

Lab 4: Tidying your dataset

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Prune the dataset

```
who1 <- who %>%  
  pivot_longer(  
    cols = new_sp_m014:newrel_f65,  
    names_to = "key",  
    values_to = "cases",  
    values_drop_na = TRUE  
  )
```

Exercise 1

Enforcing one observation per row

```
brauer2 <- brauer %>% select(-GID, -YORF, -GWEIGHT)
```

Exercise 2

```
brauer3 <- brauer2 %>%  
  pivot_longer(  
    cols = GO.05:U0.3,  
    names_to = "sample",  
    values_to = "expression",  
    values_drop_na = TRUE  
  )
```

Enforcing one column per variable and one value per cell

Exercise 3

```
brauer4 <- brauer3 %>%  
  separate(  
    col = sample,  
    into = combine("nutrient", "rate"),
```

```

    sep = 1
  )

```

```

## Warning: `combine()` was deprecated in dplyr 1.0.0.
## i Please use `vctrs::vec_c()` instead.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

```

Exercise 4

```

brauer5 <- brauer4 %>%
  separate(
    col = NAME,
    into = combine("gene_name", "biological_process", "molecular_function", "systematic_id", "n
    sep = "\\|\\|\\|"
  )

```

```

## Warning: `combine()` was deprecated in dplyr 1.0.0.
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## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

```

Exercise 5

```

brauer_tidy <- brauer5 %>%
  mutate_at(vars(gene_name:systematic_id), str_trim)

```

Visualizations using the tidy dataset

Exercise 6

```

brauer_tidy %>% filter(gene_name == "LEU1") %>%
  ggplot()+
  geom_line(aes(x=rate, y=expression, group = nutrient, color= nutrient ))

```

