

# Package ‘hubR’

September 9, 2022

**Title** Build UCSC track hubs

**Version** 0.1.5

**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,  
dplyr

**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 builds the track hub and handles all uploading to AWS S3 buckets as named in track.bucket and hub.bucket. Any changes to the bigwig file names or 'track.bucket' will require the regeneration of HMAC signatures and the hub file (rerun hubR).

**Usage**

```
hubR(
  track.bucket,
  hub.bucket,
  data.dir,
  species,
  region,
  type,
  taxonomy,
  genome,
  bigwigs = NULL,
  track.names = NULL,
  track.labels = NULL,
  colors = NULL,
  groupby = NULL,
  hub.type = "multiwig",
  output.track.file = "trackDB.txt",
  email = "nelson.johansen@alleninstitute.org"
)
```

**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
data.dir	Location of the bigwig files and where the trackDB.txt will be saved locally
species	Species information
region	Brain region information
type	Data type (ATAC, Multiome, etc.)
taxonomy	Annotation information
genome	Genome information, must be a valid UCSC genome browser genome.
bigwigs	Either a directory or vector of file names for bigwigs. If a vector, then the order of the vector will define the order of the tracks.
track.names	Short labels to give each track. If NULL the function attempts to gather from .bw file name: track.names-*.bw
track.labels	Detailed labels to give each track. If NULL the function attempts to gather from .bw file name: track.labels-*.bw
colors	Colors (in R, G, B format) to give the tracks. If NULL colors will be auto-generated.

groupby	A vector of grouping variables for the bigwigs when building composite or sea-ad tracks.
hub.type	Format of the track hub: multiwig or composite
output.track.file	Output track hub filename. Default: trackDB.txt
email	Correspondence email

**Value**

Hub URL

---

setup.aws	<i>Setup aws.s3</i>
-----------	---------------------

---

**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'

---

setup.awsccli	<i>Setup awsccli2</i>
---------------	-----------------------

---

**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, defaults to Nelson Johansens install
--------------	--

# Index

hubR, [2](#)

setup.aws, [3](#)

setup.awsccli, [3](#)