

# Package ‘GNOSIS’

November 14, 2025

**Type** Package

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

**Version** 1.9.0

**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

**git\_url** <https://git.bioconductor.org/packages/GNOSIS>

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Contents

|                  |   |
|------------------|---|
| GNOSIS . . . . . | 2 |
| Index            | 3 |

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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()
}
```

# Index

GNOSIS, [2](#)