

# Package: scoper (via r-universe)

May 26, 2026

**Type** Package

**Version** 1.5.0.999

**Date** 2026-05-25

**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 Kleinstein SH (2018) <[doi:10.1093/bioinformatics/bty235](https://doi.org/10.1093/bioinformatics/bty235)>. Nouri N and Kleinstein SH (2019) <[doi:10.1101/788620](https://doi.org/10.1101/788620)>. Gupta NT, et al. (2017) <[doi:10.4049/jimmunol.1601850](https://doi.org/10.4049/jimmunol.1601850)>.

**License** AGPL-3

**URL** <https://scoper.readthedocs.io>

**BugReports** <https://github.com/immcantation/scoper/issues>

**LazyData** true

**BuildVignettes** true

**VignetteBuilder** knitr

**Encoding** UTF-8

**LinkingTo** Rcpp

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

**Imports** alakazam (>= 1.4.1), shazam (>= 1.3.0), data.table, doParallel, dplyr (>= 1.0), fastcluster, foreach, methods, Rcpp (>= 0.12.12), rlang, scales, stats, stringi, tidyr (>= 1.0)

**Suggests** knitr, rmarkdown, testthat (>= 3.0.0)

**RoxygenNote** 7.3.3

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

**Config/pak/sysreqs**

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

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

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**RemoteUrl** <https://github.com/immcantation/scoper>

**RemoteRef** HEAD

**RemoteSha** 810ad5a174a0fa8a40d73318cd5dfdcfcff31bf8