c(treatment_list, treatment_name)
            surv_prob_list <- c(surv_prob_list, NA)
            std_error_list <- c(std_error_list, NA)
        }
    }
}

# Create the data frame
surv_probs <- data.frame(time = unlist(times_list), treatment = unlist(treatment_list),
    surv_prob = unlist(surv_prob_list), std_error_data = unlist(std_error_list))

# Replace 'treatment=' with an empty string
surv_probs$treatment <- gsub("treatment=", "", surv_probs$treatment)

# Convert the treatment variable to a factor with the specified order
surv_probs$treatment <- factor(surv_probs$treatment, levels = strains_order)

# Join the survival dataframe to strains
surv_probs <- left_join(surv_probs, strains_df, by = "treatment")

# Print the data frame
print(surv_probs)
```

```
##    time treatment  surv_prob std_error_data        species     -80
## 1    72       194 0.12244898    0.019117897  P. paralactis     194
## 2    72       200 0.02230483    0.009003784 P. fluorescens     200
## 3    72       204 0.05281690    0.013272241 P. fluorescens     204
## 4    72       205 0.07118644    0.014971038 P. fluorescens     205
## 5    72       215 0.22222222    0.024497697    P. syringae     215
## 6    72       216 0.15625000    0.021395412 P. fluorescens     216
## 7    72       220 0.17229730    0.021949800  P. paralactis     220
## 8    72       221 0.09363296    0.017828335 P. fluorescens     221
## 9    72       227 0.16949153    0.021844143 P. fluorescens     227
## 10   72       228 0.10447761    0.018684542 P. fluorescens     228
## 11   72     B728a 0.10996564    0.018339411    P. syringae   B728a
## 12   72      Cit7 0.17073171    0.022210773    P. syringae      14
## 13   72   Control 0.81678082    0.011319228        Control Control
## 14   72      pisi 0.74151436    0.022370650    P. syringae       6
##                name
## 1     field sample #8
## 2    field sample #14
## 3    field sample #17
## 4  field sample #18-1
## 5  field sample #26-1
## 6  field sample #26-2
## 7  field sample #29-2
## 8  field sample #29-3
## 9    field sample #35
## 10   field sample #36
## 11        B728a ΔFlgK
## 12               Cit7
## 13            Control
```

```
## 14                Pisi
```

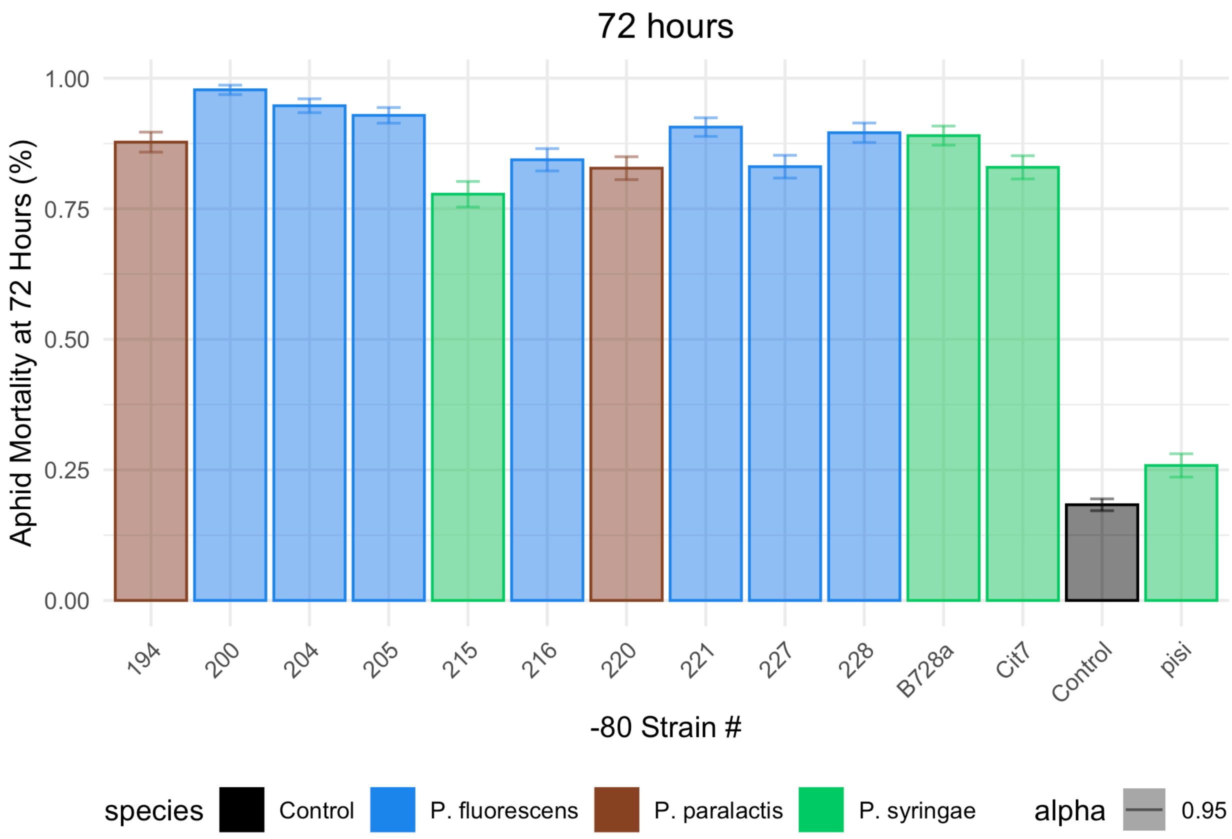
Post-hoc test for survival

```r
# Perform pairwise log-rank tests between treatment groups and the control
# group
pairwise_tests <- pairwise_survdiff(Surv(time, censored) ~ treatment, data = aphid_virulence_data)

# Print the pairwise tests
print(pairwise_tests)
```

```
##
##  Pairwise comparisons using Log-Rank test
##
## data:  aphid_virulence_data and treatment
##
##         194     200     204     205     215     216     220     221     227
## 200     2.3e-12 -       -       -       -       -       -       -       -
## 204     1.6e-08 0.26489 -       -       -       -       -       -       -
## 205     3.7e-06 0.04009 0.38289 -       -       -       -       -       -
## 215     4.6e-05 < 2e-16 < 2e-16 7.8e-16 -       -       -       -       -
## 216     0.20589 3.0e-06 0.00054 0.00915 1.3e-05 -       -       -       -
## 220     1.2e-05 0.34987 0.95899 0.61067 7.5e-10 0.04787 -       -       -
## 221     0.06597 1.7e-06 0.00063 0.01560 3.0e-08 0.57084 0.05899 -       -
## 227     0.00048 0.05275 0.34910 0.75895 1.7e-08 0.14997 0.65606 0.23547 -
## 228     0.02457 2.3e-05 0.00265 0.03730 5.6e-09 0.52684 0.02668 0.75895 0.15756
## B728a   0.30241 3.8e-15 2.0e-10 1.5e-07 0.00193 0.15635 0.00089 0.00913 0.00558
## Cit7    0.97833 6.8e-10 1.0e-06 8.4e-05 0.00044 0.38289 0.00217 0.11439 0.01459
## Control < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16
## pisi    < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16 < 2e-16
##         228     B728a   Cit7    Control
## 200     -       -       -       -
## 204     -       -       -       -
## 205     -       -       -       -
## 215     -       -       -       -
## 216     -       -       -       -
## 220     -       -       -       -
## 221     -       -       -       -
## 227     -       -       -       -
## 228     -       -       -       -
## B728a   0.00265 -       -       -
## Cit7    0.05646 0.46912 -       -
## Control < 2e-16 < 2e-16 < 2e-16 -
## pisi    < 2e-16 < 2e-16 < 2e-16 0.00042
##
## P value adjustment method: BH
```

Plot Surival Dataframe at different times

```r
surv_plot <- ggplot(data = surv_probs, aes(x = treatment, y = (1-surv_prob), color = species, fill = spe
  geom_col() +
  geom_errorbar(aes(ymin = (1-surv_prob) - std_error_data, ymax = (1-surv_prob) + std_error_data),
                width = 0.3,  # Width of error bars
                position = position_dodge(width = 0.9)) +  # Dodge bars slightly
  labs(title = "72 hours",
       x = "-80 Strain #",
       y = "Aphid Mortality at 72 Hours (%)") +
  theme_minimal() +
  scale_fill_manual(values = species_colors) +
  scale_color_manual(values = species_colors) +
  theme(plot.title = element_text(hjust = 0.5),
        axis.text.x = element_text(angle = 45, hjust = 1), legend.position = "bottom")

surv_plot
```



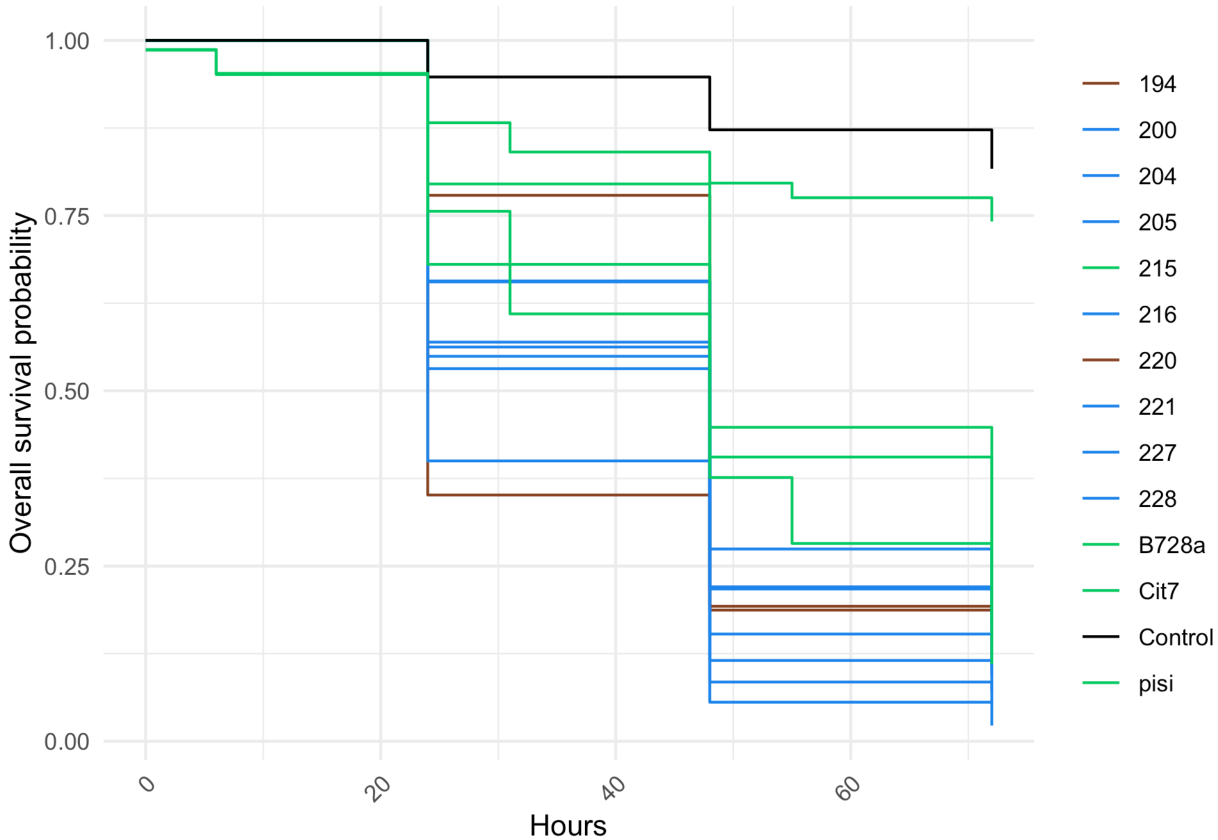
Make Kaplan-Meier Plot

Cohort Survival Curve

```r
# Plot the Kaplan-Meier survival curves
survfit2(Surv(time, censored) ~ treatment, data = aphid_virulence_data) %>%
```

```r
ggsurvfit(type = "survival") + labs(x = "Hours", y = "Overall survival probability") +
    theme_minimal() + scale_fill_manual(values = species_colors_manual) + scale_color_manual(values = sp
    theme(plot.title = element_text(hjust = 0.5), axis.text.x = element_text(angle = 45,
        hjust = 1), legend.position = "right")
```

```
## Warning: No shared levels found between `names(values)` of the manual scale and the
## data's fill values.
```



Epiphytic Growth Analysis

Calculate mean/variance epiphytic growth ability

```r
# Replace NA with a lower value or remove them for visualization Remove rows
# with NA in CFU_per_10_leafdiscs
epi_growth_clean <- epi_growth_data %>%
    filter(!is.na(CFU_per_10_leafdiscs))

# Convert CFU_per_10_leafdiscs to numeric, handling scientific notation
epi_growth_clean$CFU_per_10_leafdiscs <- as.numeric(gsub("<", "", epi_growth_clean$CFU_per_10_leafdiscs
```

```
## Warning: NAs introduced by coercion
```

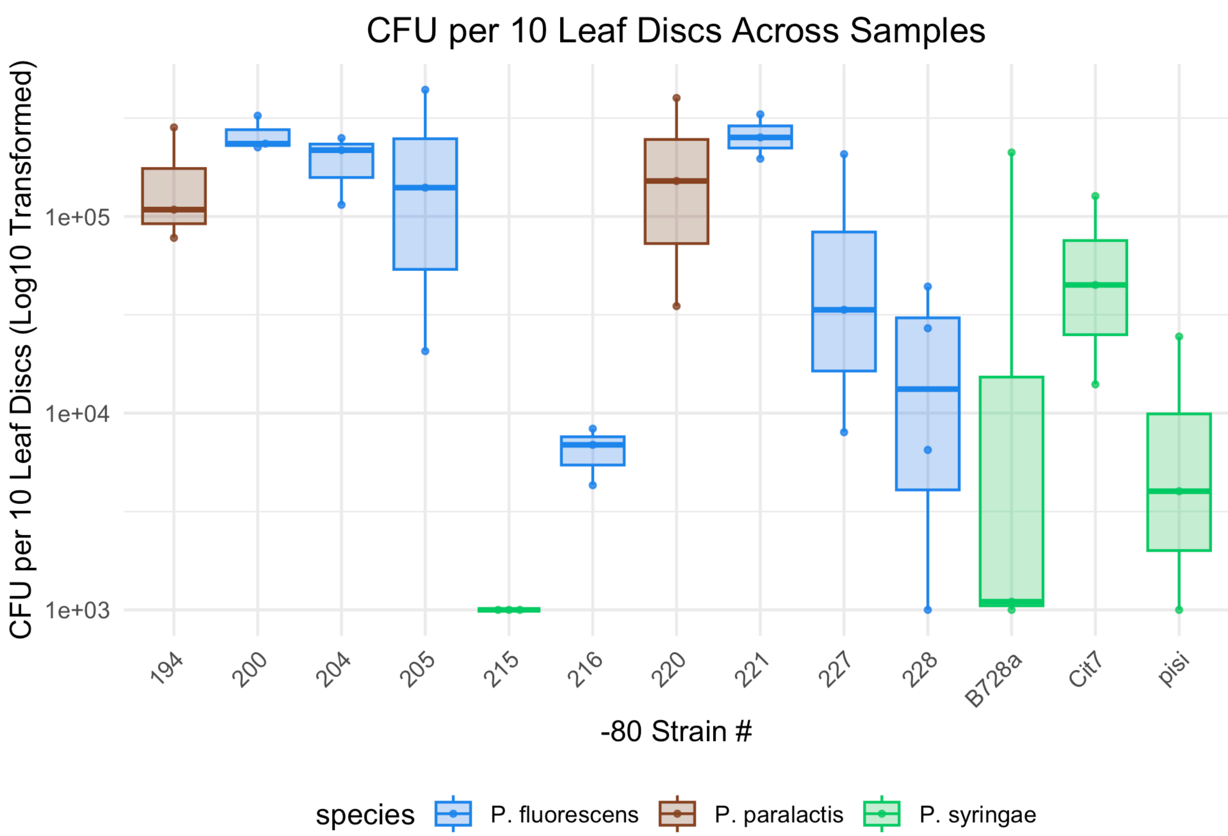
```r
# Subset data to remove unfinished strains and extract the letter part from the
# 'plant_rep' column
epi_growth_clean <- epi_growth_clean %>%
    mutate(plant_rep_letter = substr(plant_rep, 1, 1))

# Calculate the mean and SD CFU per strain for each plant rep letter and retain
# the specified columns
epi_growth_mean_per_rep <- epi_growth_clean %>%
    group_by(strain, plant_rep_letter) %>%
    summarise(mean_CFU_per_10_leafdiscs = mean(CFU_per_10_leafdiscs, na.rm = TRUE),
        sd_CFU = sd(CFU_per_10_leafdiscs, na.rm = TRUE), sample = first(sample),
        person = first(person), block = first(block), species = first(species), plant_rep = first(plant_
        .groups = "drop")

# Calculate the mean and SD CFU per strain for each plant rep letter and retain
# the specified columns
epi_growth_mean_per_strain <- epi_growth_clean %>%
    group_by(strain) %>%
    summarise(mean_CFU_per_10_leafdiscs = mean(CFU_per_10_leafdiscs, na.rm = TRUE),
        sd_CFU = sd(CFU_per_10_leafdiscs, na.rm = TRUE), sample = first(sample),
        person = first(person), block = first(block), species = first(species), plant_rep = first(plant_
        .groups = "drop")

epi_growth_mean_per_strain
```

```
## # A tibble: 13 x 8
##    strain mean_CFU_per_10_leafdiscs sd_CFU sample person block species plant_rep
##    <fct>                      <dbl>  <dbl> <chr>  <chr>  <chr> <chr>   <chr>
##  1 194                      156472. 1.43e5 194-A1 Havi   2-1   P. par~ A1
##  2 200                      261214. 1.81e5 200-A1 Havi   2-6   P. flu~ A1
##  3 204                      186888. 1.89e5 204-A1 Havi   2-3   P. flu~ A1
##  4 205                      207750  2.40e5 205-A1 Sara   3     P. flu~ A1
##  5 215                        1000  0      215-A1 Sara   3     P. syr~ A1
##  6 216                        6788. 7.61e3 216-A1 Sara   3     P. flu~ A1
##  7 220                      172543. 1.89e5 220-A1 Sara   5     P. par~ A1
##  8 221                      259556. 1.93e5 221-A1 Havi   2-7   P. flu~ A1
##  9 227                       82872. 1.53e5 227-A1 Sara   5     P. flu~ A1
## 10 228                       22875  2.37e4 228-A1 Sara   5     P. flu~ A1
## 11 B728a                     71144. 1.36e5 B728a~ Sara   4     P. syr~ A1
## 12 Cit7                      61906. 1.17e5 Cit7-~ Havi   2-3   P. syr~ A1
## 13 pisi                      11607. 3.51e4 pisi-~ Havi   2-4   P. syr~ A1
```

Plot Epiphytic Growth

```r
epi_growth_species <- ggplot(data = epi_growth_mean_per_rep, aes(x = strain, y = mean_CFU_per_10_leafdi
  geom_boxplot(outlier.shape = NA, alpha = 0.3) +
  geom_beeswarm(stroke = 0.5, size = 0.8, alpha = 0.8) +
  labs(title = "CFU per 10 Leaf Discs Across Samples",
       x = "-80 Strain #",
       y = "CFU per 10 Leaf Discs (Log10 Transformed)") +
  theme_minimal() +
```

```
  scale_fill_manual(values = species_colors) +
  scale_color_manual(values = species_colors) +
  scale_y_log10() +  # Apply log transformation to y-axis
  theme(plot.title = element_text(hjust = 0.5),
        axis.text.x = element_text(angle = 45, hjust = 1), legend.position = "bottom")

epi_growth_species
```



Epiphytic growth stats

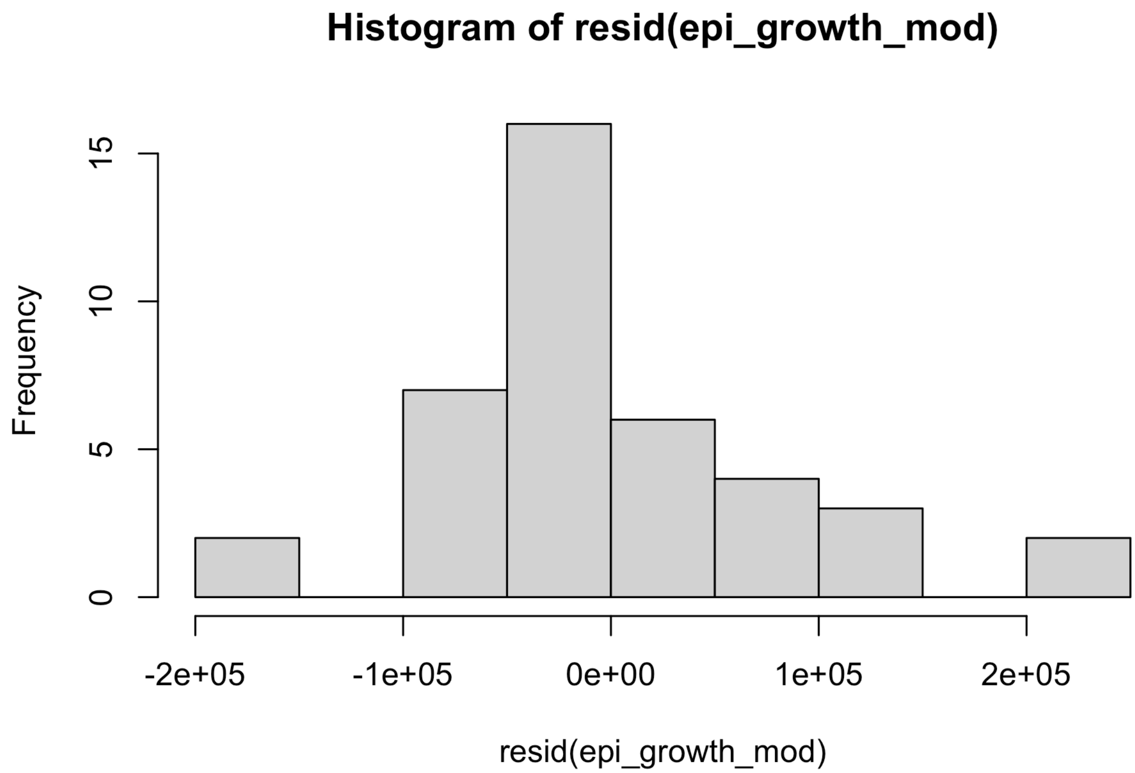
```
epi_growth_mod = lm(mean_CFU_per_10_leafdiscs ~ strain, data = epi_growth_mean_per_rep)

emmeans(epi_growth_mod, pairwise ~ strain)
```

```
## $emmeans
##  strain emmean    SE df lower.CL upper.CL
##  194    156472 58153 27    37151   275793
##  200    261214 58153 27   141893   380535
##  204    193911 58153 27    74590   313232
##  205    200222 58153 27    80901   319543
##  215      1000 58153 27  -118321   120321
##  216      6511 58153 27  -112810   125832
```

```
##  220    195467 58153 27    76146   314788
##  221    259556 58153 27   140234   378877
##  227     82872 58153 27   -36449   202193
##  228     19625 50362 27   -83710   122960
##  B728a   71144 58153 27   -48177   190466
##  Cit7    61906 58153 27   -57416   181227
##  pisi     9839 58153 27  -109482   129160
##
## Confidence level used: 0.95
##
## $contrasts
##  contrast     estimate    SE df t.ratio p.value
##  194 - 200     -104742 82241 27  -1.274  0.9829
##  194 - 204      -37439 82241 27  -0.455  1.0000
##  194 - 205      -43750 82241 27  -0.532  1.0000
##  194 - 215      155472 82241 27   1.890  0.7869
##  194 - 216      149961 82241 27   1.823  0.8218
##  194 - 220      -38994 82241 27  -0.474  1.0000
##  194 - 221     -103083 82241 27  -1.253  0.9849
##  194 - 227       73600 82241 27   0.895  0.9992
##  194 - 228      136847 76930 27   1.779  0.8434
##  194 - B728a     85328 82241 27   1.038  0.9970
##  194 - Cit7      94567 82241 27   1.150  0.9926
##  194 - pisi     146633 82241 27   1.783  0.8415
##  200 - 204       67303 82241 27   0.818  0.9997
##  200 - 205       60992 82241 27   0.742  0.9999
##  200 - 215      260214 82241 27   3.164  0.1318
##  200 - 216      254703 82241 27   3.097  0.1503
##  200 - 220       65747 82241 27   0.799  0.9998
##  200 - 221        1658 82241 27   0.020  1.0000
##  200 - 227      178342 82241 27   2.169  0.6194
##  200 - 228      241589 76930 27   3.140  0.1381
##  200 - B728a    190069 82241 27   2.311  0.5282
##  200 - Cit7     199308 82241 27   2.423  0.4582
##  200 - pisi     251375 82241 27   3.057  0.1624
##  204 - 205       -6311 82241 27  -0.077  1.0000
##  204 - 215      192911 82241 27   2.346  0.5064
##  204 - 216      187400 82241 27   2.279  0.5489
##  204 - 220       -1556 82241 27  -0.019  1.0000
##  204 - 221      -65644 82241 27  -0.798  0.9998
##  204 - 227      111039 82241 27   1.350  0.9733
##  204 - 228      174286 76930 27   2.266  0.5573
##  204 - B728a    122767 82241 27   1.493  0.9456
##  204 - Cit7     132006 82241 27   1.605  0.9132
##  204 - pisi     184072 82241 27   2.238  0.5748
##  205 - 215      199222 82241 27   2.422  0.4589
##  205 - 216      193711 82241 27   2.355  0.5003
##  205 - 220        4756 82241 27   0.058  1.0000
##  205 - 221      -59333 82241 27  -0.721  0.9999
##  205 - 227      117350 82241 27   1.427  0.9601
##  205 - 228      180597 76930 27   2.348  0.5052
##  205 - B728a    129078 82241 27   1.569  0.9246
##  205 - Cit7     138317 82241 27   1.682  0.8853
##  205 - pisi     190383 82241 27   2.315  0.5258
```

```
##  215 - 216       -5511 82241 27  -0.067  1.0000
##  215 - 220     -194467 82241 27  -2.365  0.4945
##  215 - 221     -258556 82241 27  -3.144  0.1372
##  215 - 227      -81872 82241 27  -0.996  0.9979
##  215 - 228      -18625 76930 27  -0.242  1.0000
##  215 - B728a    -70144 82241 27  -0.853  0.9995
##  215 - Cit7     -60906 82241 27  -0.741  0.9999
##  215 - pisi      -8839 82241 27  -0.107  1.0000
##  216 - 220     -188956 82241 27  -2.298  0.5368
##  216 - 221     -253044 82241 27  -3.077  0.1563
##  216 - 227      -76361 82241 27  -0.928  0.9989
##  216 - 228      -13114 76930 27  -0.170  1.0000
##  216 - B728a    -64633 82241 27  -0.786  0.9998
##  216 - Cit7     -55394 82241 27  -0.674  1.0000
##  216 - pisi      -3328 82241 27  -0.040  1.0000
##  220 - 221      -64089 82241 27  -0.779  0.9998
##  220 - 227      112594 82241 27   1.369  0.9704
##  220 - 228      175842 76930 27   2.286  0.5443
##  220 - B728a    124322 82241 27   1.512  0.9409
##  220 - Cit7     133561 82241 27   1.624  0.9068
##  220 - pisi     185628 82241 27   2.257  0.5626
##  221 - 227      176683 82241 27   2.148  0.6323
##  221 - 228      239931 76930 27   3.119  0.1441
##  221 - B728a    188411 82241 27   2.291  0.5410
##  221 - Cit7     197650 82241 27   2.403  0.4705
##  221 - pisi     249717 82241 27   3.036  0.1688
##  227 - 228       63247 76930 27   0.822  0.9997
##  227 - B728a     11728 82241 27   0.143  1.0000
##  227 - Cit7      20967 82241 27   0.255  1.0000
##  227 - pisi      73033 82241 27   0.888  0.9993
##  228 - B728a    -51519 76930 27  -0.670  1.0000
##  228 - Cit7     -42281 76930 27  -0.550  1.0000
##  228 - pisi       9786 76930 27   0.127  1.0000
##  B728a - Cit7     9239 82241 27   0.112  1.0000
##  B728a - pisi    61306 82241 27   0.745  0.9999
##  Cit7 - pisi     52067 82241 27   0.633  1.0000
##
## P value adjustment: tukey method for comparing a family of 13 estimates
```

```r
hist(resid(epi_growth_mod))
```



Combine epiphytic and virulence data

```r
# Assuming strain_stats has a column 'strain' and surv_probs has a column
# 'treatment' Rename columns if necessary to match the key for joining
epi_growth_mean_per_strain <- epi_growth_mean_per_strain %>%
    rename(treatment = strain)

# Combine strain_stats and surv_probs using left_join
epi_virulence_data <- left_join(epi_growth_mean_per_strain, surv_probs, by = "treatment")

# Print the combined data
print(epi_virulence_data)
```

```
## # A tibble: 13 x 14
##    treatment mean_CFU_per_10_leafdiscs  sd_CFU sample   person block species.x
##    <chr>                         <dbl>   <dbl> <chr>    <chr>  <chr> <chr>
##  1 194                         156472. 142871. 194-A1   Havi   2-1   P. paralac~
##  2 200                         261214. 180932. 200-A1   Havi   2-6   P. fluores~
##  3 204                         186888. 189203. 204-A1   Havi   2-3   P. fluores~
##  4 205                         207750  239592. 205-A1   Sara   3     P. fluores~
##  5 215                           1000       0  215-A1   Sara   3     P. syringae
##  6 216                           6788.   7614. 216-A1   Sara   3     P. fluores~
##  7 220                         172543. 189362. 220-A1   Sara   5     P. paralac~
```

```
##  8 221                        259556. 193140. 221-A1   Havi   2-7   P. fluores~
##  9 227                         82872. 153323. 227-A1   Sara   5     P. fluores~
## 10 228                         22875   23673. 228-A1   Sara   5     P. fluores~
## 11 B728a                       71144. 135614. B728a-A1 Sara   4     P. syringae
## 12 Cit7                        61906. 117046. Cit7-A1  Havi   2-3   P. syringae
## 13 pisi                        11607.  35081. pisi-A1  Havi   2-4   P. syringae
## # i 7 more variables: plant_rep <chr>, time <dbl>, surv_prob <dbl>,
## #   std_error_data <dbl>, species.y <chr>, `-80` <chr>, name <chr>
```

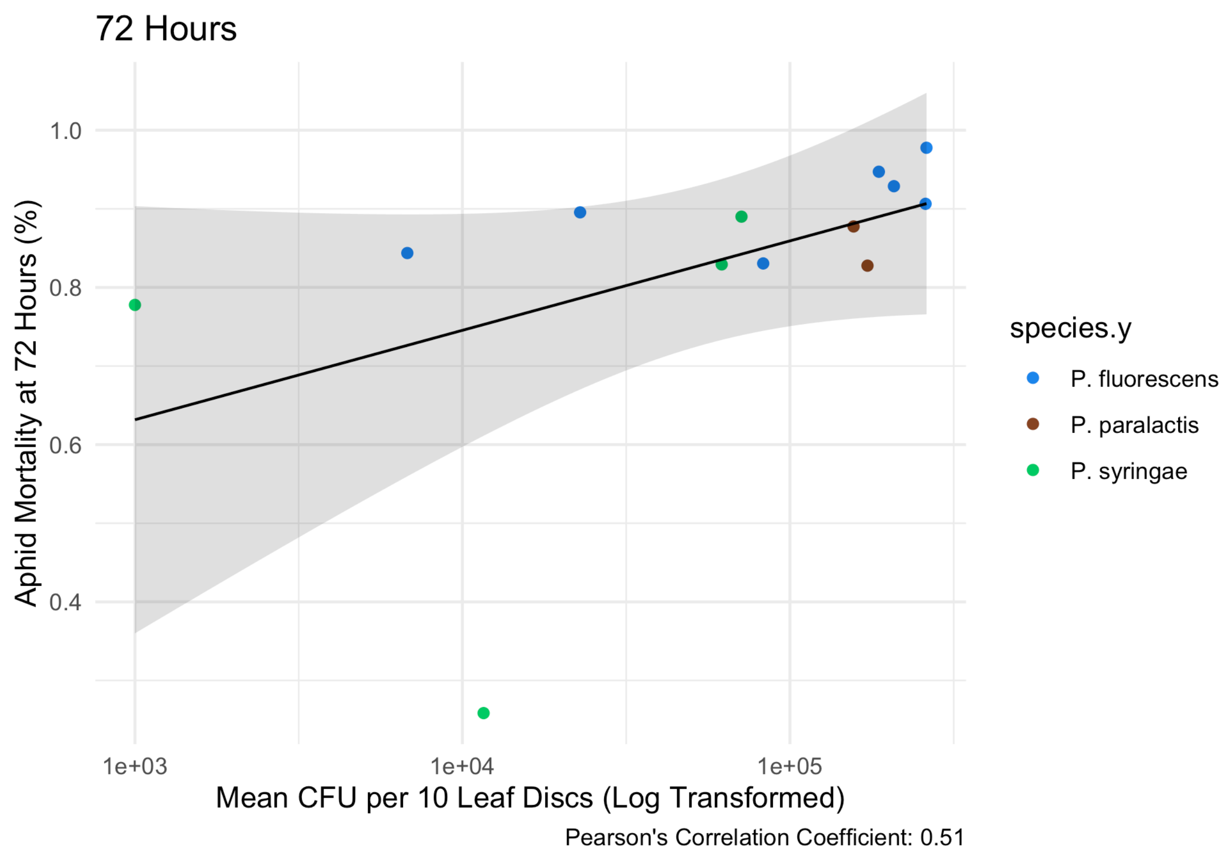
```
# Calculate correlation coefficient between survival probability and epiphytic
# growth ability
correlation <- -1 * cor(epi_virulence_data$surv_prob, epi_virulence_data$mean_CFU_per_10_leafdiscs,
    method = "pearson")
```

Plot epi virulence plot

```
# Create scatter plot for 72 hours
epi_virulence_plot_strains <- ggplot(epi_virulence_data, aes(x = mean_CFU_per_10_leafdiscs, y = 1-surv_p
  geom_point(aes(color = species.y)) +
  geom_smooth(method = "lm", se = TRUE, color = "black", fill = "black", alpha = 0.15, linewidth = 0.5)
  labs(title = "72 Hours",
       x = "Mean CFU per 10 Leaf Discs (Log Transformed)",
       y = "Aphid Mortality at 72 Hours (%)",
       caption = paste("Pearson's Correlation Coefficient:", round(correlation, 2))) +
  scale_x_continuous(trans = "log10") +  # Apply log transformation to x-axis
  scale_fill_manual(values = species_colors) +
  scale_color_manual(values = species_colors) +
  theme_minimal()

epi_virulence_plot_strains
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning: No shared levels found between `names(values)` of the manual scale and the
## data's fill values.
```



Session Information

```
devtools::session_info()
```

```
## - Session info ---------------------------------------------------------------
##  setting  value
##  version  R version 4.4.0 (2024-04-24)
##  os       macOS Ventura 13.4
##  system   x86_64, darwin20
##  ui       X11
##  language (EN)
##  collate  en_US.UTF-8
##  ctype    en_US.UTF-8
##  tz       America/New_York
##  date     2024-06-25
##  pandoc   3.1.11 @ /Applications/RStudio.app/Contents/Resources/app/quarto/bin/tools/x86_64/ (via rma
##
## - Packages -------------------------------------------------------------------
##  ! package       * version date (UTC) lib source
##  P abind           1.4-5   2016-07-21 [?] RSPM
```

```
##  P backports       1.4.1   2021-12-13 [?] CRAN (R 4.4.0)
##  P beeswarm        0.4.0   2021-06-01 [?] CRAN (R 4.4.0)
##  P bit             4.0.5   2022-11-15 [?] CRAN (R 4.4.0)
##  P bit64           4.0.5   2020-08-30 [?] CRAN (R 4.4.0)
##  P broom           1.0.6   2024-05-17 [?] CRAN (R 4.4.0)
##  P broom.helpers   1.15.0  2024-04-05 [?] CRAN (R 4.4.0)
##  P cachem          1.0.8   2023-05-01 [?] CRAN (R 4.4.0)
##  P car             3.1-2   2023-03-30 [?] RSPM
##  P carData         3.0-5   2022-01-06 [?] RSPM
##  P cellranger      1.1.0   2016-07-27 [?] CRAN (R 4.4.0)
##  P cli             3.6.2   2023-12-11 [?] CRAN (R 4.4.0)
##  P colorspace      2.1-0   2023-01-23 [?] CRAN (R 4.4.0)
##  P cowplot       * 1.1.3   2024-01-22 [?] CRAN (R 4.4.0)
##  P crayon          1.5.2   2022-09-29 [?] CRAN (R 4.4.0)
##  P data.table      1.15.4  2024-03-30 [?] CRAN (R 4.4.0)
##  P devtools      * 2.4.5   2022-10-11 [?] RSPM
##  P digest          0.6.35  2024-03-11 [?] CRAN (R 4.4.0)
##  P dplyr         * 1.1.4   2023-11-17 [?] CRAN (R 4.4.0)
##  P ellipsis        0.3.2   2021-04-29 [?] RSPM
##  P emmeans       * 1.10.2  2024-05-20 [?] RSPM
##  P estimability    1.5.1   2024-05-12 [?] RSPM
##  P evaluate        0.23    2023-11-01 [?] CRAN (R 4.4.0)
##  P fansi           1.0.6   2023-12-08 [?] CRAN (R 4.4.0)
##  P farver          2.1.2   2024-05-13 [?] CRAN (R 4.4.0)
##  P fastmap         1.1.1   2023-02-24 [?] CRAN (R 4.4.0)
##  P forcats       * 1.0.0   2023-01-29 [?] CRAN (R 4.4.0)
##  P formatR       * 1.14    2023-01-17 [?] RSPM
##  P fs              1.6.4   2024-04-25 [?] CRAN (R 4.4.0)
##  P generics        0.1.3   2022-07-05 [?] CRAN (R 4.4.0)
##  P ggbeeswarm    * 0.7.2   2023-04-29 [?] CRAN (R 4.4.0)
##  P ggplot2       * 3.5.1   2024-04-23 [?] CRAN (R 4.4.0)
##  P ggpubr        * 0.6.0   2023-02-10 [?] RSPM
##  P ggsignif        0.6.4   2022-10-13 [?] RSPM
##  P ggsurvfit     * 1.1.0   2024-05-08 [?] CRAN (R 4.4.0)
##  P glue            1.7.0   2024-01-09 [?] CRAN (R 4.4.0)
##  P gridExtra     * 2.3     2017-09-09 [?] RSPM
##  P gt              0.10.1  2024-01-17 [?] CRAN (R 4.4.0)
##  P gtable          0.3.5   2024-04-22 [?] CRAN (R 4.4.0)
##  P gtsummary     * 1.7.2   2023-07-15 [?] CRAN (R 4.4.0)
##  P here          * 1.0.1   2020-12-13 [?] CRAN (R 4.4.0)
##  P hms             1.1.3   2023-03-21 [?] CRAN (R 4.4.0)
##  P htmltools       0.5.8.1 2024-04-04 [?] CRAN (R 4.4.0)
##  P htmlwidgets     1.6.4   2023-12-06 [?] CRAN (R 4.4.0)
##  P httpuv          1.6.15  2024-03-26 [?] RSPM
##  P km.ci           0.5-6   2022-04-06 [?] RSPM
##  P KMsurv          0.1-5   2012-12-03 [?] RSPM
##  P knitr         * 1.46    2024-04-06 [?] CRAN (R 4.4.0)
##  P labeling        0.4.3   2023-08-29 [?] CRAN (R 4.4.0)
##  P later           1.3.2   2023-12-06 [?] RSPM
##  P lattice         0.22-6  2024-03-20 [?] CRAN (R 4.4.0)
##  P lifecycle       1.0.4   2023-11-07 [?] CRAN (R 4.4.0)
##  P lubridate     * 1.9.3   2023-09-27 [?] CRAN (R 4.4.0)
##  P magrittr        2.0.3   2022-03-30 [?] CRAN (R 4.4.0)
##  P Matrix          1.7-0   2024-03-22 [?] CRAN (R 4.4.0)
```

```
##  P memoise         2.0.1   2021-11-26 [?] CRAN (R 4.4.0)
##  P mgcv            1.9-1   2023-12-21 [?] CRAN (R 4.4.0)
##  P mime            0.12    2021-09-28 [?] CRAN (R 4.4.0)
##  P miniUI          0.1.1.1 2018-05-18 [?] RSPM
##  P munsell         0.5.1   2024-04-01 [?] CRAN (R 4.4.0)
##  P mvtnorm         1.2-5   2024-05-21 [?] RSPM
##  P nlme            3.1-164 2023-11-27 [?] CRAN (R 4.4.0)
##  P pacman          0.5.1   2019-03-11 [?] CRAN (R 4.4.0)
##  P paletteer     * 1.6.0   2024-01-21 [?] RSPM
##  P pillar          1.9.0   2023-03-22 [?] CRAN (R 4.4.0)
##  P pkgbuild        1.4.4   2024-03-17 [?] RSPM
##  P pkgconfig       2.0.3   2019-09-22 [?] CRAN (R 4.4.0)
##  P pkgload         1.3.4   2024-01-16 [?] RSPM
##  P profvis         0.3.8   2023-05-02 [?] RSPM
##  P promises        1.3.0   2024-04-05 [?] RSPM
##  P purrr         * 1.0.2   2023-08-10 [?] CRAN (R 4.4.0)
##  P R6              2.5.1   2021-08-19 [?] CRAN (R 4.4.0)
##  P RColorBrewer  * 1.1-3   2022-04-03 [?] CRAN (R 4.4.0)
##  P Rcpp            1.0.12  2024-01-09 [?] CRAN (R 4.4.0)
##  P readr         * 2.1.5   2024-01-10 [?] CRAN (R 4.4.0)
##  P readxl        * 1.4.3   2023-07-06 [?] CRAN (R 4.4.0)
##  P rematch2        2.1.2   2020-05-01 [?] CRAN (R 4.4.0)
##  P remotes         2.5.0   2024-03-17 [?] CRAN (R 4.4.0)
##    renv            1.0.7   2024-04-11 [1] CRAN (R 4.4.0)
##  P rlang           1.1.3   2024-01-10 [?] CRAN (R 4.4.0)
##  P rmarkdown       2.26    2024-03-05 [?] CRAN (R 4.4.0)
##  P rprojroot       2.0.4   2023-11-05 [?] CRAN (R 4.4.0)
##  P rstatix         0.7.2   2023-02-01 [?] RSPM
##  P rstudioapi      0.16.0  2024-03-24 [?] CRAN (R 4.4.0)
##  P scales          1.3.0   2023-11-28 [?] CRAN (R 4.4.0)
##  P sessioninfo     1.2.2   2021-12-06 [?] RSPM
##  P shiny           1.8.1.1 2024-04-02 [?] RSPM
##  P stringi         1.8.3   2023-12-11 [?] CRAN (R 4.4.0)
##  P stringr       * 1.5.1   2023-11-14 [?] CRAN (R 4.4.0)
##  P survival      * 3.6-4   2024-04-24 [?] CRAN (R 4.4.0)
##  P survminer     * 0.4.9   2021-03-09 [?] RSPM
##  P survMisc        0.5.6   2022-04-07 [?] RSPM
##  P tibble        * 3.2.1   2023-03-20 [?] CRAN (R 4.4.0)
##  P tidycmprsk    * 1.0.0   2023-10-30 [?] CRAN (R 4.4.0)
##  P tidyr         * 1.3.1   2024-01-24 [?] CRAN (R 4.4.0)
##  P tidyselect      1.2.1   2024-03-11 [?] CRAN (R 4.4.0)
##  P tidyverse     * 2.0.0   2023-02-22 [?] CRAN (R 4.4.0)
##  P timechange      0.3.0   2024-01-18 [?] CRAN (R 4.4.0)
##  P tzdb            0.4.0   2023-05-12 [?] CRAN (R 4.4.0)
##  P urlchecker      1.0.1   2021-11-30 [?] RSPM
##  P usethis       * 2.2.3   2024-02-19 [?] RSPM
##  P utf8            1.2.4   2023-10-22 [?] CRAN (R 4.4.0)
##  P vctrs           0.6.5   2023-12-01 [?] CRAN (R 4.4.0)
##  P vipor           0.4.7   2023-12-18 [?] CRAN (R 4.4.0)
##  P viridis       * 0.6.5   2024-01-29 [?] RSPM
##  P viridisLite   * 0.4.2   2023-05-02 [?] CRAN (R 4.4.0)
##  P vroom           1.6.5   2023-12-05 [?] CRAN (R 4.4.0)
##  P wesanderson   * 0.3.7   2023-10-31 [?] RSPM
##  P withr           3.0.0   2024-01-16 [?] CRAN (R 4.4.0)
```

```
##  P xfun            0.43    2024-03-25 [?] CRAN (R 4.4.0)
##  P xml2            1.3.6   2023-12-04 [?] CRAN (R 4.4.0)
##  P xtable          1.8-4   2019-04-21 [?] RSPM
##  P yaml            2.3.8   2023-12-11 [?] CRAN (R 4.4.0)
##  P zoo             1.8-12  2023-04-13 [?] RSPM
##
##  [1] /Users/zahavahrojer/Desktop/Cornell/Hendry Lab/pseud-epi-growth/renv/library/macos/R-4.4/x86_64-
##  [2] /Users/zahavahrojer/Library/Caches/org.R-project.R/R/renv/sandbox/macos/R-4.4/x86_64-apple-darwi
##
##  P -- Loaded and on-disk path mismatch.
##
## ------------------------------------------------------------------------------
```