

Data Analysis and Visualization Exercise 5

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3 January 2019

Setup

```
library(data.table)
library(magrittr)
library(tidyr)
```

Questions

Q1 Product dataset

The `example_product_data` file describes the number of times a person bought product “a” and “b”

```
messy_file <- file.path('extdata', 'example_product_data.csv')
messy_dt <- fread(messy_file)
messy_dt
##           name producta productb
## 1:   John Doe        NA         12
## 2:  Marry Doe         3          1
## 3: John Johnson      5          1
```

Why is this data-set messy? Which columns should a tidy version of this table have?

A1

Q2 Product dataset

Tranform `messy_dt` into a tidy from.

A2

Q3 Weather dataset

Read in the weather dataset `weather.txt`. Why is this dataset messy? How would a tidy version of it look like?

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A3

Q4 Weather dataset

Create a tidy version of the weather dataset.

A4

Q5 Scattered data across many files

The `baby-names` folder contains 258 csv-files (`1999.girl.csv`, `1999.boy.csv`, ...) which store name frequencies for a particular year and sex. Read in the data from all files into one table. *Hint*: when you read many files and gather them into one table, be sure to add a column that identifies each file. `rbindlist()`

A5

Q6

Is the data tidy? If not, tidy it up.

A6

Small case-study - cleaning up a gene-expression dataset in yeast

Here, we will read and clean up the data from the paper:

- *Bauer et.al., 2007, Coordination of Growth Rate, Cell Cycle, Stress Response, and Metabolic Activity in Yeast, MBoC*, <http://www.molbiolcell.org/content/19/1/352.abstract>

Read in the data:

```
original_dt <- fread("extdata/gene_expression.tds")
dim(original_dt)
## [1] 5537 40
head(original_dt, n = 2)
##          GID          YORF
## 1: GENE1331X A_06_P5820
## 2: GENE4924X A_06_P5866
##
## 1: SFB2          || ER to Golgi transport || molecular function unknown || YNL049C || 1082129
## 2:          || biological process unknown || molecular function unknown || YNL095C || 1086222
## GWEIGHT G0.05 G0.1 G0.15 G0.2 G0.25 G0.3 N0.05 N0.1 N0.15 N0.2 N0.25
## 1:      1 -0.24 -0.13 -0.21 -0.15 -0.05 -0.05 0.20 0.24 -0.20 -0.42 -0.14
## 2:      1 0.28 0.13 -0.40 -0.48 -0.11 0.17 0.31 0.00 -0.63 -0.44 -0.26
## N0.3 P0.05 P0.1 P0.15 P0.2 P0.25 P0.3 S0.05 S0.1 S0.15 S0.2 S0.25 S0.3
## 1: 0.09 -0.26 -0.20 -0.22 -0.31 0.04 0.34 -0.51 -0.12 0.09 0.09 0.20 0.08
## 2: 0.21 -0.09 -0.04 -0.10 0.15 0.20 0.63 0.53 0.15 -0.01 0.12 -0.15 0.32
```

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```
##      L0.05 L0.1 L0.15 L0.2 L0.25 L0.3 U0.05  U0.1 U0.15  U0.2 U0.25 U0.3
## 1:  0.18 0.18  0.13 0.20  0.17 0.11 -0.06 -0.26 -0.05 -0.28 -0.19 0.09
## 2:  0.16 0.09  0.02 0.04  0.03 0.01 -1.02 -0.91 -0.59 -0.61 -0.17 0.18
```

Column description:

- GID - gene ID
- YORF - Some other ID
- NAME - gene description composed of:
 - Gene name
 - Biological process
 - Molecular function
 - Systematic ID
 - Some other ID
- GWEIGHT - some type of weight
- G0.05, .., P0.03 - gene expression values for measured at different nutrient and growth rates:
 - Nutrients (G, N, P, ...):
 - G = Glucose
 - L = Leucine
 - P = Phosphate
 - S = Sulphate
 - N = Ammonia
 - U = Uracil
 - Growth rate (0.05, 0.3, ...)

Q6

Why is this dataset not tidy?

A6

Q7 - Transform it into a tidy form

Provide a tidy dataset in the following form:

```
##      name      biological_process      molecular_function
## 1: SFB2      ER to Golgi transport      molecular function unknown
## 2:      biological process unknown      molecular function unknown
## 3: QRI7 proteolysis and peptidolysis metalloendopeptidase activity
## 4: CFT2      mRNA polyadenylation*      RNA binding
## 5: SS02      vesicle fusion*      t-SNARE activity
## 6: PSP2      biological process unknown      molecular function unknown
##      systematic_name nutrient rate expression
## 1:      YNL049C  Glucose 0.05      -0.24
## 2:      YNL095C  Glucose 0.05      0.28
## 3:      YDL104C  Glucose 0.05      -0.02
## 4:      YLR115W  Glucose 0.05      -0.33
```

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## 5:	YMR183C	Glucose 0.05	0.05
## 6:	YML017W	Glucose 0.05	-0.69

A7