# Instructions for Installing R and R Studio, and Running the Example from the File example\_5db.r (example\_cytocon.r) with the Connected File insysbio\_db.r

### 1. Installing R

1. Go to the official R website: <https://cran.r-project.org/>.
2. Select the version of R for your operating system (Windows, macOS, Linux).
3. Download and install R, following the on-screen instructions.

### 2. Installing R Studio

1. Go to the official R Studio website: <https://posit.co/download/rstudio-desktop/>.
2. Download the R Studio Desktop version for your operating system.
3. Install R Studio, following the on-screen instructions.

### 3. Preparing the Working Directory

1. Create a folder on your computer where the example files (example\_5db.r, insysbio\_db.r, etc.) will be stored. For example, create a folder named C:/R\_Projects/Example5db.
2. Extract the api.zip folder into the created folder.
3. In the cytocon\_credentials.txt and fivedb\_credentials.txt files, enter your login and password for the databases.

### 4. Launching R Studio

1. Open R Studio.
2. In R Studio, go to the menu: ****Session**** → ****Set Working Directory**** → ****Choose Directory...****.
3. Select the folder where you saved the files (e.g., C:/R\_Projects/Example5db).

### 5. Running the Example from File example\_5db\_parameter\_for\_celltype\_plot.r

1. In R Studio, open the file example\_5db\_parameter\_for\_celltype\_plot.r To do this, go to the menu: ****File**** → ****Open File...**** and select the file example\_5db\_parameter\_for\_celltype\_plot.r.
2. Ensure that the file insysbio\_db.r is in the same folder as example\_5db\_parameter\_for\_celltype\_plot.r , as it is connected in the code.
3. Run the script example\_5db\_parameter\_for\_celltype\_plot.r . To do this, click the ****Source**** button at the top of the editor window (see the figure below).

### 6. Description of the Dictionary Saving Process and Parameter Selection

In your code, dictionaries are saved to disk so that users can later select the desired parameters (species, tissue\_types, diseases, markers) from the saved files. Let’s break down this process in detail.

#### 6.1. Saving Dictionaries to Disk

Dictionaries are saved to text files using methods of the cytoconDBManager object. Each method saves the corresponding dictionary to the specified file. For example:

fiveDBManager$saveProcessTypes(file.path(dirname(script\_path),'5db\_process\_types.r.txt'))

fiveDBManager$saveParameters(file.path(dirname(script\_path),'5db\_parameters.r.txt'))

fiveDBManager$saveCellTypes(file.path(dirname(script\_path),'5db\_cell\_types.r.txt'))

fiveDBManager$saveStimulateds(file.path(dirname(script\_path),'5db\_stimulateds.r.txt'))

fiveDBManager$savePatientStates(file.path(dirname(script\_path),'5db\_patient\_states.r.txt'))

fiveDBManager$saveProducts(file.path(dirname(script\_path),'5db\_products.r.txt'))

fiveDBManager$saveDaughterCells(file.path(dirname(script\_path),'5db\_daughter\_cells.r.txt'))

fiveDBManager$saveRegulators(file.path(dirname(script\_path),'5db\_regulators.r.txt'))

fiveDBManager$saveModifiers(file.path(dirname(script\_path),'5db\_modifiers.r.txt'))

* path\_to\_dict — The path to the folder where the files are saved. For example, this could be C:/R\_Projects/Example5db/.
* 5db\_process\_types.r.txt, 5db\_parameters.r.txt, 5db\_cell\_types.r.txt, 5db\_stimulateds.r.txt, 5db\_patient\_states.r.txt,  5db\_products.r.txt, 5db\_daughter\_cells.r.txt, 5db\_regulators.r.txt, 5db\_modifiers.r.txt — The names of the files where the corresponding dictionaries are saved.

After executing this code, four files will appear in the specified folder:

1. 5db\_process\_types.r.txt — List of process types.
2. 5db\_parameters.r.txt — List of parameters.
3. 5db\_cell\_types.r.txt — List of cell types.
4. 5db\_stimulateds.r.txt — List of stimulated cells.
5. 5db\_patient\_states.r.txt — List of patient states.
6. 5db\_products.r.txt – List of products.
7. 5db\_daughter\_cells.r.txt – List of daughter cells.
8. 5db\_regulators.r.txt – List of regulators.
9. 5db\_modifiers.r.txt – List of modifiers.

#### 6.2. User Parameter Selection

After saving the dictionaries, the user can select the desired parameters to include in the selection list. This is done using the methods selectProcessTypes, selectParameters, selectCellTypes, selectStimulated, selectPatientStates, selectProducts, selectDaughterCells, selectRegulators, selectModifiers.

For example:

user\_process\_types <- fiveDBManager$selectProcessTypes(c('Migration'))

user\_parameters <- fiveDBManager$selectParameters(c('Emax'))

user\_cell\_types <- fiveDBManager$selectCellTypes(c())

user\_stimulateds <- fiveDBManager$selectStimulated(c())

user\_patient\_states <- fiveDBManager$selectPatientStates(c())

user\_products <- fiveDBManager$selectProducts(c())

user\_daughter\_cells <- fiveDBManager$selectDaughterCells(c())

user\_regulators <- fiveDBManager$selectRegulators(c())

user\_modifiers <- fiveDBManager$selectModifiers(c())

#### 6.3. Example Usage

Suppose the user wants to select specific parameters:

* Process type : Migration.
* Parameter: Emax.

After this, the variables user\_process\_types, user\_parameters, user\_cell\_types, user\_stimulateds, user\_patient\_states, user\_products, user\_daughter\_cells, user\_regulators and user\_modifiers will contain the selected parameters, which can be used for data queries.

### 7. Checking the Results

1. After running the script, ensure that all operations were completed without errors.
2. The results of the script (if they are output to the console or saved to files) will be available in the specified folder, e.g., C:/R\_Projects/Example5db.

### 8. Conclusion

You have now successfully installed R and R Studio, prepared the working directory, and run the example from the file example\_5db.r. If errors occur, check the file paths and ensure all required packages are installed.