

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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# 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 3.5.1 Patched (2018-07-12 r74967), 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 16.04.5 LTS
- Matrix products: default
- BLAS: /home/biocbuild/bbs-3.8-bioc/R/lib/libRblas.so
- LAPACK: /home/biocbuild/bbs-3.8-bioc/R/lib/libRlapack.so
- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Loaded via a namespace (and not attached): compiler 3.5.1, tools 3.5.1

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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