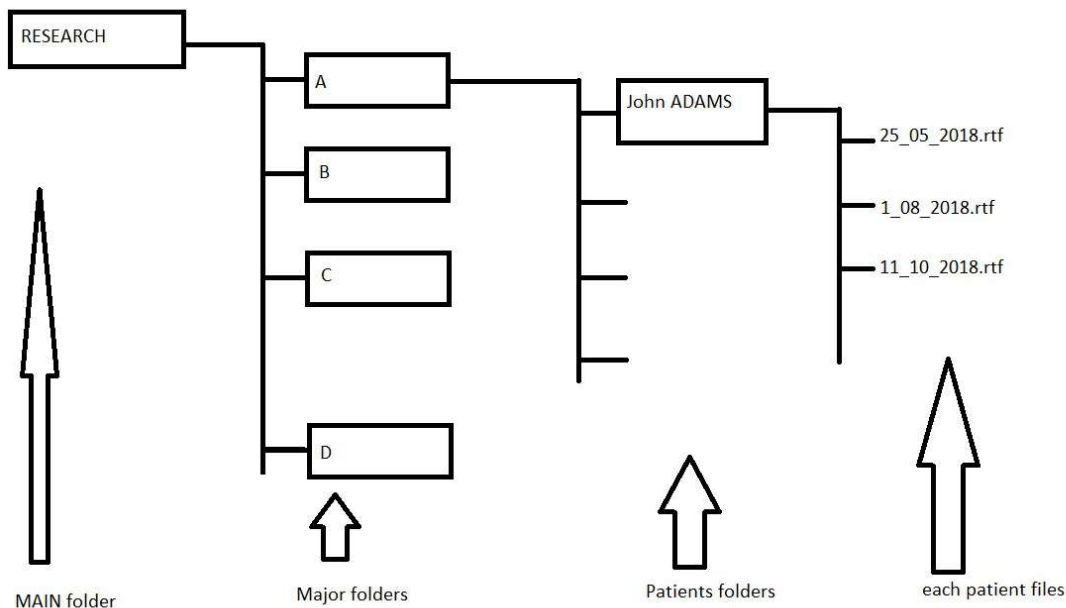


USER MANUAL

Project Retrieval

1. Unzip PR.zip into the one folder. This archive contains 4 executable files.
2. If you are new user, and need to design your research step-by-step, start PR.exe
3. At first, you should have segregated files with patient data in tree-directory system:
 - 1 folder = 1 patient and is called as patient would be called in your research (for example: patient name or ID number, of course, you can anonymize it later)
 - in every folder you can have one or more files about this one patient
 - only rich text format (rtf) files will be searched by PR algorithms
 - patient folders should be inside another folder (we called it *major folder*)
 - you can have one or more *major folders* (for example unique folder for every health center or for patients with surname starting by A, B, C, etc)
 - all of your *major folders* should be in the one separated folder (for example RESEARCH) it shouldnt contain any other folders, with other data (we called it main folder)

Tree-directory structure of database

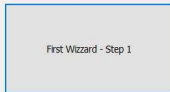


4. Now you can start work with our program. Click at STEP 1 button

Step 1

You can divide your patients on few sub-groups, for example with or without some drug. You can also don't do it, and just select all patients into one group. Use The First Wizard for this step

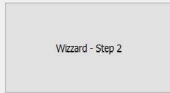
The window of main application



<--- click for begin the work with new database

Step 2

The most important thing now: input queries, which you want to add for your database. For example alphanumeric values as WBC, and CRP, and U/L values, like stroke - yes/no

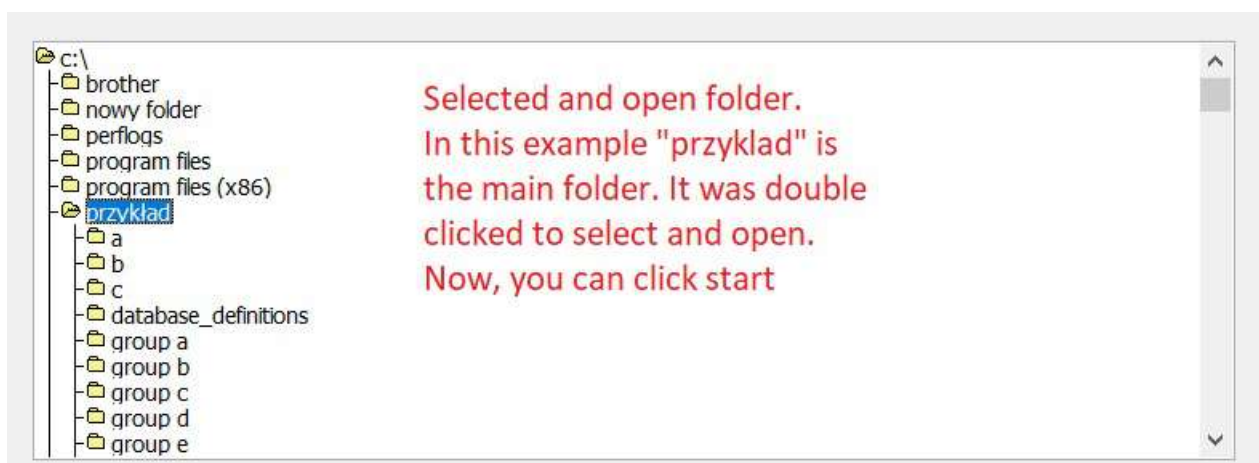
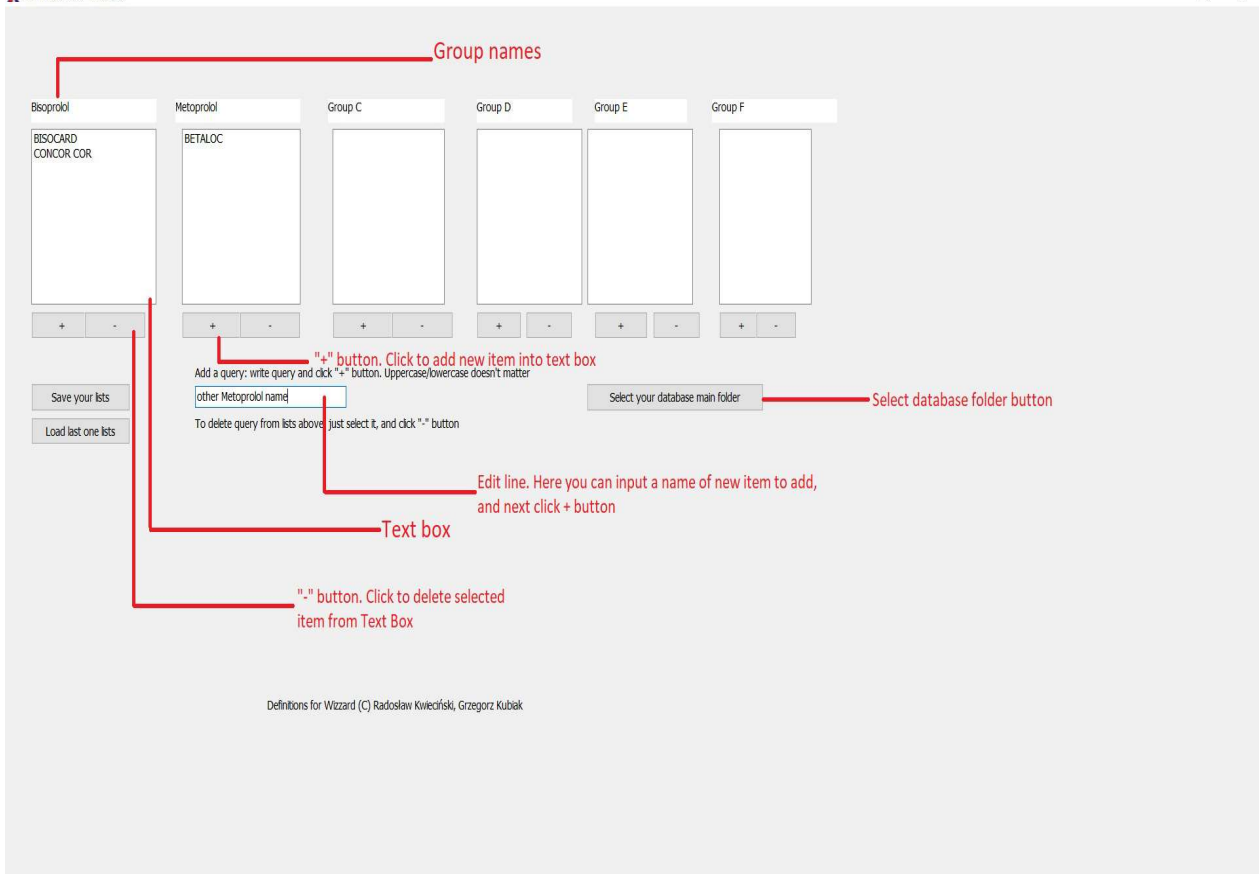


Step 3

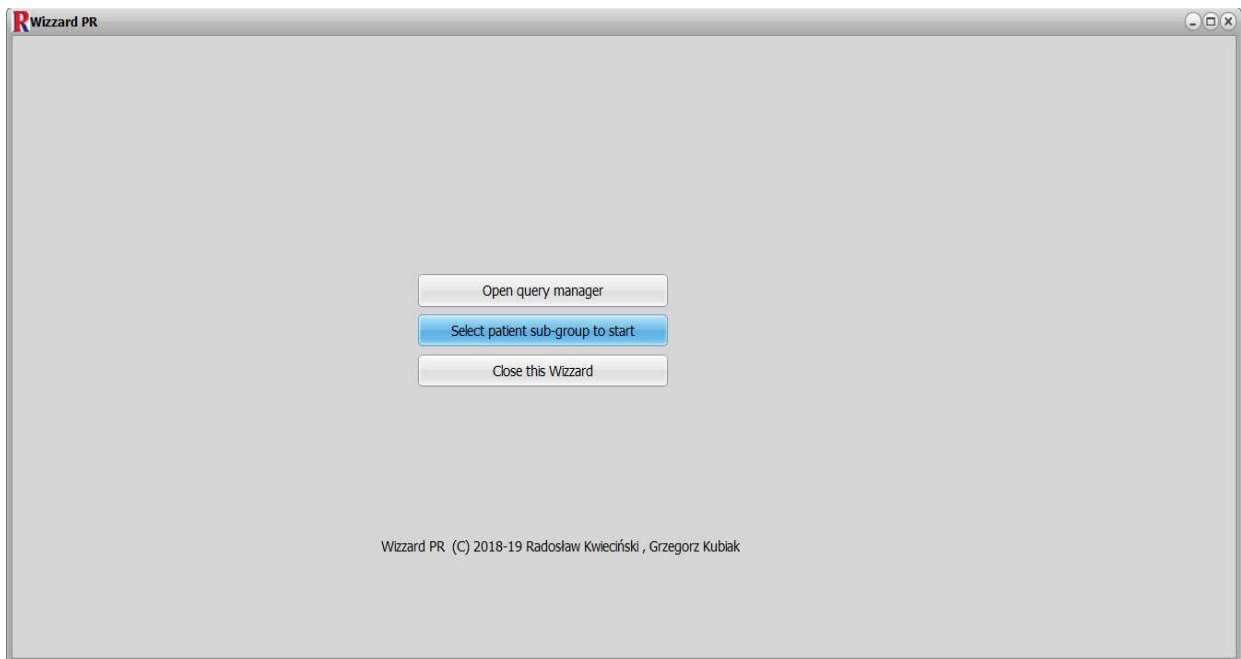
Now you have a lot of csv files - 1 patient = 1 file. You can finish work with PR now and use those databases how do you want, or compile it into bigger database: 1 sub-group of patients = 1 database



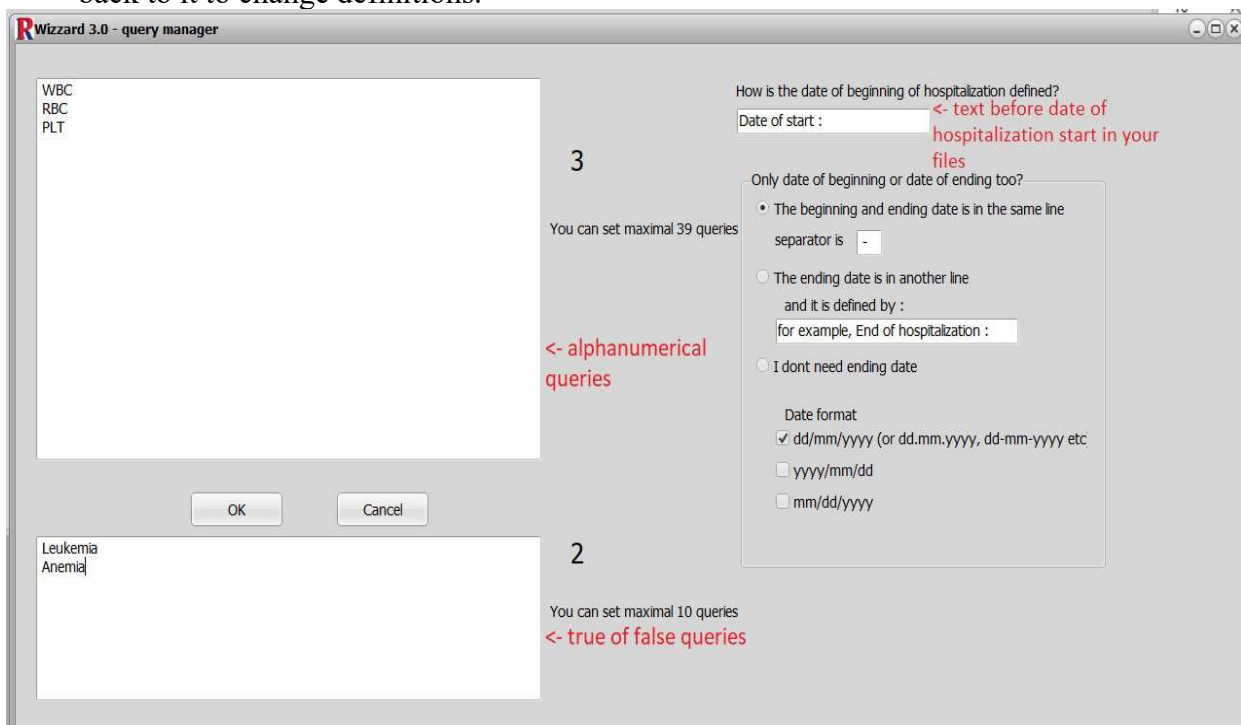
5. It will be opened Definitions window. You can decide, do you want to treat all patient as one population, or create few sub-populations. Of course, maybe you already have your patients divided. (maybe in 2 main folders like RESEARCH1 and RESEARCH2) If this case, please go to step 8. But if you want to divide them by some key-words, go to step 6
6. Definitions Wizard can divide patients by key-word presence in rtf file. For example, we wanted to select patient with different kinds of beta-blockers. You have 6 lists boxes called Group A – F. Its possible to change this names, for example for Bisoprolol, Metoprolol, Carvedilol, etc (or leukemia, anemia). Just add key-words by input text into the edit line and click „+” button under text box. You can delete selected key-words from list boxes by „-” buttons for each text box.
Every text box can have added few key-words. If algorithm will find any of them, patient would be assigned to this group. If rtf file contains key-words from more then 1 group, patient will be assigned to more then one group.
7. When you fullfill your text boxes (you dont need to declare all of them), you can save your list (for easy load it next time) ,and select main folder of your files (in our example RESEARCH) The main folder is folder contains all *major folders* (look at step 3) Open this folder as its showed at the picture below, and click start. Software will work for few minutes (it depends on your database size). When it shows message about finished task, you can close this window, and go to step 9



8. If you don't need to divide patients by key-words, just left all text boxes empty, click „select your database main folder”, open main folder of patients (like in picture above) and press start. After message about end of task, close window of Definitions Wizzard
9. Now you can find in your main folder, few new sub-folders. 6 of them will be called as your sub-populations (for ex. Group A-F), 1 will be called „outside_all_groups” and one „database_definitions”. Most of them still will be empty.
10. Click STEP 2 button in main application. The new window will be opened.
11. Now you must declare your database queries. Click „Open query manager”



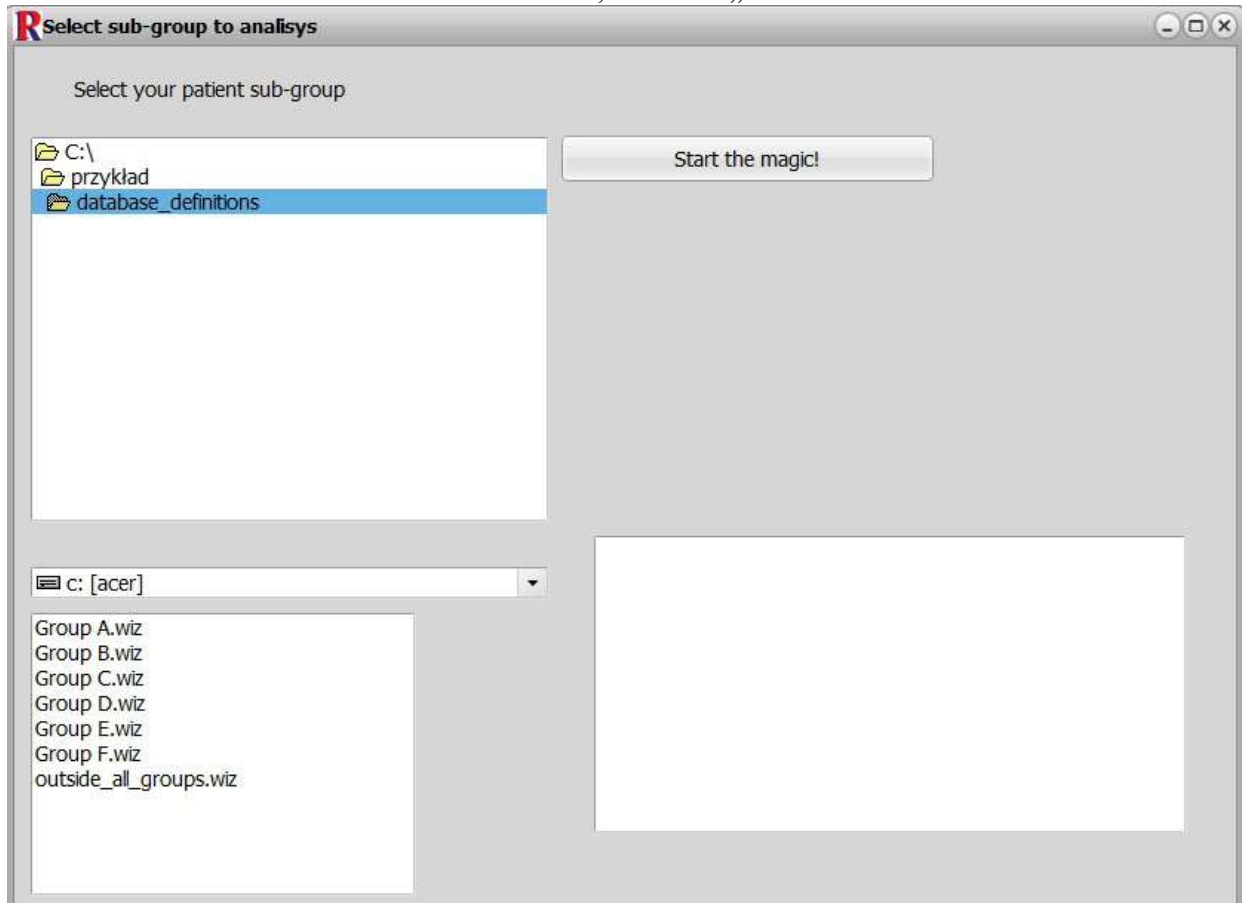
12. We divided queries on 2 kinds : - queries with alphanumerical values (like WBC, GFR, etc) and 1/0 queries (1 if query is present in a document, 0 if not). Just write queries which you need in text boxes (is a limit of 39 alphanumerical queries and 10 true/false queries). Our algorithm will search this queries in every rtf file of your database. At right side, you see tools for define how in your files is set date of hospitalization, date format, etc If you change definition of separator, be carefull, if is it with or without <space>. For example in date 27-05-2017-31-05-2017 separator is just – but in 27-05-2017 – 31-05-2017 is <space>-<space> (, - ,,) When you set all of them, click OK twice. Window will close, but you can back to it to change definitions.



13. Click the button „Select patient sub-group to start”. In new window, find your main folder, and „database_definition” in it. If you open it, you will see few files with wiz extension. They are called as your patient sub-groups. (look at step 6) You have one extra file too, its called „outside_all_groups” - its define patients without any key-words from Definition

Wizzard. It could be your control group, or you could just dont use it. But if you decided to not divide population of patients by Definition Wizzard (look at step 5) this file contains all of your patients form main folder. (so you need to use only this one file)

14. Select wiz file, which you want to start to analyze, and click „start the magic!“. This is the longest process of all procedure. This is a moment of creation of csv (coma separated value) files with patients data. When task will be finished, you can select other wiz file and start work with it. Afterall close this window ,and click „Close this Wizzard“



15. Now folders (Group A, B, C, etc) in your main folder contains a lot of csv files. Every file is a little database of searched values of one patient. 1 file = 1 patient. Because they are in separated sub-folders, you know which sub-population they belong to.
16. If you want, you can compile little csv database into bigger ones. Like 1 database for every sub-population. Just click STEP 3 button. Open folder of sub-group (like Group B) and click OK. Program will generate in this folder new csv file with data of all patients from sub-population. This database will have one more column, called NAME. As patient name, software will use file name. (so it depends how you called folders in your tree-directory structure → look at step 3)
17. Now your work with Project is really finished. You can use your database how would you want. After check it by any program like MS-Word or Open Office, you should save it in more stabile format then csv (like xls for example)