

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

Simon G. Coetzee<sup>°‡\*</sup>, Suhn K. Rhie<sup>‡</sup>, Benjamin P. Berman<sup>‡</sup>,  
Gerhard A. Coetzee<sup>‡</sup> and Houtan Noushmehr<sup>°‡†</sup>

April 12, 2014

<sup>°</sup>Faculdade de Medicina de Ribeirão Preto  
Departamento de Genética  
Universidade de São Paulo  
Ribeirão Preto, São Paulo, BRASIL

–  
<sup>‡</sup>Norris Cancer Center  
Keck School of Medicine  
University of Southern California  
Los Angeles, CA, USA

## Contents

<b>1</b>	<b>Introduction</b>	<b>2</b>
<b>2</b>	<b>Contact information</b>	<b>2</b>
<b>3</b>	<b>sessionInfo</b>	<b>2</b>

---

\*scoetzee NEAR gmail POINT com

†houtan NEAR usp POINT br

# 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 3.1.0 (2014-04-10), x86\_64-unknown-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
- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Loaded via a namespace (and not attached): tools 3.1.0

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

This document was proudly made using  $\LaTeX$  and **Sweave**.