

Package: tigger (via r-universe)

June 1, 2026

Type Package

Version 1.1.3

Date 2026-04-13

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://github.com/immcantation/tigger/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 7.3.3

Config/pak/sysreqs

libglpk-dev libbz2-dev libicu-dev liblzma-dev libxml2-dev libx11-dev xz-utils zlib1g-dev

Repository <https://immcantation.r-universe.dev>

Date/Publication 2026-04-13 19:01:21 UTC

RemoteUrl <https://github.com/immcantation/tigger>

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RemoteRef HEAD

RemoteSha 157027c0b10037161ace09e53030795f77bc2ab2