Unsupervised learning of pharmacokinetic responses

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App user guide

App setting up and run

The EMPK.jar app is written in java so you need to have java runtime environment (JRE) installed in your machine (version 8 at least). If you are not sure about the version you have installed, please type on the command line:

```
java –version
```

If you need to install another version, please type on your search engine "download java" and follow the instructions of the site.

You then need to download the app EMPK.jar from:

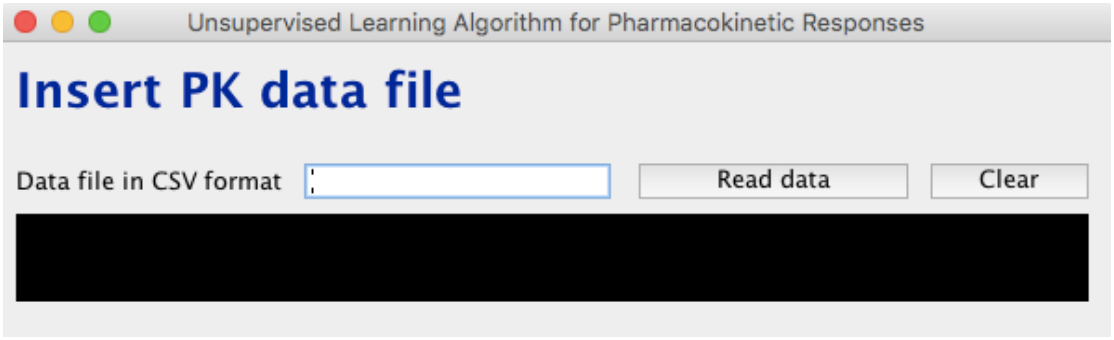
https://asmcarvalho.github.io/EMPK/

You can place it anywhere you like. To run the app open a command line and type:

```
java –jar EMPK.jar
```

Running the app

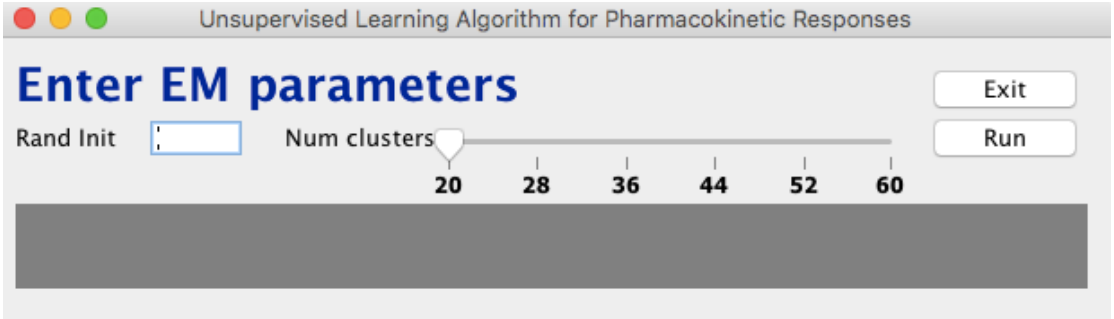
When you run the application the follow window appears:



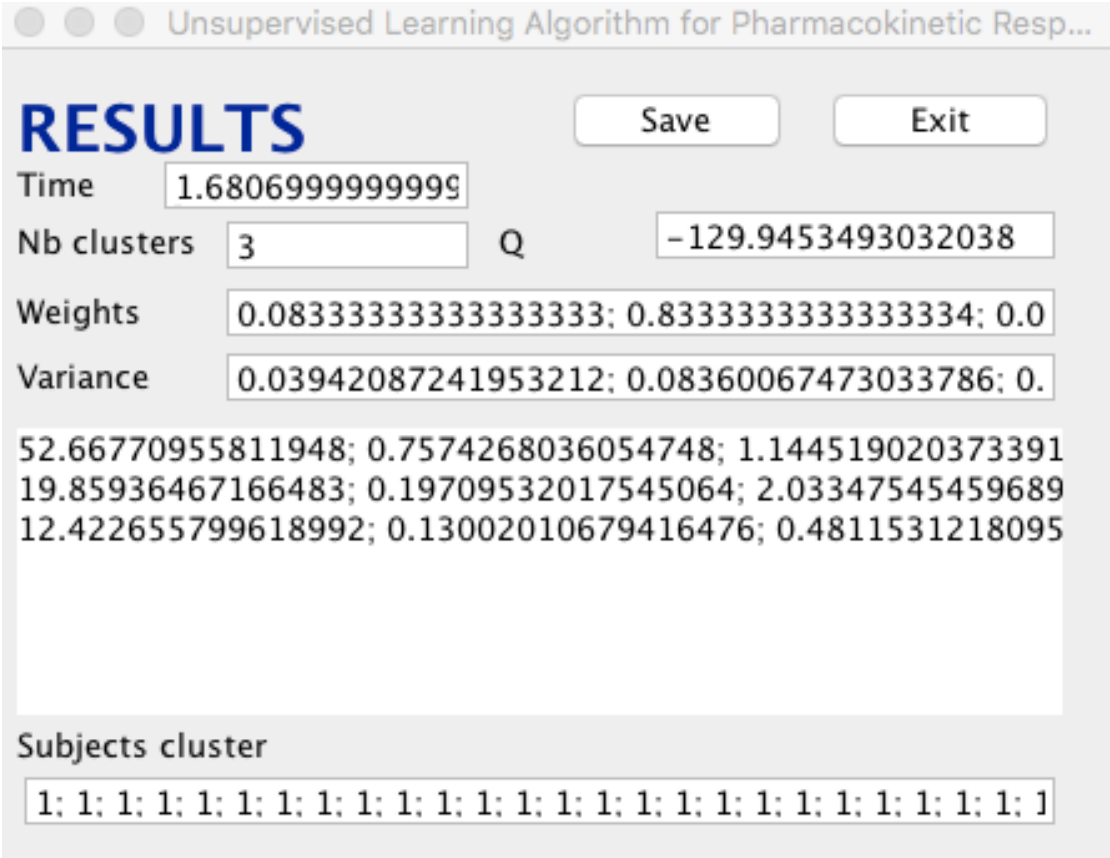
Please insert the name of the data you want to process (full name with extension); you can use, for instance, imbalanced-data/Imb-3C-50-5-5-LV.csv from the imbalance-data folder offered in the web page along with the application. Note that this file must be in the same directory as the executable

jar file; alternatively, you may pass a complete path to the file. After that press the “Read” button.

A new window appears where you have to indicate the number of random initializations (“Rand Init”) and number of initial clusters to consider (“Num clusters”); you can type, for instance, 100 and leave 20, respectively. Then press “Run”.



After pressing the “Run” button you need to wait for the results, which will appear in another window:



This is a window with the results. In:

- “Time” – average time of each random initialization.
- “Nb clusters” – number of final clusters.

- “Q” – the Q function used to evaluate the likelihood of the result against the data.
- “Weights” – weight of each clusters, separated by a semicolon.
- “Variance” – variance of each cluster separated by a semicolon.
- After the Variance it appears the parameters (\alpha, \beta_1 and \beta_2) of each retrieved clusters; each cluster in a line, with parameters separated by a semicolon.
- “Subjects cluster” – indicates the cluster of each subject.

You can also save the results by pressing in the “Save” button to a file (automatically) named Results.txt (that will appear in the same folder as the app).

In the end, please, close all windows.