# Demo of Open Refine

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## Open refine demo

(adapted from Data Carpentry materials)

Open Refine (previously Google Refine) is an open-source tool that can help you to clean-up messy datasets. It presents itself as a spreadsheet-like interface, but all operations we do to the data are recorded and can be repeated or reversed. We will show how it can be used to solve some of the issues we have highlighted previously. You can use Open Refine to build-up a data-cleaning pipeline which you can apply to multiple files. We will not go that far today though. There are some nice introductory videos

Open Refine runs in a web browser, although you do not have to be online to use it.

## Some example data

We will use some data that have been simulated to demonstrate many of the problems we have seen already. Each row represents a different patient in a fictitious study and can be downloaded from the course website. (Right-click and Save Link as....)

### Importing the data

Start the program. On Windows, Double-click on the openrefine.exe file. Java services will start on your machine, and Refine will open in your Firefox browser. On the Mac, you've probably installed the package into your Applications folder.

Note the file types Open Refine handles: TSV, CSV, \*SV, Excel (.xls .xlsx), JSON, XML, RDF as XML, Google Data documents. Support for other formats can be added with Google Refine extensions.

Once Refine is open, you'll be asked if you want to Create, Open, or Import a Project.

- Click *Browse*, find patient-data.txt
- Click *next* to open patient-data.txt Refine gives you a preview a chance to show you it understood the file. If, for example, your file was really comma-separated, the preview might look strange, you would choose the correct separator in the box shown and click "update preview."
- You should see something like...



If all looks well, click Create Project.

## **Faceting**

Faceting provides you a snapshot of the entries in a particular column and allows you to filter down to particular rows. It can also quickly highlight problems with the data.

Typically, you create a facet on a particular column. The facet summarizes the cells in that column to give you a big picture on that column, and allows you to filter to some subset of rows for which their cells in that column satisfy some constraint. That's a bit abstract, so let's jump into some examples. Before we start, how many different entries would we expect to find a column that is supposed to be just Male or Female?

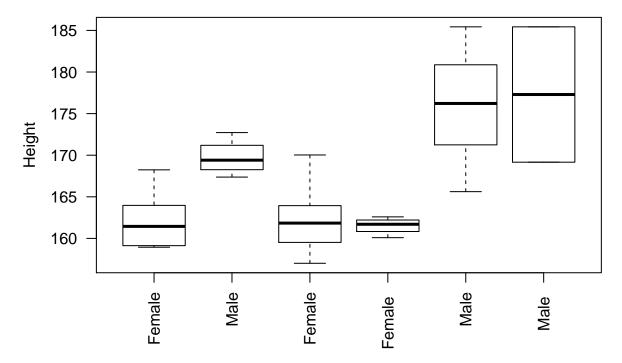
- Scroll over to the Sex column
- Click the down arrow and choose Facet -> Text facet
- In the left margin, you'll see a box containing every unique, distinct value in the Sex column and Refine shows you how many times that value occurs in the column (a count), and allows you to sort (order) your facets by name or count.

In this case, we have found  $\boldsymbol{6}$  different ways for Male or Female to be entered.

Edit. Note that at any time, in any cell of the Facet box, or data cell in the Refine window, you have access to edit and can fix an error immediately. Refine will even ask you if you'd like to make that same correction to every value it finds like that one (or not).

#### Trimming whitespace

Whitespace is when we have a blank space at the beginning, or end, of a text entry. They can be difficult to spot by-eye and for the computer Male and Male are completely distinct entries. This can have undesired consequences in a data analysis.



Fortunately, Open Refine has a straightforward solution to this problem

- Select the Sex column
- Select Edit cells
- Common transforms -> Trim trailing and leading whitespace

Now try the text facet operation from above. What do you notice?

### Clustering

Clustering in Open Refine is used to identify and consolidate similar entries into a consistent term. Let's try this on the Pet column. The first thing we will notice is that Cat and CAT are distinct entries but probably shouldn't be. We can fix that by clustering

- Select the Pet colum
- Facet -> Text Facet as before
- Now, click the *cluster* button in the top-right of the panel that shows you all the different values in this column.
- It will now suggest various groups of entries that it thinks represent the same thing. You can click the checkbox to merge into a single group and have the ability to choose the new name.
- Clicking Merge Selected and Close will perform the operation

## **Bulk-editing**

Staying with the Pet column, there is also an inconsistent way of representing missing data; with NA, None or NULL used. Languages such as R would prefer NA to be used, although in practice we can use any as long as we are consistent.

- Click on None in the Facet panel. Only rows where the value of Pet is None will be shown.
- Click on the *edit* box None value in any particular row. This will give you the chance to edit the value.
- Change the value to NA. Clicking Apply to all identical cells will change all occurences of None to NA.

• You could also try changing NULL...

## Splitting into several columns

Sometimes multiple pieces of information can be encoded in a single cell. In our particular case, the ID assigned to each patient contains a hospital identifier (either AH or SG) and a numeric ID. For some analyses we might want to quickly perform operations that take the hospital as a factor

- Select the ID column
- Edit column -> Split into several columns
- It will ask you what text character splits the IDs into different parts. In this case we specify /
- Each new column is assigned a new name automatically. You can change the names by *Edit column* 
  - -> Rename this column

## Filling missing values

The final column Date entered study was used to indicate the date at which each patient was enrolled onto the study in question. Patients were enrolled in batches. However, the person filling out the form thought it was helpful to include this information only once for each batch of new patients.

- Select the Date Entered Study column
- Select Edit cells -> Fill down
- Empty cells will now be filled with the appropriate date.

## Upper- and lower-case transformations

For consistency, we might want the text entries in a particular column to be all lower or UPPPER case.

- Select the Name column
- Edit column -> Common transformations
- You can choose To uppercase, To lowercase if required.
- However, we will use the operation To titlecase. It makes the first letter of the text *Upper case*, but the rest of the text *Lower case*.

### More-advanced text operations

Open Refine has it's own language ("General Refine Expression language (GREL)") for performing custom text operations in a column.

The Height and Weight columns are problematic because they contain the units information (kg and cm respectively). Languages such as R will interpret the values in such a column as text, and not numeric data. Simple plotting and numeric analysis will not be possible without extra manipulation.

- Select the Height column
- Select Edit cells -> Transform...
- In the Expression box, enter replace(value, "cm","")

### Things to try

- Can you split the Birth column into Year, Month and Day?
- Can you make the Smokes column suitable for analysis?
- Tidy up the Weight column for analysis

- The Race column contains one value that is very suspicious... Can you find it and change it to something suitable?
- Look at the State column and try faceting / clustering?. Are there any entries that should be joined into one? You may need to experiment with different clustering methods.

## Exporting your data / project

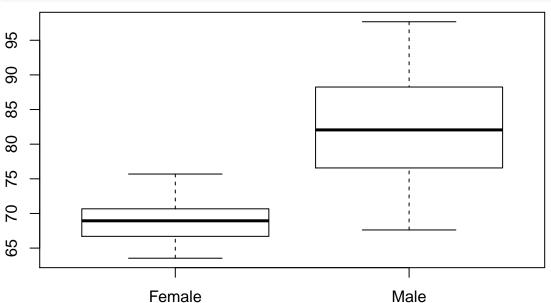
You can export the modified table into a new file:-

• Export -> Tab-separated value or Export -> Comma-separated value would seem to be sensible choices.

# Impact on analysis

Lets suppose we want to look at the difference in weight between males and females in the study.

```
patients <- read.delim("patient-data-cleaned.tsv")
boxplot(patients$Weight ~patients$Sex)</pre>
```



```
library(stringr)
patients <- read.delim("patient-data.txt")
patients$Weight <- as.numeric(str_replace_all(patients$Weight, "kg",""))
patients$Sex <- str_trim(patients$Sex)
boxplot(patients$Weight ~patients$Sex)</pre>
```

