# factorMerger

Cheat Sheet

Agnieszka Sitko [aut, cre] Przemysław Biecek [aut, ths] University of Warsaw



## **Basics**

The aim of **factorMerger** is to provide set of tools to support results from post hoc comparisons. *Post hoc* testing is an analysis performed after running *ANOVA* to examine differences between group means (of some response numeric variable) for each pair of groups (groups are defined by a factor variable).

This project arose from the need to create a method of post hoc testing which gives the hierarchical interpretation of relations between groups means. Thereby, for a given significance level we may divide groups into nonoverlapping clusters.

1.TODO: here describe more details

## **Example**

library(factorMerger)
fmAll <- mergeFactors
 (response\_variable,
 factor\_variable,
 method = "hclust",
 family = "binomial")
print(fmAll)
plotTree(fmAll,
 panel = "all",
 responsePanel = "tukey")</pre>

# FactorMerger - set of tools to support results from post hoc testing

## Four panels to see it all

#### A. The Merging Paths Plot panel

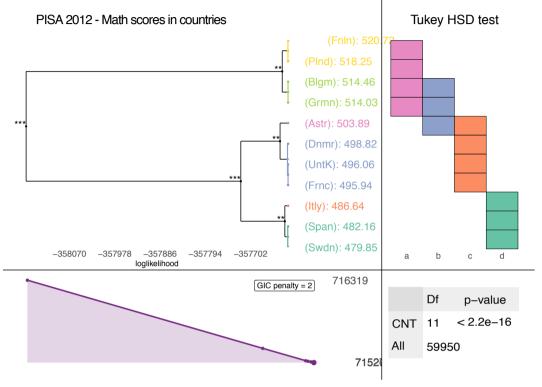
Shows the hierarchical structure of similarity between groups.

Stars presents how significant are differences between two clusters.

Height of the join corresponds to the likelihood of the combined model.

#### B. The response panel

Shows graphical summaries for group separately. Use the responsePanel argument to select the desired summary.



#### C. The GIC panel

Shows the *Generalized Information Criterion* for all models in MPP panel. Default *penalty=2* corresponds to the AIC criterion. Colours in the MPP panel corresponds to the optimal model.

### D. The summary panel

Shows the no. groups, no. observations, and the p-value for global hypothesis that parameter of interest is equall in all groups.

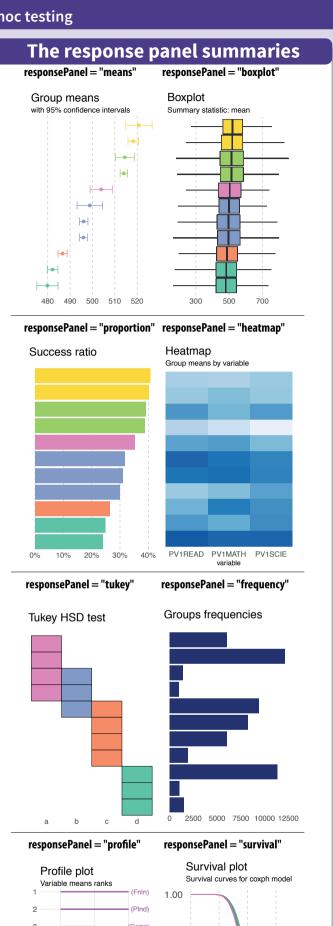
# **Level fusing plot**

The top-left plot shows level fusing paths (merging paths). With arguments **family=**, **show=**, **fuse=**, **spacing=**, one can select how to merge factors and what shall be presented on OX/OY axes.

Argument	Summary
<pre>panel = "all"</pre>	All panels
<pre>panel = "response"</pre>	Panels A and B
<pre>panel = "GIC"</pre>	Panels A and C
panel = "tree"	Only panel A

Argument	Summary
fuse = "all2all"	Compare all pairs of groups
fuse = "nearby"	Compare nearby groups
fuse = "cluster"	DMR4glm algorithm

Argument	Summary
<pre>family = "gaussian"</pre>	For 1/n-dimensional Gaussian
<pre>family = "binomial"</pre>	For binomial regression
<pre>family = "survival"</pre>	For Cox regression



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