

Supplementary Materials for ‘Mining human prostate cancer datasets: The camcAPP shiny app’

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Introduction

The camcAPP is implemented as a Shiny (Chang et al. 2017) application in R. Shiny allows the non-specialist to create publication-ready figures and tables through an intuitive online interface to the underlying R code. The source code for the entire app is available through github (M. Dunning 2017). The `dplyr` (Wickham and Francois 2016) package is used throughout for efficient data manipulation and graphics are generated using `ggplot2` (Wickham 2009). Plots can be exported as PDF or PNG file with configurable height, width and file name. Some configuration of the background colour and grid style is also possible with the *Pick a plot style* drop-down box, which changes the overall appearance of the plot using pre-defined themes in `ggplot2` and the `ggthemes` package (Arnold 2016).

Details of specific panels

Data Input and Availability

Each dataset that can be interrogated using camcAPP was previously made available through Gene Expression Omnibus (GEO). Using the GEOquery (S. Davis and Meltzer 2007) Bioconductor package, each dataset was downloaded and converted into a data object (`ExpressionSet`) compatible with Bioconductor (Huber et al. 2015) packages. Thus, each dataset is also available as a Bioconductor experimental data package and can be downloaded and interrogated independantly of camcAPP. The R code used to download and process each dataset is available in it’s respective package vignette. Below is the R code required to download the data package for the Cambridge 2015 dataset. GEO accession number and corresponding Bioconductor package names are given in Table 1. Datasets other than Cambridge 2015 can be installed by replacing `prostateCancerCamcap` with the appropriate package name.

Example of installing the prostateCancerCamcap data package in R

```
source("http://www.bioconductor.org/biocLite.R")
biocLite("prostateCancerCamcap")
```

Table 1: Summary of each dataset accessible through camcAPP, its GEO accession number and Bioconductor data package

Dataset	GEO Accession	Bioconductor Package
Cambridge 2015	GSE70770	prostateCancerCamcap
Stockholm 2015	GSE70769	prostateCancerStockholm
MSKCC 2010	GSE21032	prostateCancerTaylor
Michigan 2012	GSE35988	prostateCancerGrasso
Michigan 2005	GSE3325	prostateCancerVarambally

Uploading a gene list for interrogation

The gene-list must be presented in a tab-delimited file assumed to have a column header. Only one column is required in the file, and this must contain the official RefSeq gene symbols that are to be used in analysis. Each gene symbol must appear on a different row. If no list is uploaded, a sample list of illustrative cancer-related genes is used; AR, ESR1, HES6, MELK and STAT3. See **Figure 1**.

docker container

Docker is a system that facilitates easy deployment and sharing of software as containers to alleviate the common headache of “dependency hell” when trying to install Bioinformatics software (Boettiger 2015). We provide a docker container for those that want easy access to all the R code, packages and datasets used in the app. The latest version of Docker is available for Windows 10 and Mac OSX 10.11 or newer. Once Docker is install, the container to run camcAPP can be installed and run from a terminal window as follows.

```
docker pull markdunning/camcapp
docker run -p 8787:8787 markdunning/camcapp
```

Entering the address: <http://localhost:8787> in a web-browser will then open an RStudio session with the username and password `rstudio`. Running the following commands in the RStudio console will run the app.

```
library(shiny)
runApp("../camcAPP")
```

Gene Profile

In this panel one can produce boxplots of the expression levels of the chosen gene list across a particular study. The z-score transformation will scale all genes to an average expression level of 0 and standard deviation of 1; thus making it easier to compare the trends of different genes. A clinical covariate is used to split the samples into different groups (choice of covariates will depend on dataset). The default settings will show the gene-expression aggregated in the subgroups identified in (Ross-Adams et al. 2015) (**Figure 2**).

By default, all genes will be displayed in a grid-like display. By clicking *Composite plot?* to *No* you can view a particular gene, where the gene to be plotted is given in the *Gene to Plot* dropdown box.

An analysis of variance is also performed for each gene to see if there is evidence for a change in expression level across the different categories for selected covariate. Please note that these results such be used for guidance only.

Survival

The `party` R package (Hothorn et al. 2006) is first used on a gene-by-gene basis to see if the expression level of each gene can be split into (typically, two) distinct groups. If a p-value of < 0.05 is calculated from this preliminary analysis, then samples are assigned to groups based on their expression-level being higher or lower than the identified cut-off. If the p-value is > 0.05 , samples are assigned to low or high expression level groups based on the median expression level of the gene.

The histogram shows the distribution of expression levels for a chosen gene (defined by the *Gene to plot* drop-down) and vertical line to show the cut-off to be used to assign samples to groups (either median expression level, or the cut-off identified by recursive partitioning)

A Kaplan-Meier curve is then generated from the biochemical relapse-free times of samples in the different groups (**Figure 3**).

Note only the Cambridge 2015, Stockholm and MSKCC dataset include the appropriate clinical metadata to perform a survival analysis.

Gene Correlation

This panel can display scatter plots for all pairwise combinations of genes in the selected list. Points in the scatter plots can be coloured according to the different clinical covariates in the selected study.

Alternatively, a single gene can be selected from the gene list and the panel will display a series of scatter plots with the expression level of the selected gene on the y-axis, and each other gene in the x-axis. These scatter plots will also show the value of r^2 using either Pearson or Spearman correlation.

Heatmap

The entire gene-list is used to cluster the samples in the chosen study, and the resulting ordering of samples is displayed using a heatmap (**Figure 4**). Cells in the heatmaps are coloured blue for under-expressed genes and red for over-expressed. The default option generate a heatmap by computing Euclidean distances and applying hierarchical clustering with complete linkage. However, other popular methods (e.g. correlation-based distance) are supported. Furthermore, the rows of the heatmap (i.e. the genes in the gene-list) can be ordered according to the results of the clustering, or left in the order in which they occur in the gene-list (option *Re-order Rows?*).

We also provide some basic exploratory analysis of the sample clustering. The dendrogram of the samples can be “cut” at a specified height, h , (on the y-axis), or an unknown height that will yield a pre-determined number of clusters, k . The clinical characteristics of the samples that fall into each cluster are then tabulated. Note that the values of h and k are restricted to give between 2 and 10 clusters.

Copy Number

This panel allows the visualisation of copy-number calls from Cambridge 2015, Stockholm and MSKCC datasets (Lalonde et al. 2014). Firstly (*Frequency* option in the *Type of plot to show* drop-down menu), one can see, on a per-gene basis the percentage of samples in each of the cohorts that have an amplification or deletion of the given gene. Alternatively (*Frequency by Dataset* option in *Type of plot to show*), for a selected cohort, the number of samples may be split into different clinical subgroups and the number of per-gene deletions and amplifications for each subgroup can be tabulated.

Finally (the *Heatmap* option in *Type of plot to show*), a heatmap can be generated from the copy-number calls of all selected genes in the selected cohort. Thus, allowing the user to assess whether certain genes are amplified or deleted in the same samples (**Figure 5**).

Quick Analysis

This panel allows the boxplots, survival and copy-number analysis listed above to be performed on a single-gene rather than a gene list. The gene name must be entered into the text box, and the user can check whether the name entered is a valid gene name before clicking *Go!* to proceed with the analysis.

Figures

Figure 1

Entry point to camcAPP, including the upload point for gene lists, selecting a cohort and citation information

Figure 2

Boxplots for gene expression can be created for a list of genes. This example shows the expression profile of selected genes in the five subgroups identified in the analysis of (Ross-Adams et al. 2015).

Figure 3

Kaplan-Meier biochemical relapse-free survival plots can be created for any selected gene from the input list in an selected dataset.

Figure 4

Heatmaps for gene expression can be created from any of the datasets.

Figure 5

Copy Number (CN) plots depicting CN gain or loss can also be created.

References

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