Introduction to using gcplyr

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Getting started

`gcplyr` is a package that implements a number of functions to make it easier to import, manipulate, and analyze microbial growth from data collected in multiwell plate readers ("growth curves"). Without `gcplyr`, importing and analyzing plate reader data can be a complicated process that has to be tailored for each experiment, requiring many lines of code. With `gcplyr` many of those steps are now just a single line of code.

This document gives an introduction of how to use `gcplyr` for each step of a growth curve analysis.

To get started, you need your growth curve data file saved to your computer (.csv, .xls, or .xlsx).

Users often want to combine their data with some information on the experimental design of their plate(s). You can save this information into a tabular file as well, or you can just keep it handy to enter directly in `R` (see `vignette("incorporate_designs")`).

Let's get started by loading `gcplyr`. We're also going to load a couple other packages we'll need.

```r
library(gcplyr)

library(dplyr)
library(ggplot2)
```

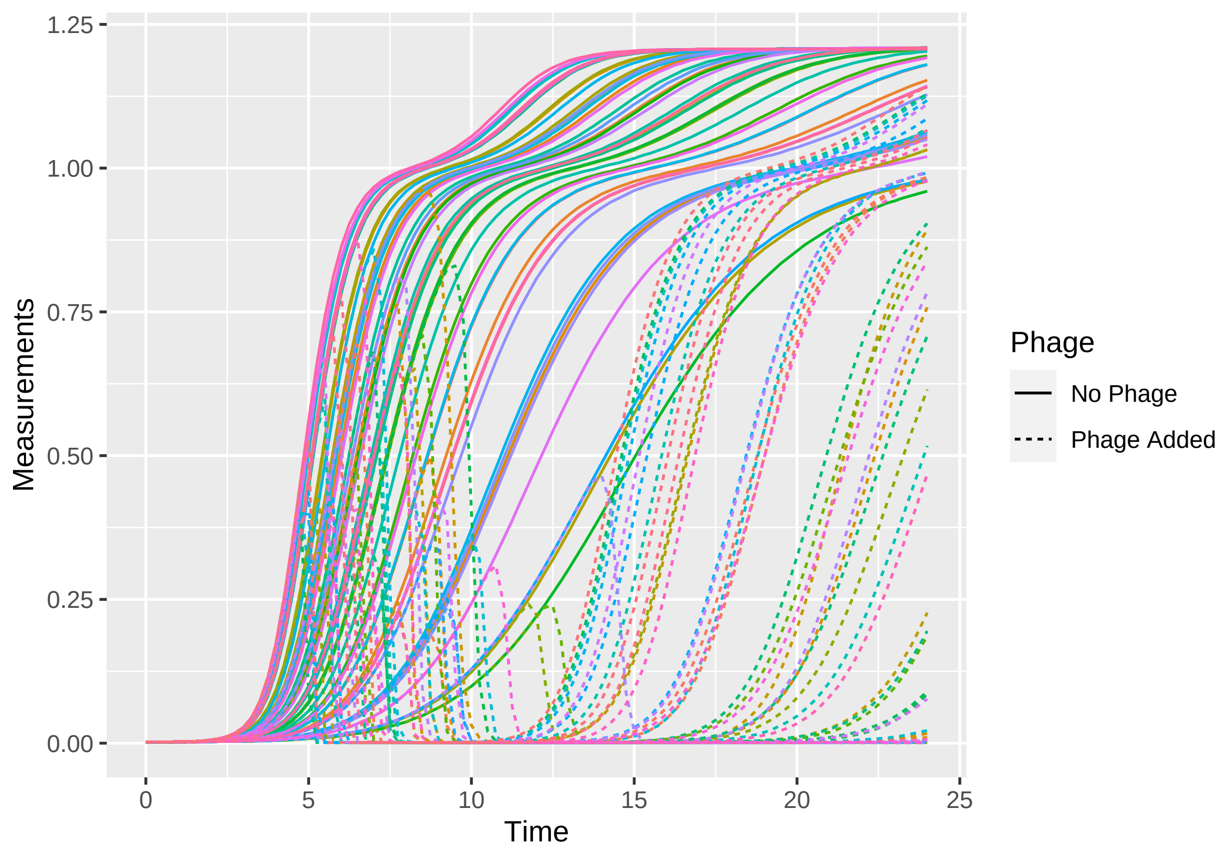
A quick demo of `gcplyr`

Before digging into the details, here's a simple demonstration of what a final `gcplyr` script can look like. This script:

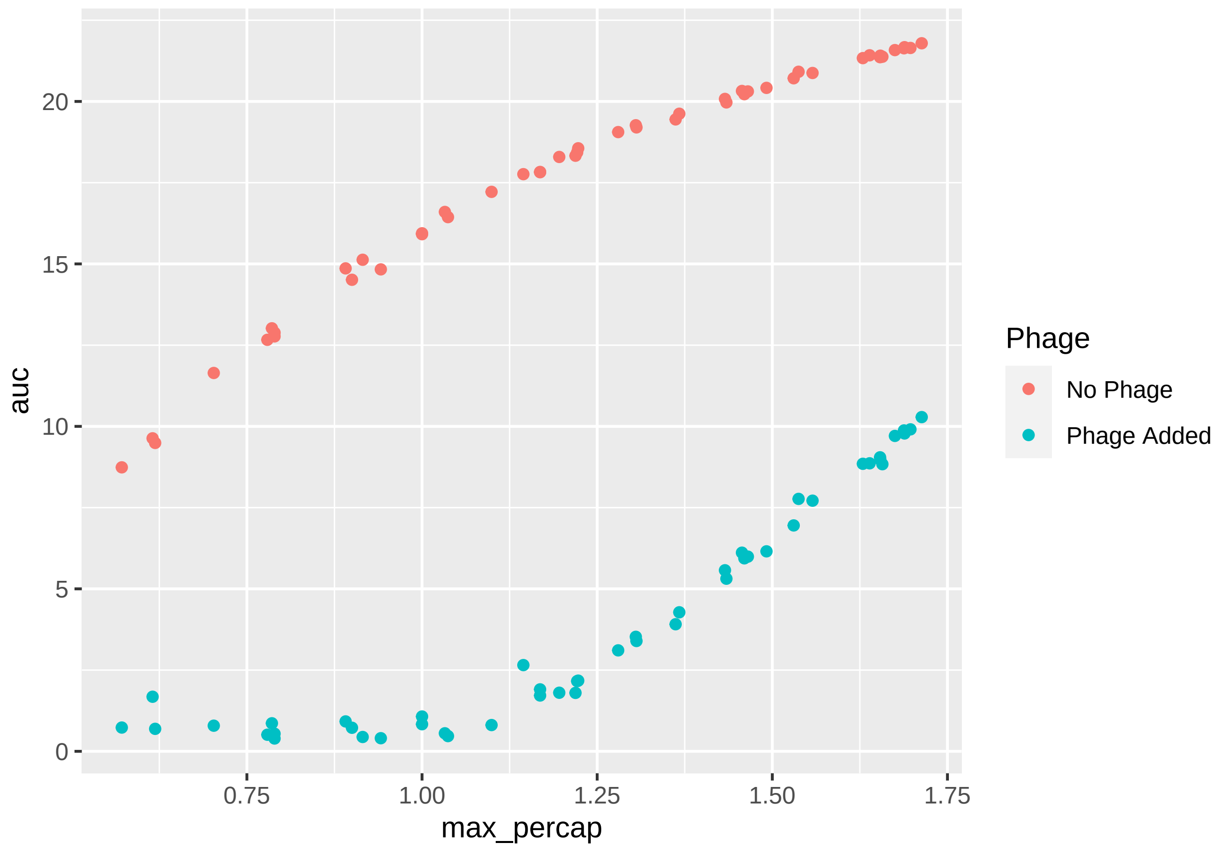
1. imports data from files created by a plate reader
2. combines it with design files created by the user
3. calculates the maximum growth rate and area-under-the-curve

Don't worry about understanding all the details of how the code works right now. Each of these steps is explained in depth in later articles.

```r
# Read in our data
#  (our plate reader data is saved in "widedata.csv")
data_wide <- read_wides(files = "widedata.csv")

# Transform our data to be tidy-shaped
data_tidy <-
  trans_wide_to_tidy(wides = data_wide, id_cols = c("file", "Time"))

# Convert our time into hours
data_tidy$Time <- as.numeric(data_tidy$Time)/3600

# Import our designs
#  (saved in the files Bacteria_strain.csv and Phage.csv)
designs <- import_blockdesigns(files = c("Bacteria_strain.csv", "Phage.csv"))

# Merge our designs and data
data_merged <- merge_dfs(data_tidy, designs)
#> Joining with `by = join_by(Well)`

# Plot the data
ggplot(data = data_merged,
       aes(x = Time, y = Measurements, color = Well)) +
  geom_line(aes(lty = Phage)) +
  guides(color = "none")
```



```
# Voila! 8 lines of code and all your data is imported & plotted!

# Calculate the per-capita growth rate over time in each well
data_merged <- mutate(
  group_by(data_merged, Well),
  percap_deriv = calc_deriv(y = Measurements, x = Time, percapita = TRUE,
                            blank = 0, window_width_n = 5))

# Calculate two common metrics of bacterial growth:
#  the maximum growth rate, saving it to a column named max_percap
#  the area-under-the-curve, saving it to a column named 'auc'
data_sum <- summarize(
  group_by(data_merged, Well, Bacteria_strain, Phage),
  max_percap = max(percap_deriv, na.rm = TRUE),
  auc = auc(y = Measurements, x = as.numeric(Time)))
#> `summarise()` has grouped output by 'Well', 'Bacteria_strain'. You can override
#> using the `.groups` argument.

# Print some of the max growth rates and auc's
head(data_sum)
#> # A tibble: 6 x 5
#> # Groups:   Well, Bacteria_strain [6]
#>   Well  Bacteria_strain Phage       max_percap   auc
#>   <chr> <chr>           <chr>            <dbl> <dbl>
#> 1 A1    Strain 1        No Phage          1.00  15.9
#> 2 A10   Strain 4        Phage Added      1.43   5.57
#> 3 A11   Strain 5        Phage Added      1.47   5.99
#> 4 A12   Strain 6        Phage Added      0.789  0.395
#> 5 A2    Strain 2        No Phage         1.31  19.3
#> 6 A3    Strain 3        No Phage         0.915 15.1

# Plot the results for max growth rate and area under the curve in
#  presence vs absence of phage
ggplot(data = data_sum,
       aes(x = max_percap, y = auc, color = Phage)) +
  geom_point()
```



What's next?

Generally, working with `gcplyr` will follow a number of steps, each of which is likely to be only one or a few lines of code in your final script. We've explained each of these steps in a page linked below. To start, we'll learn how to import our data into `R` and transform it into a convenient format.

1. Introduction: `vignette("gcplyr")`
2. **Importing and transforming data: `vignette("import_transform")`**
3. Incorporating design information: `vignette("incorporate_designs")`
4. Pre-processing and plotting your data: `vignette("preprocess_plot")`
5. Processing your data: `vignette("process")`

6. Analyzing your data: `vignette("analyze")`
7. Dealing with noise: `vignette("noise")`
8. Statistics, merging other data, and other resources: `vignette("conclusion")`