

# 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

**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

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add.buckets	<i>Create buckets</i>
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### 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	<i>Computes HMAC signatures</i>
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### 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'

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fill.hub.bucket	<i>Upload hub file to hub bucket</i>
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### 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.

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fill.track.bucket	<i>Populate track bucket with bigwigs</i>
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### 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.

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generate.track.hub	<i>Build multi-wig track hub</i>
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### 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.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 <code>create.signatures</code>
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 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

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

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```
set.bucket.permissions
```

*Update bucket permission*

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### Description

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

### Usage

```

set.bucket.permissions(
  track.bucket,
  access.key = "AKIAXEERKKJCONE3EJV0",
  secret.key = "TTGhaHb9gbWobMf+x6wcILN5f9CKfdXT1sVqrd1o"
)

```

### 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

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`setup.aws`*Setup aws.s3*

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**Description**

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

**Usage**

```
setup.aws(  
  access.key = "AKIAXEERKKJCONE3EJV0",  
  secret.key = "TTGhaHb9gbWobMf+x6wcILN5f9CKfdXT1sVqrd1o",  
  region = "us-west-2"  
)
```

**Arguments**

<code>access.key</code>	Amazon S3 access key ID
<code>secret.key</code>	Amazon S3 access key ID
<code>region</code>	Amazon S3 region: default 'us-west-2'

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