IGV-webapp

kike

12/6/2019

IGV-WebApp

I have found IGV-webapp suited for situations in which we are interested in creating a genome session browser and then share that session online via a URL with the community IGV-WebApp.

Create session from public files in Google Cloud Storage (GCS)

We are creating a JSON file that helps us building the session when we've a lot of files. We can then upload directly this json file to IGVWebApp. For the moment it's only working for bigwig files.

We just need:

- * Default session json file (mine is for hg19, but feel free to change and download it)
- * Name of the GCS bucket
- * Directory path of the folder with all files in the GCS bucket
- * csv annotation file where each row contains the name of the file (all bigwigs), and it's ID
- * Final json file name

```
annotation_file_name <- "./hg19_browser_links.csv"
small_jason_file_name <- "./igv-app-test_hg19.json"
bucket_name <- "any_bucket_name"
dir_path <- "any_dir_path"
final_json <- "./final.json"

library(RJSONIO)

annotation <- read.csv(annotation_file_name)
start_json <- start_json <-RJSONIO::fromJSON(small_jason_file_name)
tracks <- start_json$tracks</pre>
```

Annotation

head(annotation)

```
## Library ID type url
## 1 11 DO_skhds bigWig file1.bigWig
## 2 12 DO_fdfdfdf bigWig File2.bigWig
## 3 13 D3_gfgf bigWig File3.bigWig
```

```
for (i in 1:nrow(annotation))
{
   new_track <- annotation[i,]
   name <- as.character(new_track$ID)
   filename <- strsplit(as.character(new_track$url),dir_path)[[1]][2]
   format <- "bigwig"
   url <- paste("gs://",bucket_name,dir_path,filename,sep="")</pre>
```