

# Package: ClinicalVariantR (via r-universe)

September 30, 2026

**Title** Clinical Variant Interpretation Using ACMG/AMP Germline Criteria

**Version** 0.99.3

**Date** 2026-07-22

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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 and applies automated plus curator-guided ACMG criteria. The package supports streaming analysis of large call sets and exports structured per-criterion evidence with reproducibility metadata for clinical review.

**License** MIT + file LICENSE

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

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

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

**Encoding** UTF-8

**LazyData** false

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 8.0.0

**VignetteBuilder** knitr

**Depends** R (>= 4.5.0)

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

**Suggests** BiocStyle, knitr, rmarkdown, ggplot2, shinyjs, 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** 2026-07-31 05:59:19 UTC  
**RemoteUrl** https://github.com/BiocStaging/ClinicalVariantR  
**RemoteRef** HEAD  
**RemoteSha** 72cd727e3f1e64ca699d8c6630e2ff91c01fe78d

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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(...)

Arguments

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

Value

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

See Also

[ClinicalVariantRApp](#)

Examples

```
stopifnot(is.function(ClinicalVariantR))
stopifnot(is.function(ClinicalVariantRApp))
```

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|                     |                                                   |
|---------------------|---------------------------------------------------|
| ClinicalVariantRApp | <i>Alias for</i> <a href="#">ClinicalVariantR</a> |
|---------------------|---------------------------------------------------|

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**Description**

Alias for [ClinicalVariantR](#)

**Usage**

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

**Arguments**

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

**Value**

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

**Examples**

```
stopifnot(is.function(ClinicalVariantRApp))
```

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