

Package ‘GNOSIS’

February 2, 2026

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

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Author Lydia King [aut, cre] (ORCID: <<https://orcid.org/0000-0002-0696-9811>>),
Marcel Ramos [ctb]
Maintainer Lydia King <l.king18@universityofgalway.ie>

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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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