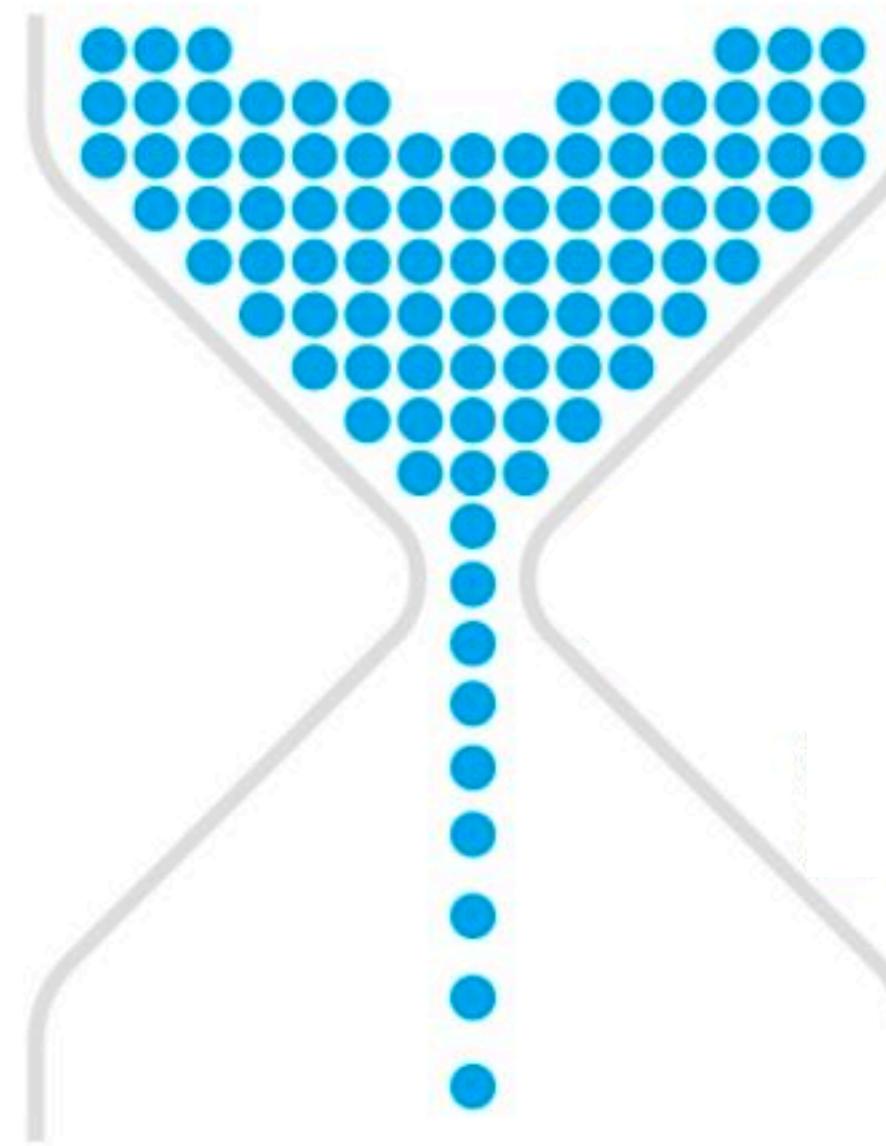




Basic R Programming

Mustafa Anil Kocak **March 4th 2024**

Why learn statistical programming?



Data is the new commodity

- We have better access to data than most of the world
- Not using it efficiently is leaving money on the table!

Analysis/analysts are typical bottlenecks

- Analysts are working one experiment at a time
- Understanding the experiment, meta-data and questions takes time

Most of the analyses are ...

- straightforward once you got the experimental thinking
- can be performed with a limited vocabulary!

Most analyses are doable with limited vocabulary

- Visualization (ggplot)**
- Vectors, lists and data tables (tibbles)**
- Libraries and how to get help**
- Loading/Saving datasets:** `data.table::fread`, `readRDS()`, `write_csv()`
- Taking a peek:** `head()`, `tail()`, `summary()`, `names()`, `View()`, `nrow()`, `table()`, `dim()`,
`summarize()`, `describe()`
- Data manipulation:** `select()`, `distinct()`, `filter()`, `group_by()`, `ungroup()`, `summarize()`,
`summarize_all()`, `arrange()`, `count()`
- Joins:** `left/right/inner/full/anti/semi_join()`
- Extra:** `top_n()`, `is.finite()`, `is.na()`, `%in%`, `paste0()`, `max()`, `min()`, `mean()`, `median()`, `sd()`,
`mad()`, `quantile()`, `is.finite()`, `toupper()`, `word()`, `n()`, `%>%`, `write_csv()`, `bind_rows()`, `c()`,
`psych::pairs.plots()`, `pheatmap()`, `reorder()`, `taiga (?)`

What is our objective?

How to draw an owl

1.



2.



1. Draw some circles

2. Draw the rest of the ~~fucking~~ owl

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Knowledge

Skill

Attitude

What is our objective?

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Knowledge

- What R is good for; tutorials, resources, lectures

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- Using what you learned in your projects next week

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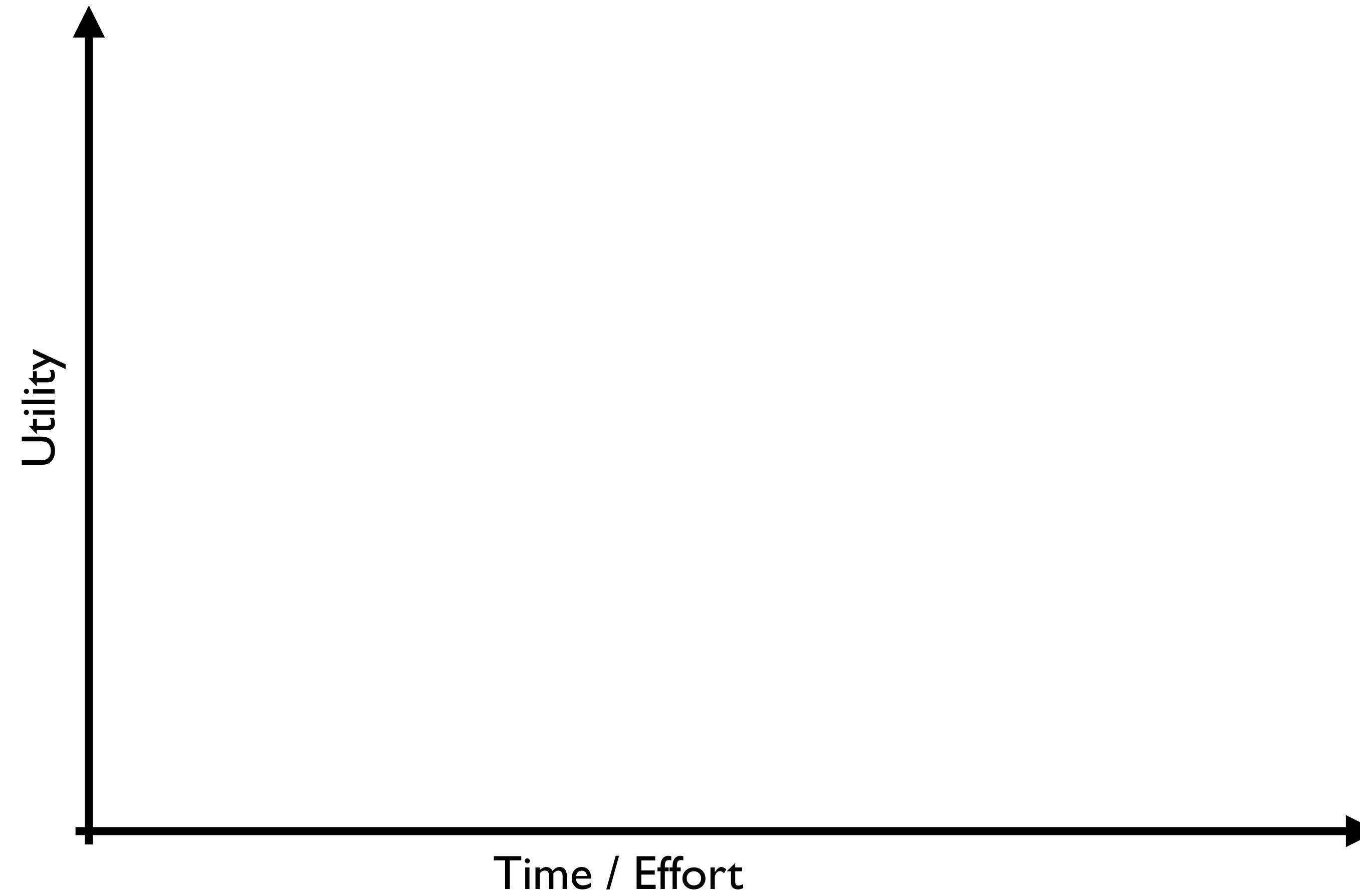
- Using what you learned in your projects next week

Attitude

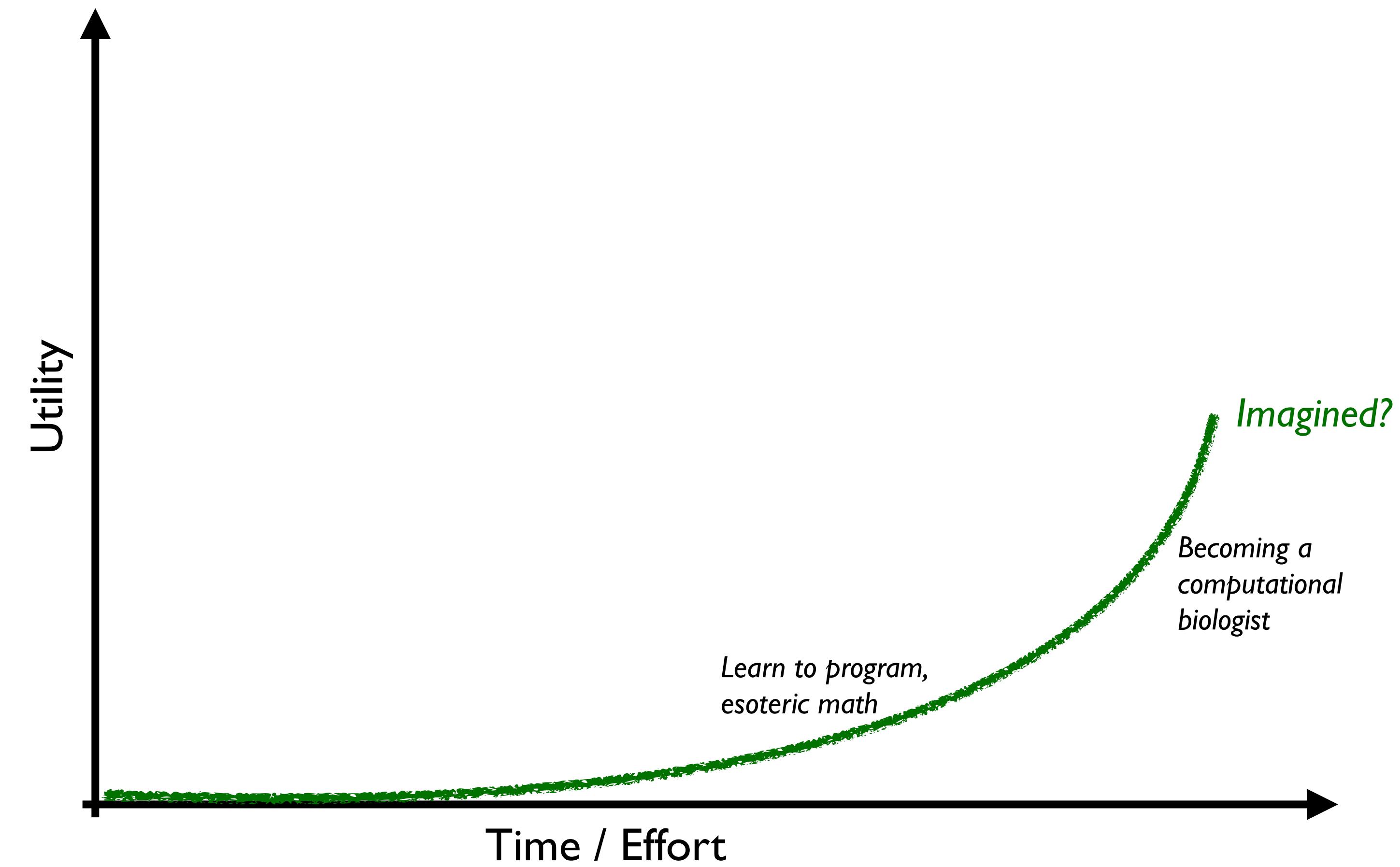
- Keep using what you learned in the bootcamp

- Having joy through playing with data!

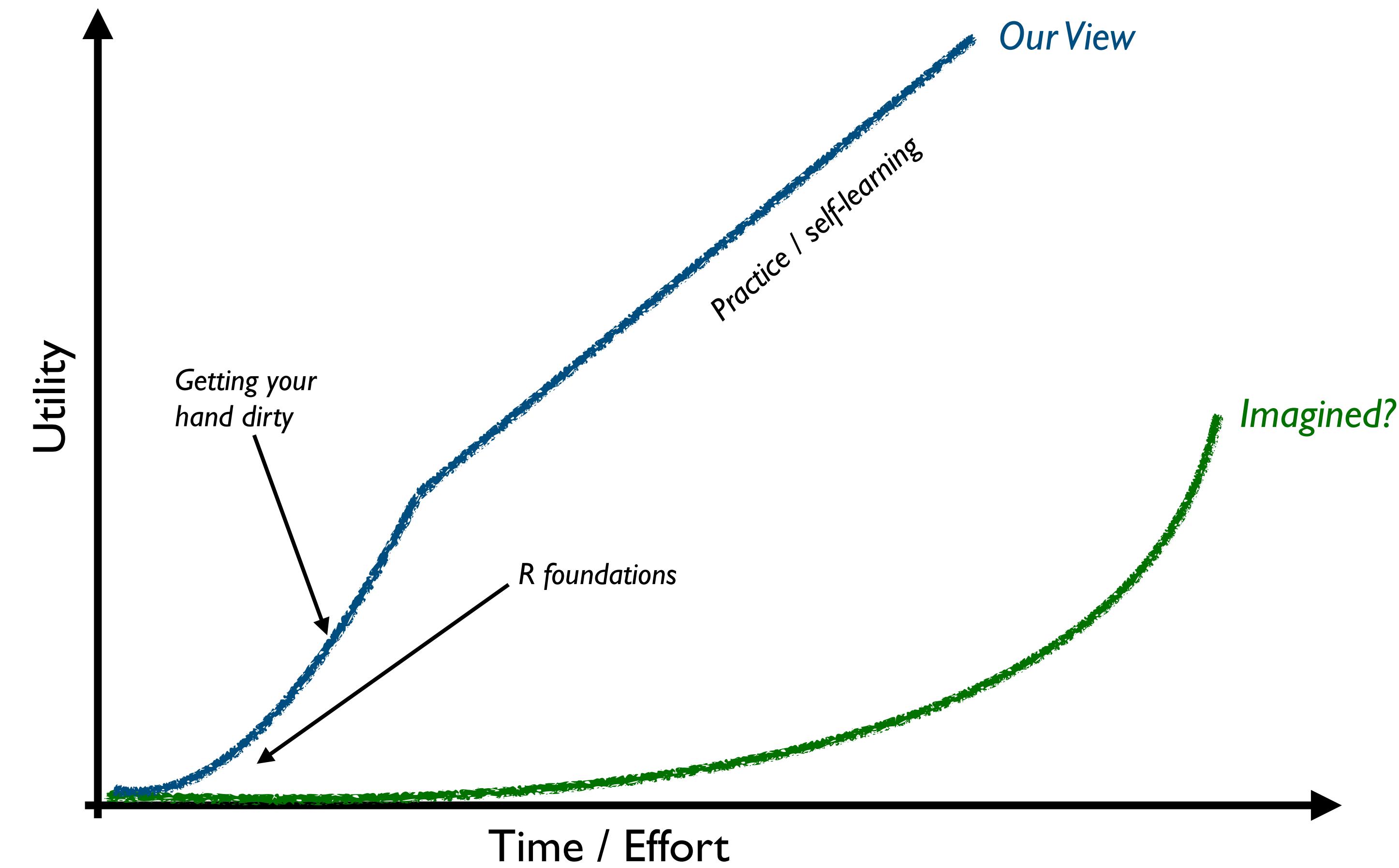
Our View of the Learning Curve



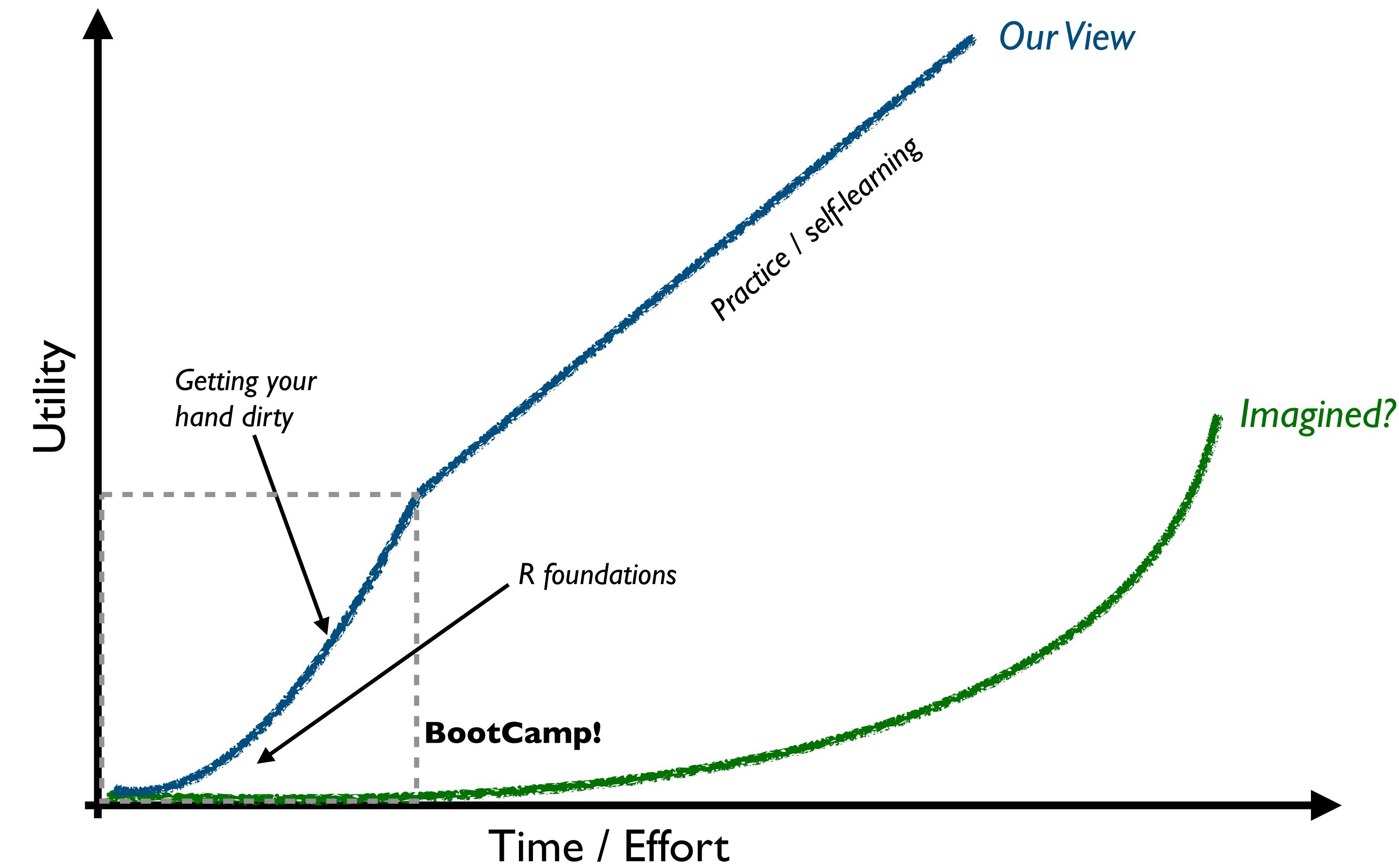
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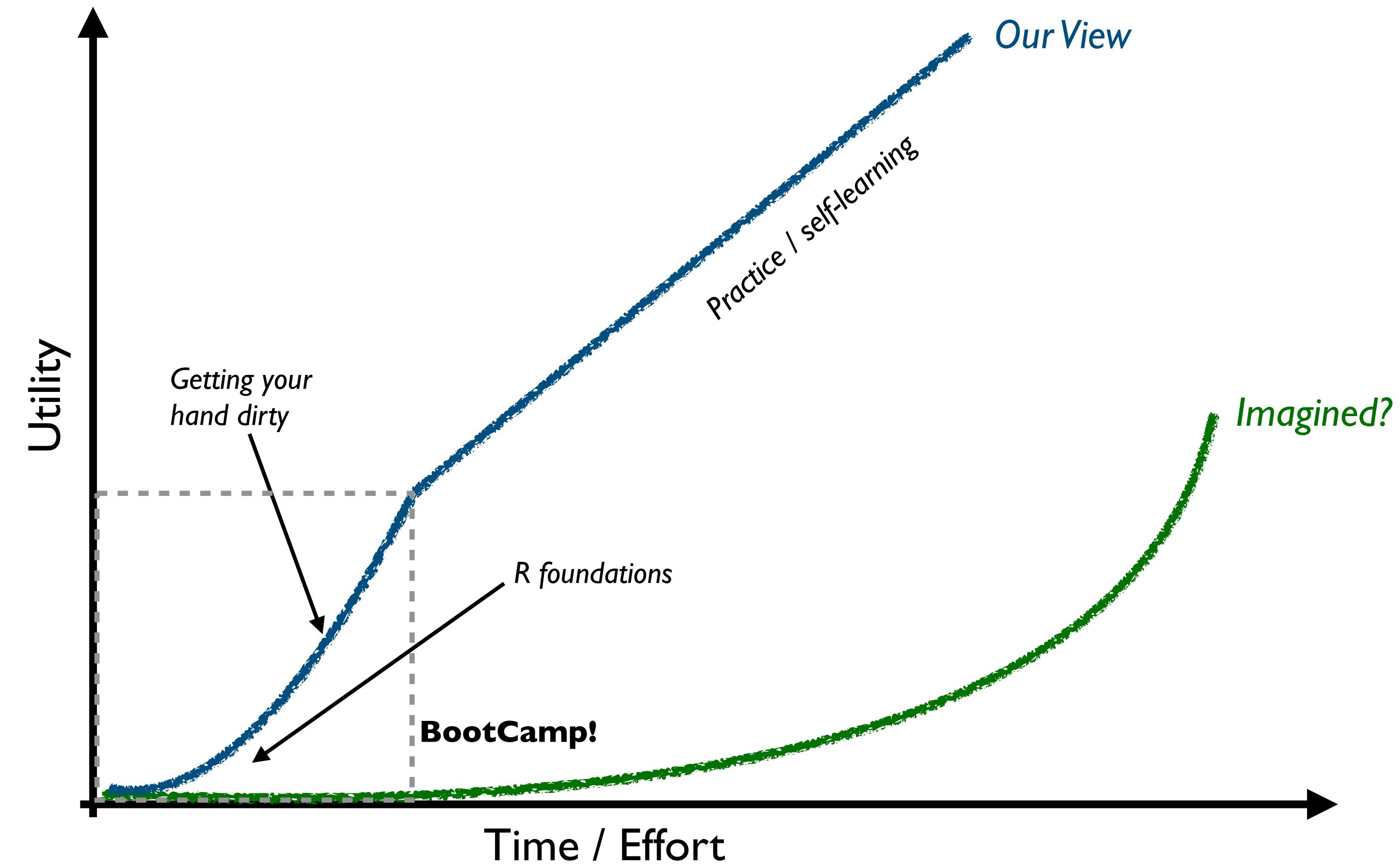


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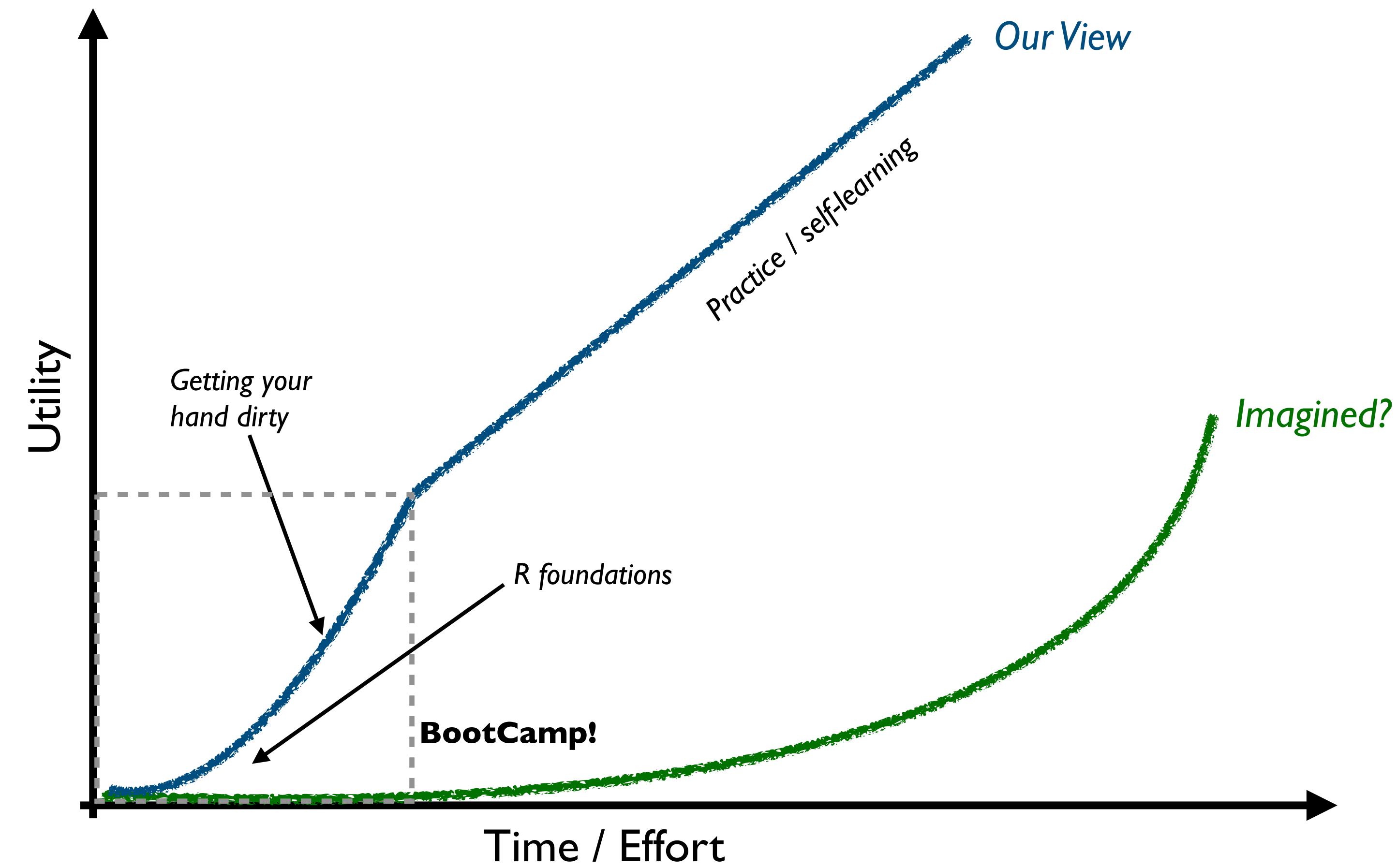
I need your help!



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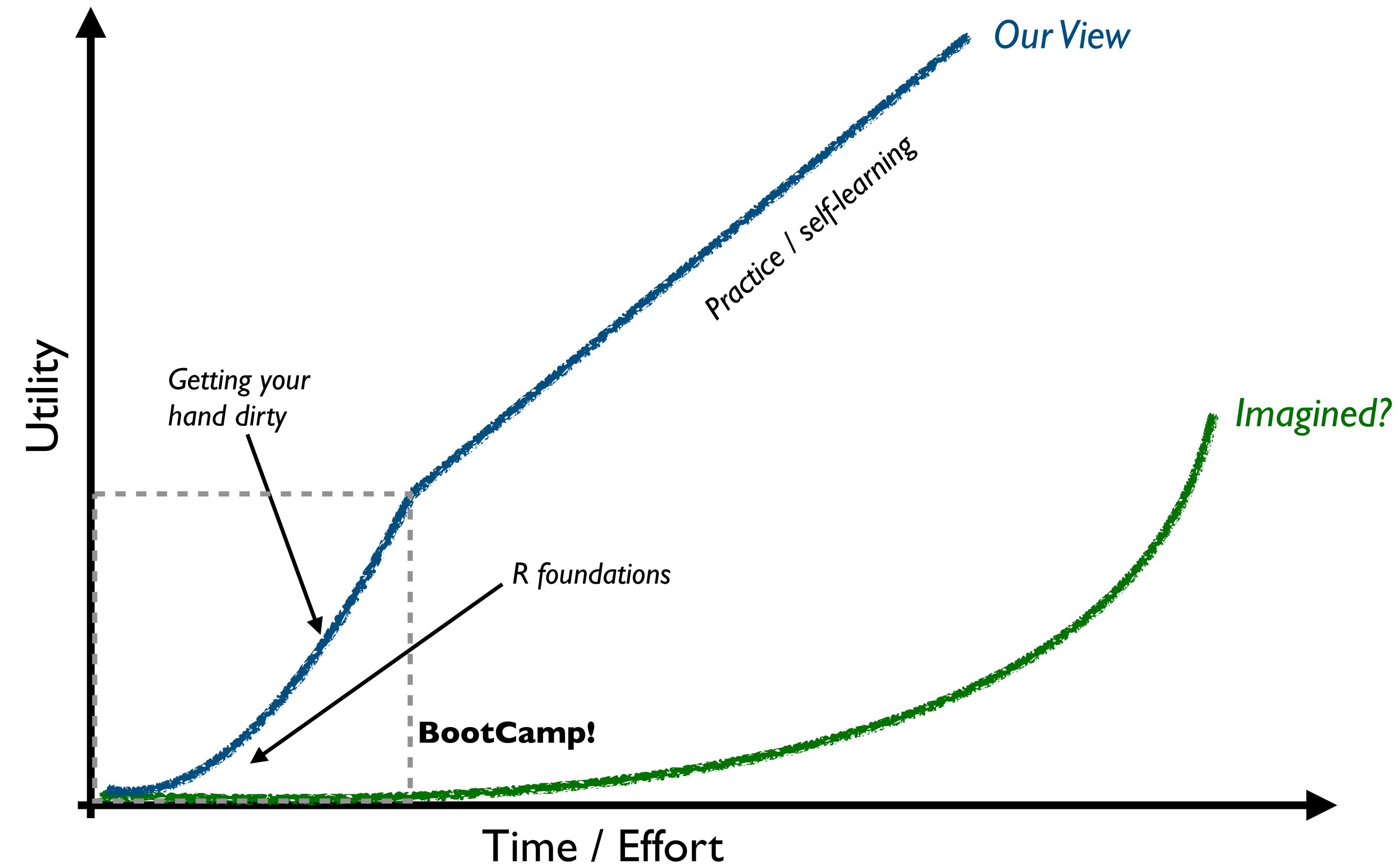
- This is my first second bootcamp



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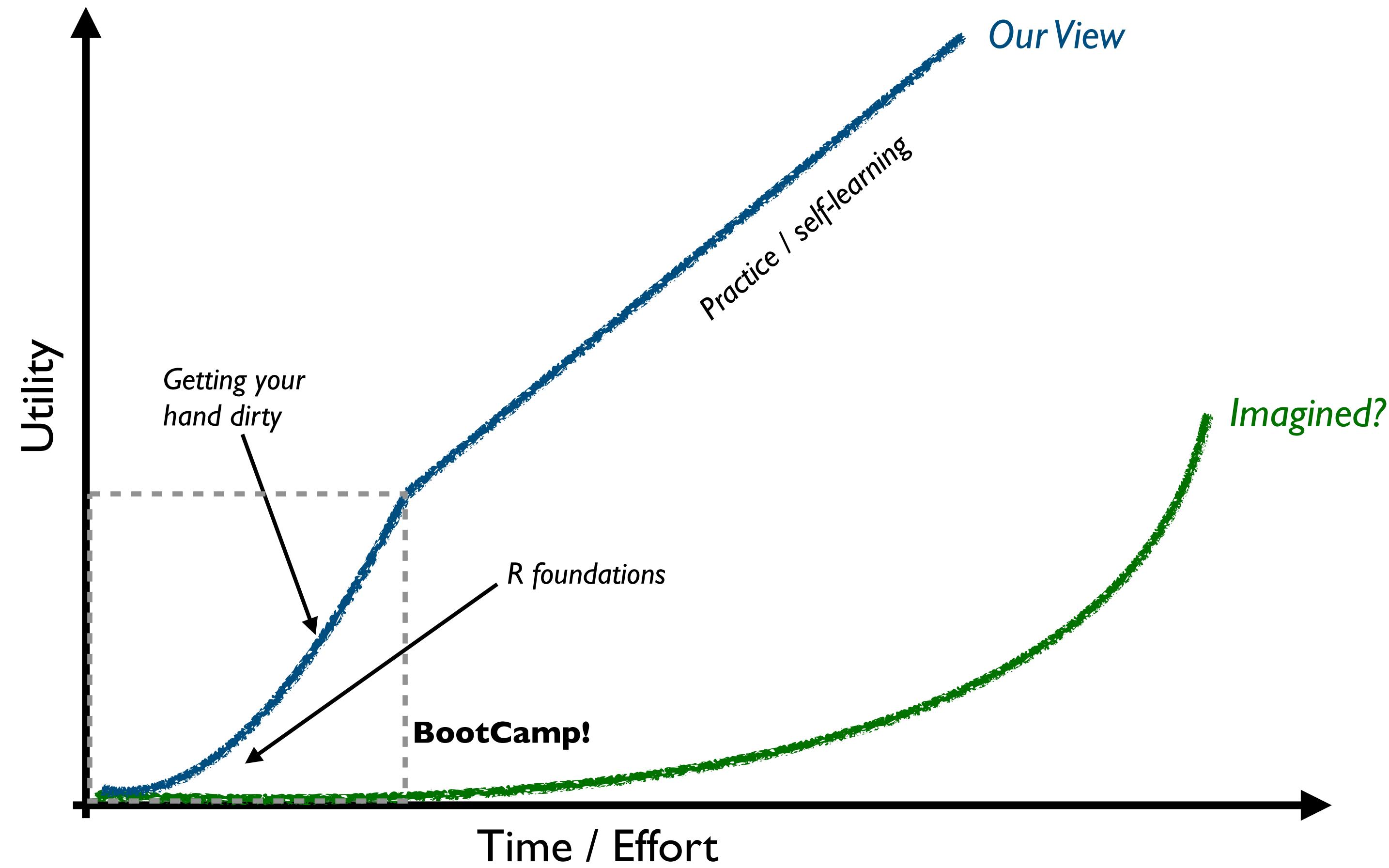
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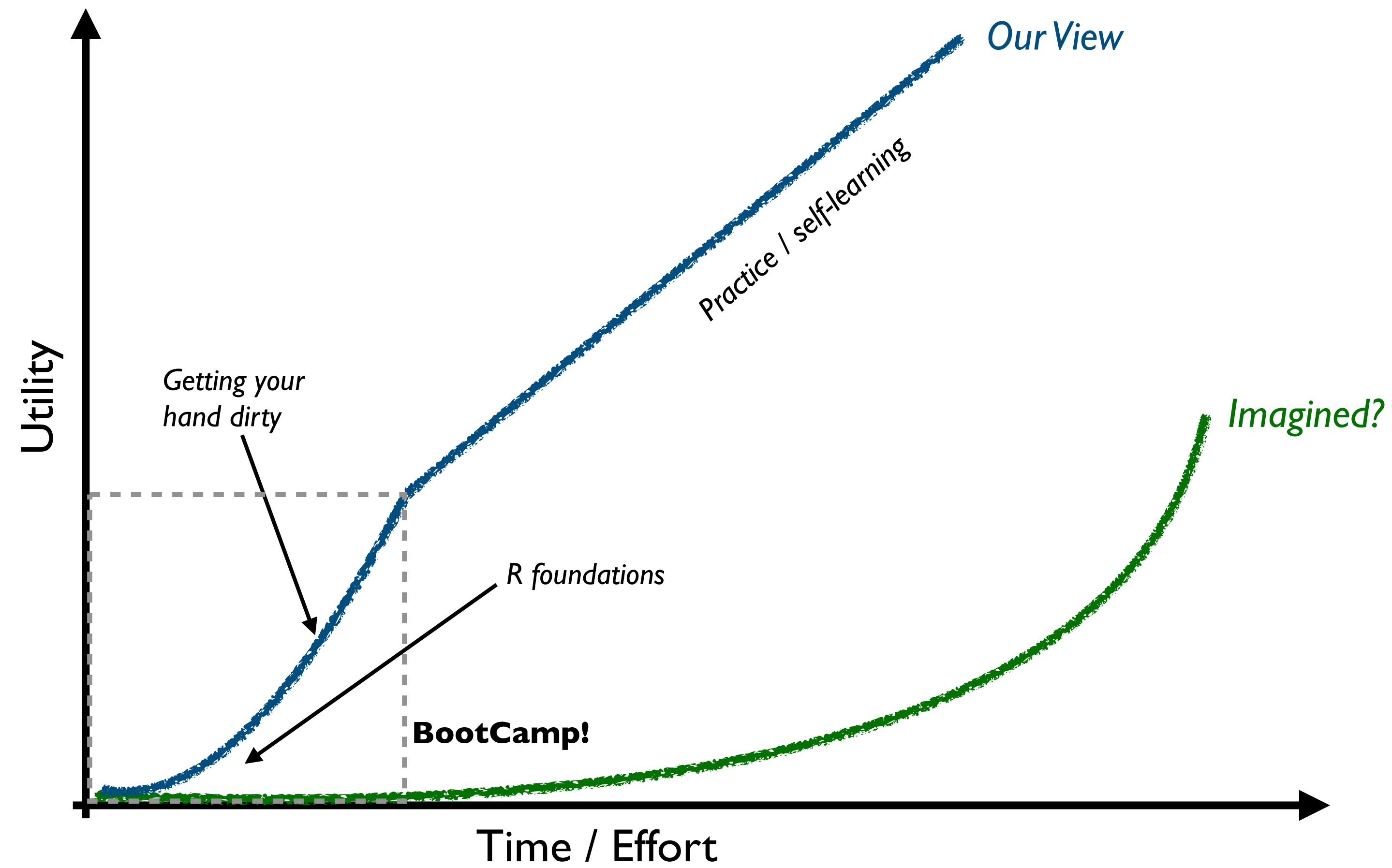
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- And I am nervous :)
- We will figure it out together



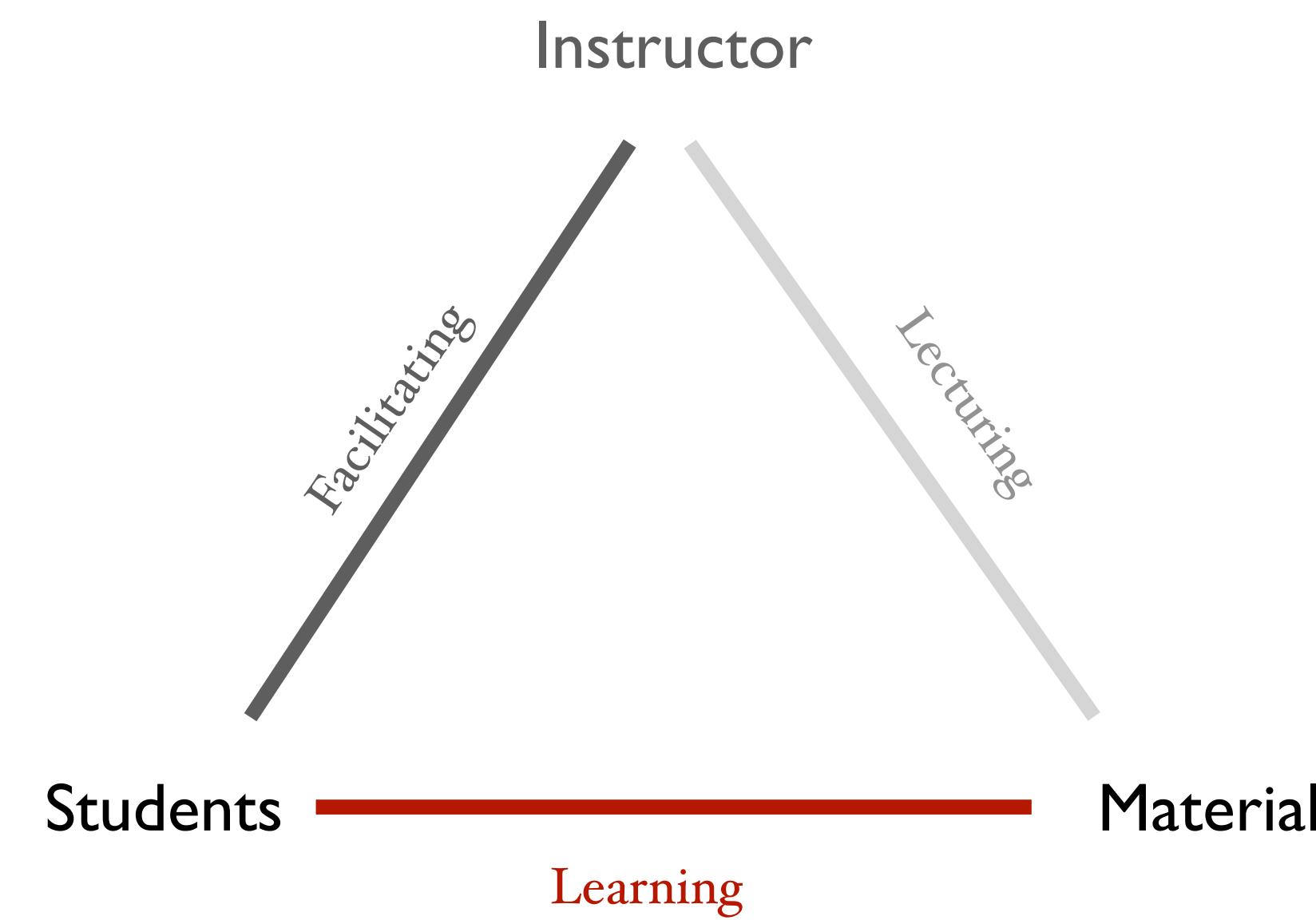
Our View of the Learning Curve

I need your help!

- This is my first second bootcamp
- And I am nervous :)
- We will figure it out together
- Please ask questions and give feedback



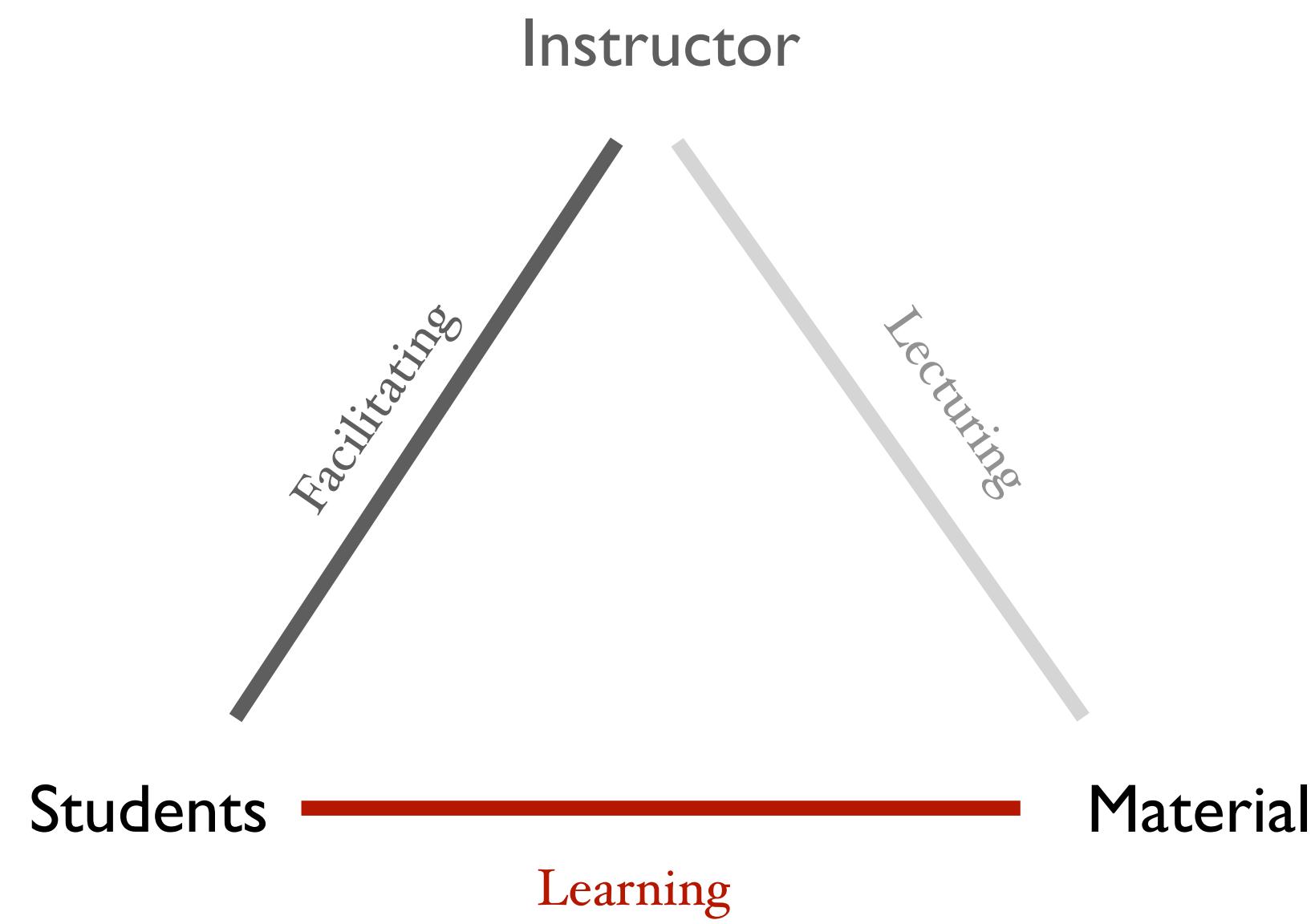
Approach



Approach

Emphasis on the practical skills

- Basics, visualization, wrangling, ...



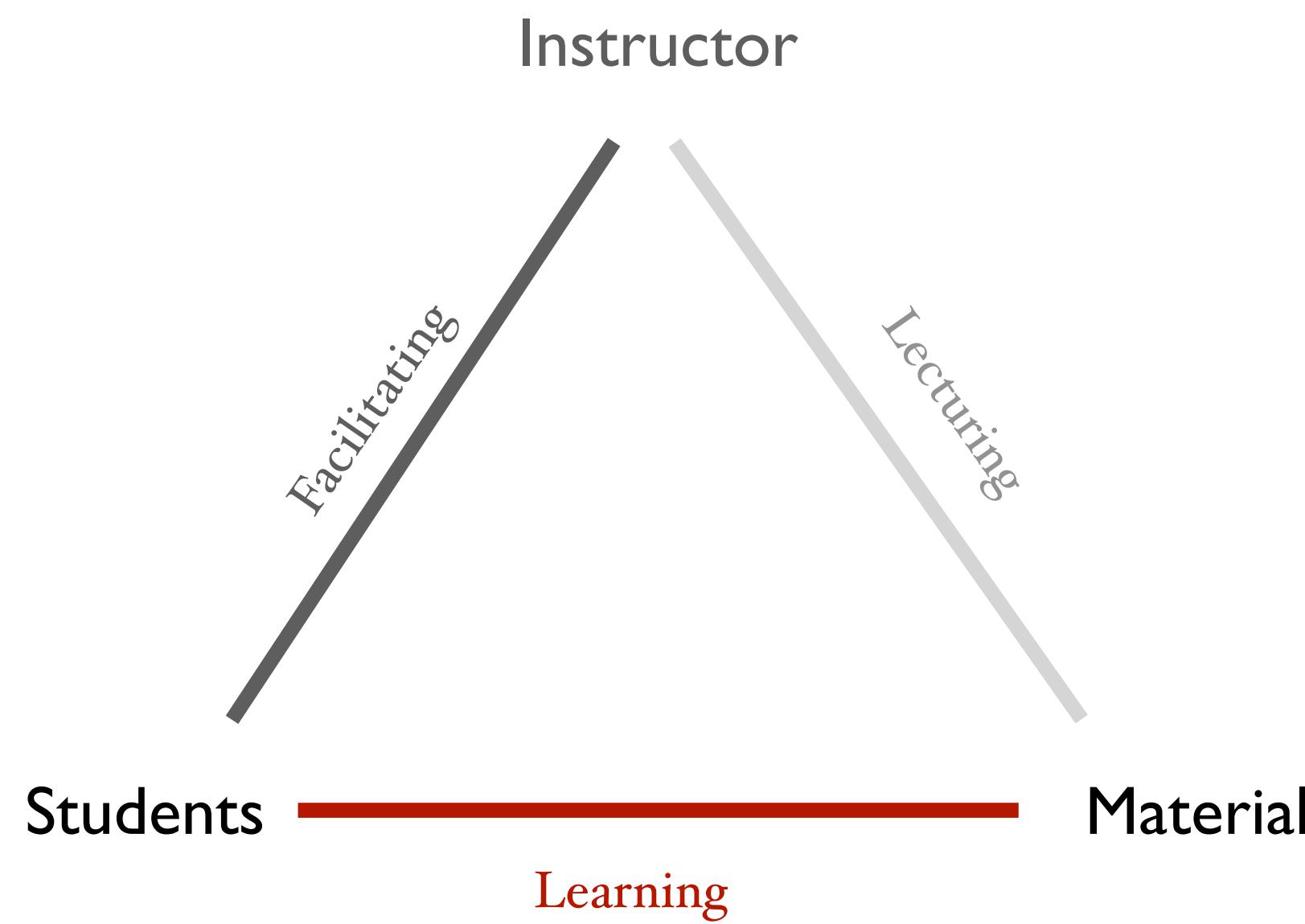
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Pointing out resources but
mostly giving the ‘need-to-know’

- Think about what else would you
like to do with R and data?



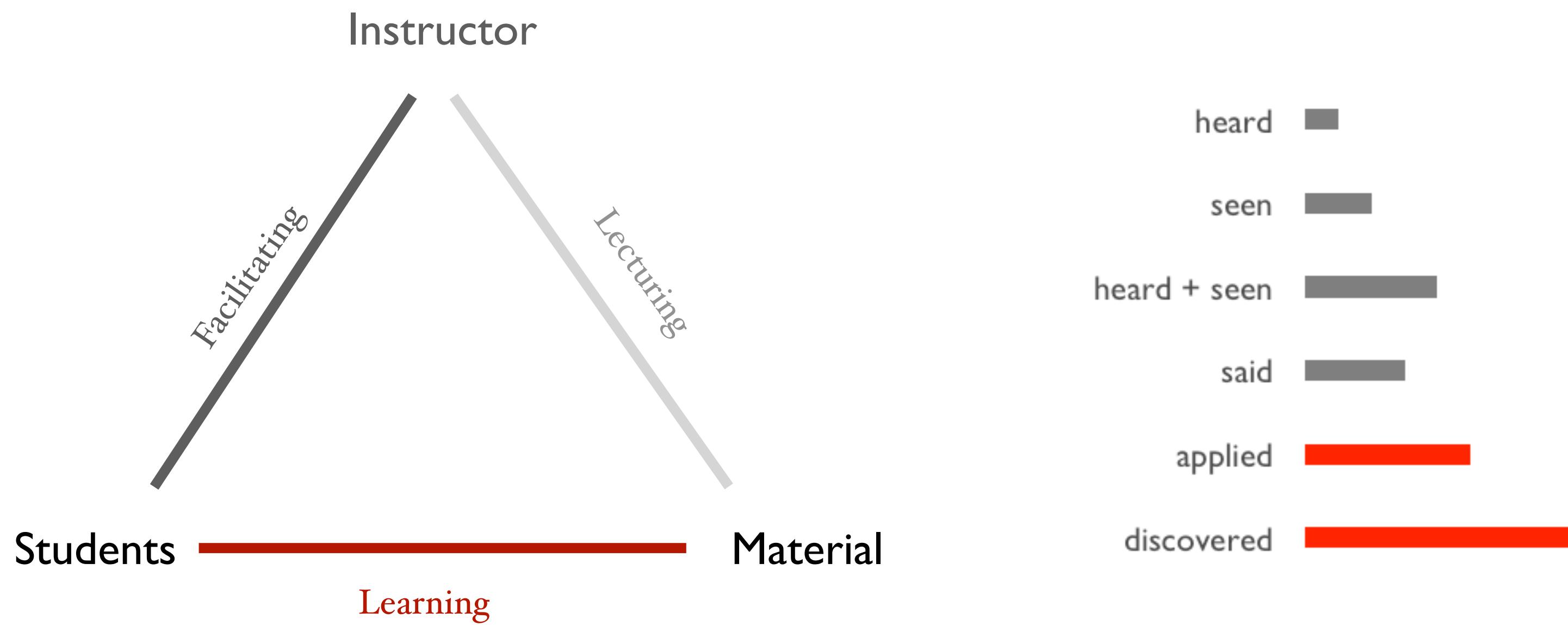
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Approach

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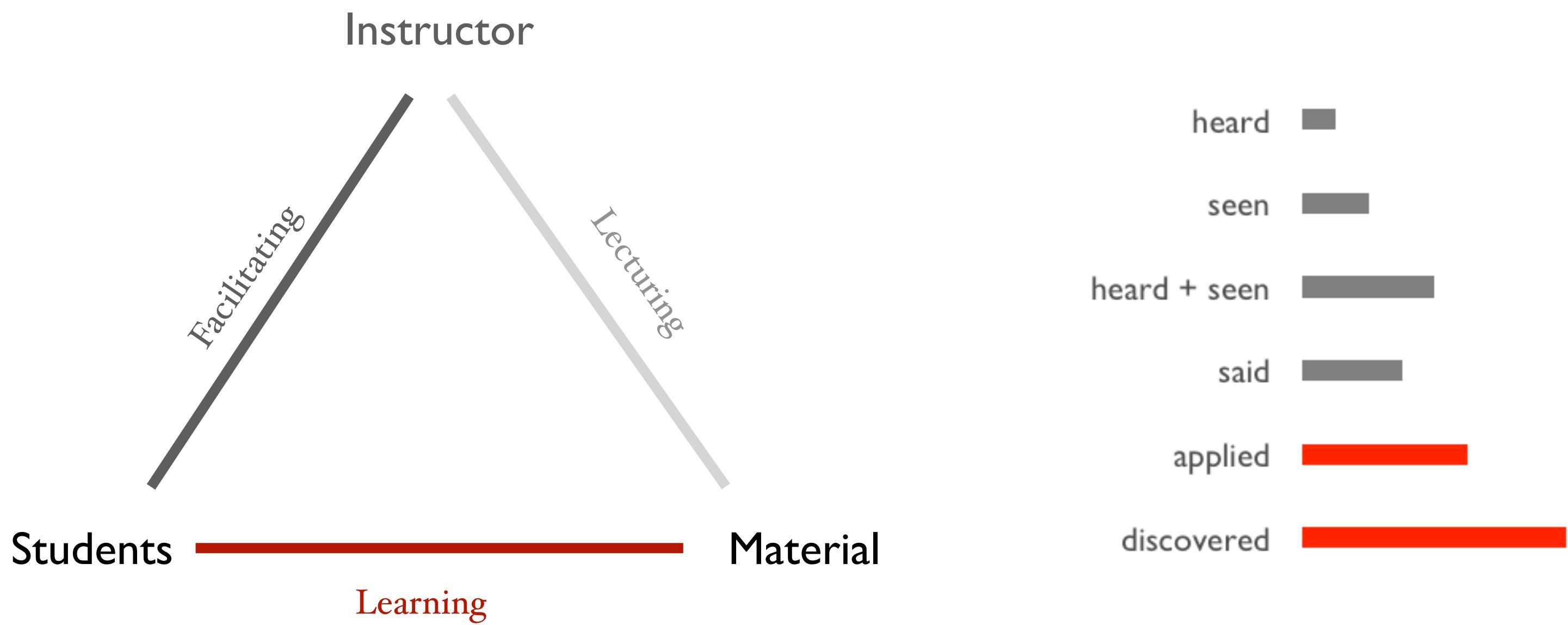
- Basics, visualization, wrangling, ...

Pointing out resources but mostly giving the 'need-to-know'

- Think about what else would you like to do with R and data?

Slides are reminders, we will write code during the sessions.

- Learn from your experience and peers!



Course Content

First Encounter with R Programming!

- R studio, scripts, markdowns
- Functions, packages, help pages
- R Objects, notation & modifying values
- Data structures, programming

Introduction to Tidyverse

- Visualization
- Wrangling
- Exploratory Data Analysis

Miscellaneous

- Practice and case studies
- Advanced data visualization
- Machine learning examples

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A hands-on introduction to basic R

The Very Basics
R Objects & Notation
Basic Programming

First Encounter with R Programming!

Freely available online:

- <https://rstudio-education.github.io/hopr/>

Little pedestrian, but great introduction.

We will skip chapters 8 and 10.

- Recommended for self-study
- Great basis, but we will significantly refine in the following sessions.



Garrett Grolemund

The Very Basics

User Interface

Objects

Functions

Writing your Own Functions

Packages

Scripts / Mark-downs

R Studio Interface

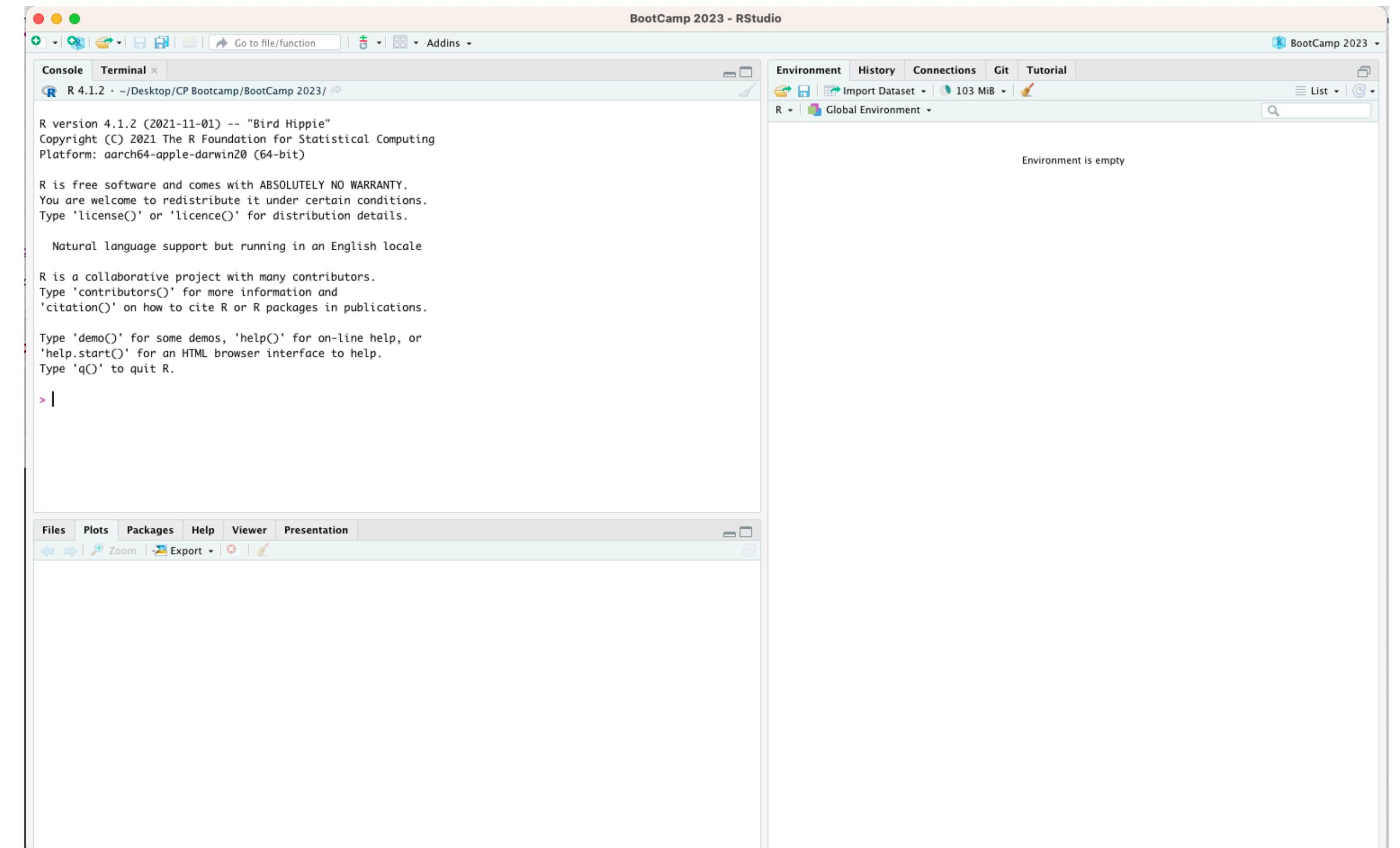
□ Interface

□ Projects

□ R as a calculator

□ Scripts and mark-downs

□ Arithmetic operators



R Objects

Variables

Vectors

Naming convention

Vector recycling

$$\begin{array}{rcl} \text{die} & * & \text{die} \\ \hline 1 & * & 1 \\ 2 & * & 2 \\ 3 & * & 3 \\ 4 & * & 4 \\ 5 & * & 5 \\ 6 & * & 6 \end{array} = \begin{array}{r} 1 \\ 4 \\ 9 \\ 16 \\ 25 \\ 36 \end{array}$$

$$\begin{array}{rcl} \text{die} & * & \text{c}(1,2) \\ \hline 1 & * & 1 \\ 2 & * & 2 \\ 3 & * & 1 \\ 4 & * & 2 \\ 5 & * & 1 \\ 6 & * & 2 \end{array} = \begin{array}{r} 1 \\ 4 \\ 4 \\ 6 \\ 6 \\ 8 \end{array}$$

Functions

□ Calling a function

□ Arguments

□ Help pages

□ Writing a function

□ Extract function

1. **The name.** A user can run the function by typing the name followed by parentheses, e.g., roll2().

3. **The arguments.** A user can supply values for these variables, which appear in the body of the function.

4. **The default values.** Optional values that R can use for the arguments if a user does not supply a value.

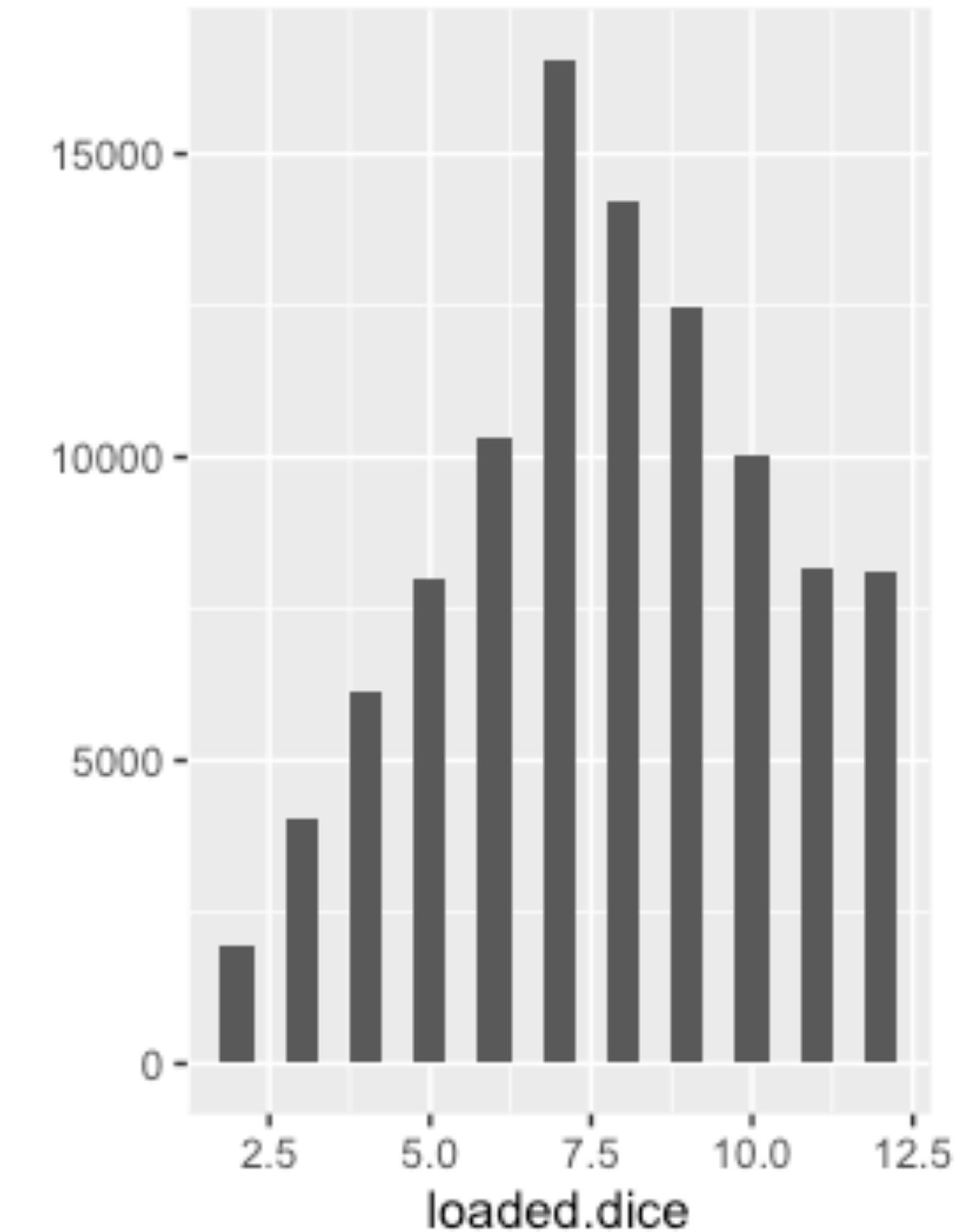
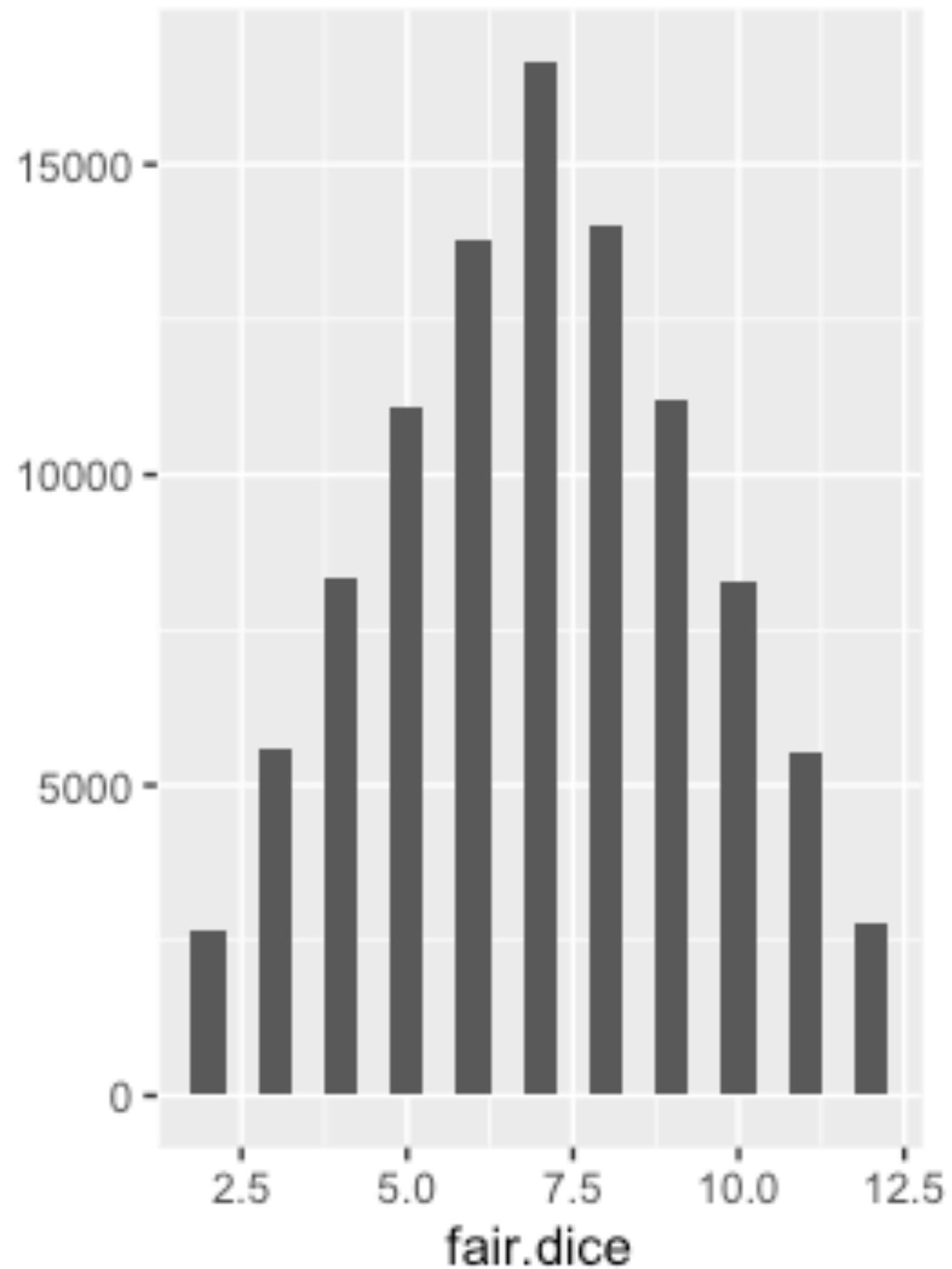
2. **The body.** R will run this code whenever a user calls the function.

```
roll2 <- function(bones = 1:6) {  
  dice <- sample(bones, size = 2,  
    replace = TRUE)  
  sum(dice)  
}
```

5. **The last line of code.** The function will return the result of the last line.

Packages

- Installing packages
- Loading packages
- Functions from a package
- Help pages re-visited
- Misc:
 - c / replicate / qplot / ctrl + c / pipe / plot_grid



R Objects & Notation

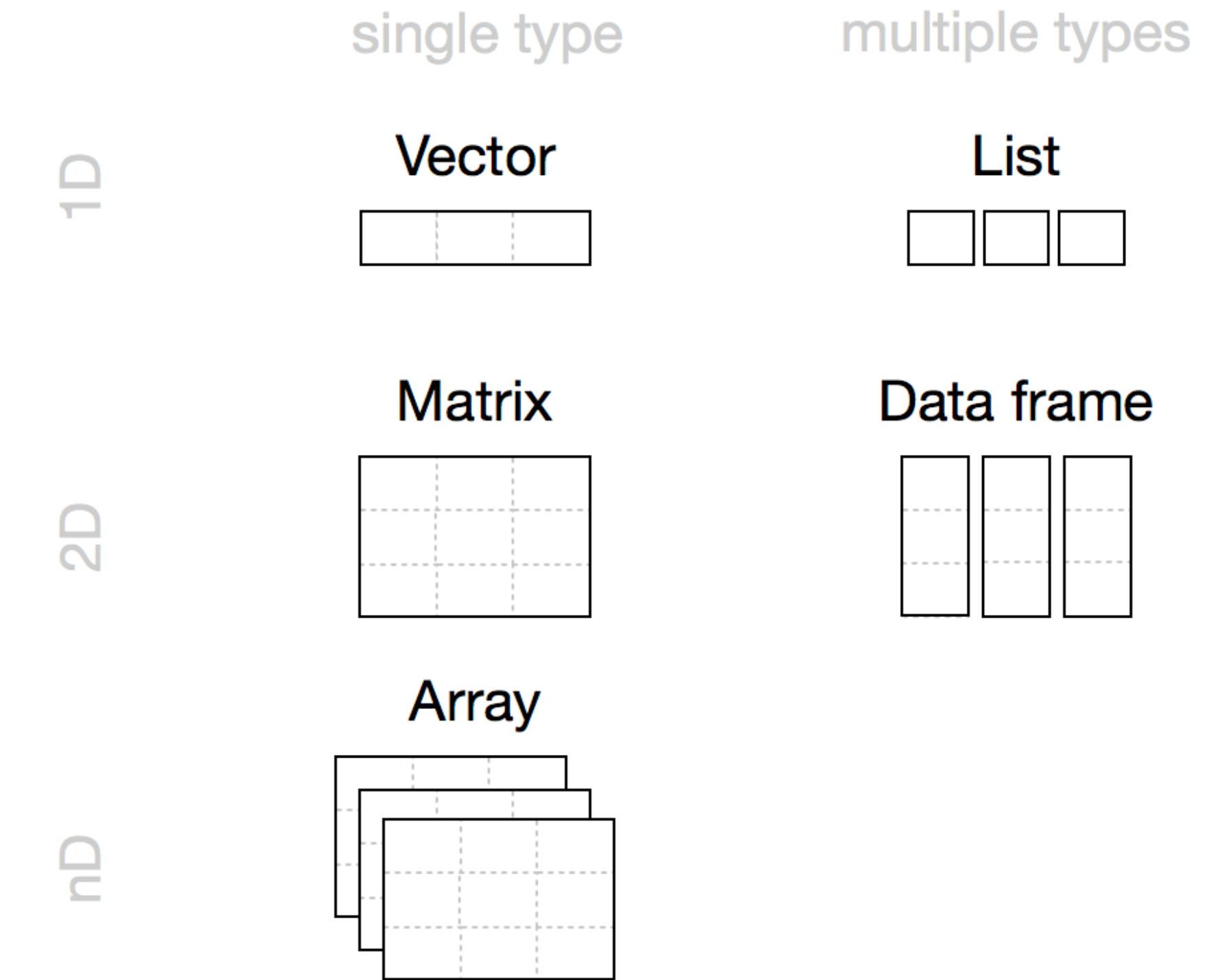
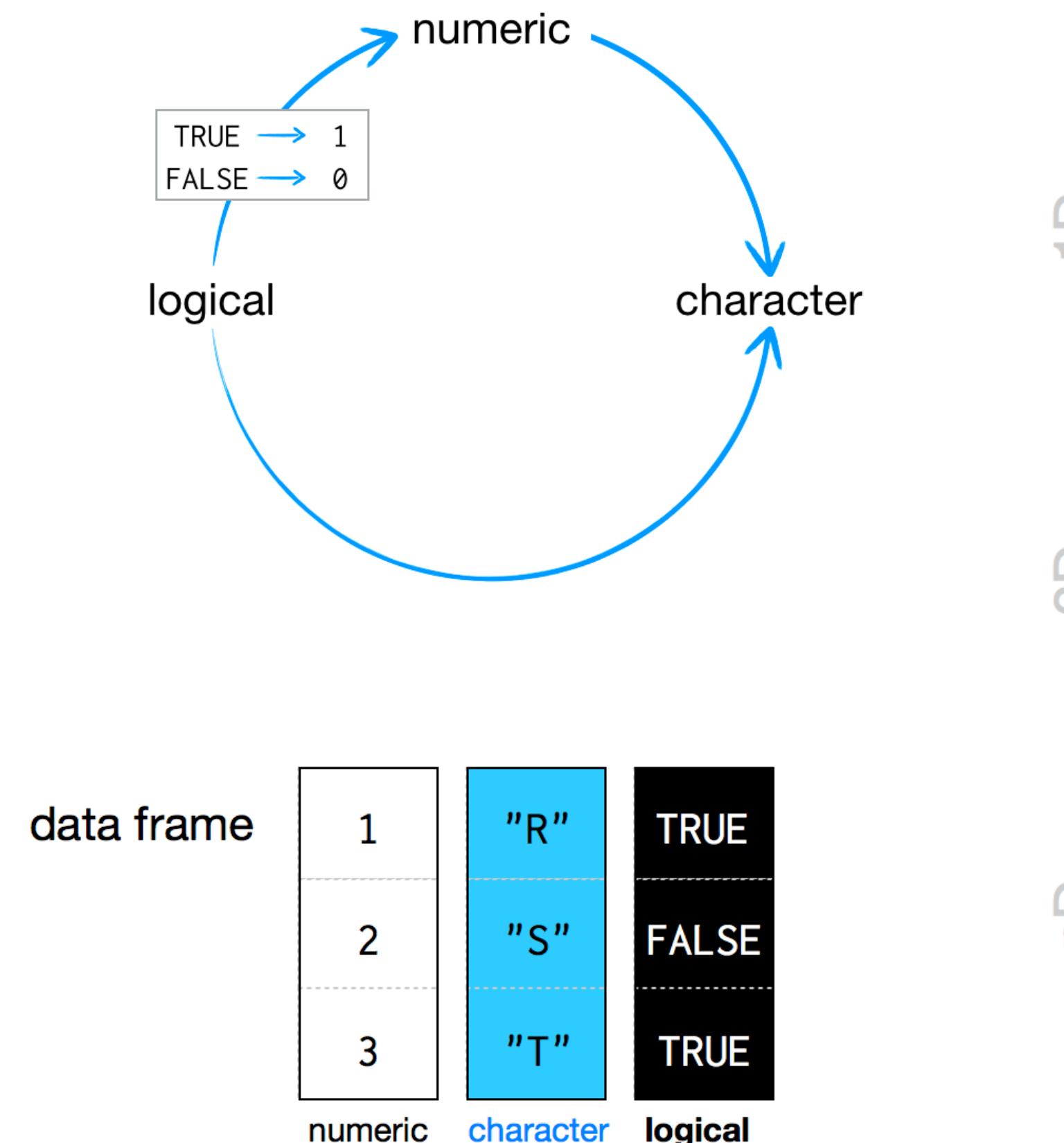
R Objects

Slicing

Modifying Values

R Objects

- Atomic vectors
- Basic types: **doubles**, integers, **characters**, **logicals**, complex, raw
- Coercion
- Matrices & arrays
- Attributes & class
- Lists & data frames
- Loading & saving data



Slicing and Modifying Values

Slicing datasets: []

`6 1 3 6 10 5`

John	1940	guitar
Paul	1941	bass
George	1943	guitar
Ringo	1940	drums

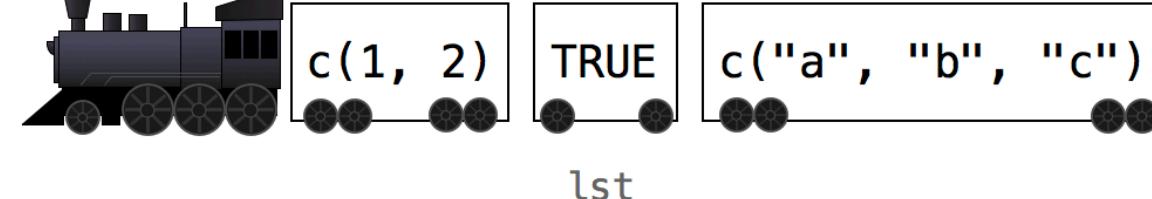
\$ and [[]] to slice lists

`vec[5]`

`df[2, c(2,3)]`

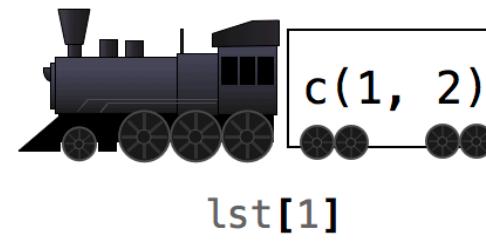
Modifying values

Changing in-place



`lst`

Logical subsetting



`lst[1]`

`c(1, 2)`

`lst[[1]]`

Missing values

`x > 2 & x < 9`

`TRUE & TRUE`

`TRUE`

`x > 2 & < 9`

`TRUE & Error!`

`Error!`

Operator	Syntax	Tests
<code>></code>	<code>a > b</code>	Is a greater than b?
<code>>=</code>	<code>a >= b</code>	Is a greater than or equal to b?
<code><</code>	<code>a < b</code>	Is a less than b?
<code><=</code>	<code>a <= b</code>	Is a less than or equal to b?
<code>==</code>	<code>a == b</code>	Is a equal to b?
<code>!=</code>	<code>a != b</code>	Is a not equal to b?
<code>%in%</code>	<code>a %in% c(a, b, c)</code>	Is a in the group c(a, b, c)?

Operator	Syntax	Tests
<code>&</code>	<code>cond1 & cond2</code>	Are both <code>cond1</code> and <code>cond2</code> true?
<code> </code>	<code>cond1 cond2</code>	Is one or more of <code>cond1</code> and <code>cond2</code> true?
<code>xor</code>	<code>xor(cond1, cond2)</code>	Is exactly one of <code>cond1</code> and <code>cond2</code> true?
<code>!</code>	<code>!cond1</code>	Is <code>cond1</code> false? (e.g., <code>!</code> flips the results of a logical test)
<code>any</code>	<code>any(cond1, cond2, cond3, ...)</code>	Are any of the conditions true?
<code>all</code>	<code>all(cond1, cond2, cond3, ...)</code>	Are all of the conditions true?

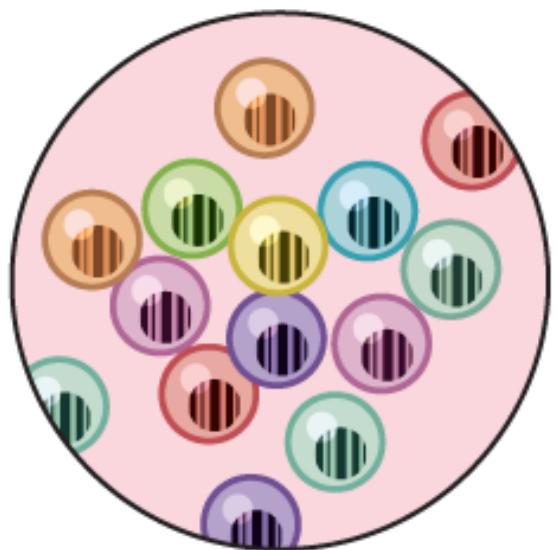
Basic Programming

Slot Machines (Conditionals)

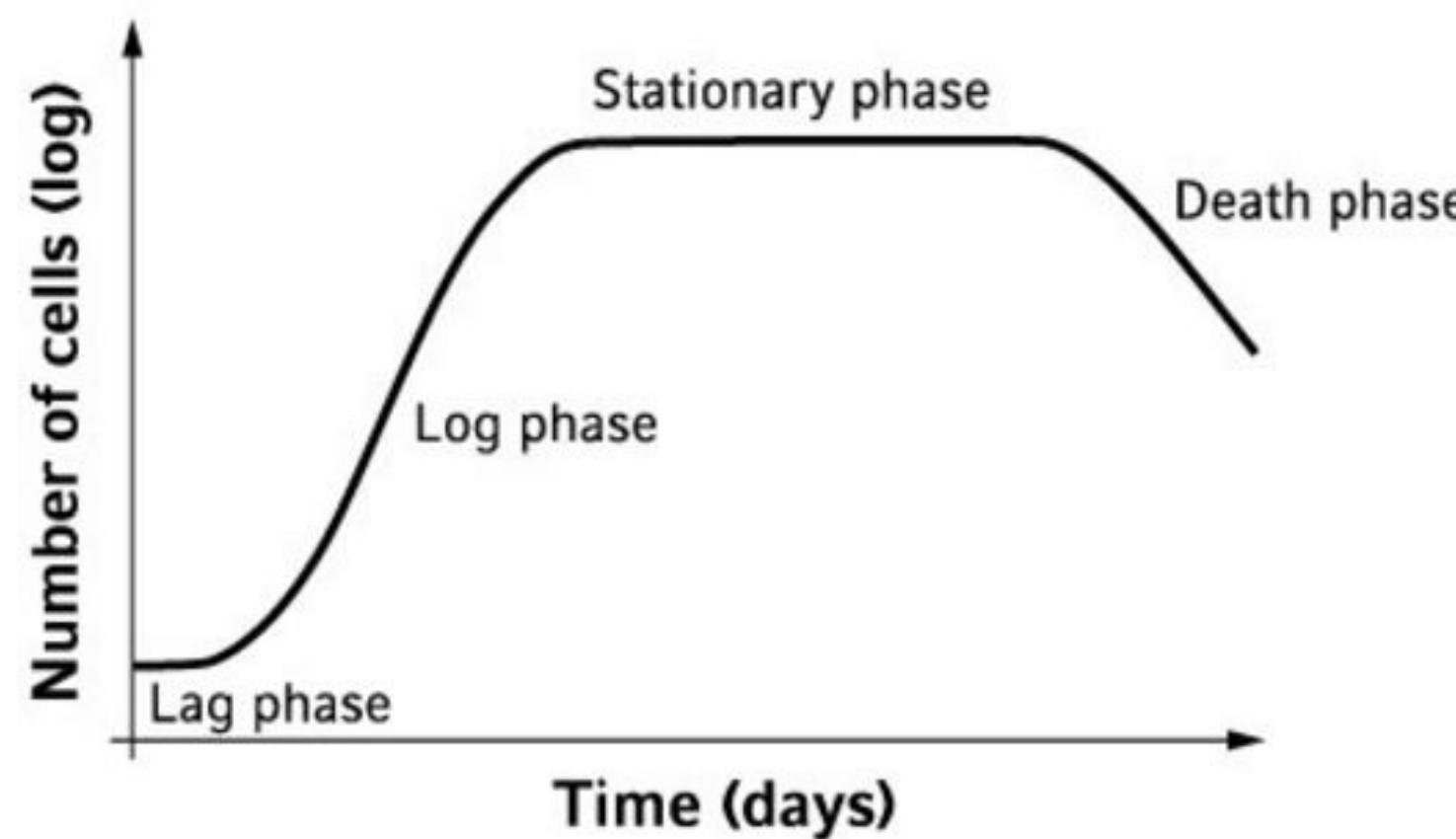
Expected Returns (Loops)

Speed

Pooled Cell Lines Example



Assay-ready
pools



- Cell Lines are characterized by**
 - Growth rates (doubling per day)
 - Initial cell count (cells)
 - Duration of lag-phase (days)
- Assay is characterized by**
 - End-point (days)
 - PCR bottleneck (cells)
 - Sequencing depth (counts)
- # of cell lines with more than 400 counts.**

Pooled Cell Lines and Conditionals

Strategy:

- Break complex tasks into simple subtasks.
- Use concrete examples.
- Describe your solutions in English, then convert them to R.

If / else statements

```
if (condition){  
  # This will run only when  
  # the condition is TRUE  
} else {  
  # This will run only when  
  # the condition is FALSE  
}
```

```
# First attempt (planning)  
simulate_experiment <- function(){  
  
  # calculate cell counts at the end-point  
lysate_cell_counts <- simulate_growth()  
  
  # simulate the pcr bottleneck  
pcr_counts <- simulate_pcr()  
  
  # simulate sequencing  
sequencing_counts <- simulate_sequencing()  
  
  # visualize final population  
hist(sequencing_counts, 100)  
  
  # count the detected cell lines  
detected_lines <- count_detected()  
}
```

Loops

- Expected values
- expand.grid
- for loops
- while loops
- repeat loops

$$E(x) = \sum_{i=1}^n (x_i \cdot P(x_i))$$

$$\begin{aligned} E(\text{die}) &= \sum_{i=1}^n (\text{die}_i \cdot P(\text{die}_i)) \\ &= 1 \cdot \frac{1}{6} + 2 \cdot \frac{1}{6} + 3 \cdot \frac{1}{6} + 4 \cdot \frac{1}{6} + 5 \cdot \frac{1}{6} + 6 \cdot \frac{1}{6} \\ &= 3.5 \end{aligned}$$

```
for (value in that) {  
  this  
}
```

```
while (condition) {  
  code  
}
```

Speed

Vectorized code

logical tests

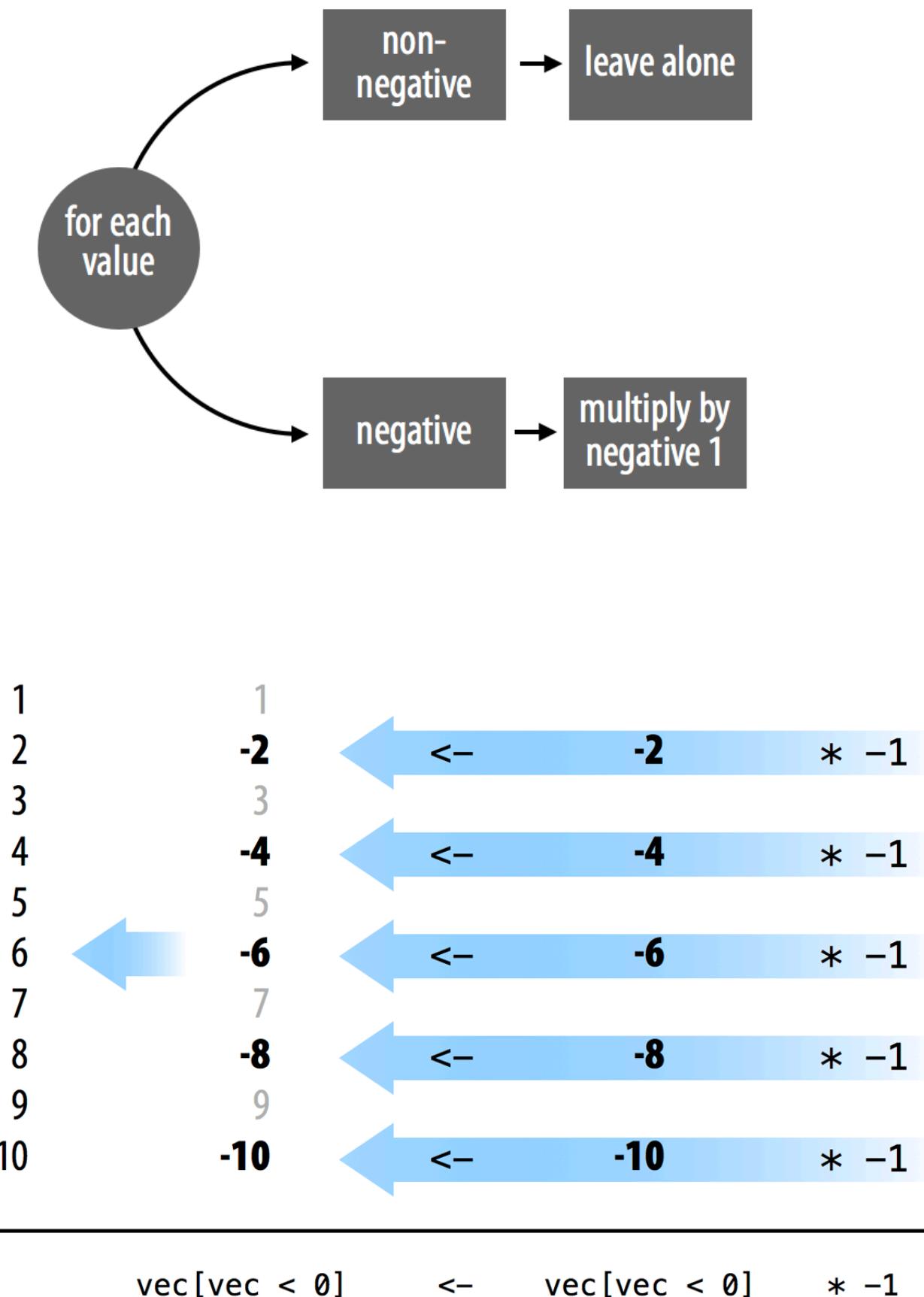
subsetting

element-wise execution

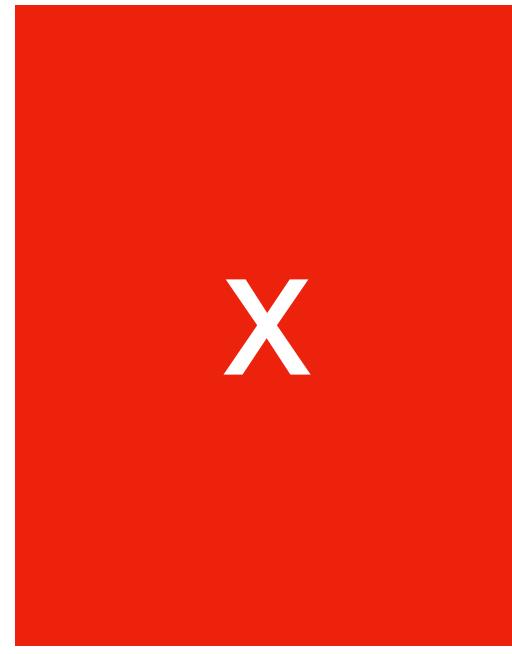
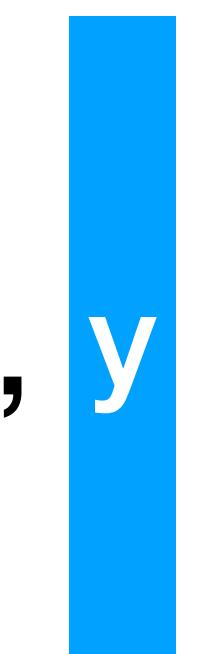
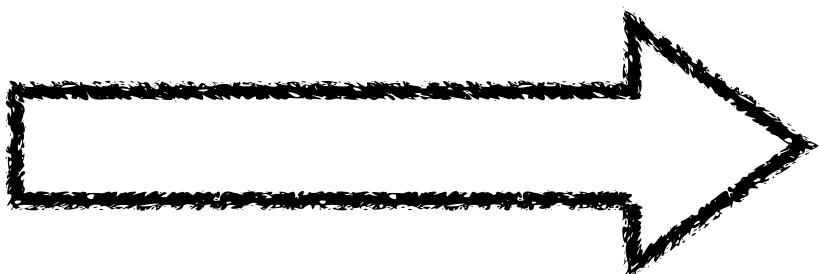
Faster for loops

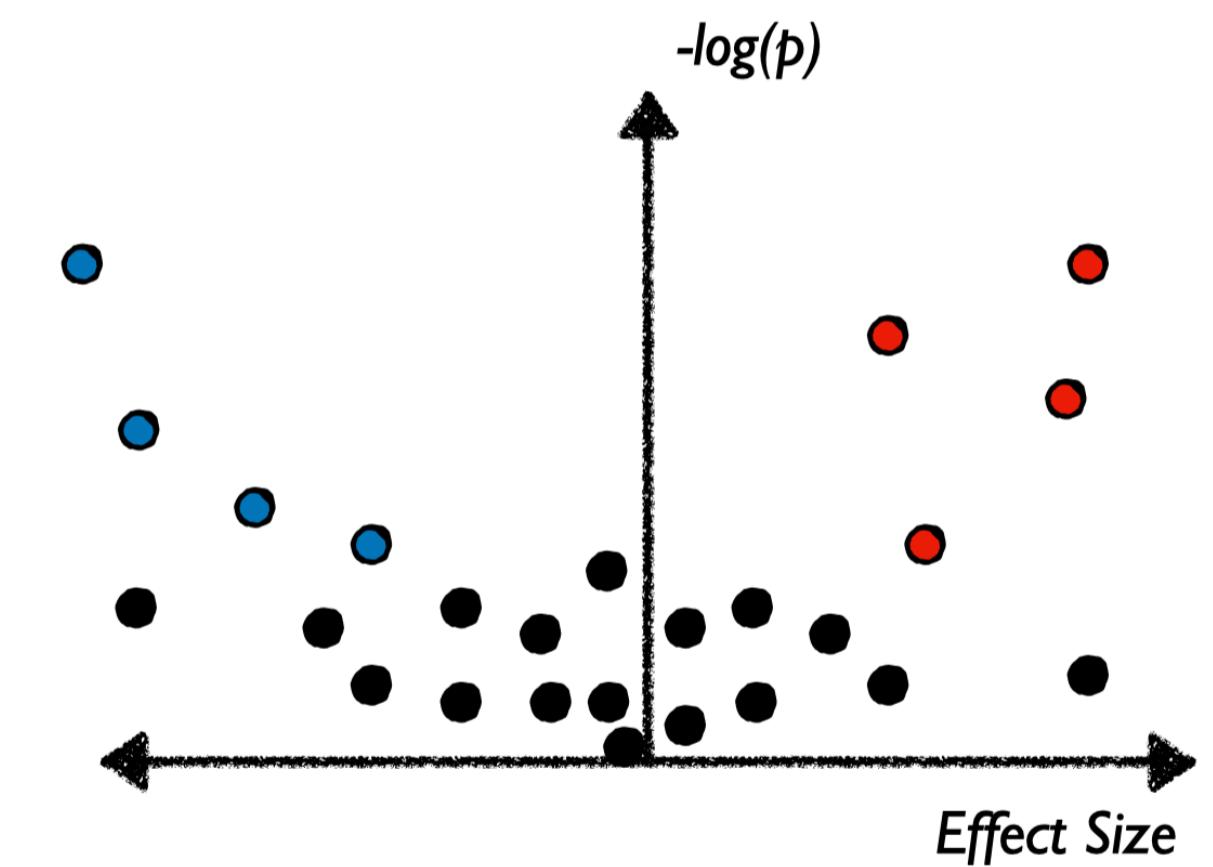
apply() and its friends

Monte Carlo simulations



Practice: Correlations and Volcano Plots

volcano( , ) 



- Are rows matching?
- What if there are missing values in X or y?
- Multiple hypothesis correction — q values (FDR)
- Bonus: Replace y with a matrix Y

$$z = r \sqrt{\frac{n-2}{1-r^2}} \sim t_{n-2}$$

Homework

1. From 2019 HW's: I & 2
2. Review all the code we wrote and Mustafa sent.

Check out chapters 7,9,11, and 12 (optional) from [HOPR](#)

3. Videos from Roger Peng

Data Types: [I](#) / [II](#) / [III](#)

Subsetting: [I](#) / [II](#) / [III](#) / [IV](#) / [V](#)

Control Structures: [I](#) / [II](#) / [III](#) / [IV](#) / [V](#)

