SCIENCE MEETS LIFE

Introduction to Data Cleaning with OpenRefine

VIB BIOINFORMATICS CORE

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Our areas of bioinformatics training comprise various topics of life sciences

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Our trainers for VIB and ELIXIR Belgium

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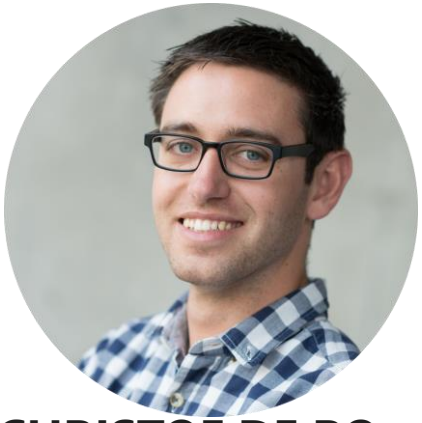

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What is OpenRefine?

A free, open source, power tool for working with messy data

Automatically tracks steps in working with data

http://openrefine.org

Large community / google group

How does OpenRefine compare with other tools?

- Compared to spreadsheets
  Basic unit of interaction is column (versus cells)
  Pro: easier to import data, explore, manipulate and export again

- Compared to scripting
  Pro: you see your data, while it is being transformed
  Con: for medium size data sets (1,000,000 rows)

- Compared to databases
  Pro: you see your data, while it is being queried
  Con: for simple data structures

What are typical use cases for OpenRefine?

- Explore unknown, new data files
- Manipulate/clean data to prepare for other tools (GREL)
- split in more granular parts
- match local data with other datasets
- get data from web services to enhance the dataset
- use as workflow tools to replay

We start OpenRefine and explore the interface together

- Create a project from the sample data
  https://ndownloader.figshare.com/files/7823341

- Exploring data by applying filters
  Faceting

  Explore the scientificName column

- What type of errors do we spot?

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We learn more about facets and their use

- Types
  Numeric facets
  Timeline facets
  Custom facets
  Scatterplot facets
- Custom facets
  e.g. by blank, text length, word, duplicates

- Group common values, filter, and bulk edit them

Exercise 1

- Using faceting, find out how many years are represented in the census.
- Is the column formatted as Number, Date, or Text? How does changing the format change the faceting display?
- Which years have the most and least observations?

We use clustering to bulk edit values

Gödel and Godel or New York and new york

- Explore the scientificName column
- Cluster: key collision method and metaphone3

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Exercise 2

- Split the column scientific name into genus and species
- Explore the Undo / Redo operations
- Which transform solves the issue?

How can we use a subset of the data

Text filter > bai

Exercise 3

- What scientific names (genus and species) are selected by searching for 'bai'?
- How would you restrict this to one of the species selected?
- How many rows are matched for each of the species?
- Use include / exclude to select entries from one of the species.
- Add custom text facet to arrive at the same selection like the text filter 'bai'
  e.g. value.toLowercase().contains("bai")

Sorting

Text, number, dates or Booleans

Exercise 4

- Continue to work with both species.
- Sort by month. How can you ensure that months are in order?
- Sort the data by plot. What years were observations recorded for the filtered set?
- How do you sort your data by month?
- How do you sort the subset in chronological order.

We examine numbers in OpenRefine

Edit cells > Common transforms on recordID

Exercise 5

- Use the full set again.
- Transform the columns recordID, dy, mo, period, plot_id to numbers.
- Edit several cells of the column 'dy' to contain text or empty cells. Explore the numeric facet on that column.
- Create a scatterplots by plotting pairs of numeric columns.
- Why does the scatterplot recordID vs period have the pattern is does?

Exercise 6

- Create a project with the bed file: syst-nocallsCG69.bed https://bit.ly/2Q9gA05

Try to determine

- a) the number of no-call regions that are larger than 1040 bases long in chromosome 21
- b) the length of the longest region in chromosome 1

Here you can find additional resources about OpenRefine

- https://datacarpentry.org/OpenRefine-ecology-lesson/06-resources/index.html

Questions?

Comments?