factorMerger: hierarchical clustering and model visualization

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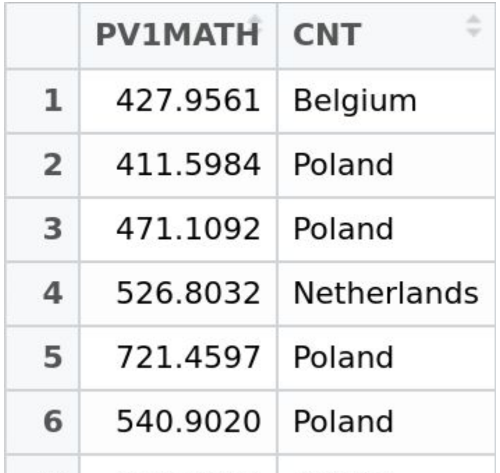
University of Warsaw, MI^2 Group

useR!2017 | 06-07-2017

Problem 1

Given a factor C (with k* levels) and a numeric response y* analyze the differences among group means of y.



	PV1MATH	CNT
1	427.9561	Belgium
2	411.5984	Poland
3	471.1092	Poland
4	526.8032	Netherlands
5	721.4597	Poland
6	540.9020	Poland

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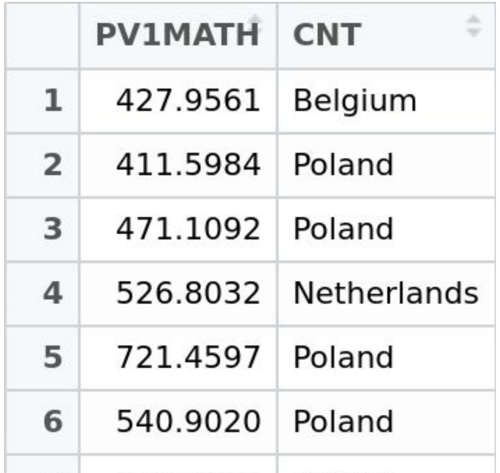

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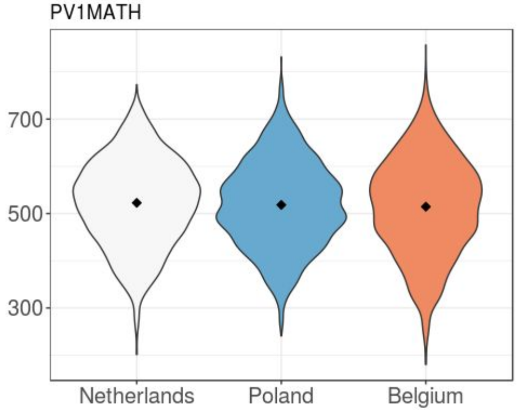

* k is greater than 2,
* y is normally distributed.

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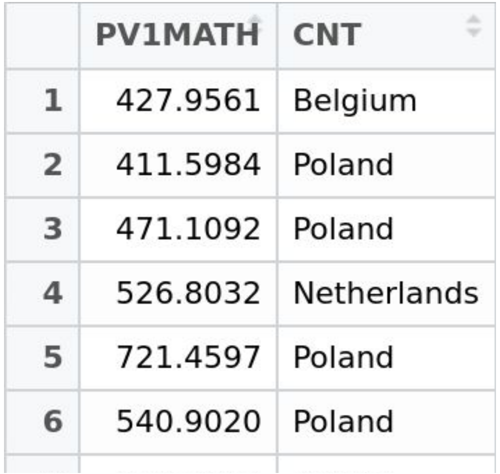

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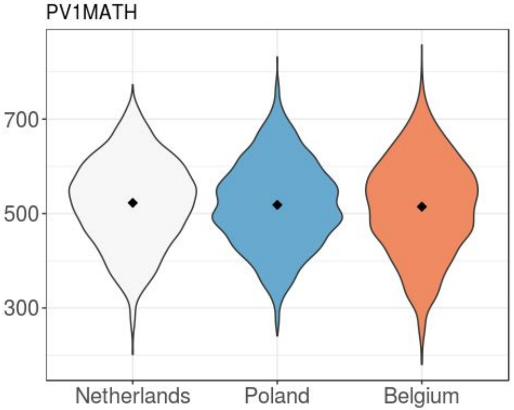
Solution

That’s easy!

Let’s run ANOVA and then post-hoc tests.



* k is greater than 2,
* y is normally distributed.

Solution

Let’s run ANOVA and then post-hoc tests.

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Let’s try this out.

Solution

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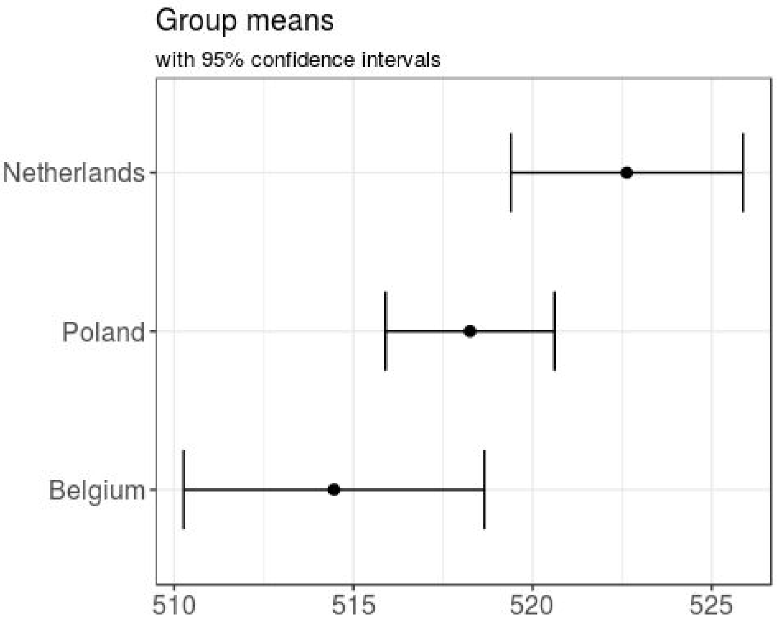
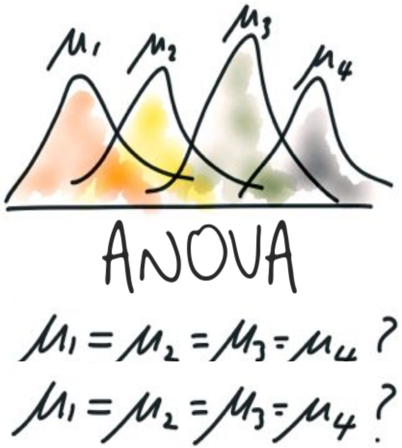
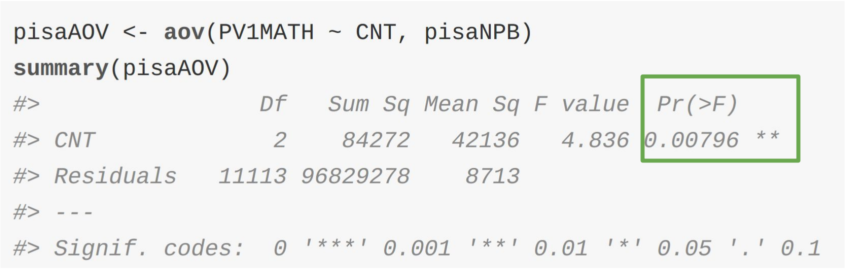




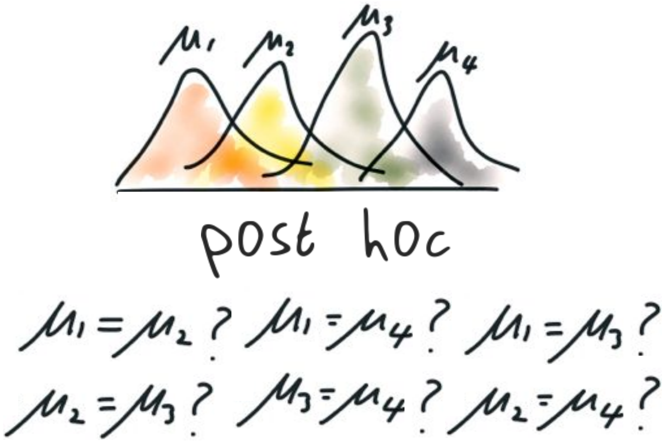


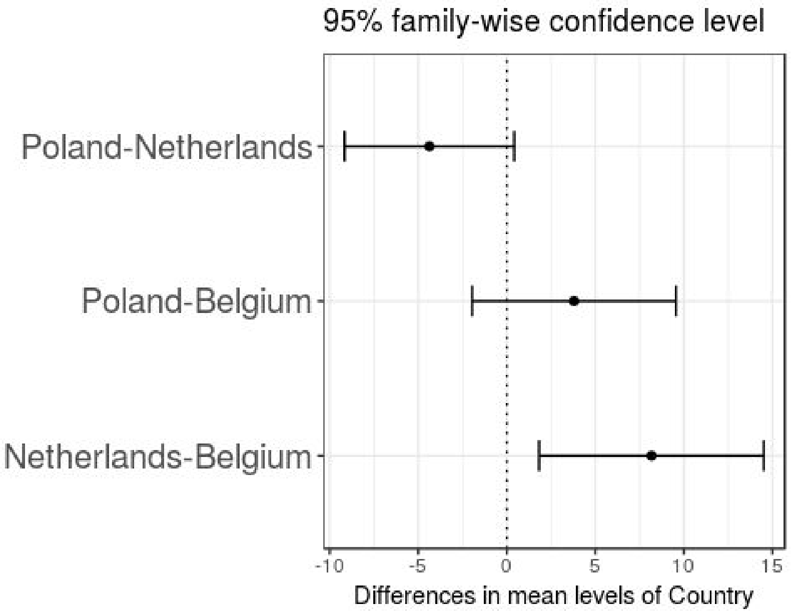
```
pisaAOV <- aov(PV1MATH ~ CNT, pisaNPB)
summary(pisaAOV)
#>                Df   Sum Sq Mean Sq F value  Pr(>F)
#> CNT             2    84272   42136   4.836 0.00796 **
#> Residuals   11113 96829278    8713
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
```

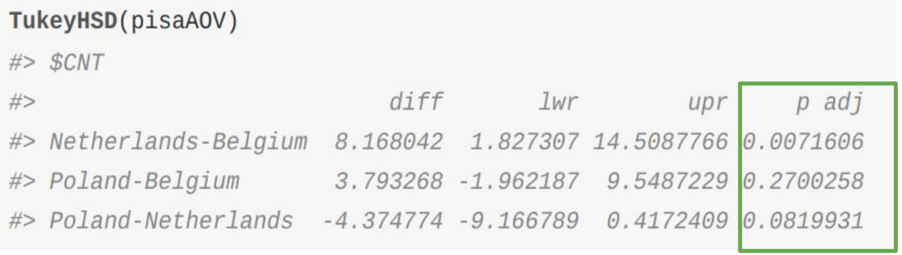
https://www.linkedin.com/pulse/anova-analysis-variance-kumar-p

Solution

Let’s run ANOVA and then post-hoc tests.


μ_1
μ_2
μ_3
μ_4
post hoc
$\mu_1 = \mu_2$? $\mu_1 = \mu_4$? $\mu_1 = \mu_3$?
$\mu_2 = \mu_3$? $\mu_3 = \mu_4$? $\mu_2 = \mu_4$?





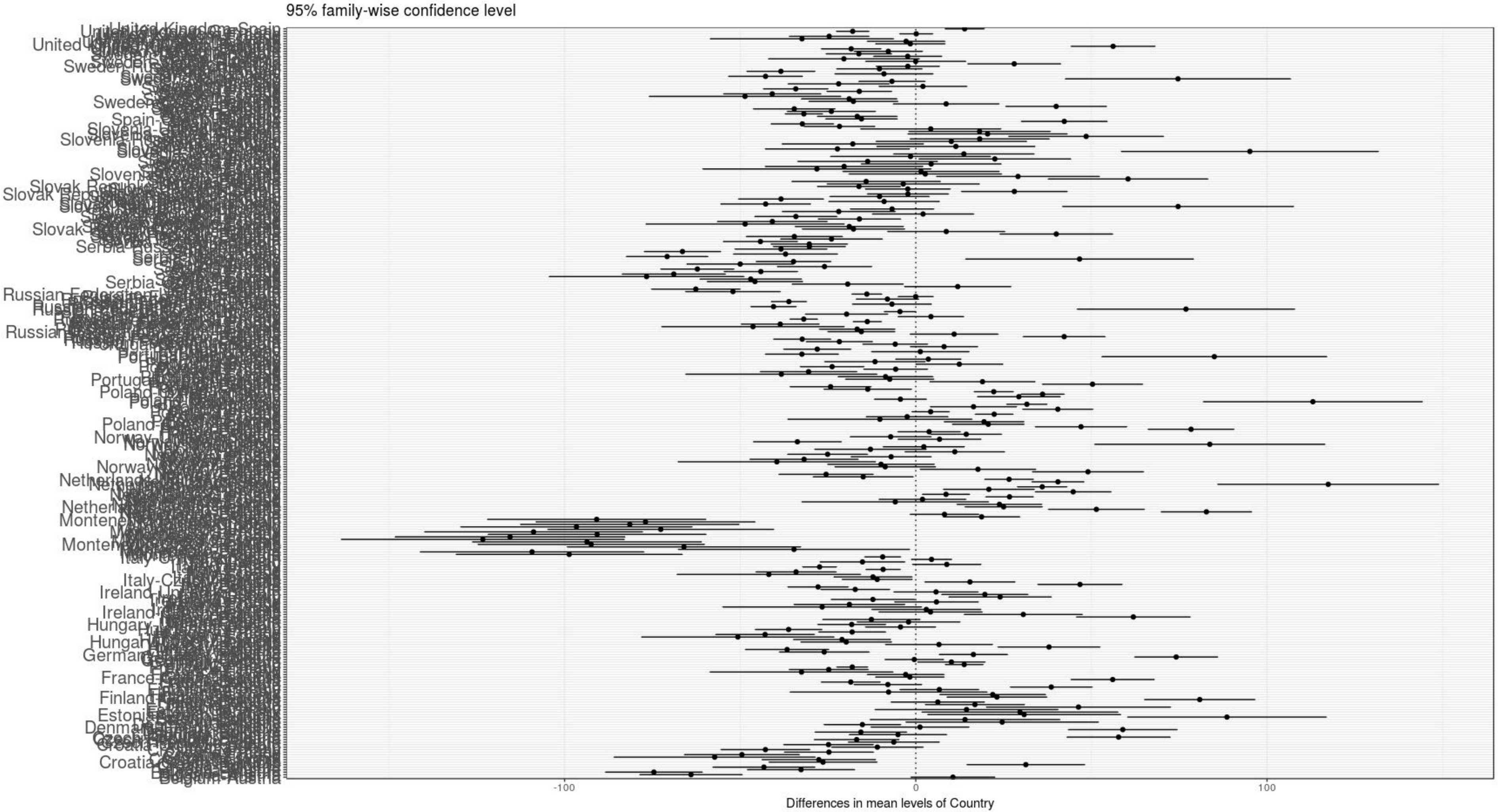
```
TukeyHSD(pisaAOV)
#> $CNT
#>                           diff       lwr        upr     p adj
#> Netherlands-Belgium   8.168042  1.827307 14.5087766 0.0071606
#> Poland-Belgium        3.793268 -1.962187  9.5487229 0.2700258
#> Poland-Netherlands   -4.374774 -9.166789  0.4172409 0.0819931
```

https://www.linkedin.com/pulse/anova-analysis-variance-kumar-p

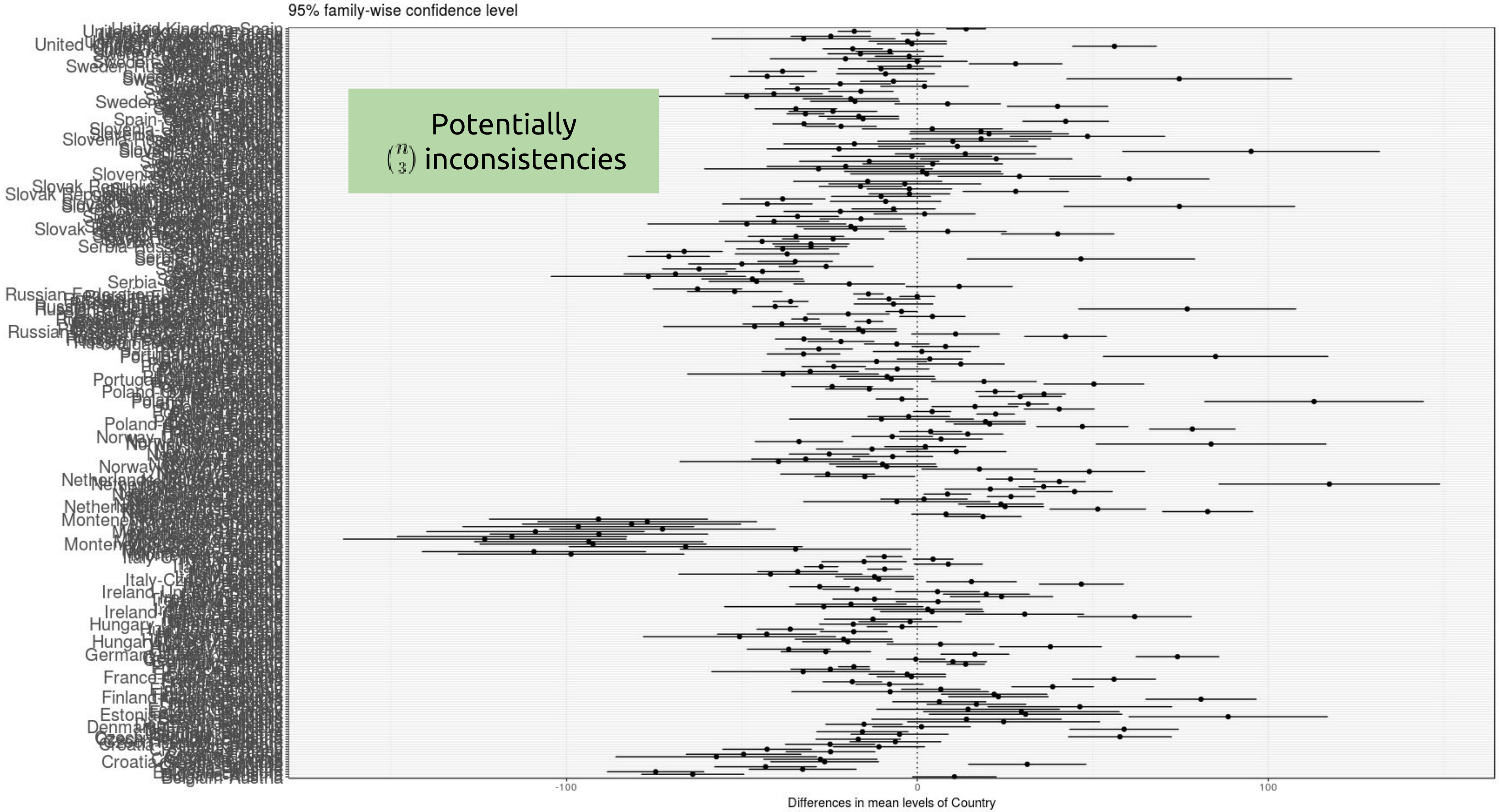
Problem 2

Given a factor *C* (with *k** levels) and
a numeric response *y** analyze the differences
among group means of *y*.

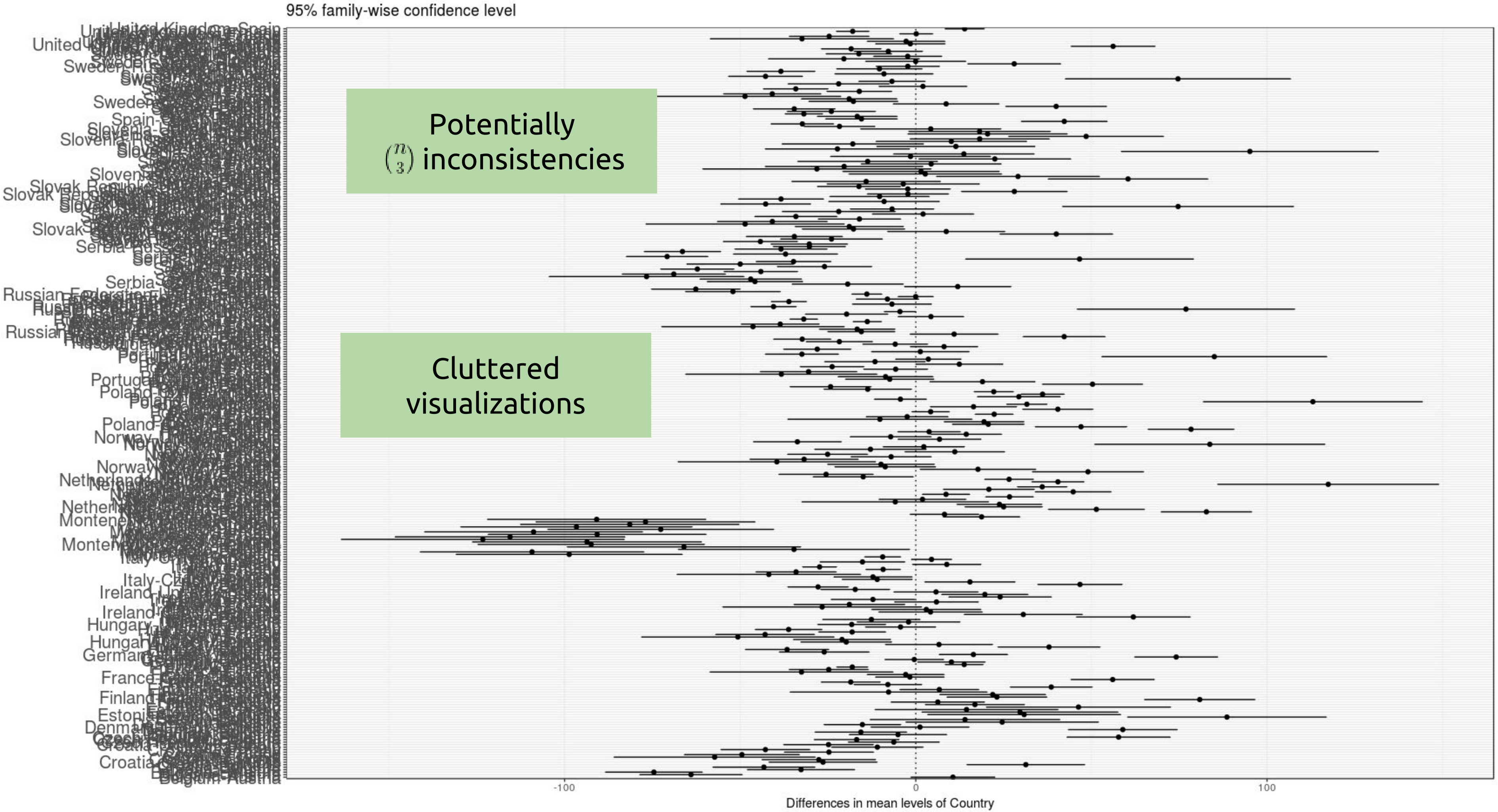
Group levels of *C* into non-overlapping clusters.



95% family-wise confidence level
-100
0
100
Differences in mean levels of Country

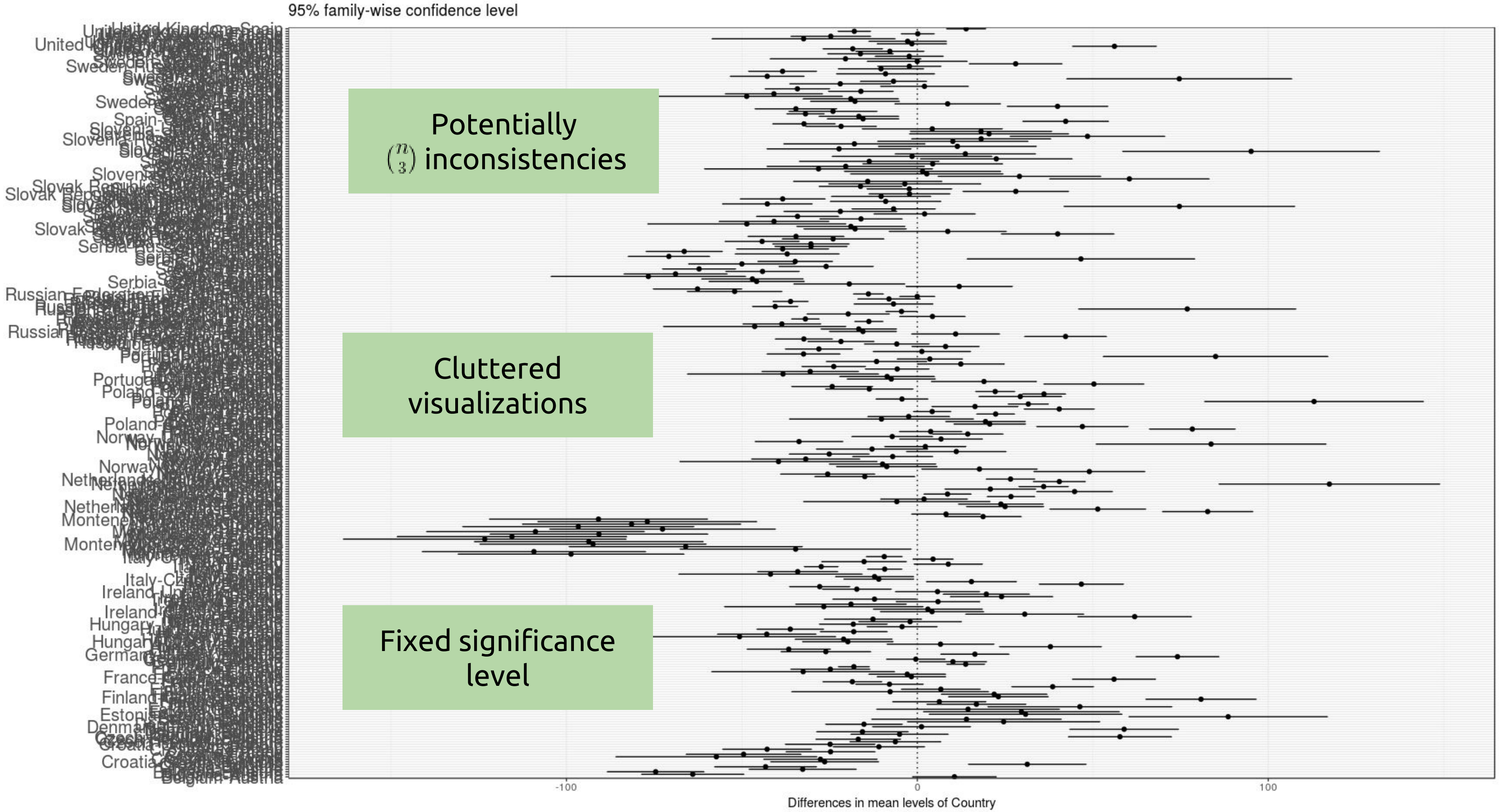


Potentially $\binom{n}{3}$ inconsistencies



Potentially $\binom{n}{3}$ inconsistencies

Cluttered visualizations

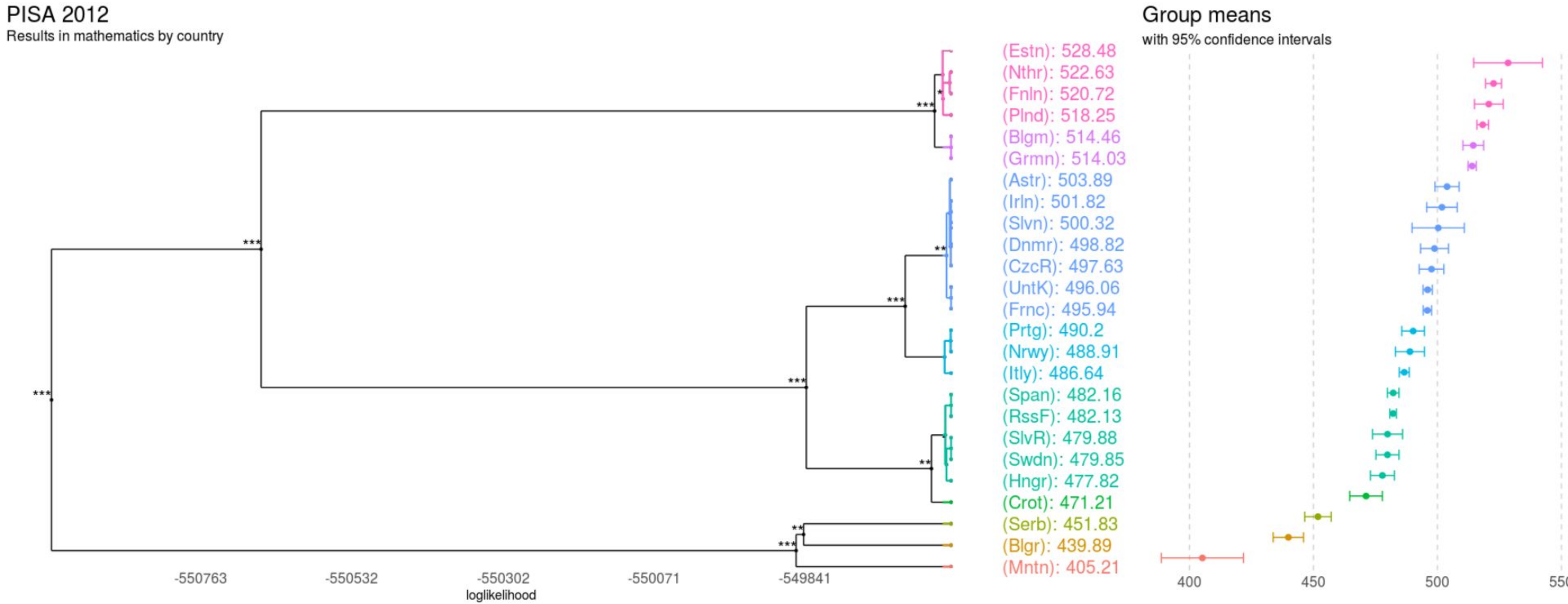


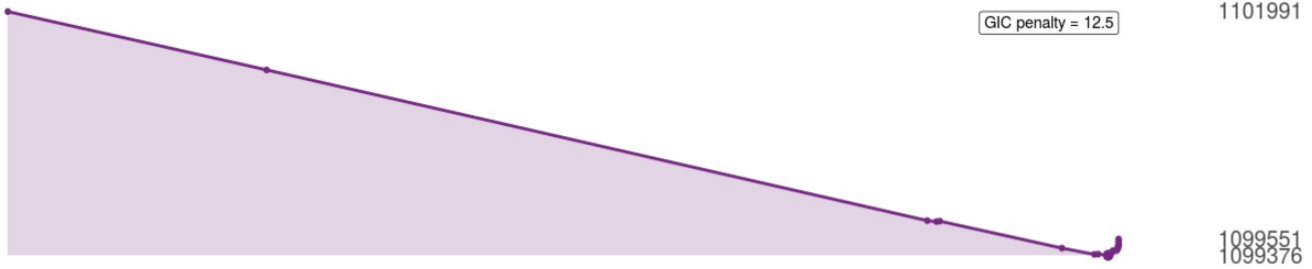
Potentially $\binom{n}{3}$ inconsistencies

Cluttered visualizations

Fixed significance level

Time for factorMerger

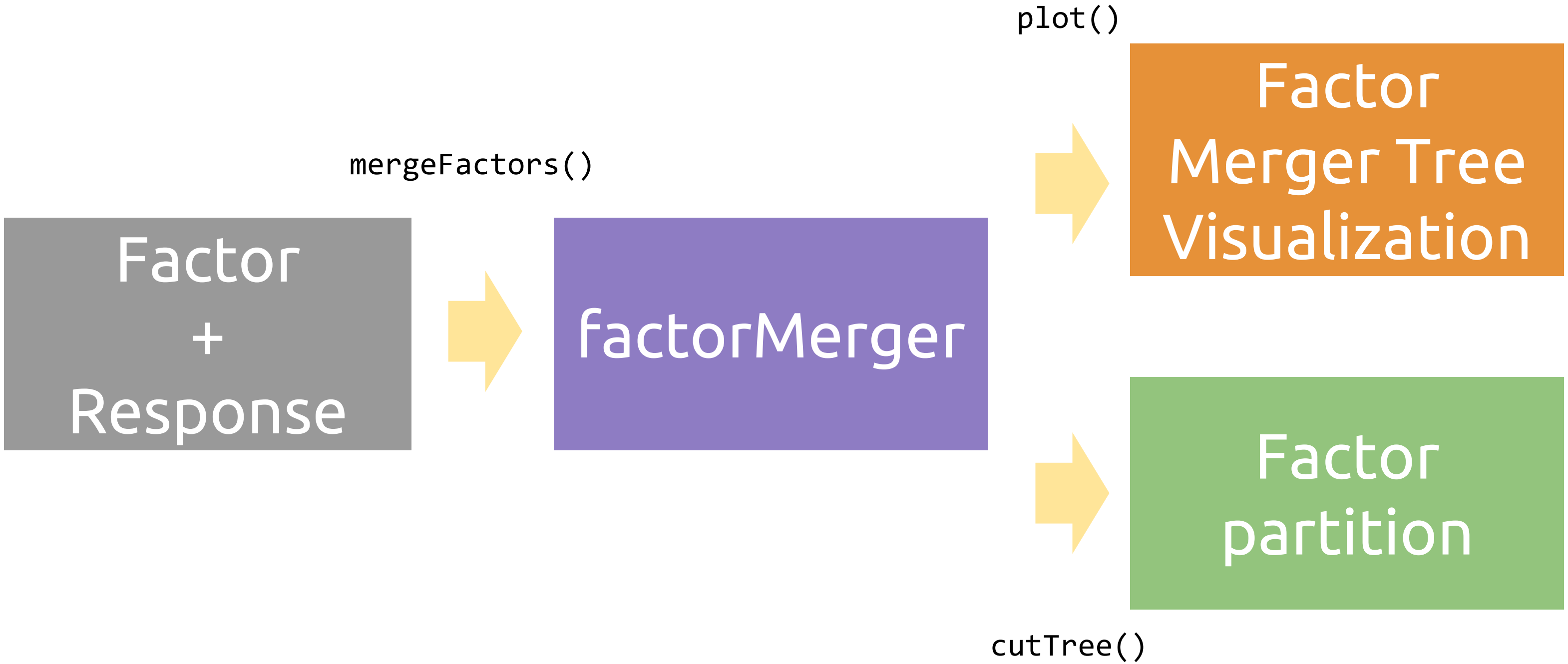




ANOVA table

	Df	F	p-value
factor	25	105939.6	< 2.2e-16
Res	92411		

Working with factorMerger



plot()

Factor Merger Tree Visualization

mergeFactors()

Factor + Response

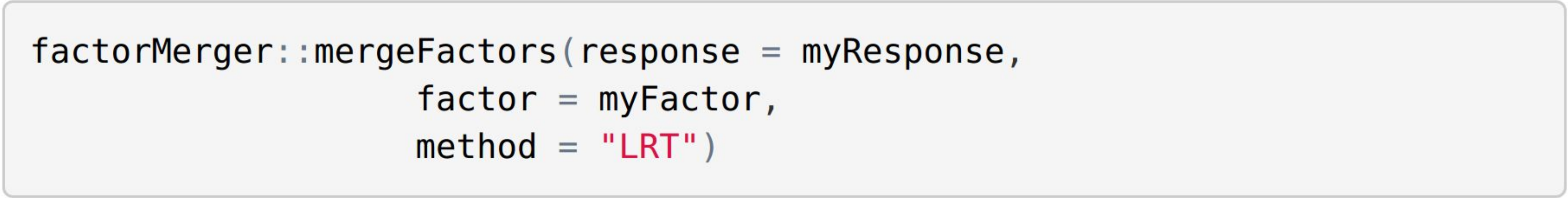
factorMerger

Factor partition

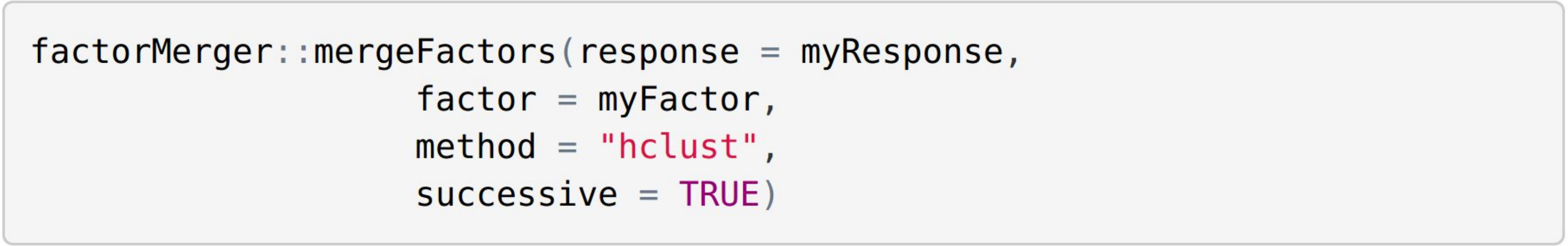
cutTree()

Merge

1. Likelihood Ratio Tests
2. Delete or Merge Regressors



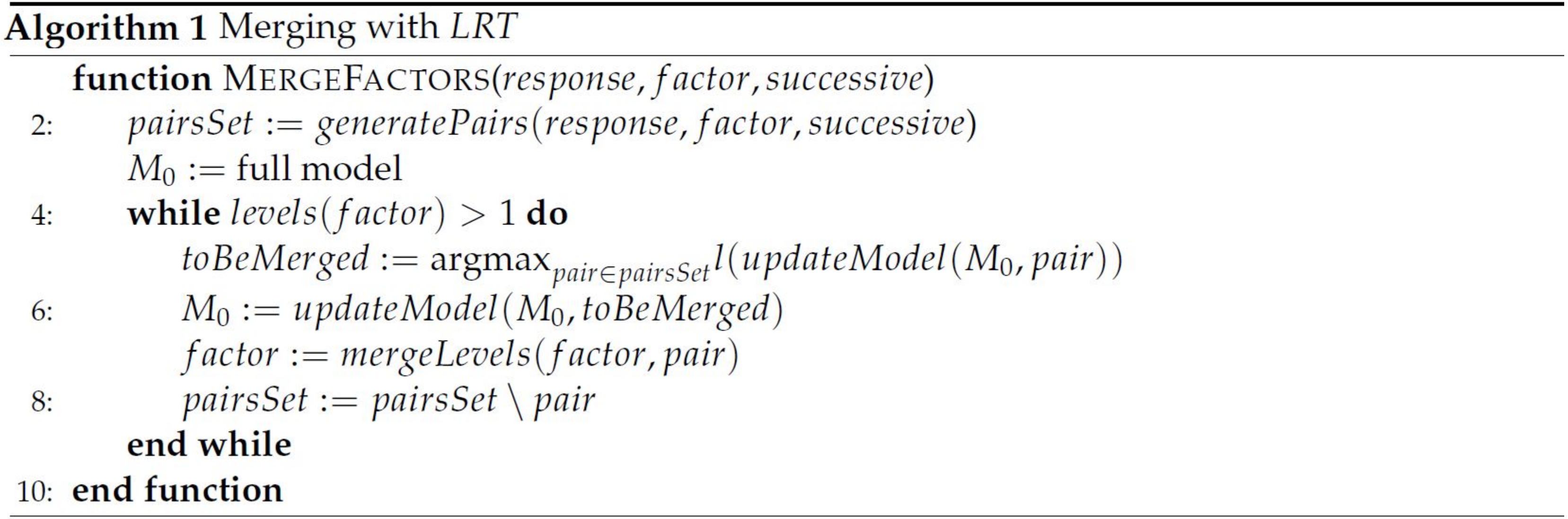
```r
factorMerger::mergeFactors(response = myResponse,
                           factor = myFactor,
                           method = "LRT")
```



```r
factorMerger::mergeFactors(response = myResponse,
                           factor = myFactor,
                           method = "hclust",
                           successive = TRUE)
```

Merge

1. Likelihood Ratio Tests
2. Delete or Merge Regressors

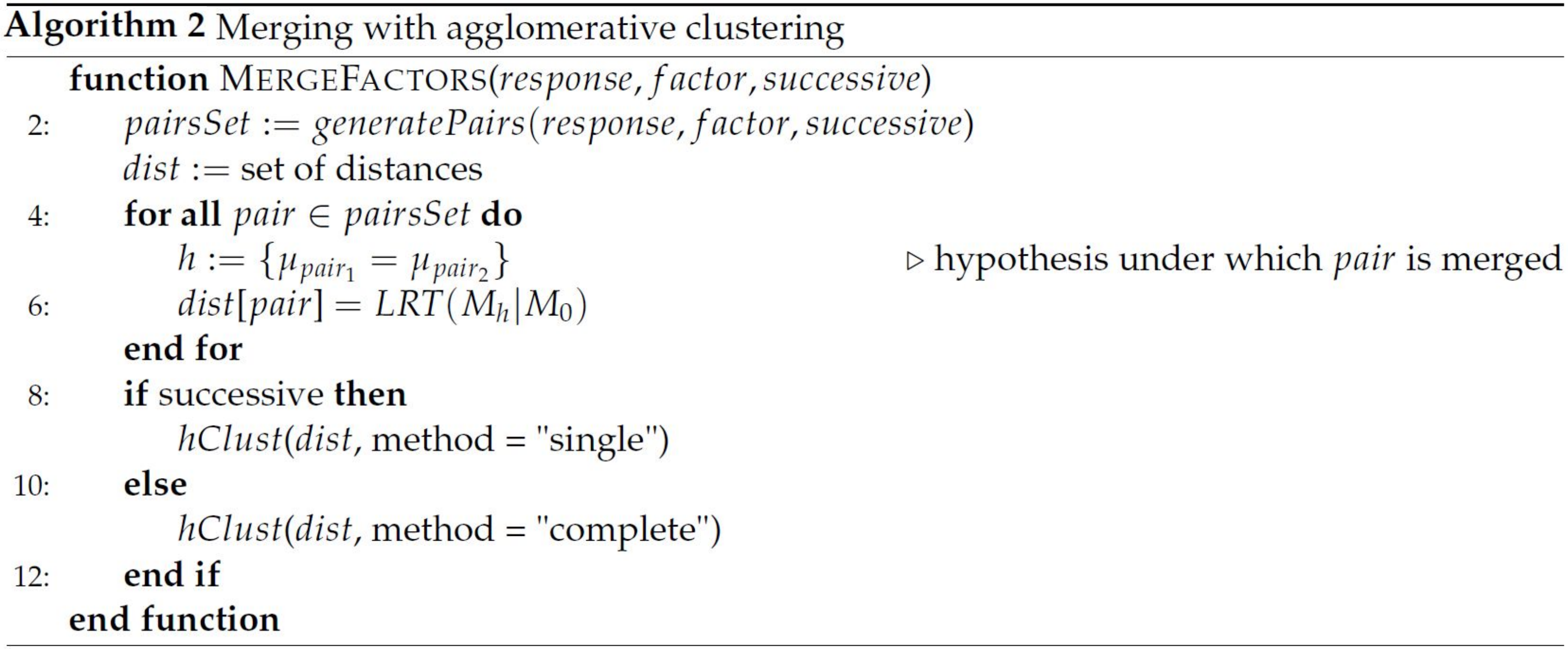


Algorithm 1 Merging with *LRT*

```
function MergeFactors($response, factor, successive$)
    $pairsSet := generatePairs(response, factor, successive)$
    $M_0 :=$ full model
    while $levels(factor) > 1$ do
        $toBeMerged := \text{argmax}_{pair \in pairsSet} l(updateModel(M_0, pair))$
        $M_0 := updateModel(M_0, toBeMerged)$
        $factor := mergeLevels(factor, pair)$
        $pairsSet := pairsSet \setminus pair$
    end while
end function
```

Merge

1. Likelihood Ratio Tests
2. Delete or Merge Regressors



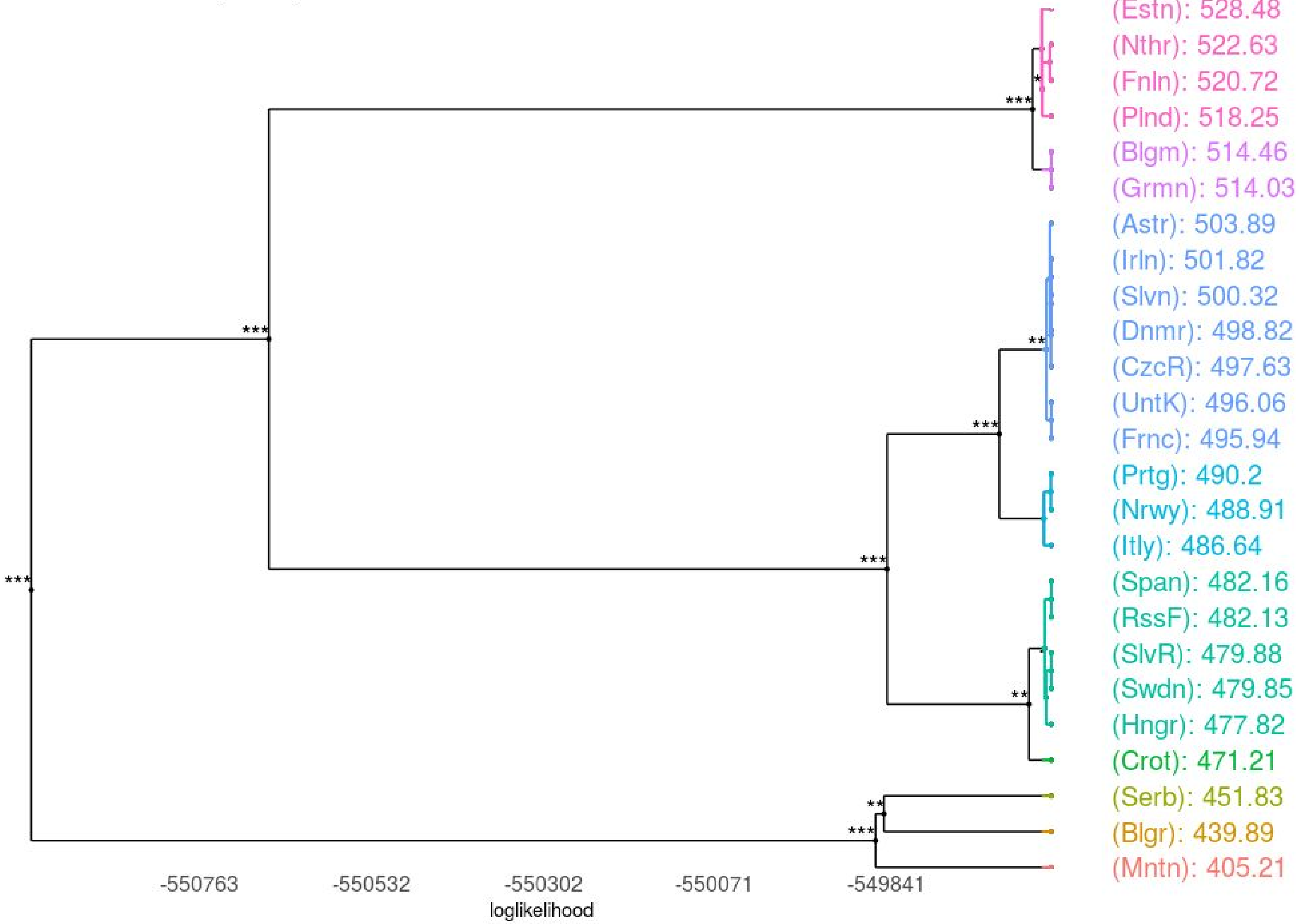
Algorithm 2 Merging with agglomerative clustering

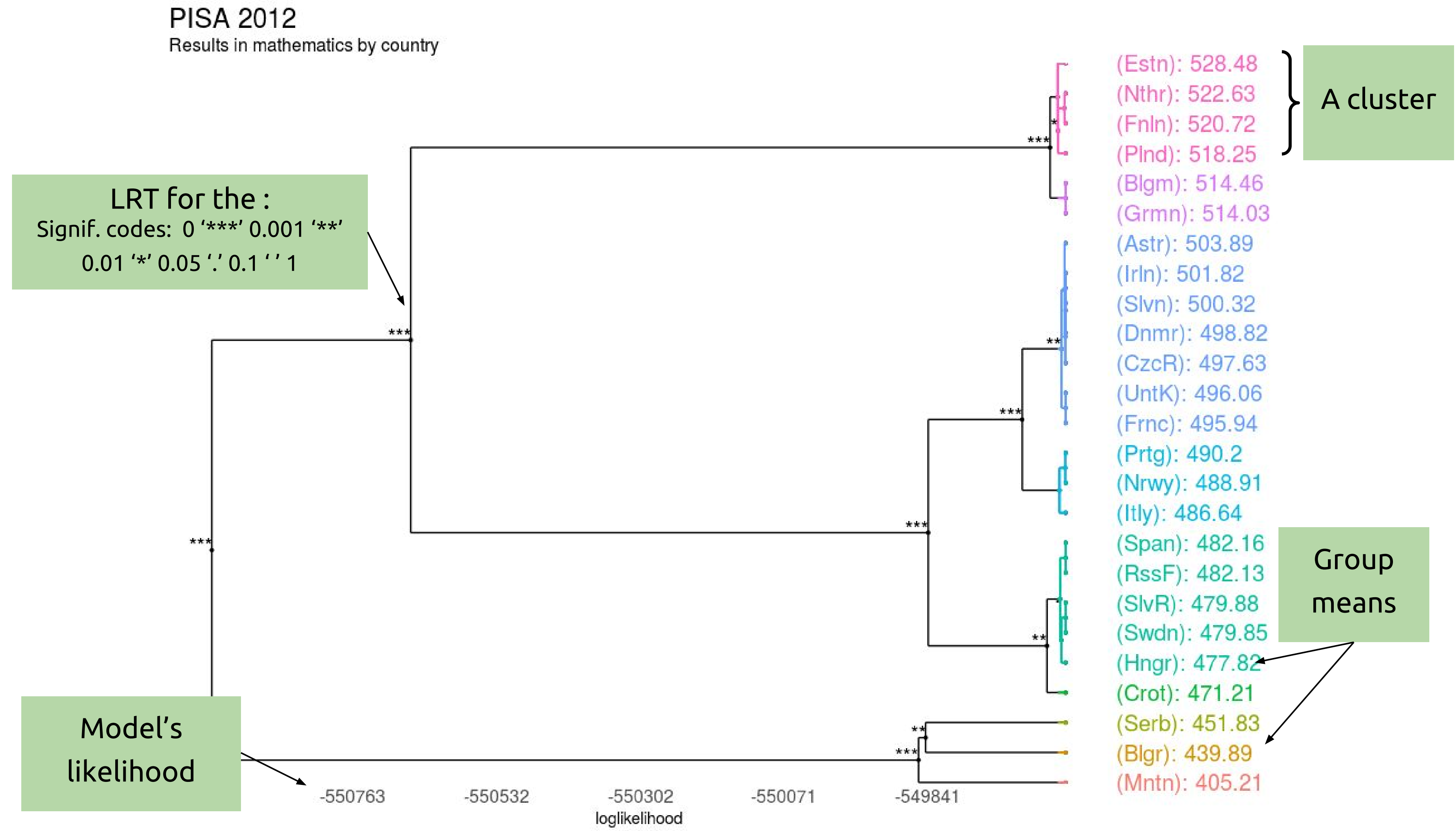
```
function MergeFactors($response, factor, successive$)
    $pairsSet := generatePairs(response, factor, successive)$
    $dist :=$ set of distances
    for all $pair \in pairsSet$ do
        $h := \{\mu_{pair_1} = \mu_{pair_2}\}$        ▷ hypothesis under which $pair$ is merged
        $dist[pair] = LRT(M_h|M_0)$
    end for
    if successive then
        $hClust(dist,$ method = "single")
    else
        $hClust(dist,$ method = "complete")
    end if
end function
```

More about the DMR algorithm: https://arxiv.org/abs/1505.04008

PISA 2012

Results in mathematics by country





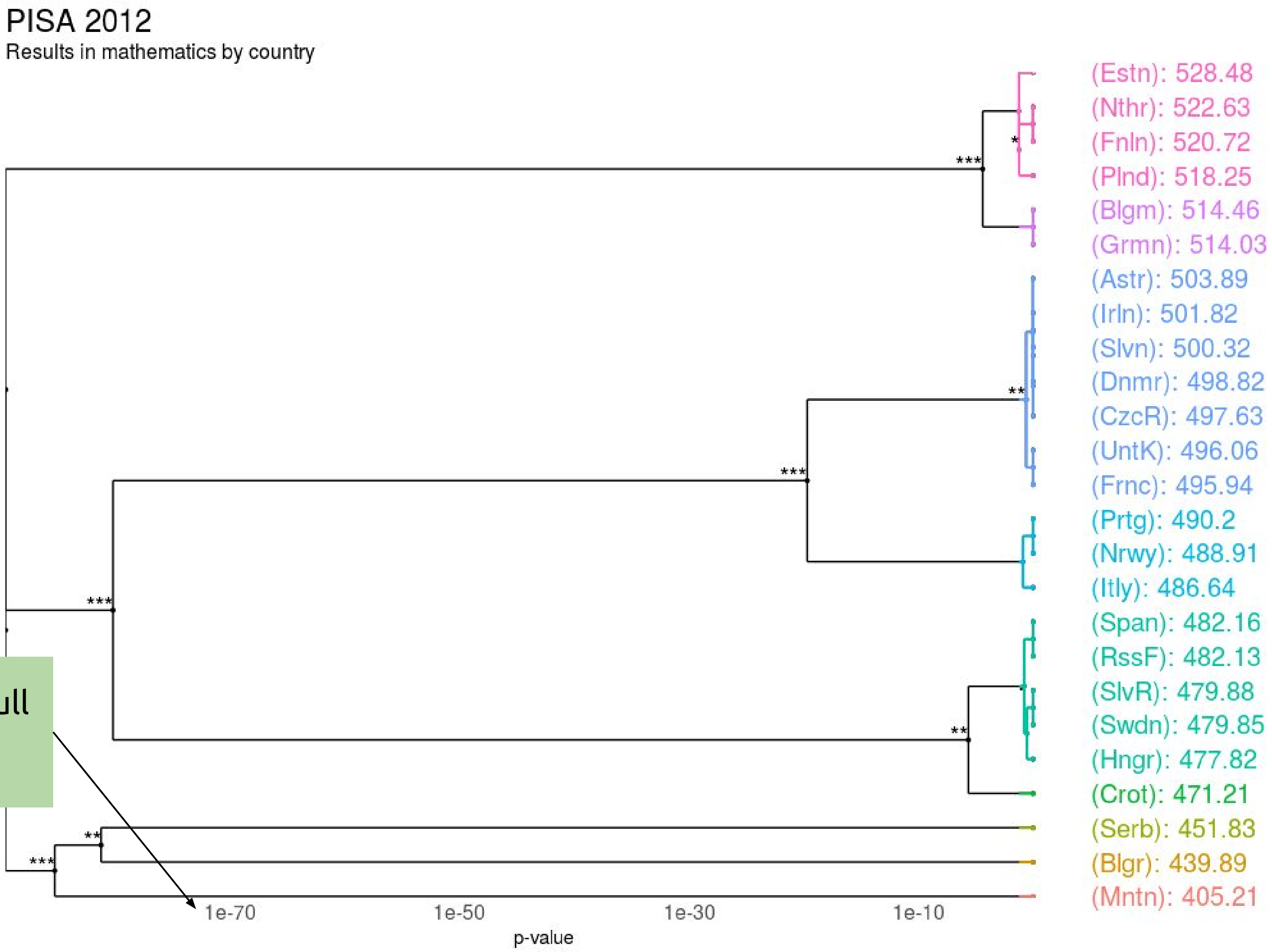
A cluster

LRT for the :

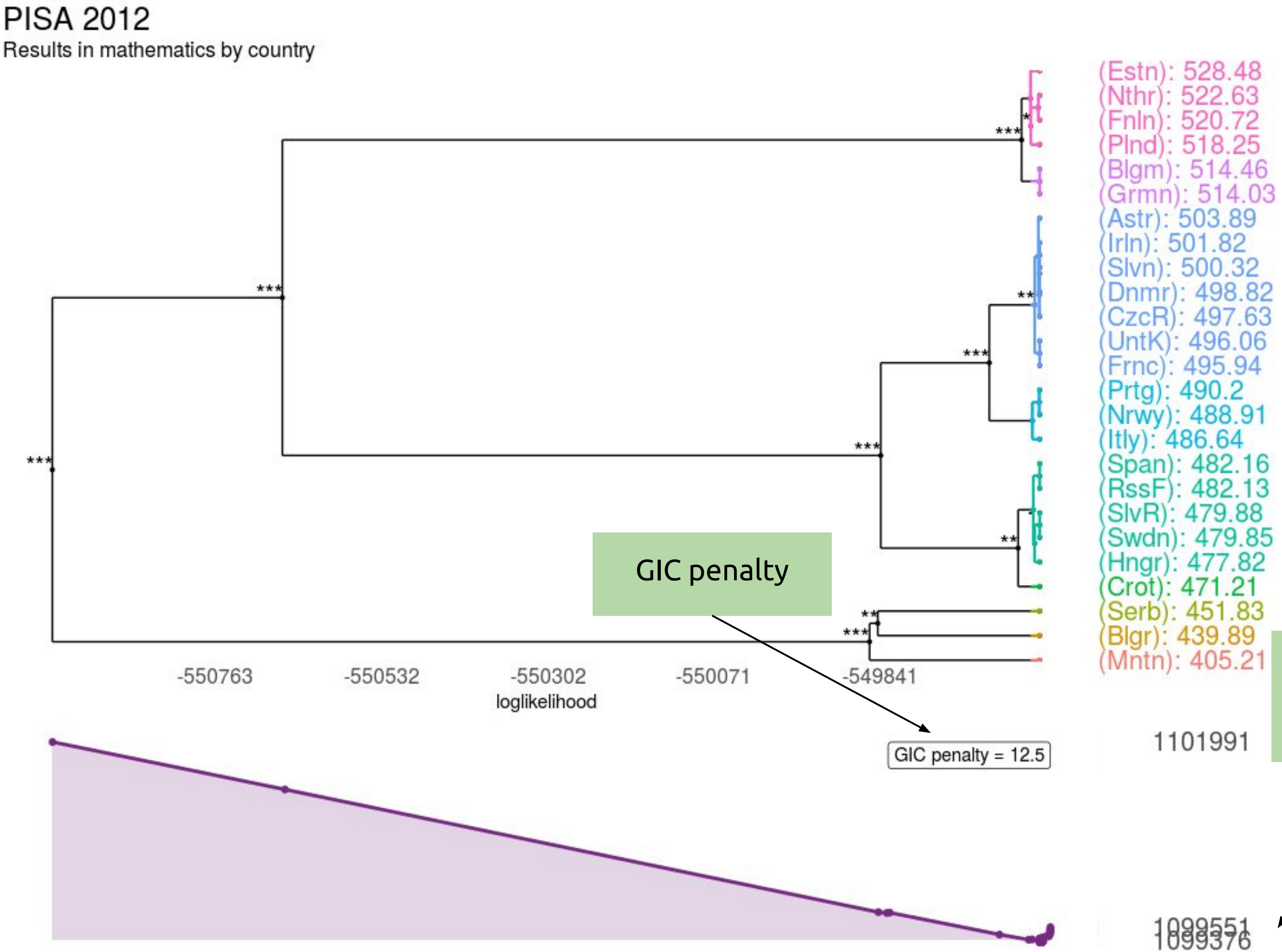
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Group means

Model's likelihood



LRT vs. full model

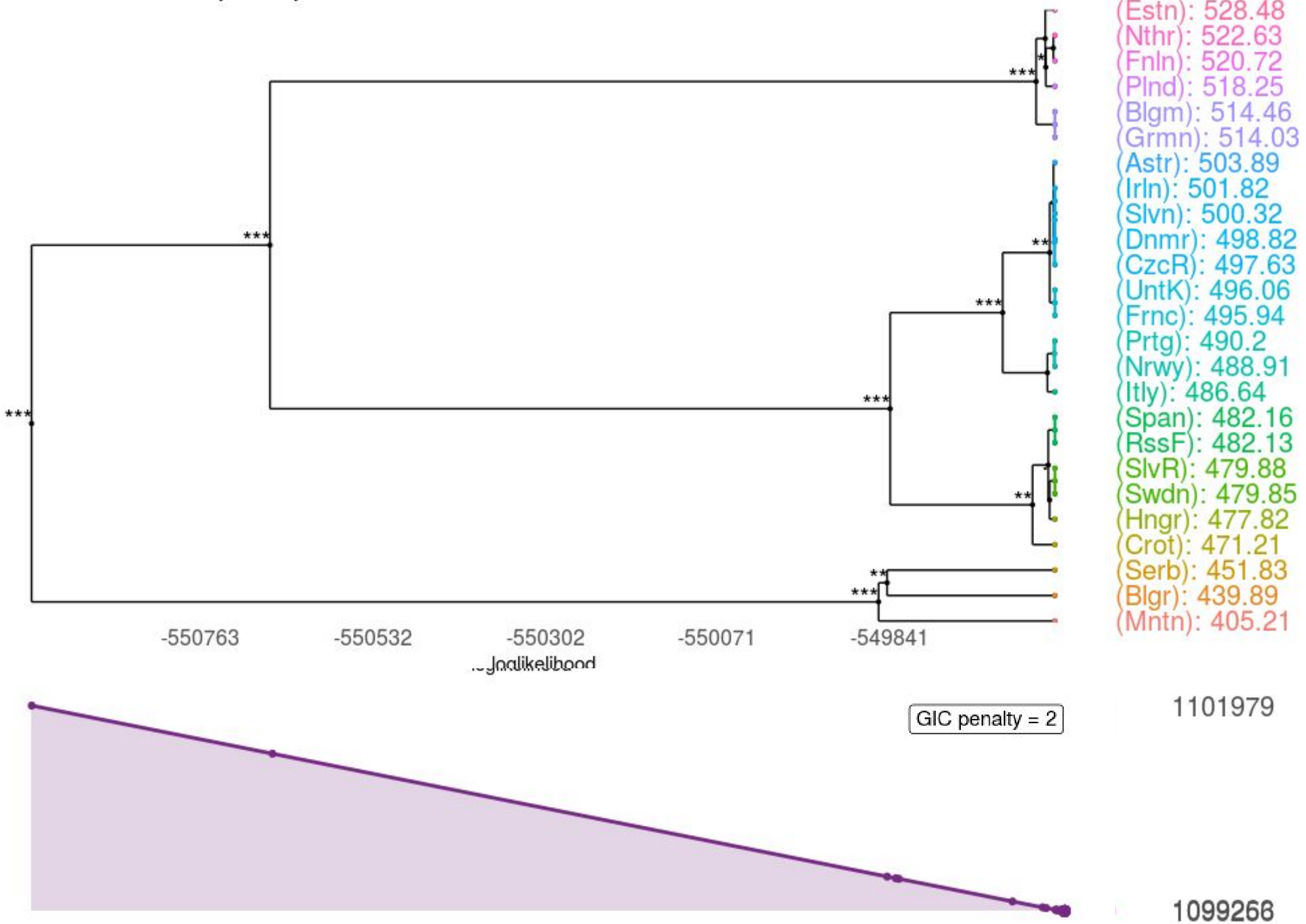


GIC penalty

Models: constant, full best

PISA 2012

Results in mathematics by country



PISA 2012

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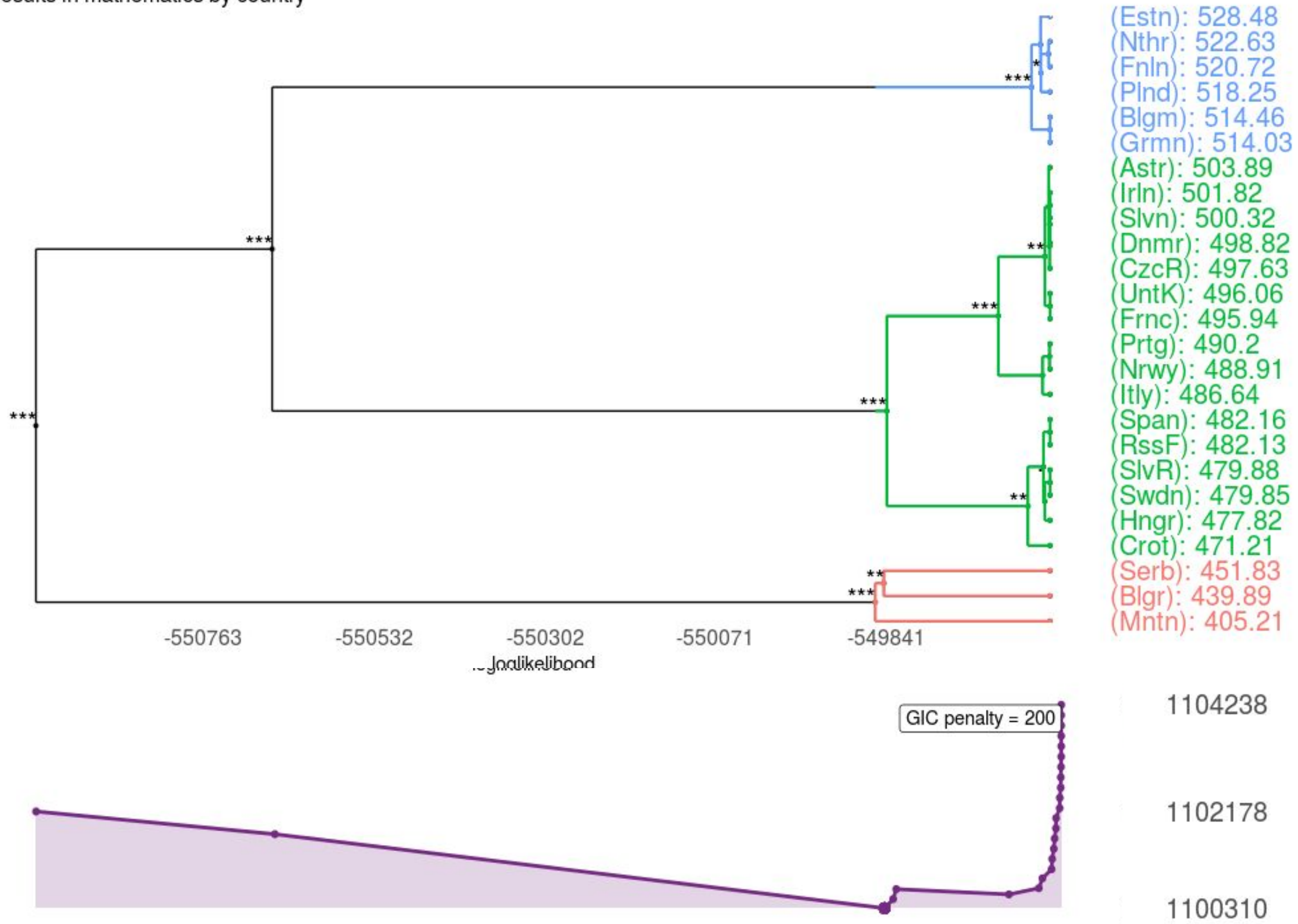
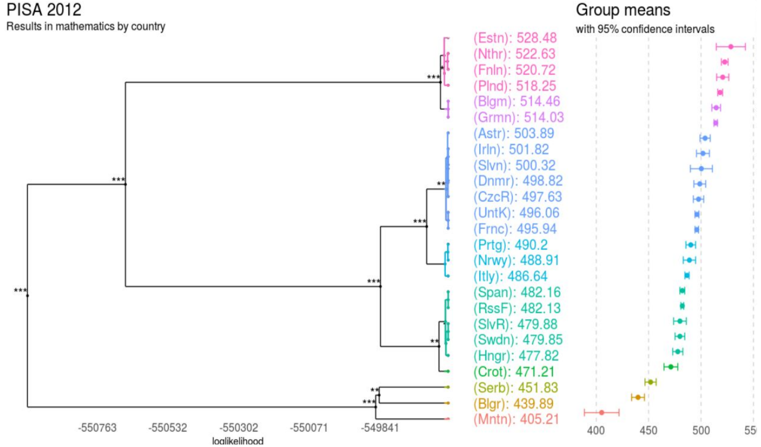


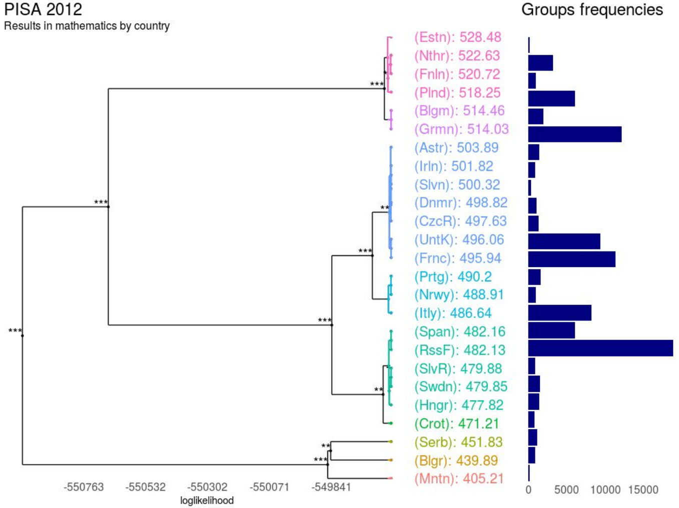


PISA 2012

Results in mathematics by country

Group means

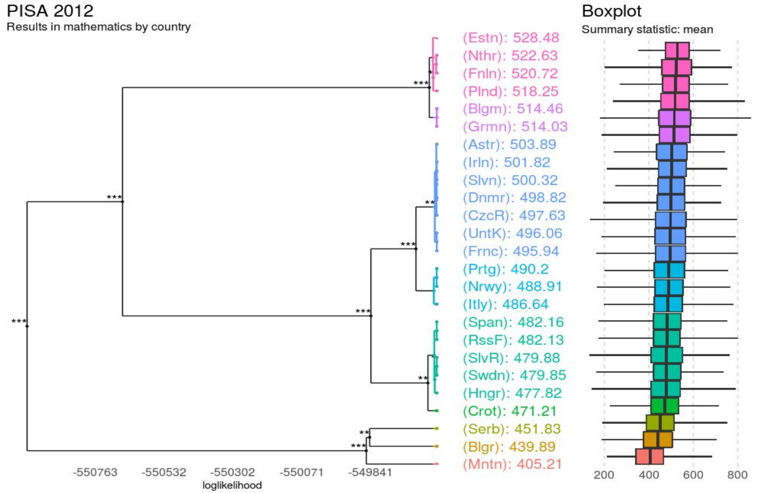
with 95% confidence intervals



PISA 2012

Results in mathematics by country

Groups frequencies

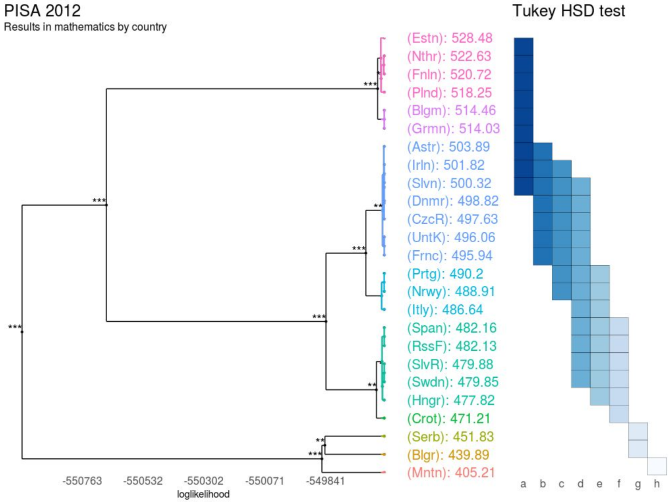


PISA 2012

Results in mathematics by country

Boxplot

Summary statistic: mean



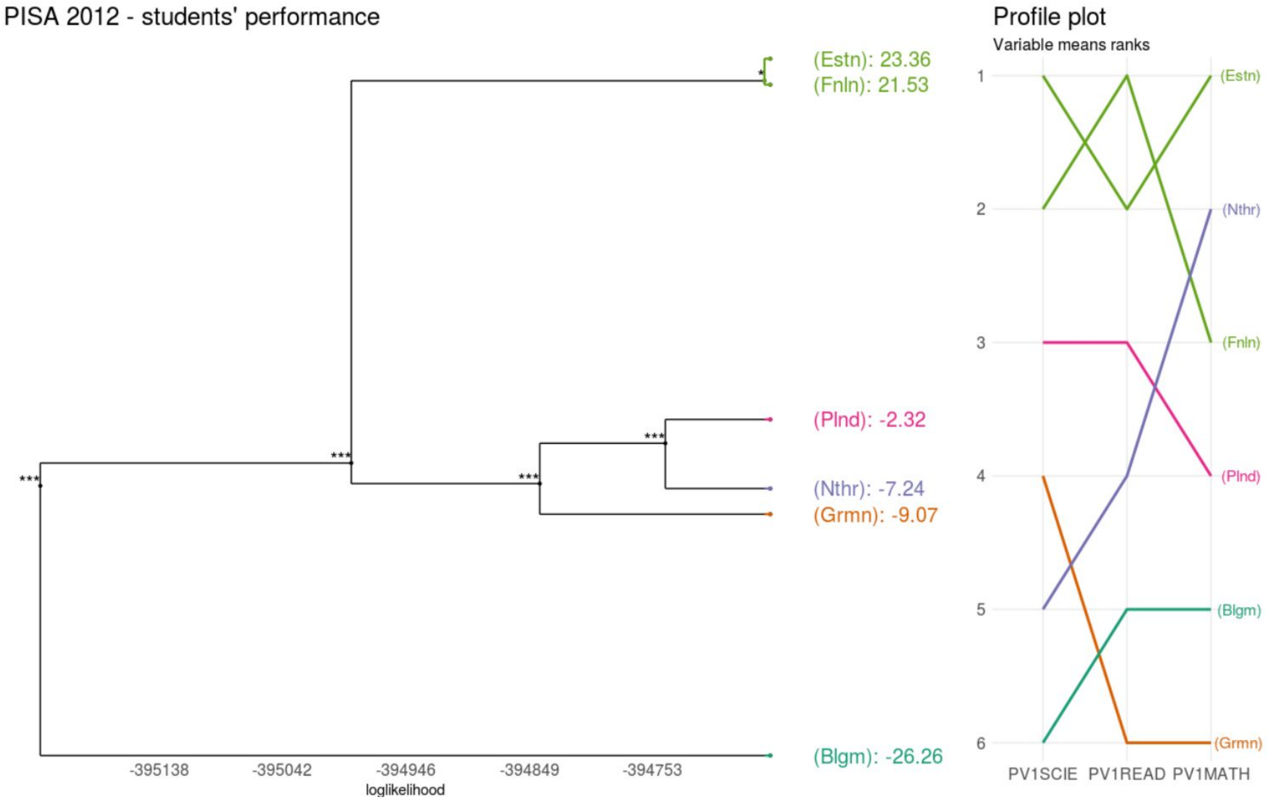
PISA 2012

Results in mathematics by country

Tukey HSD test

Other parametric models

1. multi dimensional Gaussian model,
2. binomial model,
3. survival model.



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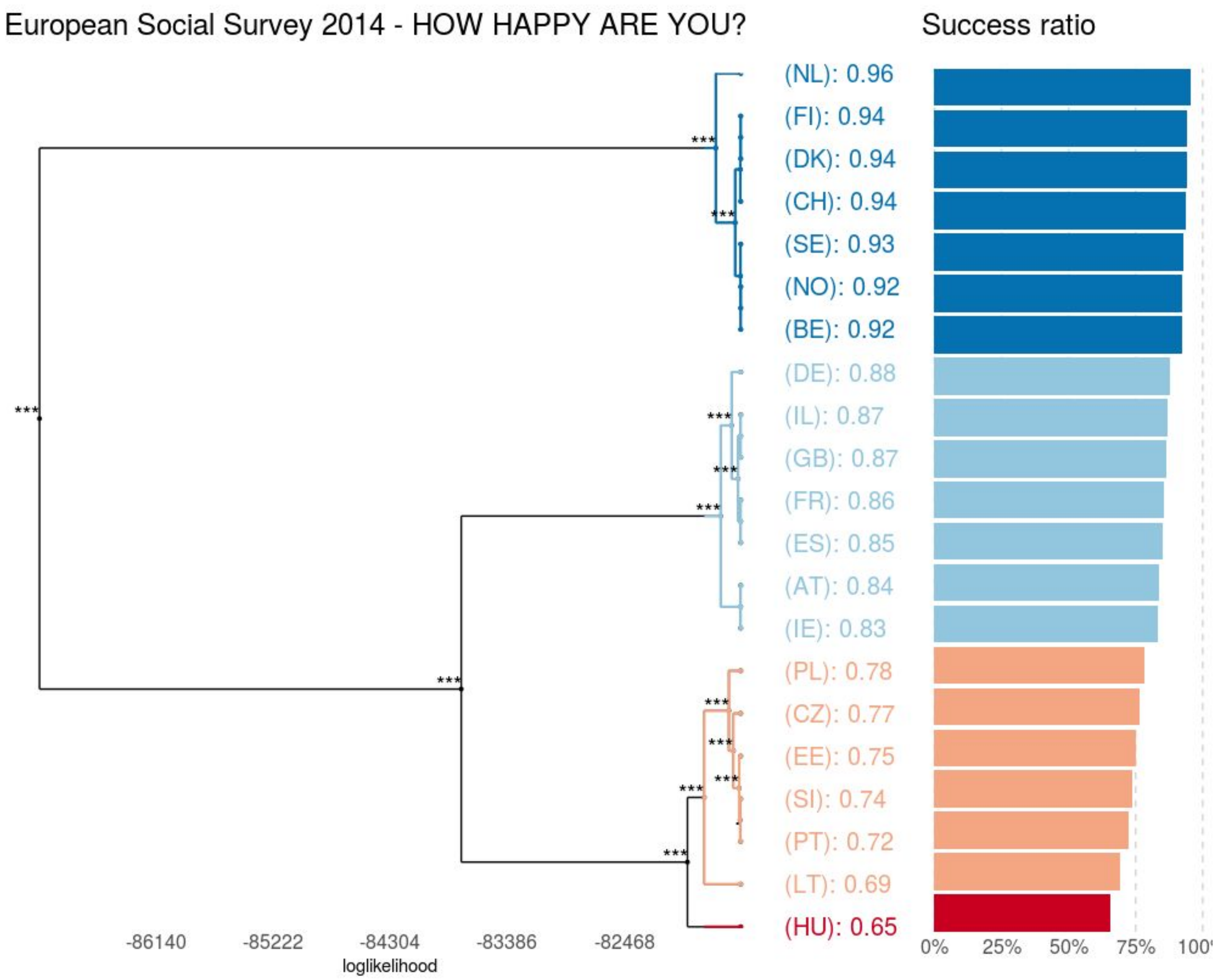

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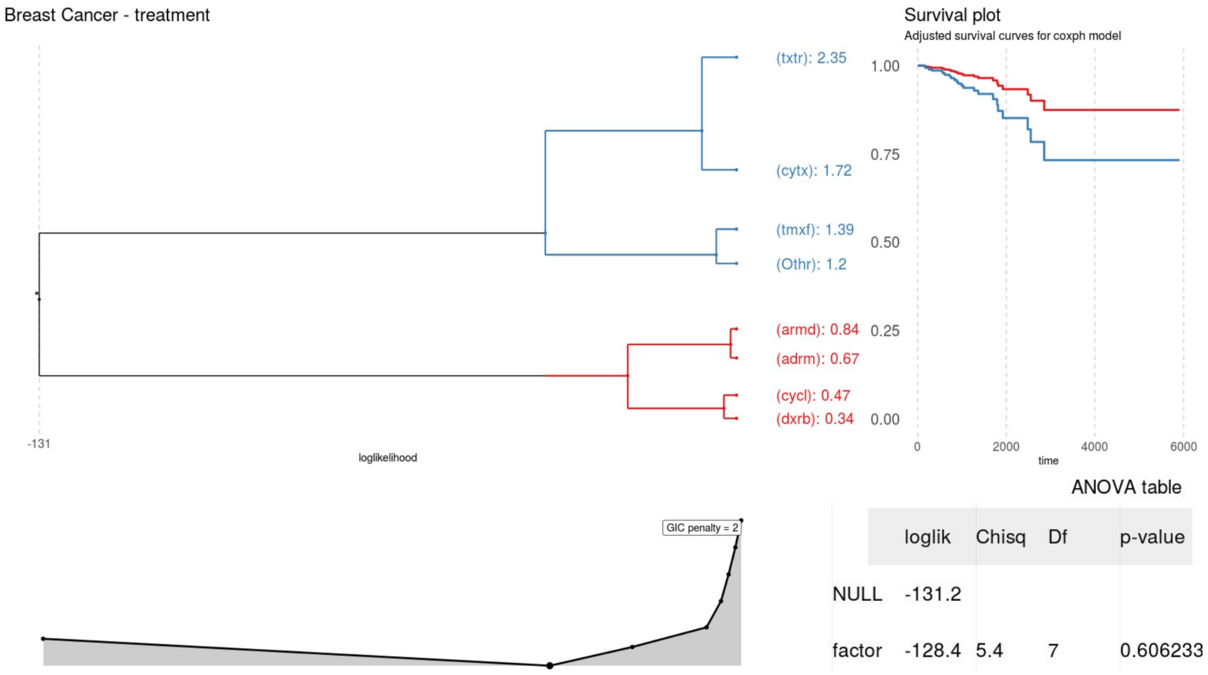
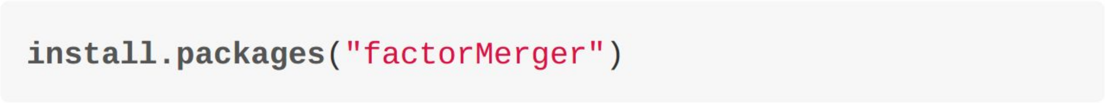


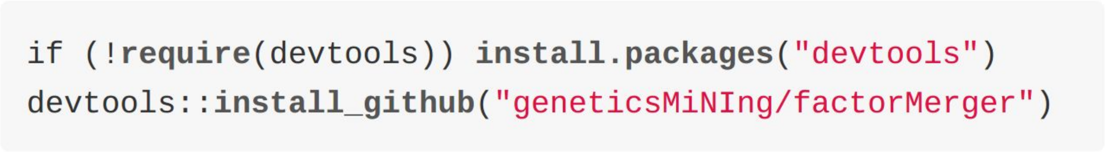
	loglik	Chisq	Df	p-value
NULL	-131.2			
factor	-128.4	5.4	7	0.606233

Install and use the package



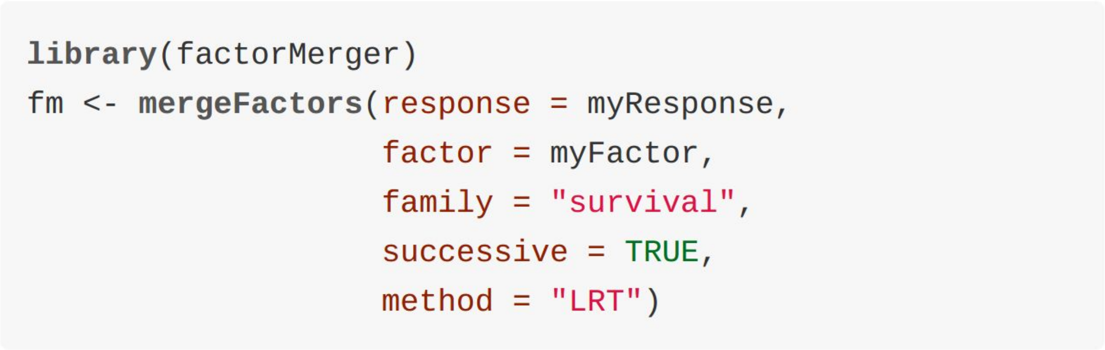
```r
install.packages("factorMerger")
```

CRAN



```r
if (!require(devtools)) install.packages("devtools")
devtools::install_github("geneticsMiNIng/factorMerger")
```

Github



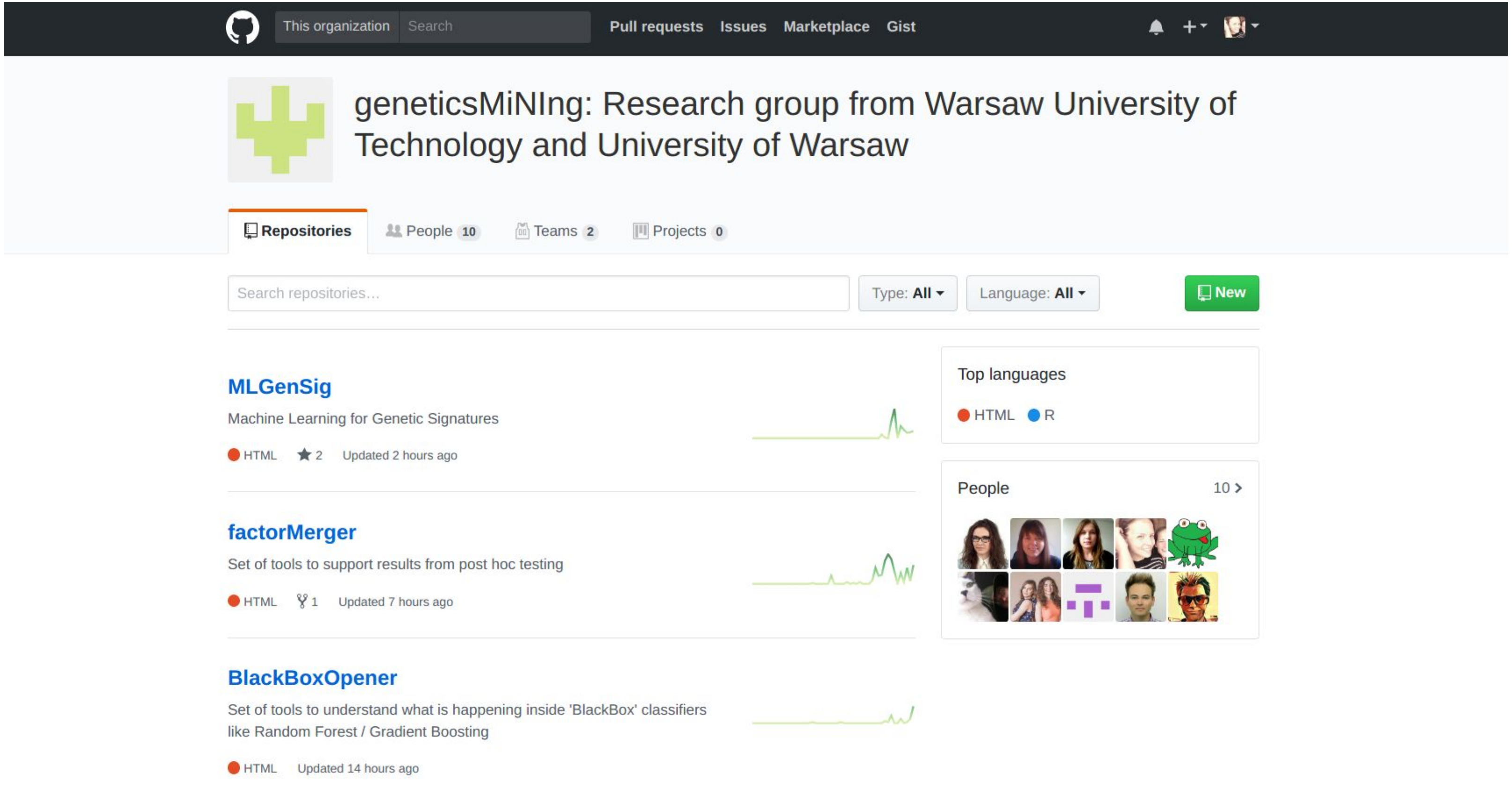
```r
library(factorMerger)
fm <- mergeFactors(response = myResponse,
                   factor = myFactor,
                   family = "survival",
                   successive = TRUE,
                   method = "LRT")
```

Find more: *https://github.com/geneticsMiNIng/factorMerger*

The aim of the factorMerger package

1. Create an algorithm which outputs an unequivocal data partition.
2. Improve visualizations.
3. Include other parametric models:
    a. multi dimensional Gaussian model,
    b. binomial model,
    c. survival model.

geneticsMiNIng



geneticsMiNIng: Research group from Warsaw University of Technology and University of Warsaw

MLGenSig

Machine Learning for Genetic Signatures

● HTML ★ 2 Updated 2 hours ago

factorMerger

Set of tools to support results from post hoc testing

● HTML 1 Updated 7 hours ago

BlackBoxOpener

Set of tools to understand what is happening inside 'BlackBox' classifiers like Random Forest / Gradient Boosting

● HTML Updated 14 hours ago

Top languages

● HTML ● R

People 10 >

Any questions?

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06-07-2017