

Gene List

Browse...

interesting-genes.txt

Upload complete

Your gene list must tab-delimited, with gene names in the first column

If no gene list is uploaded, the genes ESR1, AR and STAT3 will be used

If you want to analyse a single-gene, see the Quick Analysis tab

Choose a Dataset

Cambridge

Citation

If you use any of the images generated in a publication or presentation, please cite: *Dunning et al. Mining the human prostate cancer datasets: The camcApp shiny app. In preparation*

Please also cite the relevant publication for the dataset;

Cambridge and Stockholm

*Integration of copy number and transcriptomics provides risk stratification in prostate cancer: A discovery and validation cohort study. Ross-Adams et al. (2015) doi:10.1016/j.ebiom.2015.07.017*

MSKCC

*Integrative genomic profiling of human prostate cancer. Taylor et al. (2010) doi:10.1016/j.ccr.2010.05.026*

Michigan2005

*Integrative genomic and proteomic analysis of prostate cancer reveals signatures of metastatic progression. Varambally et al. (2005) doi:10.1016/j.ccr.2005.10.001*

Michigan2012

*The Mutational Landscape of Lethal Castrate Resistant Prostate Cancer. Grasso et al. (2012) doi:10.1038/nature11125*

About this app.....



[cruk.cam.ac.uk](http://cruk.cam.ac.uk)

This app was developed by

[Cancer Research Uk](#) [Cambridge Institute](#) [Bioinformatics Core](#)

Source code available on [github](#);

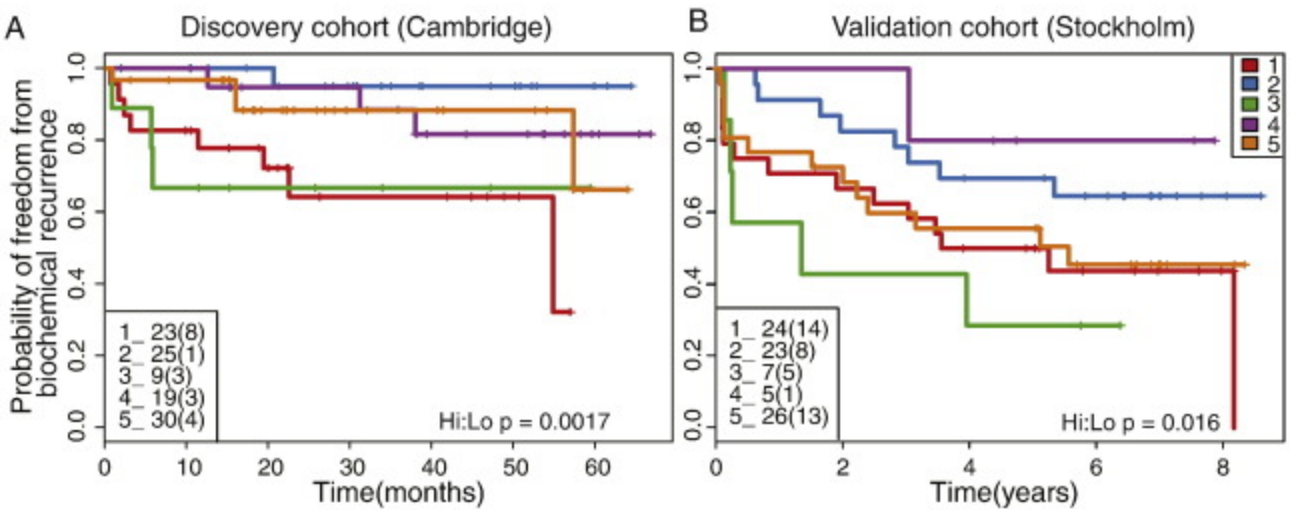
<https://github.com/crukci-bioinformatics/camcAPP>

Features

Gene Profile

Produces boxplots to visualise the distribution of the selected genes. For each dataset, you can choose which clinical variable to group the samples on

When choosing Cambridge or Stockholm, you will have the option to display the expression in the five different subtypes identified by Ross-Adams et al (2015). These subtypes were shown to have significantly different outcomes



If multiple microarray probes are found for the gene, the probe with the highest inter-quartile range (IQR) will be picked

An ANOVA analysis will also be performed to assess whether there are different expression levels in the groups you have chosen

The boxplot can be exported as a pdf or png image. An R script can be downloaded, allowing you to repeat the analysis or tweak as you wish