

# Exercise on the use of Open Refine



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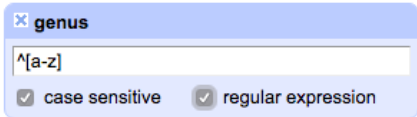
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# CONVENTIONS

*Formulas (copy-paste)*

Text in blue

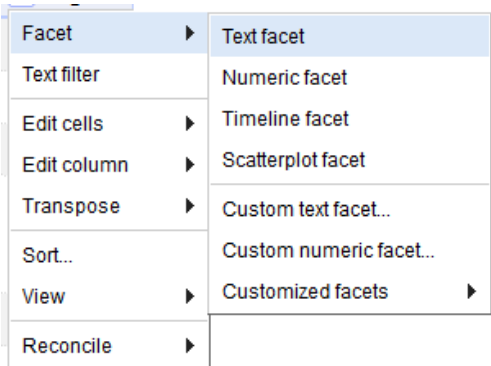
Example: ...then paste the expression `^[a-z]`



*Commands in Refine*

Text in red

Example: ...and follow the route to **Text facet**



*Column names*

Text in green

Example: ...go to column **Cat. Numb**

Show as: <b>rows</b> records		Show: 5 10 25 50 rows		
▼ All	▼ Cat. Numb.	▼ University	▼ Collector	
☆ 7.	UWP:157339	University of Guatemala	Betancur J	
☆ 8.	UWP:157339	University of Guatemala	Betancur H	
☆ 224.	UWP:122471	University of Guatemala	Vargas P	
☆ 225.	UWP:122471	University of Guatemala	Vargas I	

*Hyperlinks*

[www.gbif.org](http://www.gbif.org)

*Column menu*



## 2. BASIC USE

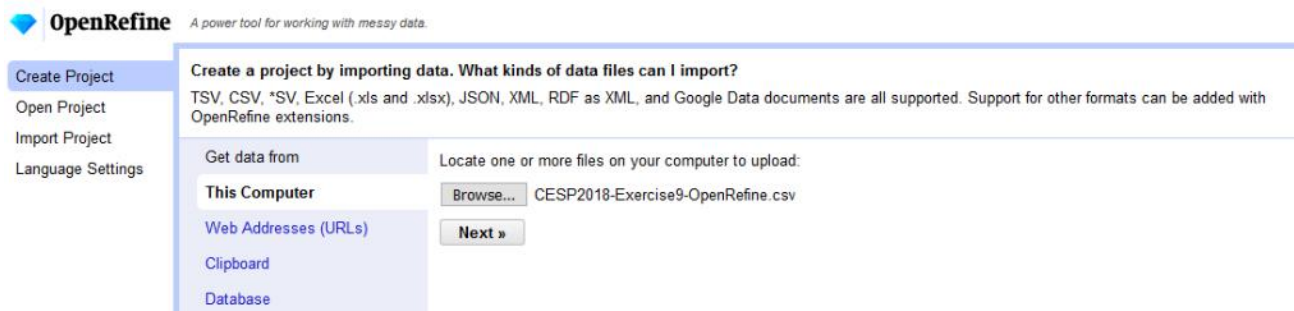
### 2.1. FILE LOADING AND PROJECTS

#### 2.1.1. Before starting

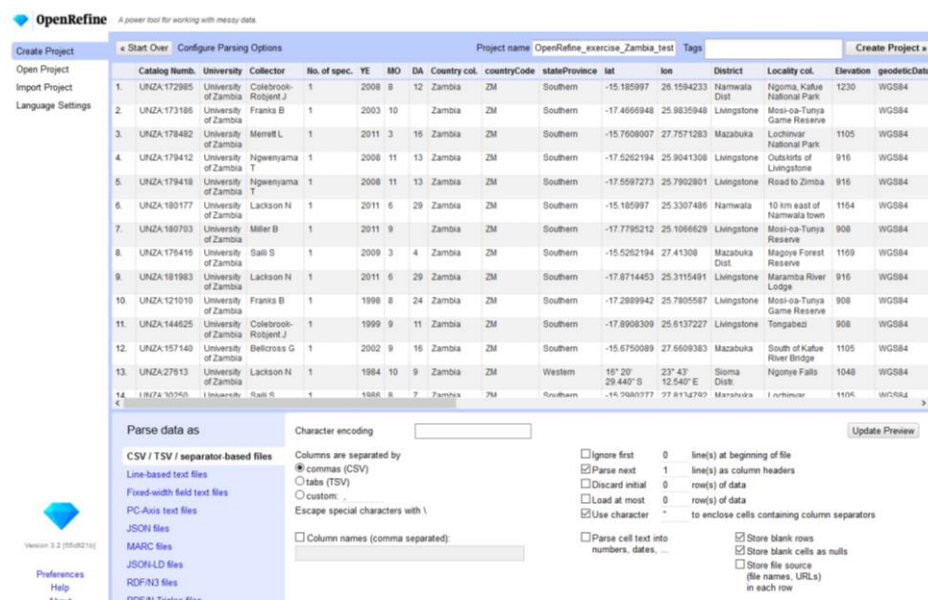
Data can be loaded from various data sources: TSV, CSV, SV, Excel (.xls and .xlsx), JSON, XML, RDF and XML data as well as Google Docs. Loading data involves two steps: the first is selecting the file, and the second is the creation of the project.

#### 2.1.2. Exercise 1. Create a project

1. Find the file Exercise-OpenRefine.csv in your course folder.
2. Open *OpenRefine* (using openrefine.exe), click on **Create Project**, and follow the route **Get data from > This Computer**, then click on **Browse**. Select the file. Click on **Next**.



3. A parsing options menu will appear. Fill in the options as shown in the picture below. Note that columns may be separated by tabs, commas or semicolons (;), so if you are not sure which delimiter your file uses, experiment with different options, until the data is split into columns correctly, as shown in the image below :



- On the top centre you can provide a **Project name**, and click **Create Project** and you will be ready to work!

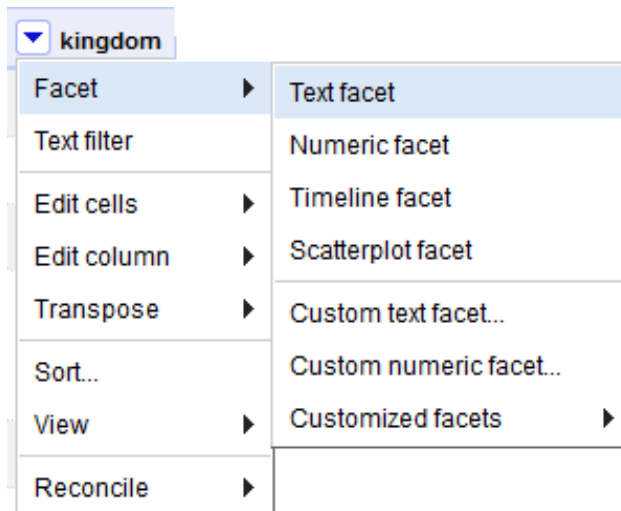
## 2.2. FACETING

### 2.2.1. Before starting

Faceting is a feature that will allow us to get a big picture overview of the data, and to filter down to just the subset of rows that we want to change or view in bulk. It facilitates the use and analysis of data and can be done with cells containing any kind of text, numbers and dates.

### 2.2.2. Exercise 2. Faceting and mass editing

- Go to column **kingdom**, and then click on the column menu  and follow the route to **Text facet** as shown below:

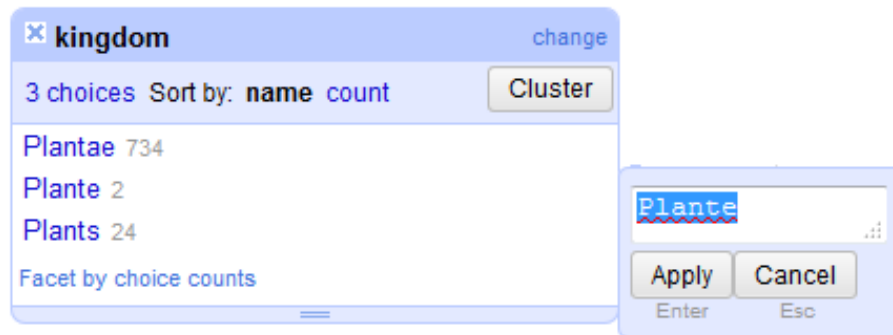


- On the left a window with the name of the column will appear, which is the facet:



Click on **count** to sort by count, then click on **name** to sort alphabetically.

- To fix the spelling mistakes (all values should be identical), place the cursor over the text in the window and click on **Edit**, then fix the error in the text box, and to save click on **Apply**.

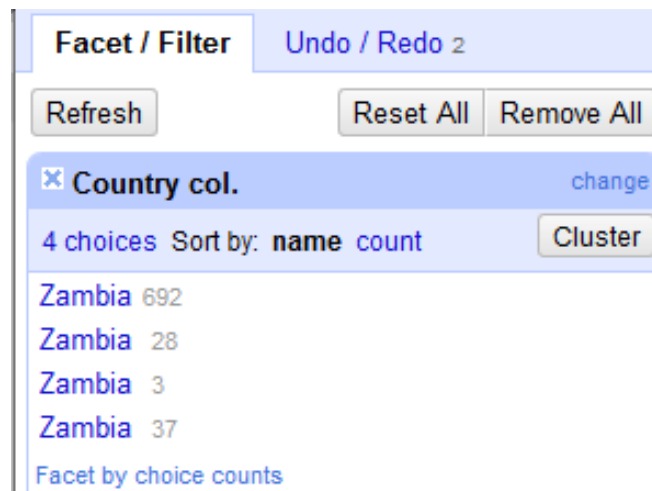


All the values will be fixed automatically in all records.


- To close a facet, click on the **x** next to the facet's name.

### 2.2.3. Exercise 3. Faceting and white spaces I

- Go to **Country col.** and click on column menu  and perform a **Text Facet**.



It appears that the country name is spelled correctly, but the facet shows four different values. This is due to the extra spaces at the end of the text.


- To fix the error in this column, go to **Country col.** and click on column menu  > **Edit Cells** > **Common transforms** > **Trim leading and trailing whitespace**. You will see a notification message:

**Text transform on 68 cells in column Country col.:  
value.trim() Undo**

- Now check the facet window: only one value will remain.

#### 2.2.4. Exercise 4. Faceting and white spaces II

- Go to column **Full name** and click on  then go to **Text facet**. Then click on **count**. The facet will show:

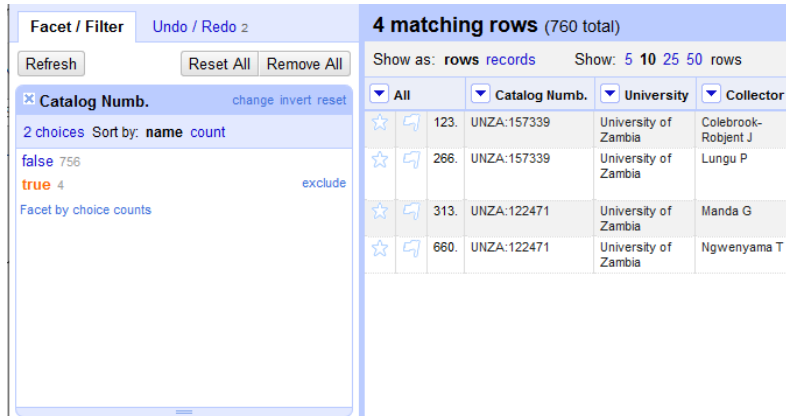
Facet / Filter		Undo / Redo 	
<input type="button" value="Refresh"/>		<input type="button" value="Reset All"/> <input type="button" value="Remove All"/>	
Full name		change	
207 choices		Sort by: name	count
		<input type="button" value="Cluster"/>	
Brachystegia spiciformis		81	
Brachystegia stipulata		41	
Isoberlinia tomentosa		30	
Brachystegia spiciformis		28	
Brachystegia boehmii		22	
Brachystegia longifolia		22	
Brachystegia microphylla		21	
Isoberlinia angolensis		20	
Brachystegia woodiana		18	
Caesalpinioideae		18	
Brachystegia glaucescens		17	
Colophospermum mopane		15	
Brachystegia bakeriana		13	
Tessmannia		10	

As seen above, *Brachystegia spiciformis* is the first item in the list with 81 specimens, but it is also present in the 4th place with 28 specimens. This is because there are additional white spaces between *Brachystegia* and *spiciformis*.

- Fix the error from the **Full name** column menu, **Edit Cells** > **Common transforms** > **Collapse consecutive whitespaces**.
- Once the whitespaces are removed, *Brachystegia spiciformis* should only appear once in the list with 109 records.

### 2.2.5. Exercise 5. Faceting and duplicates

1. Go to column catalog in **Cat. Numb.**, and follow the route **Facet** > **Customized facets** > **Duplicates facet**. The facet will show 4 duplicates
2. Click on **true**, and you'll see the values in the main window:



The screenshot shows the GBIF data interface. On the left, the 'Facet / Filter' panel is open for 'Catalog Numb.'. It shows '2 choices' sorted by 'name count'. The 'true' choice has 4 items, and the 'false' choice has 756 items. The main window displays '4 matching rows (760 total)'. The table shows the following data:

	Star	Comment	UNZA:157339	University of Zambia	Colebrook-Robjent J
123.			UNZA:157339	University of Zambia	Colebrook-Robjent J
266.			UNZA:157339	University of Zambia	Lungu P
313.			UNZA:122471	University of Zambia	Manda G
660.			UNZA:122471	University of Zambia	Ngwenyama T





3. Fix the catalog numbers using the correct values shown in the table below, by clicking on **edit** directly in the relevant cell. A window will open that allows editing of the value. Once it has been corrected, click **Apply**.

UNZA:122470	Manda G
UNZA:122471	Ngwenyama T
UNZA:157351	Colebrook-Robjent J
UNZA:157339	Lungu P

## 2.3. FILTERING

### 2.3.1. Exercise 6. Basic filter

1. Go again to **Full name** column menu and perform a **Text facet** to visualize the values, then go again to  and click on **Text filter**, perform the following filters and fix them as shown below:

Filter	How to fix	Correct value
 <p><b>Full name</b></p> <p>sp1</p> <p><input type="checkbox"/> case sensitive <input type="checkbox"/> regular expression</p>	Edit directly in the cell	Eragrostis
 <p><b>Full name</b></p> <p>SP2</p> <p><input checked="" type="checkbox"/> case sensitive <input type="checkbox"/> regular expression</p>	Edit directly in the cell, check <b>case sensitive</b>	Julbernardia
 <p><b>Full name</b></p> <p>spp</p> <p><input type="checkbox"/> case sensitive <input type="checkbox"/> regular expression</p>	<ol style="list-style-type: none"> <li>1. Go to  on <b>Full name</b>, then click <b>Edit cells &gt; Transform...</b></li> <li>2. In the text box paste the formula <code>value.replace(" spp", "")</code></li> <li>3. Click <b>OK</b></li> </ol>	Digitaria Diheteropogon Sporobolus Tessmannia

2. Remember to always close filters before continuing to the next exercise.



### 2.3.2. Exercise 7. Advanced filter I

1. Go to column **Full name** and perform a **Text filter**.
2. Check **regular expression** and **case sensitive**, then paste the expression `^[a-z]`



This regular expression filters the strings in which the first letter is lowercase.


3. **WRITE DOWN THE NUMBER OF RECORDS, AS WELL AS THE NAME IN THE FULL NAME COLUMN, THAT HAVE THE FIRST LETTER AS A LOWERCASE LETTER. YOU WILL REQUIRE THIS INFORMATION TO COMPLETE THE QUIZ.**

4. Perform a correction since the genus should be capitalized.

Note: If you want to know more about regular expressions click [here](https://github.com/OpenRefine/OpenRefine/wiki/Understanding-Regular-Expressions)  
<https://github.com/OpenRefine/OpenRefine/wiki/Understanding-Regular-Expressions>

### 2.3.3. Exercise 8. Advanced filter II

1. Go to column **Full name** and perform a **Text filter**.
2. Check **regular expression** and **case sensitive**, then paste the expression `^[A-Z].*\s[A-Z]`



This regular expression filters the strings that start with a capital letter followed by any character, then a space, then a capital letter.

3. **WRITE DOWN THE NUMBER OF RECORDS, AS WELL AS THE NAME IN THE FULL NAME COLUMN, THAT HAVE THE FIRST LETTER OF THE SECOND WORD AS AN UPPERCASE LETTER. YOU WILL REQUIRE THIS INFORMATION TO COMPLETE THE QUIZ.**

4. Perform a correction since the second word of the name should be lowercase.

Note: If you want to know more about regular expressions click [here](#) -

<https://github.com/OpenRefine/OpenRefine/wiki/Understanding-Regular-Expressions>

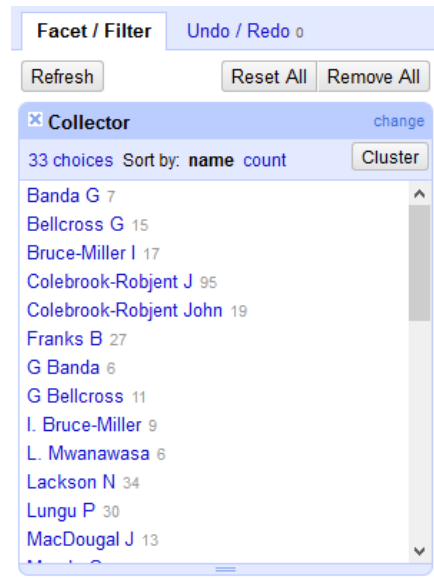
### **2.3.4. Exercise 9. Advanced filter – additional exercise on advanced filter 1**

1. Go to column **genus** and perform a **Text filter**.
2. Check **regular expression** and **case sensitive**, then paste the correct expression to be able to find the strings in which the first letter is lowercase.
3. **WRITE DOWN THE NUMBER OF RECORDS AS WELL AS THE NAME IN THE GENUS COLUMN THAT HAVE THE FIRST LETTER AS A LOWERCASE LETTER. YOU WILL REQUIRE THIS INFORMATION TO COMPLETE THE QUIZ.**
4. Perform a correction since the genus should be capitalized.

## 2.4. CLUSTERING

### 2.4.1. Exercise 9. Basic clustering

1. Go to **Collector**, then in the menu column click **Text facet**.



2. On the top right of the facet window click on **Cluster**, a new window will appear:

**Cluster & Edit column "Collector"**

This feature helps you find groups of different cell values that might be alternative representations of the same thing. For example, the two strings "New York" and "new york" are very likely to refer to the same concept and just have capitalization differences, and "Gödel" and "Godel" probably refer to the same person. [Find out more...](#)

Method: **key collision**      Keying Function: **fingerprint**      27 clusters found

Cluster Size	Row Count	Values in Cluster	Merge?	New Cell Value
2	14	<ul style="list-style-type: none"> <li>Marulanda O (10 rows)</li> <li>O. Marulanda (4 rows)</li> </ul>	<input type="checkbox"/>	Marulanda O
2	39	<ul style="list-style-type: none"> <li>Phiri S (27 rows)</li> <li>Phiri S. (12 rows)</li> </ul>	<input type="checkbox"/>	Phiri S
2	26	<ul style="list-style-type: none"> <li>Bellcross G (15 rows)</li> <li>G Bellcross (11 rows)</li> </ul>	<input type="checkbox"/>	Bellcross G
2	26	<ul style="list-style-type: none"> <li>Bruce-Miller I (17 rows)</li> <li>I. Bruce-Miller (9 rows)</li> </ul>	<input type="checkbox"/>	Bruce-Miller I
2	49	<ul style="list-style-type: none"> <li>Mwanawasa L (43 rows)</li> <li>L. Mwanawasa (6 rows)</li> </ul>	<input type="checkbox"/>	Mwanawasa L
2	13	<ul style="list-style-type: none"> <li>Banda G (7 rows)</li> <li>G Banda (6 rows)</li> </ul>	<input type="checkbox"/>	Banda G
1	30	<ul style="list-style-type: none"> <li>Lungu P (30 rows)</li> </ul>	<input type="checkbox"/>	Lungu P

Visualizations on the right:

- # Choices in Cluster**: A horizontal bar chart showing the distribution of cluster sizes. The x-axis ranges from 1 to 2.
- # Rows in Cluster**: A vertical bar chart showing the distribution of row counts. The x-axis ranges from 1 to 95.
- Average Length of Choices**: A vertical bar chart showing the distribution of average lengths. The x-axis ranges from 7 to 22.
- Length Variance of Choices**: A horizontal bar chart showing the distribution of length variances. The x-axis ranges from 0 to 0.5.

3. Now you can see information about the clusters:
  - **Cluster size**: the number of different versions that the clustering algorithm believes to be the same.
  - **Row count**: the number of records with any of the cluster values.
  - **Values in cluster**: the actual values that the algorithm believes to be the same. There is also the number of records with each particular value, and the possibility to browse the contents of the cluster in a different tab.
  - **Merge?**: check if values are to be merged into a single standard value.

- **New cell value:** the value to be applied to every record in the cluster. By default, it is the value with most records. You can also click on any value to apply that to the **New cell value**.

On the right will be a number of graphs providing additional information about the clusters. The top graph will be **#Choices in Cluster**. In our example, this will range from 1 to 2. Drag the slider to be greater than 1, so that only those 6 clusters that have more than one choice will show.

Note: If you want to know more about clustering click [here](#).

- Click on **Select All** and then on **Merge Selected & close**, you will see a notification message:

**Mass edit 167 cells in column Collector Undo**

- To fix the remaining collectors go again to **Cluster** in the facet window of **Collector**.
- In the Cluster and edit window, go to **Keying Function**, then select **metaphone3**. Again, the top graph on the right will be **#Choices in Cluster**. Drag the slider to be greater than 1, so that only those clusters that have more than one choice will show. The 3 clusters shown in the image below will be identified.

Cluster & Edit column "Collector"

This feature helps you find groups of different cell values that might be alternative representations of the same thing. For example, the two strings "New York" and "new york" are very likely to refer to the same concept and just have capitalization differences, and "Gödel" and "Godel" probably refer to the same person. [Find out more...](#)

Method **key collision** Keying Function **metaphone3** 3 clusters filtered from 24 total

Cluster Size	Row Count	Values in Cluster	Merge?	New Cell Value
2	90	<ul style="list-style-type: none"> <li>Ngwenyama T (83 rows)</li> <li>Ngwenyama T (7 rows)</li> </ul>	<input type="checkbox"/>	Ngwenyama T
2	21	<ul style="list-style-type: none"> <li>Stjernstedt R (13 rows)</li> <li>Stjernstedt RJ (8 rows)</li> </ul>	<input type="checkbox"/>	Stjernstedt R
2	114	<ul style="list-style-type: none"> <li>Colebrook-Robjert J (95 rows)</li> <li>Colebrook-Robjert John (19 rows)</li> </ul>	<input type="checkbox"/>	Colebrook-Robjert J

# Choices in Cluster

1.22 — 2

# Rows in Cluster

0 — 120

Average Length of Choices

7 — 21

Length Variance of Choices

0 — 1.5

Select All Unselect All

Export Clusters Merge Selected & Re-Cluster Merge Selected & Close Close

- Click on **Select All** and then on **Merge Selected & close**, you will see a notification message:

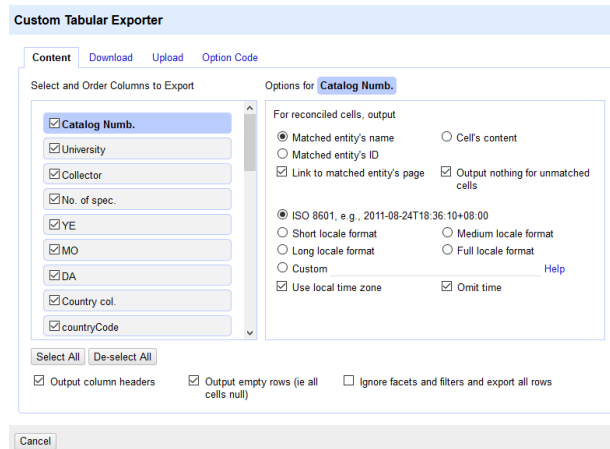
**Mass edit 225 cells in column Collector Undo**

- Your collectors are now fixed.

## 2.5. EXPORTING

You will have several options for exporting your cleaned data, but the following option is useful in most cases.

1. On the upper right corner click on **Export** and select Custom tabular exporter.
2. You will see the exportation window:



3. In the content tab you can choose the columns that you want to export, if you select **Ignore facets and filters and export all rows**, all facets and filterings will be ignored - this is useful if you forget to clear them before exporting.
4. Go to the **Download** tab and select the separator that you prefer, or whether you would like to download it as an Excel file. Don't modify the other options unless you need to. You can also **Upload** the data to a Google spreadsheet.

You can also export the whole project to open it in OpenRefine on another computer by following the route **Export > Export project**. In this case you are not downloading a data file to open in a spreadsheet or text processor, but rather a GZIP file that will only be accessible through OpenRefine.

## 3. USEFUL LINKS AND REFERENCES

- Documentation  
<https://github.com/OpenRefine/OpenRefine/wiki/Documentation-For-Users>
- Resources list for OpenRefine:  
<https://github.com/OpenRefine/OpenRefine/wiki/External-Resource>

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Exercise concept and content developed by Néstor Beltrán, and adapted for OpenRefine 3.2 and an African example by Lizanne Roxburgh.