Data Wrangling in R

Federico Lopez

November 13, 2015

Contents

An introduction to manipulating data with `tidyr` and `dplyr`

`tidyr` is designed specifically for data tidying (not general reshaping or aggregating) and works well with `dplyr` data pipelines. Tidy data ensures that values of different variables from the same observation are always paired. In tidy data:

- Each variable forms a column
- Each observation forms a row
- Each type of observational unit forms a table

For further detail see https://github.com/hadley/tidyr and https://ramnathv.github.io/pycon2014-r/explore/tidy.html

`dplyr` provides several functions for manipulating data frames. It is a new iteration of the `plyr` package, which implements the "split-apply-combine" strategy for data analysis. Here we will go over a few examples of data manipulation using `dplyr`.

Reshaping data

Gather columns into rows

```
# Install and load tidyr and dplyr
#install.packages("tidyr")
#install.packages("dplyr")
library(tidyr)
library(dplyr)

# Load the Iris data
# This data frame includes 150 obs. of 5 variables
str(iris)
```

```
## 'data.frame':    150 obs. of  5 variables:
##  $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
##  $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
##  $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
##  $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
##  $ Species     : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 ...
```

```
head(iris)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1         3.5          1.4         0.2  setosa
## 2          4.9         3.0          1.4         0.2  setosa
## 3          4.7         3.2          1.3         0.2  setosa
## 4          4.6         3.1          1.5         0.2  setosa
## 5          5.0         3.6          1.4         0.2  setosa
## 6          5.4         3.9          1.7         0.4  setosa
```

```
# Use the tbl_df from dplyr to transform a regular data frame to a tbl object
# "tbl objects only print a few rows and all the columns that fit on one screen"
# (transforming data frames into tbl_dfs is not a requirement to use dplyr)
iris <- tbl_df(iris)
iris
```

```
## Source: local data frame [150 x 5]
##
##    Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##           (dbl)       (dbl)        (dbl)       (dbl)  (fctr)
## 1           5.1         3.5          1.4         0.2  setosa
## 2           4.9         3.0          1.4         0.2  setosa
## 3           4.7         3.2          1.3         0.2  setosa
## 4           4.6         3.1          1.5         0.2  setosa
## 5           5.0         3.6          1.4         0.2  setosa
## 6           5.4         3.9          1.7         0.4  setosa
## 7           4.6         3.4          1.4         0.3  setosa
## 8           5.0         3.4          1.5         0.2  setosa
## 9           4.4         2.9          1.4         0.2  setosa
## 10          4.9         3.1          1.5         0.1  setosa
## ..          ...         ...          ...         ...     ...
```

```r
# Summarize tbl data
glimpse(iris)
```

```
## Observations: 150
## Variables: 5
## $ Sepal.Length (dbl) 5.1, 4.9, 4.7, 4.6, 5.0, 5.4, 4.6, 5.0, 4.4, 4.9,...
## $ Sepal.Width  (dbl) 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1,...
## $ Petal.Length (dbl) 1.4, 1.4, 1.3, 1.5, 1.4, 1.7, 1.4, 1.5, 1.4, 1.5,...
## $ Petal.Width  (dbl) 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1,...
## $ Species      (fctr) setosa, setosa, setosa, setosa, setosa, setosa, ...
```

```r
# Get first observation for each Species in iris data
mini.iris <- iris[c(1, 51, 101), ]
mini.iris
```

```
## Source: local data frame [3 x 5]
##
##   Sepal.Length Sepal.Width Petal.Length Petal.Width    Species
##          (dbl)       (dbl)        (dbl)       (dbl)     (fctr)
## 1          5.1         3.5          1.4         0.2     setosa
## 2          7.0         3.2          4.7         1.4 versicolor
## 3          6.3         3.3          6.0         2.5  virginica
```

```r
# Gather columns into rows (converting data from wide to long)
# Usage: gather(data, key, value, ...)
# data: A data frame.
# key, value: Names of key and value columns to create in output
# ...: Specification of columns to gather
# -Species is used to drop the Species column and gather the remaining
# columns, that is, Sepal.Length, Sepal.Width, Petal.Length, and Petal.Width
mini.irisl <- gather(mini.iris, key=flower_trait, value=measurement, -Species)
mini.irisl
```

```
## Source: local data frame [12 x 3]
##
##       Species flower_trait measurement
##        (fctr)       (fctr)       (dbl)
## 1      setosa Sepal.Length         5.1
## 2  versicolor Sepal.Length         7.0
## 3   virginica Sepal.Length         6.3
## 4      setosa  Sepal.Width         3.5
## 5  versicolor  Sepal.Width         3.2
## 6   virginica  Sepal.Width         3.3
## 7      setosa Petal.Length         1.4
## 8  versicolor Petal.Length         4.7
## 9   virginica Petal.Length         6.0
## 10     setosa  Petal.Width         0.2
## 11 versicolor  Petal.Width         1.4
## 12  virginica  Petal.Width         2.5
```

Spread rows into columns

```
# Spread rows into columns (converting data from long to wide)
mini.irisw <- spread(mini.irisl, flower_trait, measurement)
mini.irisw
```

```
## Source: local data frame [3 x 5]
##
##      Species Sepal.Length Sepal.Width Petal.Length Petal.Width
##       (fctr)        (dbl)       (dbl)        (dbl)       (dbl)
## 1     setosa          5.1         3.5          1.4         0.2
## 2 versicolor          7.0         3.2          4.7         1.4
## 3  virginica          6.3         3.3          6.0         2.5
```

Order rows by values

```
# low to high
arrange(iris, Sepal.Length)
```

```
## Source: local data frame [150 x 5]
##
##    Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##           (dbl)       (dbl)        (dbl)       (dbl)  (fctr)
## 1           4.3         3.0          1.1         0.1  setosa
## 2           4.4         2.9          1.4         0.2  setosa
## 3           4.4         3.0          1.3         0.2  setosa
## 4           4.4         3.2          1.3         0.2  setosa
## 5           4.5         2.3          1.3         0.3  setosa
## 6           4.6         3.1          1.5         0.2  setosa
## 7           4.6         3.4          1.4         0.3  setosa
## 8           4.6         3.6          1.0         0.2  setosa
## 9           4.6         3.2          1.4         0.2  setosa
## 10          4.7         3.2          1.3         0.2  setosa
## ..          ...         ...          ...         ...     ...
```

```
# high to low
arrange(iris, desc(Sepal.Length))
```

```
## Source: local data frame [150 x 5]
##
##    Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
##           (dbl)       (dbl)        (dbl)       (dbl)    (fctr)
## 1           7.9         3.8          6.4         2.0 virginica
## 2           7.7         3.8          6.7         2.2 virginica
## 3           7.7         2.6          6.9         2.3 virginica
## 4           7.7         2.8          6.7         2.0 virginica
## 5           7.7         3.0          6.1         2.3 virginica
## 6           7.6         3.0          6.6         2.1 virginica
## 7           7.4         2.8          6.1         1.9 virginica
```

```
## 8          7.3         2.9          6.3         1.8 virginica
## 9          7.2         3.6          6.1         2.5 virginica
## 10         7.2         3.2          6.0         1.8 virginica
## ..         ...         ...          ...         ...       ...
```

Rename the columns of a data frame

```
rename(iris, sp=Species)
```

```
## Source: local data frame [150 x 5]
##
##    Sepal.Length Sepal.Width Petal.Length Petal.Width     sp
##           (dbl)       (dbl)        (dbl)       (dbl) (fctr)
## 1           5.1         3.5          1.4         0.2 setosa
## 2           4.9         3.0          1.4         0.2 setosa
## 3           4.7         3.2          1.3         0.2 setosa
## 4           4.6         3.1          1.5         0.2 setosa
## 5           5.0         3.6          1.4         0.2 setosa
## 6           5.4         3.9          1.7         0.4 setosa
## 7           4.6         3.4          1.4         0.3 setosa
## 8           5.0         3.4          1.5         0.2 setosa
## 9           4.4         2.9          1.4         0.2 setosa
## 10          4.9         3.1          1.5         0.1 setosa
## ..          ...         ...          ...         ...    ...
```

Manipulating data (filter, select, mutate, bind etc.)

`dplyr` provides a function for each basic verb of data manipulation:

- `filter()` (and `slice()`)
- `arrange()`
- `select()` (and `rename()`)
- `distinct()`
- `mutate()` (and `transmute()`)
- `summarise()`
- `sample_n()` and `sample_frac()`

The data is always the first argument of the verb functions.

Subset observations (rows)

Filter

```
# Extract rows that meet logical criteria
filter(iris, Sepal.Length > 6)
```

```
## Source: local data frame [61 x 5]
##
##    Sepal.Length Sepal.Width Petal.Length Petal.Width    Species
##           (dbl)       (dbl)        (dbl)       (dbl)     (fctr)
## 1           7.0         3.2          4.7         1.4 versicolor
## 2           6.4         3.2          4.5         1.5 versicolor
## 3           6.9         3.1          4.9         1.5 versicolor
## 4           6.5         2.8          4.6         1.5 versicolor
## 5           6.3         3.3          4.7         1.6 versicolor
## 6           6.6         2.9          4.6         1.3 versicolor
## 7           6.1         2.9          4.7         1.4 versicolor
## 8           6.7         3.1          4.4         1.4 versicolor
## 9           6.2         2.2          4.5         1.5 versicolor
## 10          6.1         2.8          4.0         1.3 versicolor
## ..          ...         ...          ...         ...        ...
```

```
iris[iris$Sepal.Length > 6, ] # Using base R
```

```
## Source: local data frame [61 x 5]
##
##    Sepal.Length Sepal.Width Petal.Length Petal.Width    Species
##           (dbl)       (dbl)        (dbl)       (dbl)     (fctr)
## 1           7.0         3.2          4.7         1.4 versicolor
## 2           6.4         3.2          4.5         1.5 versicolor
## 3           6.9         3.1          4.9         1.5 versicolor
## 4           6.5         2.8          4.6         1.5 versicolor
## 5           6.3         3.3          4.7         1.6 versicolor
## 6           6.6         2.9          4.6         1.3 versicolor
## 7           6.1         2.9          4.7         1.4 versicolor
## 8           6.7         3.1          4.4         1.4 versicolor
## 9           6.2         2.2          4.5         1.5 versicolor
## 10          6.1         2.8          4.0         1.3 versicolor
## ..          ...         ...          ...         ...        ...
```

```
# Extract rows according to a factor
filter(iris, Species == "setosa")
```

```
## Source: local data frame [50 x 5]
##
##    Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##           (dbl)       (dbl)        (dbl)       (dbl)  (fctr)
## 1           5.1         3.5          1.4         0.2  setosa
## 2           4.9         3.0          1.4         0.2  setosa
## 3           4.7         3.2          1.3         0.2  setosa
## 4           4.6         3.1          1.5         0.2  setosa
## 5           5.0         3.6          1.4         0.2  setosa
## 6           5.4         3.9          1.7         0.4  setosa
## 7           4.6         3.4          1.4         0.3  setosa
## 8           5.0         3.4          1.5         0.2  setosa
## 9           4.4         2.9          1.4         0.2  setosa
## 10          4.9         3.1          1.5         0.1  setosa
## ..          ...         ...          ...         ...     ...
```

```r
subset(iris, Species == "setosa") # Using base R
```

```
## Source: local data frame [50 x 5]
##
##    Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##           (dbl)       (dbl)        (dbl)       (dbl)  (fctr)
## 1           5.1         3.5          1.4         0.2  setosa
## 2           4.9         3.0          1.4         0.2  setosa
## 3           4.7         3.2          1.3         0.2  setosa
## 4           4.6         3.1          1.5         0.2  setosa
## 5           5.0         3.6          1.4         0.2  setosa
## 6           5.4         3.9          1.7         0.4  setosa
## 7           4.6         3.4          1.4         0.3  setosa
## 8           5.0         3.4          1.5         0.2  setosa
## 9           4.4         2.9          1.4         0.2  setosa
## 10          4.9         3.1          1.5         0.1  setosa
## ..          ...         ...          ...         ...     ...
```

```r
# Provide any number of filtering conditions,
# which are joined together with & or |
filter(iris, Species == "setosa" & Sepal.Length > 5)
```

```
## Source: local data frame [22 x 5]
##
##    Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##           (dbl)       (dbl)        (dbl)       (dbl)  (fctr)
## 1           5.1         3.5          1.4         0.2  setosa
## 2           5.4         3.9          1.7         0.4  setosa
## 3           5.4         3.7          1.5         0.2  setosa
## 4           5.8         4.0          1.2         0.2  setosa
## 5           5.7         4.4          1.5         0.4  setosa
## 6           5.4         3.9          1.3         0.4  setosa
## 7           5.1         3.5          1.4         0.3  setosa
## 8           5.7         3.8          1.7         0.3  setosa
## 9           5.1         3.8          1.5         0.3  setosa
## 10          5.4         3.4          1.7         0.2  setosa
## ..          ...         ...          ...         ...     ...
```

```r
#filter(iris, Species == "setosa" & Sepal.Length > median(Sepal.Length))
# Using base R code
iris[iris$Species == "setosa" | iris$Sepal.Length > median(iris$Sepal.Length), ]
```

```
## Source: local data frame [120 x 5]
##
##    Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##           (dbl)       (dbl)        (dbl)       (dbl)  (fctr)
## 1           5.1         3.5          1.4         0.2  setosa
## 2           4.9         3.0          1.4         0.2  setosa
## 3           4.7         3.2          1.3         0.2  setosa
## 4           4.6         3.1          1.5         0.2  setosa
## 5           5.0         3.6          1.4         0.2  setosa
## 6           5.4         3.9          1.7         0.4  setosa
```

```
## 7           4.6         3.4          1.4         0.3  setosa
## 8           5.0         3.4          1.5         0.2  setosa
## 9           4.4         2.9          1.4         0.2  setosa
## 10          4.9         3.1          1.5         0.1  setosa
## ..          ...         ...          ...         ...     ...
```

Remove duplicate rows

```
# Remove duplicate rows
# Show duplicated rows: duplicated(iris)
distinct(iris)
```

```
## Source: local data frame [149 x 5]
##
##    Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##           (dbl)       (dbl)        (dbl)       (dbl)  (fctr)
## 1           5.1         3.5          1.4         0.2  setosa
## 2           4.9         3.0          1.4         0.2  setosa
## 3           4.7         3.2          1.3         0.2  setosa
## 4           4.6         3.1          1.5         0.2  setosa
## 5           5.0         3.6          1.4         0.2  setosa
## 6           5.4         3.9          1.7         0.4  setosa
## 7           4.6         3.4          1.4         0.3  setosa
## 8           5.0         3.4          1.5         0.2  setosa
## 9           4.4         2.9          1.4         0.2  setosa
## 10          4.9         3.1          1.5         0.1  setosa
## ..          ...         ...          ...         ...     ...
```

Randomly select rows

```
# Randomly select fraction of rows
sample_frac(iris, 0.5, replace=TRUE)
```

```
## Source: local data frame [75 x 5]
##
##    Sepal.Length Sepal.Width Petal.Length Petal.Width    Species
##           (dbl)       (dbl)        (dbl)       (dbl)     (fctr)
## 1           5.1         3.5          1.4         0.3     setosa
## 2           5.2         2.7          3.9         1.4 versicolor
## 3           5.1         3.4          1.5         0.2     setosa
## 4           5.4         3.0          4.5         1.5 versicolor
## 5           5.9         3.0          5.1         1.8  virginica
## 6           6.3         2.9          5.6         1.8  virginica
## 7           5.8         2.7          4.1         1.0 versicolor
## 8           6.5         3.0          5.2         2.0  virginica
## 9           6.1         2.6          5.6         1.4  virginica
## 10          6.1         2.8          4.0         1.3 versicolor
## ..          ...         ...          ...         ...        ...
```

```r
# Randomly select n rows
sample_n(iris, 10, replace=TRUE)
```

```
## Source: local data frame [10 x 5]
##
##    Sepal.Length Sepal.Width Petal.Length Petal.Width    Species
##           (dbl)       (dbl)        (dbl)       (dbl)     (fctr)
## 1           6.5         3.2          5.1         2.0  virginica
## 2           4.9         3.1          1.5         0.1     setosa
## 3           5.5         2.5          4.0         1.3 versicolor
## 4           4.5         2.3          1.3         0.3     setosa
## 5           5.3         3.7          1.5         0.2     setosa
## 6           7.2         3.0          5.8         1.6  virginica
## 7           5.5         3.5          1.3         0.2     setosa
## 8           7.7         3.8          6.7         2.2  virginica
## 9           5.7         2.8          4.1         1.3 versicolor
## 10          5.6         2.8          4.9         2.0  virginica
```

```r
# Select rows by position
slice(iris, 10:15)
```

```
## Source: local data frame [6 x 5]
##
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##          (dbl)       (dbl)        (dbl)       (dbl)  (fctr)
## 1          4.9         3.1          1.5         0.1  setosa
## 2          5.4         3.7          1.5         0.2  setosa
## 3          4.8         3.4          1.6         0.2  setosa
## 4          4.8         3.0          1.4         0.1  setosa
## 5          4.3         3.0          1.1         0.1  setosa
## 6          5.8         4.0          1.2         0.2  setosa
```

Subset variables (columns)

Select columns by complete or partial name, drop variables

```r
# Select columns by name
select(iris, Sepal.Width, Petal.Length, Species)
```

```
## Source: local data frame [150 x 3]
##
##    Sepal.Width Petal.Length Species
##          (dbl)        (dbl)  (fctr)
## 1          3.5          1.4  setosa
## 2          3.0          1.4  setosa
## 3          3.2          1.3  setosa
## 4          3.1          1.5  setosa
## 5          3.6          1.4  setosa
## 6          3.9          1.7  setosa
## 7          3.4          1.4  setosa
```

```
## 8          3.4          1.5  setosa
## 9          2.9          1.4  setosa
## 10         3.1          1.5  setosa
## ..         ...          ...     ...
```

```
# Select columns whose name starts with a character string
select(iris, starts_with("Petal"))
```

```
## Source: local data frame [150 x 2]
##
##    Petal.Length Petal.Width
##           (dbl)       (dbl)
## 1           1.4         0.2
## 2           1.4         0.2
## 3           1.3         0.2
## 4           1.5         0.2
## 5           1.4         0.2
## 6           1.7         0.4
## 7           1.4         0.3
## 8           1.5         0.2
## 9           1.4         0.2
## 10          1.5         0.1
## ..          ...         ...
```

```
# Select columns whose name ends with a character string
select(iris, ends_with("Length"))
```

```
## Source: local data frame [150 x 2]
##
##    Sepal.Length Petal.Length
##           (dbl)        (dbl)
## 1           5.1          1.4
## 2           4.9          1.4
## 3           4.7          1.3
## 4           4.6          1.5
## 5           5.0          1.4
## 6           5.4          1.7
## 7           4.6          1.4
## 8           5.0          1.5
## 9           4.4          1.4
## 10          4.9          1.5
## ..          ...          ...
```

```
# Select columns whose names are in a group of names
#select(iris, one_of("Species"))

# Drop variables
select(iris, -starts_with("Petal"))
```

```
## Source: local data frame [150 x 3]
##
##    Sepal.Length Sepal.Width Species
```

```
##           (dbl)       (dbl)  (fctr)
## 1           5.1         3.5  setosa
## 2           4.9         3.0  setosa
## 3           4.7         3.2  setosa
## 4           4.6         3.1  setosa
## 5           5.0         3.6  setosa
## 6           5.4         3.9  setosa
## 7           4.6         3.4  setosa
## 8           5.0         3.4  setosa
## 9           4.4         2.9  setosa
## 10          4.9         3.1  setosa
## ..          ...         ...     ...
```

```
select(iris, -contains("etal"))
```

```
## Source: local data frame [150 x 3]
##
##    Sepal.Length Sepal.Width Species
##           (dbl)       (dbl)  (fctr)
## 1           5.1         3.5  setosa
## 2           4.9         3.0  setosa
## 3           4.7         3.2  setosa
## 4           4.6         3.1  setosa
## 5           5.0         3.6  setosa
## 6           5.4         3.9  setosa
## 7           4.6         3.4  setosa
## 8           5.0         3.4  setosa
## 9           4.4         2.9  setosa
## 10          4.9         3.1  setosa
## ..          ...         ...     ...
```

```
select(iris, -Petal.Length, -Petal.Width)
```

```
## Source: local data frame [150 x 3]
##
##    Sepal.Length Sepal.Width Species
##           (dbl)       (dbl)  (fctr)
## 1           5.1         3.5  setosa
## 2           4.9         3.0  setosa
## 3           4.7         3.2  setosa
## 4           4.6         3.1  setosa
## 5           5.0         3.6  setosa
## 6           5.4         3.9  setosa
## 7           4.6         3.4  setosa
## 8           5.0         3.4  setosa
## 9           4.4         2.9  setosa
## 10          4.9         3.1  setosa
## ..          ...         ...     ...
```

```
select(iris, -(Sepal.Length:Petal.Length))
```

```
## Source: local data frame [150 x 2]
```

```
##
##    Petal.Width Species
##          (dbl)  (fctr)
## 1          0.2  setosa
## 2          0.2  setosa
## 3          0.2  setosa
## 4          0.2  setosa
## 5          0.2  setosa
## 6          0.4  setosa
## 7          0.3  setosa
## 8          0.2  setosa
## 9          0.2  setosa
## 10         0.1  setosa
## ..         ...     ...
```

```
# Using base R
# iris$Species <- NULL
# iris[["Species"]] <- NULL
# iris[,"Species"]  <- NULL
# iris[[5]] <- NULL
# iris[,5] <- NULL
# iris <- subset(iris, select=-Species)
```

Summarize data

```
summarise(group_by(iris, Species), mean(Sepal.Length))
```

```
## Source: local data frame [3 x 2]
##
##      Species mean(Sepal.Length)
##       (fctr)              (dbl)
## 1     setosa              5.006
## 2 versicolor              5.936
## 3  virginica              6.588
```

```
# Apply summary function to each column
summarise_each(iris, funs(mean))
```

```
## Source: local data frame [1 x 5]
##
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##          (dbl)       (dbl)        (dbl)       (dbl)   (dbl)
## 1     5.843333    3.057333        3.758    1.199333      NA
```

```
iris %>%
  select(-Species) %>%
  summarise_each(funs(mean))
```

```
## Source: local data frame [1 x 4]
##
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width
##          (dbl)       (dbl)        (dbl)       (dbl)
## 1     5.843333    3.057333        3.758    1.199333
```

Group data

```
# Group data into rows with the same value of Species
group_by(iris, Species)
```

```
## Source: local data frame [150 x 5]
## Groups: Species [3]
##
##    Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##           (dbl)       (dbl)        (dbl)       (dbl)  (fctr)
## 1           5.1         3.5          1.4         0.2  setosa
## 2           4.9         3.0          1.4         0.2  setosa
## 3           4.7         3.2          1.3         0.2  setosa
## 4           4.6         3.1          1.5         0.2  setosa
## 5           5.0         3.6          1.4         0.2  setosa
## 6           5.4         3.9          1.7         0.4  setosa
## 7           4.6         3.4          1.4         0.3  setosa
## 8           5.0         3.4          1.5         0.2  setosa
## 9           4.4         2.9          1.4         0.2  setosa
## 10          4.9         3.1          1.5         0.1  setosa
## ..          ...         ...          ...         ...     ...
```

```
# Remove grouping information from data frame
ungroup(iris)
```

```
## Source: local data frame [150 x 5]
##
##    Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##           (dbl)       (dbl)        (dbl)       (dbl)  (fctr)
## 1           5.1         3.5          1.4         0.2  setosa
## 2           4.9         3.0          1.4         0.2  setosa
## 3           4.7         3.2          1.3         0.2  setosa
## 4           4.6         3.1          1.5         0.2  setosa
## 5           5.0         3.6          1.4         0.2  setosa
## 6           5.4         3.9          1.7         0.4  setosa
## 7           4.6         3.4          1.4         0.3  setosa
## 8           5.0         3.4          1.5         0.2  setosa
## 9           4.4         2.9          1.4         0.2  setosa
## 10          4.9         3.1          1.5         0.1  setosa
## ..          ...         ...          ...         ...     ...
```

Make new variables

```
# Compute and append one or more new columns
mutate(iris, sepal=Sepal.Length + Sepal.Width)
```

```
## Source: local data frame [150 x 6]
##
##    Sepal.Length Sepal.Width Petal.Length Petal.Width Species sepal
##           (dbl)       (dbl)        (dbl)       (dbl)  (fctr) (dbl)
## 1           5.1         3.5          1.4         0.2  setosa   8.6
## 2           4.9         3.0          1.4         0.2  setosa   7.9
## 3           4.7         3.2          1.3         0.2  setosa   7.9
## 4           4.6         3.1          1.5         0.2  setosa   7.7
## 5           5.0         3.6          1.4         0.2  setosa   8.6
## 6           5.4         3.9          1.7         0.4  setosa   9.3
## 7           4.6         3.4          1.4         0.3  setosa   8.0
## 8           5.0         3.4          1.5         0.2  setosa   8.4
## 9           4.4         2.9          1.4         0.2  setosa   7.3
## 10          4.9         3.1          1.5         0.1  setosa   8.0
## ..          ...         ...          ...         ...     ...   ...
```

```
mutate(iris, logSepal.Length=log10(Sepal.Length))
```

```
## Source: local data frame [150 x 6]
##
##    Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##           (dbl)       (dbl)        (dbl)       (dbl)  (fctr)
## 1           5.1         3.5          1.4         0.2  setosa
## 2           4.9         3.0          1.4         0.2  setosa
## 3           4.7         3.2          1.3         0.2  setosa
## 4           4.6         3.1          1.5         0.2  setosa
## 5           5.0         3.6          1.4         0.2  setosa
## 6           5.4         3.9          1.7         0.4  setosa
## 7           4.6         3.4          1.4         0.3  setosa
## 8           5.0         3.4          1.5         0.2  setosa
## 9           4.4         2.9          1.4         0.2  setosa
## 10          4.9         3.1          1.5         0.1  setosa
## ..          ...         ...          ...         ...     ...
## Variables not shown: logSepal.Length (dbl)
```

```
# Using base R
# iris[["logSepal.Length"]] <- log10(iris$Sepal.Length)
# iris[,"logSepal.Length"] <- log10(iris$Sepal.Length)
# iris$logSepal.Length <- log10(iris$Sepal.Length)

# Drop existing variables
transmute(iris, logSepal.Length=log10(Sepal.Length))
```

```
## Source: local data frame [150 x 1]
##
##    logSepal.Length
##              (dbl)
## 1        0.7075702
## 2        0.6901961
## 3        0.6720979
## 4        0.6627578
## 5        0.6989700
## 6        0.7323938
```

```
## 7        0.6627578
## 8        0.6989700
## 9        0.6434527
## 10       0.6901961
## ..             ...
```

```
# Compute one or more new columns. Drop original columns
transmute(iris, sepal=Sepal.Length + Sepal.Width)
```

```
## Source: local data frame [150 x 1]
##
##    sepal
##    (dbl)
## 1    8.6
## 2    7.9
## 3    7.9
## 4    7.7
## 5    8.6
## 6    9.3
## 7    8.0
## 8    8.4
## 9    7.3
## 10   8.0
## ..   ...
```

Combine data sets

```
a <- data_frame(x1=c("A", "B", "C"), x2=c(1, 2, 3))
a
```

```
## Source: local data frame [3 x 2]
##
##      x1    x2
##   (chr) (dbl)
## 1     A     1
## 2     B     2
## 3     C     3
```

```
b <- data_frame(x1=c("A", "B", "D"), x3=c("T", "F", "T"))
b
```

```
## Source: local data frame [3 x 2]
##
##      x1    x3
##   (chr) (chr)
## 1     A     T
## 2     B     F
## 3     D     T
```

```r
# Join matching rows from b to a
left_join(a, b, by="x1")
```

```
## Source: local data frame [3 x 3]
##
##      x1    x2    x3
##   (chr) (dbl) (chr)
## 1     A     1     T
## 2     B     2     F
## 3     C     3    NA
```

```r
# Join matching rows from a to b
right_join(a, b, by="x1")
```

```
## Source: local data frame [3 x 3]
##
##      x1    x2    x3
##   (chr) (dbl) (chr)
## 1     A     1     T
## 2     B     2     F
## 3     D    NA     T
```

```r
# Join data. Retain only rows in both sets
inner_join(a, b, by="x1")
```

```
## Source: local data frame [2 x 3]
##
##      x1    x2    x3
##   (chr) (dbl) (chr)
## 1     A     1     T
## 2     B     2     F
```

```r
# Join data. Retain all values, all rows
full_join(a, b, by="x1")
```

```
## Source: local data frame [4 x 3]
##
##      x1    x2    x3
##   (chr) (dbl) (chr)
## 1     A     1     T
## 2     B     2     F
## 3     C     3    NA
## 4     D    NA     T
```

```r
# All rows in a that have a match in b
semi_join(a, b, by="x1")
```

```
## Source: local data frame [2 x 2]
##
##      x1    x2
##   (chr) (dbl)
## 1     A     1
## 2     B     2
```

```
# All rows in a that do not have a match in b
anti_join(a, b, by="x1")
```

```
## Source: local data frame [1 x 2]
##
##      x1    x2
##   (chr) (dbl)
## 1     C     3
```

Set operations

These expect the x and y inputs to have the same variables, and treat the observations like sets.

```
y <- data_frame(x1=c("A", "B", "C"), x2=c(1, 2, 3))
z <- data_frame(x1=c("B", "C", "D"), x2=c(2, 3, 4))
str(y)
```

```
## Classes 'tbl_df', 'tbl' and 'data.frame':    3 obs. of  2 variables:
##  $ x1: chr  "A" "B" "C"
##  $ x2: num  1 2 3
```

```
glimpse(y)
```

```
## Observations: 3
## Variables: 2
## $ x1 (chr) "A", "B", "C"
## $ x2 (dbl) 1, 2, 3
```

```
y
```

```
## Source: local data frame [3 x 2]
##
##      x1    x2
##   (chr) (dbl)
## 1     A     1
## 2     B     2
## 3     C     3
```

```
z
```

```
## Source: local data frame [3 x 2]
##
##      x1    x2
##   (chr) (dbl)
## 1     B     2
## 2     C     3
## 3     D     4
```

```r
# Rows that appear in both y and z
intersect(y, z)
```

```
## Source: local data frame [2 x 2]
##
##      x1    x2
##   (chr) (dbl)
## 1     B     2
## 2     C     3
```

```r
# Rows that appear in either or both y and z
union(y, z)
```

```
## Source: local data frame [4 x 2]
##
##      x1    x2
##   (chr) (dbl)
## 1     D     4
## 2     C     3
## 3     B     2
## 4     A     1
```

```r
# Rows that appear in y but not z
setdiff(y, z)
```

```
## Source: local data frame [1 x 2]
##
##      x1    x2
##   (chr) (dbl)
## 1     A     1
```

Binding

```r
# Append z to y as new rows
bind_rows(y, z)
```

```
## Source: local data frame [6 x 2]
##
##      x1    x2
##   (chr) (dbl)
## 1     A     1
## 2     B     2
## 3     C     3
## 4     B     2
## 5     C     3
## 6     D     4
```

```
# Append z to y as new columns. Caution: matches rows by position
bind_cols(y, z)
```

```
## Source: local data frame [3 x 4]
##
##      x1    x2    x1    x2
##   (chr) (dbl) (chr) (dbl)
## 1     A     1     B     2
## 2     B     2     C     3
## 3     C     3     D     4
```

For further information on `dplyr`:
https://cran.r-project.org/web/packages/dplyr/index.html
http://blog.rstudio.org/2014/01/17/introducing-dplyr/
http://www.dataschool.io/dplyr-tutorial-for-faster-data-manipulation-in-r/

Using `magrittr` to create pipelines

According to its documentation (https://github.com/smbache/magrittr), the `magrittr` package offers a set of operators which promote semantics that will improve your code by:

- structuring sequences of data operations left-to-right (as opposed to from the inside and out),
- avoiding nested function calls,
- minimizing the need for local variables and function definitions, and
- making it easy to add steps anywhere in the sequence of operations.

A simple example:

```
#install.packages("magrittr")
library(magrittr)
iris %>% head(4)
```

```
## Source: local data frame [4 x 5]
##
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##          (dbl)       (dbl)        (dbl)       (dbl)  (fctr)
## 1          5.1         3.5          1.4         0.2  setosa
## 2          4.9         3.0          1.4         0.2  setosa
## 3          4.7         3.2          1.3         0.2  setosa
## 4          4.6         3.1          1.5         0.2  setosa
```

The pipe operator `%>%` passes the object on left hand side as first argument of function on righthand side. `dplyr` imports the `%>%` operator from `magrittr`.

```
iris %>%
  filter(Species == "setosa") %>%
  select(Sepal.Length, Sepal.Width) %>%
  head(10)
```

```
## Source: local data frame [10 x 2]
##
##    Sepal.Length Sepal.Width
##           (dbl)       (dbl)
## 1           5.1         3.5
## 2           4.9         3.0
## 3           4.7         3.2
## 4           4.6         3.1
## 5           5.0         3.6
## 6           5.4         3.9
## 7           4.6         3.4
## 8           5.0         3.4
## 9           4.4         2.9
## 10          4.9         3.1
```

```
iris %>%
  group_by(Species) %>%
  summarise(avg=mean(Sepal.Width)) %>%
  arrange(avg)
```

```
## Source: local data frame [3 x 2]
##
##      Species   avg
##       (fctr) (dbl)
## 1 versicolor 2.770
## 2  virginica 2.974
## 3     setosa 3.428
```

There are also functions that do not have a data argument, for which it is useful to expose the variables in the data. This is done with the `%$%` operator:

```
iris %>%
  filter(Sepal.Length > mean(Sepal.Length)) %$%
  cor(Sepal.Length, Sepal.Width)
```

```
## [1] 0.3361992
```

Which country experienced the sharpest 5-year drop in life expectancy?

```
#install.packages("gapminder")
library(gapminder)
```

```
## Warning: package 'gapminder' was built under R version 3.1.3
```

```
gtbl <- tbl_df(gapminder)
glimpse(gtbl)
```

```
## Observations: 1,704
## Variables: 6
## $ country   (fctr) Afghanistan, Afghanistan, Afghanistan, Afghanistan,...
## $ continent (fctr) Asia, Asia, Asia, Asia, Asia, Asia, Asia, Asia, Asi...
```

```
## $ year      (dbl) 1952, 1957, 1962, 1967, 1972, 1977, 1982, 1987, 1992...
## $ lifeExp   (dbl) 28.801, 30.332, 31.997, 34.020, 36.088, 38.438, 39.8...
## $ pop       (dbl) 8425333, 9240934, 10267083, 11537966, 13079460, 1488...
## $ gdpPercap (dbl) 779.4453, 820.8530, 853.1007, 836.1971, 739.9811, 78...
```

```
#worstle <-
gtbl %>%
  group_by(continent, country) %>%
  select(country, year, continent, lifeExp) %>%
  # lag(): copy with values lagged by 1
  mutate(le.delta=lifeExp - lag(lifeExp)) %>%
  summarize(worstle.delta=min(le.delta, na.rm=TRUE)) %>%
  filter(min_rank(worstle.delta) < 2) %>%
  arrange(worstle.delta)
```

```
## Source: local data frame [5 x 3]
## Groups: continent [5]
##
##   continent     country worstle.delta
##      (fctr)      (fctr)         (dbl)
## 1    Africa      Rwanda       -20.421
## 2  Americas El Salvador        -1.511
## 3      Asia    Cambodia        -9.097
## 4    Europe  Montenegro        -1.464
## 5   Oceania   Australia         0.170
```

```
#worstle
```

What is the correlation between life expectancy and year within each country?

```
# Fit a linear regression within country
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 3.1.3
```

```
str(gapminder)
```

```
## 'data.frame':    1704 obs. of  6 variables:
##  $ country  : Factor w/ 142 levels "Afghanistan",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ continent: Factor w/ 5 levels "Africa","Americas",..: 3 3 3 3 3 3 3 3 3 3 ...
##  $ year     : num  1952 1957 1962 1967 1972 ...
##  $ lifeExp  : num  28.8 30.3 32 34 36.1 ...
##  $ pop      : num  8425333 9240934 10267083 11537966 13079460 ...
##  $ gdpPercap: num  779 821 853 836 740 ...
```

```
ggplot(gapminder, aes(x=year, y=lifeExp, colour=continent)) +
  geom_jitter() +
  geom_smooth(lwd=1.5, method="lm")
```


```
# Calculate overall correlation between year and life expectancy
(ov.cor <- gapminder %$%
  cor(year, lifeExp))
```

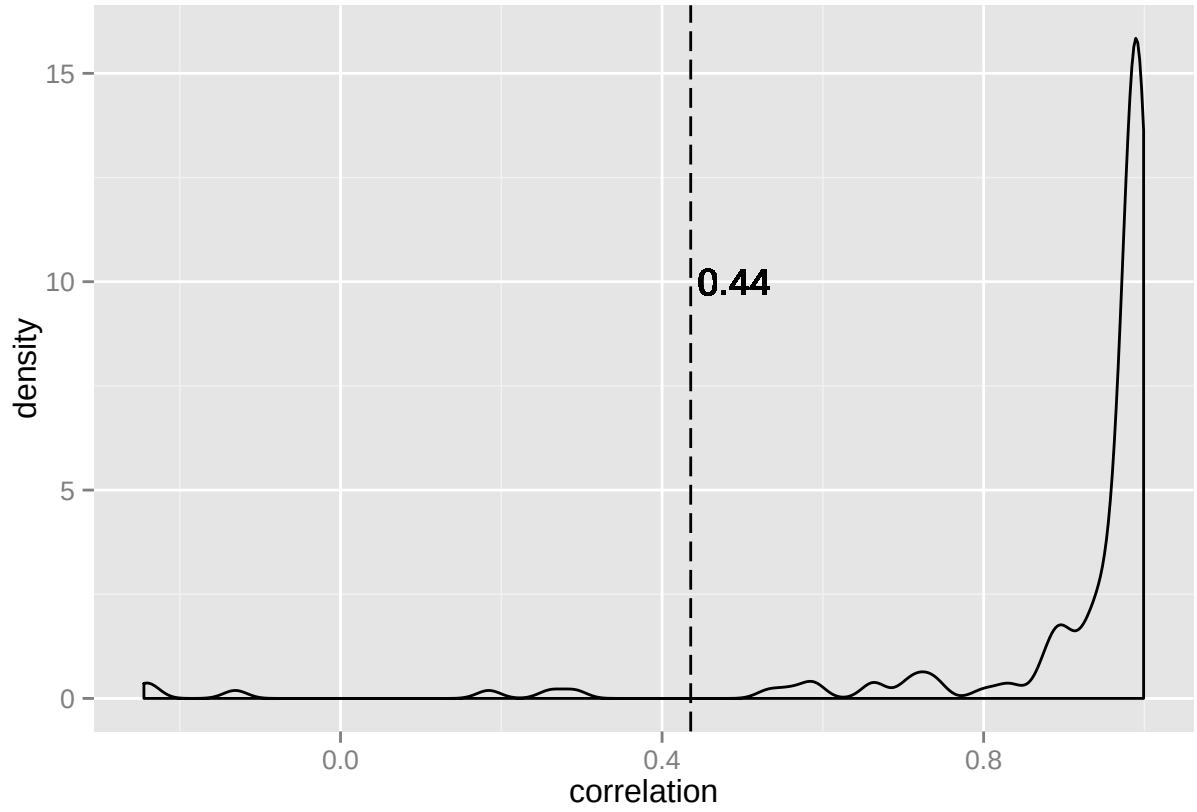
```
## [1] 0.4356112
```

```
#> [1] 0.4356112
# Calculate correlation within each country
(gcor <- gapminder %>%
  group_by(country) %>%
  summarize(correlation=cor(year, lifeExp)))
```

```
## Source: local data frame [142 x 2]
##
##        country correlation
##         (fctr)       (dbl)
## 1  Afghanistan   0.9735051
## 2      Albania   0.9542420
## 3      Algeria   0.9925307
## 4       Angola   0.9422392
## 5    Argentina   0.9977816
## 6    Australia   0.9897716
## 7      Austria   0.9960592
## 8      Bahrain   0.9832293
## 9   Bangladesh   0.9946662
```

```
## 10     Belgium   0.9972665
## ..         ...         ...
```

```r
# The correlation between life expectancy and year is
# much higher within countries
ggplot(gcor, aes(x=correlation)) +
  geom_density() +
  geom_vline(xintercept=ov.cor, linetype="longdash") +
  geom_text(data=NULL, x=ov.cor, y=10, label=round(ov.cor, 2),
            hjust=-0.1)
```



Pattern matching and replacement

Some content included here taken from https://github.com/STAT545-UBC

Position of pattern within the string

- `^`: start of the string.
- `$`: end of the string.
- `\b`: empty string at either edge of a word. Don't confuse it with ^ $ which marks the edge of a string.
- `\B`: empty string provided it is not at an edge of a word.

Operators

- `.`: matches any single character, as shown in the first example.
- `[...]`: a character list, matches any one of the characters inside the square brackets. We can also use - inside the brackets to specify a range of characters.
- `[^...]`: an inverted character list, similar to [...], but matches any characters except those inside the square brackets.
- `\`: suppress the special meaning of metacharacters in regular expression, i.e. `$ * + . ? [ ] ^ { } | ( ) \`, similar to its usage in escape sequences. Since `\` itself needs to be escaped in R, we need to escape these metacharacters with double backslash like `\\$`.
- `|`: an "or" operator, matches patterns on either side of the `|`.
- `(...)`: grouping in regular expressions. This allows you to retrieve the bits that matched various parts of your regular expression so you can alter them or use them for building up a new string. Each group can than be refer using `\\N`, with N being the No. of `(...)` used. This is called backreference.

```
# Find matches for a string
?grep
bee.spp <- c("Apis cerana", "Apis koschevnikovi", "Apis mellifera",
  "Apis nigrocincta", "Bombus atratus", "Bombus dahlbomii",
  "Bombus fervidus", "Bombus lapidarius", "Bombus ruderatus",
  "Bombus rupestris")

i <- grep("Bombus", bee.spp)
cat("'Bombus' appears", length(bee.spp[i]), "times")
```

```
## 'Bombus' appears 6 times
```

```
i
```

```
## [1]  5  6  7  8  9 10
```

```
bee.spp[i]
```

```
## [1] "Bombus atratus"    "Bombus dahlbomii"  "Bombus fervidus"
## [4] "Bombus lapidarius" "Bombus ruderatus"  "Bombus rupestris"
```

```
# Replace specified values
gsub(" ", "_", bee.spp)
```

```
##  [1] "Apis_cerana"        "Apis_koschevnikovi" "Apis_mellifera"
##  [4] "Apis_nigrocincta"   "Bombus_atratus"     "Bombus_dahlbomii"
##  [7] "Bombus_fervidus"    "Bombus_lapidarius"  "Bombus_ruderatus"
## [10] "Bombus_rupestris"
```

```
#grep -oE "^>.*\|" sequence.fasta
#grep -oE "\|.*\|" ants.fasta
```