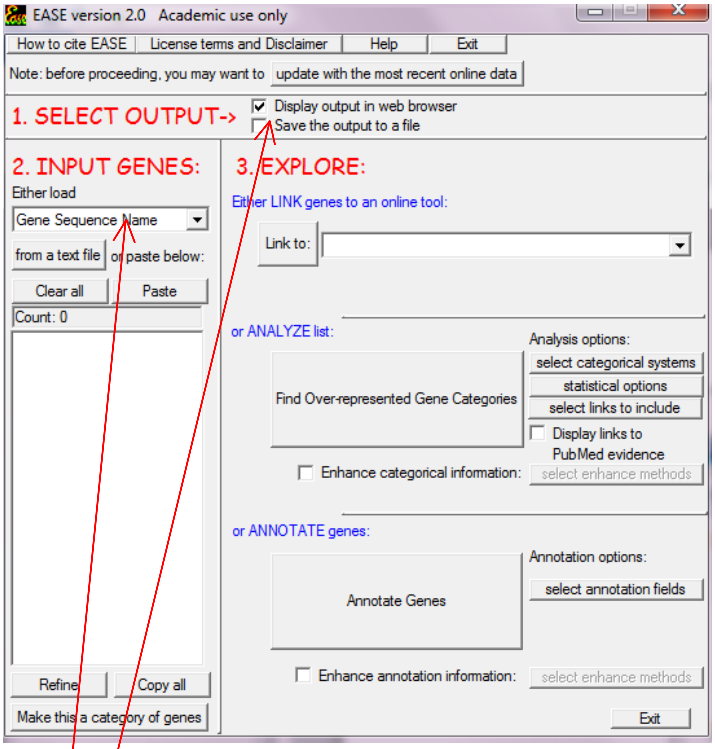
How to use EASE and EASE manager

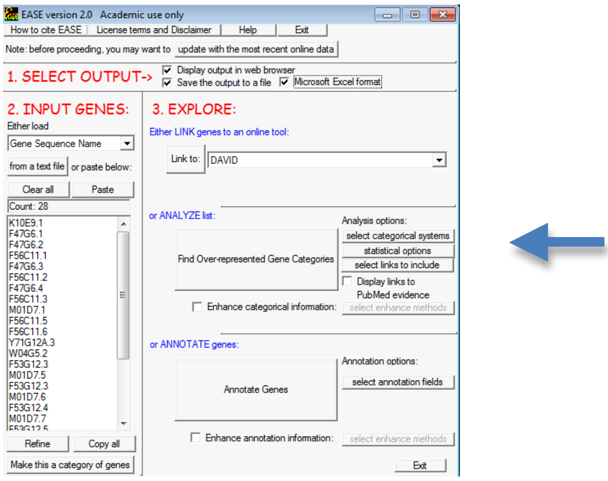
1. Using EASE

EASE is a complicated application with many options. This document does not in any way aim to explain all the possibilities EASE offers, but rather is a quick guide to one simple analysis method. **EASE is a third-party application for which we have absolutely no responsibility**. Please refer to the EASE “Help” pages for more detailed advice. To start, in the folder “EASE” double click on the application EASE. The following window will appear:



☑ Display output in web browser
☐ Save the output to a file
Gene Sequence Name
Count: 0

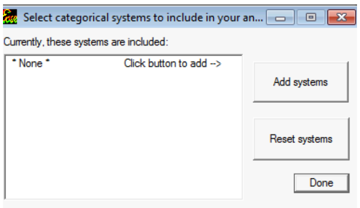
1. Choose your output (you can save it as an excel file)
2. Paste your input gene list (i.e. your genes of interest) and chose the format of the gene names



☑ Display output in web browser
☑ Save the output to a file ☑ Microsoft Excel format
Gene Sequence Name
Count: 28
K10E9.1
F47G6.1
F47G6.2
F56C11.1
F47G6.3
F56C11.2
F47G6.4
F56C11.3
M01D7.1
F56C11.5
F56C11.6
Y71G12A.3
W04G5.2
F53G12.3
M01D7.5
F53G12.3
M01D7.6
F53G12.4
M01D7.7
Link to: DAVID

3. Select your annotation list (categorical systems)

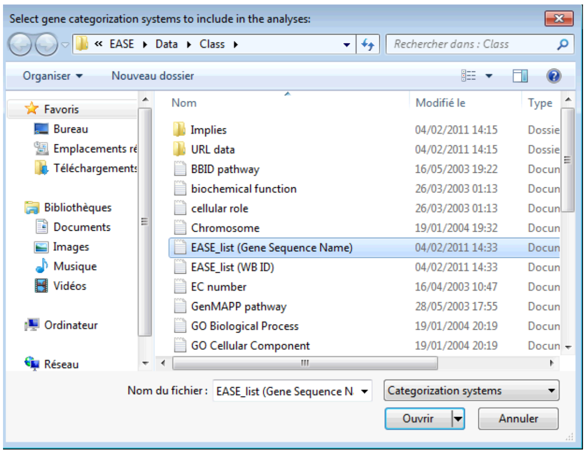
This brings up this box:


Select categorical systems to include in your an...

Currently, these systems are included:

* None * Click button to add -->

Click “Add systems” and you should have a dialogue box like this:


Select gene categorization systems to include in the analyses:

« EASE ▸ Data ▸ Class ▸

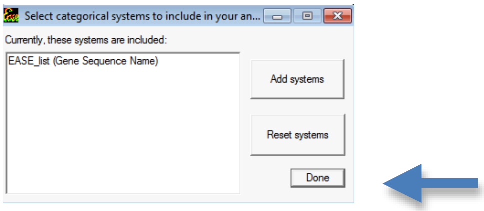
Rechercher dans : Class

Nom	Modifié le	Type
Implies	04/02/2011 14:15	Dossie
URL data	04/02/2011 14:15	Dossie
BBID pathway	16/05/2003 19:22	Docun
biochemical function	26/03/2003 01:13	Docun
cellular role	26/03/2003 01:13	Docun
Chromosome	19/01/2004 19:32	Docun
EASE_list (Gene Sequence Name)	04/02/2011 14:33	Docun
EASE_list (WB ID)	04/02/2011 14:33	Docun
EC number	16/04/2003 10:47	Docun
GenMAPP pathway	28/05/2003 17:55	Docun
GO Biological Process	19/01/2004 20:19	Docun
GO Cellular Component	19/01/2004 20:19	Docun

Nom du fichier : EASE_list (Gene Sequence N

Categorization systems

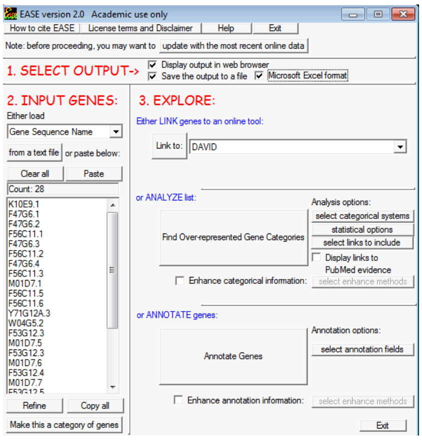
If you want to use your in-house bibliographic annotations, generated using EASE Manager and are using Gene Sequence Names, then click on “EASE_list (Gene Sequence Names)”. And then you can either “Add systems” to use other annotation lists, or just hit “Done”:


Select categorical systems to include in your an...

Currently, these systems are included:

EASE_list (Gene Sequence Name)

This takes you back to


EASE version 2.0 Academic use only

Note: before proceeding, you may want to update with the most recent online data

1. SELECT OUTPUT->
☑ Display output in web browser
☑ Save the output to a file ☑ Microsoft Excel format

2. INPUT GENES:

Either load

Gene Sequence Name

from a text file or paste below:

Count: 28

K10E9.1
F47G6.1
F47G6.2
F56C11.1
F47G6.3
F56C11.2
F47G6.4
F56C11.3
M01D7.1
F56C11.5
F56C11.6
Y71G12A.3
W04G5.2
F53G12.3
M01D7.5
F53G12.3
M01D7.6
F53G12.4
M01D7.7

3. EXPLORE:

Either LINK genes to an online tool:

Link to: DAVID

or ANALYZE list:

Analysis options:

☐ Display links to PubMed evidence

☐ Enhance categorical information:

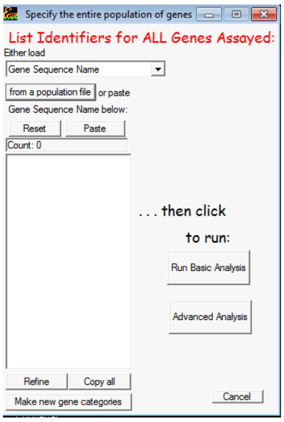
or ANNOTATE genes:

Annotation options:

☐ Enhance annotation information:

where for a simple analysis, after you have set the “statistical options”(e.g. Fisher exact for p values), you hit “Find Over-represented Gene Categories”.

This in turn brings up another window:


Specify the entire population of genes

List Identifiers for ALL Genes Assayed:

Either load

Gene Sequence Name

or paste

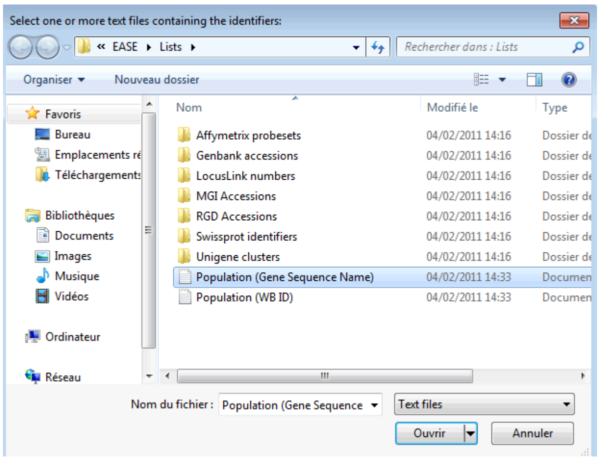
Gene Sequence Name below:

Count: 0

. . . then click

to run:

Clicking on “from a population file” (the list that the annotations of your input gene list are compared to) should give you this window:


Select one or more text files containing the identifiers:

« EASE ▸ Lists ▸

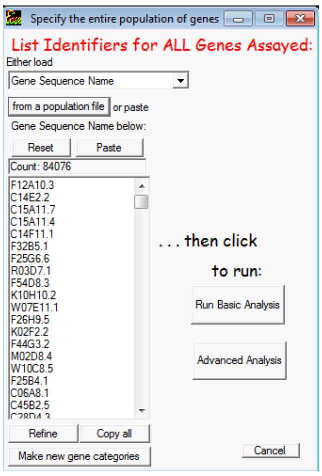
Rechercher dans : Lists

Nom	Modifié le	Type
Affymetrix probesets	04/02/2011 14:16	Dossier de
Genbank accessions	04/02/2011 14:16	Dossier de
LocusLink numbers	04/02/2011 14:16	Dossier de
MGI Accessions	04/02/2011 14:16	Dossier de
RGD Accessions	04/02/2011 14:16	Dossier de
Swissprot identifiers	04/02/2011 14:16	Dossier de
Unigene clusters	04/02/2011 14:16	Dossier de
Population (Gene Sequence Name)	04/02/2011 14:33	Documen
Population (WB ID)	04/02/2011 14:33	Documen

Nom du fichier : Population (Gene Sequence

Text files

If you are using Gene Sequence Names, click on “Population (Gene Sequence Names)”, which then will take you back to


Specify the entire population of genes

List Identifiers for ALL Genes Assayed:

Either load

Gene Sequence Name

or paste

Gene Sequence Name below:

Count: 84076

F12A10.3
C14E2.2
C15A11.7
C15A11.4
C14F11.1
F32B5.1
F25G6.6
R03D7.1
F54D8.3
K10H10.2
W07E11.1
F26H9.5
K02F2.2
F44G3.2
M02D8.4
W10C8.5
F25B4.1
C06A8.1
C45B2.5

. . . then click

to run:

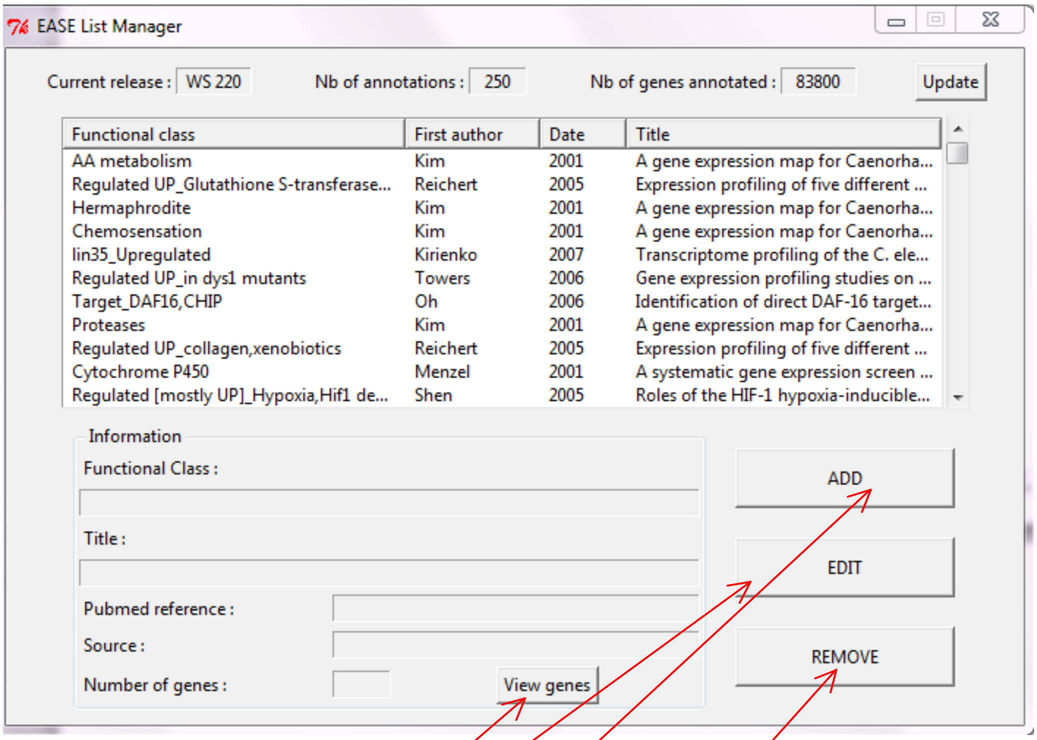
Click on “Run Basic Analysis”. You will be asked to name the result file and choose where to save it (if you selected “save as a file”). That’s it!

2. How to use EASE manager :

In the folder WBConverter__Client__Windows directory, double click on EASE manager.

The programme will connect to the server and update the bibliographic annotation list. A message will appear:

“Update in progress. Please wait.” Click ok and wait until you see the annotations in the window. The example below is our in-house list:



Current release : WS 220   Nb of annotations : 250   Nb of genes annotated : 83800

Functional class	First author	Date	Title
AA metabolism	Kim	2001	A gene expression map for Caenorha...
Regulated UP_Glutathione S-transferase...	Reichert	2005	Expression profiling of five different ...
Hermaphrodite	Kim	2001	A gene expression map for Caenorha...
Chemosensation	Kim	2001	A gene expression map for Caenorha...
lin35_Upregulated	Kirienko	2007	Transcriptome profiling of the C. ele...
Regulated UP_in dys1 mutants	Towers	2006	Gene expression profiling studies on ...
Target_DAF16,CHIP	Oh	2006	Identification of direct DAF-16 target...
Proteases	Kim	2001	A gene expression map for Caenorha...
Regulated UP_collagen,xenobiotics	Reichert	2005	Expression profiling of five different ...
Cytochrome P450	Menzel	2001	A systematic gene expression screen ...
Regulated [mostly UP]_Hypoxia,Hif1 de...	Shen	2005	Roles of the HIF-1 hypoxia-inducible...

You can now:

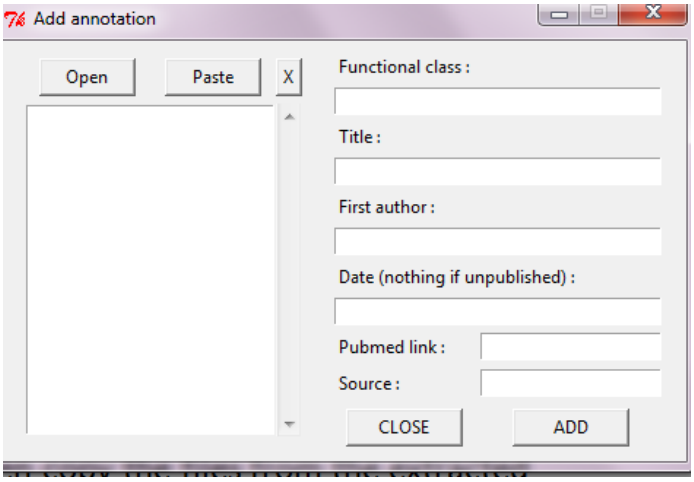
- look at the gene lists
- edit annotations
- remove annotation (password required*)
- add annotations

* By default the password is "admin_annot" (without the quotes); this can be changed if required by editing the “EASE Manager.py” file the at the line

elif (passwd.get() != "admin_annot") :

But don’t try unless you really know what you’re doing!

If you add annotations, a new window will open:



Fill in ALL the fields on the right. As ever, it is far, far easier to include this data at the start than at some later date. And without it, the gene lists cannot be checked, and may need to be deleted. For “functional class”, be as precise and infomative as possible. “Title” is the title of the paper from which the data has been taken. If the data has not been published, enter “Unpublished”. This is important for filtering the list. For the date, if unpublished, leave this blank, otherwise, just put in the year. Cut and paste the Pubmed URL, and in “Source” enter exactly where the data comes from (e.g. Table 3; Figure 1; Table S7; etc).

NB. You must avoid any special characters (eg: °, (as in 25°), quotes, carriage return, tab, etc) in the annotations (in the name of the publication, the author, etc). When you add an annotation, do check carefully that the text does not contain any non-standard alphanumerical characters. This is important!

Then paste your gene list. To be accurate, these **MUST be in WB ID format of the Freeze used by the current EASE list!** So use the Wormbase Converter first to get the correct format and version. You can copy and paste directly from Wormbase Converter to EASE Manager.

Click on “Add”. A message will inform you that the new annotations have been sent to the server Remember: Anything you alter will modify the list on the server!!!!