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 strain colors Define your strains
strains <- c("194", "200", "204", "205", "215", "216", "220", "221", "227", "228",
    "B728a", "Cit7", "Control", "pisi")

# Generate colors using the 'grDevices::Set 2' palette
set2_colors <- as.character(paletteer_c("grDevices::Dark 3", length(strains)))

# Create a named vector for strain colors, with 'Control' as black
```

```
strain_colors <- setNames(c(set2_colors), strains)

species_colors <- c(`P. fluorescens` = "dodgerblue2", `P. syringae` = "springgreen3",
    `P. paralactis` = "sienna4")
```

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

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.
```

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

```
# 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(24, 48, 72)
km_summary <- summary(km_fit, times = time_points)

# Initialize empty lists to store the results
times_list <- list()
treatment_list <- list()
surv_prob_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])
        } else {
            times_list <- c(times_list, t)
            treatment_list <- c(treatment_list, treatment_name)
            surv_prob_list <- c(surv_prob_list, NA)
        }
    }
}

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

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

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

```
##    time treatment  surv_prob
## 1    24       194 0.77891156
## 2    48       194 0.18707483
## 3    72       194 0.12244898
## 4    24       200 0.53159851
## 5    48       200 0.05576208
## 6    72       200 0.02230483
## 7    24       204 0.54929577
## 8    48       204 0.08450704
## 9    72       204 0.05281690
## 10   24       205 0.56949153
## 11   48       205 0.11525424
## 12   72       205 0.07118644
## 13   24       215 0.79513889
## 14   48       215 0.44791667
## 15   72       215 0.22222222
## 16   24       216 0.56250000
## 17   48       216 0.27430556
## 18   72       216 0.15625000
## 19   24       220 0.35135135
## 20   48       220 0.19256757
## 21   72       220 0.17229730
## 22   24       221 0.65543071
## 23   48       221 0.21722846
## 24   72       221 0.09363296
## 25   24       227 0.40000000
## 26   48       227 0.22033898
## 27   72       227 0.16949153
## 28   24       228 0.65671642
## 29   48       228 0.15298507
```

```
## 30   72       228 0.10447761
## 31   24     B728a 0.68041237
## 32   48     B728a 0.40549828
## 33   72     B728a 0.10996564
## 34   24      Cit7 0.75609756
## 35   48      Cit7 0.37630662
## 36   72      Cit7 0.17073171
## 37   24   Control 0.94777397
## 38   48   Control 0.87243151
## 39   72   Control 0.81678082
## 40   24      pisi 0.88250653
## 41   48      pisi 0.79634465
## 42   72      pisi 0.74151436
```

```r
# subset data by time
surv_probs_72 <- surv_probs %>%
    filter(time == 72)

# If you need to save it to a file, you can use the following command
# write.csv(surv_probs, 'survival_probabilities.csv', row.names = FALSE)
```

Post-hoc test for survival

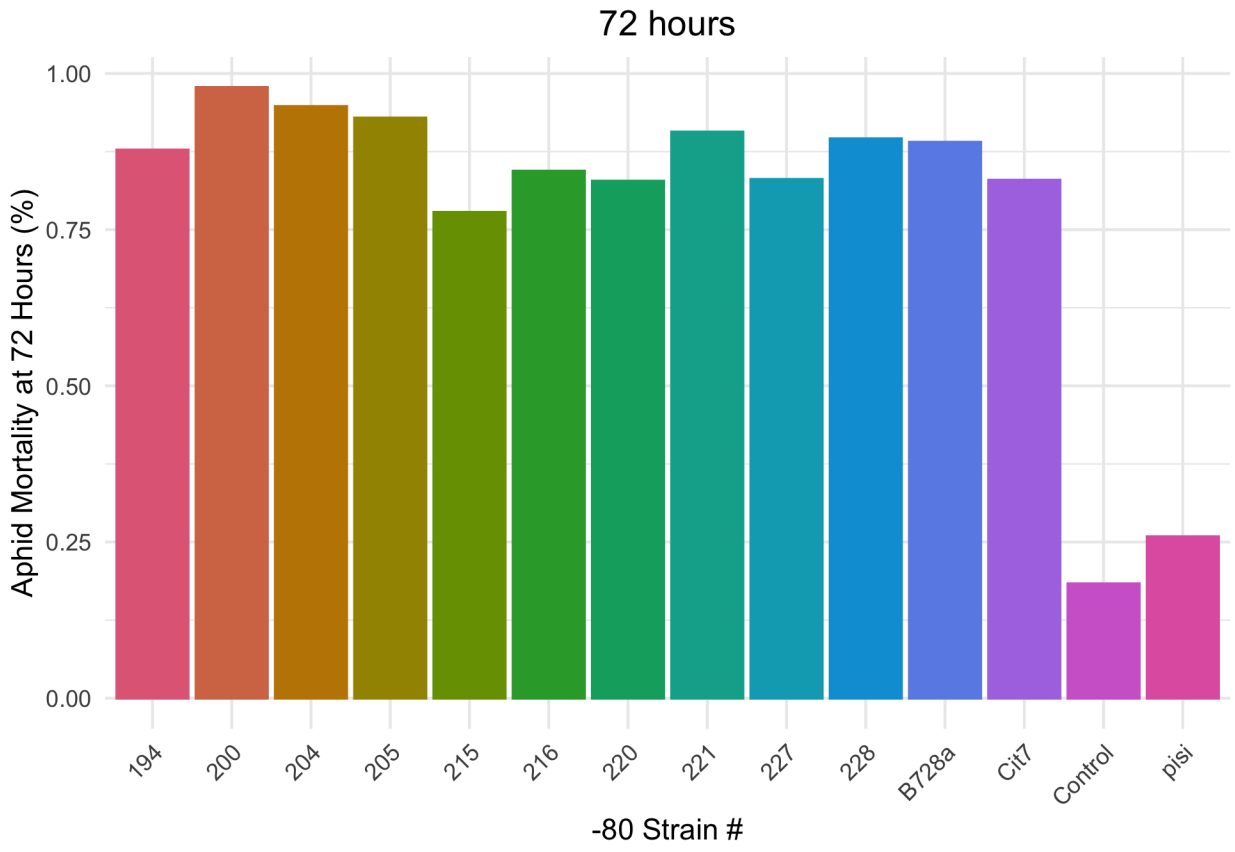
```r
# Perform pairwise log-rank tests between treatment groups and the control
# group
pairwise_tests <- pairwise_survdiff(Surv(time, censored) ~ treatment, data = aphid_virulence_data)

# 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

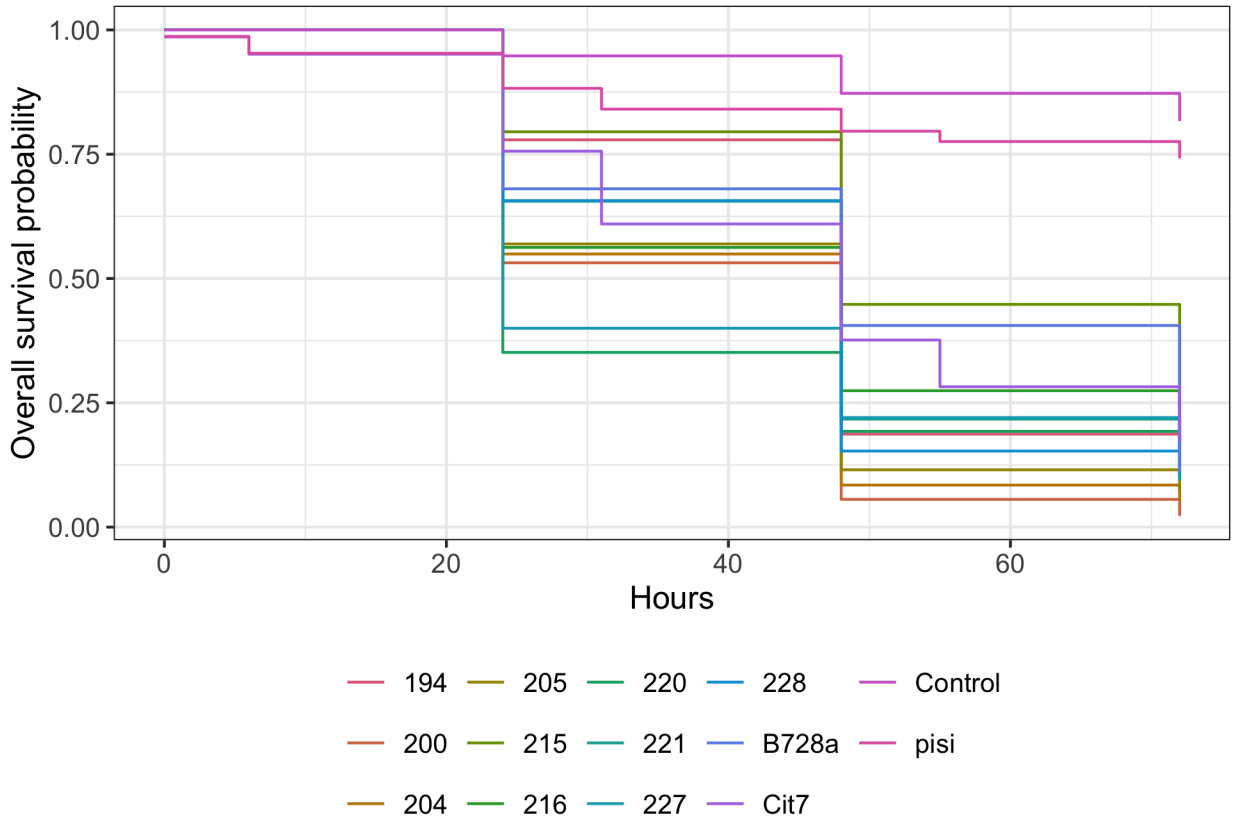
```
surv_plot_72 <- ggplot(data = surv_probs_72, aes(x = treatment, y = (1 - surv_prob),
    color = treatment, fill = treatment)) + geom_col() + labs(title = "72 hours",
    x = "-80 Strain #", y = "Aphid Mortality at 72 Hours (%)") + theme_minimal() +
    scale_fill_manual(values = strain_colors) + scale_color_manual(values = strain_colors) +
    theme(plot.title = element_text(hjust = 0.5), axis.text.x = element_text(angle = 45,
        hjust = 1), legend.position = "none")

surv_plot_72
```



Make Kaplan-Meier Plot

Cohort Survival Curve

```
survfit2(Surv(time, censored) ~ treatment, data = aphid_virulence_data) %>%
    ggsurvfit() + labs(x = "Hours", y = "Overall survival probability") + scale_color_manual(values = s
```



Epiphytic Growth Analysis

Calculate mean/variance epiphytic growth ability

```
# Replace NA with a lower value or remove them for visualization Remove rows
# with NA in CFU_per_10_leafdiscs
epi_growth_clean <- pseud_epi_growth_2024summer_R %>%
    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
```

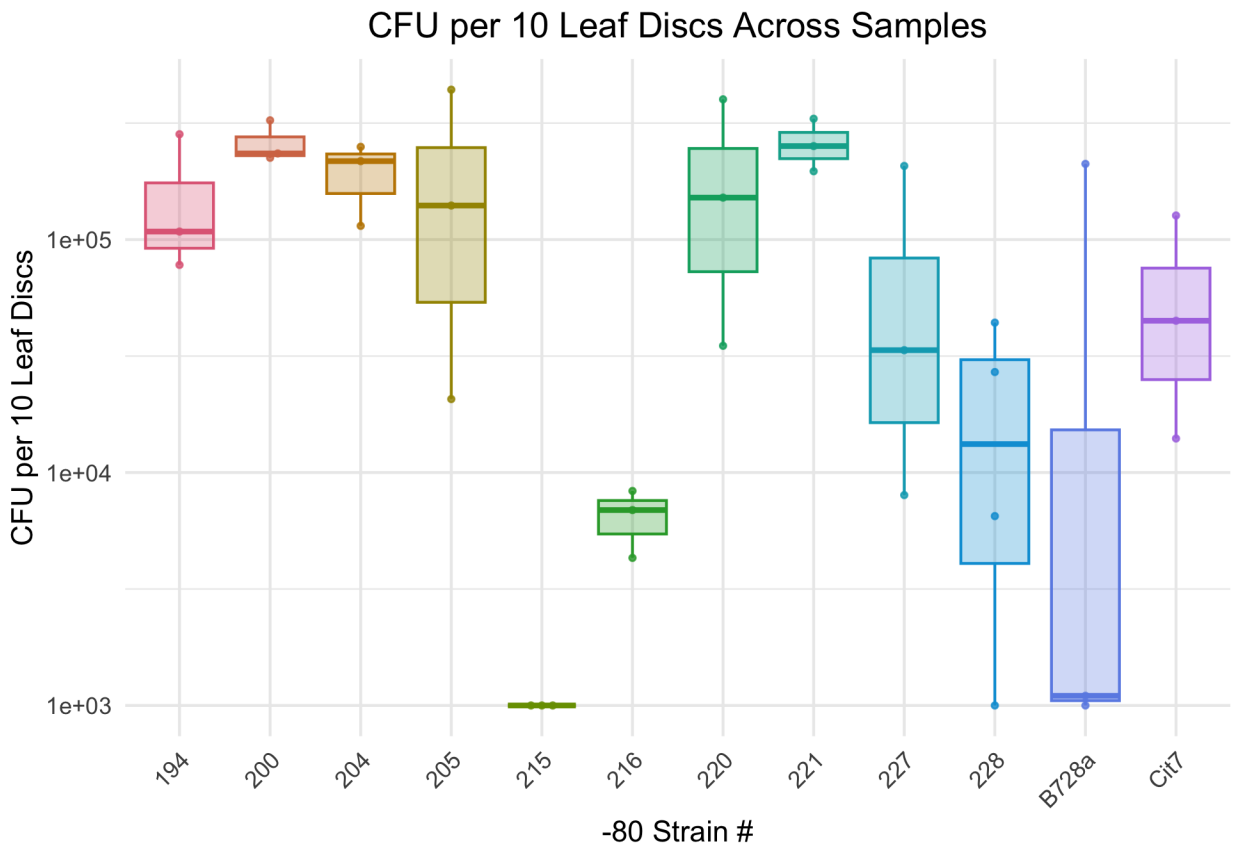
```
# Subset data to remove unfinished strains and extract the letter part from the
# 'plant_rep' column
epi_growth_clean <- epi_growth_clean %>%
    filter(!strain %in% c("pisi")) %>%
    mutate(plant_rep_letter = substr(plant_rep, 1, 1))

# Calculate the mean and SD CFU per strain for each plant rep letter and retain
# the specified columns
```

```r
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
```

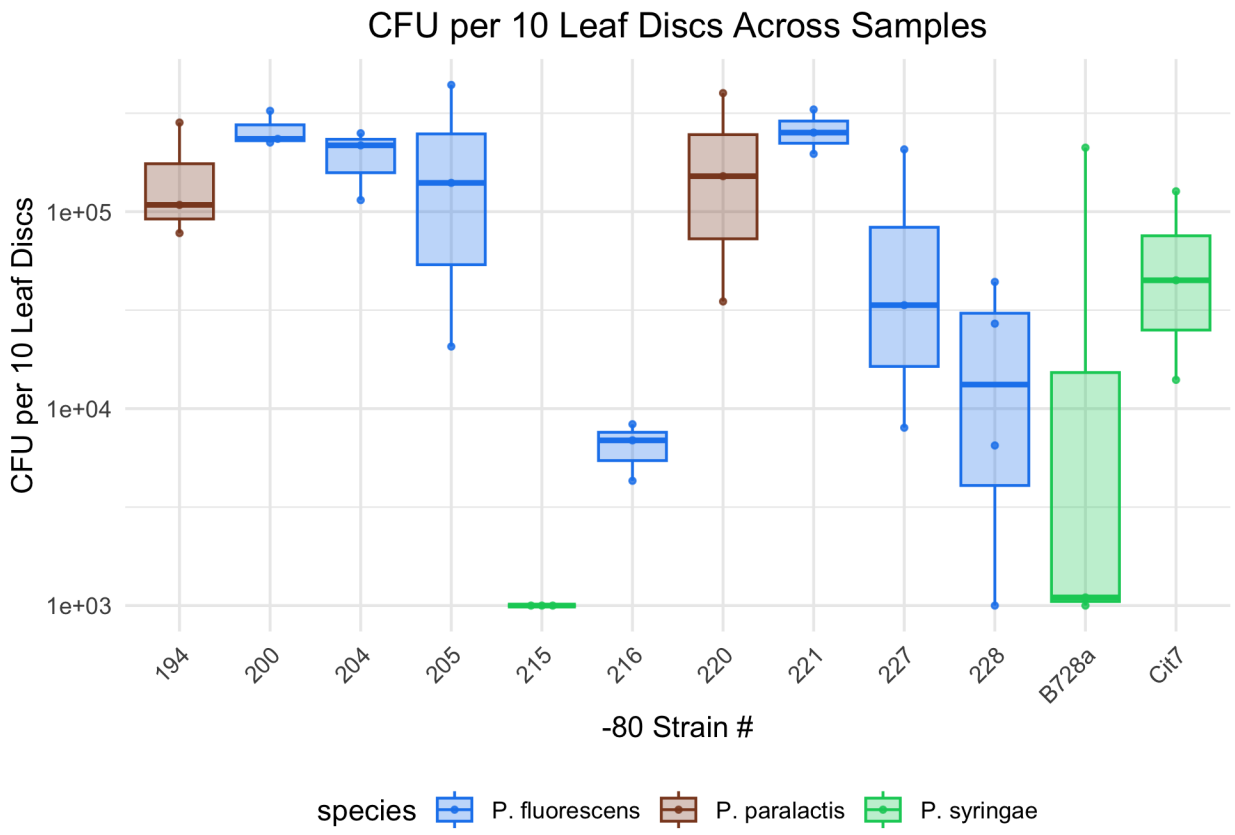
```
## # A tibble: 12 x 8
##    strain mean_CFU_per_10_leafdiscs sd_CFU sample person block species plant_rep
##    <chr>                      <dbl>  <dbl> <chr>  <chr>  <chr> <chr>   <chr>
##  1 194                      156472. 1.43e5 194-A1 Havi   2-1   P. par~ A1
##  2 200                      261214. 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
```

Plot Epiphytic Growth

```r
epi_growth_strain <- ggplot(data = epi_growth_mean_per_rep, aes(x = strain, y = mean_CFU_per_10_leafdis
  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") +
  theme_minimal() +
  scale_fill_manual(values = strain_colors) +
  scale_color_manual(values = strain_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 = "none")

epi_growth_strain
```




```
epi_growth_species <- ggplot(data = epi_growth_mean_per_rep, aes(x = strain, y = mean_CFU_per_10_leafdis
  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") +
  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
```



Epiphutic growth stats

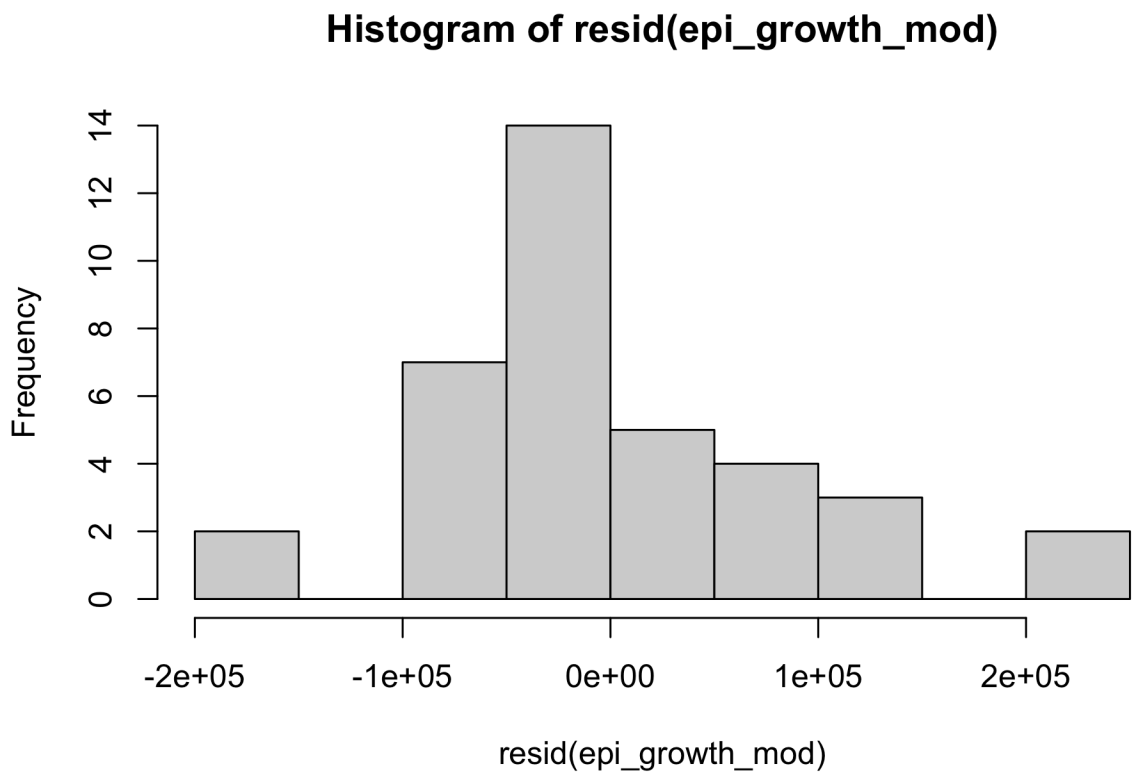
```
epi_growth_mod = lm(mean_CFU_per_10_leafdiscs ~ strain, data = epi_growth_mean_per_rep)

emmeans(epi_growth_mod, pairwise ~ strain)
```

```
## $emmeans
##  strain emmean    SE df lower.CL upper.CL
##  194    156472 60399 25    32079   280866
##  200    261214 60399 25   136820   385608
##  204    193911 60399 25    69518   318305
##  205    200222 60399 25    75829   324616
##  215      1000 60399 25  -123394   125394
##  216      6511 60399 25  -117882   130905
##  220    195467 60399 25    71073   319860
##  221    259556 60399 25   135162   383949
##  227     82872 60399 25   -41521   207266
##  228     19625 52307 25   -88103   127353
##  B728a   71144 60399 25   -53249   195538
##  Cit7    61906 60399 25   -62488   186299
##
## Confidence level used: 0.95
##
```

```
## $contrasts
##  contrast     estimate    SE df t.ratio p.value
##  194 - 200    -104742 85417 25  -1.226  0.9813
##  194 - 204     -37439 85417 25  -0.438  1.0000
##  194 - 205     -43750 85417 25  -0.512  1.0000
##  194 - 215     155472 85417 25   1.820  0.7929
##  194 - 216     149961 85417 25   1.756  0.8259
##  194 - 220     -38994 85417 25  -0.457  1.0000
##  194 - 221    -103083 85417 25  -1.207  0.9834
##  194 - 227      73600 85417 25   0.862  0.9990
##  194 - 228     136847 79900 25   1.713  0.8463
##  194 - B728a    85328 85417 25   0.999  0.9963
##  194 - Cit7     94567 85417 25   1.107  0.9914
##  200 - 204      67303 85417 25   0.788  0.9995
##  200 - 205      60992 85417 25   0.714  0.9998
##  200 - 215     260214 85417 25   3.046  0.1529
##  200 - 216     254703 85417 25   2.982  0.1725
##  200 - 220      65747 85417 25   0.770  0.9996
##  200 - 221       1658 85417 25   0.019  1.0000
##  200 - 227     178342 85417 25   2.088  0.6349
##  200 - 228     241589 79900 25   3.024  0.1596
##  200 - B728a   190069 85417 25   2.225  0.5480
##  200 - Cit7    199308 85417 25   2.333  0.4808
##  204 - 205      -6311 85417 25  -0.074  1.0000
##  204 - 215     192911 85417 25   2.258  0.5271
##  204 - 216     187400 85417 25   2.194  0.5678
##  204 - 220      -1556 85417 25  -0.018  1.0000
##  204 - 221     -65644 85417 25  -0.769  0.9996
##  204 - 227     111039 85417 25   1.300  0.9715
##  204 - 228     174286 79900 25   2.181  0.5758
##  204 - B728a   122767 85417 25   1.437  0.9441
##  204 - Cit7    132006 85417 25   1.545  0.9127
##  205 - 215     199222 85417 25   2.332  0.4814
##  205 - 216     193711 85417 25   2.268  0.5213
##  205 - 220       4756 85417 25   0.056  1.0000
##  205 - 221     -59333 85417 25  -0.695  0.9999
##  205 - 227     117350 85417 25   1.374  0.9584
##  205 - 228     180597 79900 25   2.260  0.5260
##  205 - B728a   129078 85417 25   1.511  0.9237
##  205 - Cit7    138317 85417 25   1.619  0.8861
##  215 - 216      -5511 85417 25  -0.065  1.0000
##  215 - 220    -194467 85417 25  -2.277  0.5158
##  215 - 221    -258556 85417 25  -3.027  0.1586
##  215 - 227     -81872 85417 25  -0.959  0.9974
##  215 - 228     -18625 79900 25  -0.233  1.0000
##  215 - B728a   -70144 85417 25  -0.821  0.9993
##  215 - Cit7    -60906 85417 25  -0.713  0.9998
##  216 - 220    -188956 85417 25  -2.212  0.5563
##  216 - 221    -253044 85417 25  -2.962  0.1788
##  216 - 227     -76361 85417 25  -0.894  0.9986
##  216 - 228     -13114 79900 25  -0.164  1.0000
##  216 - B728a   -64633 85417 25  -0.757  0.9997
##  216 - Cit7    -55394 85417 25  -0.649  0.9999
##  220 - 221     -64089 85417 25  -0.750  0.9997
```

```
##  220 - 227      112594 85417 25   1.318  0.9686
##  220 - 228      175842 79900 25   2.201  0.5635
##  220 - B728a    124322 85417 25   1.455  0.9394
##  220 - Cit7     133561 85417 25   1.564  0.9066
##  221 - 227      176683 85417 25   2.068  0.6470
##  221 - 228      239931 79900 25   3.003  0.1659
##  221 - B728a    188411 85417 25   2.206  0.5603
##  221 - Cit7     197650 85417 25   2.314  0.4927
##  227 - 228       63247 79900 25   0.792  0.9995
##  227 - B728a     11728 85417 25   0.137  1.0000
##  227 - Cit7      20967 85417 25   0.245  1.0000
##  228 - B728a    -51519 79900 25  -0.645  0.9999
##  228 - Cit7     -42281 79900 25  -0.529  1.0000
##  B728a - Cit7     9239 85417 25   0.108  1.0000
##
## P value adjustment: tukey method for comparing a family of 12 estimates
```

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



Combine epiphytic and virulence data

```
# Assuming strain_stats has a column 'strain' and surv_probs has a column
# 'treatment' Rename columns if necessary to match the key for joining
```

```r
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)
```

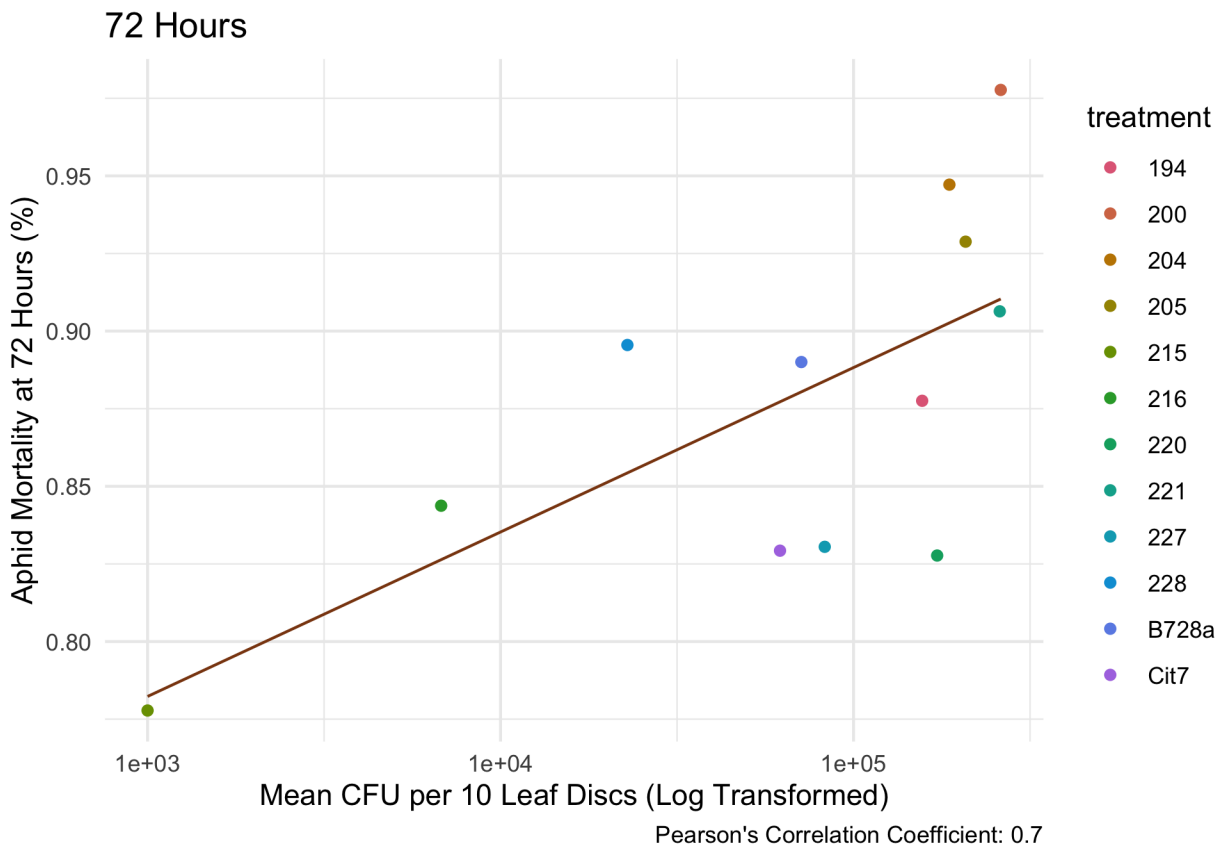
```
## # A tibble: 36 x 10
##    treatment mean_CFU_per_10_leaf~1 sd_CFU sample person block species plant_rep
##    <chr>                      <dbl>  <dbl> <chr>  <chr>  <chr> <chr>   <chr>
##  1 194                      156472. 1.43e5 194-A1 Havi   2-1   P. par~ A1
##  2 194                      156472. 1.43e5 194-A1 Havi   2-1   P. par~ A1
##  3 194                      156472. 1.43e5 194-A1 Havi   2-1   P. par~ A1
##  4 200                      261214. 1.81e5 200-A1 Havi   2-6   P. flu~ A1
##  5 200                      261214. 1.81e5 200-A1 Havi   2-6   P. flu~ A1
##  6 200                      261214. 1.81e5 200-A1 Havi   2-6   P. flu~ A1
##  7 204                      186888. 1.89e5 204-A1 Havi   2-3   P. flu~ A1
##  8 204                      186888. 1.89e5 204-A1 Havi   2-3   P. flu~ A1
##  9 204                      186888. 1.89e5 204-A1 Havi   2-3   P. flu~ A1
## 10 205                      207750  2.40e5 205-A1 Sara   3     P. flu~ A1
## # i 26 more rows
## # i abbreviated name: 1: mean_CFU_per_10_leafdiscs
## # i 2 more variables: time <dbl>, surv_prob <dbl>
```

```r
subset_data_72 <- epi_virulence_data %>%
    filter(time == 72)

# Calculate correlation coefficient between survival probability and epiphytic
# growth ability
correlation_72 <- -1 * cor(subset_data_72$surv_prob, subset_data_72$mean_CFU_per_10_leafdiscs,
    method = "pearson")
```

Plot it for different times

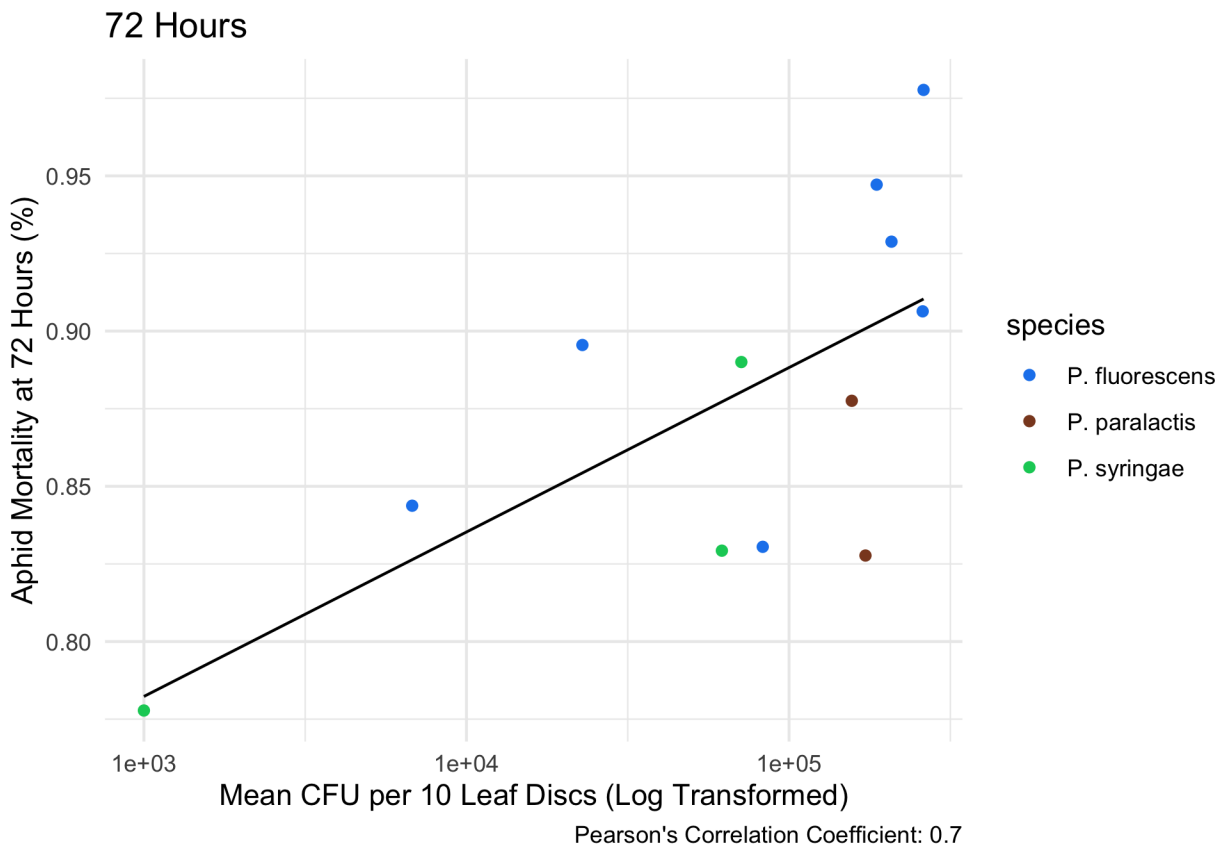
```r
# Create scatter plot for 72 hours
epi_virulence_plot_strains <- ggplot(subset_data_72, aes(x = mean_CFU_per_10_leafdiscs, y = 1-surv_prob
  geom_point(aes(color = treatment)) +
  geom_smooth(method = "lm", se = FALSE, color = "chocolate4", linewidth = 0.5) +
  labs(title = "72 Hours",
       x = "Mean CFU per 10 Leaf Discs (Log Transformed)",
       y = "Aphid Mortality at 72 Hours (%)",
       caption = paste("Pearson's Correlation Coefficient:", round(correlation_72, 2))) +
  scale_x_continuous(trans = "log10") +  # Apply log transformation to x-axis
  scale_color_manual(values = strain_colors) +
  theme_minimal()

epi_virulence_plot_strains
```

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




```
epi_virulence_plot_species <- ggplot(subset_data_72, aes(x = mean_CFU_per_10_leafdiscs, y = (1-surv_prob
  geom_point(aes(color = species)) +
  geom_smooth(method = "lm", se = FALSE, color = "black", 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_72, 2))) +
  scale_color_manual(values = species_colors) +
  scale_x_continuous(trans = "log10") +  # Apply log transformation to x-axis
    theme_minimal()

epi_virulence_plot_species
```

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



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     2024-06-18
##  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 prismatic       1.1.2   2024-04-10 [?] 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-darw
##
##  P -- Loaded and on-disk path mismatch.
##
## ------------------------------------------------------------------------------
```