

Importing and transforming data

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Where are we so far?

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3. Incorporating design information: `vignette("incorporate_designs")`
4. Pre-processing and plotting your data: `vignette("preprocess_plot")`

5. Processing your data: `vignette("process")`
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8. Statistics, merging other data, and other resources: `vignette("conclusion")`

Previously, we gave an overview and quick demonstration of what `gcplyr` can do. Here, we're going to start going into more detail just how you can carry out each step of an analysis with your own data.

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

```
library(gcplyr)
```

Data layouts

With the previous demonstration in mind, let's dig into some more details of how your input data might be organized and what `gcplyr` does. Growth curve data and design elements can be organized in one of three different tabular layouts: block-shaped, wide-shaped, and tidy-shaped, described below.

Tidy-shaped data is the best layout for analyses, but most plate readers output block-shaped or wide-shaped data, and most user-created design files will be block-shaped. Thus, `gcplyr` works by reshaping block-shaped into wide-shaped data, and wide-shaped data into tidy-shaped data, then running any analyses.

So, what are these three data layouts, and how can you tell which of them your data is in?

Block-shaped

In block-shaped data, the organization of the data corresponds directly with the layout of the physical multi-well plate it was generated from. For instance, a data point from the third row and fourth column of the `data.frame` will be from the well in the third row and fourth column in the physical plate. Because of this, a timeseries of growth curve data that is block-shaped will consist of many separate block-shaped `data.frames`, each corresponding to a single timepoint.

For example, here is a block-shaped `data.frame` of a 96-well plate (with “...” indicating Columns 4 - 10, not shown). In this example, all the data shown would be from a single timepoint.

	Column 1	Column 2	Column 3	...	Column 11	Column 12
Row A	0.060	0.083	0.086	...	0.082	0.085
Row B	0.099	0.069	0.065	...	0.066	0.078
Row C	0.081	0.071	0.070	...	0.064	0.084
Row D	0.094	0.075	0.065	...	0.067	0.087
Row E	0.052	0.054	0.072	...	0.079	0.065
Row F	0.087	0.095	0.091	...	0.075	0.058
Row G	0.095	0.079	0.099	...	0.063	0.075
Row H	0.056	0.069	0.070	...	0.053	0.078

Wide-shaped

In wide-shaped data, each column of the dataframe corresponds to a single well from the plate, and each row of the dataframe corresponds to a single timepoint. Typically, headers contain the well names.

For example, here is a wide-shaped dataframe of a 96-well plate (here, “...” indicates the 91 columns A4 - H10, not shown). Each row of this dataframe corresponds to a single timepoint.

Time	A1	A2	A3	...	H11	H12
0	0.060	0.083	0.086	...	0.053	0.078
1	0.012	0.166	0.172	...	0.106	0.156
2	0.024	0.332	0.344	...	0.212	0.312
3	0.048	0.664	0.688	...	0.424	0.624
4	0.096	1.128	0.976	...	0.848	1.148
5	0.162	1.256	1.152	...	1.096	1.296
6	0.181	1.292	1.204	...	1.192	1.352
7	0.197	1.324	1.288	...	1.234	1.394

Tidy-shaped

In tidy-shaped data, there is a single column that contains all the plate reader measurements, with each unique measurement having its own row. Additional columns specify the timepoint, which well the data comes from, and any other design elements.

Note that, in tidy-shaped data, the number of rows equals the number of wells times the number of timepoints. For instance, with a 96 well plate and 100 timepoints, that will be 9600 rows. (Yes, that’s a lot of rows! But don’t worry, tidy-shaped data is the best format for downstream analyses.) Tidy-shaped data is common in a number of R packages, including `ggplot`, where it’s sometimes called a “long” format. If you want to read more about tidy-shaped data and why it’s ideal for analyses, see: Wickham, Hadley. Tidy data. The Journal of Statistical Software, vol. 59, 2014.

Timepoint	Well	Measurement
1	A1	0.060
1	A2	0.083
1	A3	0.086
...
7	H10	1.113
7	H11	1.234
7	H12	1.394

Importing data

Once you’ve determined what format your data is in, you can begin importing it using the `read_*` or `import_*` functions of `gcplyr`.

If your data is block-shaped: use `import_blockmeasures` and start in the next section: **Importing block-shaped data**

If your data is wide-shaped: use `read_wides` and skip down to the **Importing wide-shaped data** section

If your data is already tidy-shaped: use `read_tidys` and skip down to the **Importing tidy-shaped data** section.

Importing block-shaped data

To import block-shaped data, use the `import_blockmeasures` function. `import_blockmeasures` only requires a list of filenames (or relative file paths) and **will return a wide-shaped data.frame** that you can save in R.

A basic example

Here's a simple example. First, we need to create a series of example block-shaped .csv files. **Don't worry how this code works.** When working with real growth curve data, these files would be output by the plate reader. All you need to do is put the file names in R in a vector, here we've stored the file names in `temp_filenames`.

```
#This code just creates a series of block-shaped example files
#Don't worry about how it works - when working with real growth
#curves data, all these files would be created by the plate reader
temp_filenames <-
  paste("Plate1-",
        paste(example_widedata_noiseless$Time %/% 3600,
              formatC((example_widedata_noiseless$Time %/% 3600) %/% 60,
                      width = 2, flag = 0),
              formatC((example_widedata_noiseless$Time %/% 3600) %/% 60,
                      width = 2, flag = 0),
              sep = "_"), ".csv", sep = "")
for (i in 1:length(temp_filenames)) {
  temp_filenames[i] <- strsplit(temp_filenames[i], split = "\\")(1)[
    length(strsplit(temp_filenames[i], split = "\\")(1))]
}
for (i in 1:length(temp_filenames)) {
  write.table(
    cbind(
      matrix(c("", "", "", "", "A", "B", "C", "D", "E", "F", "G", "H"),
            nrow = 12),
      rbind(rep("", 12),
            matrix(c("Time", example_widedata_noiseless$Time[i], rep("", 10)),
                  ncol = 12),
            rep("", 12),
            matrix(1:12, ncol = 12),
            matrix(
              example_widedata_noiseless[i, 2:ncol(example_widedata_noiseless)],
              ncol = 12))
    ),
    file = temp_filenames[i], quote = FALSE, row.names = FALSE, sep = ",",
    col.names = FALSE)
}
```

If you've saved all the files to a single folder, you can easily get a vector with all their names using `list.files`. If your folder contains other files, you can specify a regular expression `pattern` to limit it to just those you want to import:

```
#Here we print all the files we're going to read
list.files(pattern = "Plate1.*csv")
#> [1] "Plate1-0_00_00.csv" "Plate1-0_15_00.csv" "Plate1-0_30_00.csv" "Plate1-0_45_00.csv"
#> [5] "Plate1-1_00_00.csv" "Plate1-1_15_00.csv" "Plate1-1_30_00.csv" "Plate1-1_45_00.csv"
#> [9] "Plate1-10_00_00.csv" "Plate1-10_15_00.csv" "Plate1-10_30_00.csv" "Plate1-10_45_00.csv"
#> [13] "Plate1-11_00_00.csv" "Plate1-11_15_00.csv" "Plate1-11_30_00.csv" "Plate1-11_45_00.csv"
#> [17] "Plate1-12_00_00.csv" "Plate1-12_15_00.csv" "Plate1-12_30_00.csv" "Plate1-12_45_00.csv"
#> [21] "Plate1-13_00_00.csv" "Plate1-13_15_00.csv" "Plate1-13_30_00.csv" "Plate1-13_45_00.csv"
#> [25] "Plate1-14_00_00.csv" "Plate1-14_15_00.csv" "Plate1-14_30_00.csv" "Plate1-14_45_00.csv"
#> [29] "Plate1-15_00_00.csv" "Plate1-15_15_00.csv" "Plate1-15_30_00.csv" "Plate1-15_45_00.csv"
```

```
#> [33] "Plate1-16_00_00.csv" "Plate1-16_15_00.csv" "Plate1-16_30_00.csv" "Plate1-16_45_00.csv"
#> [37] "Plate1-17_00_00.csv" "Plate1-17_15_00.csv" "Plate1-17_30_00.csv" "Plate1-17_45_00.csv"
#> [41] "Plate1-18_00_00.csv" "Plate1-18_15_00.csv" "Plate1-18_30_00.csv" "Plate1-18_45_00.csv"
#> [45] "Plate1-19_00_00.csv" "Plate1-19_15_00.csv" "Plate1-19_30_00.csv" "Plate1-19_45_00.csv"
#> [49] "Plate1-2_00_00.csv" "Plate1-2_15_00.csv" "Plate1-2_30_00.csv" "Plate1-2_45_00.csv"
#> [53] "Plate1-20_00_00.csv" "Plate1-20_15_00.csv" "Plate1-20_30_00.csv" "Plate1-20_45_00.csv"
#> [57] "Plate1-21_00_00.csv" "Plate1-21_15_00.csv" "Plate1-21_30_00.csv" "Plate1-21_45_00.csv"
#> [61] "Plate1-22_00_00.csv" "Plate1-22_15_00.csv" "Plate1-22_30_00.csv" "Plate1-22_45_00.csv"
#> [65] "Plate1-23_00_00.csv" "Plate1-23_15_00.csv" "Plate1-23_30_00.csv" "Plate1-23_45_00.csv"
#> [69] "Plate1-24_00_00.csv" "Plate1-3_00_00.csv" "Plate1-3_15_00.csv" "Plate1-3_30_00.csv"
#> [73] "Plate1-3_45_00.csv" "Plate1-4_00_00.csv" "Plate1-4_15_00.csv" "Plate1-4_30_00.csv"
#> [77] "Plate1-4_45_00.csv" "Plate1-5_00_00.csv" "Plate1-5_15_00.csv" "Plate1-5_30_00.csv"
#> [81] "Plate1-5_45_00.csv" "Plate1-6_00_00.csv" "Plate1-6_15_00.csv" "Plate1-6_30_00.csv"
#> [85] "Plate1-6_45_00.csv" "Plate1-7_00_00.csv" "Plate1-7_15_00.csv" "Plate1-7_30_00.csv"
#> [89] "Plate1-7_45_00.csv" "Plate1-8_00_00.csv" "Plate1-8_15_00.csv" "Plate1-8_30_00.csv"
#> [93] "Plate1-8_45_00.csv" "Plate1-9_00_00.csv" "Plate1-9_15_00.csv" "Plate1-9_30_00.csv"
#> [97] "Plate1-9_45_00.csv"

#Here we save them to the temp_filenames variable
temp_filenames <- list.files(pattern = "Plate1.*csv")
```

Here's what one of the files looks like (where the values are absorbance/optical density):

```
print_df(read.csv(temp_filenames[1], header = FALSE, colClasses = "character"))
#>
#>   Time      0
#>
#>    1      2      3      4      5      6      7      8      9     10     11     12
#> A 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> B 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> C 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> D 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> E 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> F 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> G 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> H 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
```

This file corresponds to all the reads for a single plate taken at the very first timepoint. We can see that the second row of the file contains some metadata about the timepoint when this plate read was taken. Then, the data itself starts with column headers on row 4 and rownames in column 1.

If we want to read these files into R, we simply provide `import_blockmeasures` with the vector of file names, and save the result to some R object (here, `imported_blockdata`). Since our data doesn't start on the first row and column of the file, we simply need to specify what row/column it does start on using the `startrow`, `startcol`, `endrow`, and `endcol` arguments. (`import_blockmeasures` assumes that your data starts on the first row and column and ends on the last row and column, so you don't have to specify when your data meets those criteria).

```
#Now let's read it with import_blockmeasures
imported_blockdata <- import_blockmeasures(
  files = temp_filenames, startrow = 4)

head(imported_blockdata, c(6, 8))
```

```
#>      block_name  A1    A2    A3    A4    A5    A6    A7
#> 1 Plate1-0_00_00 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> 2 Plate1-0_15_00 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> 3 Plate1-0_30_00 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> 4 Plate1-0_45_00 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> 5 Plate1-1_00_00 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> 6 Plate1-1_15_00 0.002 0.003 0.002 0.003 0.003 0.002 0.002
```

Here we can see that `import_blockmeasures` has created a wide-shaped R object containing the data from all of our reads. It has also added the file names under the `block_name` column, so that we can easily track which row came from which file.

If you're looking at your data in Excel or a similar spreadsheet program, you'll notice that the columns aren't nicely numbered. Instead, they're coded by letter. Rather than have to count by hand what columns your data starts and ends on, just specify the column by letter and `import_blockmeasures` will translate that to a number for you! (in this example we don't have to specify a start column, since the data starts in the first column, but I do so just to show this letter-style functionality).

```
#We can specify rows or columns by Excel-style letters too
imported_blockdata <- import_blockmeasures(
  files = temp_filenames,
  startrow = 4, startcol = "A")
```

Specifying metadata

Sometimes, your input files will have information you want to import that's not included in the main block of data. For instance, with block-shaped data the timepoint is nearly always specified somewhere in the input file. `import_blockmeasures` can include that information as well via the `metadata` argument.

For example, let's return to our most-recent example files:

```
print_df(read.csv(temp_filenames[1], header = FALSE, colClasses = "character"))
#>
#>   Time      0
#>
#>      1      2      3      4      5      6      7      8      9     10     11     12
#> A 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> B 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> C 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> D 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> E 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> F 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> G 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> H 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
```

In these files, the timepoint information was located in the 2nd row and 3rd column. Here's how we could specify that metadata in our `import_blockmeasures` command:

```
#Reading the blockcurves files with metadata included
imported_blockdata <- import_blockmeasures(
  files = temp_filenames,
  startrow = 4,
  metadata = list("time" = c(2, 3)))
```

```
head(imported_blockdata, c(6, 8))
#>      block_name time    A1    A2    A3    A4    A5    A6
#> 1 Plate1-0_00_00    0 0.002 0.002 0.002 0.002 0.002 0.002
#> 2 Plate1-0_15_00  900 0.002 0.002 0.002 0.002 0.002 0.002
#> 3 Plate1-0_30_00 1800 0.002 0.002 0.002 0.002 0.002 0.002
#> 4 Plate1-0_45_00 2700 0.002 0.002 0.002 0.002 0.002 0.002
#> 5 Plate1-1_00_00 3600 0.002 0.002 0.002 0.002 0.002 0.002
#> 6 Plate1-1_15_00 4500 0.002 0.003 0.002 0.003 0.003 0.002
```

You can see that the metadata you specified has been added as a column in our output `data.frame`. When specifying metadata, the metadata argument must be a list of named vectors. Each vector should have two elements specifying the location of the metadata in the input files: the first element is the row, the second element is the column.

And just like how you can specify `startrow`, `startcol`, etc. with Excel-style lettering, the location of metadata can also be specified with Excel-style lettering.

```
#Reading the blockcurves files with metadata included
imported_blockdata <- import_blockmeasures(
  files = temp_filenames,
  startrow = 4,
  metadata = list("time" = c(2, "C")))
```

Reading multiple blocks from a single file

`import_blockmeasures` can also import multiple blocks from a single file, which some plate readers may output. In this case, you simply have to specify a vector of rows and columns that define the location of each block within the file.

First, let's create an example file. **Don't worry about how this code works**, normally this file would be created by the plate reader.

```
#This code just creates an example file with multiple blocks
#Don't worry about how it works - when working with real growth
#curves data, this would be created by the plate reader
write_blocks(read_blocks(files = temp_filenames,
  startrow = 4,
  metadata = list("time" = c(2, "C"))),
  file = "blocks_single.csv",
  output_format = "single",
  block_name_location = "file")
```

Let's take a look at what the file looks like:

```
print_df(head(read.csv("blocks_single.csv", header = FALSE,
  colClasses = "character"),
  c(20, 8)))
#> block_name Plate1-0_00_00
#>      time      0
#>           1      2      3      4      5      6      7
#>      A      0.002 0.002 0.002 0.002 0.002 0.002 0.002
#>      B      0.002 0.002 0.002 0.002 0.002 0.002 0.002
```

```

#>      C      0.002 0.002 0.002 0.002 0.002 0.002 0.002
#>      D      0.002 0.002 0.002 0.002 0.002 0.002 0.002
#>      E      0.002 0.002 0.002 0.002 0.002 0.002 0.002
#>      F      0.002 0.002 0.002 0.002 0.002 0.002 0.002
#>      G      0.002 0.002 0.002 0.002 0.002 0.002 0.002
#>      H      0.002 0.002 0.002 0.002 0.002 0.002 0.002
#>
#> block_name Plate1-0_15_00
#>      time      900
#>      1      2      3      4      5      6      7
#>      A      0.002 0.002 0.002 0.002 0.002 0.002 0.002
#>      B      0.002 0.002 0.002 0.002 0.002 0.002 0.002
#>      C      0.002 0.002 0.002 0.002 0.002 0.002 0.002
#>      D      0.002 0.002 0.002 0.002 0.002 0.002 0.002
#>      E      0.002 0.002 0.002 0.002 0.002 0.002 0.002

```

We can see that the first block has some metadata above it, then the block of data itself. After that there's an empty row before the next block starts. In fact, if we look at the whole file, we'll notice that all the blocks go from column 1 ("A" in Excel) to column 13 ("M" in Excel), they start on rows 3, 15, 27, 39, etc, and end on rows 11, 23, 35, 47, etc. When we look in the file, we can also see that the very last block starts on row 1155 and ends on row 1163. Let's read this information in using `import_blockmeasures` (in this example we don't *have* to specify a start column, since the data starts in the first column, but I do to be explicit):

```

imported_blockdata <- import_blockmeasures(
  "blocks_single.csv",
  startrow = seq(from = 3, to = 1155, by = 12),
  endrow = seq(from = 11, to = 1163, by = 12),
  startcol = 1, endcol = 13)

```

Here we've used the built-in R function `seq` to generate the full vector of `startrows` and `endrows`. If we take a look, we can see that it's been read successfully:

```

head(imported_blockdata, c(6, 8))
#>      block_name  A1    A2    A3    A4    A5    A6    A7
#> 1 blocks_single 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> 2 blocks_single 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> 3 blocks_single 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> 4 blocks_single 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> 5 blocks_single 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> 6 blocks_single 0.002 0.003 0.002 0.003 0.003 0.002 0.002

```

Now let's add some metadata. Because we're reading from a single file, we need to specify the metadata slightly differently. Instead of the metadata being a single vector `c(row,column)` with the location, it's going to be a list of two vectors, one with the row numbers, and one with the column numbers.

Going back to the file, we can see that the time of the block is saved in the second column, in rows 2, 14, 26, 38, ... through 1154.

```

imported_blockdata <- import_blockmeasures(
  "blocks_single.csv",
  startrow = seq(from = 3, to = 1155, by = 12),
  endrow = seq(from = 11, to = 1163, by = 12),
  startcol = 1, endcol = 13,
  metadata = list("time" = list(seq(from = 2, to = 1154, by = 12), 2)))

```


And now if we take a look at the resulting object, we can see that the time metadata has been incorporated.

```
head(imported_blockdata, c(6, 8))
#>      block_name time      A1      A2      A3      A4      A5      A6
#> 1 blocks_single    0 0.002 0.002 0.002 0.002 0.002 0.002
#> 2 blocks_single  900 0.002 0.002 0.002 0.002 0.002 0.002
#> 3 blocks_single 1800 0.002 0.002 0.002 0.002 0.002 0.002
#> 4 blocks_single 2700 0.002 0.002 0.002 0.002 0.002 0.002
#> 5 blocks_single 3600 0.002 0.002 0.002 0.002 0.002 0.002
#> 6 blocks_single 4500 0.002 0.003 0.002 0.003 0.003 0.002
```

Notes for more advanced use

Note that `import_blockmeasures` is essentially a wrapper function that calls `read_blocks`, `uninterleave`, and `trans_block_to_wide`. Any arguments for those functions can be passed to `import_blockmeasures`.

If you find yourself needing even more control over the process of importing block-shaped measures files, each of the functions is available for users to call themselves. So you can run the steps manually, first reading with `read_blocks`, separating plates as needed with `uninterleave`, then transforming to wide with `trans_block_to_wide`.

What to do next

Now that you've imported your block-shaped data, you'll need to transform it for later analyses. Jump directly to the **Transforming data** section.

Importing wide-shaped data

To import wide-shaped data, use the `read_wides` function. `read_wides` only requires a filename (or vector of filenames, or relative file paths) and will return a `data.frame` (or list of `data.frames`) that you can save in R.

A basic example

Here's a simple example. First, we need to create an example wide-shaped .csv file. **Don't worry how this code works.** When working with real growth curve data, these files would be output by the plate reader. All you need to do is know the file name(s) to put in your R code. In this example, the file name is `widedata.csv`.

```
#This code just creates a wide-shaped example file where the data doesn't
#start on the first row.
#Don't worry about how it works - when working with real growth
#curves data, this file would be created by the plate reader
temp_example_widedata <- example_widedata_noiseless
colnames(temp_example_widedata) <- paste("V", 1:ncol(temp_example_widedata),
                                         sep = "")
modified_example_widedata <-
  rbind(
    as.data.frame(matrix("", nrow = 4, ncol = ncol(example_widedata_noiseless))),
    colnames(example_widedata_noiseless),
```

```
temp_example_widedata)
modified_example_widedata[1:2, 1:2] <-
  c("Experiment name", "Start date", "Experiment_1", as.character(Sys.Date()))

write.table(modified_example_widedata, file = "widedata.csv",
            row.names = FALSE, col.names = FALSE, sep = ",")
write.table(modified_example_widedata, file = "widedata2.csv",
            row.names = FALSE, col.names = FALSE, sep = ",")
```

Here's what the start of the file looks like (where the values are absorbance/optical density):

```
#Let's take a peek at what this file looks like
print_df(head(read.csv("widedata.csv", header = FALSE,
                      colClasses = "character"),
           c(10, 10)))
#> Experiment name Experiment_1
#>      Start date 2023-01-30
#>
#>
#>      Time      A1      B1      C1      D1      E1      F1      G1      H1      A2
#>      0      0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#>      900      0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#>      1800      0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#>      2700      0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#>      3600      0.002 0.002 0.002 0.003 0.003 0.002 0.002 0.003 0.002
```

This file contains all the reads for a single plate taken across all timepoints. We can see that the first two rows contain some metadata saved by the plate reader, like the name of the experiment and the date of the experiment. Then, we can see that the data starts on the 5th row with a header. The first column contains the timepoint information, and each subsequent column corresponds to a well in the plate.

If we want to read this file into R, we simply provide `read_wides` with the file name, and save the result to some R object (here, `imported_widedata`). Since our data doesn't start on the first row and column of the file, we simply need to specify what row/column it does start on using the `startrow`, `startcol`, `endrow`, and `endcol` arguments. (`read_wides` assumes that your data starts on the first row and column and ends on the last row and column, so you don't have to specify when you data meets those criteria. Also note that `header = TRUE` by default').

```
imported_widedata <- read_wides(files = "widedata.csv", startrow = 5)
```

The resulting `data.frame` looks like this:

```
head(imported_widedata, c(6, 10))
#>      file Time      A1      B1      C1      D1      E1      F1      G1      H1
#> 6 widedata   0 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> 7 widedata  900 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> 8 widedata 1800 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> 9 widedata 2700 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002 0.002
#> 10 widedata 3600 0.002 0.002 0.002 0.003 0.003 0.002 0.002 0.003
#> 11 widedata 4500 0.002 0.003 0.002 0.003 0.003 0.002 0.003 0.003
```

Note that `read_wides` automatically saves the filename the data was imported from into the first column of the output `data.frame`. This is done to ensure that later on, `data.frames` from multiple plates can be combined without fear of losing the identity of each plate.

If you're looking at your data in Excel or a similar spreadsheet program, you'll notice that the columns aren't nicely numbered. Instead, they're coded by letter. Rather than have to count by hand what columns your data starts and ends on, just specify the column by letter and `read_wides` will translate that to a number for you! (in this example we don't have to specify a start column, since the data starts in the first column, but I do so just to show this letter-style functionality).

```
imported_widedata <- read_wides(files = "widedata.csv",
                                startrow = 5, startcol = "A")
```

Note that if you have multiple files you'd like to read in, you can do so directly with a single `read_wides` command. In this case, `read_wides` will return a list containing all the data.frames:

```
#If we had multiple wide-shaped data files to import
imported_widedata <- read_wides(files = c("widedata.csv", "widedata2.csv"))
```

Specifying metadata

Sometimes, your input files will have information you want to import that's not included in the main block of data. For instance, many readers will output information like the experiment name and date into a header in the file. `read_wides` can include that information as well via the `metadata` argument.

The `metadata` argument should be a list of named vectors. Each vector should be of length 2, with the first entry specifying the row and the second entry specifying the column where the metadata is located.

For example, in our previous example files, the experiment name was located in the 2nd row, 2nd column, and the start date was located in the 3rd row, 2nd column. Here's how we could specify that metadata:

```
imported_widedata <- read_wides(files = "widedata.csv",
                                startrow = 5,
                                metadata = list("experiment_name" = c(1, 2),
                                                  "start_date" = c(2, 2)))
head(imported_widedata, c(6, 8))
#>      file experiment_name start_date Time    A1    B1    C1    D1
#> 6 widedata Experiment_1 2023-01-30    0 0.002 0.002 0.002 0.002
#> 7 widedata Experiment_1 2023-01-30  900 0.002 0.002 0.002 0.002
#> 8 widedata Experiment_1 2023-01-30 1800 0.002 0.002 0.002 0.002
#> 9 widedata Experiment_1 2023-01-30 2700 0.002 0.002 0.002 0.002
#> 10 widedata Experiment_1 2023-01-30 3600 0.002 0.002 0.002 0.003
#> 11 widedata Experiment_1 2023-01-30 4500 0.002 0.003 0.002 0.003
```

And just like how you can specify `startrow`, `startcol`, etc. with Excel-style lettering, the location of metadata can also be specified with Excel-style lettering.

```
imported_widedata <- read_wides(files = "widedata.csv",
                                startrow = 5,
                                metadata = list("experiment_name" = c(1, "B"),
                                                  "start_date" = c(2, "B")))
```

Reading multiple wides from a single file

In the rare case that you have multiple wide-shaped datasets saved into a single file, `read_wides` can import that as well. Refer to the earlier section **Reading multiple blocks from a single file**, since the syntax for such operations is the same for `read_wides` as it is for `import_blockmeasures`.

What to do next

Now that you've imported your wide-shaped data, you'll need to transform it for later analyses. Continue on to the **Transforming data** section.

Importing tidy-shaped data

To import tidy-shaped data, you could use the built-in R functions like `read.table`. However, if you need a few more options, you can use the `gcplyr` function `read_tidys`. Unlike the built-in option, `read_tidys` can import multiple tidy-shaped files at once, can add the filename as a column in the resulting `data.frame`, and can handle files where the tidy-shaped information doesn't start on the first row and column.

`read_tidys` only requires a filename (or vector of filenames, or relative file paths) and will return a `data.frame` (or list of `data.frames`) that you can save in R.

If you've read in your tidy-shaped data, you won't need to transform it, so you can skip down to the **What's next?** section.

Transforming data

Now that you've gotten your data into the R environment, we need to transform it before we can do analyses. To reiterate, this is necessary because most plate readers that generate growth curve data outputs it in block-shaped or wide-shaped files, but tidy-shaped `data.frames` are the best shape for analyses and required by `gcplyr`.

You can transform your `data.frames` using the `trans_*` functions in `gcplyr`.

Transforming from wide-shaped to tidy-shaped

If the data you've read into the R environment is wide-shaped (or you've gotten wide-shaped data by transforming your originally block-shaped data), you'll transform it to tidy-shaped using `trans_wide_to_tidy`.

First, you need to provide `trans_wide_to_tidy` with the R object created by `read_wides` or by `trans_block_to_wide`.

Then, you have to specify one of: * the columns your data (the spectrophotometric measures) are in via `data_cols` * what columns your non-data (e.g. time and other information) are in via `id_cols`

```
imported_blocks_now_tidy <- trans_wide_to_tidy(  
  wides = imported_blockdata,  
  id_cols = c("block_name", "time"))  
  
imported_wides_now_tidy <- trans_wide_to_tidy(  
  wides = imported_widedata,  
  id_cols = c("file", "experiment_name", "start_date", "Time"))  
  
print(head(imported_blocks_now_tidy), row.names = FALSE)  
#>   block_name time Well Measurements  
#> blocks_single 0   A1      0.002  
#> blocks_single 0   A2      0.002  
#> blocks_single 0   A3      0.002  
#> blocks_single 0   A4      0.002
```

```
#> blocks_single    0    A5    0.002  
#> blocks_single    0    A6    0.002
```

What's next?

Now that you've imported and transformed your data to be tidy-shaped, you likely want to incorporate some design information on what went into each well (and plate). Alternatively, if you'd like to skip that step for now, you can go directly to pre-processing and plotting your data

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")`