Quor

Adriano Polpo* Carlos A. de B. Pereira†
Cassio P. de Campos‡

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Abstract

This text provides a minimalistic usage guide for the `Quor` package, driven by an example on how to use its main function.

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1 Introduction

This document presents the `Quor` package for `R` (R Core Team, 2012a), for more details see Pereira et al. (2014). It is an open source software under GPLv3. We illustrate trough examples how to use the main function in the package.

The package aims at performing a statistical analysis based on the confidence statement for the ordering of populations' quantiles. We considered non-parametric methods based on the order statistics using exact distributions, without the need of any asymptotic result. Numerical issues might happen when the number of samples is high (many hundreds), but it should nevertheless provide reasonable results.

2 Installing the package

In case you have not yet done so, the first thing to do before using the functions is to install and to load the library. The package can be obtained from http://code.google.com/p/quor/.

To install the package from the source file we use

*Federal University of São Carlos; email: polpo@ufscar.br
†University of São Paulo; email: cpereira@ime.usp.br
‡Queen's University Belfast; email: cassiopc@acm.org

```
> install.packages("Quor_VERSION.tar.gz",
+                  repos=NULL,type="source")
```

For more details on installing R or R packages please see R Core Team (2012b). After the package has been installed, one should "load" it by using the command

```
> library("Quor")
```

3 Confidence statement

Consider that $X_j = \{X_{j1}, \ldots, X_{jn_j}\}$, $j = 1, \ldots, g$, are independent identically distributed continuous random variables, and $X_1, \ldots, X_g$ is an arrangement of size g, that is, we have a sample for each one of the g different groups with size n_j. We are interested in evaluating the confidence level of the statement $Q_1 < Q_2 < \cdots < Q_g$, where Q_i represents a given quantile for the population i (they do not need to be the same). The function `conf.statement` gets groups from the g populations, one or more orderings to be evaluated, and the quantiles of interest for each population. The method is able to deal efficiently with many variables at the same time (as long as groups have the same length across different variables, but obviously not necessarily across groups).

Example 1 Pre-operative Gleason score provides valuable prognosis in cases of prostate cancer. However, for patients in the scale Gleason 7, it does not work as well. This might be because Gleason 7 tumors display great morphological heterogeneity among regions. The data set has microarray data of gene *RPS28* for both recurrent (R) and non-recurrent (NR) Gleason 7 prostate cancer patients. The following commands evaluate the confidence statement for the population median M_1 of the recurrent patients against the population median M_2 of the non-recurrent patients. By default, both $M_1 < M_2$ and $M_2 < M_1$ statements are evaluated.

```
> data(gleason7)
> d <- list(x1 = gleason7[1:5,1], x2 = gleason7[,2])
> conf.statement(d,verbose=FALSE)

CALL:  conf.statement ( d,FALSE )
------------------------------------------------------------
Confidence Statement of ordered population quantiles:
```

```
Number of permutations: 2
Number of groups: 2
Number of variables: 1
Logscale: FALSE

1 2  :  0.963025689125061
2 1  :  0.00104683637619019
Best :  0.963025689125061

Total time spent: 0.001 seconds
------------------------------------------------------------
```

4 Remarks

This simple document shows basic use of the `Quor` package. We invite the user to the help pages (available with the package) for more details about the parameters and to the technical paper which explains the method in detail.

References

R Core Team (2012a). *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria. ISBN: 3-900051-07-0.

R Core Team (2012b). *R Installation and Administration*. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-09-7.

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