Introduction to Data Analysis

Lecture 01

Agenda

- Course content
- Motivation for R in data analysis

Course description

- This is a course for students and researchers who have data or starting to gather data in their research work.
- This course deals on how to handle, manage, analyze, and visualize data in health and biomedical research.

Course objectives

1. To answer research questions using data
2. To learn basic concepts in data wrangling, exploratory data analysis, statistical analysis, reproducible research, and data communication for publication
3. To write codes involving real life datasets using the R language

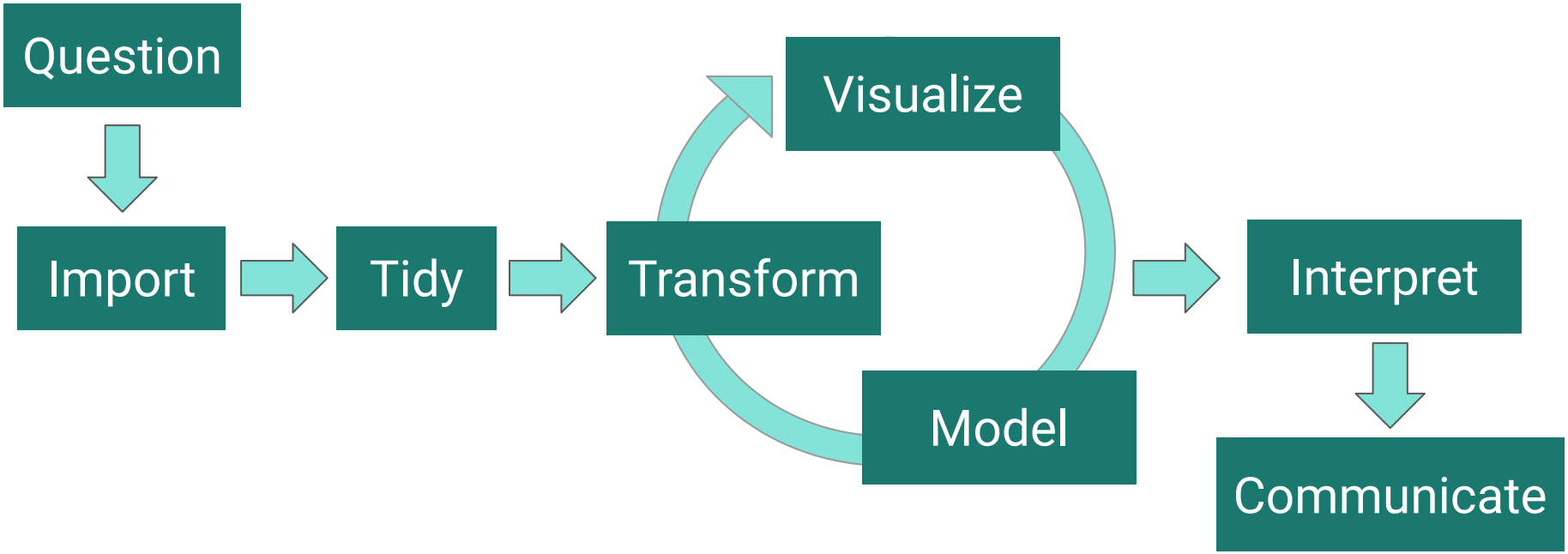
Course format

- Classes will be conducted online via Google Meet
- Lectures with hands-on exercises
- Mondays, 10:00~11:00 AM

Course schedule

Week	Date	Topic
1	07 Dec 2020	Introduction to Data Analysis
2	14 Dec 2020	From Variables to Data Frames
3	21 Dec 2020	Control Flow
4	18 Jan 2021	Importing Data
5	25 Jan 2021	Cleaning Data
6	01 Feb 2021	Tidying Data
7	08 Feb 2021	Transforming Data
8	15 Feb 2021	Merging Data
9	22 Feb 2021	Exploratory Data Analysis
10	01 Mar 2021	Statistical Inference
11	08 Mar 2021	Statistical Modeling I
12	15 Mar 2021	Statistical Modeling II
13	22 Mar 2021	Data Visualization
14	29 Mar 2021	Data Communication

Motivation



Modified from https://r4ds.had.co.nz/explore-intro.html#explore-intro

Reproducible data analysis

- Data analysis can be repeated by others (transparent and reproducible)
- Analogous to lab protocol
- Journal requirement to submit data and code

Avoid using Excel!

- Difficult to separate the data from the process
- Difficult to follow the logic behind the analysis
- Formulas are hidden in cells, can be accidentally deleted or overwritten
- Prone to formatting errors

Avoid using Excel!

BBC Sign in Home News Sport Reel Worklife

NEWS

Home | US Election | Coronavirus | Video | World | Asia | UK | Business | Tech | Science

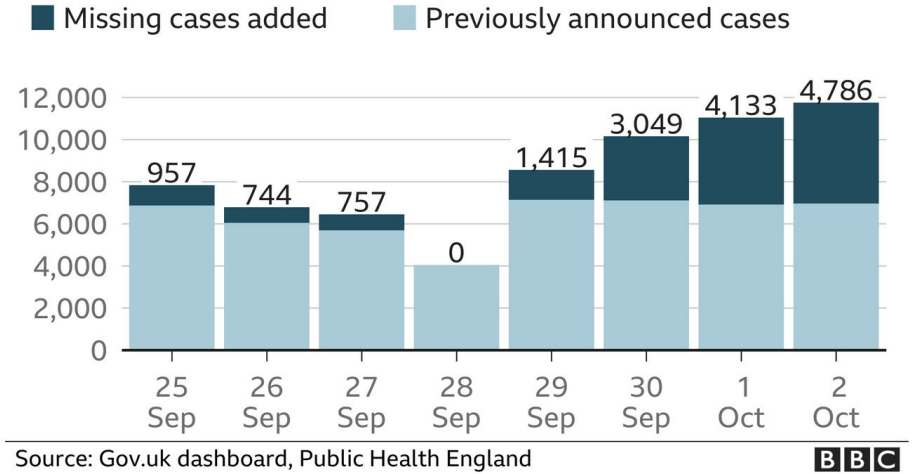
UK | England | N. Ireland | Scotland | Wales | Local News

Covid: Test error 'should never have happened' - Hancock

5 October

Thousands of missing coronavirus cases added after reporting problem

Number of new coronavirus cases by date reported



Source: Gov.uk dashboard, Public Health England

BBC

Avoid using Excel!

Ziemann *et al. Genome Biology* (2016) 17:177
DOI 10.1186/s13059-016-1044-7

Genome Biology

COMMENT Open Access

Gene name errors are widespread in the scientific literature

Mark Ziemann[1], Yotam Eren[1,2] and Assam El-Osta[1,3*]

Abstract

The spreadsheet software Microsoft Excel, when used with default settings, is known to convert gene names to dates and floating-point numbers. A programmatic scan of leading genomics journals reveals that approximately one-fifth of papers with supplementary Excel gene lists contain erroneous gene name conversions.

Keywords: Microsoft Excel, Gene symbol, Supplementary data

Abbreviations: GEO, Gene Expression Omnibus; JIF, journal impact factor

The problem of Excel software (Microsoft Corp., Redmond, WA, USA) inadvertently converting gene symbols to dates and floating-point numbers was originally described in 2004 [1]. For example, gene symbols such as *SEPT2* (Septin 2) and *MARCH1* [Membrane-Associated Ring Finger (C3HC4) 1, E3 Ubiquitin Protein Ligase] are converted by default to '2-Sep' and '1-Mar', respectively. Furthermore, RIKEN identifiers were described to be automatically converted to floating point numbers (i.e. from accession '2310009E13' to '2.31E+13'). Since

frequently reused. Our aim here is to raise awareness of the problem.

We downloaded and screened supplementary files from 18 journals published between 2005 and 2015 using a suite of shell scripts. Excel files (.xls and.xlsx suffixes) were converted to tabular separated files (tsv) with ssconvert (v1.12.9). Each sheet within the Excel file was converted to a separate tsv file. Each column of data in the tsv file was screened for the presence of gene symbols. If the first 20 rows of a column contained five or more gene symbols, then it was suspected to be a list of gene symbols, and then a regular expression (regex) search of the entire column was applied to identify gene symbol errors. Official gene symbols from Ensembl version 82, accessed November 2015, were obtained for *Arabidopsis thaliana*, *Caenorhabditis elegans*, *Drosophila melanogaster*, *Danio rerio*, *Escherichia coli*, *Gallus gallus*, *Homo sapiens*, *Mus musculus*, *Oryza sativa* and *Saccharomyces cerevisiae* [2]. The regex search used was similar to that described previously by Zeeberg and colleagues [1], with the added screen for dates in other formats (e.g. DD/MM/YY and MM-DD-YY). To expedite analysis of supplementary files from multi-disciplinary journals, we limited the articles screened to those that have the keyword 'genome' in the title or abstract (*Science*, *Nature* and *PLoS One*). Excel files (.xls and.xlsx) deposited

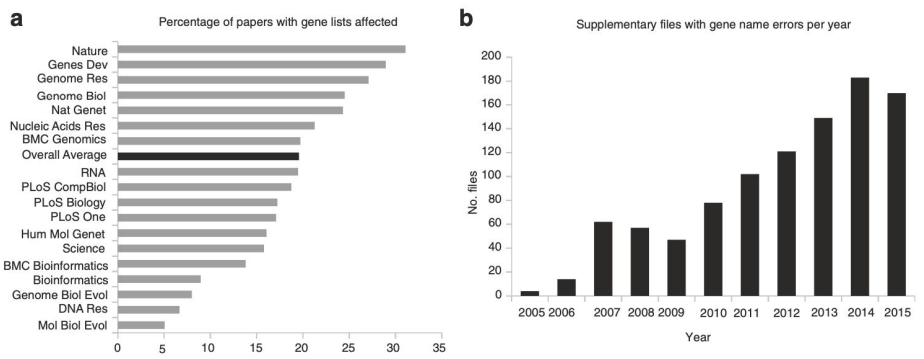
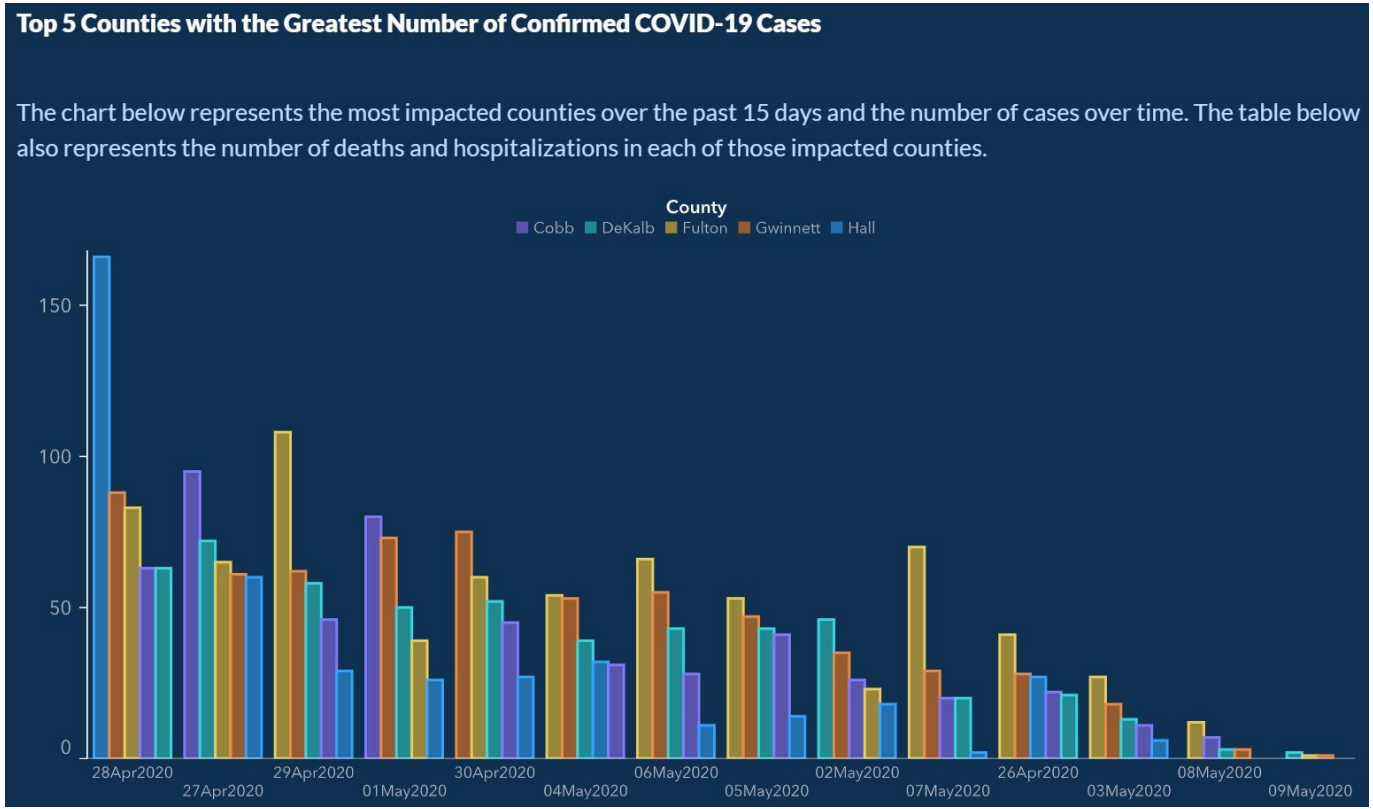


Fig. 1 Prevalence of gene name errors in supplementary Excel files. **a** Percentage of published papers with supplementary gene lists in Excel files affected by gene name errors. **b** Increase in gene name errors by year

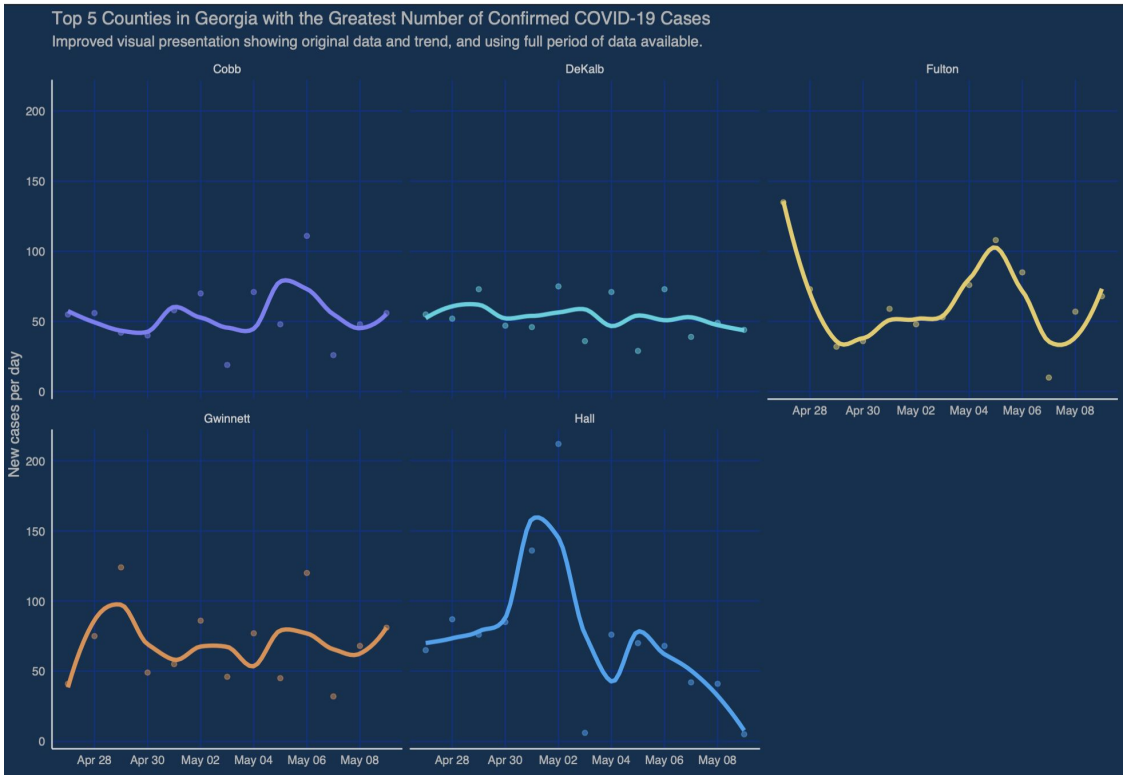
Data analysis gone wrong !



Department of Public Health, Georgia, USA

https://statmodeling.stat.columbia.edu/2020/05/18/hey-i-think-somethings-wrong-with-this-graph/

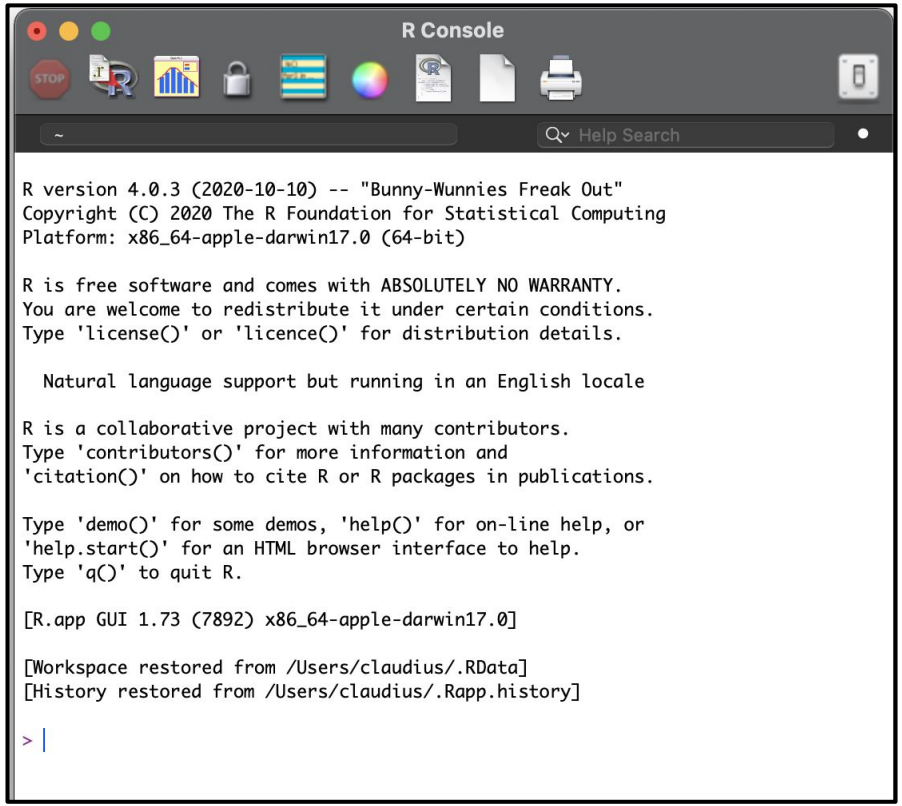
Better visualization using “small multiples”



https://www.r-bloggers.com/2020/05/ordering-bars-within-their-clumps-in-a-bar-chart-by-ellis2013nz/

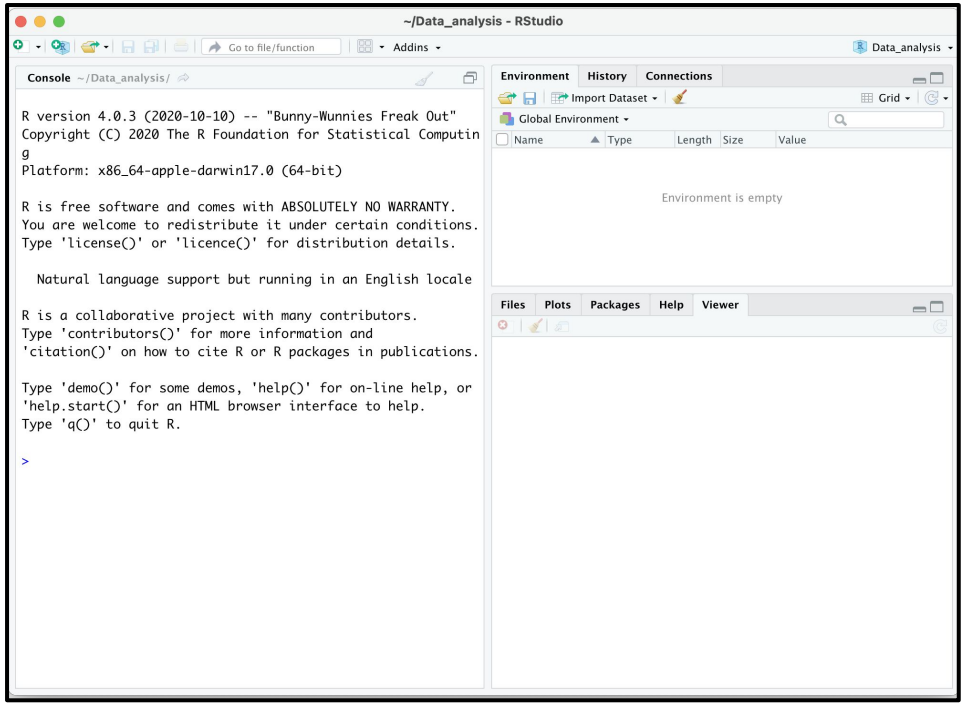
Why R?

- Free software and open-source
- Environment for statistical computing and graphics
- Simple programming language based on S (1976)
- Comprehensive set packages from accessing data, cleaning, analysis, and reporting
- Community of developers
- Easy to install packages



R under GUI using RStudio

- Easy to use interface
- Console is where you can type commands and see output
- Workspace tab shows all active objects
- History tab shows a list of commands recently used
- Files tab shows all files and folders in your workspace
- Plots tab show all graphs
- Packages tab will list of series of packages
- Help tab to see additional information



How R works?

- R creates objects in memory and saves them in a file called .RData
- Commands are recorded in an .Rhistory file (recall by pressing arrow up or down)
- Recalled commands may be edited
- Commands may be abandoned by pressing <Esc>
- To end your session, type q() or just kill the window
- Use of **working directory**: each project is associated with a working folder containing all data, scripts, output files, figures, etc.

Hands-on exercises using R

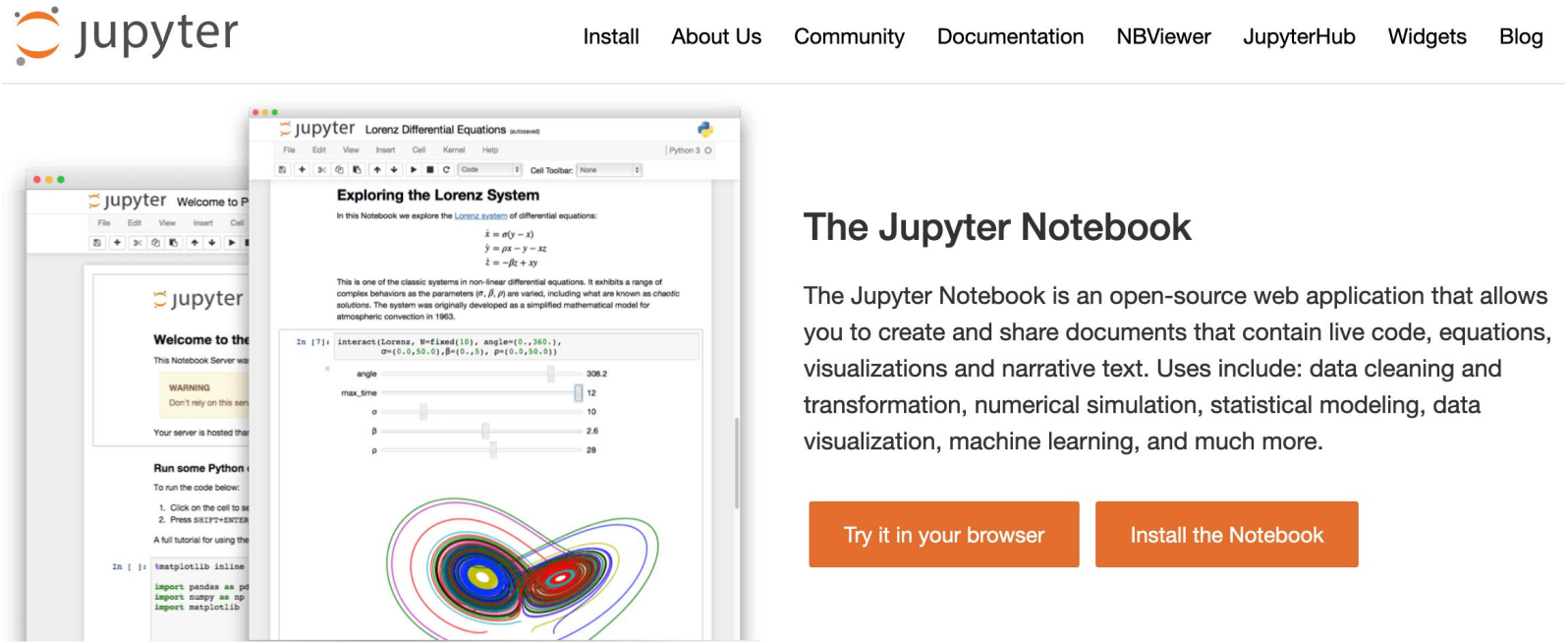
- Focus on real-life data, e.g. COVID-19 dataset at Johns Hopkins University
- Clean messy data
- Explore data
- Visualize data
- Do basic statistical analyses
- Generate models
- Generate publication ready figures
- Communicate results

Using R for documentation

- virtual “lab notebook”
- R Script, R Markdown, R Notebook, Jupyter
- For capturing what you did, codes, results, figures, conclusions
- For collaborating with other team members, your boss, future you!
- For submitting to journals as part of publication (reproducibility)

Using Jupyter

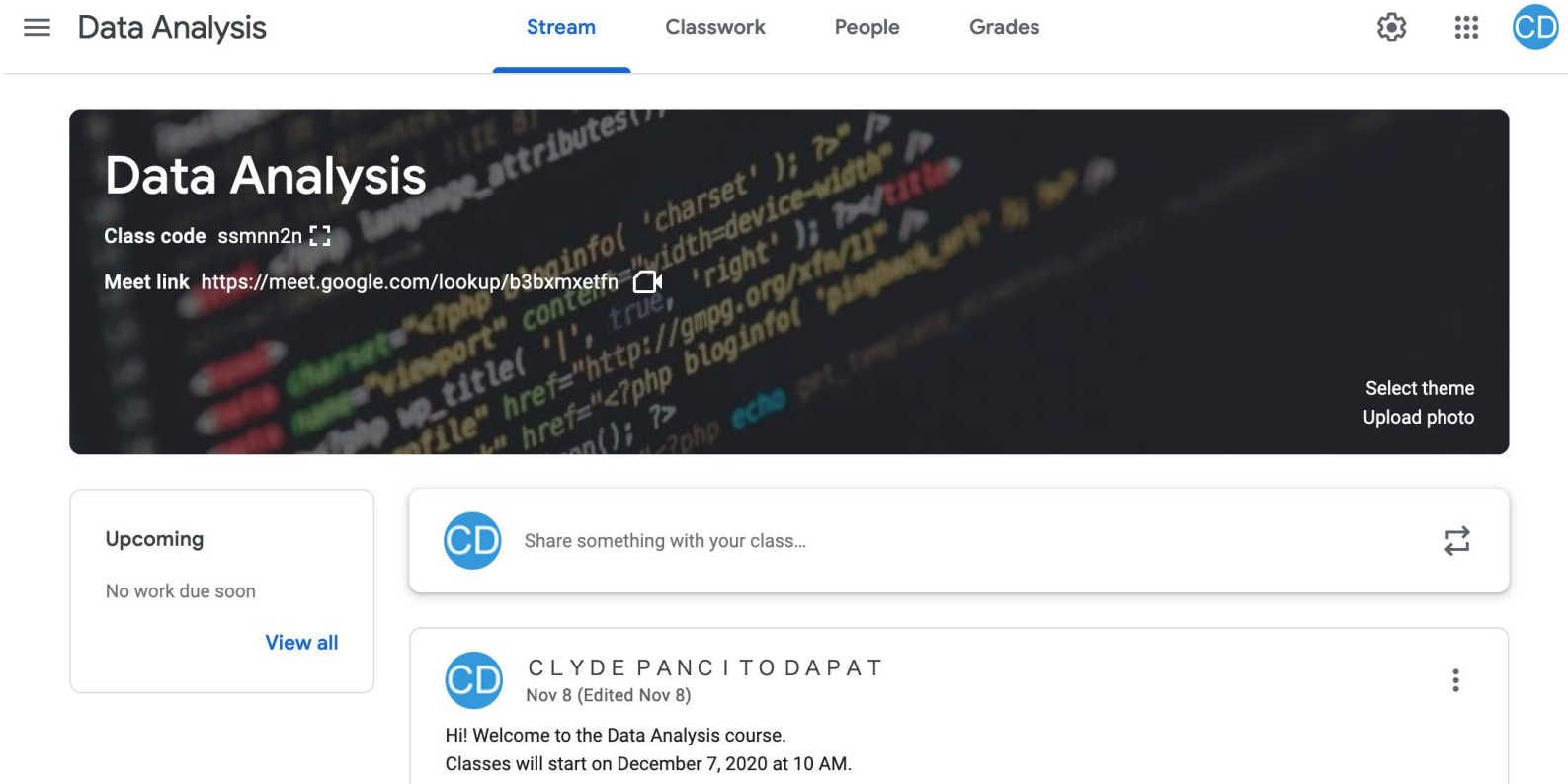
- For hands-on exercises in this course



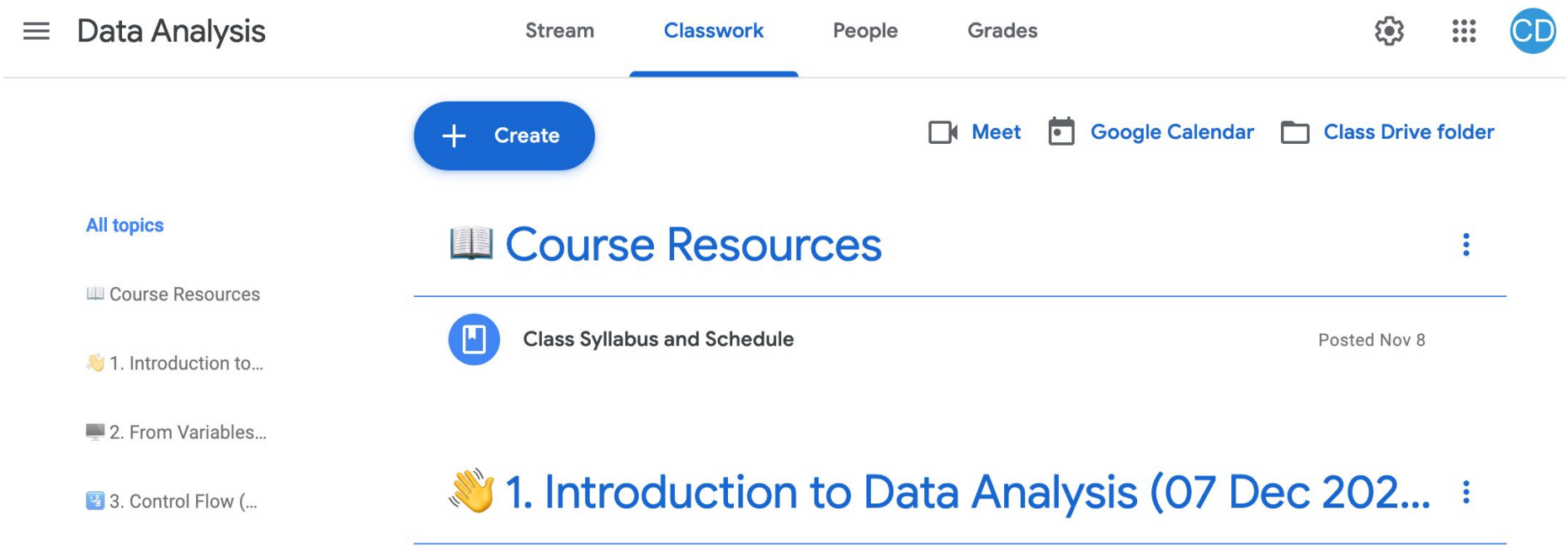
What is not covered in this course?

- Crafting a research question
- Gathering data
- Teaching computer to learn from data

Google Classroom



Google Classroom



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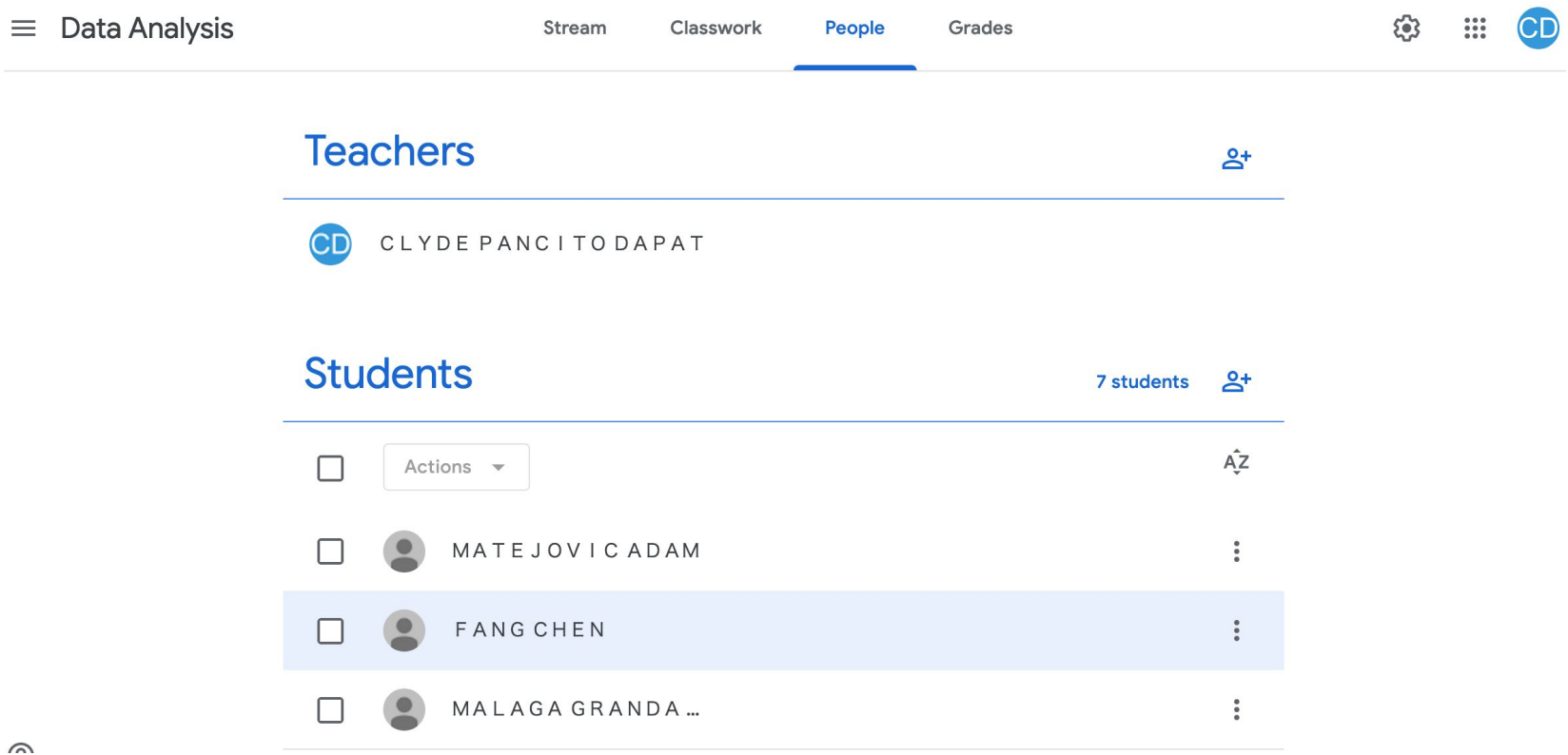

Course Project

- Describe your project question
- Plan in answering your project question
- Present code, figures, results, and conclusion
- Class presentation at end of course

Things to do

- Install R, RStudio, Jupyter and R kernel (installation guide available in Classwork tab of Google Classroom)
- Take the course survey

Take away message

- Use R for data analysis
- Data analysis should be reproducible