Package ‘GNOSIS’

May 4, 2026

Type Package

Title Genomics explorer using statistical and survival analysis in R

Version 1.11.0

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

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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`>

Contents

`GNOSIS` *#' Initialise GNOSIS*

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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