

# User manual, data integration and interactions

MSc Applied Bioinformatics,

Marie Schmit

# Database population

To execute the script for database population, you need to have java installed. In an IDE, open and run DataBasePopulating.java (folder Database, dataBaseParsingPopulation, src). You can also open it in a terminal, writing: javac DataBasePopulating.java.

A browser window will then appear, allowing you to choose the vcf file that you want to save in the database. Select the file, click the button “open” and wait. It can take some time, depending on the size of the vcf file.

# Run REST API

Open a terminal in folder REST\_API, where javascript scripts are saved. Create a new npm project: npm init.

Install the following dependencies (see also package.json):

* Express: npm install express –save
* Body parser: npm install body-parser –save
* Sqlite3: npm install sqlite3 –save
* R script: npm install r-script (or npm install r-script-with-bug-fixes)

Once the dependencies are installed, run the script, writing: node server.js. This should send the following message: Application deployed on port 3000. You can now open your browser to type urls.

# Display density plot with R, plumber

To display density plot, you need to open the script variant\_density.R (folder REST API) in an IDE. Make sure that you install the following packages:

* Plumber
* Ggplot2
* Jsonlite
* Httr

Deploy the R API by typing: plumber::plumb("variant\_density.R")$run(port = 3000) in your console. Make sure that your server is activated (node server.js). The end-point to display density plot is usable.

# End points of API

api/genomes