Package: scoper (via r-universe)

September 11, 2024

Type Package

Version 1.3.1.999

Date 2024-08-01

Title Spectral Clustering-Based Method for Identifying B Cell Clones

Description Provides a computational framework for identification of B
cell clones from Adaptive Immune Receptor Repertoire sequencing
(AIRR-Seq) data. Three main functions are included
(identicalClones, hierarchicalClones, and spectralClones) that
perform clustering among sequences of BCRs/IGs (B cell
receptors/immunoglobulins) which share the same V gene, J gene
and junction length. Nouri N and Klein-
stein SH (2018) <doi:10.1093/bioinformatics/bty235>. Nouri N and Kleinstein SH
(2019) <doi:10.1101/788620>. Gupta NT, et al. (2017) <doi:10.4049/jimmunol.1601850>.

License AGPL-3

URL https://scoper.readthedocs.io

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

LazyData true

BuildVignettes true

VignetteBuilder knitr

Encoding UTF-8

LinkingTo Rcpp

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

Imports alakazam (>= 1.3.0), shazam (>= 1.2.0), data.table,
doParallel, dplyr (>= 1.0), foreach, methods, Rcpp (>=
0.12.12), rlang, scales, stats, stringi, tidyr (>= 1.0)

Suggests knitr, rmarkdown, testthat

RoxygenNote 7.3.1

Collate 'Data.R' 'Scoper.R' 'Functions.R' 'RcppExports.R'

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

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

RemoteRef HEAD
RemoteSha 7446db426974407e2ff50d6584ab354ccac7ca85