

S1 File. User Manual

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1. INTRODUCTION

HIGH-THROUGHPUT TABULAR DATA PROCESSOR (HTDP) is Java application that is intended to facilitate data exploration and reduction tasks in large text files resulting from high throughput technologies, e.g. massively parallel sequencing or microarrays. The software has been optimized for microarray and deep parallel sequencing data, however it can accept any character delimited tabular data sets. In the latter case the first row of the data set should be designated as header row and should contain the names of the corresponding columns. HTDP can also import, process and convert Variant Call Format (VCF) files ver. 4.0, 4.1 and 4.2 (<http://www.1000genomes.org/wiki/Analysis/Variant%20Call%20Format/vcf-variant-call-format-version-41>).

HTDP provides quick filtering functionality and can process data consisting of single or multiple input files. Files in different supported formats can be processed at the same time. The processed data can be exported as tab delimited file. The user interface provides two modes of operation: “basic mode” (default) and “advanced mode”.

Data filtering in the basic mode is carried out via selection of search terms from the pull down list or manual input of alphanumeric strings into a simple form (up to 8 queries). Data filtering in the advanced mode is carried out based on user defined unlimited queries. Subsequent queries are added to the queue, which constitutes a set of filtering criteria. This set of filtering criteria is applied to every row in the input file(s).

HTDP is distributed under GPL License version 3.0.

Nullsoft Scriptable Install System (NSIS, <https://sourceforge.net/projects/nsis/>) was used to generate windows installer. NSIS is licensed as zlib/libpng licensed software with parts licensed under bzip2 and Common Public License version 1.0. The installer automates installation process and is applicable in Windows only.

Apache Derby database (Apache License, Version 2.0) is required to compile HTDP (<http://db.apache.org/derby/>).

2. INSTALLATION AND RUNNING

2.1 System requirements:

- Windows XP, Windows 7 or Linux with Java run time environment v. 1.6 or later (64-bit version)*.
- At least 1 GB of RAM, depending on the amount of input data and complexity of queries.

*Default Java version is 32-bit and its maximum theoretical heap limit is 4GB. To increase the amount of allocated memory and therefore the performance of this program, the 64-bit version should be used.

2.2 Windows (automated installation):

- Run the installation program (htdpinstaller.exe) and follow the on screen tips.
- The installation program will create program group “**HIGH-THROUGHPUT TABULAR DATA PROCESSOR**” in Windows Start Menu.
- The program group contains the shortcut to the “**HIGH-THROUGHPUT TABULAR DATA PROCESSOR**” as well as to the uninstall program.
- Additional shortcut to the “HIGH-THROUGHPUT TABULAR DATA PROCESSOR” will be created on Windows desktop.

2.3 Windows (manual installation):

Copy **HTDP.jar** file and **lib** folder from the installation archive to selected folder on local hard drive. Run the program using the following command:

```
"java -Xmx800M -jar "/path/to/the/program/folder/HTDP.jar"
```

2.4 Linux:

Copy **HTDP.jar** file from the installation archive to selected folder on local hard drive. Run the program using the following command:

```
"java -Xmx800M -jar "/path/to/the/program/folder/HTDP.jar"
```

3. INPUT FILE FORMAT AND LIMITS:

The following file formats can be imported and processed:

- **Any Tabular Text File** with a single line header row present or absent. File has to contain at least four row of the data to be correctly recognized and opened. This includes **Variant Call Format (VCF)** ver. 4.0, 4.1 and 4.2 (<http://www.1000genomes.org/wiki/Analysis/Variant%20Call%20Format/vcf-variant-call-format-version-41>) and other uncompressed text data formats like BED, BED detail, PSL, GFF, Personal Genome SNP, ENCODE RNA elements: BED6 + 3 scores, ENCODE narrowPeak: Narrow (or Point-Source) Peaks, ENCODE broadPeak: Broad Peaks (or Regions), ENCODE gappedPeak: Gapped Peaks (or Regions), ENCODE peptideMapping: BED6+4, detailed formats description: <https://genome.ucsc.edu/FAQ/FAQformat.html>. The column delimiter character may be defined by user (tab, space, comma or any other) similarly to the comment indicator. Maximal number of simultaneously opened files and data rows depends on memory installed in the system. Some example limitations are presented in table 1.

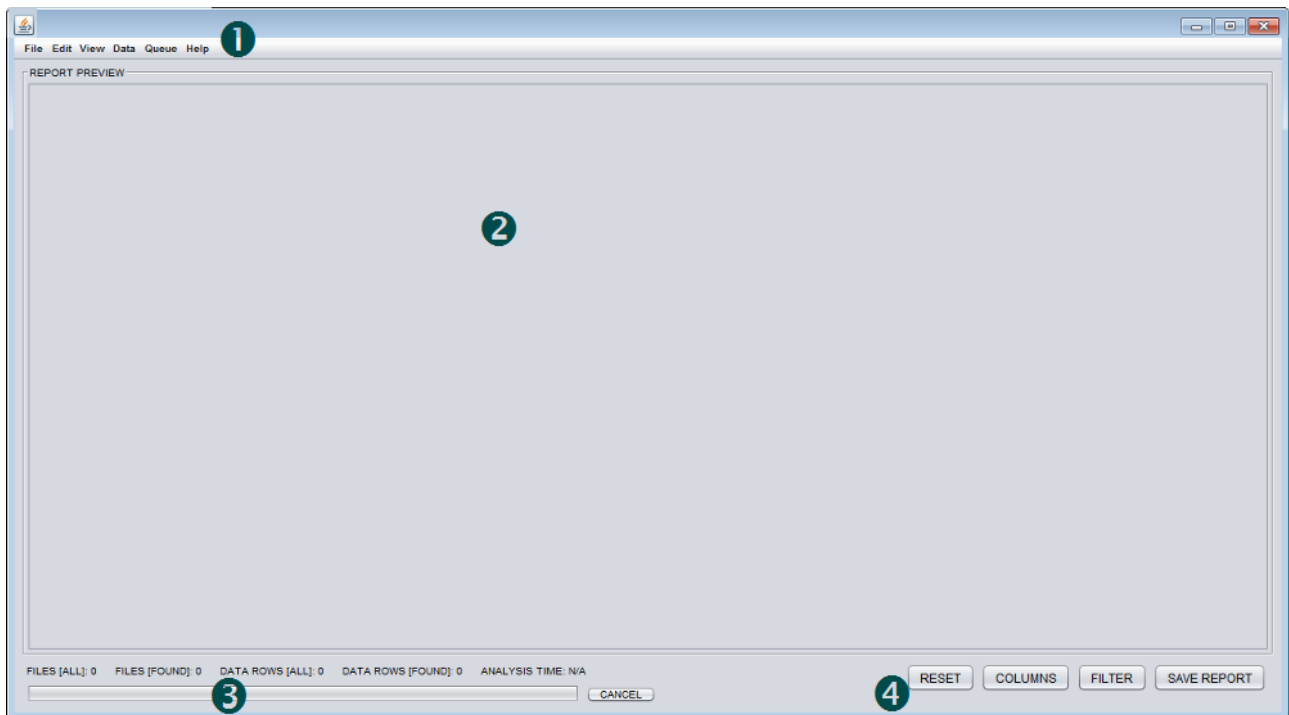
Table 1. Sample memory requirement and performance test results.

Allocated memory (max. RAM usage allowed)	Max input file size (format)	Rows	Additional information
4 GB	228,4 MB (VCF) ^a	1 750 000	Opening time: about 6 min. Simple query (get unique rows only on the basis of selected column contents): 8 sec.
8 GB	457,9 MB (VCF) ^a	3 500 000	Opening time: about 9 min. Simple query (get unique rows only on the basis of selected column content): 21 sec.
16 GB	918,7 MB (VCF) ^a	7 000 000	Opening time: about 17 min. Simple query (get unique rows only on the basis of selected column content): 46 sec.
4GB	184,8 MB (TDTF) ^a	4 800 000	Opening time: about 2 min. Simple query (get unique rows only on the basis of selected column content): 48 sec.
8 GB	388,4 MB (TDTF) ^a	9 700 000	Opening time: about 4 min. Simple query (get unique rows only on the basis of selected column content): 95 sec.
16 GB	704,9 MB (TDTF) ^a	17 500 000	Opening time: about 6 min. Simple query (get unique rows only on the basis of selected column content): 2 min.

Methodology: Linux (Debian 8) 'split' command was used to split large files into the desired number of rows as indicated in the table. Java 'Xmx' parameter was used to set java virtual machine accessible memory limit. All tests were carried out on a workstation equipped with Intel Xeon E5-1650v3 3,5GHz processor.

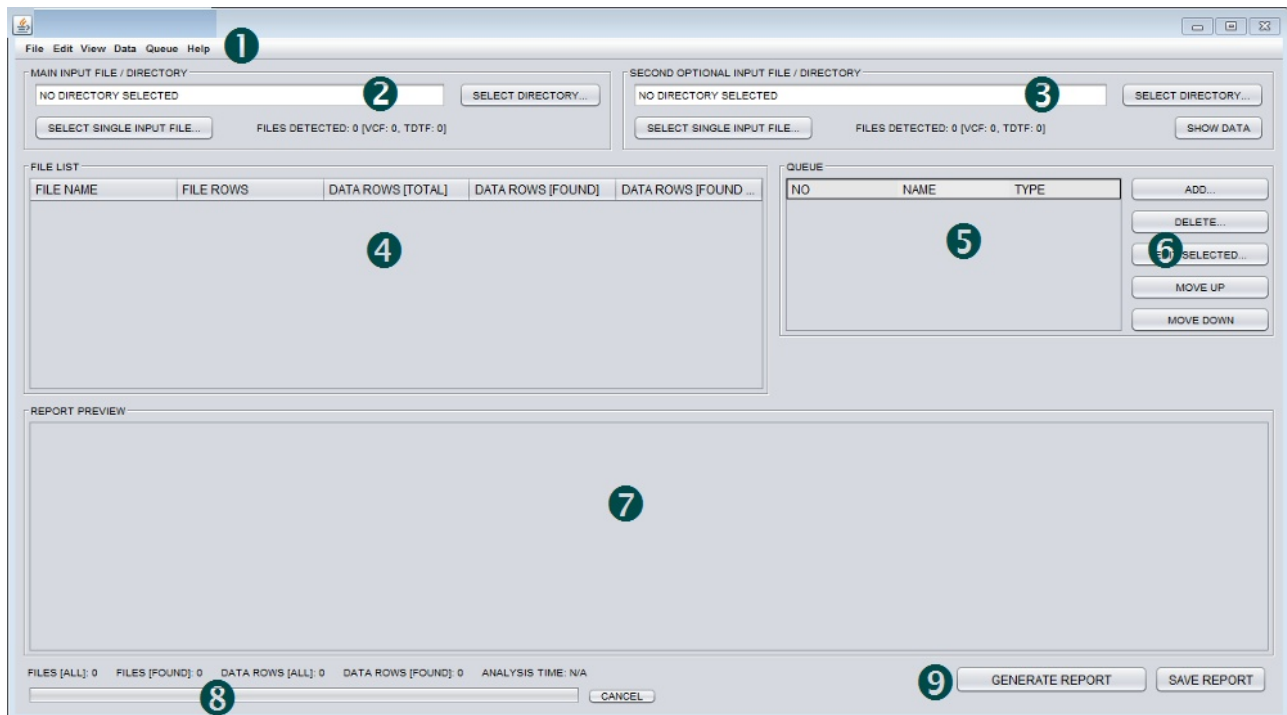
^a TDTF and VCF files are both character-delimited files. However, VCF files often have richer annotation compared to simple tab-delimited files, as well as VCF files utilize multiple delimiters (tabs, colons and semicolons) in a single file. Hence, VCF and TDTF files were subjected to the test separately to illustrate differences in the initial processing time during file opening. The tab delimited text file (TDTF) (6 columns) and VCF file (32 columns) were used.

4. THE MAIN WINDOW OF THE PROGRAM – BASIC MODE



- ① – Pull down text menu with program options
- ② – Preview of the data, before and after filtering (**REPORT PREVIEW**)
- ③ – Information and status bar
- ④ – The buttons for column and file operations (**RESET, COLUMN, FILTER, SAVE REPORT**)

5. THE MAIN WINDOW OF THE PROGRAM – ADVANCED MODE

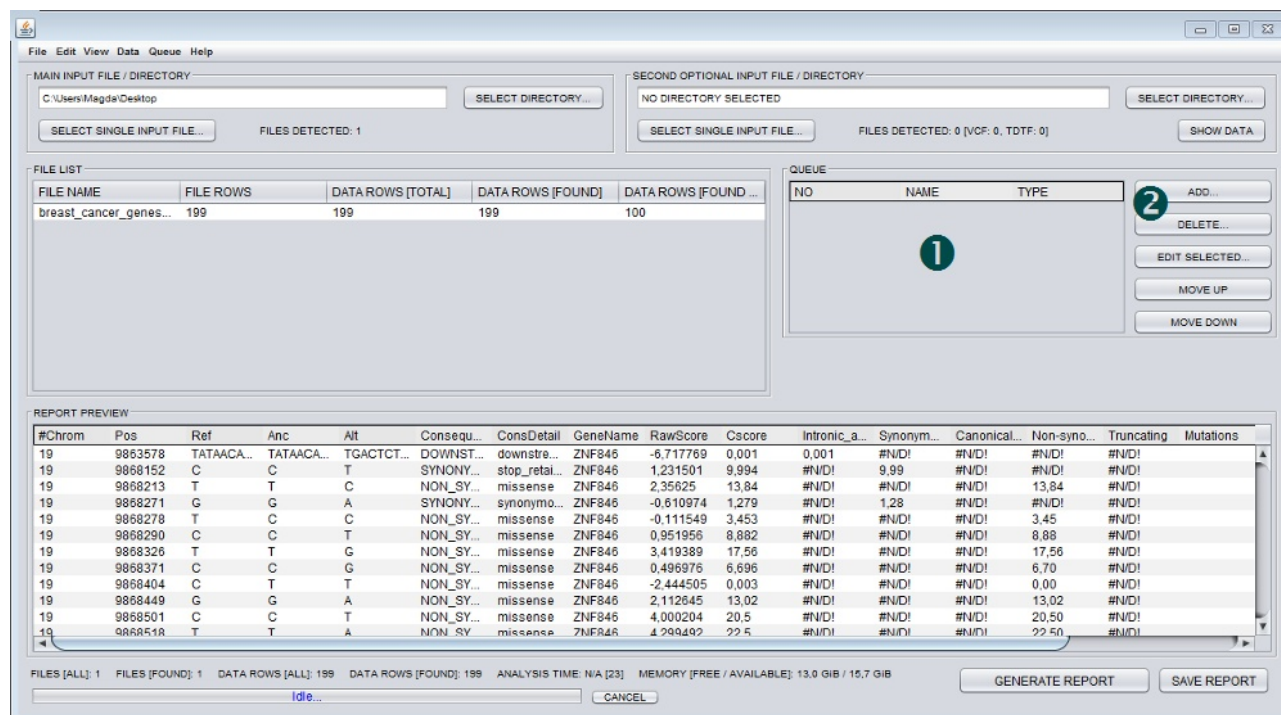


- 1 – Pull down text menu with program options
- 2 – Input data folder selection form (**MAIN INPUT FILE / DIRECTORY**)
- 3 – Selection form for the second file or folder (**SECOND, OPTIONAL INPUT FILE / DIRECTORY**)
- 4 – List of imported files (**FILE LIST**)
- 5 – The list of user specified queries (**QUEUE**)
- 6 – Query queue control section
- 7 – Preview of the resulting data table (**REPORT PREVIEW**)
- 8 – Information and status bar
- 9 – The buttons for file operations (**GENERATE REPORT, SAVE REPORT**)

6. QUERY CONFIGURATION WINDOW – ADVANCED MODE

The **QUERY SETUP** window is available only in the advanced mode. It enables forming subsequent, complex queries.

To set up a query, click the **ADD** button in the query queue control section (❷). Subsequently added queries will show up as a list in the **QUEUE** field (❶).



In the present version of the program the **QUERY SETUP** window has six tabs corresponding to the different types of queries that can be handled by the program (see 7.6 FILTERING THE INPUT FILE(S) section):

- **DATA PREPROCESSING.**
- **SIMPLE FILTER.**
- **LOCATION FILTER.**
- **EXTERNAL DATA FILTER / MERGER.**
- **EXTERNAL DATA FILTER / MERGER (LOCATION).**
- **SAMPLE FILTER.**

DATA PREPROCESSING tab is selected by default.

The screenshot shows a 'QUERY SETUP' dialog box with several tabs: 'DATA PREPROCESSING', 'SIMPLE FILTER', 'LOCATION FILTER', 'EXTERNAL DATA FILTER / MERGER', 'EXTERNAL DATA FILTER / MERGER (LOCATION)', and 'SAMPLE FILTER'. The 'DATA PREPROCESSING' tab is active. Below the tabs, there is a 'QUERY NAME' field containing 'DATA PREPROCESSING' and a 'QUERY DESCRIPTION' field. The main configuration area on the left includes: 'FILTER UNIQUE / NOT UNIQUE ROWS' with 'SELECT' set to 'unique' and 'ROWS' set to 'in all data'; 'SAMPLE COLUMNS' with four 'no data' dropdowns; 'ON THE BASE OF COLUMNS' with four 'no data' dropdowns; and 'EXCLUDING COLUMNS' with four 'no data' dropdowns. At the bottom right, there are 'ADD QUERY' and 'Cancel' buttons.

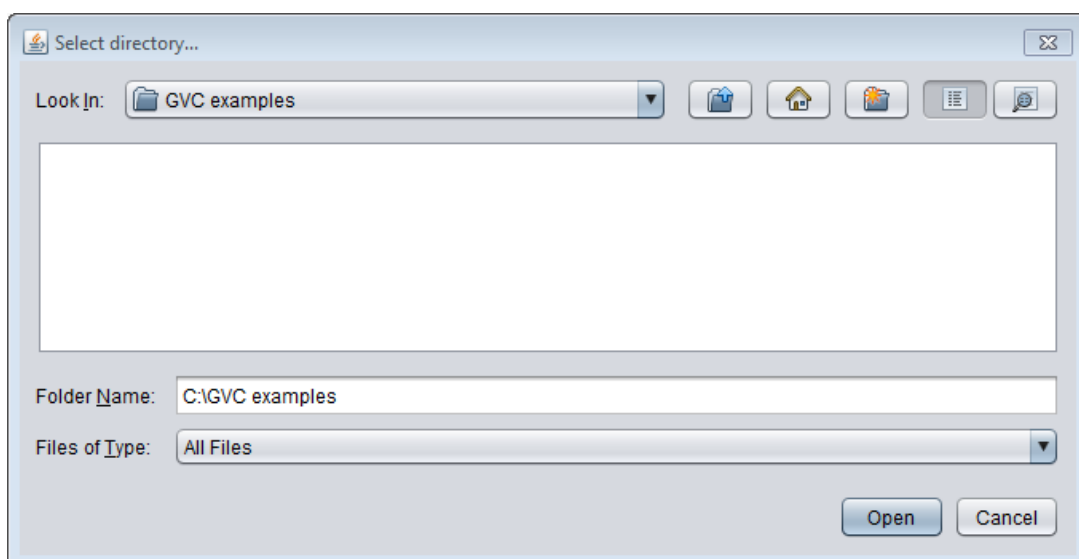
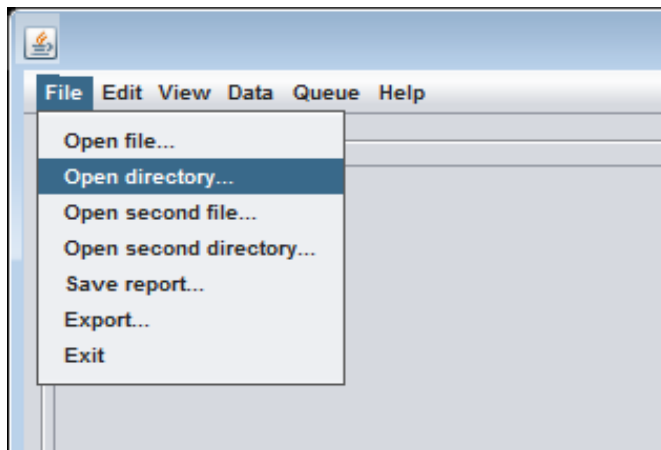
7. BASIC MODE – USAGE

The **BASIC MODE** is intended for simple tasks, specifically for viewing the combined data from multiple files and simplified alphanumeric filtering which may however consist of several steps linked by Boolean operators.

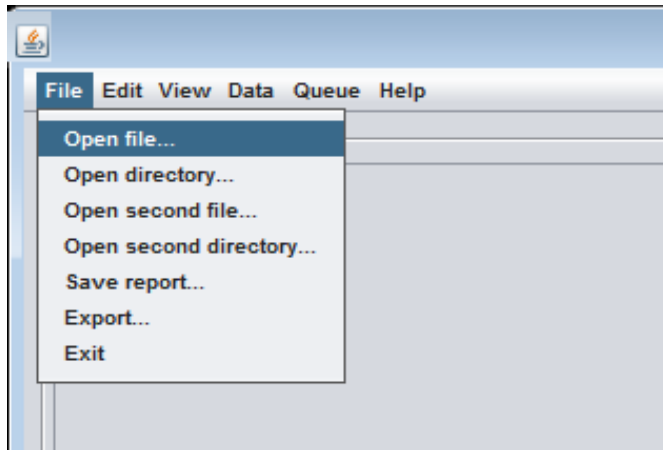
7.1 FILE IMPORT

To import file(s) which will be subjected to filtering:

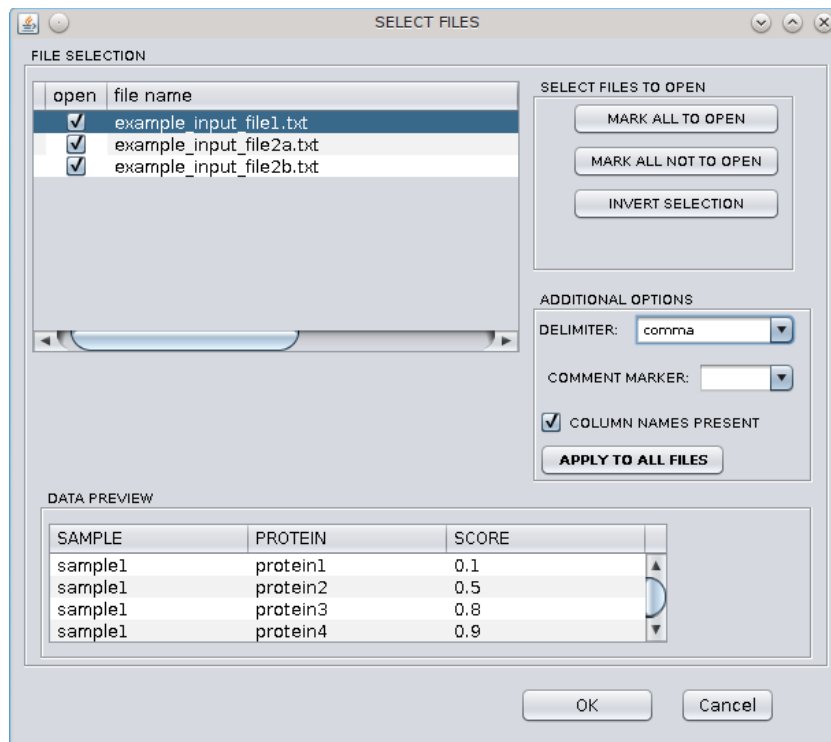
- 1 Copy the input files to a single directory. Select **File > Open directory** menu option and point to this directory in **Select directory** window. The supported data formats are automatically detected and listed upon data import.



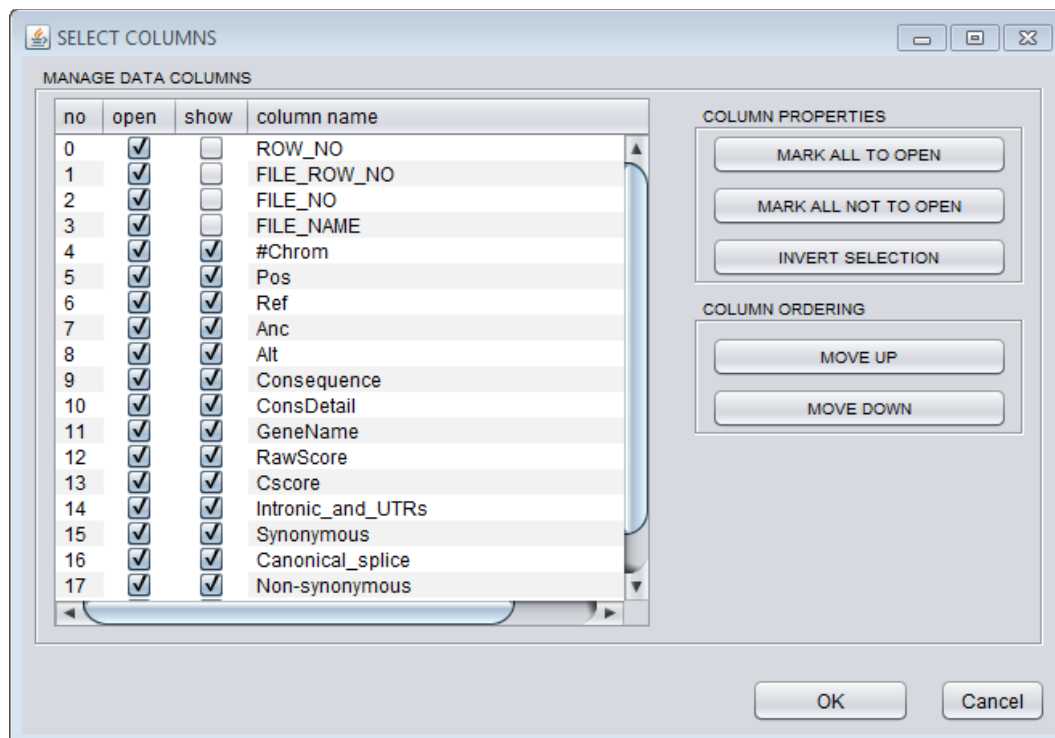
Alternatively, a single file can be imported. To accomplish it, select **File > Open file** menu option and point the file in **Select single file** window.



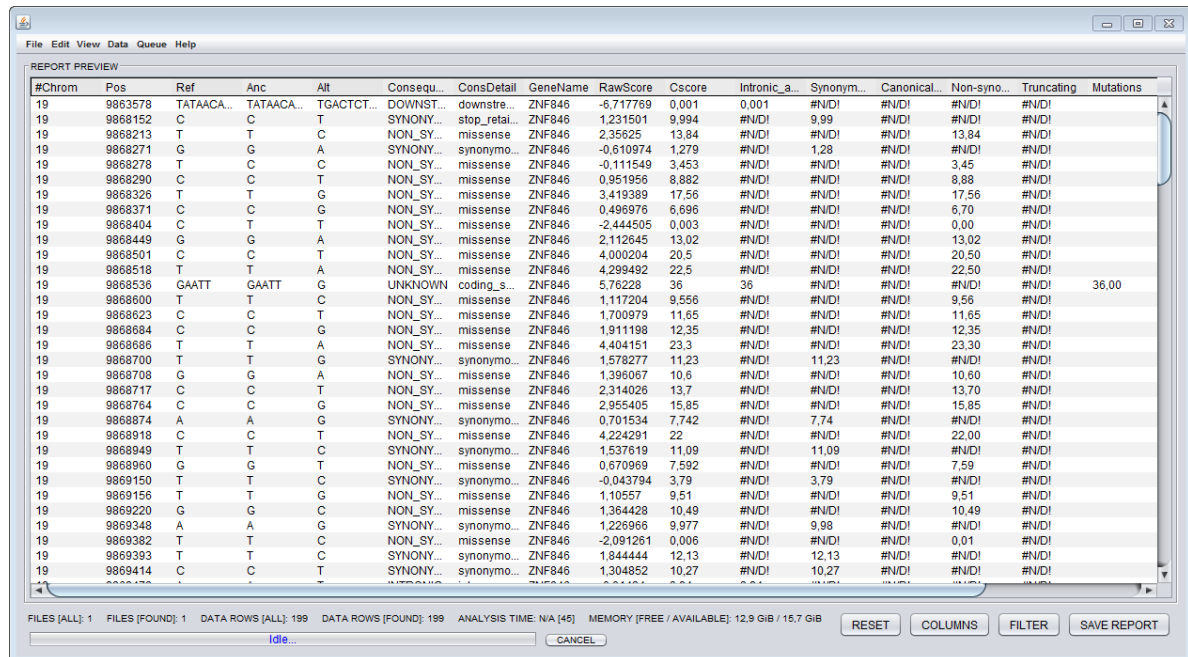
- 2 The status bar displays file import progress information in real time. The import time depends on the total size of the import files and available computing power and RAM.
- 3 In the **SELECT FILES** window mark the files from the import directory to open. Using buttons in **SELECT FILES TO OPEN** subfield it is possible to simultaneously select or deselect for opening all detected files (**MARK ALL TO OPEN / MARK ALL NOT TO OPEN**) or to invert the selection of files (**INVERT SELECTION**). Column delimiter and comment marker may be set independently for each opened file with data preview. The predefined values may be selected using the menu or simply typed in menu field and confirmed by pressing enter key. Selected settings may be applied to all opened files (by pressing **APPLY TO ALL FILES** button) or set to each file separately.



In the **SELECT COLUMNS** window select the data columns to be imported from the input file(s) using the same buttons as in the previous window (**MARK ALL TO OPEN**, **MARK ALL NOT TO OPEN** and **INVERT SELECTION**). Optionally, reorganize the data columns with **MOVE UP** and **MOVE DOWN** buttons in **COLUMN ORDERING** subfield.



- 4 When the file import has been completed, the **REPORT PREVIEW** is generated, which contains the combined data from the imported files.



The screenshot shows a software window titled "REPORT PREVIEW" with a menu bar (File, Edit, View, Data, Queue, Help). The window contains a table with 15 columns: #Chrom, Pos, Ref, Anc, Alt, Consequ..., ConsDetail, GeneName, RawScore, Cscore, Intronic_a..., Synonym..., Canonical..., Non-syno..., Truncating, and Mutations. The table lists genomic data for chromosome 19, including positions, reference and alternative alleles, consequences, and scores. At the bottom, a status bar displays: FILES [ALL]: 1, FILES [FOUND]: 1, DATA ROWS [ALL]: 199, DATA ROWS [FOUND]: 199, ANALYSIS TIME: N/A [45], MEMORY [FREE / AVAILABLE]: 12.9 GIB / 15.7 GIB. There are buttons for "RESET", "COLUMNS", "FILTER", and "SAVE REPORT".

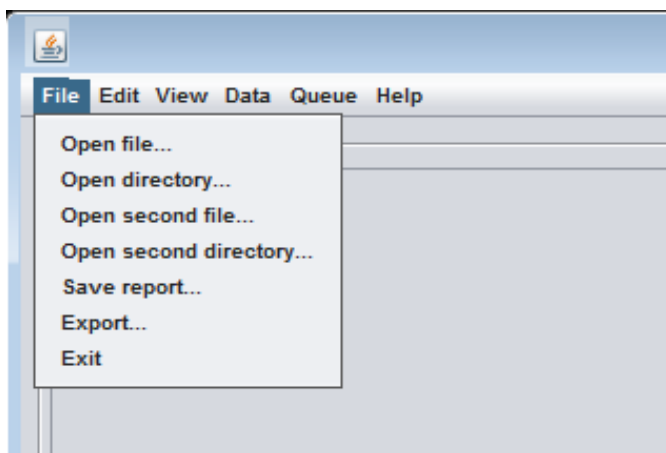
#Chrom	Pos	Ref	Anc	Alt	Consequ...	ConsDetail	GeneName	RawScore	Cscore	Intronic_a...	Synonym...	Canonical...	Non-syno...	Truncating	Mutations
19	9863578	TATAACA...	TATAACA...	TGACTCT...	DOWNST...	downstre...	ZNF846	-6,717769	0,001	0,001	#N/D!	#N/D!	#N/D!	#N/D!	
19	9868152	C	C	T	SYNONY...	stop_retai...	ZNF846	1,231501	9,994	#N/D!	9,99	#N/D!	#N/D!	#N/D!	
19	9868213	T	T	C	NON_SY...	missense	ZNF846	2,35625	13,84	#N/D!	#N/D!	#N/D!	13,84	#N/D!	
19	9868271	G	G	A	SYNONY...	synonymo...	ZNF846	-0,610974	1,279	#N/D!	1,28	#N/D!	#N/D!	#N/D!	
19	9868278	T	C	C	NON_SY...	missense	ZNF846	-0,111549	3,453	#N/D!	#N/D!	#N/D!	3,45	#N/D!	
19	9868290	C	C	T	NON_SY...	missense	ZNF846	0,951956	8,882	#N/D!	#N/D!	#N/D!	8,88	#N/D!	
19	9868326	T	T	G	NON_SY...	missense	ZNF846	3,419389	17,56	#N/D!	#N/D!	#N/D!	17,56	#N/D!	
19	9868371	C	C	G	NON_SY...	missense	ZNF846	0,496976	6,696	#N/D!	#N/D!	#N/D!	6,70	#N/D!	
19	9868404	C	T	T	NON_SY...	missense	ZNF846	-2,444505	0,003	#N/D!	#N/D!	#N/D!	0,00	#N/D!	
19	9868449	G	G	A	NON_SY...	missense	ZNF846	2,112645	13,02	#N/D!	#N/D!	#N/D!	13,02	#N/D!	
19	9868501	C	C	T	NON_SY...	missense	ZNF846	4,000204	20,5	#N/D!	#N/D!	#N/D!	20,50	#N/D!	
19	9868518	T	T	A	NON_SY...	missense	ZNF846	4,299492	22,5	#N/D!	#N/D!	#N/D!	22,50	#N/D!	
19	9868536	GAATT	GAATT	G	UNKNOWN	coding_s...	ZNF846	5,76228	36	36	#N/D!	#N/D!	#N/D!	#N/D!	36,00
19	9868600	T	T	C	NON_SY...	missense	ZNF846	1,117204	9,556	#N/D!	#N/D!	#N/D!	9,56	#N/D!	
19	9868623	C	C	T	NON_SY...	missense	ZNF846	1,700979	11,65	#N/D!	#N/D!	#N/D!	11,65	#N/D!	
19	9868684	C	C	G	NON_SY...	missense	ZNF846	1,911198	12,35	#N/D!	#N/D!	#N/D!	12,35	#N/D!	
19	9868686	T	T	A	NON_SY...	missense	ZNF846	4,404151	23,3	#N/D!	#N/D!	#N/D!	23,30	#N/D!	
19	9868700	T	T	G	SYNONY...	synonymo...	ZNF846	1,578277	11,23	#N/D!	11,23	#N/D!	#N/D!	#N/D!	
19	9868708	G	G	A	NON_SY...	missense	ZNF846	1,396067	10,6	#N/D!	#N/D!	#N/D!	10,60	#N/D!	
19	9868717	C	C	T	NON_SY...	missense	ZNF846	2,314026	13,7	#N/D!	#N/D!	#N/D!	13,70	#N/D!	
19	9868764	C	C	G	NON_SY...	missense	ZNF846	2,955405	15,85	#N/D!	#N/D!	#N/D!	15,85	#N/D!	
19	9868874	A	A	G	SYNONY...	synonymo...	ZNF846	0,701534	7,742	#N/D!	7,74	#N/D!	#N/D!	#N/D!	
19	9868918	C	C	T	NON_SY...	missense	ZNF846	4,224291	22	#N/D!	#N/D!	#N/D!	22,00	#N/D!	
19	9868949	T	T	C	SYNONY...	synonymo...	ZNF846	1,537619	11,09	#N/D!	11,09	#N/D!	#N/D!	#N/D!	
19	9868960	G	G	T	NON_SY...	missense	ZNF846	0,670969	7,592	#N/D!	#N/D!	#N/D!	7,59	#N/D!	
19	9869150	T	T	C	SYNONY...	synonymo...	ZNF846	-0,043794	3,79	#N/D!	3,79	#N/D!	#N/D!	#N/D!	
19	9869156	T	T	G	NON_SY...	missense	ZNF846	1,10557	9,51	#N/D!	#N/D!	#N/D!	9,51	#N/D!	
19	9869220	G	G	C	NON_SY...	missense	ZNF846	1,364428	10,49	#N/D!	#N/D!	#N/D!	10,49	#N/D!	
19	9869348	A	A	G	SYNONY...	synonymo...	ZNF846	1,226966	9,977	#N/D!	9,98	#N/D!	#N/D!	#N/D!	
19	9869382	T	T	C	NON_SY...	missense	ZNF846	-2,091261	0,006	#N/D!	#N/D!	#N/D!	0,01	#N/D!	
19	9869393	T	T	C	SYNONY...	synonymo...	ZNF846	1,844444	12,13	#N/D!	12,13	#N/D!	#N/D!	#N/D!	
19	9869414	C	C	T	SYNONY...	synonymo...	ZNF846	1,304852	10,27	#N/D!	10,27	#N/D!	#N/D!	#N/D!	

7.2 MAIN VIEW

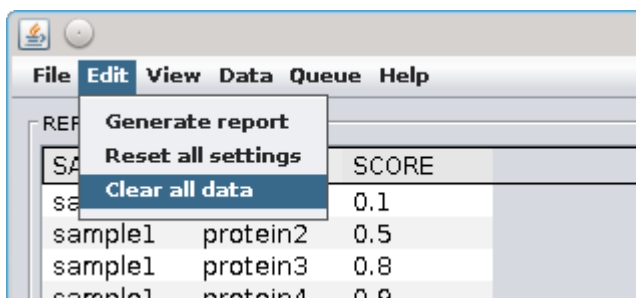
7.2.1 PULL DOWN MENU

At the top of the main window there is a pull down menu with six program menus, namely **File**, **Edit**, **View**, **Data**, **Queue** and **Help**.

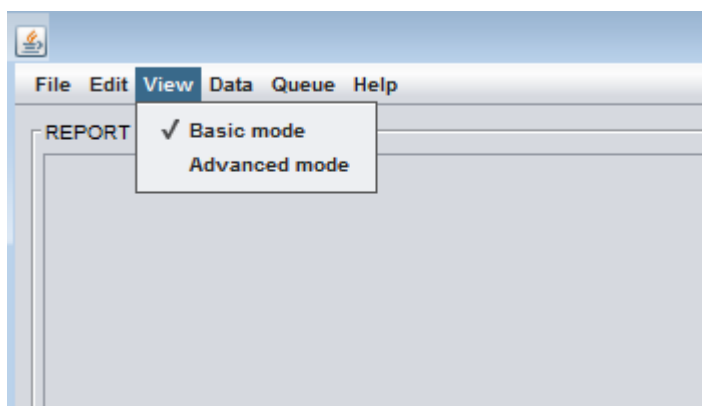
File menu refers to following operations on files – opening a single file, opening a directory with files, opening second file or directory, saving report with processed data and exiting the program.



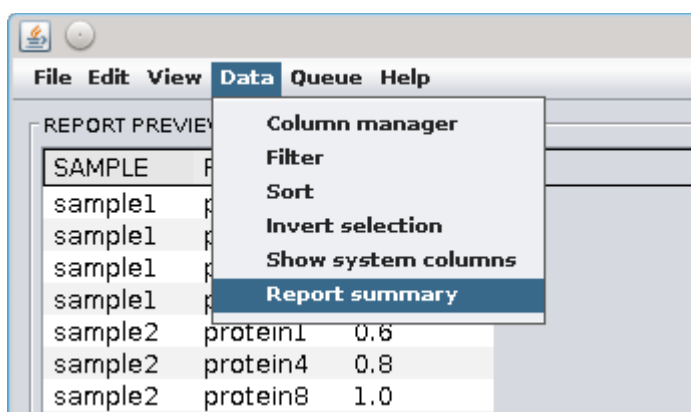
Making use of **Edit** menu, the global data changes can be done – such as carrying out the filtering task and generating a resulting report or resetting all settings. Clearing all actually loaded data is also possible.



Switching between the basic and advanced mode is available via **View** menu.

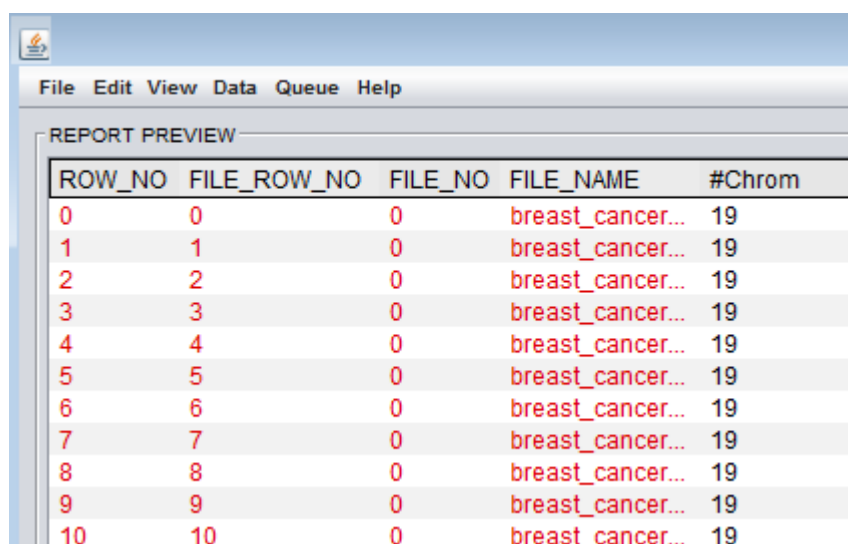


Functions designed for data processing are provided in **Data** menu. Functions called **Column manager**, **Sort** and **Filter** are also available via buttons in the bottom right of the main window (see 7.5 COLUMN MANAGEMENT, 7.4 COLUMN SORTING or 7.6 FILTERING THE INPUT FILE(S) section, respectively).



Under **Data** menu it is also possible to reverse the output with regards to the applied filtering criteria using **Invert selection** function. The invert selection function is intended for control purposes, i.e. to provide an insight into data that is removed by the filters.

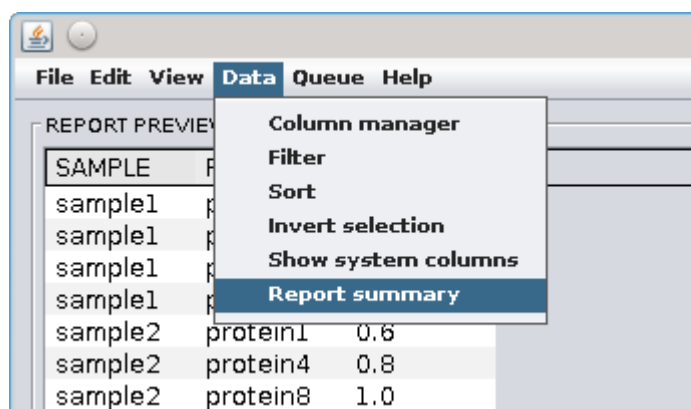
Show system columns function is intended to determine whether system columns are displayed or hidden. System columns, called **ROWS_NO**, **FILE_ROW_NO**, **FILE_NO** and **FILE_NAME**, are created automatically by the program to keep track of the original records in the imported files. **Show system columns** function is mainly helpful when working with multiple files at the same time.

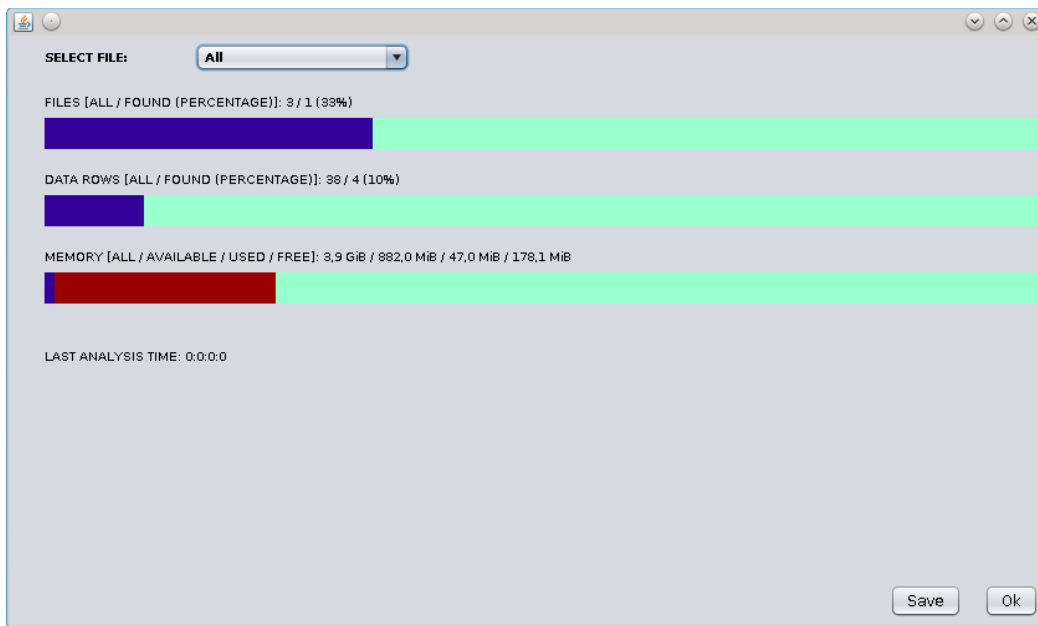


The screenshot shows a window titled 'REPORT PREVIEW' with a menu bar (File, Edit, View, Data, Queue, Help). Below the menu bar is a table with the following columns: ROW_NO, FILE_ROW_NO, FILE_NO, FILE_NAME, and #Chrom. The table contains 11 rows of data, all with the same values: ROW_NO from 0 to 10, FILE_ROW_NO from 0 to 10, FILE_NO as 0, FILE_NAME as 'breast_cancer...', and #Chrom as 19.

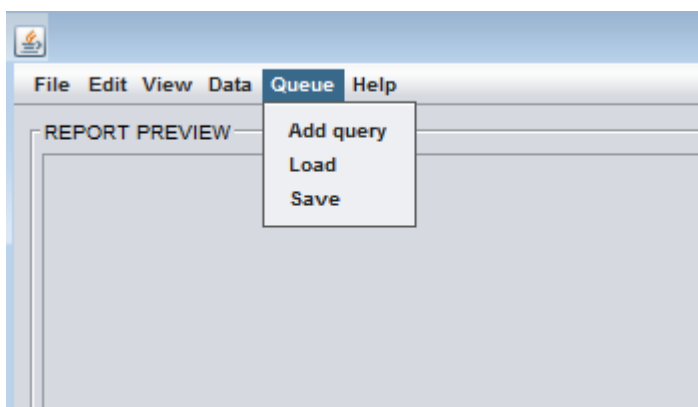
ROW_NO	FILE_ROW_NO	FILE_NO	FILE_NAME	#Chrom
0	0	0	breast_cancer...	19
1	1	0	breast_cancer...	19
2	2	0	breast_cancer...	19
3	3	0	breast_cancer...	19
4	4	0	breast_cancer...	19
5	5	0	breast_cancer...	19
6	6	0	breast_cancer...	19
7	7	0	breast_cancer...	19
8	8	0	breast_cancer...	19
9	9	0	breast_cancer...	19
10	10	0	breast_cancer...	19

Report summary gives some useful information about last task run time, system memory and processed files (number of rows/number of selected rows). These data can be exported to tab delimited text file for additional use. Additionally, there are graphical bars where these simple informations are graphically presented (total number of files, data rows, system memory are signed with green, actual selected files, data rows, and memory used with blue and maximal java memory limit with red).

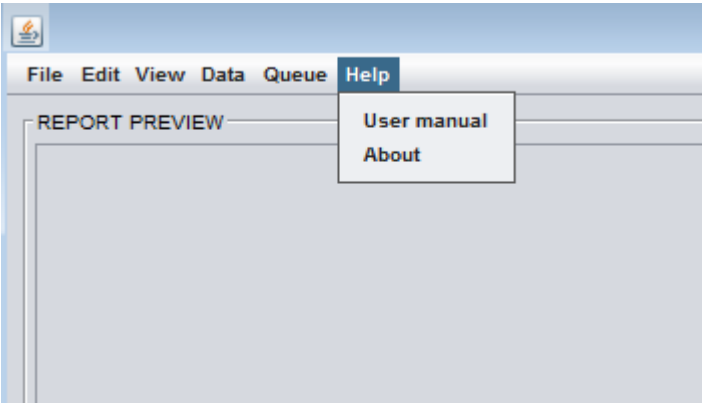




Add query function under **Queue** menu facilitates adding a query with regard to imported data. It is also possible to save a query consisting of particular parameters for further analyses and to load the previously saved query if needed (see 7.8 SAVING QUERIES and 7.9 LOADING QUERIES sections).



Information about the **HIGH-THROUGHPUT TABULAR DATA PROCESSOR** and this **user manual** is accessible via **Help** menu.



7.2.2 REPORT PREVIEW

In the basic mode the main portion of the application window is occupied by the **REPORT PREVIEW** table.

A screenshot of the application window showing the 'REPORT PREVIEW' table. The table has 15 columns: ROW_NO, FILE_ROW_NO, FILE_NAME, #Chrom, Pos, Ref, Anc, Alt, Consequ..., ConsDetail, GeneName, RawScore, Cscore, Intronic_a..., and Synonyr. The table contains 31 rows of data, all from 'breast_cancer...' files. The status bar at the bottom shows 'FILES [ALL]: 1', 'FILES [FOUND]: 1', 'DATA ROWS [ALL]: 199', 'DATA ROWS [FOUND]: 199', 'ANALYSIS TIME: N/A [8]', and 'MEMORY [FREE / AVAILABLE]: 13.4 GiB / 15.7 GiB'. There are buttons for 'RESET', 'COLUMNS', 'FILTER', 'SAVE REPORT', and 'CANCEL'.

Table is updated in real time along with execution of the filtering (see 7.6 FILTERING FILES section). The table can be sorted by any column after clicking the column name or selecting **Data > Sort** menu option (see 7.4 COLUMN SORTING section).

This table is also editable – double click on certain field, type some text and the modified content will be saved.

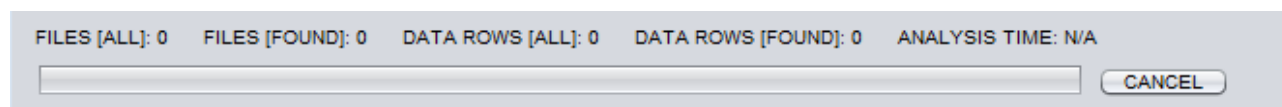
7.2.3 INFORMATION AND STATUS BAR

The information bar, located at the bottom of the main window, shows aggregate data statistics:

- Number of imported files (**FILES [ALL]**).
- Number of imported files which have retained at least one row of data after the filtering has been applied (**FILES [FOUND]**).
- The total number of rows in all imported files prior to filtering (**DATA ROWS [ALL]**).
- The total number of rows in all imported files which are retained after the filtering criteria have been applied (**DATA ROWS [FOUND]**).
- Total analysis time after completion of all items in the query queue (**ANALYSIS TIME**).

Status bar is located below aggregate data statistics and shows progress of the analysis in real time.

The **CANCEL** button allows to abort an ongoing operation.



7.2.4 THE CONTROL BUTTONS

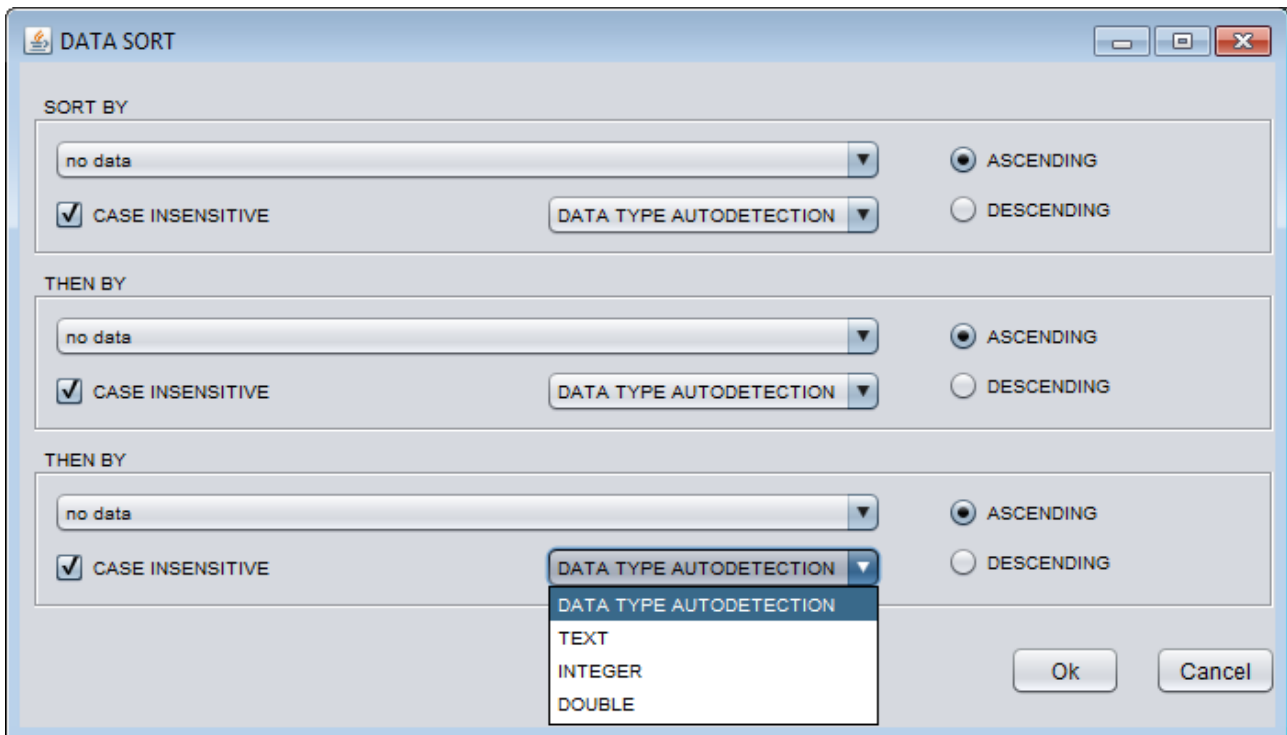
These four buttons, namely **RESET**, **COLUMN**, **FILTER** and **SAVE REPORT**, are located in the bottom right corner of the main window. They are created to facilitate operations on columns and files. The specific functions are described in the following sections: 7.6. CANCELLING OF CHANGES, 7.4. COLUMN MANAGEMENT, 7.5. FILTERING THE INPUT FILE(S), 7.7. SAVING FILTERED FILE(S), respectively.

7.3

7.4 COLUMN SORTING

To rearrange the data set with respect to one or more columns select **Data > Sort** in pull down menu or click on any column name in the header line in the **REPORT PREVIEW** field. The **DATA SORT** window which is opened facilitates sorting by up to the three

columns at a time, in ascending or descending manner and in case insensitive (by default) or sensitive way.

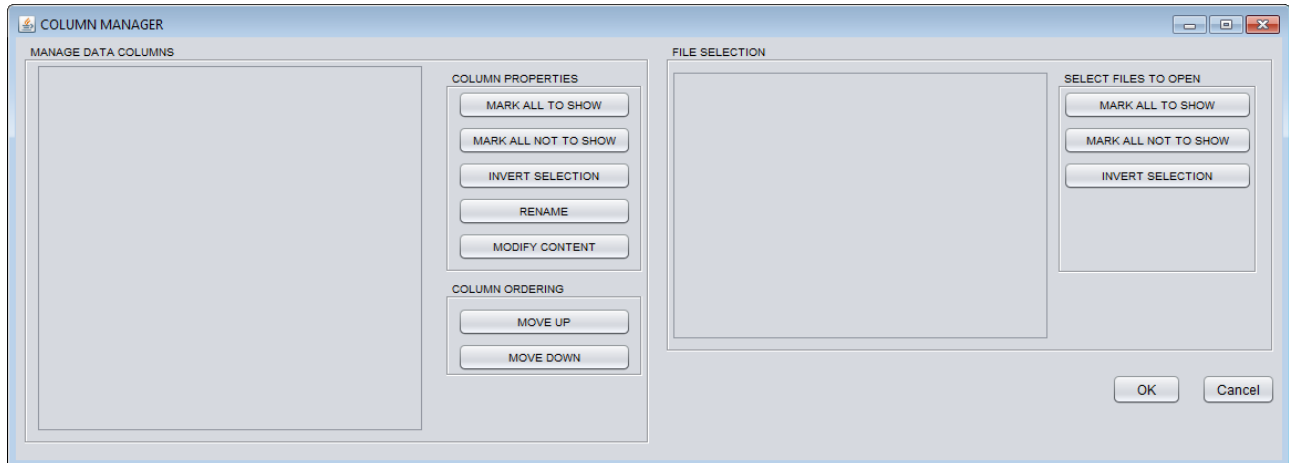


The type of data in the column(s) subjected to sorting is detected automatically (**DATA TYPE AUTODETECTION**), but can be also selected by hand as **TEXT**, **INTEGER** or **DOUBLE** (double-precision floating-point numbers, namely decimals).

7.5 COLUMN MANAGEMENT

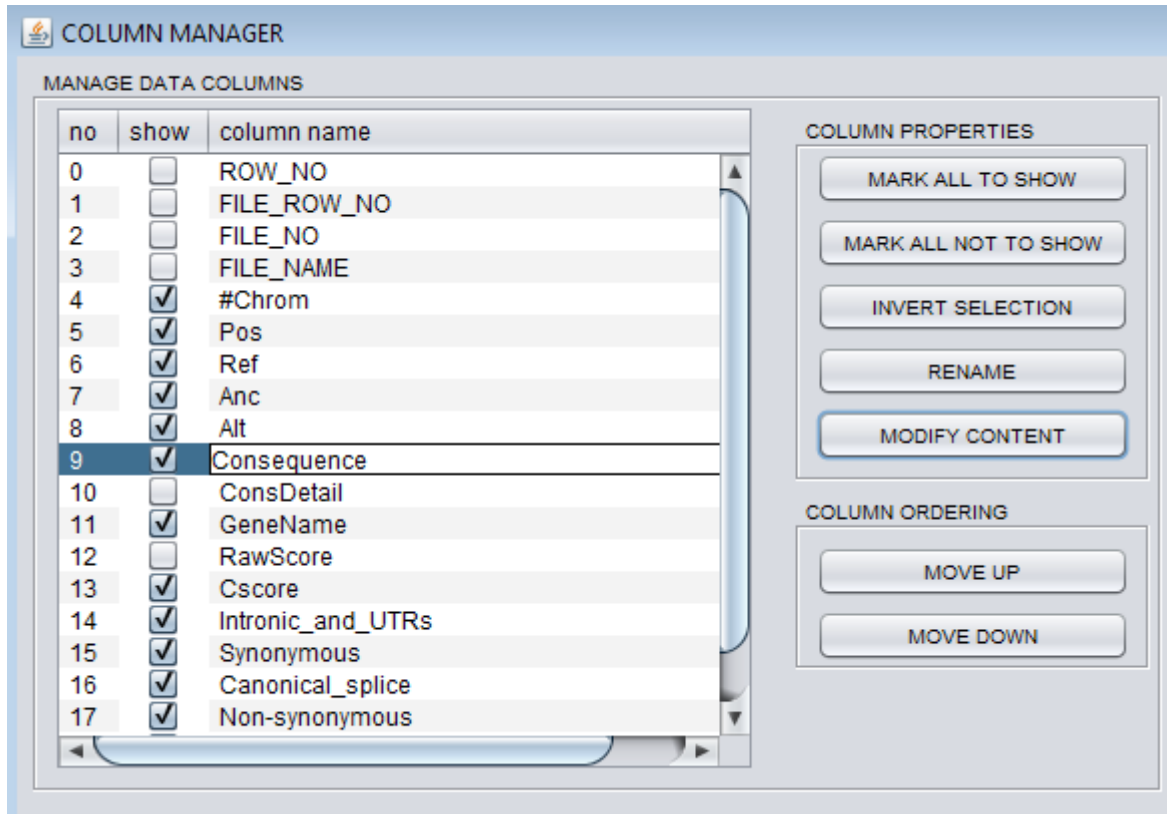
Column(s) and file(s) management is possible via the **COLUMN MANAGER** window. To open it, select **Data > Column manager** in pull down menu or click on **COLUMNS** button in the main screen.

This window consists of two main fields – **MANAGE DATA COLUMNS** and **FILE SELECTION**.



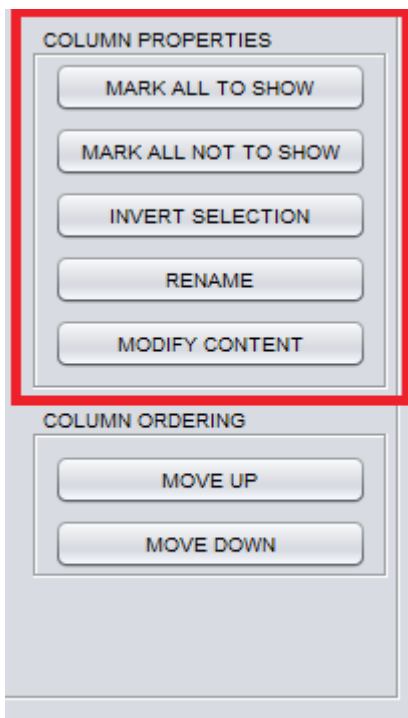
7.5.1 MANAGE DATA COLUMNS field

Here it is possible to change columns' settings / visibility that have been chosen during file(s) import.

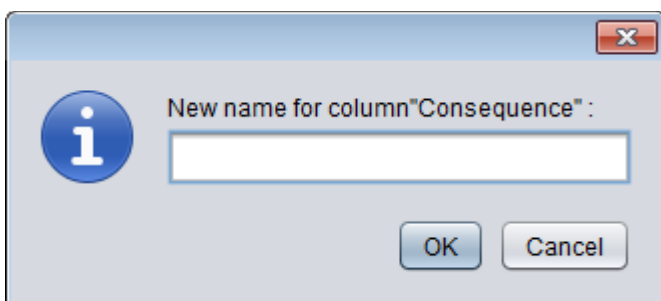


7.5.1.1 COLUMN PROPERTIES subfield

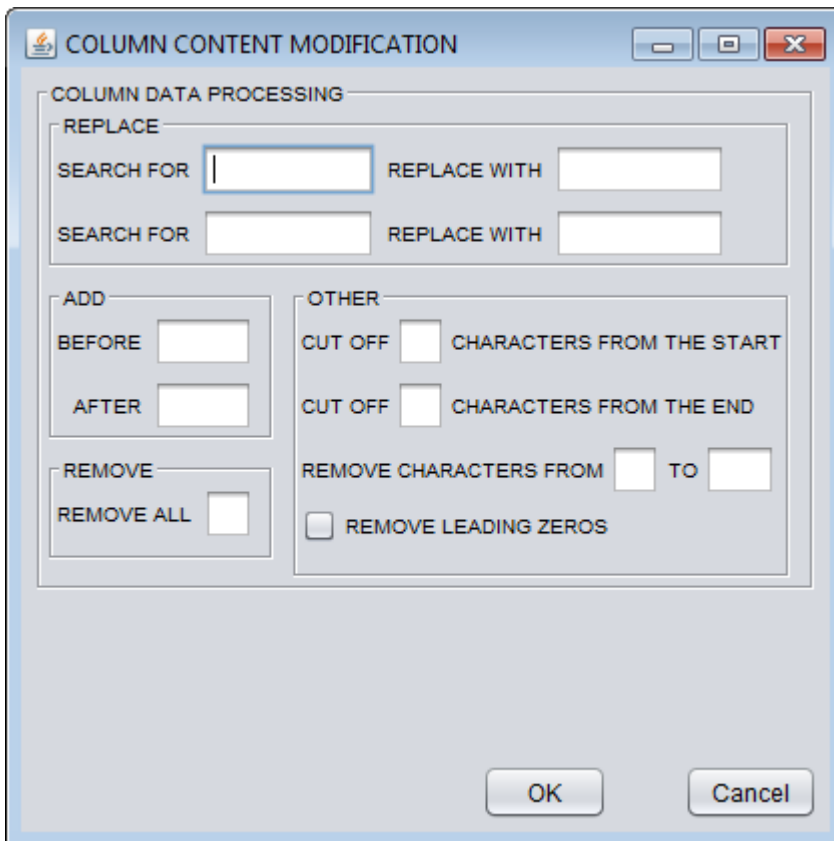
To customize browsing the data by hiding or showing again selected column(s), uncheck or check the corresponding selection field(s). For this purpose also **MARK ALL TO SHOW**, **MARK ALL NOT TO SHOW** and **INVERT SELECTION** buttons can be used. Hidden columns are not deleted from the data set though and are taken into account during every data processing step.



Every column name can be altered in two ways – by double clicking on it or by using the **RENAME** button. The latter opens a new window to define the new name of particular column.



MODIFY CONTENT button opens a window called **COLUMN CONTENT MODIFICATION**, which is intended to transform the data in all fields / cells from the selected column.



The screenshot shows a dialog box titled "COLUMN CONTENT MODIFICATION" with standard Windows window controls (minimize, maximize, close). The dialog is divided into several sections for data processing:

- COLUMN DATA PROCESSING** (Section Header)
- REPLACE** (Section Header)
 - Two rows of input fields: "SEARCH FOR" followed by a text box, and "REPLACE WITH" followed by a text box.
- ADD** (Section Header)
 - Two rows of input fields: "BEFORE" followed by a text box, and "AFTER" followed by a text box.
- REMOVE** (Section Header)
 - A checkbox labeled "REMOVE ALL".
- OTHER** (Section Header)
 - Two rows of checkboxes and text: "CUT OFF" followed by a checkbox and "CHARACTERS FROM THE START", and "CUT OFF" followed by a checkbox and "CHARACTERS FROM THE END".
 - A row of text: "REMOVE CHARACTERS FROM" followed by a text box, "TO", and another text box.
 - A checkbox labeled "REMOVE LEADING ZEROS".

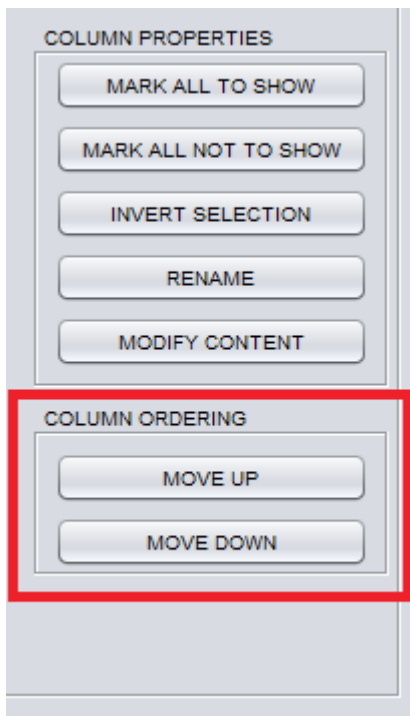
At the bottom right of the dialog are two buttons: "OK" and "Cancel".

Following changes are available here:

- Searching and replacing alphanumeric strings (**SEARCH FOR ... REPLACE WITH ...**).
- Adding alphanumeric strings before and/or after (**ADD – BEFORE ... and AFTER ...**).
- Removing specified expression from every data row (**REMOVE ALL ...**).
- Trimming the ends of the alphanumeric strings (**CUT OFF ... CHARACTERS FROM THE START / END**) or cutting the characters within the alphanumeric strings at the specified positions (**REMOVE CHARACTERS FROM ... TO ...**).
- Removing of so called “leading zeros”, eg. 000023 to 23 (**REMOVE LEADING ZEROS** checkbox).

7.5.1.2 COLUMN ORDERING subfield

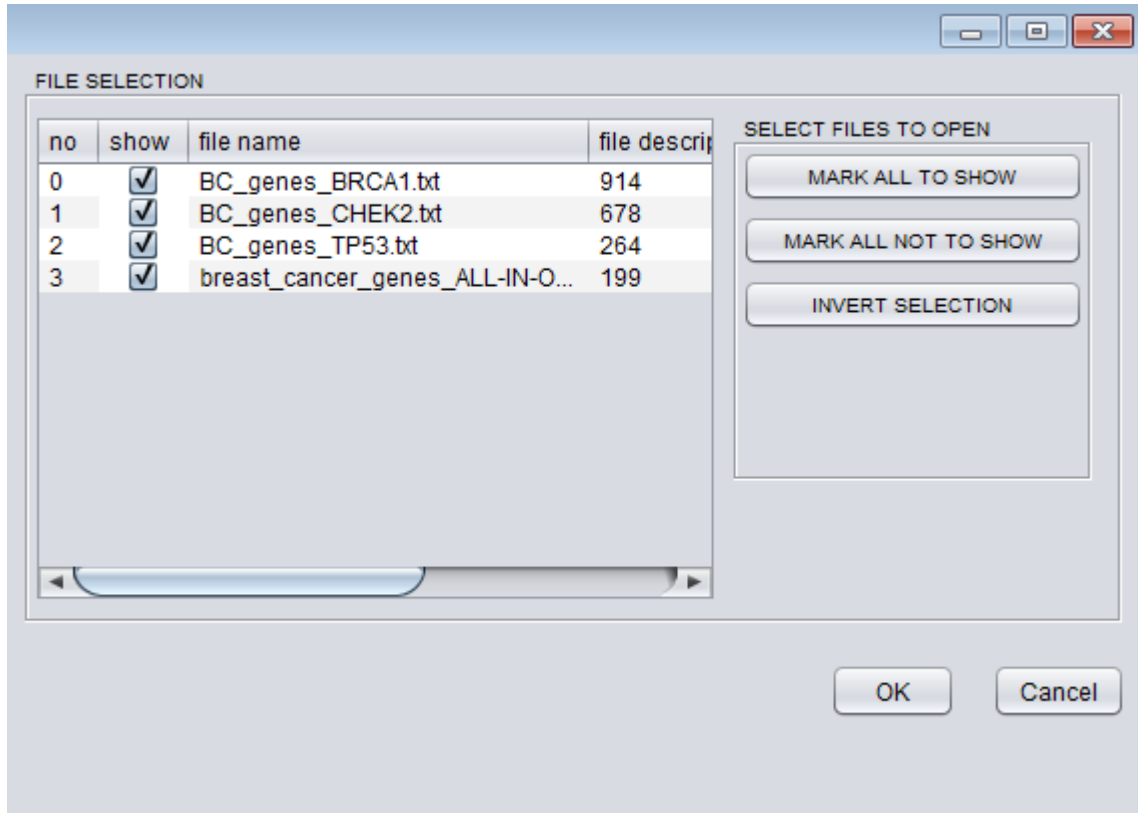
The order of columns displayed in **DATA PREVIEW** field (at the main window) can be changed. For this purpose, choose the column name and click **MOVE UP** or **MOVE DOWN** button. Every click changes the column's location by one position forward or backward.



7.5.2 FILE SELECTION field

In this field it is possible to hide or unhide previously imported data set(s). As in case of column selection, mark a checkbox of matched file(s) with cursor or use **MARK ALL TO SHOW**, **MARK ALL NOT TO SHOW** and **INVERT SELECTION** buttons.

Hidden files are not deleted from the data set though, and are taken into account during every data processing step.



7.6 FILTERING THE INPUT FILE(S)

In the basic mode, filtering applies to the simplified alphanumeric processing of the data.

The **SIMPLE FILTER** window is displayed when the **FILTER** button has been pressed or **Data > Filter** in the pull down menu has been selected.

The SIMPLE FILTER window is a dialog box with a title bar containing the text "SIMPLE FILTER" and standard window controls (minimize, maximize, close). The main area of the dialog is a table with four columns: "OPERAND", "COLUMN NAME", "CONDITION", and "VALUE". The table has eight rows. The first row has "AND" in the OPERAND column, "Consequence" in the COLUMN NAME column, and "no data" in the VALUE column. The second row has "AND" in the OPERAND column, "Consequence" in the COLUMN NAME column, and "no data" in the VALUE column. The third row has "AND" in the OPERAND column, "Consequence" in the COLUMN NAME column, and "no data" in the VALUE column. The fourth row has "AND" in the OPERAND column, "Consequence" in the COLUMN NAME column, and "no data" in the VALUE column. The fifth row has "AND" in the OPERAND column, "Consequence" in the COLUMN NAME column, and "no data" in the VALUE column. The sixth row has "AND" in the OPERAND column, "Consequence" in the COLUMN NAME column, and "no data" in the VALUE column. The seventh row has "AND" in the OPERAND column, "Consequence" in the COLUMN NAME column, and "no data" in the VALUE column. The eighth row has "AND" in the OPERAND column, "Consequence" in the COLUMN NAME column, and "no data" in the VALUE column. Below the table, there is a "FILES:" label followed by a dropdown menu showing "All". There are two checkboxes: "CASE INSENSITIVE" and "REMOVE DUPLICATES". At the bottom, there are three buttons: "RESET", "OK", and "Cancel".

OPERAND	COLUMN NAME	CONDITION	VALUE
AND	Consequence		no data
			no data
			no data
			no data
			no data
			no data
			no data
			no data

FILES: All

☐ CASE INSENSITIVE ☐ REMOVE DUPLICATES

RESET OK Cancel

Up to 8 columns, chosen from the **COLUMN NAME** pull down lists, can be filtered. For this purpose following conditions are available in the **CONDITION** pull down list: "=", "<", ">", "<=", ">=", "<>", "Contains", "Does not contain", "Begins with", "Does not begin with", "Ends with", "Does not end with".

CONDITION

=

>

>=

<>

Contains

Does not c...

Begins with

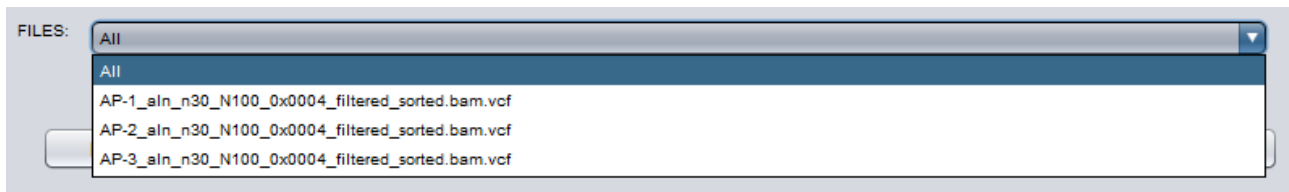
Ends with

The subsequent filtering steps can be linked by **AND** or **OR** Boolean operators present in **OPERAND** drop-down list at each line.

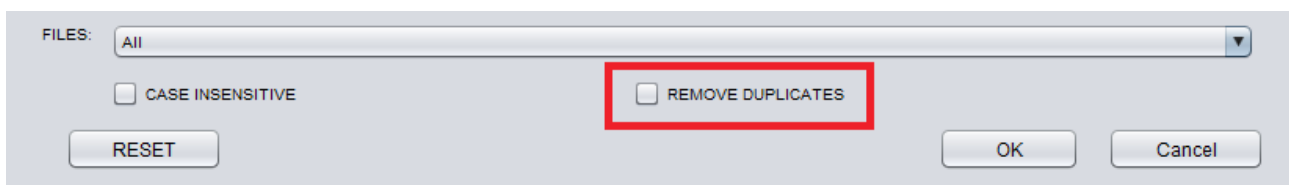
SIMPLE FILTER

OPERAND	COLUMN NAME

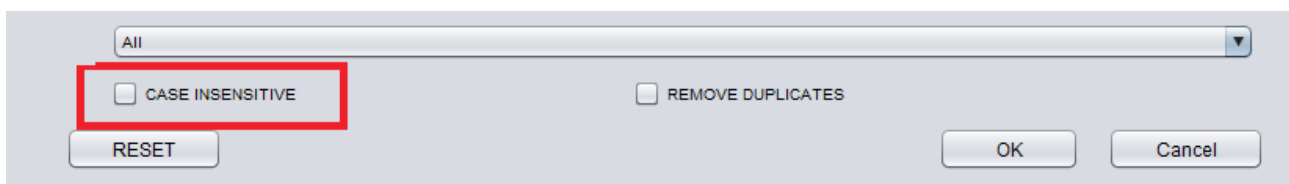
The filtering task can be limited to the selected file with **FILES** drop-down list. By default it is performed for all imported files.



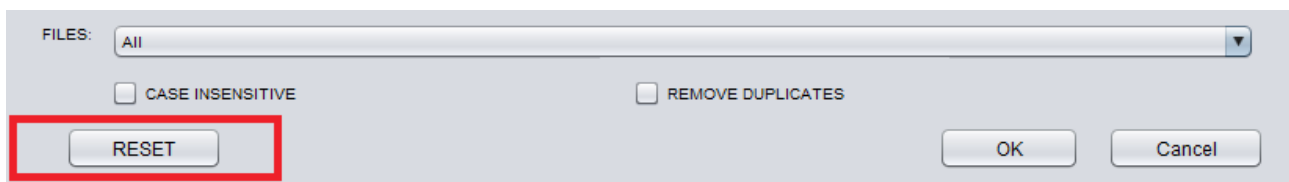
It is also possible to remove duplicate rows from the input data (**REMOVE DUPLICATES** checkbox).



All operations are case sensitive unless specified otherwise by checking the **CASE INSENSITIVE** box.



All entered filtering criteria can be cancelled using the **RESET** button.



The described functions were used in example 4 (stage 5) in S2 Text. **CANCELLING OF INTRODUCED CHANGES**

The **RESET** button, which is situated in the operation buttons' panel, restores the data to the original layout. It can be also done using the **Reset all settings** option from the **Edit** pull down menu.

It does not apply to permanently introduced changes – namely using **MODIFY CONTENT** and **RENAME** functions in **COLUMN MANAGER** window (see 7.5.1.1 COLUMN PROPERTIES subfield section).

REPORT PREVIEW

ROW_NO	FILE_ROW_NO	FILE_NO	FILE_NAME	#Chrom	Pos	Ref	Anc	Alt	Consequ...	ConsDetail	GeneName	RawScore	Cscore	Intronic_a...	Synonymr
0	0	0	breast_cancer...	19	9863578	TATAACA...	TATAACA...	TGACTCT...	DOWNST...	downstre...	ZNF846	-6.717769	0.001	0.001	#N/D!
1	1	0	breast_cancer...	19	9868152	C	C	T	SYNONY...	stop_retal...	ZNF846	1.231501	9.994	#N/D!	9.99
2	2	0	breast_cancer...	19	9868213	T	T	C	NON_SY...	missense	ZNF846	2.35625	13.84	#N/D!	#N/D!
3	3	0	breast_cancer...	19	9868271	G	G	A	SYNONY...	synonymo...	ZNF846	-0.610974	1.279	#N/D!	1.28
4	4	0	breast_cancer...	19	9868278	T	C	C	NON_SY...	missense	ZNF846	-0.111549	3.453	#N/D!	#N/D!
5	5	0	breast_cancer...	19	9868290	C	C	T	NON_SY...	missense	ZNF846	0.951956	8.882	#N/D!	#N/D!
6	6	0	breast_cancer...	19	9868326	T	T	G	NON_SY...	missense	ZNF846	3.419389	17.56	#N/D!	#N/D!
7	7	0	breast_cancer...	19	9868371	C	C	G	NON_SY...	missense	ZNF846	0.496976	6.696	#N/D!	#N/D!
8	8	0	breast_cancer...	19	9868404	C	T	T	NON_SY...	missense	ZNF846	-2.444505	0.003	#N/D!	#N/D!
9	9	0	breast_cancer...	19	9868449	G	G	A	NON_SY...	missense	ZNF846	2.112645	13.02	#N/D!	#N/D!
10	10	0	breast_cancer...	19	9868501	C	C	T	NON_SY...	missense	ZNF846	4.000204	20.5	#N/D!	#N/D!
11	11	0	breast_cancer...	19	9868518	T	T	A	NON_SY...	missense	ZNF846	4.299492	22.5	#N/D!	#N/D!
12	12	0	breast_cancer...	19	9868536	GAATT	GAATT	G	UNKNOWN	coding_s...	ZNF846	5.76228	36	#N/D!	#N/D!
13	13	0	breast_cancer...	19	9868600	T	T	C	NON_SY...	missense	ZNF846	1.117204	9.556	#N/D!	#N/D!
14	14	0	breast_cancer...	19	9868623	C	C	T	NON_SY...	missense	ZNF846	1.700979	11.65	#N/D!	#N/D!
15	15	0	breast_cancer...	19	9868684	C	C	G	NON_SY...	missense	ZNF846	1.911198	12.35	#N/D!	#N/D!
16	16	0	breast_cancer...	19	9868686	T	T	A	NON_SY...	missense	ZNF846	4.404151	23.3	#N/D!	#N/D!
17	17	0	breast_cancer...	19	9868700	T	T	G	SYNONY...	synonymo...	ZNF846	1.578277	11.23	#N/D!	11.23
18	18	0	breast_cancer...	19	9868708	G	G	A	NON_SY...	missense	ZNF846	1.396067	10.6	#N/D!	#N/D!
19	19	0	breast_cancer...	19	9868717	C	C	T	NON_SY...	missense	ZNF846	2.314026	13.7	#N/D!	#N/D!
20	20	0	breast_cancer...	19	9868764	C	C	G	NON_SY...	missense	ZNF846	2.955405	15.85	#N/D!	#N/D!
21	21	0	breast_cancer...	19	9868874	A	A	G	SYNONY...	synonymo...	ZNF846	0.701534	7.742	#N/D!	7.74
22	22	0	breast_cancer...	19	9868918	C	C	T	NON_SY...	missense	ZNF846	4.224291	22	#N/D!	#N/D!
23	23	0	breast_cancer...	19	9868949	T	T	C	SYNONY...	synonymo...	ZNF846	1.537619	11.09	#N/D!	11.09
24	24	0	breast_cancer...	19	9868960	G	G	T	NON_SY...	missense	ZNF846	0.670969	7.592	#N/D!	#N/D!
25	25	0	breast_cancer...	19	9869150	T	T	C	SYNONY...	synonymo...	ZNF846	-0.043794	3.79	#N/D!	3.79
26	26	0	breast_cancer...	19	9869156	T	T	G	NON_SY...	missense	ZNF846	1.10557	9.51	#N/D!	#N/D!
27	27	0	breast_cancer...	19	9869220	G	G	C	NON_SY...	missense	ZNF846	1.364428	10.49	#N/D!	#N/D!
28	28	0	breast_cancer...	19	9869348	A	A	G	SYNONY...	synonymo...	ZNF846	1.226966	9.977	#N/D!	9.98
29	29	0	breast_cancer...	19	9869382	T	T	C	NON_SY...	missense	ZNF846	-2.091261	0.006	#N/D!	#N/D!
30	30	0	breast_cancer...	19	9869393	T	T	C	SYNONY...	synonymo...	ZNF846	1.844444	12.13	#N/D!	12.13
31	31	0	breast_cancer...	19	9869414	C	C	T	SYNONY...	synonymo...	ZNF846	1.304852	10.27	#N/D!	10.27

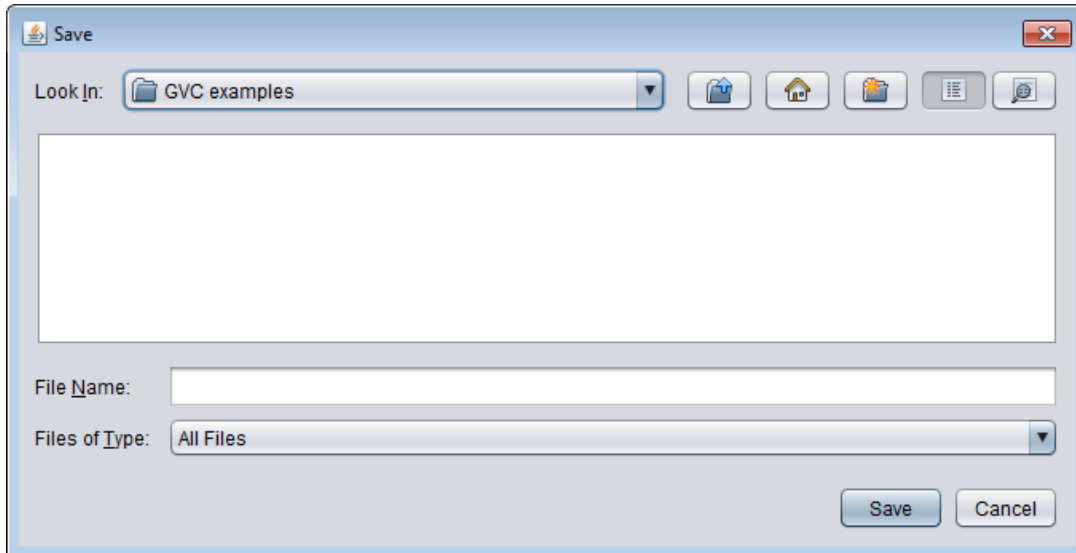
FILES [ALL]: 1 FILES [FOUND]: 1 DATA ROWS [ALL]: 199 DATA ROWS [FOUND]: 199 ANALYSIS TIME: N/A [8] MEMORY [FREE / AVAILABLE]: 13.4 GIB / 15.7 GIB

RESET COLUMNS FILTER SAVE REPORT

7.7 SAVING FILTERED FILE(S)

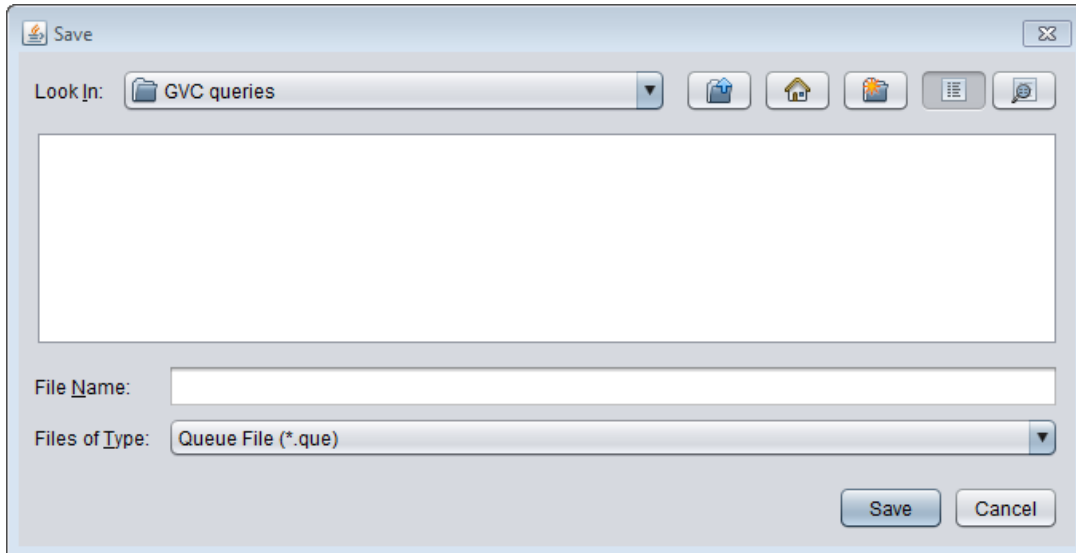
The filtered data can be saved to the output file by clicking the **SAVE REPORT** button in the main window or **File > Save Report** in pull down menu.

In the Save window the file directory and name are specified. The file is saved in tab delimited format only.



7.8 SAVING QUERIES

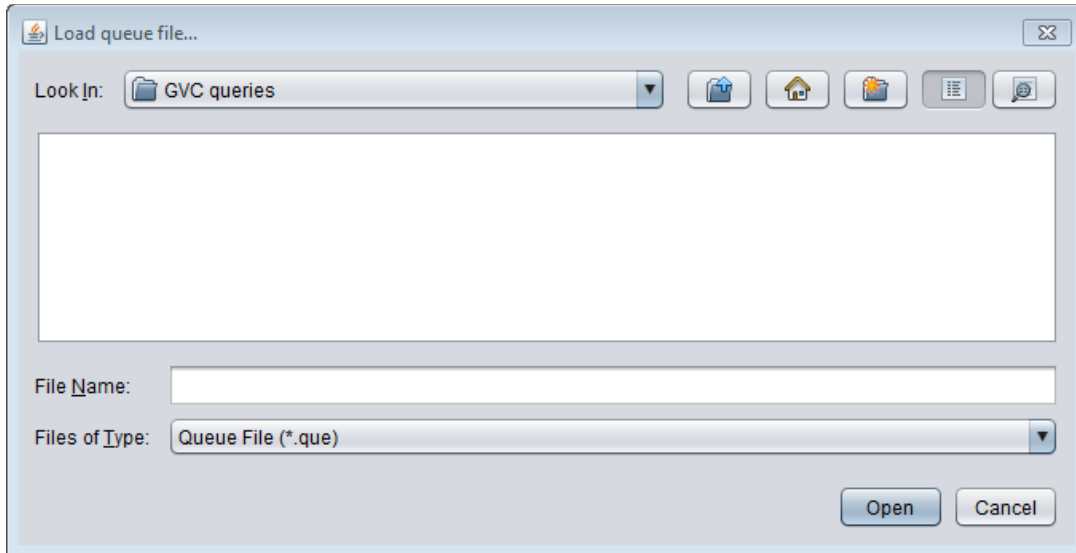
Every implemented set of filtering parameters can be saved for further analyses. For this purpose select **Queue > Save** in pull down menu in the main window. In the **SAVE** window the query file directory and name are specified. The file is saved in the internal format (.que extension).



7.9 LOADING QUERIES

Previously saved query can be loaded by selecting **Queue > Load**. The **Load queue file** window is opened to point to the particular directory with .que file.

To successfully use the queue file, it should be consistent with previously loaded data, particularly in terms of columns' names.



8. ADVANCED MODE – USAGE

The **ADVANCED MODE** is intended for complex tasks that can be performed on the unlimited number of files, simultaneously. For example, the following procedures can be carried out: searching for unique/redundant samples, at the same time for multiple alphanumerical strings, for specified locus, filtering file with regard to any data from external data files or filtering on the base of column defined samples..

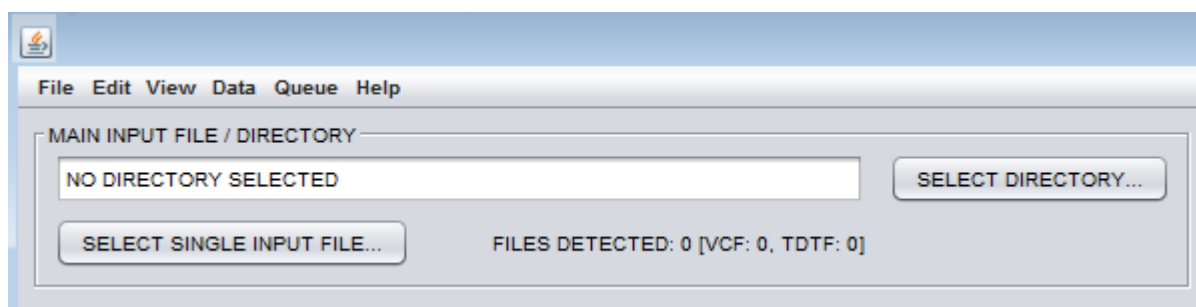
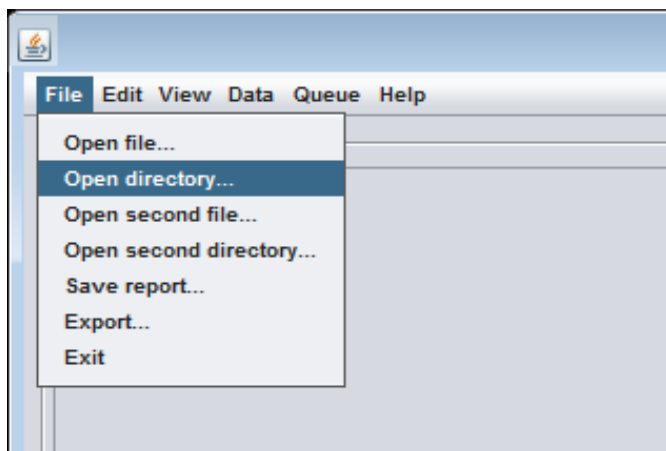
8.1 FILE IMPORT

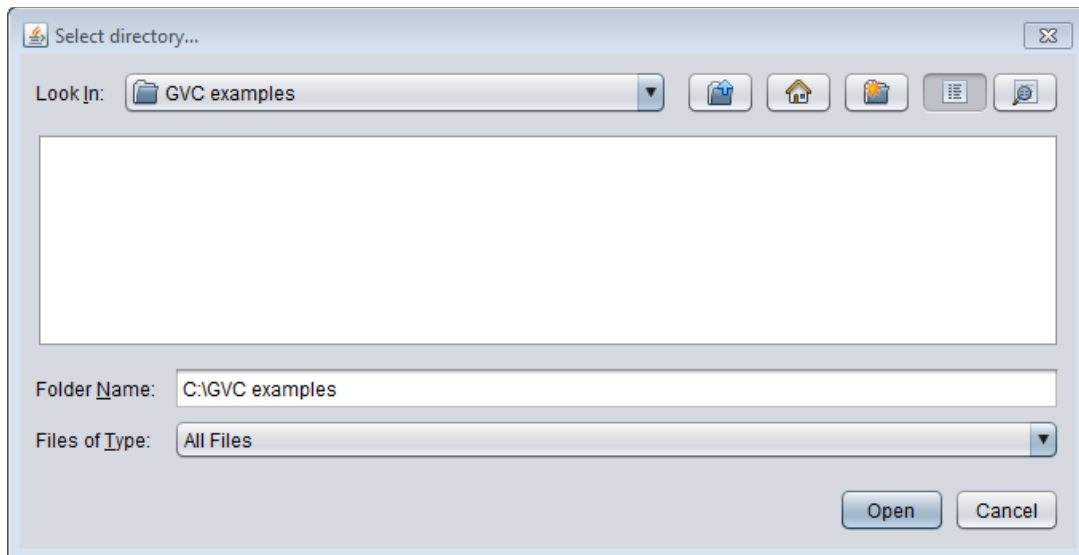
To import file(s) that will be subjected to filtering:

- 1 Copy the input files to a single directory. Select **File > Open directory** menu option or click on **SELECT DIRECTORY** button and point to this directory in **Select directory** window.

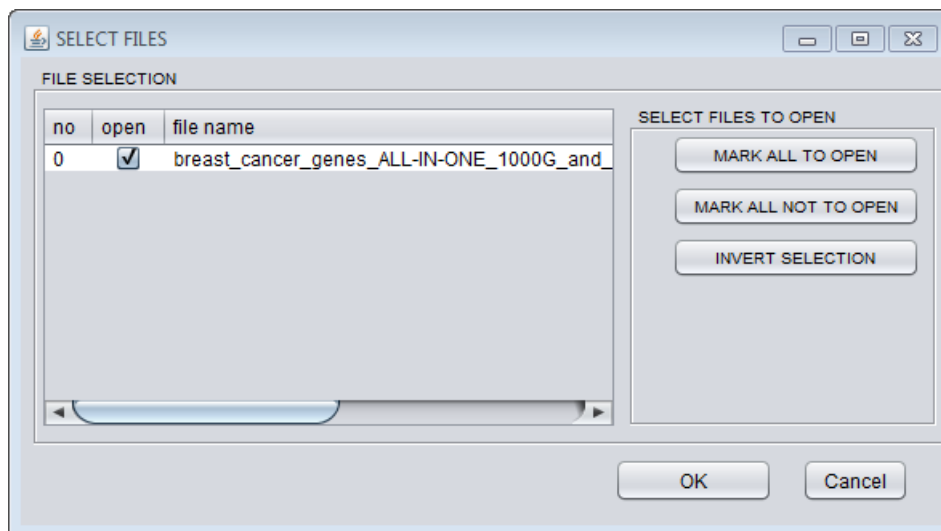
The supported data formats are automatically detected and listed upon data import.

Alternatively, a single file can be imported. To accomplish it, select **File > Open file** menu option or click on **SELECT SINGLE INPUT FILE** button and point to the file in **Select single file** window.



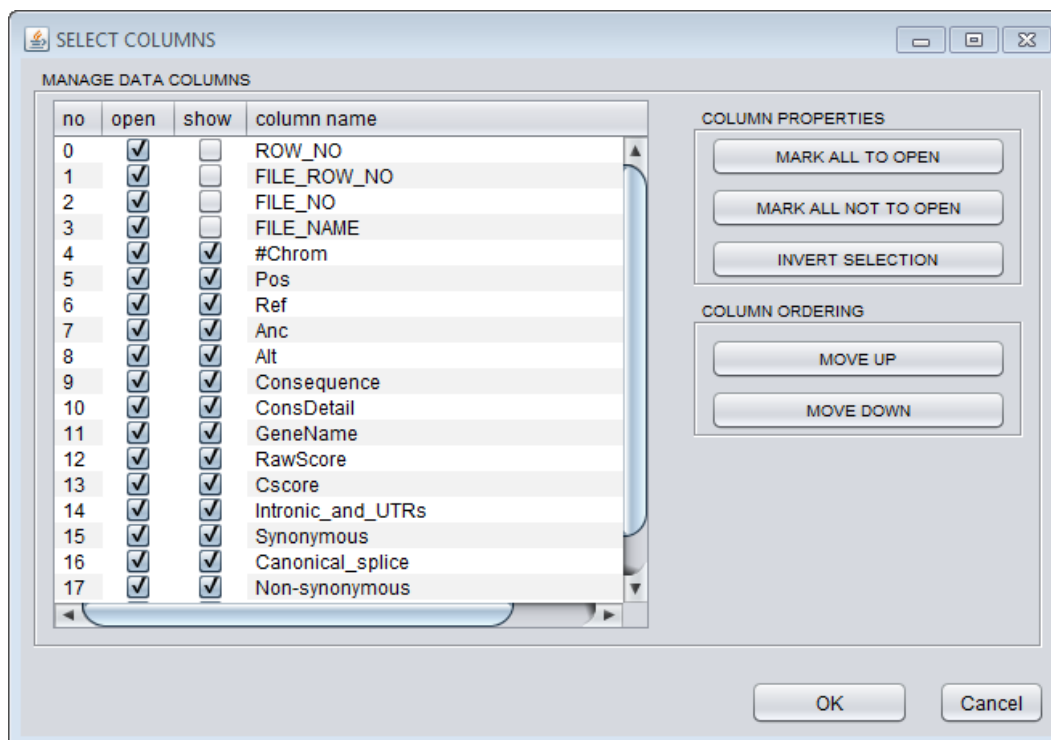


- 2 The status bar displays file import progress information in real time. The import time depends on the total size of the import files and available computing power and RAM.
- 3 In the **SELECT FILES** window mark the files from the import directory to open. Using buttons in **SELECT FILES TO OPEN** subfield it is possible to simultaneously select or deselect for opening all detected files (**MARK ALL TO OPEN** / **MARK ALL NOT TO OPEN**) or to invert the selection of files (**INVERT SELECTION**).



- 4 In the **SELECT COLUMNS** window select the data columns to be imported from the input files using the same buttons like in the previous window (**MARK ALL TO OPEN**, **MARK ALL TO NOT OPEN** and **INVERT SELECTION**).

Optionally, the data columns can be reorganized with the **MOVE UP** and **MOVE DOWN** buttons (in **COLUMN ORDERING** subfield).



- When the file import has been completed, the imported files along with the corresponding summaries are displayed in the **FILE LIST** and above the status bar. At the same time the **REPORT PREVIEW** is generated, which contains the combined data from the imported files.

The screenshot displays a software window with a menu bar (File, Edit, View, Data, Queue, Help) and a toolbar. The interface is divided into several sections:

- MAIN INPUT FILE / DIRECTORY:** Shows the path "C:\Users\Magda\Desktop" and "FILES DETECTED: 4".
- SECOND OPTIONAL INPUT FILE / DIRECTORY:** Shows "NO DIRECTORY SELECTED" and "FILES DETECTED: 0 [VCF: 0, TDTF: 0]".
- FILE LIST:** A table listing imported files and their row counts.
- QUEUE:** A section for managing the import queue with buttons like ADD, DELETE, EDIT, MOVE UP, and MOVE DOWN.
- REPORT PREVIEW:** A detailed table showing genomic data for BRCA1 genes, including chromosome, position, reference, and scores.
- Status Bar:** Displays summary statistics: FILES [ALL]: 4, FILES [FOUND]: 4, DATA ROWS [ALL]: 2055, DATA ROWS [FOUND]: 2055, ANALYSIS TIME: N/A [< 1], MEMORY [FREE / AVAILABLE]: 13.0 GIB / 15.7 GIB.

FILE LIST Data:

FILE NAME	FILE ROWS	DATA ROWS [TOTAL]	DATA ROWS [FOUND]	DATA ROWS [FOUND ...]
BC_genes_BRCA1.txt	914	914	100	
BC_genes_CHEK2.txt	678	678	100	
BC_genes_TP53.txt	264	264	100	
breast_cancer_genes...	199	199	100	

REPORT PREVIEW Data (Sample Rows):

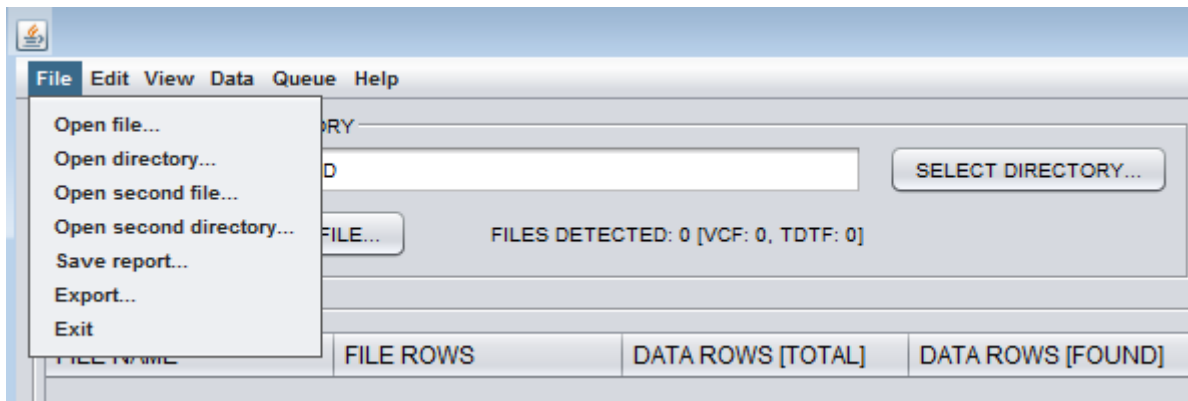
ROW_NO	FILE_ROW_NO	FILE_NO	FILE_NAME	#Chrom	Pos	Ref	Anc	Alt	Consequ...	ConsDetail	GeneName	RawScore	Cscore	Intronic_a...	Synonymr
71	71	0	BC_genes_B...	17	41203326	G	G	A	INTRONIC	intron	BRCA1	0.166896	4.898	4.898	#NDI
72	72	0	BC_genes_B...	17	41203388	G	G	A	INTRONIC	intron	BRCA1	1.632536	11.42	11.42	#NDI
73	73	0	BC_genes_B...	17	41203591	T	C	C	INTRONIC	intron	BRCA1	-0.28328	2.645	2.645	#NDI

8.2 MAIN VIEW

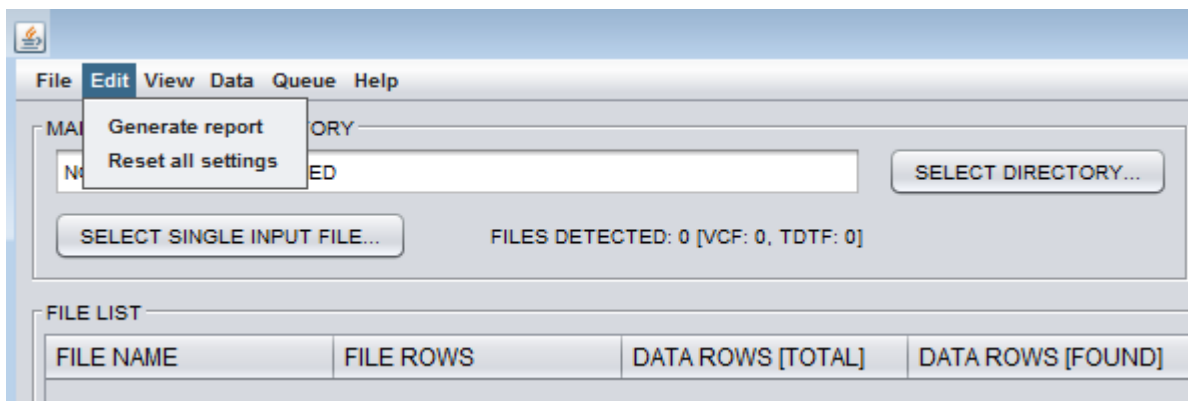
8.2.1 PULL DOWN MENU

At the top of the main window there is a pull down menu with six program menus, namely **File**, **Edit**, **View**, **Data**, **Queue** and **Help**.

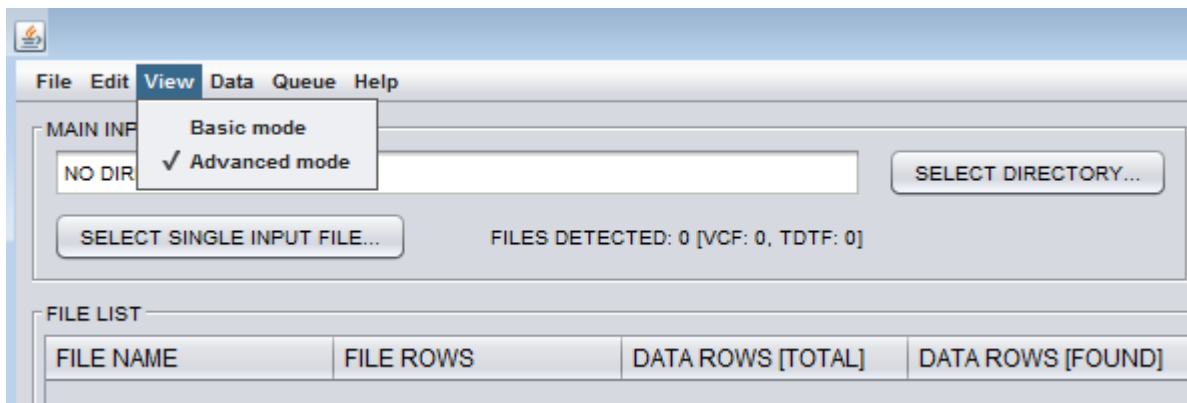
File menu refers to following operations on files – opening a single file, opening a directory with files, opening second file or directory, saving report with processed data and exiting the program.



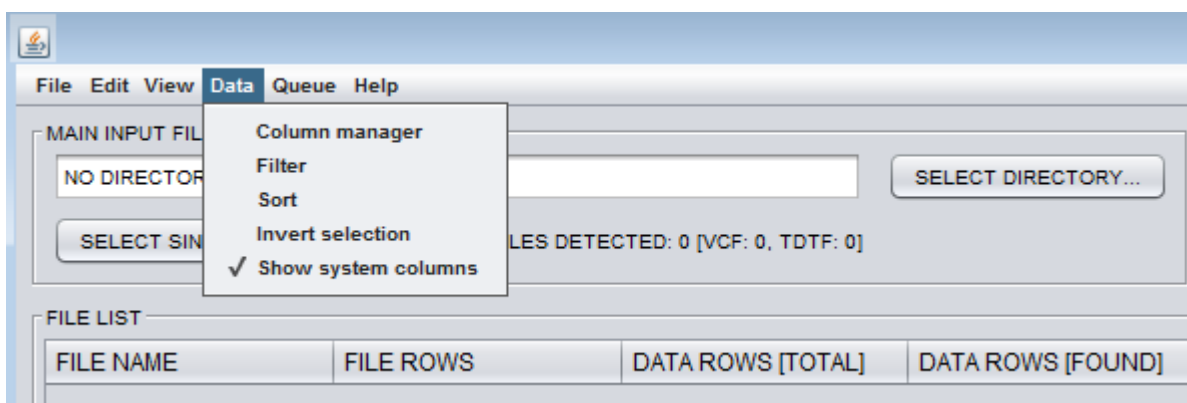
Making use of **Edit** menu, the global data changes can be done – such as carrying out the filtering task and generating a resulting report or resetting all settings.



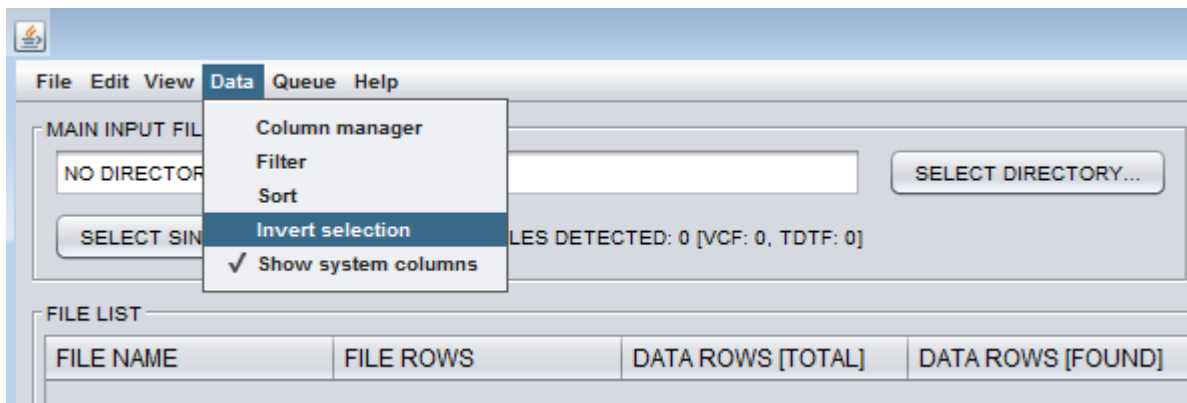
Switching between the advanced and basic mode is available via **View** menu.



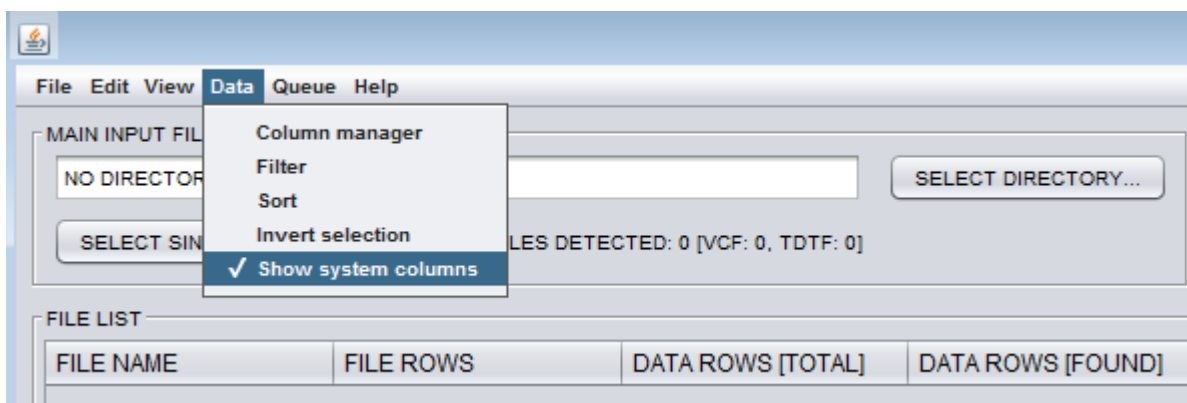
Functions designed for data processing are provided in **Data** menu. Functions called **Column manager**, **Sort** and **Filter** are described in 8.4. COLUMN MANAGEMENT, 8.3. SORTING OF COLUMNS and 8.5. FILTERING THE INPUT FILE(S) section, respectively.



Under **Data** menu it is also possible to reverse the output with regards to the applied filtering criteria using **Invert selection** function. The invert selection function is intended for control purposes, i.e. to provide an insight into data that is removed by the filters.

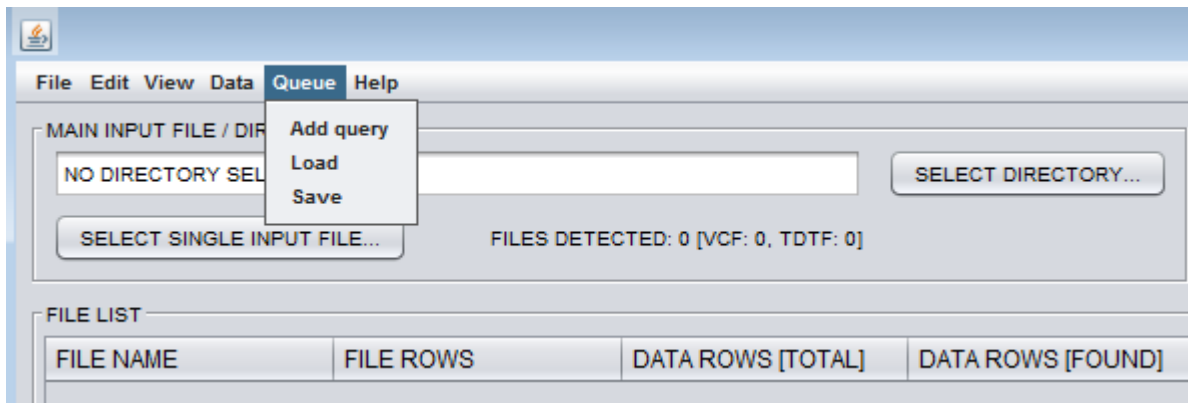


Show system columns function is intended to determine whether system columns are displayed or hidden. System columns, called **ROWS_NO**, **FILE_ROW_NO**, **FILE_NO** and **FILE_NAME**, are created automatically by the program to keep track of the original records in the imported files. **Show system columns** function is mainly helpful when working with multiple files at the same time.

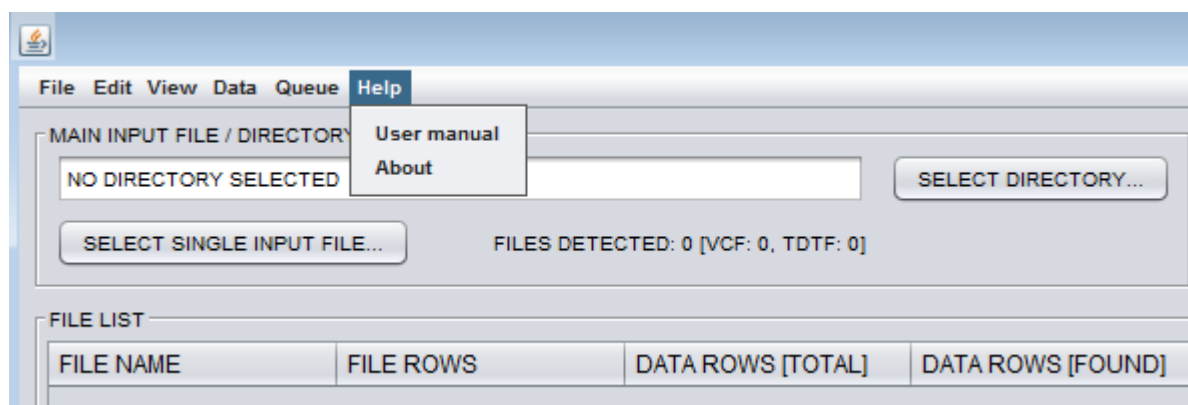


REPORT PREVIEW				
ROW_NO	FILE_ROW_NO	FILE_NO	FILE_NAME	#Chrom
0	0	0	breast_cancer...	19
1	1	0	breast_cancer...	19
2	2	0	breast_cancer...	19
3	3	0	breast_cancer...	19
4	4	0	breast_cancer...	19
5	5	0	breast_cancer...	19
6	6	0	breast_cancer...	19
7	7	0	breast_cancer...	19
8	8	0	breast_cancer...	19
9	9	0	breast_cancer...	19
10	10	0	breast_cancer...	19

Add query function under **Queue** menu facilitates adding a query with regard to imported data. It is also possible to save a query consisting of particular parameters for further analyses and to load the previously saved query if needed (see 7.8 SAVING QUERIES and 7.9. LOADING QUERIES sections).

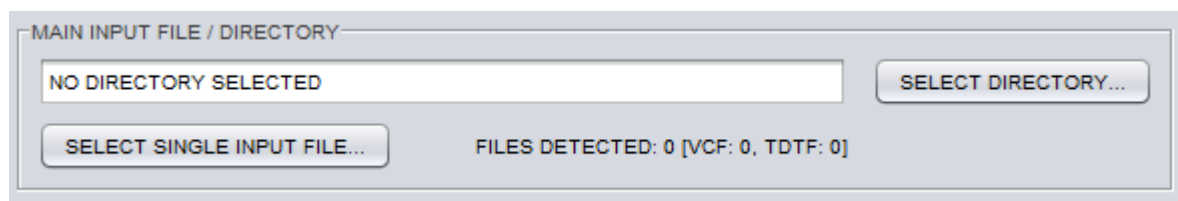


Information about the **HIGH-THROUGHPUT TABULAR DATA PROCESSOR** and this **user manual** is accessible via **Help** menu.



8.2.2 MAIN INPUT FILE / DIRECTORY field

This field facilitates opening a single file (**SELECT SINGLE INPUT FILE**) or directory with files (**SELECT DIRECTORY**) intended for processing. For details see 8.1 FILE IMPORT section.



8.2.3 SECOND, OPTIONAL FILE / DIRECTORY field

Here, it is possible to open an additional file (**SELECT SINGLE INPUT FILE**) or directory with files (**SELECT DIRECTORY**). All operations are similar to those in the **MAIN INPUT FILE / DIRECTORY** field.

The **SHOW DATA** button provides a preview of the new data set.

SECOND OPTIONAL INPUT FILE / DIRECTORY

NO DIRECTORY SELECTED

SELECT DIRECTORY...

SELECT SINGLE INPUT FILE...

FILES DETECTED: 0 [VCF: 0, TDTF: 0]

SHOW DATA

8.2.4 FILE LIST field

This field contains a list of imported files. Besides files names (**FILE NAME** column), the following information is provided:

- The number of rows in the input file (**FILE ROWS**).
- The total number of data rows (**DATA ROWS [TOTAL]**) – in the case of tab delimited text files the values in **FILE ROWS** and **DATA ROWS [TOTAL]** are always equal, while for VCF files these values may be different.
- The number of rows which are retained after the filtering criteria have been applied (**DATA ROWS [FOUND]**).
- Percentage of rows which are retained after the filtering criteria have been applied (**DATA ROWS [FOUND (%)]**), i.e. **DATA ROWS [FOUND]** vs. **DATA ROWS [TOTAL]**.

FILE LIST				
FILE NAME	FILE ROWS	DATA ROWS [TOTAL]	DATA ROWS [FOUND]	DATA ROWS [FOUND ...]
BC_genes_BRCA1.txt	914	914	63	6
BC_genes_CHEK2.txt	678	678	16	2
BC_genes_TP53.txt	264	264	10	3
breast_cancer_genes...	199	199	22	11

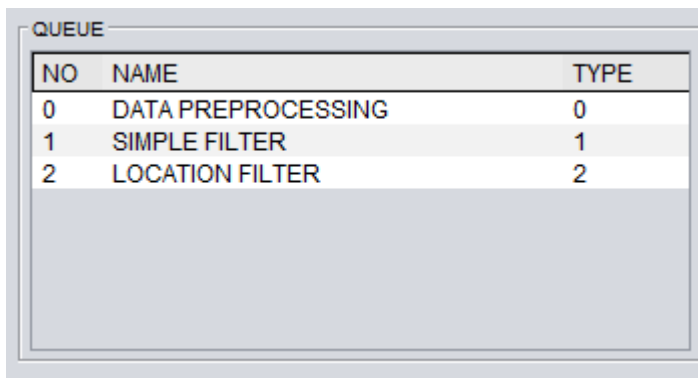
The list is updated in real time along with execution of user queries (see 8.4 FILTERING THE INPUT FILE(S) section). It can be also sorted by any column after clicking the column name (see 8.3 SORTING OF COLUMNS section).

8.2.5 QUEUE field

8.2.5.1 QUEUE subfield

This subfield displays the list of user-defined queries.

Each query is automatically denoted by subsequent number (**NO** column) along with user-defined identifier (**NAME**). Each query is also tagged with a query type (**TYPE** column) according to the name of the tab in **QUERY CONFIGURATION** window containing filtering parameters (see 6 QUERY CONFIGURATION WINDOW – ADVANCED MODE section). Queries are implemented in the order in which they have been added to the list. There are no limits with regard to the number of queries.

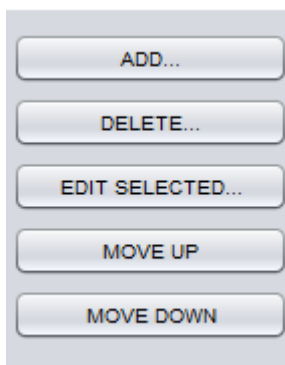


The screenshot shows a window titled "QUEUE" containing a table with three columns: NO, NAME, and TYPE. The table lists three queries: 0 DATA PREPROCESSING (TYPE 0), 1 SIMPLE FILTER (TYPE 1), and 2 LOCATION FILTER (TYPE 2). Below the table is a large empty rectangular area.

NO	NAME	TYPE
0	DATA PREPROCESSING	0
1	SIMPLE FILTER	1
2	LOCATION FILTER	2

8.2.5.2 QUERY QUEUE CONTROL SECTION

Five buttons located on the right side of the **QUEUE** subfield allow query queue management.



ADD button opens query configuration window to set filtering rules (see **8.4 FILTERING THE INPUT FILE(S)** section). Subsequently added queries will show up in the list.

Removal of every added query is possible using the **DELETE** button.

Click on a specific query in **QUEUE** field and then on **EDIT SELECTED** button to modify the content of this query. Afterwards, the **QUERY SETUP** window will be displayed again to introduce all changes.

Using **MOVE UP** and **MOVE DOWN** buttons the order of queries in the queue can be changed.

8.2.6 REPORT PREVIEW

The **REPORT PREVIEW** field displays the preview of the resulting data table.

REPORT PREVIEW															
ROW_NO	FILE_ROW_NO	FILE_NO	FILE_NAME	#Chrom	Pos	Ref	Anc	Alt	Consequ...	ConsDetail	GeneName	RawScore	Cscore	Intronic_a...	Synonymr
1355	441	1	BC_genes_C...	22	29121013	G	G	T	NON_SY...	missense...	CHEK2	2,932784	15,77	#ND!	#ND!
1356	442	1	BC_genes_C...	22	29121018	C	C	T	NON_SY...	missense...	CHEK2	1,964469	12,53	#ND!	#ND!
1357	443	1	BC_genes_C...	22	29121019	G	G	A	NON_SY...	missense...	CHEK2	3,371204	17,36	#ND!	#ND!
1358	444	1	BC_genes_C...	22	29121087	A	A	G	NON_SY...	missense...	CHEK2	4,093588	21,1	#ND!	#ND!
1424	510	1	BC_genes_C...	22	29126425	C	C	T	NON_SY...	missense...	CHEK2	-1,914662	0,008	#ND!	#ND!
1466	552	1	BC_genes_C...	22	29130456	G	G	A	NON_SY...	missense...	CHEK2	1,814893	12,03	#ND!	#ND!
1468	554	1	BC_genes_C...	22	29130637	C	C	T	NON_SY...	missense...	CHEK2	0,485389	6,634	#ND!	#ND!
1469	555	1	BC_genes_C...	22	29130657	C	C	T	NON_SY...	missense...	CHEK2	1,360916	10,48	#ND!	#ND!
1615	23	2	BC_genes_TP...	17	7573948	C	C	G	NON_SY...	missense...	TP53	-1,595425	0,014	#ND!	#ND!
1647	55	2	BC_genes_TP...	17	7576911	G	G	C	NON_SY...	missense...	TP53	1,539529	11,1	#ND!	#ND!
1653	61	2	BC_genes_TP...	17	7577046	C	C	T	NON_SY...	missense...	TP53	2,258414	13,51	#ND!	#ND!
1654	62	2	BC_genes_TP...	17	7577069	C	C	T	NON_SY...	missense...	TP53	0,804706	8,231	#ND!	#ND!

This table is updated in real time along with execution of the filtering (see 8.4 FILTERING THE INPUT FILE(S) section). It can be sorted by any column after clicking the column name (see 8.3 SORTING OF COLUMNS section).

This table is also editable – double click on certain field, type some text and modified content will be saved.

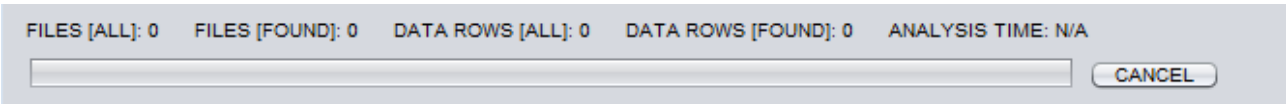
8.2.7 INFORMATION AND STATUS BAR

The information bar, located at the bottom of the main window, shows aggregate data statistics:

- Number of imported files (**FILES [ALL]**).
- Number of imported files which have retained at least one row of data after the filtering has been applied (**FILES [FOUND]**).
- The total number of rows in all imported files prior to filtering (**DATA ROWS [ALL]**).
- The total number of rows in all imported files which are retained after the filtering criteria have been applied (**DATA ROWS [FOUND]**).
- Total analysis time after completion of all items in the query queue (**ANALYSIS TIME**).

Status bar is located below aggregate data statistics and shows progress of the analysis in real time.

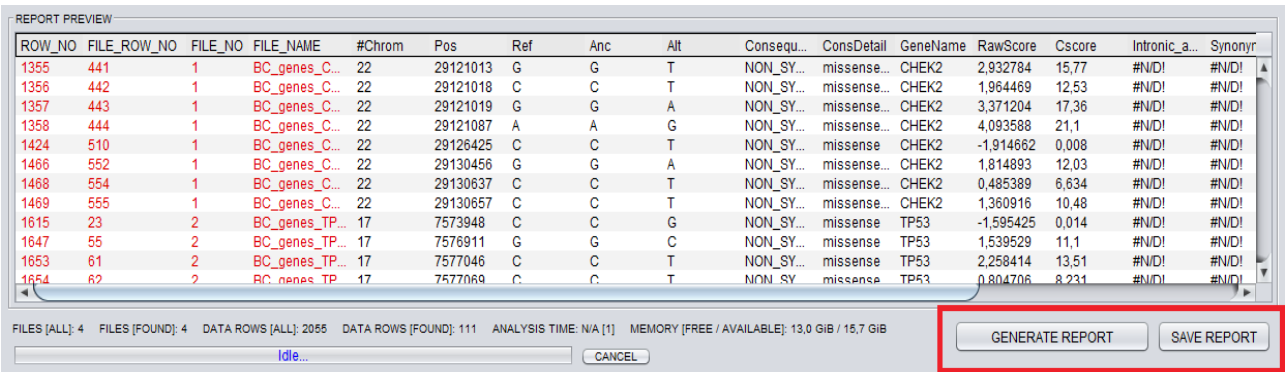
The **CANCEL** button allows user to abort an ongoing operation.



8.2.8 FILE OPERATIONS BUTTONS

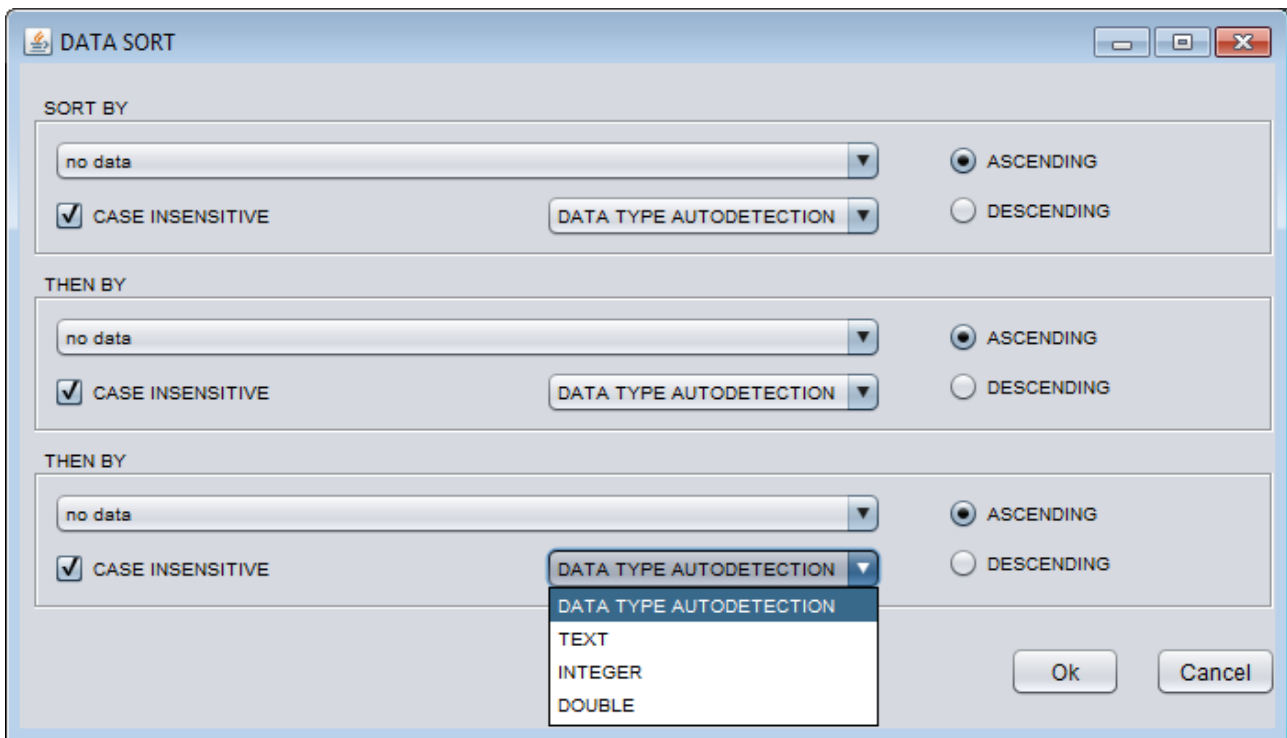
GENERATE REPORT button commences data analysis. The status bar will display data processing progress information in real time and after completion the **REPORT PREVIEW** will be refreshed.

SAVE REPORT opens a dialog box to specify the output file name and folder (see 8.7 SAVING FILTERED FILE(S) section). The output data is saved as tab delimited file.



8.3 SORTING OF COLUMNS

To rearrange the data set with respect to one or more columns, select **Data > Sort** in pull down menu or click on any column name in the header line in the **REPORT PREVIEW** field. The **DATA SORT** window which is opened, facilitates sorting by up to the three columns at a time, in ascending or descending manner and in case insensitive (by default) or case sensitive way.



The type of data in the column(s) subjected to sorting is detected automatically (**DATA TYPE AUTODETECTION**), but can be also selected by hand as **TEXT**, **INTEGER** or **DOUBLE** (double-precision floating-point numbers, namely decimals).**COLUMNS MANAGEMENT**

Column(s) and file(s) management is possible via **COLUMN MANAGER** window. To open the window select **Data > Column manager** in pull down menu.

This window consists of two fields – **MANAGE DATA COLUMNS** and **FILE SELECTION**.

COLUMN MANAGER

MANAGE DATA COLUMNS

no	show	column name
0	<input checked="" type="checkbox"/>	ROW_NO
1	<input checked="" type="checkbox"/>	FILE_ROW_NO
2	<input checked="" type="checkbox"/>	FILE_NO
3	<input checked="" type="checkbox"/>	FILE_NAME
4	<input checked="" type="checkbox"/>	#Chrom
5	<input checked="" type="checkbox"/>	Pos
6	<input checked="" type="checkbox"/>	Ref
7	<input checked="" type="checkbox"/>	Anc
8	<input checked="" type="checkbox"/>	Alt
9	<input checked="" type="checkbox"/>	Consequence
10	<input checked="" type="checkbox"/>	ConsDetail
11	<input checked="" type="checkbox"/>	GeneName
12	<input checked="" type="checkbox"/>	RawScore
13	<input checked="" type="checkbox"/>	Cscore
14	<input checked="" type="checkbox"/>	Intronic_and_UTRs
15	<input checked="" type="checkbox"/>	Synonymous
16	<input checked="" type="checkbox"/>	Canonical_splice
17	<input checked="" type="checkbox"/>	Non-synonymous

COLUMN PROPERTIES

MARK ALL TO SHOW

MARK ALL NOT TO SHOW

INVERT SELECTION

RENAME

MODIFY CONTENT

COLUMN ORDERING

MOVE UP

MOVE DOWN

FILE SELECTION

no	show	file name	file descrip
0	<input checked="" type="checkbox"/>	BC_genes_BRCA1.txt	914
1	<input checked="" type="checkbox"/>	BC_genes_CHEK2.txt	678
2	<input checked="" type="checkbox"/>	BC_genes_TP53.txt	264
3	<input checked="" type="checkbox"/>	breast_cancer_genes_ALL-IN-O...	199

SELECT FILES TO OPEN

MARK ALL TO SHOW

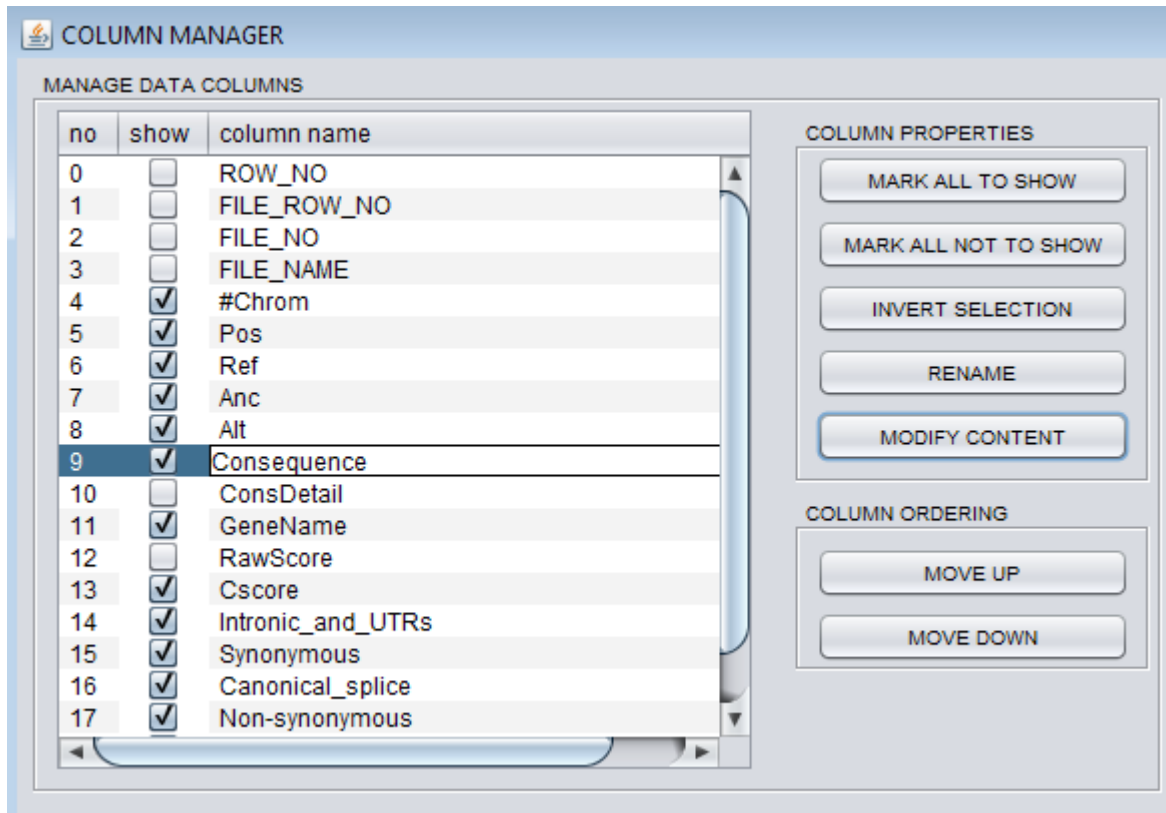
MARK ALL NOT TO SHOW

INVERT SELECTION

OKCancel

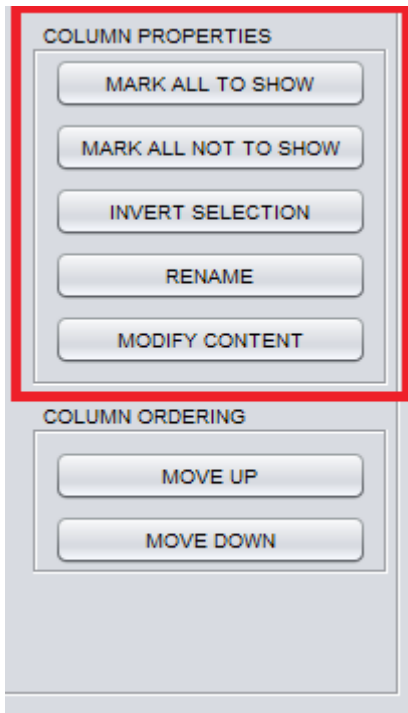
8.3.1 MANAGE DATA COLUMNS field

Here it is possible to change columns' settings that have been chosen during file(s) import.

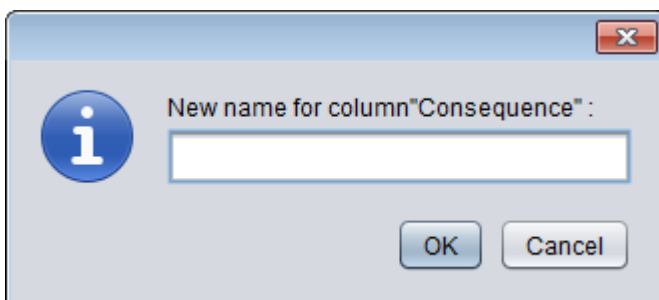


8.3.1.1 COLUMN PROPERTIES subfield

To customize browsing the data by hiding or showing again selected column(s), uncheck or check the corresponding selection field(s). For this purpose also **MARK ALL TO SHOW**, **MARK ALL NOT TO SHOW** and **INVERT SELECTION** buttons can be used. Hidden columns are not deleted from the data set though and are taken into account during every data processing step.



Every column name can be altered in two ways – by double clicking on it or by using the **RENAME** button. The latter opens the next window to define the new name of a specific column.



MODIFY CONTENT button opens a window called **COLUMN CONTENT MODIFICATION**, which is intended to transform the data in all fields / cells from the selected column.

The screenshot shows a Windows-style dialog box titled "COLUMN CONTENT MODIFICATION". Inside, there is a section labeled "COLUMN DATA PROCESSING". This section contains several groups of controls:

- REPLACE:** Two rows of "SEARCH FOR" and "REPLACE WITH" text boxes.
- ADD:** Two text boxes labeled "BEFORE" and "AFTER".
- REMOVE:** A "REMOVE ALL" checkbox.
- OTHER:** Three checkboxes: "CUT OFF ... CHARACTERS FROM THE START", "CUT OFF ... CHARACTERS FROM THE END", and "REMOVE CHARACTERS FROM ... TO ...". Below these is a "REMOVE LEADING ZEROS" checkbox.

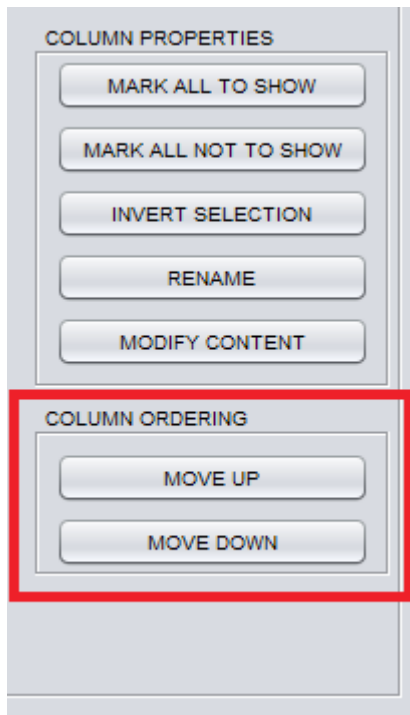
At the bottom of the dialog are "OK" and "Cancel" buttons.

Following changes are available here:

- Searching and replacing alphanumeric strings (**SEARCH FOR ... REPLACE WITH ...**).
- Adding alphanumeric strings before and/or after (**ADD – BEFORE ... and AFTER ...**).
- Removing specified expression from every data row (**REMOVE ALL ...**).
- Trimming the ends of the alphanumeric strings (**CUT OFF ... CHARACTERS FROM THE START / END**) or cutting the characters within the alphanumeric strings at the specified positions (**REMOVE CHARACTERS FROM ... TO ...**).
- Removing of so called “leading zeros”, eg. 000023 to 23 (**REMOVE LEADING ZEROS** checkbox).

8.3.1.2 COLUMN ORDERING subfield

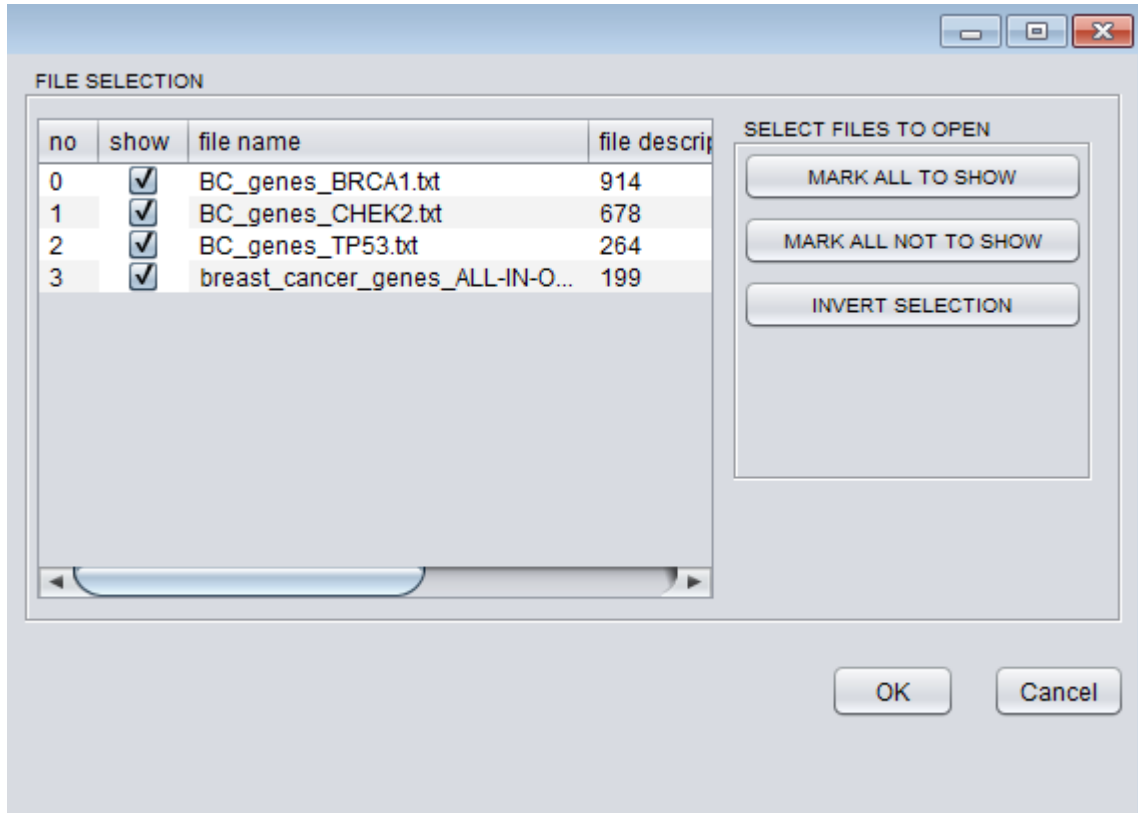
The order of columns displayed in **DATA PREVIEW** field (at the main window) can be changed. For this purpose, point the column name and click **MOVE UP** or **MOVE DOWN** button.



8.3.2 FILE SELECTION field

In this field it is possible to hide or unhide previously imported data set(s). As in case of column selection, click on a checkbox of matched file(s) or use **MARK ALL TO SHOW**, **MARK ALL NOT TO SHOW** and **INVERT SELECTION** buttons.

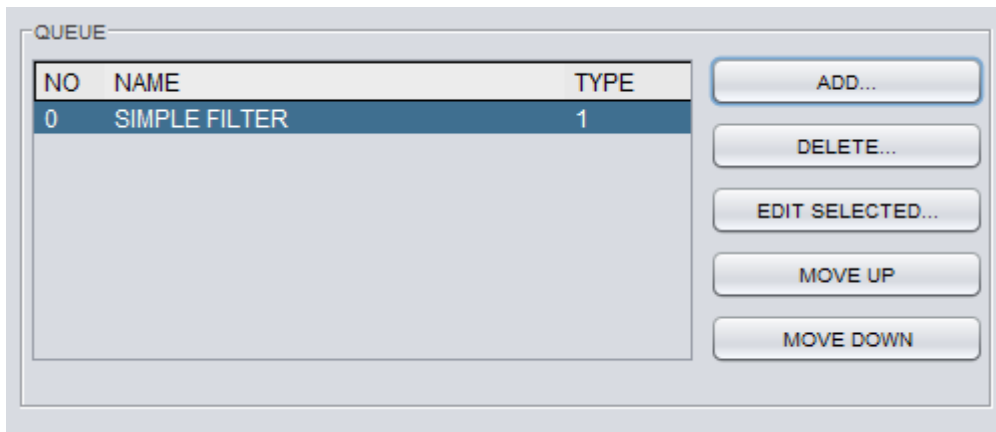
Hidden files are not deleted from the data set though, and are taken into account during every data processing step.



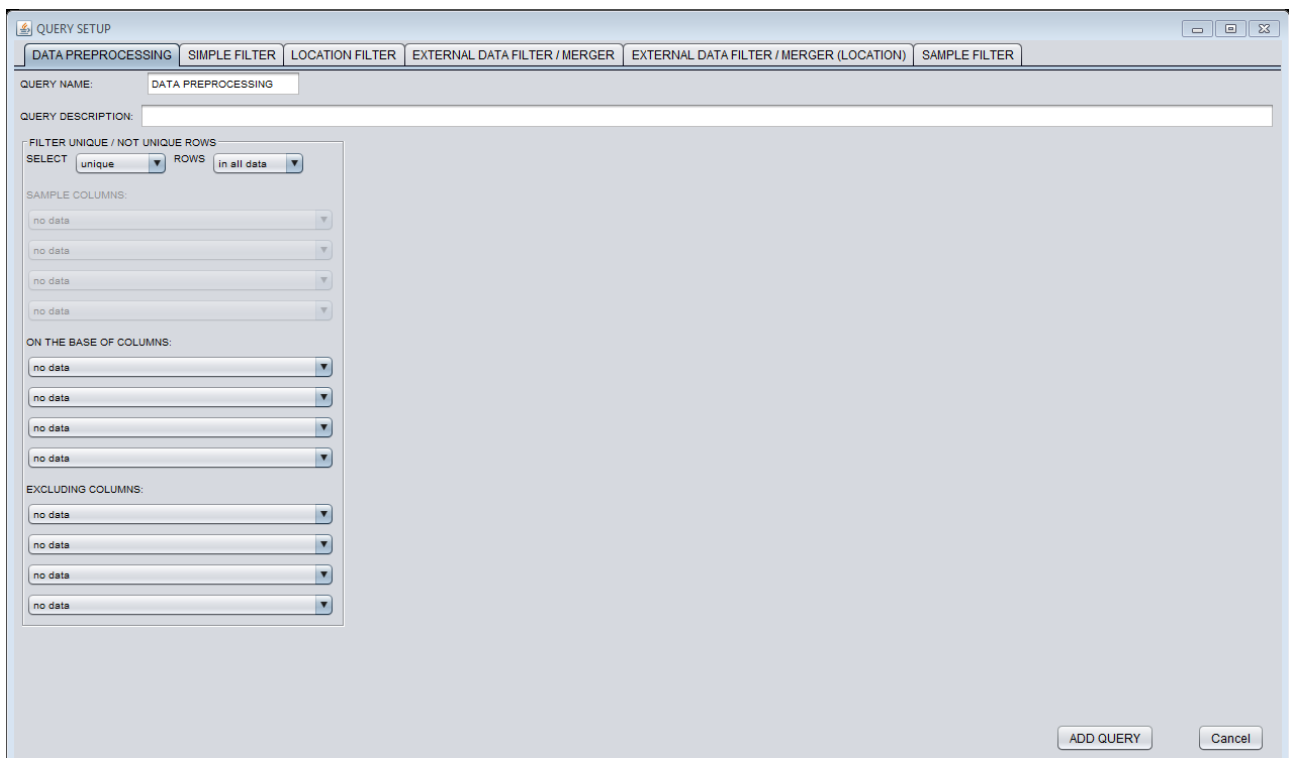
8.4 FILTERING THE INPUT FILE(S)

Advanced mode enables filtering which is carried out based on unlimited number of complex queries.

To set up filtering, click the **ADD** button in the query queue control section.



Subsequently, the **QUERY SETUP** window is opened that facilitates adding the queries.



QUERY SETUP window has six tabs corresponding to different types of queries that can be handled by the program:

- **DATA PREPROCESSING.**
- **SIMPLE FILTER.**
- **LOCATION FILTER.**
- **EXTERNAL DATA FILTER / MERGER.**
- **EXTERNAL DATA FILTER / MERGER (LOCATION).**
- **SAMPLE FILTER.**

Single query should only consist of parameters selected in one tab, as settings defined simultaneously in other tabs will not be executed. Consequently, the list of filtering criteria will be longer, but more legible.

8.4.1 DATA PREPROCESSING

DATA PREPROCESSING form is selected by default. This form is intended for global operations on the entire data sets.

The screenshot shows the 'QUERY SETUP' dialog box with the 'DATA PREPROCESSING' tab selected. The 'QUERY NAME' field is set to 'DATA PREPROCESSING'. The 'QUERY DESCRIPTION' field is empty. The 'FILTER UNIQUE / NOT UNIQUE ROWS' section has 'SELECT' set to 'unique' and 'ROWS' set to 'in all data'. The 'SAMPLE COLUMNS' section has four dropdown menus, all set to 'no data'. The 'ON THE BASE OF COLUMNS' section has four dropdown menus, all set to 'no data'. The 'EXCLUDING COLUMNS' section has four dropdown menus, all set to 'no data'. At the bottom right, there are 'ADD QUERY' and 'Cancel' buttons.

QUERY NAME and **QUERY DESCRIPTION** entry fields allow to assign the optional name and a short description to the query.

This screenshot shows the top portion of the 'QUERY SETUP' dialog box. The 'QUERY NAME' field contains 'DATA PREPROCESSING' and the 'QUERY DESCRIPTION' field is empty. The tabs at the top are 'DATA PREPROCESSING', 'SIMPLE FILTER', 'LOCATION FILTER', 'EXTERNAL DATA FILTER / MERGER', 'EXTERNAL DATA FILTER / MERGER (LOCATION)', and 'SAMPLE FILTER'.

By using **SELECT** pull down menu only unique or redundant rows (occurring in the data more than once) can be retained.
 The choice can be based on the unique/redundant rows in the entire data set, in each file separately or in each sample.

FILTER UNIQUE / NOT UNIQUE ROWS

SELECT unique ROWS in all data

SAMPLE unique
not unique

FILTER UNIQUE / NOT UNIQUE ROWS

SELECT unique ROWS in all data

SAMPLE COLUMNS: in all data
in each file
in each sample

The uniqueness/redundancy can be determined based on the contents of the entire row (by default) or based on up to four indicated data column(s) (**ON THE BASE OF COLUMNS** subfield).

ON THE BASE OF COLUMNS:

Four empty dropdown menus for selecting columns.

Alternatively, it is possible to determine the uniqueness/redundancy based on the contents of the entire row, but with the exclusion of up to four selected columns in the data (**EXCLUDING COLUMNS** subfield).

EXCLUDING COLUMNS:

▼

▼

▼

▼

The described functions were used in example 1 in S2 Text. All needed example files were deposited on Open Science Framework (<https://osf.io/pw2dx/>) and are publicly available.

SIMPLE FILTER

SIMPLE FILTER refers to modifications and further filtering of the data stored in the indicated column.

QUERY SETUP
[Icons]

DATA PREPROCESSING
SIMPLE FILTER
LOCATION FILTER
EXTERNAL DATA FILTER / MERGER
EXTERNAL DATA FILTER / MERGER (LOCATION)
SAMPLE FILTER

QUERY NAME: SIMPLE FILTER

QUERY DESCRIPTION:

[1] SELECT COLUMN

COLUMN

no data ▼

[2] INPUT DATA PREPROCESSING

REPLACE

SEARCH FOR

REPLACE WITH

SEARCH FOR

REPLACE WITH

ADD

BEFORE

CUT OFF ☐ CHARACTERS FROM THE START

AFTER

CUT OFF ☐ CHARACTERS FROM THE END

REMOVE

REMOVE ALL ☐

REMOVE CHARACTERS FROM TO

☐ REMOVE LEADING ZEROS

PREVIEW

OTHER DATA

REFRESH

☒ MAKE CHANGES PERMANENT

[3] QUERY SETUP

NUMERIC DATA SEARCH

SEARCH FOR

<

TEXTUAL DATA SEARCH

SEARCH FOR

no data ▼

CONDITION

▼

☐ CASE INSENSITIVE

LIST

No	Value

ADD

REMOVE

MOVE UP

MOVE DOWN

AUTO FILL

☐ AND ABOVE

OTHER FILES

▼

All

☐ INVERT SELECTION

ADD QUERY

Cancel

8.4.1.1 COLUMN SELECTION field

The first field, called **COLUMN SELECTION**, is used for choice of the column which will be subjected to filtering. Pull down menu located here contains the list of all columns included in the data set.

The screenshot shows a software window titled "QUERY SETUP" with three tabs: "DATA PREPROCESSING", "SIMPLE FILTER", and "LOCATION FIL". The "SIMPLE FILTER" tab is active. Below the tabs, there are two input fields: "QUERY NAME:" with the text "SIMPLE FILTER" and "QUERY DESCRIPTION:" which is empty. Below these fields is a section titled "[1] SELECT COLUMN" with a sub-label "COLUMN". This section contains a list box with a scroll bar. The list box has "ROW_NO" selected at the top, and the following items are visible in the list: "ROW_NO", "FILE_ROW_NO", "FILE_NO", "FILE_NAME", "#Chrom", "Pos", "Ref", and "Anc".

Column Name
ROW_NO
FILE_ROW_NO
FILE_NO
FILE_NAME
#Chrom
Pos
Ref
Anc

8.4.1.2 INPUT DATA PREPROCESSING field

In this field, data from the selected column can be prepared to the main filtering task.

[2] INPUT DATA PREPROCESSING

REPLACE

SEARCH FOR REPLACE WITH

SEARCH FOR REPLACE WITH

ADD

BEFORE

AFTER

REMOVE

REMOVE ALL ☐

OTHER

CUT OFF CHARACTERS FROM THE START

CUT OFF CHARACTERS FROM THE END

REMOVE CHARACTERS FROM TO

☐ REMOVE LEADING ZEROS

PREVIEW

☒ MAKE CHANGES PERMANENT

OTHER DATA

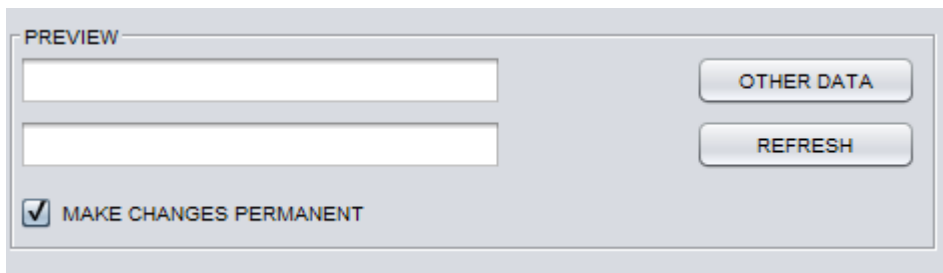
REFRESH

These preparatory operations include:

- Searching for alphanumeric strings to replace them with other phrases (**SEARCH FOR ... REPLACE WITH ...**).
-
- Adding alphanumeric strings before and/or after expressions in the rows (**ADD – BEFORE ...** and **AFTER ...**).
-
- Trimming the beginnings or ends of the alphanumeric strings (**CUT OFF ... CHARACTERS FROM THE START / END**) or cutting the characters within the alphanumeric strings at the specified positions (**REMOVE CHARACTERS FROM ... TO ...**).
-
- Removing of so called “leading zeros”, eg. 000023 to 23 (**REMOVE LEADING ZEROS** checkbox).
-
- Removing specified expression from every data row (**REMOVE ALL...**).

The **PREVIEW** subfield shows a preview of introduced changes in the selected column and randomly selected row of data. The first line shows the original data and the second line presents the same data after processing.

The preview is updated upon introduction of any change in the **INPUT DATA PREPROCESSING** field, or can be enforced by clicking the **REFRESH** button. Also other exemplary rows of data can be drawn by clicking the **OTHER DATA** button.



The screenshot shows a user interface for a 'PREVIEW' section. It contains two empty text input fields stacked vertically. To the right of these fields are two buttons: 'OTHER DATA' and 'REFRESH'. Below the input fields is a checkbox labeled 'MAKE CHANGES PERMANENT', which is currently checked.

If the **MAKE CHANGES PERMANENT** box is not checked, the changes introduced in the **INPUT DATA PREPROCESSING** field have temporary character and facilitate customization of data for the **QUERY SETUP** field. In this case, after filtering has been applied, the actual data is not changed (the change is introduced temporarily then the original content is restored).

8.4.1.3 QUERY SETUP field

The query setup field serves for setting up the main filtering parameters. These parameters may refer to numeric or alphanumeric data, which are included in already chosen data column. Filtering can be done on data from one selected file from the dataset as well as on data from all loaded files.

[3] QUERY SETUP

NUMERIC DATA SEARCH

> [] < []

TEXTUAL DATA SEARCH

SEARCH FOR []

CONDITION [] ☐ CASE INSENSITIVE

LIST

No	Value
----	-------

ADD
REMOVE
MOVE UP
MOVE DOWN
AUTO FILL

☐ AND ABOVE

OTHER

FILES [All]

☐ INVERT SELECTION

NUMERIC DATA SEARCH subfield provides searching for values less or greater than specified or values within the specified range.

[3] QUERY SETUP

NUMERIC DATA SEARCH

> [] < []

> [] < []

>= []

TEXTUAL DATA SEARCH

SEARCH FOR []

CONDITION [] ☐ CASE INSENSITIVE

In the **TEXTUAL DATA SEARCH** subfield the data can be checked for matches with the specified alphanumeric substring.

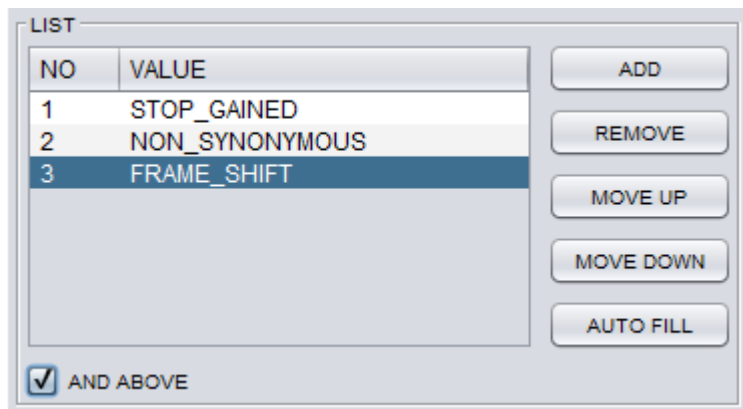
Type the text to be searched or use the pull down list called **SEARCH FOR** to choose one of the expressions occurring in column. Furthermore, to specify the filtering task, following operators are available in the **CONDITION** pull down list: "=", "<", ">", "<=", ">=", "<>", "Contains", "Does not contain", "Begins with", "Does not begin with", "Ends with", "Does not end with".

Operations can be executed in case sensitive or insensitive way, respectively, which is defined using **CASE INSENSITIVE** checkbox.

The image shows a software dialog box titled "TEXTUAL DATA SEARCH". It contains the following elements:

- A "SEARCH FOR" dropdown menu.
- A "CONDITION" dropdown menu that is open, showing a list of operators: ">", "<=", ">=", "<>", "Contains", "Does not contain", "Begins with", and "Does not begin".
- A "CASE INSENSITIVE" checkbox.
- A list box on the left with columns "No" and "Value".
- Buttons on the right: "ADD", "REMOVE", "MOVE UP", "MOVE DOWN", and "AUTO FILL".
- An "AND ABOVE" checkbox at the bottom left.

More complex filtering tasks can utilize the **LIST** feature. It allows to simultaneously look for more than one expression from the column selected in the first step of **SIMPLE FILTER**.



NO	VALUE
1	STOP_GAINED
2	NON_SYNONYMOUS
3	FRAME_SHIFT

Buttons: ADD, REMOVE, MOVE UP, MOVE DOWN, AUTO FILL

☒ AND ABOVE

Each item in the list is added by clicking the **ADD** button. Subsequent items are shown denoted with a number (in the **NO** column) and a text to be searched (in the **VALUE** column).

To delete a particular item from the list click on it and then on the **REMOVE** button. An operation window will be displayed to confirm this action.

The order of listed expressions can be changed by using the **MOVE UP** and **MOVE DOWN** buttons. Select the item and then click on one of these two buttons. Every click changes the item's location by one position forward or backward.

The **AUTO FILL** function can be used to automatically create a list of all contents occurring in the indicated column.

The **LIST** can be utilized in 3 various ways:

- Without selecting any of the items in the list – in this case the contents of the selected column will be searched for the presence of either item in the list.
- With selecting an item in the list – in this case the contents of the selected column will be searched with regard to the conditions as defined by the selected item in the list.
- With selecting an item in the list and clicking the **AND ABOVE** checkbox – in this case the contents of selected column will be searched with regard to the conditions as defined by the selected item in the list as well as the items preceding the selected item in the list.

The described functions were used in example 2 (stage 7), 3 (stage 8) and 4 (stage 2 and 3) in S2 Text. All needed example files were deposited on Open Science Framework (<https://osf.io/pw2dx/>) and are publicly available.

8.4.2 LOCATION FILTER

LOCATION FILTER is useful to search for a data on the basis of the locus.

The screenshot shows the 'QUERY SETUP' dialog box with the 'LOCATION FILTER' tab selected. The dialog has a title bar with standard window controls. Below the title bar are several tabs: 'DATA PREPROCESSING', 'SIMPLE FILTER', 'LOCATION FILTER' (active), 'EXTERNAL DATA FILTER / MERGER', 'EXTERNAL DATA FILTER / MERGER (LOCATION)', and 'SAMPLE FILTER'. The main area is divided into two columns. The left column, labeled '[1] SELECT COLUMN OR CREATE LOCUS', contains a dropdown menu for 'MULTIPLE COLUMN LOCUS' (currently set to 'no data'), followed by three dropdown menus for 'CHROMOSOME COLUMN', 'START POSITION COLUMN', and 'STOP POSITION COLUMN' (all set to 'no data'). Below these is a text input for 'STOP POSITION = START POSITION +' and a checkbox for 'STOP POS. = START POS. + STOP POS. COL. VALUE LENGTH'. The right column, labeled '[2] LOCUS SEARCH', contains a 'CHROMOSOME' dropdown (set to 'All'), and three text inputs for 'START POS.', 'LENGTH', and 'STOP POS.'. There is also an 'OVERLAP AT LEAST (%)' input set to '0'. At the bottom left is a 'PREVIEW' section with 'CHROMOSOME:', 'START POS.', and 'STOP POS.' labels and corresponding input fields, along with an 'OTHER DATA' button. At the bottom right are 'UPDATE QUERY' and 'Cancel' buttons.

8.4.2.1 SELECT COLUMN OR CREATE A LOCUS field

The first field, called **SELECT COLUMN OR CREATE A LOCUS**, is designed to define the format of location data. It can be done in two ways – there are two options in the pull down menu:

- Using **MULTIPLE COLUMN LOCUS** – indicate which columns (presented in the pull down lists) refer to the number of the chromosome (**CHROMOSOME COLUMN**), start position (**STARTING POSITION COLUMN**) and stop position (**STOP POSITION COLUMN**), respectively.

Alternatively, the stop position can be created by adding any number to the start position. Therefore all loci will have the same length (**STOP POSITION = START POSITION + ...**).

[1] SELECT COLUMN OR CREATE LOCUS

MULTIPLE COLUMN LOCUS ▼

MULTIPLE COLUMN LOCUS

CHROMOSOME COLUMN

#Chrom ▼

START POSITION COLUMN

Pos ▼

STOP POSITION COLUMN

▼

STOP POSITION = START POSITION + 1

- Using **SINGLE COLUMN LOCUS** – indicate, which column contains complete information about the locus and then choose its format from the pull down list (**LOCUS COLUMN FORMAT**). Four different formats are available:
 - ✓ Chromosome: start – stop.
 - ✓ Chromosome start stop.
 - ✓ Chromosome – start – stop.
 - ✓ Chromosome: start : stop.

[1] SELECT COLUMN OR CREATE LOCUS

SINGLE COLUMN LOCUS ▼

ONE COLUMN LOCUS

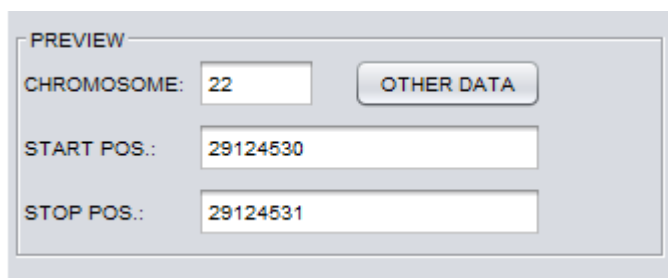
COLUMN

▼

LOCUS COLUMN FORMAT

CHR:START-STOP ▼

PREVIEW subfield, located below, displays the preview of locus data based on the one randomly chosen row. The other exemplary rows can be drawn by clicking the **OTHER DATA** button.



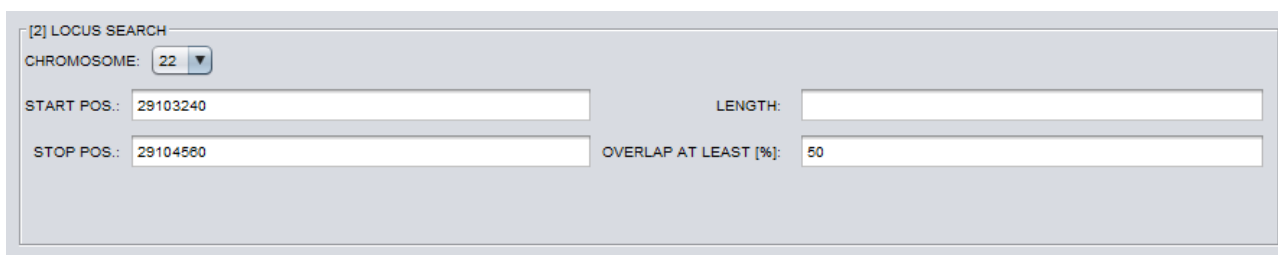
The screenshot shows a 'PREVIEW' section with a light blue border. Inside, there are three input fields: 'CHROMOSOME:' with the value '22', 'START POS.:' with the value '29124530', and 'STOP POS.:' with the value '29124531'. To the right of the 'CHROMOSOME' field is a button labeled 'OTHER DATA'.

8.4.2.2 LOCUS SEARCH field

LOCUS SEARCH is created to select the rows containing particular locus data. The search can be done with regard to one chromosome or all chromosomes present in the data – to determine it, there is a **CHROMOSOME** pull down list.

This option may be used in 3 main ways:

- To look for a specified locus, the **START POS.** and **STOP POS.** entry fields must be filled.
- To look for a locus of defined length, the **START POS.** must be completed as well as the number of nucleotides in the **LENGTH** entry field.
- To look for a particular percentage overlap with the specified locus, the **START POS.** and **STOP POS.** entry fields must be filled along with the **OVERLAP [%]** entry field.



The screenshot shows a '[2] LOCUS SEARCH' section with a light blue border. It contains four input fields: 'CHROMOSOME:' with a pull-down menu showing '22', 'START POS.:' with the value '29103240', 'STOP POS.:' with the value '29104580', and 'LENGTH:' which is empty. Below the 'STOP POS.:' field is a label 'OVERLAP AT LEAST [%]:' followed by an input field containing the value '50'.

The described functions were used in example 1, 4 in S2 Text. All needed example files were deposited on Open Science Framework (<https://osf.io/pw2dx/>) and are publicly available. **EXTERNAL DATA FILTER/MERGER**

EXTERNAL DATA FILTER/MERGER form enables two main actions:

- Filtering the main file, namely particular column(s), on the basis of up to four columns from the additional file.
- Merging the matching data from external file(s) with the main file.

QUERY SETUP

DATA PREPROCESSING | SIMPLE FILTER | LOCATION FILTER | EXTERNAL DATA FILTER / MERGER | EXTERNAL DATA FILTER / MERGER (LOCATION) | SAMPLE FILTER

QUERY NAME:

QUERY DESCRIPTION:

SELECT COLUMNS AND CONDITION

COLUMNS

COLUMN

ADDITIONAL COLUMNS (OPTIONAL)

CONDITION

COLUMNS [EXTERNAL DATA]

COLUMN

ADDITIONAL COLUMNS (OPTIONAL)

☐ CASE INSENSITIVE

SELECT ACTION

SELECT COLUMNS

☐ DO NOT FILTER - MERGE ONLY

☐ REPEAT DATA ROW WHEN MORE THAN ONE EXTERNAL DATA ROWS MATCH

ADDITIONAL COLUMNS AND STATISTICS

☐ ADD BASIC STATISTICS

☐ ADD COLUMN

INPUT COLUMN

OUTPUT

☐ ADD COLUMN

INPUT COLUMN

OUTPUT

8.4.2.3 SELECT COLUMNS AND CONDITION field

Here, a set of columns from the main file and external data is chosen to define the filtering/merging criteria.

SELECT COLUMNS AND CONDITION

COLUMNS

COLUMN

ADDITIONAL COLUMNS (OPTIONAL)

CONDITION

COLUMNS [EXTERNAL DATA]

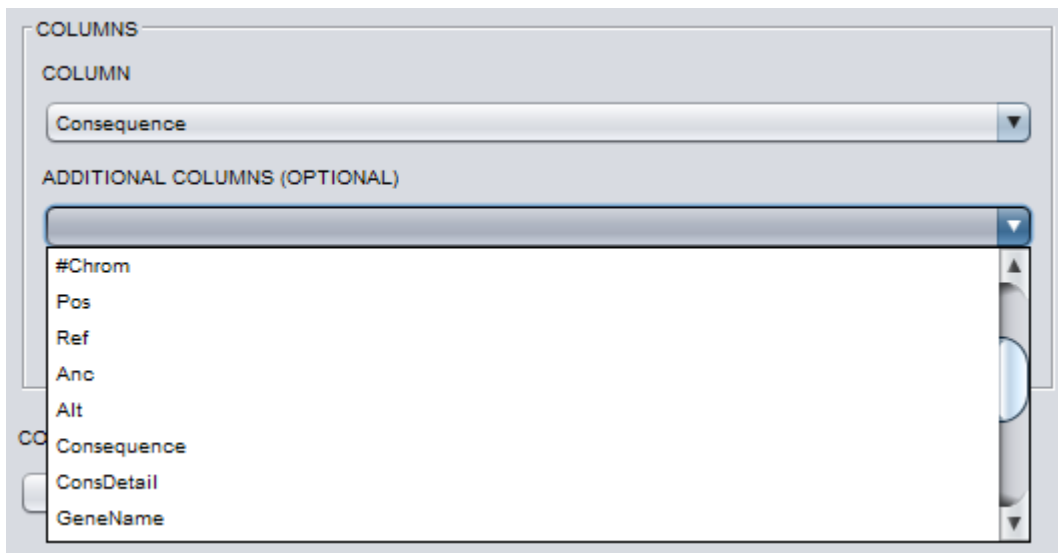
COLUMN

ADDITIONAL COLUMNS (OPTIONAL)

☐ CASE INSENSITIVE

SHOW DATA

In the first step choose from one up to four columns from the main file ((**COLUMN**) and **ADDITIONAL COLUMNS (OPTIONAL)** from the **COLUMNS** subfield). An input dataset, which is created in this way, will be subjected to processing.



Using the pull down list called **CONDITION**, define the condition with regard to the filtering or merging task. There are 12 following options here, including simple mathematical signs and expressions – “=”, “<”, “>”, “=<”, “=>”, “<>”, “Contains”, “Does not contain”, “Begins with”, “Does not begin with”, “Ends with” and “Does not end with”.



Finally, select from one up to four columns from external data file(s) (**COLUMN (EXTERNAL DATA)** and **ADDITIONAL COLUMNS (OPTIONAL)** which are located in the **COLUMNS [EXTERNAL FILE]** subfield). To facilitate the choice of columns, especially from several files, the **SHOW DATA** button is available to display the preview of the external dataset.

Moreover, filtering or merging on the basis of selected columns may be done in case insensitive way (**CASE INSENSITIVE** checkbox).

COLUMNS [EXTERNAL DATA]

COLUMN

Consequence

ADDITIONAL COLUMNS (OPTIONAL)

ConsDetail

☐ CASE INSENSITIVE

SHOW DATA

8.4.2.4 SELECT ACTION field

The **SELECT ACTION** is intended to determine the data processing operation.

The major step is to select one of three following alternatives:

- **FILTER ONLY** – data from the main file will be filtered on the basis of previously chosen condition and set of columns from the external file(s).
- **ADD ALL COLUMNS FROM EXTERNAL DATA MATCHING ROWS** – all previously selected columns that contain information matching defined criteria will be appended to the input dataset.
- **ADD SELECTED COLUMNS FROM EXTERNAL DATA MATCHING ROWS** – only selected columns from matching rows will be appended to the input dataset. Here, the **SELECT COLUMNS** subfield is active to choose up to three columns using pull down lists.

SELECT ACTION

FILTER ONLY

SELECT COLUMNS

☐ DO NOT FILTER - MERGE ONLY

☐ REPEAT DATA ROW WHEN MORE THAN ONE EXTERNAL DATA ROWS MATCH

ADDITIONAL COLUMNS AND STATISTICS

☐ ADD BASIC STATISTICS

☐ ADD COLUMN

INPUT COLUMN

OUTPUT **LIST FOUND VALUES (A,B,C)**

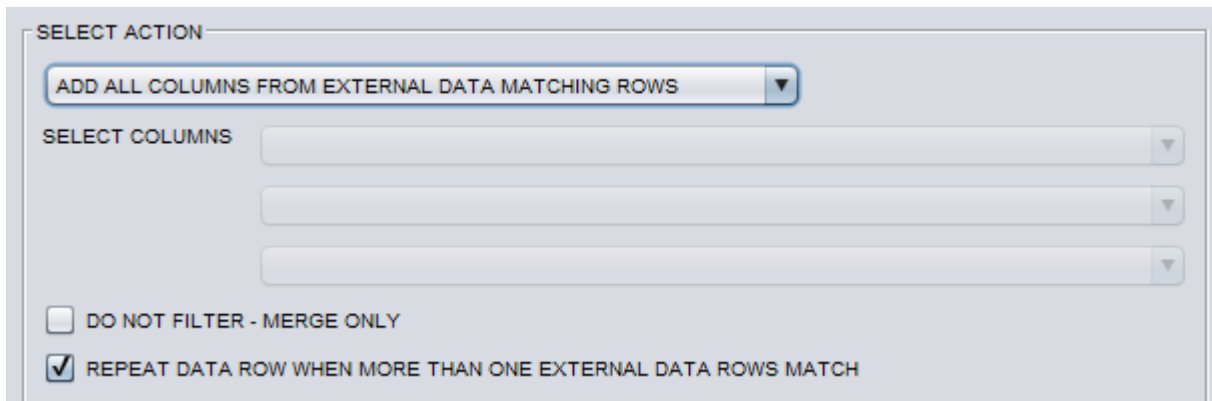
☐ ADD COLUMN

INPUT COLUMN

OUTPUT **LIST FOUND VALUES (A,B,C)**

While merging files together, all rows from the main file that do not have matching data in the external file, will be filtered out and thus not visible. To keep all rows from the main file the **DO NOT FILTER – MERGE ONLY** option is useful. If the checkbox is marked, to every

row from the main file which does not have any matching data in the external file, empty fields will be inserted in places corresponding to columns from the external file. This option is available for both adding actions – **ADD ALL COLUMNS FROM EXTERNAL DATA MATCHING ROWS** and **ADD SELECTED COLUMNS FROM EXTERNAL DATA MATCHING ROWS**.



SELECT ACTION

ADD ALL COLUMNS FROM EXTERNAL DATA MATCHING ROWS ▼

SELECT COLUMNS

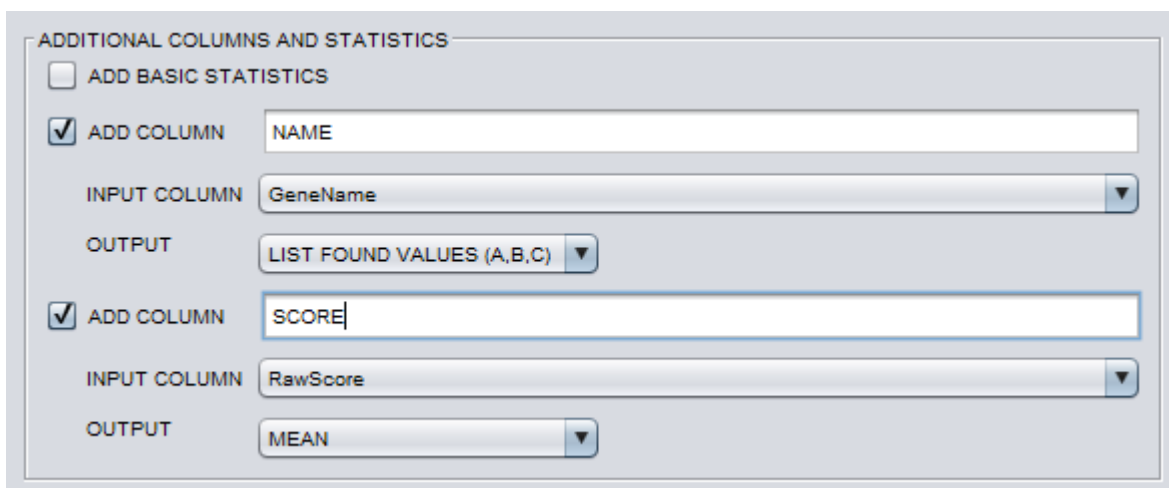
DO NOT FILTER - MERGE ONLY ☐

REPEAT DATA ROW WHEN MORE THAN ONE EXTERNAL DATA ROWS MATCH ☒

REPEAT DATA WHEN MORE THAN ONE EXTERNAL DATA ROWS MATCH checkbox is automatically marked while selecting the merging action. This option is designed to highlight the repeated occurrence of the same data row in the external file(s) – when two or more matching data rows (based on the condition and set of columns) are found in external dataset they will be repeated also after combining the data. If this option is inactive, only the first occurrence of matching data in external file, will be shown.

8.4.2.5 ADDITIONAL COLUMNS AND STATISTICS subfield

This subfield facilitates adding further information to the newly created in this form dataset.



ADDITIONAL COLUMNS AND STATISTICS

ADD BASIC STATISTICS ☐

ADD COLUMN ☒ NAME

INPUT COLUMN GeneName ▼

OUTPUT LIST FOUND VALUES (A,B,C) ▼

ADD COLUMN ☒ SCORE

INPUT COLUMN RawScore ▼

OUTPUT MEAN ▼

The **ADD COLUMN** checkbox enables appending a single column from external file to existing dataset. Any column, containing the data of interest, can be chosen, even that is not directly related to the main column(s) from the **SELECT COLUMNS AND CONDITION** field.

In the **NAME** entry field the title of the new column has to be entered. Then, from the **INPUT COLUMN** pull down list, one column from the external file is selected. Finally, the **OUTPUT** pull down list specifies the way of presenting the data from matching rows. There are four different possibilities:

- **LIST FOUND VALUES (A,B,C)** – if there is more than one matching result, all of them will be listed, separated with commas.
- **LIST FOUND VALUES (A;B;C)** – all of matching results will be listed, separated with semicolons.
- **MEAN** – the mean value of matching results will be calculated and presented if the data format is appropriate.
- **MEDIAN** – the median value of matching results will be calculated and presented if the data format is appropriate.

The described functions were used in example 1 and 2 (stage 9) in S2 Text. All needed example files were deposited on Open Science Framework (<https://osf.io/pw2dx/>) and are publicly available. **EXTERNAL DATA FILTER/MERGER (LOCATION)**

EXTERNAL DATA FILTER/MERGER (LOCATION) form is very similar to the **EXTERNAL DATA FILTER/MERGER** as it also enables two main actions, but they are performed only taking the locus data into account:

- Filtering the main file, namely particular column(s), on the basis of up to four columns from the additional file.
- Merging the matching data from external file(s) with the main file.

QUERY SETUP

DATA PREPROCESSING SIMPLE FILTER LOCATION FILTER EXTERNAL DATA FILTER / MERGER EXTERNAL DATA FILTER / MERGER (LOCATION) SAMPLE FILTER

QUERY NAME: EXTERNAL DATA FILTER / ME

QUERY DESCRIPTION:

SELECT COLUMN OR CREATE LOCUS

MULTIPLE COLUMN LOCUS

MULTIPLE COLUMN LOCUS

CHROMOSOME COLUMN

START POSITION COLUMN

STOP POSITION COLUMN

STOP POSITION = START POSITION +

PREVIEW

CHROMOSOME: OTHER DATA

START POS.: OTHER DATA

STOP POS.: OTHER DATA

SELECT COLUMN OR CREATE LOCUS (EXTERNAL DATA)

MULTIPLE COLUMN LOCUS

MULTIPLE COLUMN LOCUS

CHROMOSOME COLUMN

START POSITION COLUMN

STOP POSITION COLUMN

STOP POSITION = START POSITION +

SHOW DATA

CONDITION

OVERLAPS AT LEAST 0 % OF MAIN DATA LOCATION

SELECT ACTION

FILTER ONLY

SELECT COLUMNS

DO NOT FILTER - MERGE ONLY

REPEAT DATA ROW WHEN MORE THAN ONE EXTERNAL DATA ROWS MATCH

ADDITIONAL COLUMNS AND STATISTICS

ADD BASIC STATISTICS

ADDITIONAL COLUMN NAME

INPUT COLUMN

OUTPUT LIST FOUND VALUES (A,B,C)

ADDITIONAL COLUMN NAME

INPUT COLUMN

OUTPUT LIST FOUND VALUES (A,B,C)

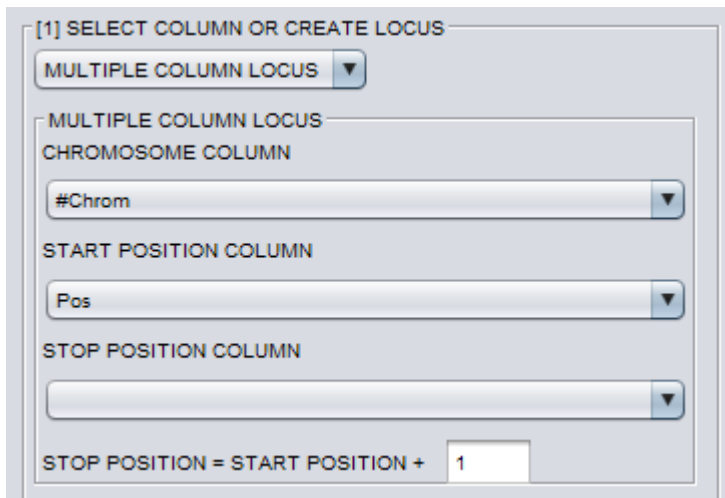
ADD QUERY Cancel

8.4.2.6 SELECT COLUMN OR CREATE LOCUS field

This field works in the same way as in **LOCATION FILTER** form. It is created to set the format of location data using one of the two ways available in the pull down menu:

- Using **MULTIPLE COLUMN LOCUS** – indicate which columns (presented in the pull down lists) refer to the number of the chromosome (**CHROMOSOME COLUMN**), start position (**STARTING POSITION COLUMN**) and stop position (**STOP POSITION COLUMN**), respectively.

Alternatively, the stop position can be created by adding any number to the start position. Therefore all loci will have the same length (**STOP POSITION = START POSITION + ...**).



[1] SELECT COLUMN OR CREATE LOCUS

MULTIPLE COLUMN LOCUS ▼

MULTIPLE COLUMN LOCUS

CHROMOSOME COLUMN

#Chrom ▼

START POSITION COLUMN

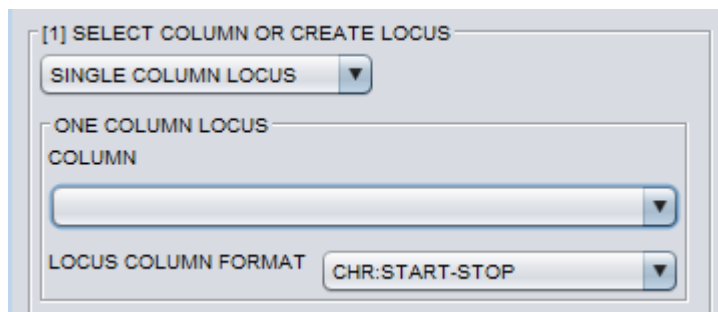
Pos ▼

STOP POSITION COLUMN

▼

STOP POSITION = START POSITION + 1

- Using **SINGLE COLUMN LOCUS** – indicate, which column contains complete information about the locus and then choose its format from the pull down list (**LOCUS COLUMN FORMAT**). Four different formats are available:
 - ✓ Chromosome: start – stop.
 - ✓ Chromosome start stop.
 - ✓ Chromosome – start – stop.
 - ✓ Chromosome: start : stop.



[1] SELECT COLUMN OR CREATE LOCUS

SINGLE COLUMN LOCUS ▼

ONE COLUMN LOCUS

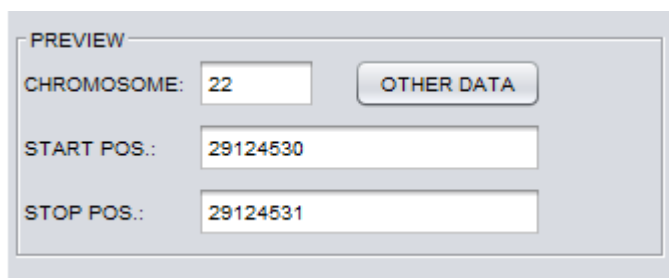
COLUMN

▼

LOCUS COLUMN FORMAT

CHR:START-STOP ▼

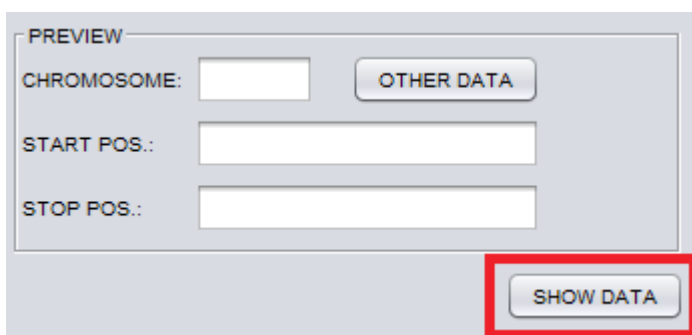
PREVIEW subfield, located below, displays the preview of locus data based on the one randomly chosen row. The other exemplary rows can be drawn by clicking the **OTHER DATA** button.

A screenshot of a web interface titled "PREVIEW". It contains three input fields: "CHROMOSOME:" with the value "22", "START POS.:" with the value "29124530", and "STOP POS.:" with the value "29124531". To the right of the "CHROMOSOME:" field is a button labeled "OTHER DATA".

8.4.2.7 SELECT COLUMN OR CREATE LOCUS (EXTERNAL DATA) field

This field refers to setting the format of location data in the external data file(s). All options operate as in the previous field (**SELECT COLUMN OR CREATE LOCUS**).

The additional button, called **SHOW DATA**, displays the preview of the external dataset to facilitate the choice of proper columns.

A screenshot of a web interface titled "PREVIEW". It contains three input fields: "CHROMOSOME:", "START POS.:", and "STOP POS.:". To the right of the "CHROMOSOME:" field is a button labeled "OTHER DATA". Below the input fields, there is a button labeled "SHOW DATA" which is highlighted with a red rectangular border.

8.4.2.8 CONDITION field

CONDITION field consists of four pull down lists to determine subsequent processing criteria.

The first one is used to choose if the main file will be analyzed for overlapping or containing certain location data as there are four options – **OVERLAPS**, **DOES NOT OVERLAP**, **CONTAINS**, **DOES NOT CONTAIN**.

Containing refers to fully lying inside the particular location and overlapping to lying even partially.

The second pull down list refers to the scope of the overlap or containing – **AT LEAST** and **AT MOST** are the alternatives here.

The third one enables selection of the percentage value from 0 to 100 for **AT LEAST** or **AT MOST** option.

The last pull down menu is to choose the objective of the condition – location data from the main file (**MAIN DATA LOCATION**), from the external file (**EXTERNAL DATA LOCATION**) or including both of these datasets (**BOTH**). **BOTH** option is built up of two loops of analysis – the first one filters the main file and then the second one searches for matching data among them.

CONDITION

OVERLAPS (selected) | AT LEAST (selected) | 25 (selected) % OF | MAIN DATA LOCATION (selected)

OVERLAPS
DOES NOT OVERLAP
CONTAINS
DOES NOT CONTAIN

AT LEAST
AT MOST

0
5
10
15
20
25 (selected)
30
35

MAIN DATA LOCATION
EXTERNAL DATA LOCATION
BOTH

8.4.2.9 SELECT ACTION field

The **SELECT ACTION** subfield is identical with that present in **EXTERNAL DATA FILTER/MERGER** form and is intended to determine the data processing operation. The major step is to select one of three following alternatives:

- **FILTER ONLY** – data from the main file will be filtered on the basis of previously chosen condition and set of columns from the external file(s).
- **ADD ALL COLUMNS FROM EXTERNAL DATA MATCHING ROWS** – all previously selected columns that contain information matching defined criteria will be appended to the input dataset.
- **ADD SELECTED COLUMNS FROM EXTERNAL DATA MATCHING ROWS** – only selected columns from matching rows will be appended to the input dataset. Here, the **SELECT COLUMNS** subfield is active to choose up to three columns using pull down lists.

SELECT ACTION

FILTER ONLY ▼

SELECT COLUMNS ▼
 ▼
 ▼

☐ DO NOT FILTER - MERGE ONLY

☐ REPEAT DATA ROW WHEN MORE THAN ONE EXTERNAL DATA ROWS MATCH

ADDITIONAL COLUMNS AND STATISTICS

☐ ADD BASIC STATISTICS

☐ ADD COLUMN

INPUT COLUMN ▼

OUTPUT **LIST FOUND VALUES (A,B,C)** ▼

☐ ADD COLUMN

INPUT COLUMN ▼

OUTPUT **LIST FOUND VALUES (A,B,C)** ▼

While merging files together, all rows from the main file that do not have matching data in the external file, will be filtered out and thus not visible. To keep all rows from the main file the **DO NOT FILTER – MERGE ONLY** option is useful. If the checkbox is marked, to every row from the main file which does not have any matching data in the external file, empty fields will be inserted in places corresponding to columns from the external file. This option is available for both adding actions – **ADD ALL COLUMNS FROM EXTERNAL DATA MATCHING ROWS** and **ADD SELECTED COLUMNS FROM EXTERNAL DATA MATCHING ROWS**.

SELECT ACTION

ADD ALL COLUMNS FROM EXTERNAL DATA MATCHING ROWS ▼

SELECT COLUMNS ▼
 ▼
 ▼

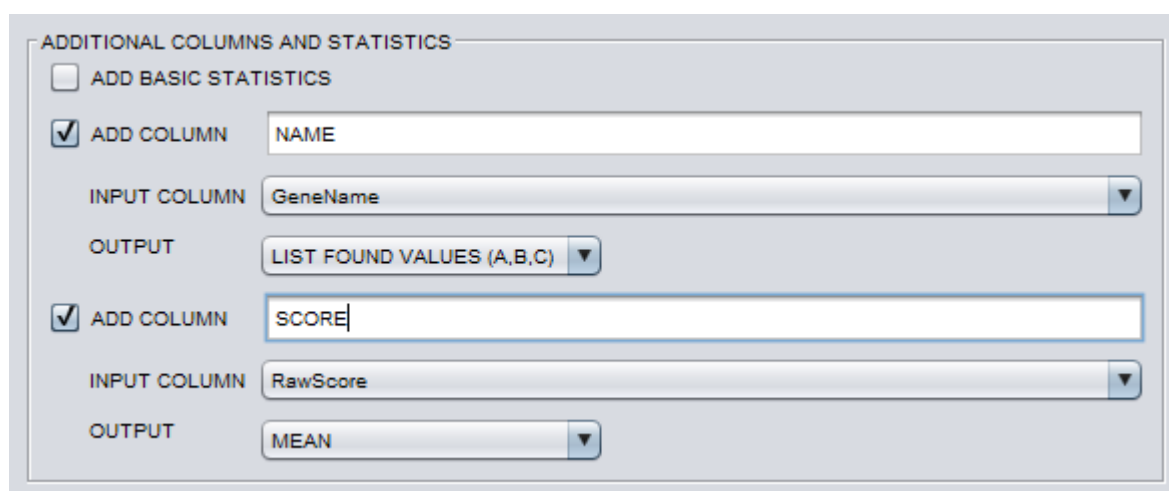
☐ DO NOT FILTER - MERGE ONLY

☒ REPEAT DATA ROW WHEN MORE THAN ONE EXTERNAL DATA ROWS MATCH

REPEAT DATA WHEN MORE THAN ONE EXTERNAL DATA ROWS MATCH checkbox is automatically marked while selecting the merging action. This option is designed to highlight the repeated occurrence of the same data row in the external file(s) – when two or more matching data rows (based on the condition and set of columns defining a locus) are found in external dataset they will be repeated also after combining the data. If this option is inactive, only the first occurrence of matching data in external file, will be shown.

8.4.2.10 ADDITIONAL COLUMNS AND STATISTICS subfield

ADDITIONAL COLUMNS AND STATISTICS subfield facilitates adding further information to the newly created in this form dataset.



The screenshot shows a software interface titled "ADDITIONAL COLUMNS AND STATISTICS". It contains two main sections. The first section has a checkbox labeled "ADD BASIC STATISTICS" which is unchecked. Below it is a checked checkbox labeled "ADD COLUMN". To the right of this checkbox is a text input field containing the word "NAME". Below the text field are two dropdown menus: "INPUT COLUMN" with "GeneName" selected, and "OUTPUT" with "LIST FOUND VALUES (A,B,C)" selected. The second section also has a checked checkbox labeled "ADD COLUMN". To its right is a text input field containing the word "SCORE". Below this text field are two more dropdown menus: "INPUT COLUMN" with "RawScore" selected, and "OUTPUT" with "MEAN" selected.

If **ADD BASIC STATISTICS** checkbox is active, an extra column will be added to the dataset – containing the overall number of external data rows that matches the main file based on the chosen column(s) and condition.

The **ADD COLUMN** checkbox enables appending a single column from external file to existing dataset. Any column, containing the data of interest, can be chosen, even that is not directly related to the main column(s) from the **SELECT COLUMNS AND CONDITION** field.

In the **NAME** entry field the title of the new column has to be entered. Then, from the **INPUT COLUMN** pull down list, one column from the external file is selected. Finally, the **OUTPUT** pull down list specifies the way of presenting the data from matching rows. There are four different possibilities:

- **LIST FOUND VALUES (A,B,C)** – if there is more than one matching result, all of them will be listed, separated with commas.

- **LIST FOUND VALUES (A;B;C)** – all of matching results will be listed, separated with semicolons.
- **MEAN** – the mean value of matching results will be calculated and presented if the data format is appropriate.
- **MEDIAN** – the median value of matching results will be calculated and presented if the data format is appropriate.

The described functions were used in example 1, 2 (stage 2), 3 (stage 3,6 and 7) and 4 (stage 4) in S2 Text. All needed example files were deposited on Open Science Framework (<https://osf.io/pw2dx/>) and are publicly available. **SAMPLE FILTER**

The last form from the **QUERY SETUP** window is designed for filtering with regard to differences in samples.

Here, sample is an individual object that can be defined by up to four columns from **SAMPLE COLUMNS** pull down lists. Columns, that will be examined, have to be chosen using **ANALYSED COLUMNS** pull down lists. Also, the maximal number of columns is four.

In order to specify the query, the **QUERY** subfield is located below. The first pull down list is intended for the selection of the condition – **is present**, **is not present**, **select largest**, **select smallest**. In case of the presence/absence condition – the second pull down list is to choose the percentage of samples (**from 1 to 100%**) for it.

QUERY

is present ▼	IN	100 ▼	% OF SAMPLES	[0/0 SAMPLES]
is present				
is not present				
select largest				
select smallest				

The described functions were used in example 1 in S2 Text. All needed example files were deposited on Open Science Framework (<https://osf.io/pw2dx/>) and are publicly available.

8.5 GENERATING REPORT

After setting the filtering parameters in the **QUEUE** field, the analysis will be carried out with the click on **GENERATE REPORT** button from the main view or **Edit > Generate report** in the main menu.

REPORT PREVIEW																
ROW_NO	FILE_ROW_NO	FILE_NO	FILE_NAME	#Chrom	Pos	Ref	Anc	Alt	Consequ...	ConsDetail	GeneName	RawScore	Cscore	Intronic_a...	Synonymr	
1355	441	1	BC_genes_C...	22	29121013	G	G	T	NON_SY...	missense...	CHEK2	2,932784	15,77	#ND!	#ND!	
1356	442	1	BC_genes_C...	22	29121018	C	C	T	NON_SY...	missense...	CHEK2	1,964469	12,53	#ND!	#ND!	
1357	443	1	BC_genes_C...	22	29121019	G	G	A	NON_SY...	missense...	CHEK2	3,371204	17,36	#ND!	#ND!	
1358	444	1	BC_genes_C...	22	29121087	A	A	G	NON_SY...	missense...	CHEK2	4,093588	21,1	#ND!	#ND!	
1424	510	1	BC_genes_C...	22	29126425	C	C	T	NON_SY...	missense...	CHEK2	-1,914662	0,008	#ND!	#ND!	
1466	552	1	BC_genes_C...	22	29130456	G	G	A	NON_SY...	missense...	CHEK2	1,814893	12,03	#ND!	#ND!	
1468	554	1	BC_genes_C...	22	29130637	C	C	T	NON_SY...	missense...	CHEK2	0,485389	6,634	#ND!	#ND!	
1469	555	1	BC_genes_C...	22	29130657	C	C	T	NON_SY...	missense...	CHEK2	1,360916	10,48	#ND!	#ND!	
1615	23	2	BC_genes_TP...	17	7573948	C	C	G	NON_SY...	missense...	TP53	-1,595425	0,014	#ND!	#ND!	
1647	55	2	BC_genes_TP...	17	7576911	G	G	C	NON_SY...	missense...	TP53	1,539529	11,1	#ND!	#ND!	
1653	61	2	BC_genes_TP...	17	7577046	C	C	T	NON_SY...	missense...	TP53	2,258414	13,51	#ND!	#ND!	
1654	62	2	BC_genes_TP...	17	7577069	C	C	T	NON_SY...	missense...	TP53	0,804706	8,231	#ND!	#ND!	

FILES [ALL]: 4 FILES [FOUND]: 4 DATA ROWS [ALL]: 2055 DATA ROWS [FOUND]: 111 ANALYSIS TIME: N/A [1] MEMORY [FREE / AVAILABLE]: 13.0 GIB / 15.7 GIB

Idle...

CANCEL

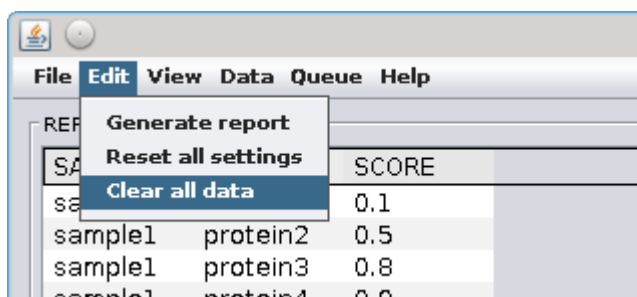
GENERATE REPORT

SAVE REPORT

8.6 CANCELLING OF INTRODUCED CHANGES

To restore the data to the original layout, the **Reset all settings** option from the **Edit** pull down menu should be used.

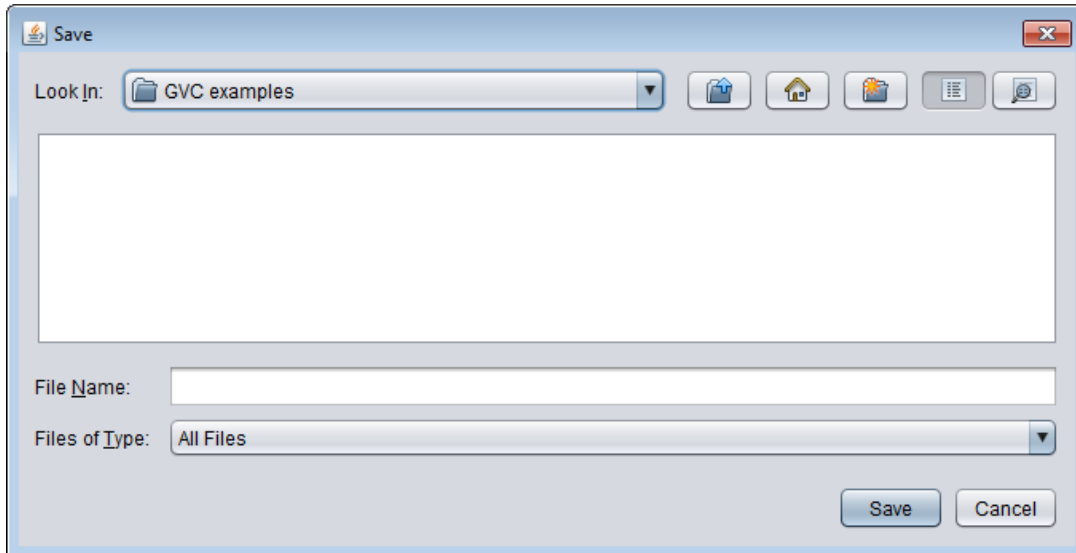
It does not apply to permanently introduced changes – namely using **MODIFY CONTENT** and **RENAME** functions in **COLUMN MANAGER** window (see 8.3.1.1 COLUMN PROPERTIES subfield section) as well as all data modifications set in the **INPUT DATA PREPROCESSING** field from the **SIMPLE FILTER** tab (see 8.4.1.2 INPUT DATA PREPROCESSING field).



8.7 SAVING FILTERED FILE(S)

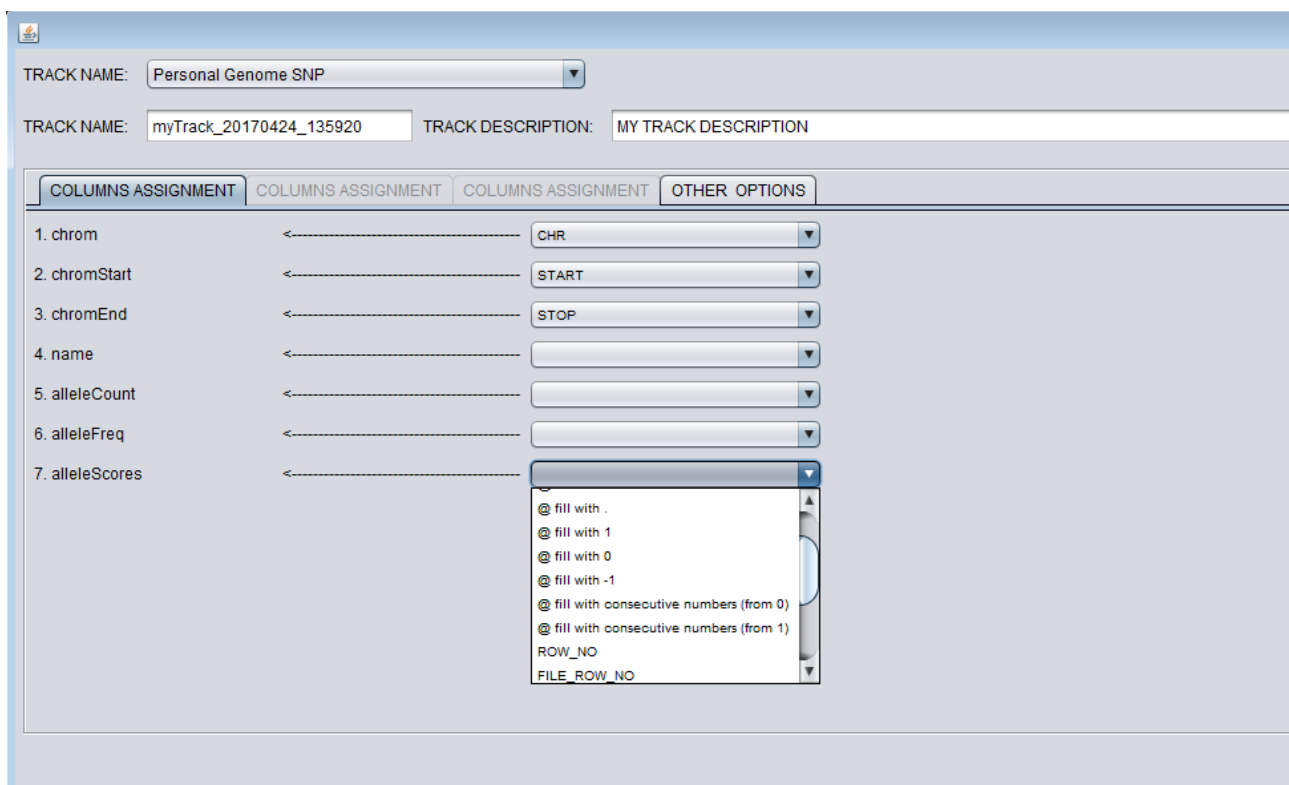
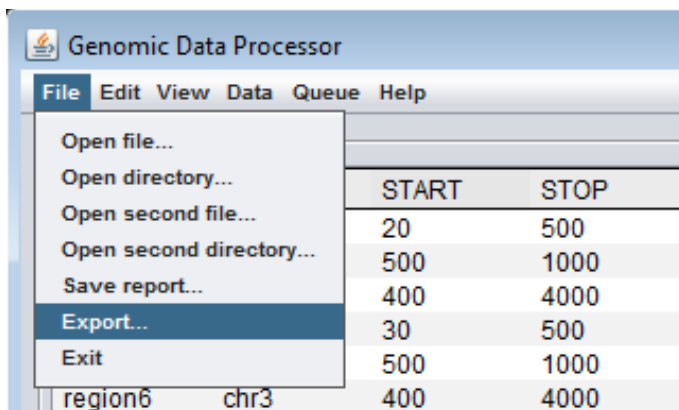
The filtered data can be saved to the output file by clicking the **SAVE REPORT** button in the main window or **File > Save Report** in pull down menu.

In the Save window the file directory and name are specified. The file is saved in table delimited format only.



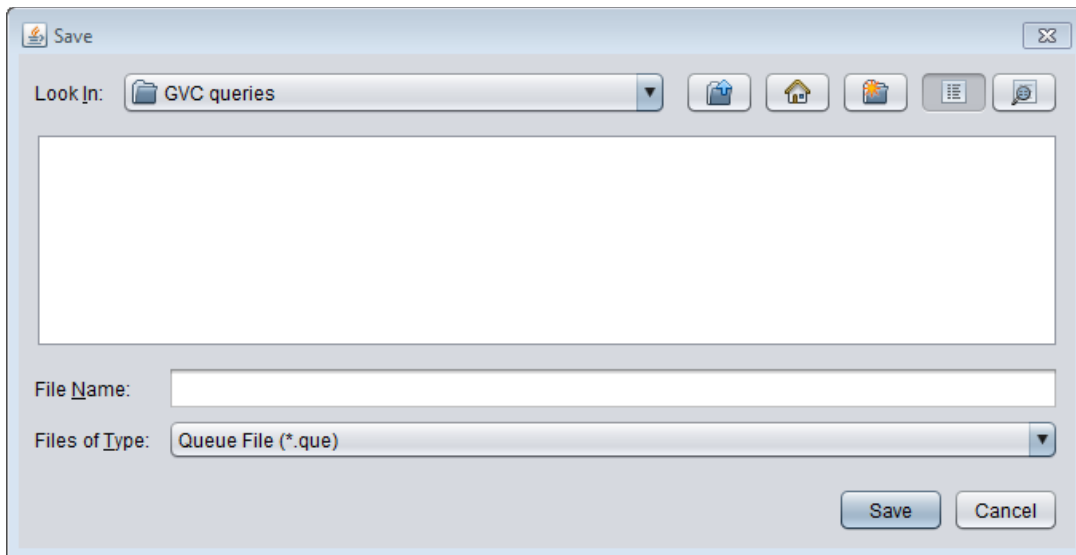
8.8 EXPORTING FILTERED FILE(S)

The filtered data can be exported to many formats (BED, BED detail, PSL, GFF, Personal Genome SNP, ENCODE RNA elements: BED6 + 3 scores, ENCODE narrowPeak: Narrow (or Point-Source) Peaks, ENCODE broadPeak: Broad Peaks (or Regions), ENCODE gappedPeak: Gapped Peaks (or Regions), ENCODE peptideMapping: BED6+4). Detailed formats description: <https://genome.ucsc.edu/FAQ/FAQformat.html>). Export can be done by clicking the **File > Export...** in pull down menu. Data columns should be assigned to the format-specific, required columns names before data exporting. Only assigned data columns are exported.



8.9 SAVING QUERIES

Every implemented set of filtering parameters can be saved for further analyses. For this purpose select **Queue > Save** in pull down menu in the main window. In the **Save** window the query file directory and name are specified. The file is saved in the internal format (.que extension).



8.10 LOADING QUERIES

Previously saved query can be loaded by selecting **Queue > Load**. The Load queue file window is opened to point to the particular directory with .que file.

To successfully use the queue file, it should be consistent with previously loaded data, particularly in terms of columns' names.

