## Finding statistics you can trust

### Jeff Leek

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## Sources of statistical software

```
biostat.jhsph.edu/~jleek/code/twitterMap.R
                                                                             http://biostat.jhsph.edu/~jleek/code/twitterMap.R
Apps 🚜 Simply Statistics 🏏 simplystats 🔯 Google Scholar 🦫 Google Music 👩 welch confer<mark>ence 🛵 google drive 🤛 google music</mark>
An R function to make a personalized map of people you follow and who follow you on twitter.
    R functions Copyright (C) 2011 Jeff Leek (jtleek@gmail.com), and the Simply Statistics Blog
    (http://simplystatistics.tumblr.com, http://twitter.com/simplystats)
    This program is free software: you can redistribute it and/or modify
    it under the terms of the GNU General Public License as published by
    the Free Software Foundation, either version 3 of the License, or
    (at your option) any later version.
    This program is distributed in the hope that it will be useful,
    but WITHOUT ANY WARRANTY; without even the implied warranty of
    MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE. See the
    GNU General Public License for more details, see <a href="http://www.gnu.org/licenses/">http://www.gnu.org/licenses/</a>>.
    These functions depend on the packages: twitteR, maps, geosphere, and RColorBrewer. It will
    attempt to install them if they are not installed when you source this function. Care
    should be used when using this function since the twitteR API has rate limiting in place.
    If you have a large number of followers, or run the function many times, you may be
    rate limited.
```

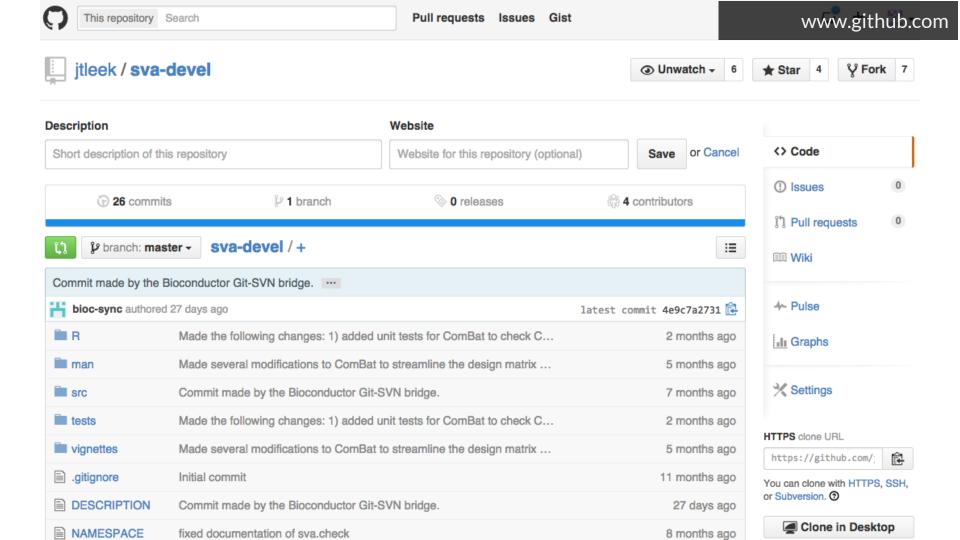
```
How to use:
    # Source the function
    source("http://biostat.jhsph.edu/~jleek/code/twitterMap.R")

# Make your twittermap
    twitterMap("simplystats")

#If your location can't be found or latitude longitude can't be calculated
    #choose a bigger city near you. The list of cities used by twitterMap
    #can be found like so:
    data(world.cities)
    grep("Baltimore",world.cities[,1])
```

# Then make the map using that big city

twitterMap("simplystats", userLocation="Baltimore")





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### <u>ABCDEFGHIJKLMNOPQRSTUVWXYZ</u>

A3: Accurate, Adaptable, and Accessible Error Metrics for Predictive Models

<u>abc</u> Tools for Approximate Bayesian Computation (ABC)

ABCanalysis Computed ABC Analysis

<u>abc.data</u> Data Only: Tools for Approximate Bayesian Computation (ABC)

<u>abcdeFBA</u> ABCDE\_FBA: A-Biologist-Can-Do-Everything of Flux Balance Analysis with this package

ABCExtremes ABC Extremes

ABCoptim Implementation of Artificial Bee Colony (ABC) Optimization
ABCp2 Approximate Bayesian Computational model for estimating P2

abctools Tools for ABC analyses

abd The Analysis of Biological Data
abf2 Load Gap-Free Axon ABF2 Files
abind Combine Multidimensional Arrays

<u>abn</u> Data Modelling with Additive Bayesian Networks

abundant Abundant regression and high-dimensional principal fitted components

acc Processes Accelerometer Data

<u>accelerometry</u> Functions for Processing Minute-to-Minute Accelerometer Data

AcceptanceSampling Creation and evaluation of Acceptance Sampling Plans

ACCLMA ACC & LMA Graph Plotting accrual Bayesian Accrual Prediction

accrued Visualization tools for partially accruing data

ACD Categorical data analysis with complete or missing responses

ace() and avas() for selecting regression transformations

acid Analysing Conditional Distributions of Income
acm4r Align-and-Count Method comparisons of RFLP data

ACNE Affymetrix SNP Probe-Summarization using Non-Negative Matrix Factorization

acnr Annotated Copy-Number Regions

Modelling dependence with multivariate Archimax (or any user-defined continuous) copulas

ran.rstudio.com/index.html

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### sva

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### Surrogate Variable Analysis

Bioconductor version: Release (3.1)

The sva package contains functions for removing batch effects and other unwanted variation in highthroughput experiment. Specifically, the sva package contains functions for the identifying and building surrogate variables for high-dimensional data sets. Surrogate variables are covariates constructed directly from high-dimensional data (like gene expression/RNA sequencing/methylation/brain imaging data) that can be used in subsequent analyses to adjust for unknown, unmodeled, or latent sources of noise. The sya package can be used to remove artifacts in three ways: (1) identifying and estimating surrogate variables for unknown sources of variation in high-throughput experiments (Leek and Storey 2007 PLoS Genetics, 2008 PNAS), (2) directly removing known batch effects using ComBat (Johnson et al. 2007 Biostatistics) and (3) removing batch effects with known control probes (Leek 2014 biorXiv). Removing batch effects and using surrogate variables in differential expression analysis have been shown to reduce dependence, stabilize error rate estimates, and improve reproducibility, see (Leek and Storey 2007 PLoS Genetics, 2008 PNAS or Leek et al. 2011 Nat. Reviews Genetics).

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#### Workflows »

Common Bioconductor workflows include:

- Oligonucleotide Arrays
- High-throughput Sequencing
- Counting Reads for Differential Expression (parathyroideSE vignette)
- Annotation
- Annotating Variants
- Annotating Ranges
- Flow Cytometry and other assays
- Candidate Binding Sites for Known Transcription Factors
- · Cloud-enabled cis-eQTL search and annotation
- · RNA-Seg workflow: gene-level exploratory analysis and differential expression
- Changing genomic coordinate systems with rtracklayer::liftOver
- Mass spectrometry and proteomics data analysis

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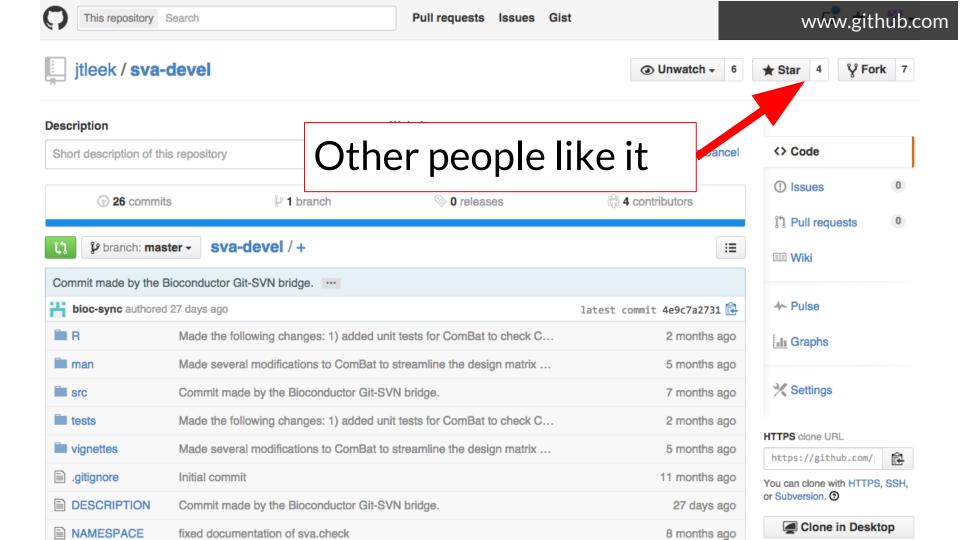
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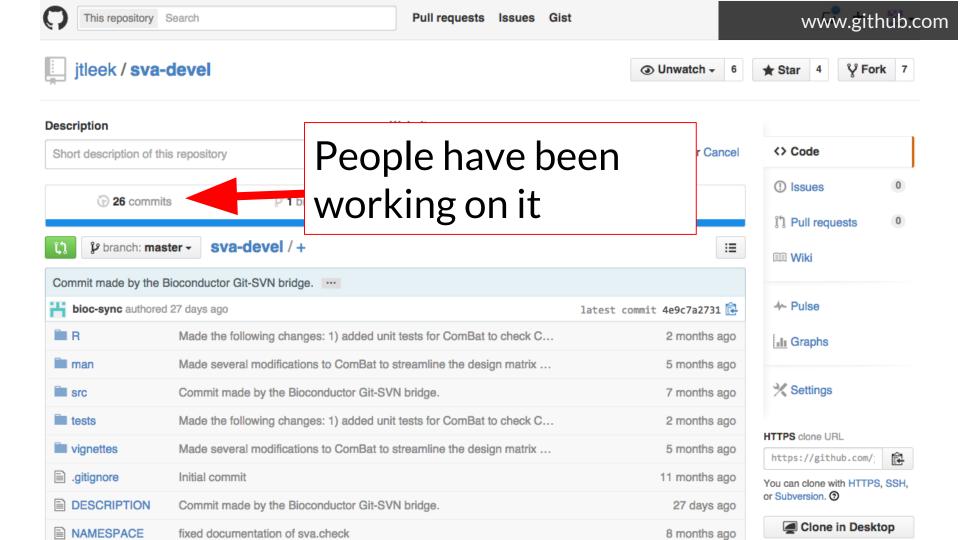
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