

Package ‘hubR’

January 7, 2022

Title Build UCSC track hubs

Version 0.0.0.9000

URL <https://github.com/>

Description Takes a list of bigwig file names, Amazon S3 bucket info and generates a UCSC genome browser track hub along with necessary hmac signatures.

License GPL-3

Imports openssl, digest, RCurl, RColorBrewer

Suggests knitr, rmarkdown, testthat

Encoding UTF-8

VignetteBuilder knitr

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

NeedsCompilation no

Author Nelson Johansen [aut, cre]

Maintainer Nelson Johansen <nelson.johansen@alleninstitute.org>

R topics documented:

create.signatures	1
generate.track.hub	2
hubR	3

create.signatures	<i>Computes HMAC signatures</i>
-------------------	---------------------------------

Description

This function takes in a vector of bigwig file names and Amazon S3 credentials to generate hmac signatures to access .bw files.

Usage

```
create.signatures(track.dir, secret.key, bigwigs)
```

Arguments

track.dir	Amazon S3 bucket name that stores the .bw files
secret.key	Amazon S3 secret access key
bigwigs	Bigwig file names which exactly match those in 'track.dir'

generate.track.hub *Build multi-wig track hub*

Description

This function loads a file as a matrix. It assumes that the first column contains the rownames and the subsequent columns are the sample identifiers. Any rows with duplicated row names will be dropped with the first one being kept.

Usage

```
generate.track.hub(
  hmac.encoded,
  track.dir,
  access.key,
  bigwigs,
  pseudo.names,
  long.labels,
  colors,
  species,
  region,
  type,
  cluster,
  genome,
  output.track.file,
  email
)
```

Arguments

hmac.encoded	Bigwig file signatures computed with <code>create.signatures</code>
track.dir	Amazon S3 bucket name that stores the .bw files
access.key	Amazon S3 access key ID
bigwigs	Bigwig file names which exactly match those in 'track.dir'
pseudo.names	Short labels to give each track. If NULL the function attempts to gather from .bw file name: pseudo.names-*.bw
long.labels	Detailed labels to give each track. If NULL the function attempts to gather from .bw file name: long.labels-*.bw
colors	Colors (in R, G, B format) to give the tracks. If NULL colors will be auto-generated.
species	Species information
region	Brain region information

type	Data type (ATAC, Multiome, etc.)
cluster	Cluster label information
genome	Genome information
output.track.file	Output track hub filename. Default: trackDB.txt
email	Correspondence email

Value

A matrix of the infile

hubR	<i>Builds a track hub for the UCSC genome browser</i>
------	---

Description

This function takes in a vector of bigwig file names along associated metadata and Amazon S3 credentials. It assumes the user has created an S3 bucket 'track.dir' where the bigwig files will be accessible on S3. Any changes to the bigwig file names or 'track.dir' will require the regeneration of HMAC signatures and the hub file.

Usage

```
hubR(
  track.dir,
  access.key,
  secret.key,
  bigwigs,
  pseudo.names = NULL,
  long.labels = NULL,
  colors = NULL,
  species,
  region,
  type,
  cluster,
  genome,
  output.track.file = "trackDB.txt",
  email = ""
)
```

Arguments

track.dir	Amazon S3 bucket name that stores the .bw files
access.key	Amazon S3 access key ID
secret.key	Amazon S3 secret access key
bigwigs	Bigwig file names which exactly match those in 'track.dir'
pseudo.names	Short labels to give each track. If NULL the function attempts to gather from .bw file name: pseudo.names-*.bw

<code>long.labels</code>	Detailed labels to give each track. If NULL the function attempts to gather from .bw file name: <code>long.labels-*.bw</code>
<code>colors</code>	Colors (in R, G, B format) to give the tracks. If NULL colors will be auto-generated.
<code>species</code>	Species information
<code>region</code>	Brain region information
<code>type</code>	Data type (ATAC, Multiome, etc.)
<code>cluster</code>	Cluster label information
<code>genome</code>	Genome information
<code>output.track.file</code>	Output track hub filename. Default: <code>trackDB.txt</code>
<code>email</code>	Correspondence email