Pre-processing and plotting data

Mike Blazanin

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So far, we've imported and transformed our measures, then combined them with our design information. Now we're going to do some final pre-processing steps and show how to easily plot our data with `ggplot`.

If you haven't already, load the necessary packages.

```
library(gcplyr)

library(dplyr)
library(ggplot2)
library(lubridate)
#>
#> Attaching package: 'lubridate'
#> The following objects are masked from 'package:base':
#>
#>     date, intersect, setdiff, union
```

```
# This code was previously explained
# Here we're re-running it so it's available for us to work with
example_tidydata <- trans_wide_to_tidy(example_widedata_noiseless,
                                       id_cols = "Time")
ex_dat_mrg <- merge_dfs(example_tidydata, example_design_tidy)
#> Joining with `by = join_by(Well)`
```

Pre-processing

Now that we have our data and designs merged, we're almost ready to start processing and analyzing them. However, first we need to carry out any necessary pre-processing steps, like excluding wells that were contaminated or empty, and converting time formats to numeric.

Pre-processing: excluding data

In some cases, we want to remove some of the wells from our growth curves data before we carry on with downstream analyses. For instance, they may have been left empty, contained negative controls, or were contaminated. We can use `dplyr`'s `filter` function to remove those wells that meet criteria we want to exclude.

For instance, let's imagine that we realized that we put the wrong media into Well B1, and that strain 13 was contaminated. To exclude them from our analyses, we can simply:

```
example_data_and_designs_filtered <-
  filter(ex_dat_mrg,
         Well != "B1", Bacteria_strain != "Strain 13")
head(example_data_and_designs_filtered)
#>   Time Well Measurements Bacteria_strain    Phage
#> 1    0   A1        0.002        Strain 1 No Phage
#> 2    0   D1        0.002       Strain 19 No Phage
#> 3    0   E1        0.002       Strain 25 No Phage
#> 4    0   F1        0.002       Strain 31 No Phage
#> 5    0   G1        0.002       Strain 37 No Phage
#> 6    0   H1        0.002       Strain 43 No Phage
```

Pre-processing: converting dates & times into numeric

Growth curve data produced by a plate reader often encodes the timestamp information as a string (e.g. "2:45:11" for 2 hours, 45 minutes, and 11 seconds), while downstream analyses need timestamp information as a numeric (e.g. number of seconds elapsed). Luckily, others have written great packages that make it easy to convert from common date-time text formats into plain numeric formats. Here, we'll see how to use `lubridate` to do so:

First we have to create a data frame with time saved as it might be by a plate reader.

```
ex_dat_mrg <- make_example(vignette = 4, example = 1)
#> Joining with `by = join_by(Well)`

head(ex_dat_mrg)
#>      Time Well Measurements Bacteria_strain    Phage
#> 1 0:00:00   A1        0.002        Strain 1 No Phage
```

```
#> 2 0:00:00   B1         0.002        Strain 7 No Phage
#> 3 0:00:00   C1         0.002       Strain 13 No Phage
#> 4 0:00:00   D1         0.002       Strain 19 No Phage
#> 5 0:00:00   E1         0.002       Strain 25 No Phage
#> 6 0:00:00   F1         0.002       Strain 31 No Phage
```

We can see that our `Time` aren't written in an easy numeric. Instead, they're in a format that's easy for a human to understand (but unfortunately not very usable for analysis).

Let's use `lubridate` to convert this text into a usable format. `lubridate` has a whole family of functions that can parse text with hour, minute, and/or second components. You can use `hms` if your text contains hour, minute, and second information, `hm` if it only contains hour and minute information, and `ms` if it only contains minute and second information.

Once `hms` has parsed the text, we'll use `time_length` to convert the output of `hms` into a pure numeric value. By default, `time_length` returns in units of seconds, but you can change that by changing the `unit` argument to `time_length`.

```
# We have previously loaded lubridate, but if you haven't already then
# make sure to add the line:
#    library(lubridate)

ex_dat_mrg$Time <- time_length(hms(ex_dat_mrg$Time), unit = "hour")

head(ex_dat_mrg)
#>   Time Well Measurements Bacteria_strain    Phage
#> 1    0   A1        0.002        Strain 1 No Phage
#> 2    0   B1        0.002        Strain 7 No Phage
#> 3    0   C1        0.002       Strain 13 No Phage
#> 4    0   D1        0.002       Strain 19 No Phage
#> 5    0   E1        0.002       Strain 25 No Phage
#> 6    0   F1        0.002       Strain 31 No Phage
```

And now we can see that we've gotten nice numeric `Time` values! So we can proceed with the next steps of the analysis.

Plotting your data

Once your data has been merged and times have been converted to numeric, we can easily plot our data using the `ggplot2` package. That's because `ggplot2` was specifically built on the assumption that data would be tidy-shaped, which ours is! We won't go into depth on how to use `ggplot` here, but there are three main commands to the plot below:

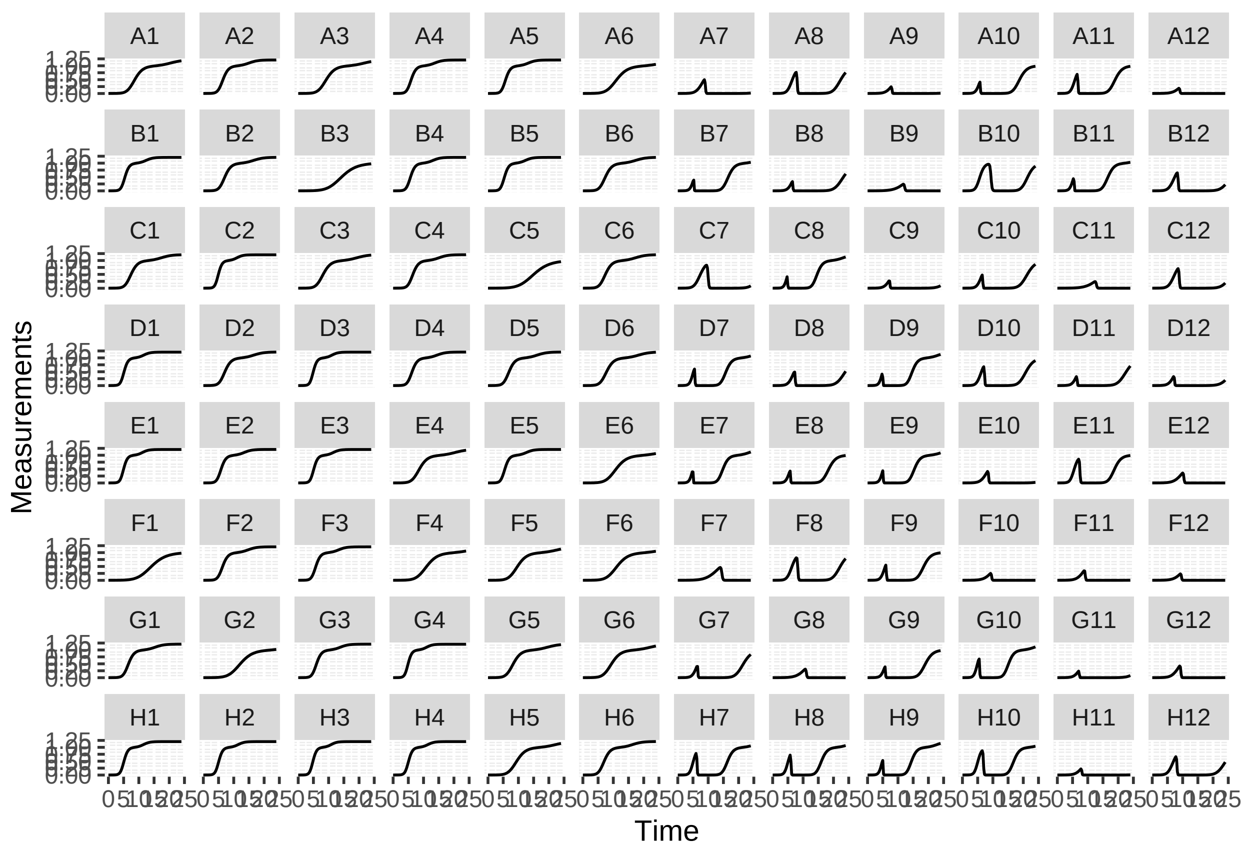
- `ggplot` - the ggplot function is where you specify the `data.frame` you would like to use and the *aes*thetics of the plot (the x and y axes you would like)
- `geom_line` - tells `ggplot` how we would like to plot the data, in this case with a line (another common `geom` for time-series data is `geom_point`)
- `facet_wrap` - tells `ggplot` to plot each Well in a separate facet

We'll be using this format to plot our data throughout the remainder of this vignette

```r
# We have previously loaded ggplot2, but if you haven't already then
# make sure to add the line:
#     library(ggplot2)

# First, we'll reorder the Well levels so they plot in the correct order
ex_dat_mrg$Well <-
  factor(ex_dat_mrg$Well,
         levels = paste0(rep(LETTERS[1:8], each = 12), 1:12))

ggplot(data = ex_dat_mrg, aes(x = Time, y = Measurements)) +
  geom_line() +
  facet_wrap(~Well, nrow = 8, ncol = 12)
```



Generally speaking, **from here on you should plot your data frequently**, and in every way you can think of! **After every processing and analysis step, visualize both the input data and output data** to understand what the processing and analysis steps are doing and whether they are the right choices for your particular data (this vignette will be doing that too!)

What's next?

Now that you've pre-processed and visualized your data, it's time to process (in most cases) and analyze (pretty much always) it!

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