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 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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add.buckets   *Create buckets*

Description

This function creates a track and hub bucket on Amazon S3

Usage

```
add.buckets(track.bucket, hub.bucket)
```

Arguments

track.bucket	Name to be given for track bucket on Amazon S3. (Must be all lower-case)
hub.bucket	Name to be given for hub bucket on Amazon S3. (Must be all lower-case)

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create.signatures   *Computes HMAC signatures*

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.bucket, secret.key, bigwigs)
```

Arguments

track.bucket	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.bucket'

---

fill.hub.bucket   *Upload hub file to hub bucket*

Description

This function takes as input the data directory and file name for the hub file and uploads it to the hub bucket.

Usage

```
fill.hub.bucket(data.dir, hub.file, hub.bucket)
```

Arguments

data.dir	Directory where the bigwig files
hub.file	Hub file produced by hubR
hub.bucket	Name of the hub bucket on Amazon S3.

---

fill.track.bucket *Populate track bucket with bigwigs*

Description

This function takes as input the data directory and file names for the bigwig files and uploads them to the track bucket.

Usage

```
fill.track.bucket(data.dir, bigwigs, track.bucket)
```

Arguments

data.dir	Directory where the bigwig files exist
bigwigs	Names of the bigwig files
track.bucket	Name of the track bucket on Amazon S3.

---

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 kepted.

Usage

```
generate.track.hub(
  hmac.encoded,
  track.bucket,
  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 `create.signatures`
`track.bucket`	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.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
`output.track.file`	
	Output track hub filename. Default: trackDB.txt
`email`	Correspondence email

Value

A matrix of the infile

`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,
  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.bucket`	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.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
`output.track.file`	
	Output track hub filename. Default: trackDB.txt
`email`	Correspondence email

`set.bucket.permissions`

Update bucket permission

Description

This function is intended to update the track bucket to be completly private

Usage

```
set.bucket.permissions(track.bucket, access.key, secret.key)
```

Arguments

`track.bucket`	Name of the track bucket on Amazon S3.
`access.key`	Amazon S3 access key ID
`secret.key`	Amazon S3 access key ID

---

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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