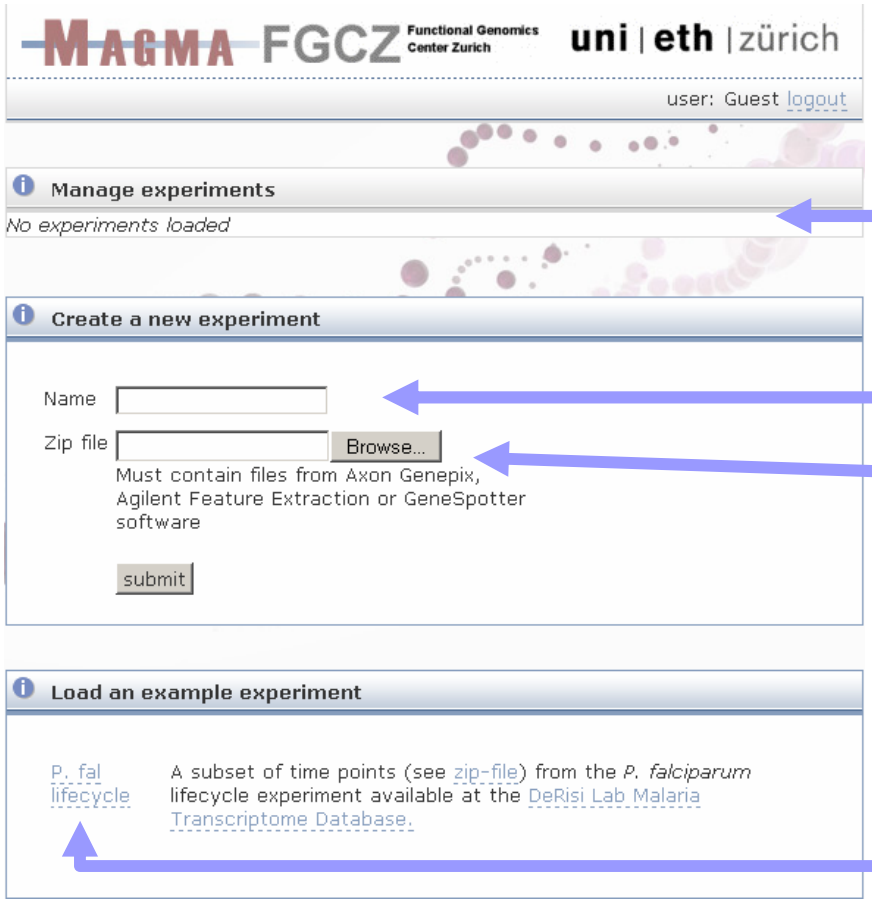
MAGMA

With MAGMA, lists of differentially expressed genes are generated in 4 simple steps:

- **Upload** – Provide the data files packed in a zip-file
- **Annotation** – Name the experimental conditions and assign them to the data files
- **Normalization** – Normalize the two channels in each file relative to each other; this step is optional
- **Analysis** – Select the conditions to compare and let Bioconductor's *limma* package find the differentially expressed genes using linear models

MAGMA
Manage Experiments Page

This page is presented to you after login.



At your first login you will not yet have any experiments

Create a new experiment by

giving it a name

providing a zip file that contains 2-Channel hybridization data; supported data formats Axon .gpr, Agilent .txt, and GeneSpotter .tbl files

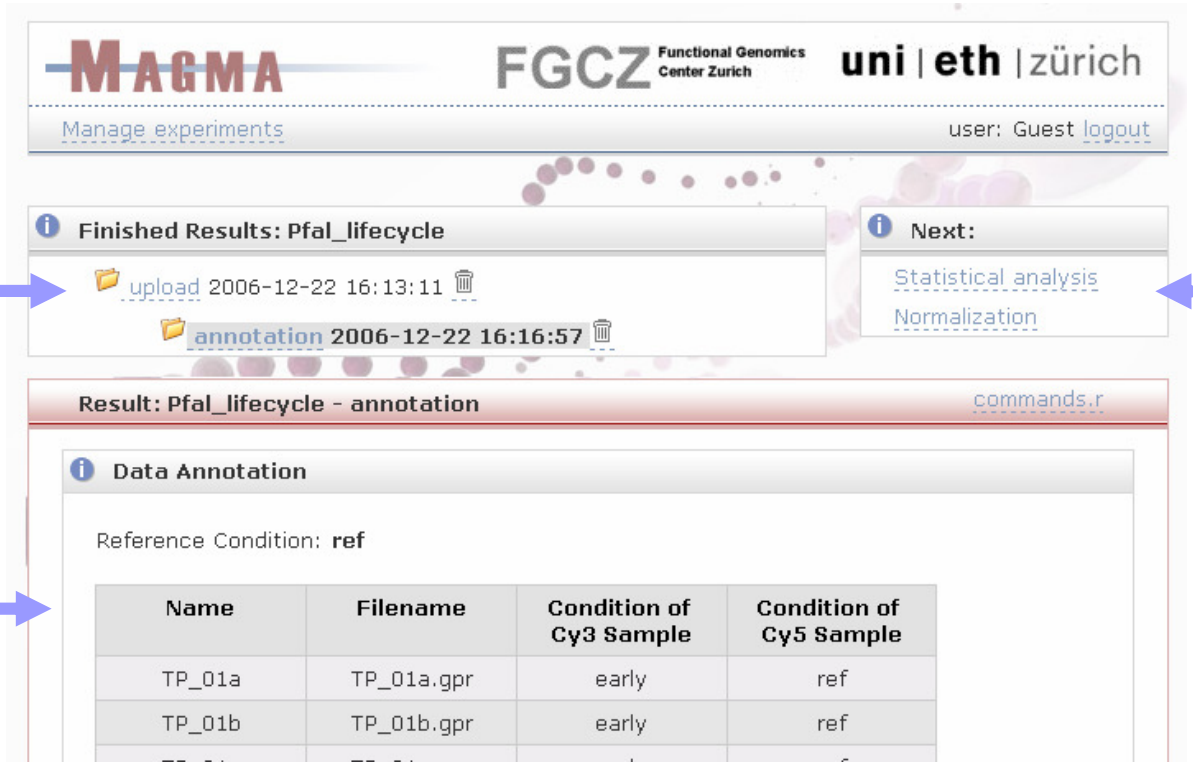
Alternatively have a look at an already processed example experiment

MAGMA
Standard Page Layout

Navigate to the results generated by the previous steps of your analysis

Select the Next processing step

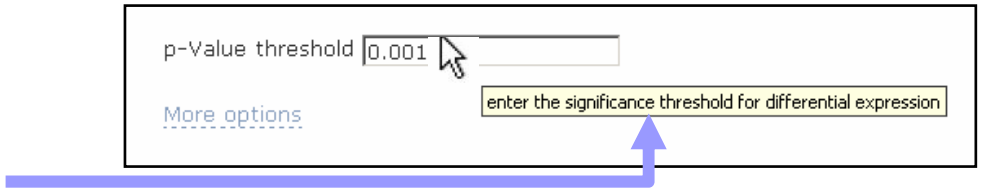
Browse the results of your current step



MAGMA
Getting Help

- PDF Documentation is available from: http://www.magma-fgcz.unizh.ch/pages/help/index.html

- Tooltip help: Moving your mouse over input fields shows up short tooltips



- Move the mouse pointer over the info icons in the title bars. This brings up short help paragraphs