# Instruction for Installing Julia

1. Download Julia:
   * Visit the official Julia website: <https://julialang.org/downloads/>.
   * Select the appropriate version for your operating system (Windows, macOS, Linux).
2. Install Julia:
   * ****Windows****: Run the downloaded installer and follow the on-screen instructions.
   * ****macOS****: Open the downloaded .dmg file and drag Julia.app to the "Applications" folder.
   * ****Linux****: Extract the archive and add the path to the Julia executable to the PATH environment variable.
3. Launch Julia:
   * After installation, open a terminal (or command prompt) and type julia to start an interactive Julia session. Extract api.zip into any directory.

## Setting Up the fivedb\_credentials.txt File

The fivedb\_credentials.txt file must contain your login and password for database access. The file format is as follows:

login password

Where login is your username and password is your password. Ensure there is a single space between the login and password.

## Description of Dictionaries

The dictionaries will appear after the first run.The dictionaries are saved so users can review the available elements in the database. This helps understand which values can be used when forming database queries. Each dictionary contains a specific type of data used for filtering and selecting information from the database. Below is a description of each dictionary:

1. ****5db\_process\_types.jl.txt****:
   * Contains a list of all available process types in the database.
   * Example: "Migration", "Proliferation", "Apoptosis".
   * Used to select process types to include in the query (user\_process\_types).
2. ****5db\_parameters.jl.txt****:
   * Contains a list of all available parameters in the database.
   * Example: "Emax", "EC50", "Hill Coefficient".
   * Used to select parameters to include in the query (user\_parameters).
3. ****5db\_cell\_types.jl.txt****:
   * Contains a list of all cell types available in the database.
   * Example: "T-cells", "B-cells", "Eosinophils".
   * Used to select cell types to include in the query (user\_cell\_types).
4. ****5db\_stimulateds.jl.txt****:
   * Contains a list of all stimulators or conditions that can be applied to cells.
   * Example: "IL-2", "TNF-alpha", "No stimulation".
   * Used to select stimulation conditions to include in the query (user\_stimulateds).
5. ****5db\_patient\_states.jl.txt****:
   * Contains a list of all patient states available in the database.
   * Example: "Healthy", "Cancer", "Autoimmune disease".
   * Used to select patient states to include in the query (user\_patient\_states).
6. ****5db\_products.jl.txt****:
   * Contains a list of all products (e.g., proteins, cytokines) that can be measured or studied.
   * Example: "IFN-gamma", "IL-6", "VEGF".
   * Used to select products to include in the query (user\_products).
7. ****5db\_regulators.jl.txt****:
   * Contains a list of all regulators (e.g., molecules that influence processes).
   * Example: "p53", "NF-kB", "STAT3".
   * Used to select regulators to include in the query (user\_regulators).
8. ****5db\_modifiers.jl.txt****:
   * Contains a list of all modifiers (e.g., substances that alter cell behavior).
   * Example: "Drug A", "Inhibitor B", "Enhancer C".
   * Used to select modifiers to include in the query (user\_modifiers).
9. ****5db\_daughter\_cells.jl.txt****:
   * Contains a list of all daughter cell types that may result from processes (e.g., cell division).
   * Example: "Differentiated T-cells", "Activated B-cells".
   * Used to select daughter cell types to include in the query (user\_daughter\_cells).

## Purpose of Selection Lists

The selection lists are used to filter data when querying the database. They allow you to specify which data you want to retrieve. For example:

* user\_process\_types: Select process types (e.g., "Migration").
* user\_parameters: Select parameters (e.g., "Emax").
* user\_cell\_types: Select cell types (e.g., "Eosinophils").
* user\_stimulateds: Select stimulation conditions (e.g., "IL-2").
* user\_patient\_states: Select patient states (e.g., "Healthy").
* user\_products: Select products (e.g., "IFN-gamma").
* user\_regulators: Select regulators (e.g., "p53").
* user\_modifiers: Select modifiers (e.g., "Drug A").
* user\_daughter\_cells: Select daughter cell types (e.g., "Differentiated T-cells").

## How to Run the Script and Expected Results

1. ****Running the Script****:
   * Ensure all required packages are installed and the fivedb\_credentials.txt file is configured.
   * Open a terminal and navigate to the directory containing your script.
   * Run the script using the command:

julia your\_script.jl

1. ****Script Output****:
   * The script will connect to the database and load the necessary dictionaries.
   * Save the dictionaries as text files in the current directory.
   * Execute a database query using the specified filters.
   * Clean the data by removing rows with missing values (NA).
   * Generate a probability density plot for the selected data.
   * Display the cleaned data and the plot on the screen.

### Example Output

* The console will display the cleaned data retrieved from the database.
* A probability density plot will be shown, visualizing the distribution of values for the selected parameter (e.g., "Emax") and process type (e.g., "Migration"). This process allows you to analyze database data and visualize it for further study.