

Package: ClinicalVariantR (via r-universe)

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Title ACMG/AMP Germline Variant Interpretation from Annotated VCF Files

Version 0.99.0

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Description ClinicalVariantR is an interactive Shiny platform for evidence-based germline variant classification under ACMG/AMP 2015 guidelines. It accepts VEP-, SnpEff-, or ANNOVAR-annotated VCF files, applies automated and curator-guided ACMG criteria, supports streaming analysis of large call sets, and exports structured per-criterion evidence with reproducibility metadata.

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URL <https://github.com/safarafique/ClinicalVariantR>

BugReports <https://github.com/safarafique/ClinicalVariantR/issues>

biocViews Software, VariantAnnotation, Genetics, Sequencing, Classification, Visualization, GUI

Encoding UTF-8

LazyData false

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

VignetteBuilder knitr

Depends R (>= 4.5.0)

Imports shiny (>= 1.8.0), bslib, DT, data.table, readr, jsonlite, VariantAnnotation, methods, stats, utils

Suggests BiocStyle, knitr, rmarkdown, testthat (>= 3.0.0), BiocCheck, shinytest2

Config/testthat/edition 3

Config/Needs/website BiocStyle
SystemRequirements Optional: bcftools for accelerated VCF streaming on Linux/WSL.
Config/pak/sysreqs cmake make libbz2-dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev libx11-dev xz-utils zlib1g-dev
Repository https://biocstaging.r-universe.dev
Date/Publication 2026-07-16 09:40:22 UTC
RemoteUrl https://github.com/BiocStaging/ClinicalVariantR
RemoteRef HEAD
RemoteSha 2c08894bfba4c5dd5aa1f1e066898d62a9918a13

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ClinicalVariantR	<i>Build the ClinicalVariantR Shiny application</i>
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Description

Returns a Shiny app object for ACMG/AMP germline variant classification. Following Bioconductor Shiny guidelines, this function **returns** the app and does not launch it. Call shiny::runApp() yourself.

Usage

```
ClinicalVariantR(...)  
  
ClinicalVariantRApp(...)
```

Arguments

... Reserved for future options (currently ignored).

Value

A shiny.appobj created by shiny::shinyApp().

See Also

[ClinicalVariantRApp](#)

Examples

```
stopifnot(is.function(ClinicalVariantR))  
# To launch interactively:  
# shiny::runApp(ClinicalVariantR())
```

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