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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Author Welliton Souza [aut, cre], Benilton Carvalho [ctb], Cristiane Rocha [ctb], Elizabeth Borgognoni [ctb]
Maintainer Welliton Souza <well309@gmail.com>
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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)

Welliton Souza, Benilton Carvalho, Cristiane Rocha, Elizabeth Borgognoni
Maintainer: Welliton Souza <well309@gmail.com>

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 through 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

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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