# panelmap: A data visualization tool for summarizing categorical and continuous data types for known groups

panelmap

Arshi Arora - github.com/arorarshi/panelmap

## Introduction

Memorial Sloan-Kettering

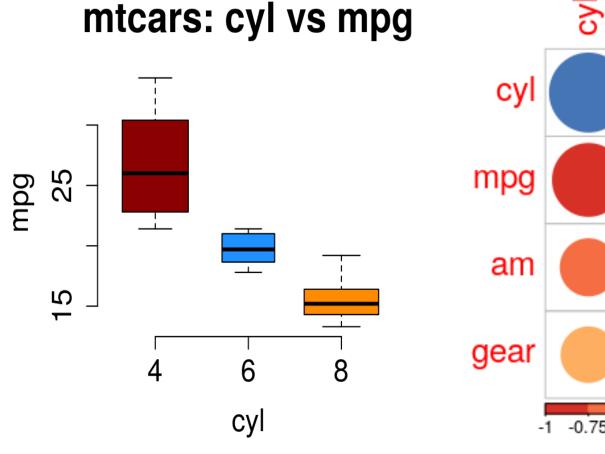
Cancer Center

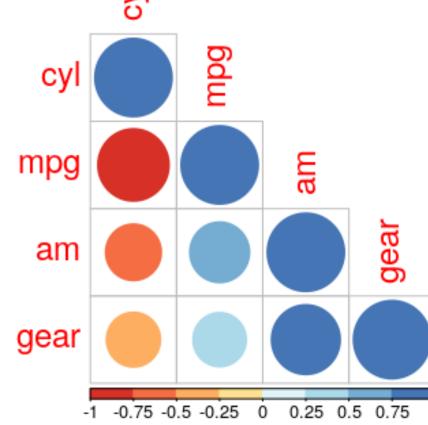
We often come across grouped data in our analyses. These groups can be either pre-defined or arrived analytically via k-means, hierarchical clustering, etc. For example, case: control, high-risk: low-risk, etc.

panelmap is a data visualization tool for viewing grouped data and its differential features in single and multi-panel layouts. It is a visual aid for understanding associations and trends in the dataset at a glance instead of tabular representation or trying to infer multiple plots.

### Motivation

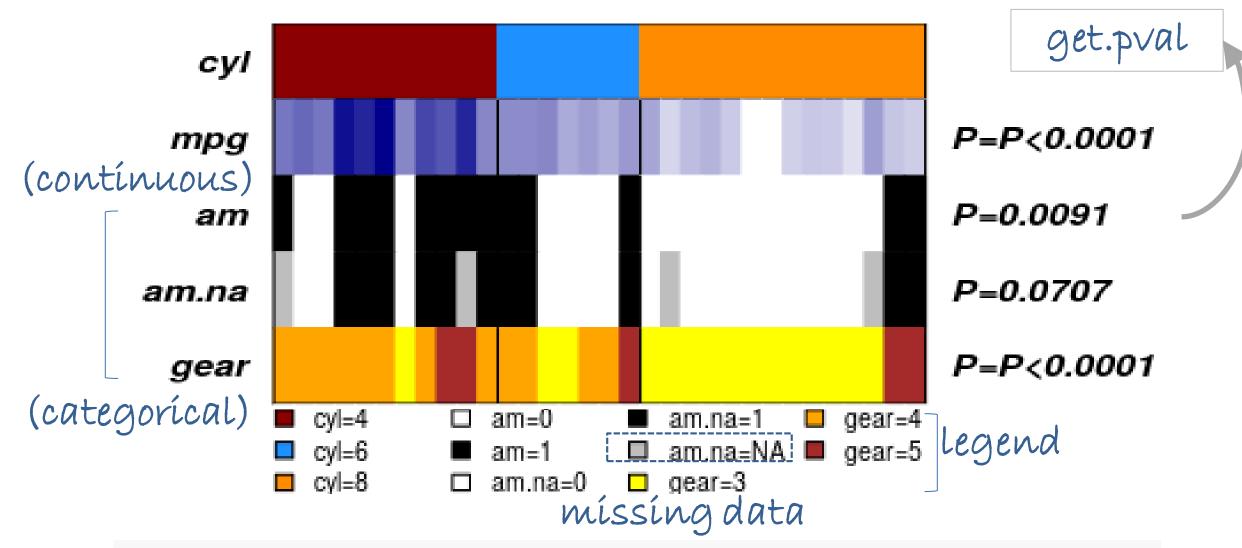
Relationships between various observations in the mtcars dataset can be summarized as follows-





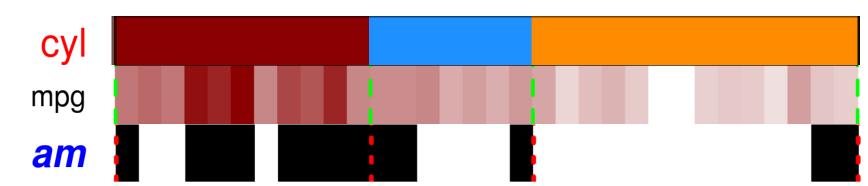
# panelmap

Instead we can visualize via a *panelmap* plot, the relationship between with cyl and other variables in the mtcars dataset.



tab=<u>makepanel</u>(gr=cyl,gr.name="cyl,gr.col=1:3,mat=mat,ma t.col= mat.col,mat.type=mat.type,border=TRUE, legend=TRUE ,get.pval= TRUE) #returns panelmap plot and a summary statistic table

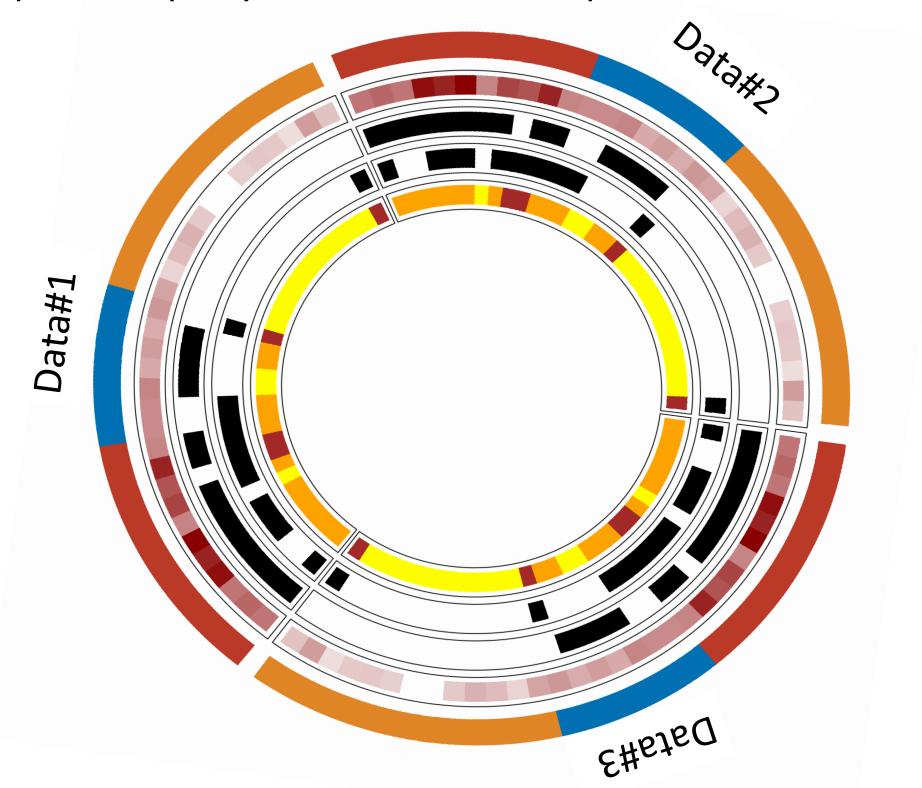
Visual tweaks and various customizations are available in panlemap.



panelmap provides a rich pool of functions to annotate, perform statistical tests, annotate missingness, automate legends, while allowing for various customizations to the user for generating rich and publication quality visualizations.

#### circomap

Multiple data types can be visualized by a multi panlemap layout, called circomap



# References

- 1. Gu, Z. circlize implements and enhances circular visualization in R. Bioinformatics 2014.
- 2. Arora, Arshi, et al. "Pan-cancer identification of clinically relevant genomic subtypes using outcomeweighted integrative clustering." bioRxiv (2020).

Arshi Arora, aroraa@mskcc.org Research Biostatistician II Memorial Sloan Kettering Cancer Center

