

Package: tigger (via r-universe)

September 2, 2024

Type Package

Version 1.1.1.999

Date 2024-08-14

Title Infers Novel Immunoglobulin Alleles from Sequencing Data

Description Infers the V genotype of an individual from immunoglobulin (Ig) repertoire sequencing data (AIRR-Seq, Rep-Seq). Includes detection of any novel alleles. This information is then used to correct existing V allele calls from among the sample sequences. Citations: Gadala-Maria, et al (2015) [doi:10.1073/pnas.1417683112](https://doi.org/10.1073/pnas.1417683112), Gadala-Maria, et al (2019) [doi:10.3389/fimmu.2019.00129](https://doi.org/10.3389/fimmu.2019.00129).

License AGPL-3

URL <http://tigger.readthedocs.io>

BugReports <https://bitbucket.org/kleinsteintigger/issues>

LazyData true

BuildVignettes true

VignetteBuilder knitr

Encoding UTF-8

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

Imports alakazam (>= 1.3.0), dplyr (>= 1.0.0), doParallel, foreach, graphics, gridExtra, gtools, iterators, lazyeval, parallel, rlang, stats, stringi, tidyr (>= 1.1.0), utils

Suggests knitr, rmarkdown, testthat

RoxygenNote 7.3.2

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

RemoteUrl <https://bitbucket.org/kleinsteintigger>

RemoteRef HEAD

RemoteSha 87d69a0b370559ef0c5a805436141bb3a2e432fd