Package 'GA4GHshiny'

November 9, 2026

Type Package

Title Shiny application for interacting with GA4GH-based data servers

Version 1.34.0

Description GA4GHshiny package provides an easy way to interact with data servers based on Global Alliance for Genomics and Health (GA4GH) genomics API through a Shiny application. It also integrates with Beacon Network.

License GPL-3

Depends GA4GHclient

Imports AnnotationDbi, BiocGenerics, dplyr, DT, Seqinfo, GenomeInfoDb, openxlsx, GenomicFeatures, methods, purrr, S4Vectors, shiny, shinyjs, tidyr, shinythemes

Suggests BiocStyle, org.Hs.eg.db, knitr, rmarkdown, testthat, TxDb.Hsapiens.UCSC.hg19.knownGene

LazyData TRUE

RoxygenNote 7.3.2

VignetteBuilder knitr

URL https://github.com/labbcb/GA4GHshiny

BugReports https://github.com/labbcb/GA4GHshiny/issues

biocViews GUI

git_url https://git.bioconductor.org/packages/GA4GHshiny

git_branch RELEASE_3_23

git_last_commit c5b6b20

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-08

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`GA4GHshiny-package` *Shiny application for interacting with GA4GH-based data servers*

Description

GA4GHshiny package provides an easy way to interact with data servers based on Global Alliance for Genomics and Health (GA4GH) Genomics API through a Shiny application. It also integrates with Beacon Network.

Author(s)

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`app` *Open web application*

Description

Web application for interacting with GA4GH API data servers.

Usage

```
app(host, orgDb = NA_character_, txDb = NA_character_,
  serverName = "GA4GHshiny")
```

Arguments

`host`	Character vector of an URL of GA4GH API data server endpoint.
`orgDb`	character vector of an org.Db package.
`txDb`	character vector of a TxDb package.
`serverName`	character vector of the server name. Default: GA4GHshiny.

Details

This application is dependent of which data the server provides trough GA4GH API. If some of tables or graphic charts not appear, the server connected may not provide the necessary data. For example, INFO data.

Value

Shiny application object.

Examples

```
if (interactive()) {
  library(org.Hs.eg.db)
  library(TxDb.Hsapiens.UCSC.hg19.knownGene)
  app("http://1kgenomes.ga4gh.org/", orgDb = "org.Hs.eg.db",
    txDb = "TxDb.Hsapiens.UCSC.hg19.knownGene")
}
```

---

countGenotype *Count genotype*

Description

Summarize a list of genotype data. Variant calls with no coverage (./.) do not enter in this count.

Usage

```
countGenotype(genotype)
```

Arguments

genotype	list of integer vectors of length 2.

Value

data.frame of 1 row containing the columns below.

- ref.homozygous reference homosygous (e.g. 0/0);
- alt.heterozygous alternate heterozygous (e.g. 0/1, 1/2);
- ref.homozygous reference homozygous (e.g. 1/1, 2/2);
- total the sum of the three previous columns.

Examples

```
countGenotype(genotype = list(c(0,0), c(0,1), c(1,2), c(1,1), c(2,2)))
```

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