

Using the FunciSNP data package
'FunciSNP: An R/Bioconductor Tool
Integrating Functional Non-coding Datasets with
Genetic Association Studies to
Identify Candidate Regulatory SNPs'

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Contents

1	Introduction	2
2	Contact information	2
3	sessionInfo	2

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1 Introduction

This is a simple data package, to be used with the *FunciSNP* package. Please refer to the *FunciSNP* vignette for more details.

2 Contact information

Questions or comments, please contact Simon G. Coetzee (scoetzee NEAR gmail POINT com) or Houtan Noushmehr, PhD (houtan NEAR usp POINT br).

3 sessionInfo

- R version 3.4.2 (2017-09-28), x86_64-pc-linux-gnu
- Locale: LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=en_US.UTF-8, LC_COLLATE=C, LC_MONETARY=en_US.UTF-8, LC_MESSAGES=en_US.UTF-8, LC_PAPER=en_US.UTF-8, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=en_US.UTF-8, LC_IDENTIFICATION=C
- Running under: Ubuntu 16.04.3 LTS
- Matrix products: default
- BLAS: /home/biocbuild/bbs-3.6-bioc/R/lib/libRblas.so
- LAPACK: /home/biocbuild/bbs-3.6-bioc/R/lib/libRlapack.so
- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Loaded via a namespace (and not attached): compiler 3.4.2, tools 3.4.2

Our recent paper describing FunciSNP and FunciSNP.data can be found in the Journal Nucleic Acids Research (doi:10.1093/nar/gks542).

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