Package 'hubR'

February 18, 2022

Title Build UCSC track hubs

Version 0.1.1

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 neccessary hmac signatures.

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Depends openssl,
digest,
RCurl,
aws.s3,
RColorBrewer

Suggests knitr,
rmarkdown,
testthat

Encoding UTF-8

LazyData true

VignetteBuilder knitr

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

R topics documented:

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hubR   *Builds a track hub for the UCSC genome browser*

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.bucket' where the bigwig files will be accessible on S3. Any changes to the bigwig file names or 'track.bucket' will require the regeneration of HMAC signatures and the hub file.

Usage

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

Arguments

track.bucket	Amazon S3 bucket name that stores the .bw files
hub.bucket	Amazon S3 bucket name that stores the track hub .txt file
bigwigs	Bigwig file names which exactly match those in 'track.bucket'
pseudo.names	Short labels to give each track. If NULL the function attemps to gather from .bw file name: pseudo.names-*.bw
long.labels	Detailed labels to give each track. If NULL the function attemps 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, must be a valid UCSC genome browser genome.
data.dir	Location of the bigwig files and where the trackDB.txt will be saved locally
output.track.file	
	Output track hub filename. Default: trackDB.txt
email	Correspondence email

Value

Hub URL

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setup.aws	*Setup aws.s3*

Description

This function takes in the users AWS credentials and primes aws.s3.

Usage

```
setup.aws(access.key, secret.key, region = "us-west-2")
```

Arguments

access.key	Amazon S3 access key ID
secret.key	Amazon S3 access key ID
region	Amazon S3 region: default 'us-west-2'

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setup.awscli	*Setup awscli2*

Description

This function adds an awscli2 install to the users PATH

Usage

```
setup.awscli(
  awscli.path = "/allen/programs/celltypes/workgroups/hct/NelsonJ/Home/v2/2.4.9/bin"
)
```

Arguments

awscli.path	directory where awscli2 was installed

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