Package ‘GA4GHshiny’

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Type Package
Title Shiny application for interacting with GA4GH-based data servers
Version 1.26.0
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.
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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.

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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.
countGenotype

Value

Shiny application object.

Examples

```r
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

```r
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

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