## R Basics

Tomasz Mądry

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### Overview

- ► Important R libraries
  - dplyr
  - ggplot2 + scales
    stringr
- Exercises

## dplyr - Introduction

#### Overview

dplyr is a grammar of data manipulation, providing a consistent set of verbs that help you solve the most common data manipulation challenges:

```
mutate() # adds new variables that are functions of existing variables
select() # picks variables based on their names.
filter() # picks cases based on their values.
summarise() # reduces multiple values down to a single summary.
arrange() # changes the ordering of the rows.
```

These all combine naturally with group\_by() which allows you to perform any operation "by group".

#### More info

https://dplyr.tidyverse.org/

## dplyr - Data set preview

#### Load exemplary data set:

```
data(mtcars)
```

#### Preview the data:

```
head(mtcars, 6) # display first 6 rows
```

```
## Mazda RX4 Wag 21.0 6 160 110 3.90 2.620 16.46 0 1 4 4 4 ## Mazda RX4 Wag 21.0 6 160 110 3.90 2.875 17.02 0 1 4 4 4 ## Datsun 710 22.8 4 108 93 3.85 2.320 18.61 1 1 1 4 4 1 ## Hornet 4 Drive 21.4 6 258 110 3.08 3.215 19.44 1 0 3 1 ## Hornet Sportabout 18.7 8 360 175 3.15 3.440 17.02 0 0 0 3 1 ## Valiant 18.1 6 225 105 2.76 3.460 20.22 1 0 0 3 1
```

# dplyr - Data set preview

```
tail(mtcars, 2) # display last 2 rows
##
                mpg cyl disp hp drat wt qsec vs am gear carb
## Maserati Bora 15.0 8 301 335 3.54 3.57 14.6 0 1 5
## Volvo 142E 21.4 4 121 109 4.11 2.78 18.6 1 1 4 2
nrow(mtcars) # display number of rows
## [1] 32
ncol(mtcars) # display number of cols
## [1] 11
```

Pipe (ctrl + shift + M):

```
%>% # magrittr pipe
```

Output from the left function is passed as input to right function:

```
mtcars %>% head()
```

```
##
                  mpg cyl disp hp drat wt qsec vs am gear carb
## Mazda RX4
                  21.0
                        6 160 110 3.90 2.620 16.46 0 1
## Mazda RX4 Wag
                  21.0 6 160 110 3.90 2.875 17.02 0 1
                                                             4
## Datsun 710
              22.8 4 108 93 3.85 2.320 18.61 1 1
## Hornet 4 Drive
                  21.4 6 258 110 3.08 3.215 19.44 1 0
## Hornet Sportabout 18.7 8 360 175 3.15 3.440 17.02 0 0
                                                             2
## Valiant
                  18.1
                        6 225 105 2.76 3.460 20.22 1
```

## dplyr - Subset rows: filter()

Select rows meeting certain conditions.

Example: Cars with 6 cylinders

```
mtcars %>% filter(cyl == 6) %>% head(6)
```

```
## Mazda RX4 21.0 6 160.0 110 3.90 2.620 16.46 0 1 4 4 ## Mazda RX4 Wag 21.0 6 160.0 110 3.90 2.875 17.02 0 1 4 4 ## Hornet 4 Drive 21.4 6 258.0 110 3.08 3.215 19.44 1 0 3 1 ## Valiant 18.1 6 225.0 105 2.76 3.460 20.22 1 0 3 1 ## Merc 280 19.2 6 167.6 123 3.92 3.440 18.30 1 0 4 4 ## Merc 280C 17.8 6 167.6 123 3.92 3.440 18.90 1 0 4 4
```

## dplyr - Choose columns: select()

Pick specific columns from the dataset.

Example: Select mpg, cyl, and hp columns

```
mtcars %>% select(mpg, cyl, hp) %>% head(6)
```

```
## Mazda RX4 21.0 6 110
## Mazda RX4 Wag 21.0 6 110
## Datsun 710 22.8 4 93
## Hornet 4 Drive 21.4 6 110
## Hornet Sportabout 18.7 8 175
## Valiant 18.1 6 105
```

## dplyr - Add/modify columns: mutate()

Create new columns or modify existing ones.

Example: Calculate fuel consumption in liters per 100 km

```
mtcars %>%
  select(mpg, cyl) %>%
  mutate("1 per 100km" = round((235.215 / mpg), 0)) %>%
  head(6)
```

```
##
                   mpg cyl l per 100km
                  21.0 6
## Mazda RX4
                                  11
## Mazda RX4 Wag
                  21.0 6
                                  11
              22.8 4
## Datsun 710
                                  10
## Hornet 4 Drive 21.4 6
                                  11
## Hornet Sportabout 18.7 8
                                  13
## Valiant
                  18.1
                                 13
```

```
dplyr - Sort rows: arrange()
```

Order rows by column values ascending or descending.

Example: Sort cars by mpg descending

```
mtcars %>%
arrange(desc(mpg)) %>%
head(6)
```

```
## Toyota Corolla 33.9 4 71.1 65 4.22 1.835 19.90 1 1 4 1 ## Fiat 128 32.4 4 78.7 66 4.08 2.200 19.47 1 1 4 1 ## Honda Civic 30.4 4 75.7 52 4.93 1.615 18.52 1 1 4 2 ## Lotus Europa 30.4 4 95.1 113 3.77 1.513 16.90 1 1 5 2 ## Fiat X1-9 27.3 4 79.0 66 4.08 1.935 18.90 1 1 4 1 ## Porsche 914-2 26.0 4 120.3 91 4.43 2.140 16.70 0 1 5 2
```

# dplyr - Aggregate data by groups: group\_by() + summarize()

Group data and compute summary statistics per group.

Example: Average mpg per cylinder count

```
## # A tibble: 3 x 3

## cyl avg_mpg count

## <dbl> <dbl> <int>
## 1 4 26.7 11

## 2 6 19.7 7

## 3 8 15.1 14
```

```
dplyr - Alternative for group_by() + summarize()
```

Grouping can be done within summarize() function.

Example: Average mpg per cylinder count

```
mtcars %>%
summarize(.by = cyl,
    avg_mpg = mean(mpg),
    count = n())
```

```
## cyl avg_mpg count
## 1 6 19.74286 7
## 2 4 26.66364 11
## 3 8 15.10000 14
```

# dplyr - Remove duplicate rows distinct()

Returns unique rows from a data frame.

Example: Get unique combinations of cylinders and gears:

```
mtcars %>% select(cyl, gear) %>% distinct()
```

| ## |                   | cyl | gear |
|----|-------------------|-----|------|
| ## | Mazda RX4         | 6   | 4    |
| ## | Datsun 710        | 4   | 4    |
| ## | Hornet 4 Drive    | 6   | 3    |
| ## | Hornet Sportabout | 8   | 3    |
| ## | Toyota Corona     | 4   | 3    |
| ## | Porsche 914-2     | 4   | 5    |
| ## | Ford Pantera L    | 8   | 5    |
| ## | Ferrari Dino      | 6   | 5    |

## dplyr - Rename columns rename()

Changes column names in a data frame.

Example: Rename mpg to miles\_per\_gallon

```
mtcars %>%
select(mpg, cyl, disp, hp) %>%
rename(miles_per_gallon = mpg) %>%
head(6)
```

```
dplyr - Rename columns pull()
```

Useful for quickly extracting a single column.

Example: Get the  ${\tt mpg}$  column as a vector

```
mtcars %>%
head(6) %>%
pull(mpg)
```

```
## [1] 21.0 21.0 22.8 21.4 18.7 18.1
```

## dplyr - Perform operations row-by-row rowwise()

Applies functions across columns for each row.

Example: Calculate row-wise average of mpg, hp, and wt

```
mtcars %>%
head(2) %>%
select(mpg, hp, wt) %>%
rowwise() %>%
mutate(avg_value = mean(c(mpg, hp, wt)))
```

## dplyr - Conditional column creation if\_else()

 $\label{prop:vectorized} Vectorized\ conditional\ logic\ (used\ inside\ mutate()).$ 

Example: Label cars as "high" or "low"  ${\tt mpg}$ 

```
mtcars %>%
  tail(4) %>%
  select(mpg, hp) %>%
  mutate(mpg_type = if_else(mpg > 20, "high", "low"))
```

```
## mpg hp mpg_type
## Ford Pantera L 15.8 264 low
## Ferrari Dino 19.7 175 low
## Maserati Bora 15.0 335 low
## Volvo 142E 21.4 109 high
```

## ggplot2 - Introduction

<code>ggplot2</code> is a powerful and flexible R package for creating declarative, layered graphics. It is based on the Grammar of Graphics, which allows users to build plots step-by-step by adding components.

#### Key Features:

- Intuitive syntax using + to add layers
- ▶ Supports a wide range of plots: scatter, bar, line, boxplot, histogram, etc.
- ► Enables layered plotting (data + geoms + stats + scales + themes)
- ▶ Powerful faceting system for multi-panel plots
- ▶ Highly customizable aesthetics (color, size, shape, labels, etc.)

# ggplot2 - Core functions

- ▶ ggplot() creates a plotting object
- ▶ geom\_\*() add geometric objects (points, bars, lines)
- ▶ aes() define aesthetic mappings (e.g., x, y, color)
- ▶ facet\_wrap() / facet\_grid() split plots by variables
- scale\_\*() control axes, colors, and legends
- ▶ theme\_\*() customize non-data elements (background, font)

### More info

https://ggplot2.tidyverse.org/

#### scales - Introduction

scales is an R package that provides tools to customize how data values are mapped to visual properties (like axes, colors, and labels) in plots—especially those created with ggplot2.

#### Key Features:

- Format numbers and dates for axis labels (e.g., currency, percentages, commas)
- ► Create and customize color palettes and gradients
- ▶ Apply transformations (log, reverse, square root) to scales
- ► Generate breaks and labels automatically or manually for axes
- ▶ Support for continuous, discrete, and date/time scales

### scales - Core functions

- Label functions: label\_dollar(), label\_percent(), label\_comma(), etc. format axis and legend labels
- Color scales: scale\_color\_gradient(), scale\_fill\_brewer(), etc. define color mappings
- Transformations: trans\_new(), built-in like log\_trans(), reverse\_trans() modify scale behavior
- ▶ Breaks and limits: control where ticks and labels appear on axes

#### More info

https://scales.r-lib.org/

### ggplot2 + scales: diamonds data set

A data set containing the prices and other attributes of almost 54,000 diamonds. Part of the ggplot2 package.

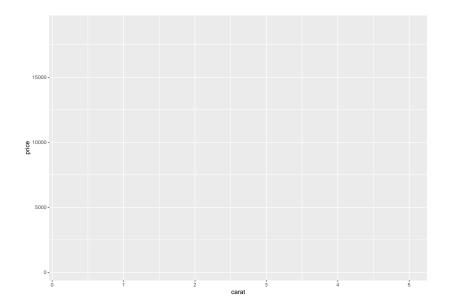
### Key columns:

- price: price in US dollars
- carat: weight of the diamond
- cut, color, clarity: quality metrics
- x, y, z: dimensions

```
## # A tibble: 3 x 10
##
    carat cut color clarity depth table price
                                              X
##
    <dbl> <ord> <ord> <ord> <dbl> <dbl> <int> <dbl> <dbl> <dbl> <</pre>
## 1 0.23 Ideal E
                    SI2 61.5
                                       326 3.95 3.98 2.43
                                   55
## 2 0.21 Premium E
                    SI1 59.8
                                   61 326 3.89 3.84 2.31
## 3 0.23 Good E
                    VS1
                            56.9
                                   65 327 4.05 4.07
                                                     2.31
```

# ggplot2 + scales: plot base

```
ggplot(data = diamonds, aes(x = carat, y = price))
```



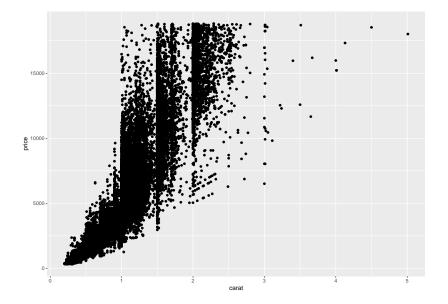
ggplot2 + scales: geoms

Add layers to represent data.

- ▶ geom\_point() scatterplot
- geom\_bar(), geom\_col() bar charts
- geom\_histogram() histogram
- geom\_boxplot() boxplot

ggplot2 + scales: geom\_point()

```
ggplot(data = diamonds, aes(x = carat, y = price)) + geom_point()
```

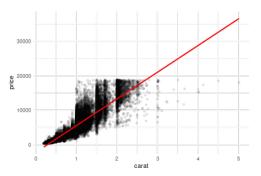


# ggplot2 + scales: Stats (stat\_\*)

Statistical transformations.

stat\_smooth(method = "lm") - regression line

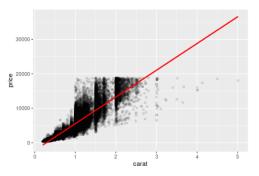
```
ggplot(diamonds, aes(carat, price)) +
  geom_point(alpha = 0.1) +
  stat_smooth(formula = y ~ x, method = "lm", col = "red") +
  theme_minimal() # select nice theme here
```



### ggplot2 + scales: Themes

Control non-data visuals (font, background, gridlines).

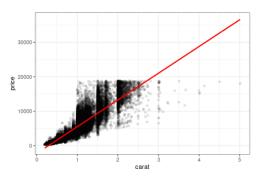
```
ggplot(diamonds, aes(carat, price)) +
  geom_point(alpha = 0.1) +
  stat_smooth(formula = y ~ x, method = "lm", col = "red")
```



### ggplot2 + scales: Themes

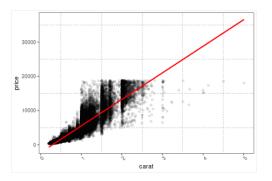
Control non-data visuals (font, background, gridlines).

```
ggplot(diamonds, aes(carat, price)) +
  geom_point(alpha = 0.1) +
  stat_smooth(formula = y ~ x, method = "lm", col = "red") +
  theme_bw()
```



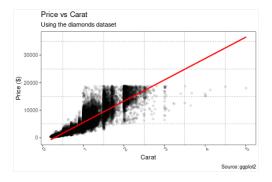
### ggplot2 + scales: Themes

Control non-data visuals (font, background, gridlines).



# ggplot2 + scales: Labels and Titles

```
labs(title = "Price vs Carat",
    subtitle = "Using the diamonds dataset",
    x = "Carat", y = "Price ($)",
    caption = "Source: ggplot2")
```

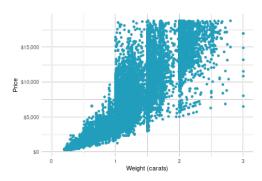


### ggplot2 + scales: Scales

Control axes and legends.

```
xlab("Weight (carats)") +
ylab("Price") +
scale_x_continuous(breaks = seq(0, 3, 0.5))
scale_y_continuous(labels = scales::label_dollar()) # or simply: scales::dollar
```

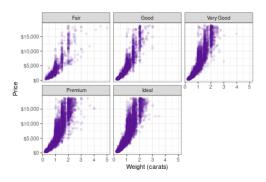
## Warning: Removed 32 rows containing missing values or values outside the sca
## ('geom\_point()').



## ggplot2 + scales: Facets

Split data into subplots.

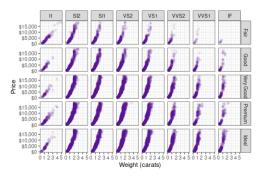
▶ facet\_wrap(~cut)



## ggplot2 + scales: Facets

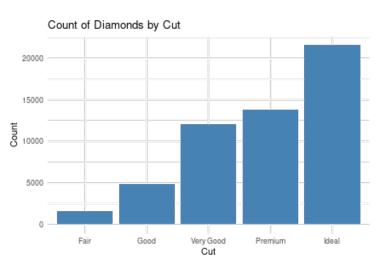
Split data into subplots.

facet\_grid(cut ~ clarity)



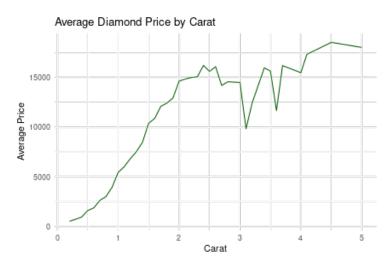
# Additional geometrics: geom\_bar

Count of diamonds by cut.



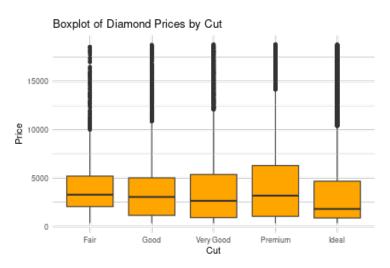
# Additional geometrics: geom\_line

Average price by carat.



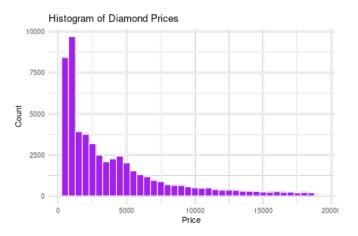
# Additional geometrics: geom\_boxplot

Price distribution by cut.



# Additional geometrics: geom\_histogram

Distribution of diamond prices.



## stringr - Introduction

stringr is an R package designed to make working with strings (character data) easier, consistent, and more user-friendly. It provides a cohesive set of functions that simplify common string manipulation tasks such as detecting, extracting, replacing, and splitting strings.

| Function          | Purpose                                       |
|-------------------|---|
| str_length()      | Returns the number of characters in a string  |
| str_sub()         | Extracts substrings based on position         |
| str_detect()      | Checks if a pattern exists in a string        |
| str_subset()      | Extracts strings that match a pattern         |
| str_replace()     | Replaces the first match of a pattern         |
| str_replace_all() | Replaces all matches of a pattern             |
| str_split()       | Splits strings into pieces based on a pattern |
| str_trim()        | Removes leading and trailing whitespace       |

## stringr - Examples

```
library(stringr)
text <- "The quick brown fox jumps over the lazy dog."
# Detect if 'fox' is in the string
str_detect(text, "fox")
## [1] TRUE
# Extract the first 9 characters
str_sub(text, 1, 9)
## [1] "The quick"
# Replace 'fox' with 'cat'
str_replace(text, "fox", "cat")
```

## [1] "The quick brown cat jumps over the lazy dog."

# stringr in real-life: modify gene\_ids

```
df <- tibble(gene_id = c("ENSG00000000457.14", "ENSG0000000005.6", "ENSG000000
            biotype = c("protein_coding", "protein_coding", "lncRNA"))
df
## # A tibble: 3 x 2
##
    gene id
                      biotype
##
    <chr>
                       <chr>>
## 1 ENSG0000000457.14 protein_coding
## 2 ENSG0000000005.6 protein coding
## 3 ENSG00000310545.1 lncRNA
df %>% mutate(gene_id = str_remove(gene_id, "\\.\\d+$"))
## # A tibble: 3 x 2
##
    gene id biotype
##
    <chr>
                 <chr>
## 1 ENSG0000000457 protein coding
## 2 ENSG00000000005 protein coding
## 3 ENSG00000310545 lncRNA
```

## stringr in real-life: modify biotypes

```
df
## # A tibble: 3 x 2
##
     gene_id
                        biotype
##
     <chr>>
                        <chr>>
## 1 ENSG0000000457.14 protein_coding
## 2 ENSG00000000005.6
                        protein_coding
## 3 ENSG00000310545.1
                        lncRNA
df %>% mutate(biotype = str_replace(biotype, "protein_coding", "pc"))
## # A tibble: 3 x 2
##
     gene_id
                        biotype
##
     <chr>>
                        <chr>>
## 1 ENSG0000000457.14 pc
## 2 ENSG00000000005.6
                        DC
## 3 ENSG00000310545.1
                        lncRNA
```



### Excercise 1:

## iris Dataset: Average Sepal Length by Species

Dataset: iris

Task:

- Use dplyr to compute the average sepal length per species.
- ▶ Use ggplot2 to create a bar plot of the results.

Hint: Use geom\_bar(stat = "identity") or geom\_col()!

### Excercise 2:

### mtcars: Horsepower vs MPG by Cylinders

Dataset: mtcars

Task:

- Use dplyr to group by the number of cylinders (cyl) and compute the average mpg and hp.
- Create a scatter plot of avg horsepower vs avg mpg, colored by number of cylinders.

**Hint:** Use factor(cyl) for color aesthetics.

### Excercise 3:

## ToothGrowth: Effect of Dose on Tooth Length

Dataset: ToothGrowth

Task:

- Use dplyr to calculate mean tooth length for each dose.
- Create a line plot showing tooth length vs dose, colored by supplement type (supp).

**Hint:** Don't forget to group\_by both: dose and supp!

### Excercise 4:

## CO2: Uptake Rate by Treatment

Dataset: CO2

- ▶ Filter for Type == "Quebec".
- Use dplyr to get average uptake per treatment and concentration.
- Use ggplot2 to plot a line graph of uptake vs concentration for each treatment.

Excercise 5:

### ChickWeight: Growth Over Time

Dataset: ChickWeight

- ▶ Use dplyr to filter for a few selected chicks (e.g., Chick %in% c(1, 5, 10)).
- Use ggplot2 to create a line plot of weight over time per chick.

### Excercise 6:

### mtcars: Boxplot of MPG by Transmission

Dataset: mtcars

- Use dplyr to mutate am to a factor labeled "Automatic" and "Manual".
- Create a boxplot of mpg by transmission type (am).

### Excercise 7:

### iris: Sepal Width Distribution

Dataset: iris

- Use ggplot2 to make a histogram of sepal width, filled by species.
- Use facet\_wrap() to show separate plots per species.

### Excercise 8:

### USArrests: Violent Crime by Region

Dataset: USArrests

Task:

- Add a column for region (use state.region from base R, it matches row names of USArrests).
- ▶ Use dplyr to get average murder and assault rate per region.
- ▶ Create a bar plot of average assault rate per region.

Hint: To match regions use: state.region[match(rownames(.), state.name)]

### Excercise 9:

## Titanic Survival (from titanic package or datasets::Titanic)

Dataset: as.data.frame(Titanic)

- Use dplyr to calculate survival rate per class and sex.
- ▶ Use ggplot2 to create a stacked bar plot showing survival by class and sex.