Package: shazam (via r-universe)

August 31, 2024

Type Package

Version 1.2.1.999

Date 2024-08-01

Title Immunoglobulin Somatic Hypermutation Analysis

Description Provides a computational framework for analyzing mutations
in immunoglobulin (Ig) sequences. Includes methods for Bayesian
estimation of antigen-driven selection pressure, mutational
load quantification, building of somatic hypermutation (SHM)
models, and model-dependent distance calculations. Also
includes empirically derived models of SHM for both mice and
humans. Citations: Gupta and Vander Heiden, et al (2015)
<doi:10.1093/bioinformatics/btv359>, Yaari, et al (2012)
<doi:10.1093/nar/gks457>, Yaari, et al (2013)
<doi:10.3389/fimmu.2013.00358>, Cui, et al (2016)
<doi:10.4049/jimmunol.1502263>.

License AGPL-3

URL http://shazam.readthedocs.io

BugReports https://bitbucket.org/kleinstein/shazam/issues

LazyData true

BuildVignettes true

VignetteBuilder knitr, rmarkdown

Encoding UTF-8

Depends R (>= 4.0), ggplot2 (>= 3.4.0)

Imports alakazam (>= 1.3.0), ape, diptest, doParallel, dplyr (>= 1.0),
foreach, graphics, grid, igraph (>= 1.5.0), iterators,
KernSmooth, lazyeval, MASS, methods, parallel, progress, rlang,
scales, seqinr, stats, stringi (>= 1.1.3), tidyr, tidyselect,
utils

Suggests knitr, rmarkdown, testthat

Collate 'Shazam.R' 'Core.R' 'RegionDefinitions.R' 'Baseline.R'
'ConvertNumbering.R' 'MutationProfiling.R' 'Deprecated.R'
'DistToNearest.R' 'MutationDefinitions.R' 'RegionsExtend.R'
'Shmulate.R' 'TargetingModels.R' 'kedd.R'

RoxygenNote 7.3.1

Repository https://ssnn-airr.r-universe.dev

RemoteUrl https://bitbucket.org/kleinstein/shazam

RemoteRef HEAD

RemoteSha ce27e4098f8e25022a0fee9ece08b6bd9981ca2f