

BioR — Class 2 Easy Challenge (Tidyr + Joins)

Goal: tidy a wide table, parse IDs, join metadata, flag missing values, export a summary table.

What to submit

```
setwd("folder/where/the/BioR_class/Field_Challenge_easy")  
  
biomass_wide <- read.csv("biomass_wide.csv", header = TRUE)  
  
site_meta <- read.csv("site_meta.csv", header = TRUE)
```

If your CSVs use semicolon separators use: `read.csv2`

Tasks (20–30 minutes)

- A) Wide -> long: `pivot_longer()` day_0/day_7/day_14 into columns day (numeric) and biomass.
- B) Parse IDs: split sample_id into site, treatment, rep using `separate()`.
- C) Join metadata: add location with `left_join(site_meta, by = 'site')`.
- D) Missingness: create `missing_biomass = is.na(biomass)`.
- E) Summary + export: compute mean biomass per site x treatment x day (use `na.rm=TRUE`) and export `outputs/mean_biomass.csv`.

Bonus (optional, 5 minutes)

- Create a cleaned wide table again with `pivot_wider()`: rows = site,treatment,rep; columns = day_0/day_7/day_14.

Hints

- Use `readr::parse_number(day)` to convert 'day_14' -> 14 after `pivot_longer()`.
- Use `left_join()` so you keep all measurements even if metadata are missing.
- Create the outputs folder if needed: `dir.create('outputs', showWarnings = FALSE)`.