

# 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 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

## R topics documented:

hubR . . . . .	2
setup.aws . . . . .	3
setup.awsccli . . . . .	3
<b>Index</b>	<b>4</b>

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 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, 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	<i>Setup aws.s3</i>
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**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.awsccli	<i>Setup awsccli2</i>
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**Description**

This function adds an awsccli2 install to the users PATH

**Usage**

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

**Arguments**

awsccli.path	directory where awsccli2 was installed
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# Index

hubR, [2](#)

setup.aws, [3](#)

setup.awsccli, [3](#)