Package ‘GA4GHshiny’

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Type Package
Title Shiny application for interacting with GA4GH-based data servers
Version 1.24.0
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
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    openxlsx, GenomicFeatures, methods, purrr, S4Vectors, shiny,
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    TxDb.Hsapiens.UCSC.hg19.knownGene
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VignetteBuilder knitr
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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.

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**app**

*Open web application*

**Description**

Web application for interacting with GA4GH API data servers.

**Usage**

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

**Arguments**

- `host`: Character vector of an URL of GA4GH API data server endpoint.
- `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**

`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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