

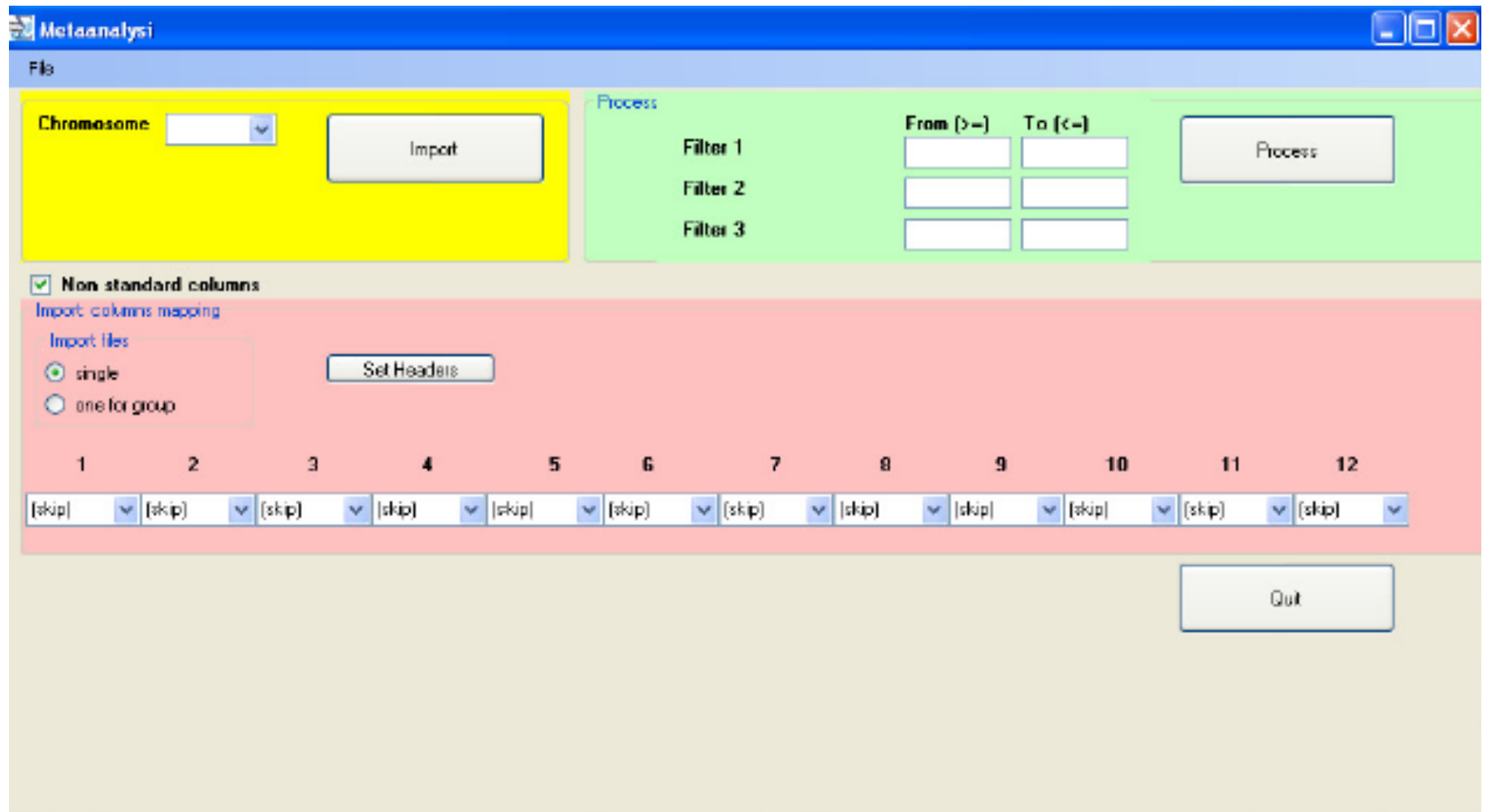
Meta-analysis tool

Installing the tool

- The meta-analysis tool can be downloaded from the TreatOA website (www.treatoa.eu)
- To install, double click on 'Metanalisi.exe'
- Select 'run' and decide in which directory you wish the programme to be installed
- The tool will open automatically upon successful installation

NOTE

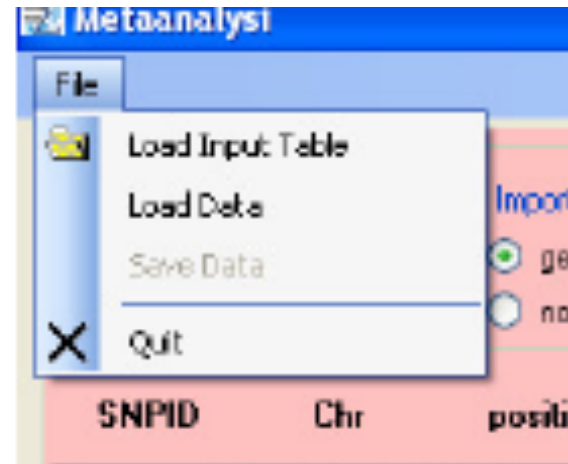
Keep [output.empty](#), [metanalisi.empty](#) and [HanEskinPvalueTable.txt](#) in the application folder!



The Meta-analysis Tool

Format of files to import

- Load Data imports from a pre-existing database (.mdb)
- Load input table allows importation of **single** and **multiple** files
- Tab or space delimited
- Two import modes
 - Standard
 - Custom



Importing: Columns

Compulsory columns:

1. SNP (the unique identifier of the row)
2. Beta
3. SE (Non numeric data will lead to the automatic skipping of the line with no warning given)

If a compulsory column is missing from one of the files a warning is issued and the import procedure will abort.

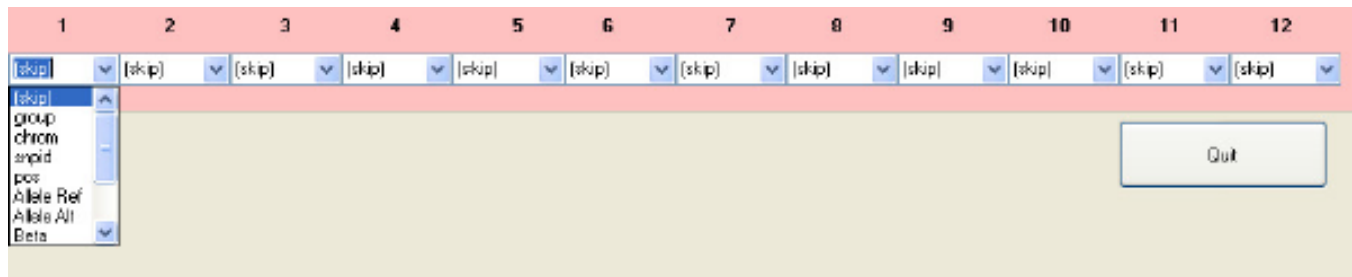
Optional columns:

1. Group (specifies the population in the case of a single file import)
2. CHR (Chromosome)
3. POS (Position)
4. EFFECT_ALLELE (Effect allele (REF))
5. NON_EFFECT_ALLELE (Non effect allele (ALT))

If an optional column is missing in any file the import is not affected, and no warning is given.

Selecting columns

- Use the red box (below) to specify which column you are using



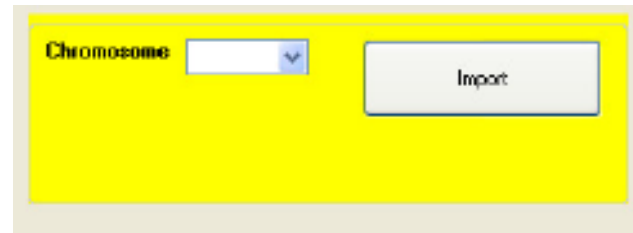
- Each column has a drop down menu to select from (skip, group, chr, snpid, pos, ref_allele, alt_allele, beta, SE, Filters1,2,3)

Single input files

- In the custom columns format it is possible to have a single input file rather than multiple input files
- With a single input file the group information (i.e. Population) should be contained in a column
- with multiple input files the group name is assumed to be the name of the input file

Multiple input files

- All “.txt” files contained in the chosen directory will be imported (one file per population (aka ‘group’))
- It is also possible to filter by chromosome: only the data of the chosen chromosome will be imported (useful to avoid memory issues)



- In a custom import of multiple datasets, the columns in each of the files must be in the same order otherwise a warning is issued. You can abort or keep going if you consider the variation in the header text irrelevant
- If effect (REF) and non effect (ALT) alleles are imported, the program will issue a warning in the case of two different files showing a different REF-ALT pair at the same position **but** the import procedure will not be interrupted

Applying filters

The screenshot shows a user interface for applying filters. It features a light green background with a title 'Process' in blue text at the top left. Below the title, there are three rows labeled 'Filter 1', 'Filter 2', and 'Filter 3'. Each row has two input fields: 'From (>=)' and 'To (<=)'. To the right of these input fields is a grey button labeled 'Process'.

- You can apply up to **three** filters
 1. Select these from the red box with a list of columns
 2. In the green box (above) choose the range you wish to retain
 3. Click 'process' to apply the selected filters

Processing the imported data

- Processing will use the tabulated PValues from the HanEskinPvalueTable.txt
- It is possible to load another PValues table using the file menu prior to processing
- If filters have been selected, these will be applied during the processing phase
- Results will be displayed in a data grid

Exporting the processed data

- **Cut and paste**

Into any program direct from the data grid

- **Access**

The program will ask for a location for the output and generate an .mdb access 2000 database format containing a Tab results table filled with the output.

NOTE

Please note that the output.empty model access DB should be in the program directory for this export to work

- **Excel**

Export directly into an Excel worksheet. Microsoft Excel should be installed in the computer for this option to work

- **Text**

Export to a tab delimited text file. If an existing file is chosen it will be overwritten

The web-based version

META ANALYSIS TOOL

Home

About

BROWSE TO YOUR INPUT FILES #ID LO-D THEN ONE AT A TIME. PRESS IMPORT DONE WHEN FINISHED

Chromosome: 9

Browse...

Import file into meta analysis tool

Import done

Custom Columns

**The online version follows the same format as
described for the stand alone tool**

NOTE

Select the chromosome AFTER files have been imported!!

Customising columns

META ANALYSIS TOOL

Home About

Import files: single one for each group

Browse...

| SNPID | Chr | position | coded_all | noncoded_all | strand_genome | Beta | SE | Pval | AF_coded_all |
|----------|----------|----------|-----------|--------------|---------------|----------|----------|----------|--------------|
| (skip) ▾ | (skip) ▾ | (skip) ▾ | (skip) ▾ | (skip) ▾ | (skip) ▾ | (skip) ▾ | (skip) ▾ | (skip) ▾ | (skip) ▾ |

Done **Restart** **Standard Columns**

PRESS DONE WHEN FINISHED SETTING COLUMNS FORMAT

Memory Issues

- The computations are all done in memory
- Loading huge input files can lead to out of memory exceptions
- The only workaround for out of memory situations is
 - to process the file on a machine with more hardware resources
 - to split the input file and process it independently