

# Package: GNOSIS (via r-universe)

May 29, 2026

**Type** Package

**Title** Genomics explorer using statistical and survival analysis in R

**Version** 1.10.0

**Description** GNOSIS incorporates a range of R packages enabling users to efficiently explore and visualise clinical and genomic data obtained from cBioPortal. GNOSIS uses an intuitive GUI and multiple tab panels supporting a range of functionalities. These include data upload and initial exploration, data recoding and subsetting, multiple visualisations, survival analysis, statistical analysis and mutation analysis, in addition to facilitating reproducible research.

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**Imports** DT, fontawesome, shinycssloaders, cBioPortalData, shinyjs, reshape2, RColorBrewer, survival, survminer, stats, compareGroups, rpart, partykit, DescTools, car, rstatix, fabricatr, shinylogs, magrittr

**Depends** R (>= 4.3.0), shiny, shinydashboard, shinydashboardPlus, dashboardthemes, shinyWidgets, shinymeta, tidyverse, operator.tools, maftools

**Suggests** BiocStyle, knitr, rmarkdown

**biocViews** Software, ShinyApps, Survival, GUI

**BugReports** <https://github.com/Lydia-King/GNOSIS/issues>

**URL** <https://github.com/Lydia-King/GNOSIS/>

**Video** <https://doi.org/10.5281/zenodo.5788544>

**VignetteBuilder** knitr

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.2.3

**Config/pak/sysreqs** libcairo2-dev cmake libfontconfig1-dev libfreetype6-dev libfribidi-dev libgmp3-dev make libharfbuzz-dev libbz2-dev libicu-dev libjpeg-dev liblzma-dev libpng-dev libsecret-1-dev libtiff-dev libuv1-dev libwebp-dev libxml2-dev libmpfr-dev libssl-dev libx11-dev xz-utils zlib1g-dev

**Repository** <https://bioc-release.r-universe.dev>  
**Date/Publication** 2026-04-28 13:01:52 UTC  
**RemoteUrl** <https://github.com/bioc/GNOSIS>  
**RemoteRef** RELEASE\_3\_23  
**RemoteSha** 9027d72da7eb2f41fcb377bd3df8f9675aa32aa0

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GNOSIS	<i>#' Initialise GNOSIS</i>
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### Description

The shiny app will allow the user to explore and analyse clinical and copy number data uploaded manually or selected from a dataframe containing datasets available through cBioPortal.

### Usage

```
GNOSIS(...)
```

### Arguments

```
... Further arguments to the runApp function
```

### Details

Note. This shiny app is an updated version of the app published in [HRB Open Research](#). For details on version updates see NEWS.

### Value

Mainly called for the side effect of displaying the shiny app in a browser

### Examples

```
if (interactive()) {
  GNOSIS()
}
```

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