# Package: InPAS (via r-universe)

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**Title** Identify Novel Alternative PolyAdenylation Sites (PAS) from RNA-seq data

**Version** 2.21.1

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**Description** Alternative polyadenylation (APA) is one of the important post- transcriptional regulation mechanisms which occurs in most human genes. InPAS facilitates the discovery of novel APA sites and the differential usage of APA sites from RNA-Seq data. It leverages cleanUpdTSeq to fine tune identified APA sites by removing false sites.

**biocViews** Alternative Polyadenylation, Differential Polyadenylation Site Usage, RNA-seq, Gene Regulation, Transcription

**License** GPL (>= 2)

**Imports** AnnotationDbi,batchtools,Biobase,Biostrings,BSgenome,cleanUpdTSeq, depmixS4,dplyr,flock,future,future.apply,GenomeInfoDb,GenomicRanges, GenomicFeatures, ggplot2, IRanges, limma, magrittr,methods,parallelly, plyranges, preprocessCore, readr,reshape2, RSQLite, Seqinfo, stats, S4Vectors, utils

**Depends** R (>= 3.5)

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addChr2Exclude *Add a globally-applied requirement for filtering out scaffolds from all analysis*

## Description

This function will set the default requirement of filtering out scaffolds from all analysis.

## Usage

```
addChr2Exclude(chr2exclude = c("chrM", "MT", "Pltd", "chrPltd"))
```

## Arguments

| | |
|---|---|
| chr2exclude | A character vector, NA or NULL, specifying chromosomes or scaffolds to be excluded for InPAS analysis. `chrM` and alternative scaffolds representing different haplotypes should be excluded. |

addInPASEnsDb *Add a globally defined EnsDb to some InPAS functions.*

## Description

Add a globally defined EnsDb to some InPAS functions.

## Usage

```
addInPASEnsDb(EnsDb = NULL)
```

## Arguments

| | |
|---|---|
| EnsDb | An object of ensembldb::EnsDb |

addInPASGenome *Add a globally defined genome to all InPAS functions.*

## Description

This function will set the genome across all InPAS functions.

## Usage

```
addInPASGenome(genome = NULL)
```

## Arguments

| | |
|---|---|
| genome | A BSgenome object indicating the default genome to be used for all InPAS functions. This value is stored as a global environment variable. This can be overwritten on a per-function basis using the given function's genome parameter. |

addInPASOutputDirectory *Add a globally defined output directory to some InPAS functions.*

## Description

Add a globally defined output directory to some InPAS functions.

## Usage

```
addInPASOutputDirectory(outdir = NULL)
```

## Arguments

| | |
|---|---|
| outdir | A character(1) vector, a path with write permission for storing InPAS analysis results. If it doesn't exist, it will be created. |

addInPASTxDb *Add a globally defined TxDb for InPAS functions.*

## Description

Add a globally defined TxDb for InPAS functions.

## Usage

```
addInPASTxDb(TxDb = NULL)
```

## Arguments

| | |
|---|---|
| TxDb | An object of GenomicFeatures::TxDb |

## Examples

```
library("TxDb.Hsapiens.UCSC.hg19.knownGene")
addInPASTxDb(TxDb = TxDb.Hsapiens.UCSC.hg19.knownGene)
```

addLockName *Add a filename for locking a SQLite database*

## Description

Add a filename for locking a SQLite database

## Usage

```
addLockName(filename = NULL)
```

## Arguments

| | |
|---|---|
| filename | A character(1) vector, specifyong a path to a file for locking. |

assemble_allCov *Assemble coverage files for a given chromosome for all samples*

## Description

Process individual sample-chromosome-specific coverage files in an experiment into a file containing a list of chromosome-specific Rle coverage of all samples

## Usage

```
assemble_allCov(
  sqlite_db,
  seqname,
  outdir = getInPASOutputDirectory(),
  genome = getInPASGenome()
)
```

## Arguments

| | |
|---|---|
| sqlite_db | A path to the SQLite database for InPAS, i.e. the output of setup_sqlitedb() |
| seqname | A character(1) vector, the name of a chromosome/scaffold |
| outdir | A character(1) vector, a path with write permission for storing InPAS analysis results. If it doesn't exist, it will be created. |
| genome | An object of BSgenome::BSgenome |

## Value

A list of paths to per-chromosome coverage files of all samples.

- seqname, chromosome/scaffold name
  - tag1, name tag for sample1
  - tag2, name tag for sample2
  - tagN, name tag for sampleN

## Author(s)

Haibo Liu

## Examples

```
if (interactive()) {
  library(BSgenome.Mmusculus.UCSC.mm10)
  genome <- BSgenome.Mmusculus.UCSC.mm10
  bedgraphs <- system.file("extdata", c(
    "Baf3.extract.bedgraph",
    "UM15.extract.bedgraph"
  ),
```

```
  package = "InPAS"
  )
  tags <- c("Baf3", "UM15")
  metadata <- data.frame(
    tag = tags,
    condition = c("Baf3", "UM15"),
    bedgraph_file = bedgraphs
  )
  outdir <- tempdir()
  write.table(metadata,
    file = file.path(outdir, "metadata.txt"),
    sep = "\t", quote = FALSE, row.names = FALSE
  )

  sqlite_db <- setup_sqlitedb(
    metadata = file.path(
      outdir,
      "metadata.txt"
    ),
    outdir
  )
  coverage <- list()
  addLockName(filename = tempfile())
  for (i in seq_along(bedgraphs)) {
    coverage[[tags[i]]] <- get_ssRleCov(
      bedgraph = bedgraphs[i],
      tag = tags[i],
      genome = genome,
      sqlite_db = sqlite_db,
      outdir = outdir,
      chr2exclude = "chrM"
    )
  }
  chr_coverage <- assemble_allCov(sqlite_db,
    seqname = "chr6",
    outdir = outdir,
    genome = genome
  )
}
```

---

`extract_UTR3Anno` *extract 3' UTR information from a GenomicFeatures::TxDb object*

---

## Description

extract 3' UTR information from a GenomicFeatures::TxDb object. The 3'UTR is defined as the last 3'UTR fragment for each transcript and it will be cut if there is any overlaps with other exons.

## Usage

```
extract_UTR3Anno(
  sqlite_db,
  TxDb = getInPASTxDb(),
  edb = getInPASEnsDb(),
  genome = getInPASGenome(),
  outdir = getInPASOutputDirectory(),
  chr2exclude = getChr2Exclude(),
  MAX_EXONS_GAP = 10000L
)
```

## Arguments

| | |
|---|---|
| sqlite_db | A path to the SQLite database for InPAS, i.e. the output of setup_sqlitedb(). |
| TxDb | An object of GenomicFeatures::TxDb |
| edb | An object of ensembldb::EnsDb |
| genome | An object of BSgenome::BSgenome |
| outdir | A character(1) vector, a path with write permission for storing InPAS analysis results. If it doesn't exist, it will be created. |
| chr2exclude | A character vector, NA or NULL, specifying chromosomes or scaffolds to be excluded for InPAS analysis. chrM and alternative scaffolds representing different haplotypes should be excluded. |
| MAX_EXONS_GAP | An integer(1) vector, maximal gap sizes between the last known CP sites to a nearest downstream exon. Default is 10 kb for mammalian genomes. For other species, user need to adjust this parameter. |

## Details

A good practice is to perform read alignment using a reference genome from Ensembl/GenCode including only the primary assembly and build a TxDb and EnsDb using the GTF/GFF files downloaded from the same source as the reference genome, such as BioMart/Ensembl/GenCode. For instruction, see Vignette of the GenomicFeatures. The UCSC reference genomes and their annotation packages can be very cumbersome.

## Value

An object of GenomicRanges::GRangesList, containing GRanges for extracted 3' UTRs, and the corresponding last CDSs and next.exon.gap for each chromosome/scaffold. Chromosome

## Author(s)

Jianhong Ou, Haibo Liu

## Examples

```
library("EnsDb.Hsapiens.v86")
library("BSgenome.Hsapiens.UCSC.hg19")
library("GenomicFeatures")
## set a sqlite database
bedgraphs <- system.file("extdata", c(
  "Baf3.extract.bedgraph",
  "UM15.extract.bedgraph"
),
package = "InPAS"
)
tags <- c("Baf3", "UM15")
metadata <- data.frame(
  tag = tags,
  condition = c("Baf3", "UM15"),
  bedgraph_file = bedgraphs
)
outdir <- tempdir()

write.table(metadata,
  file = file.path(outdir, "metadata.txt"),
  sep = "\t", quote = FALSE, row.names = FALSE
)
sqlite_db <- setup_sqlitedb(
  metadata =
    file.path(outdir, "metadata.txt"),
  outdir
)

samplefile <- system.file("extdata",
  "hg19_knownGene_sample.sqlite",
  package = "GenomicFeatures"
)
TxDb <- loadDb(samplefile)
edb <- EnsDb.Hsapiens.v86
genome <- BSgenome.Hsapiens.UCSC.hg19
addInPASOutputDirectory(outdir)
seqnames <- seqnames(BSgenome.Hsapiens.UCSC.hg19)
chr2exclude <- c(
  "chrM", "chrMT",
  seqnames[grepl("_(hap\\d+|fix|alt)$",
    seqnames,
    perl = TRUE
  )]
)
utr3 <- extract_UTR3Anno(sqlite_db, TxDb, edb,
  genome = genome,
  chr2exclude = chr2exclude,
  outdir = tempdir(),
  MAX_EXONS_GAP = 10000L
)
```

`filter_testOut` *filter 3' UTR usage test results*

## Description

filter results of `test_dPDUI()`

## Usage

```
filter_testOut(
  res,
  gp1,
  gp2,
  outdir = getInPASOutputDirectory(),
  background_coverage_threshold = 2,
  P.Value_cutoff = 0.05,
  adj.P.Val_cutoff = 0.05,
  dPDUI_cutoff = 0.2,
  PDUI_logFC_cutoff = log2(1.5)
)
```

## Arguments

| | |
|---|---|
| `res` | a UTR3eSet object, output of `test_dPDUI()` |
| `gp1` | tag names involved in group 1. gp1 and gp2 are used for filtering purpose if both are specified; otherwise only other specified thresholds are used for filtering. |
| `gp2` | tag names involved in group 2 |
| `outdir` | A character(1) vector, a path with write permission for storing InPAS analysis results. If it doesn't exist, it will be created. |
| `background_coverage_threshold` | background coverage cut off value. for each group, more than half of the long form should greater than background_coverage_threshold. for both group, at least in one group, more than half of the short form should greater than background_coverage_threshold. |
| `P.Value_cutoff` | cutoff of P value |
| `adj.P.Val_cutoff` | cutoff of adjust P value |
| `dPDUI_cutoff` | cutoff of dPDUI |
| `PDUI_logFC_cutoff` | cutoff of PDUI log2 transformed fold change |

## Value

A data frame converted from an object of GenomicRanges::GRanges.

## Author(s)

Jianhong Ou, Haibo Liu

## See Also

test_dPDUI()

## Examples

```
library(limma)
path <- system.file("extdata", package = "InPAS")
load(file.path(path, "eset.MAQC.rda"))
tags <- colnames(eset@PDUI)
g <- factor(gsub("\\..*$", "", tags))
design <- model.matrix(~ -1 + g)
colnames(design) <- c("Brain", "UHR")
contrast.matrix <- makeContrasts(
  contrasts = "Brain-UHR",
  levels = design
)
res <- test_dPDUI(
  eset = eset,
  method = "limma",
  normalize = "none",
  design = design,
  contrast.matrix = contrast.matrix
)
filter_testOut(res,
  gp1 = c("Brain.auto", "Brain.phiX"),
  gp2 = c("UHR.auto", "UHR.phiX"),
  background_coverage_threshold = 2,
  P.Value_cutoff = 0.05,
  adj.P.Val_cutoff = 0.05,
  dPDUI_cutoff = 0.3,
  PDUI_logFC_cutoff = .59
)
```

---

# find_minMSEDistr *Visualization of MSE profiles, 3' UTR coverage and minimal MSE distribution*

---

## Description

Visualization of MSE profiles, 3' UTR coverage and minimal MSE distribution

## Usage

```
find_minMSEDistr(
  CPs,
  outdir = NULL,
  MSE.plot = "MSE.pdf",
  coverage.plot = "coverage.pdf",
  min.MSE.to.end.distr.plot = "min.MSE.to.end.distr.pdf"
)
```

## Arguments

| | |
|---|---|
| CPs | A list, output from search_proximalCPs() or adjust_distalCPs() or adjust_proximalCPs() |
| outdir | A character(1) vector, specifying the output directory |
| MSE.plot | A character(1) vector, specifying a PDF file name for outputting plots of MSE profiles. No directory path is allowed. |
| coverage.plot | A character(1) vector, specifying a PDF file name for outputting per-sample coverage profiles. No directory path is allowed. |
| min.MSE.to.end.distr.plot | A character(1) vector, specifying a PDF file name for outputting histograms showing minimal MSE distribution relative to longer 3' UTR end. No directory path is allowed. |

---

# get_chromosomes *Identify chromosomes/scaffolds for CP site discovery*

---

## Description

Identify chromosomes/scaffolds which have both coverage and annotated 3' utr3 for CP site discovery

## Usage

```
get_chromosomes(utr3, sqlite_db)
```

## Arguments

| | |
|---|---|
| utr3 | An object of GenomicRanges::GRangesList. An output of extract_UTR3Anno(). |
| sqlite_db | A path to the SQLite database for InPAS, i.e. the output of setup_sqlitedb(). |

## Value

A vector of characters, containing names of chromosomes/scaffolds for CP site discovery

## Examples

```
library(BSgenome.Mmusculus.UCSC.mm10)
genome <- BSgenome.Mmusculus.UCSC.mm10
data(utr3.mm10)
utr3 <- split(utr3.mm10, seqnames(utr3.mm10), drop = TRUE)
bedgraphs <- system.file("extdata", c(
  "Baf3.extract.bedgraph",
  "UM15.extract.bedgraph"
),
package = "InPAS"
)
tags <- c("Baf3", "UM15")
metadata <- data.frame(
  tag = tags,
  condition = c("Baf3", "UM15"),
  bedgraph_file = bedgraphs
)
outdir <- tempdir()
write.table(metadata,
  file = file.path(outdir, "metadata.txt"),
  sep = "\t", quote = FALSE, row.names = FALSE
)

sqlite_db <- setup_sqlitedb(
  metadata = file.path(
    outdir,
    "metadata.txt"
  ),
  outdir
)
addLockName(filename = tempfile())
coverage <- list()
for (i in seq_along(bedgraphs)) {
      coverage[[tags[i]]] <- get_ssRleCov(
      bedgraph = bedgraphs[i],
      tag = tags[i],
      genome = genome,
      sqlite_db = sqlite_db,
      outdir = outdir,
      chr2exclude = "chrM"
    )
}
get_chromosomes(utr3, sqlite_db)
```

---

`get_lastCDSUTR3` *Extract the last unspliced region of each transcript*

---

## Description

Extract the last unspliced region of each transcript from a TxDb. These regions could be the last 3'UTR exon for transcripts whose 3' UTRs are composed of multiple exons or last CDS regions

and 3'UTRs for transcripts whose 3'UTRs and last CDS regions are on the same single exon.

## Usage

```
get_lastCDSUTR3(
  TxDb = getInPASTxDb(),
  genome = getInPASGenome(),
  chr2exclude = getChr2Exclude(),
  outdir = getInPASOutputDirectory(),
  MAX_EXONS_GAP = 10000
)
```

## Arguments

| | |
|---|---|
| TxDb | An object of GenomicFeatures::TxDb |
| genome | An object of BSgenome::BSgenome |
| chr2exclude | A character vector, NA or NULL, specifying chromosomes or scaffolds to be excluded for InPAS analysis. chrM and alternative scaffolds representing different haplotypes should be excluded. |
| outdir | A character(1) vector, a path with write permission for storing InPAS analysis results. If it doesn't exist, it will be created. |
| MAX_EXONS_GAP | An integer(1) vector, maximal gap sizes between the last known CP sites to a nearest downstream exon. Default is 10 kb for mammalian genomes. For other species, user need to adjust this parameter. |

## Value

A BED file with 6 columns: chr, chrStart, chrEnd, name, score, and strand.

---

# get_regionCov *Get coverage for 3' UTR and last CDS regions on a single chromosome*

---

## Description

Get coverage for 3' UTR and last CDS regions on a single chromosome

## Usage

```
get_regionCov(
  chr.utr3,
  sqlite_db,
  outdir = getInPASOutputDirectory(),
  phmm = FALSE,
  min.length.diff = 200
)
```

### Arguments

| | |
|---|---|
| chr.utr3 | An object of GenomicRanges::GRanges, one element of an output of extract_UTR3Anno() |
| sqlite_db | A path to the SQLite database for InPAS, i.e. the output of setup_sqlitedb(). |
| outdir | A character(1) vector, a path with write permission for storing InPAS analysis results. If it doesn't exist, it will be created. |
| phmm | A logical(1) vector, indicating whether data should be prepared for singleSample analysis? By default, FALSE |
| min.length.diff | An integer(1) vector, specifying minimal length difference between proximal and distal APA sites which should be met to be considered for differential APA analysis. Default is 200 bp. |

### Value

coverage view in GRanges

### Author(s)

Jianhong Ou, Haibo Liu

---

## get_ssRleCov *Get Rle coverage from a bedgraph file for a sample*

---

### Description

Get RLe coverage from a bedgraph file for a sample

### Usage

```
get_ssRleCov(
  bedgraph,
  tag,
  genome = getInPASGenome(),
  sqlite_db,
  future.chunk.size = NULL,
  outdir = getInPASOutputDirectory(),
  chr2exclude = getChr2Exclude()
)
```

### Arguments

| | |
|---|---|
| bedgraph | A path to a bedGraph file |
| tag | A character(1) vector, a name tag used to label the bedgraph file. It must match the tag specified in the metadata file used to setup the SQLite database |

genome — an object BSgenome::BSgenome. To make things easy, we suggest users creating a BSgenome::BSgenome instance from the reference genome used for read alignment. For details, see the documentation of `BSgenomeForge::forgeBSgenomeDataPkg()`.

sqlite_db — A path to the SQLite database for InPAS, i.e. the output of `setup_sqlitedb()`.

future.chunk.size — The average number of elements per future ("chunk"). If Inf, then all elements are processed in a single future. If NULL, then argument future.scheduling = 1 is used by default. Users can set future.chunk.size = total number of elements/number of cores set for the backend. See the future.apply package for details. You may adjust this number based based on the available computing resource: CPUs and RAM. This parameter affects the time for converting coverage from bedgraph to Rle.

outdir — A character(1) vector, a path with write permission for storing InPAS analysis results. If it doesn't exist, it will be created.

chr2exclude — A character vector, NA or NULL, specifying chromosomes or scaffolds to be excluded for InPAS analysis. `chrM` and alternative scaffolds representing different haplotypes should be excluded.

## Value

A data frame, as described below.

**tag** the sample tag

**chr** chromosome name

**coverage_file** path to Rle coverage files for each chromosome per sample tag

## Author(s)

Jianhong Ou, Haibo Liu

## Examples

```
if (interactive()) {
  library(BSgenome.Mmusculus.UCSC.mm10)
  genome <- BSgenome.Mmusculus.UCSC.mm10
  bedgraphs <- system.file("extdata", c(
    "Baf3.extract.bedgraph",
    "UM15.extract.bedgraph"
  ),
  package = "InPAS"
  )
  tags <- c("Baf3", "UM15")
  metadata <- data.frame(
    tag = tags,
    condition = c("Baf3", "UM15"),
    bedgraph_file = bedgraphs
  )
  outdir <- tempdir()
  write.table(metadata,
```

```
    file = file.path(outdir, "metadata.txt"),
    sep = "\t", quote = FALSE, row.names = FALSE
  )

  sqlite_db <- setup_sqlitedb(
    metadata = file.path(
      outdir,
      "metadata.txt"
    ),
    outdir
  )
  addLockName()
  coverage_info <- get_ssRleCov(
    bedgraph = bedgraphs[1],
    tag = tags[1],
    genome = genome,
    sqlite_db = sqlite_db,
    outdir = outdir,
    chr2exclude = "chrM"
  )
  # check read coverage depth
  db_connect <- dbConnect(drv = RSQLite::SQLite(), dbname = sqlite_db)
  dbReadTable(db_connect, "metadata")
  dbDisconnect(db_connect)
}
```

---

`get_usage4plot` *prepare coverage data and fitting data for plot*

---

## Description

prepare coverage data and fitting data for plot

## Usage

```
get_usage4plot(gr, proximalSites, sqlite_db, hugeData)
```

## Arguments

| | |
|---|---|
| `gr` | An object of GenomicRanges::GRanges |
| `proximalSites` | An integer(n) vector, specifying the coordinates of proximal CP sites. Each of the proximal sites must match one entry in the GRanges object, `gr`. |
| `sqlite_db` | A path to the SQLite database for InPAS, i.e. the output of `setup_sqlitedb()`. |
| `hugeData` | A logical(1), indicating whether it is huge data |

## Value

An object of GenomicRanges::GRanges with metadata:

| | |
|---|---|
| `dat` | A data.frame, first column is the position, the other columns are Coverage and value |
| `offset` | offset from the start of 3' UTR |

## Author(s)

Jianhong Ou, Haibo Liu

## Examples

```
library(BSgenome.Mmusculus.UCSC.mm10)
library(TxDb.Mmusculus.UCSC.mm10.knownGene)
genome <- BSgenome.Mmusculus.UCSC.mm10
TxDb <- TxDb.Mmusculus.UCSC.mm10.knownGene

## load UTR3 annotation and convert it into a GRangesList
data(utr3.mm10)
utr3 <- split(utr3.mm10, seqnames(utr3.mm10), drop = TRUE)

bedgraphs <- system.file("extdata", c(
  "Baf3.extract.bedgraph",
  "UM15.extract.bedgraph"
),
package = "InPAS"
)
tags <- c("Baf3", "UM15")
metadata <- data.frame(
  tag = tags,
  condition = c("baf", "UM15"),
  bedgraph_file = bedgraphs
)
outdir <- tempdir()
write.table(metadata,
  file = file.path(outdir, "metadata.txt"),
  sep = "\t", quote = FALSE, row.names = FALSE
)

sqlite_db <- setup_sqlitedb(
  metadata = file.path(
    outdir,
    "metadata.txt"
  ),
  outdir
)
addLockName(filename = tempfile())
coverage <- list()
for (i in seq_along(bedgraphs)) {
  coverage[[tags[i]]] <- get_ssRleCov(
    bedgraph = bedgraphs[i],
```

```
    tag = tags[i],
    genome = genome,
    sqlite_db = sqlite_db,
    outdir = outdir,
    chr2exclude = "chrM"
  )
}
data4CPsSearch <- setup_CPsSearch(sqlite_db,
  genome,
  chr.utr3 = utr3[["chr6"]],
  seqname = "chr6",
  background = "10K",
  TxDb = TxDb,
  hugeData = TRUE,
  outdir = outdir
)

gr <- GRanges("chr6", IRanges(128846245, 128850081), strand = "-")
names(gr) <- "chr6:128846245-128850081"
data4plot <- get_usage4plot(gr,
  proximalSites = 128849148,
  sqlite_db,
  hugeData = TRUE
)
plot_utr3Usage(
  usage_data = data4plot,
  vline_color = "purple",
  vline_type = "dashed"
)
```

---

`get_UTR3eSet` *prepare 3' UTR coverage data for usage test*

---

## Description

generate a UTR3eSet object with PDUI information for statistic tests

## Usage

```
get_UTR3eSet(
  sqlite_db,
  normalize = c("none", "quantiles", "quantiles.robust", "mean", "median"),
  ...,
  singleSample = FALSE
)
```

## Arguments

| | |
|---|---|
| `sqlite_db` | A path to the SQLite database for InPAS, i.e. the output of `setup_sqlitedb()`. |

| | |
|---|---|
| normalize | A character(1) vector, spcifying the normalization method. It can be "none", "quantiles", "quantiles.robust", "mean", or "median" |
| ... | parameter can be passed into preprocessCore::normalize.quantiles.robust() |
| singleSample | A logical(1) vector, indicating whether data is prepared for analysis in a single-Sample mode? Default, FALSE |

## Value

An object of UTR3eSet which contains following elements: usage: an GenomicRanges::GRanges object with CP sites info. PDUI: a matrix of PDUI PDUI.log2: log2 transformed PDUI matrix short: a matrix of usage of short form long: a matrix of usage of long form if singleSample is TRUE, one more element, signals, will be included.

## Author(s)

Jianhong Ou, Haibo Liu

## Examples

```
if (interactive()) {
  library(BSgenome.Mmusculus.UCSC.mm10)
  library(TxDb.Mmusculus.UCSC.mm10.knownGene)
  genome <- BSgenome.Mmusculus.UCSC.mm10
  TxDb <- TxDb.Mmusculus.UCSC.mm10.knownGene

  ## load UTR3 annotation and convert it into a GRangesList
  data(utr3.mm10)
  utr3 <- split(utr3.mm10, seqnames(utr3.mm10), drop = TRUE)

  bedgraphs <- system.file("extdata", c(
    "Baf3.extract.bedgraph",
    "UM15.extract.bedgraph"
  ),
  package = "InPAS"
  )
  tags <- c("Baf3", "UM15")
  metadata <- data.frame(
    tag = tags,
    condition = c("Baf3", "UM15"),
    bedgraph_file = bedgraphs
  )
  outdir <- tempdir()
  write.table(metadata,
    file = file.path(outdir, "metadata.txt"),
    sep = "\t", quote = FALSE, row.names = FALSE
  )

  sqlite_db <- setup_sqlitedb(metadata = file.path(
    outdir,
    "metadata.txt"
  ), outdir)
```

```
addLockName(filename = tempfile())
coverage <- list()
for (i in seq_along(bedgraphs)) {
  coverage[[tags[i]]] <- get_ssRleCov(
    bedgraph = bedgraphs[i],
    tag = tags[i],
    genome = genome,
    sqlite_db = sqlite_db,
    outdir = outdir,
    chr2exclude = "chrM"
  )
}

data4CPsSearch <- setup_CPsSearch(sqlite_db,
  genome,
  chr.utr3 = utr3[["chr6"]],
  seqname = "chr6",
  background = "10K",
  TxDb = TxDb,
  hugeData = TRUE,
  outdir = outdir,
  minZ = 2,
  cutStart = 10,
  MINSIZE = 10,
  coverage_threshold = 5
)
## polyA_PWM
load(system.file("extdata", "polyA.rda", package = "InPAS"))

## load the Naive Bayes classifier model from the cleanUpdTSeq package
library(cleanUpdTSeq)
data(classifier)

CPs <- search_CPs(
  seqname = "chr6",
  sqlite_db = sqlite_db,
  genome = genome,
  MINSIZE = 10,
  window_size = 100,
  search_point_START = 50,
  search_point_END = NA,
  cutEnd = 0,
  adjust_distal_polyA_end = TRUE,
  long_coverage_threshold = 2,
  PolyA_PWM = pwm,
  classifier = classifier,
  classifier_cutoff = 0.8,
  shift_range = 100,
  step = 5,
  outdir = outdir
)
utr3_cds_cov <- get_regionCov(
  chr.utr3 = utr3[["chr6"]],
```

```
    sqlite_db,
    outdir,
    phmm = FALSE
  )
  eSet <- get_UTR3eSet(sqlite_db,
    normalize = "none",
    singleSample = FALSE
  )
  test_out <- test_dPDUI(
    eset = eSet,
    method = "fisher.exact",
    normalize = "none",
    sqlite_db = sqlite_db
  )
}
```

---

`getChr2Exclude` *Get a globally-applied requirement for filtering scaffolds.*

---

## Description

This function will get the default requirement of filtering scaffolds.

## Usage

```
getChr2Exclude()
```

---

`getInPASEnsDb` *Get the globally defined EnsDb.*

---

## Description

Get the globally defined EnsDb.

## Usage

```
getInPASEnsDb()
```

## Value

An object of ensembldb::EnsDb

`getInPASGenome` *Get the globally defined genome*

## Description

This function will retrieve the genome that is currently in use by InPAS.

## Usage

```
getInPASGenome()
```

`getInPASOutputDirectory` *Get the path to a output directory for InPAS analysis*

## Description

Get the path to a output directory for InPAS analysis

## Usage

```
getInPASOutputDirectory()
```

## Value

a normalized path to a output directory for InPAS analysis

`getInPASSQLiteDb` *Get the path to an SQLite database*

## Description

Get the path to an SQLite database

## Usage

```
getInPASSQLiteDb()
```

## Value

A path to an SQLite database

## getInPASTxDb *Get the globally defined TxDb.*

### Description

Get the globally defined TxDb.

### Usage

```
getInPASTxDb()
```

### Value

An object of GenomicFeatures::TxDb

### Examples

```
library("TxDb.Hsapiens.UCSC.hg19.knownGene")
addInPASTxDb(TxDb = TxDb.Hsapiens.UCSC.hg19.knownGene)
getInPASTxDb()
```

## getLockName *Get the path to a file for locking the SQLite database*

### Description

Get the path to a file for locking the SQLite database

### Usage

```
getLockName()
```

### Value

A path to a file for locking

InPAS *A package for identifying novel Alternative PolyAdenylation Sites (PAS) based on RNA-seq data*

## Description

The InPAS package provides three categories of important functions: parse_TxDb, extract_UTR3Anno, get_ssRleCov, assemble_allCov, get_UTR3eSet, test_dPDUI, run_singleSampleAnalysis, run_singleGroupAnalysis, run_limmaAnalysis, filter_testOut, get_usage4plot, setup_GSEA, run_coverageQC

### functions for retrieving 3' UTR annotation

parse_TxDb, extract_UTR3Anno, get_lastCDSUTR3

### functions for processing read coverage data

assemble_allCov, get_ssRleCov, run_coverageQC, setup_parCPsSearch

### functions for alternative polyadenylation site analysis

test_dPDUI, run_singleSampleAnalysis, run_singleGroupAnalysis, run_limmaAnalysis, filter_testOut, get_usage4plot

parse_TxDb *Extract gene models from a TxDb object*

## Description

Extract gene models from a TxDb object and annotate last 3' UTR exons and the last CDSs

## Usage

```
parse_TxDb(
  sqlite_db = NULL,
  TxDb = getInPASTxDb(),
  edb = getInPASEnsDb(),
  genome = getInPASGenome(),
  chr2exclude = getChr2Exclude(),
  outdir = getInPASOutputDirectory()
)
```

## Arguments

| | |
|---|---|
| sqlite_db | A path to the SQLite database for InPAS, i.e. the output of setup_sqlitedb(). It can be NULL. |
| TxDb | An object of GenomicFeatures::TxDb |
| edb | An object of ensembldb::EnsDb |
| genome | An object of BSgenome::BSgenome |
| chr2exclude | A character vector, NA or NULL, specifying chromosomes or scaffolds to be excluded for InPAS analysis. chrM and alternative scaffolds representing different haplotypes should be excluded. |
| outdir | A character(1) vector, a path with write permission for storing InPAS analysis results. If it doesn't exist, it will be created. |

## Details

A good practice is to perform read alignment using a reference genome from Ensembl/GenCode including only the primary assembly and build a TxDb using the GTF/GFF files downloaded from the same source as the reference genome, such as BioMart/Ensembl/GenCode. For instruction, see Vignette of the GenomicFeatures. The UCSC reference genomes and their annotation can be very cumbersome.

## Value

A GenomicRanges::GRanges object for gene models

## Author(s)

Haibo Liu

## Examples

```
library("EnsDb.Hsapiens.v86")
library("BSgenome.Hsapiens.UCSC.hg19")
library("GenomicFeatures")

## set a sqlite database
bedgraphs <- system.file("extdata", c(
  "Baf3.extract.bedgraph",
  "UM15.extract.bedgraph"
),
package = "InPAS"
)
tags <- c("Baf3", "UM15")
metadata <- data.frame(
  tag = tags,
  condition = c("Baf3", "UM15"),
  bedgraph_file = bedgraphs
)
outdir <- tempdir()
write.table(metadata,
```

```
  file = file.path(outdir, "metadata.txt"),
  sep = "\t", quote = FALSE, row.names = FALSE
)
sqlite_db <- setup_sqlitedb(
  metadata =
    file.path(outdir, "metadata.txt"),
  outdir
)

samplefile <- system.file("extdata",
  "hg19_knownGene_sample.sqlite",
  package = "GenomicFeatures"
)
TxDb <- loadDb(samplefile)
edb <- EnsDb.Hsapiens.v86
genome <- BSgenome.Hsapiens.UCSC.hg19
seqnames <- seqnames(BSgenome.Hsapiens.UCSC.hg19)
chr2exclude <- c(
  "chrM", "chrMT",
  seqnames[grepl("_(hap\\d+|fix|alt)$",
    seqnames,
    perl = TRUE
  )]
)
parsed_Txdb <- parse_TxDb(sqlite_db, TxDb, edb, genome,
  chr2exclude = chr2exclude
)
```

---

`plot_utr3Usage` *Visualize the dPDUI events using ggplot2*

---

## Description

Visualize the dPDUI events by plotting the MSE, and total coverage per group along 3' UTR regions with dPDUI using ggplot2::geom_line.

## Usage

```
plot_utr3Usage(usage_data, vline_color = "purple", vline_type = "dashed")
```

## Arguments

| | |
|---|---|
| `usage_data` | An object of GenomicRanges::GRanges, an output from `get_usage4plot()`. |
| `vline_color` | color for vertical line showing position of predicated proximal CP site. Default, purple. |
| `vline_type` | line type for vertical line showing position of predicated proximal CP site. Default, dashed. See ggplot2 linetype. |

## Value

A ggplot object for refined plotting

## Author(s)

Haibo Liu

## See Also

For example, see `get_usage4plot()`.

---

`run_coverageQC` *Quality control on read coverage over gene bodies and 3UTRs*

---

## Description

Calculate coverage over gene bodies and 3UTRs. This function is used for quality control of the coverage.The coverage rate can show the complexity of RNA-seq library.

## Usage

```
run_coverageQC(
  sqlite_db,
  TxDb = getInPASTxDb(),
  edb = getInPASEnsDb(),
  genome = getInPASGenome(),
  cutoff_readsNum = 1,
  cutoff_expdGene_cvgRate = 0.1,
  cutoff_expdGene_sampleRate = 0.5,
  chr2exclude = getChr2Exclude(),
  which = NULL,
  future.chunk.size = 1,
  ...
)
```

## Arguments

| | |
|---|---|
| `sqlite_db` | A path to the SQLite database for InPAS, i.e. the output of `setup_sqlitedb()`. |
| `TxDb` | An object of GenomicFeatures::TxDb |
| `edb` | An object of ensembldb::EnsDb |
| `genome` | An object of BSgenome::BSgenome |
| `cutoff_readsNum` | cutoff reads number. If the coverage in the location is greater than cutoff_readsNum,the location will be treated as covered by signal |

`cutoff_expdGene_cvgRate`
: cutoff_expdGene_cvgRate and cutoff_expdGene_sampleRate are the parameters used to calculate which gene is expressed in all input dataset. cutoff_expdGene_cvgRateset the cutoff value for the coverage rate of each gene; cutoff_expdGene_sampleRateset the cutoff value for ratio of numbers of expressed and all samples for each gene. for example, by default, cutoff_expdGene_cvgRate=0.1 and cutoff_expdGene_sampleRate=0.5,suppose there are 4 samples, for one gene, if the coverage rates by base are:0.05, 0.12, 0.2, 0.17, this gene will be count as expressed gene because mean(c(0.05,0.12, 0.2, 0.17) > cutoff_expdGene_cvgRate) > cutoff_expdGene_sampleRate if the coverage rates by base are: 0.05, 0.12, 0.07, 0.17, this gene will be count as unexpressed gene because mean(c(0.05, 0.12, 0.07, 0.17) > cutoff_expdGene_cvgRate)<= cutoff_expdGene_sampleRate

`cutoff_expdGene_sampleRate`
: See cutoff_expdGene_cvgRate

`chr2exclude`
: A character vector, NA or NULL, specifying chromosomes or scaffolds to be excluded for InPAS analysis. `chrM` and alternative scaffolds representing different haplotypes should be excluded.

`which`
: an object of GenomicRanges::GRanges or NULL. If it is not NULL, only the exons overlapping the given ranges are used. For fast data quality control, set which to Granges for one or a few large chromosomes.

`future.chunk.size`
: The average number of elements per future ("chunk"). If Inf, then all elements are processed in a single future. If NULL, then argument future.scheduling = 1 is used by default. Users can set future.chunk.size = total number of elements/number of cores set for the backend. See the future.apply package for details.

`...`
: Not used yet

## Value

A data frame as described below.

**gene.coverage.rate** overage per base for all genes

**expressed.gene.coverage.rate** coverage per base for expressed genes

**UTR3.coverage.rate** coverage per base for all 3' UTRs

**UTR3.expressed.gene.subset.coverage.rate** coverage per base for 3' UTRs of expressed genes

**rownames** the names of coverage

## Author(s)

Jianhong Ou, Haibo Liu

## Examples

```
if (interactive()) {
  library("BSgenome.Mmusculus.UCSC.mm10")
  library("TxDb.Mmusculus.UCSC.mm10.knownGene")
```

```
library("EnsDb.Mmusculus.v79")

genome <- BSgenome.Mmusculus.UCSC.mm10
TxDb <- TxDb.Mmusculus.UCSC.mm10.knownGene
edb <- EnsDb.Mmusculus.v79

bedgraphs <- system.file("extdata", c(
  "Baf3.extract.bedgraph",
  "UM15.extract.bedgraph"
),
package = "InPAS"
)
tags <- c("Baf3", "UM15")
metadata <- data.frame(
  tag = tags,
  condition = c("Baf3", "UM15"),
  bedgraph_file = bedgraphs
)
outdir <- tempdir()
write.table(metadata,
  file = file.path(outdir, "metadata.txt"),
  sep = "\t", quote = FALSE, row.names = FALSE
)

sqlite_db <- setup_sqlitedb(
  metadata = file.path(
    outdir,
    "metadata.txt"
  ),
  outdir
)
tx <- parse_TxDb(
  sqlite_db = sqlite_db,
  TxDb = TxDb,
  edb = edb,
  genome = genome,
  outdir = outdir,
  chr2exclude = "chrM"
)
addLockName(filename = tempfile())
coverage <- list()
for (i in seq_along(bedgraphs)) {
  coverage[[tags[i]]] <- get_ssRleCov(
    bedgraph = bedgraphs[i],
    tag = tags[i],
    genome = genome,
    sqlite_db = sqlite_db,
    outdir = outdir,
    chr2exclude = "chrM"
  )
}
chr_coverage <- assemble_allCov(sqlite_db,
  seqname = "chr6",
```

```
    outdir,
    genome
  )
  run_coverageQC(sqlite_db, TxDb, edb, genome,
    chr2exclude = "chrM",
    which = GRanges("chr6",
      ranges = IRanges(98013000, 140678000)
    )
  )
}
```

---

search_CPs *Estimate the CP sites for UTRs on a given chromosome*

---

## Description

Estimate the CP sites for UTRs on a given chromosome

## Usage

```
search_CPs(
  seqname,
  sqlite_db,
  genome = getInPASGenome(),
  MINSIZE = 10,
  window_size = 200,
  search_point_START = 100,
  search_point_END = NA,
  cutEnd = NA,
  filter.last = TRUE,
  adjust_distal_polyA_end = FALSE,
  long_coverage_threshold = 2,
  PolyA_PWM = NA,
  classifier = NA,
  classifier_cutoff = 0.8,
  shift_range = 100,
  step = 2,
  outdir = getInPASOutputDirectory(),
  silence = FALSE,
  cluster_type = c("interactive", "multicore", "torque", "slurm", "sge", "lsf",
    "openlava", "socket"),
  template_file = NULL,
  mc.cores = 1,
  future.chunk.size = 50,
 resources = list(walltime = 3600 * 8, ncpus = 4, mpp = 1024 * 4, queue = "long", memory
    = 4 * 4 * 1024),
  DIST2ANNOAPAP = 500,
  DIST2END = 1000,
```

```
  output.all = FALSE
)
```

## Arguments

| | |
|---|---|
| seqname | A character(1) vector, specifying a chromososome/scaffold name |
| sqlite_db | A path to the SQLite database for InPAS, i.e. the output of setup_sqlitedb(). |
| genome | A BSgenome::BSgenome object |
| MINSIZE | A integer(1) vector, specifying the minimal length in bp of a short/proximal 3' UTR. Default, 10 |
| window_size | An integer(1) vector, the window size for novel distal or proximal CP site searching. default: 200. |
| search_point_START | A integer(1) vector, starting point relative to the 5' extremity of 3' UTRs for searching for proximal CP sites |
| search_point_END | A integer(1) vector, ending point relative to the 3' extremity of 3' UTRs for searching for proximal CP sites |
| cutEnd | An integer(1) vector a numeric(1) vector. What percentage or how many nucleotides should be removed from 5' extremities before searching for proximal CP sites? It can be a decimal between 0, and 1, or an integer greater than 1. 0.1 means 10 percent, 25 means cut first 25 bases |
| filter.last | A logical(1), whether to filter out the last valley, which is likely the 3' end of the longer 3' UTR if no novel distal CP site is detected and the 3' end excluded by setting cutEnd/search_point_END is small. |
| adjust_distal_polyA_end | A logical(1) vector. If true, distal CP sites are subject to adjustment by the Naive Bayes classifier from the cleanUpdTSeq::cleanUpdTSeq-package |
| long_coverage_threshold | An integer(1) vector, specifying the cutoff threshold of coverage for the terminal of long form 3' UTRs. If the coverage of first 100 nucleotides is lower than coverage_threshold, that transcript will be not considered for further analysis. Default, 2. |
| PolyA_PWM | An R object for a position weight matrix (PWM) for a hexamer polyadenylation signal (PAS), such as AAUAAA. |
| classifier | An R object for Naive Bayes classifier model, like the one in the cleanUpdTSeq package. |
| classifier_cutoff | A numeric(1) vector. A cutoff of probability that a site is classified as true CP sites. The value should be between 0.5 and 1. Default, 0.8. |
| shift_range | An integer(1) vector, specifying a shift range for adjusting the proximal and distal CP sites. Default, 50. It determines the range flanking the candidate CP sites to search the most likely real CP sites. |
| step | An integer (1) vector, specifying the step size used for adjusting the proximal or distal CP sites using the Naive Bayes classifier from the cleanUpdTSeq package. Default 1. It can be in the range of 1 to 10. |

`outdir` A character(1) vector, a path with write permission for storing the CP sites. If it doesn't exist, it will be created.

`silence` A logical(1), indicating whether progress is reported or not. By default, FALSE

`cluster_type` A character (1) vector, indicating the type of cluster job management systems. Options are "interactive","multicore", "torque", "slurm", "sge", "lsf", "openlava", and "socket". see batchtools vignette

`template_file` A charcter(1) vector, indicating the template file for job submitting scripts when cluster_type is set to "torque", "slurm", "sge", "lsf", or "openlava".

`mc.cores` An integer(1), number of cores for making multicore clusters or socket clusters using **batchtools**, and for `parallel::mclapply()`

`future.chunk.size`
The average number of elements per future ("chunk"). If Inf, then all elements are processed in a single future. If NULL, then argument future.scheduling = 1 is used by default. Users can set future.chunk.size = total number of elements/number of cores set for the backend. See the future.apply package for details. Default, 50. This parameter is used to split the candidate 3' UTRs for alternative SP sites search.

`resources` A named list specifying the computing resources when cluster_type is set to "torque", "slurm", "sge", "lsf", or "openlava". See batchtools vignette

`DIST2ANNOAPAP` An integer, specifying a cutoff for annotate MSE valleys with known proximal APAs in a given downstream distance. Default is 500.

`DIST2END` An integer, specifying a cutoff of the distance between last valley and the end of the 3' UTR (where MSE of the last base is calculated). If the last valley is closer to the end than the specified distance, it will not be considered because it is very likely due to RNA coverage decay at the end of mRNA. Default is 1200. User can consider a value between 1000 and 1500, depending on the library preparation procedures: RNA fragmentation and size selection.

`output.all` A logical(1), indicating whether to output entries with only single CP site for a 3' UTR. Default, FALSE.

## Value

An object of GenomicRanges::GRanges containing distal and proximal CP site information for each 3' UTR if detected.

## Author(s)

Jianhong Ou, Haibo Liu

## See Also

`search_proximalCPs()`, `adjust_proximalCPs()`, `adjust_proximalCPsByPWM()`, `adjust_proximalCPsByNBC()`, `get_PAscore()`, `get_PAscore2()`

## Examples

```
if (interactive()) {
  library(BSgenome.Mmusculus.UCSC.mm10)
  library(TxDb.Mmusculus.UCSC.mm10.knownGene)
  genome <- BSgenome.Mmusculus.UCSC.mm10
  TxDb <- TxDb.Mmusculus.UCSC.mm10.knownGene

  ## load UTR3 annotation and convert it into a GRangesList
  data(utr3.mm10)
  utr3 <- split(utr3.mm10, seqnames(utr3.mm10), drop = TRUE)

  bedgraphs <- system.file("extdata", c(
    "Baf3.extract.bedgraph",
    "UM15.extract.bedgraph"
  ),
  package = "InPAS"
  )
  tags <- c("Baf3", "UM15")
  metadata <- data.frame(
    tag = tags,
    condition = c("Baf3", "UM15"),
    bedgraph_file = bedgraphs
  )
  outdir <- tempdir()
  write.table(metadata,
    file = file.path(outdir, "metadata.txt"),
    sep = "\t", quote = FALSE, row.names = FALSE
  )

  sqlite_db <- setup_sqlitedb(metadata = file.path(
    outdir,
    "metadata.txt"
  ), outdir)
  addLockName(filename = tempfile())
  coverage <- list()
  for (i in seq_along(bedgraphs)) {
    coverage[[tags[i]]] <- get_ssRleCov(
      bedgraph = bedgraphs[i],
      tag = tags[i],
      genome = genome,
      sqlite_db = sqlite_db,
      outdir = outdir,
      chr2exclude = "chrM"
    )
  }
  data4CPsSearch <- setup_CPsSearch(sqlite_db,
    genome,
    chr.utr3 = utr3[["chr6"]],
    seqname = "chr6",
    background = "10K",
    TxDb = TxDb,
    hugeData = TRUE,
```

```
    outdir = outdir,
    minZ = 2,
    cutStart = 10,
    MINSIZE = 10,
    coverage_threshold = 5
  )
  ## polyA_PWM
  load(system.file("extdata", "polyA.rda", package = "InPAS"))

  ## load the Naive Bayes classifier model from the cleanUpdTSeq package
  library(cleanUpdTSeq)
  data(classifier)
  ## the following setting just for demo.
  if (.Platform$OS.type == "window") {
    plan(multisession)
  } else {
    plan(multicore)
  }
  CPs <- search_CPs(
    seqname = "chr6",
    sqlite_db = sqlite_db,
    genome = genome,
    MINSIZE = 10,
    window_size = 100,
    search_point_START = 50,
    search_point_END = NA,
    cutEnd = 0,
    filter.last = TRUE,
    adjust_distal_polyA_end = TRUE,
    long_coverage_threshold = 2,
    PolyA_PWM = pwm,
    classifier = classifier,
    classifier_cutoff = 0.8,
    shift_range = 100,
    step = 5,
    outdir = outdir
  )
}
```

---

`set_globals` *Set up global variables for an InPAS analysis*

---

## Description

Set up global variables for an InPAS analysis

## Usage

```
set_globals(
  genome = NULL,
```

```
  TxDb = NULL,
  EnsDb = NULL,
  outdir = NULL,
  chr2exclude = c("chrM", "MT", "Pltd", "chrPltd"),
  lockfile = tempfile(tmpdir = getInPASOutputDirectory())
)
```

## Arguments

| | |
|---|---|
| genome | An object BSgenome::BSgenome. To make things easy, we suggest users creating a BSgenome::BSgenome instance from the reference genome used for read alignment. For details, see the documentation of `BSgenomeForge::forgeBSgenomeDataPkg()`. |
| TxDb | An object of GenomicFeatures::TxDb |
| EnsDb | An object of ensembldb::EnsDb |
| outdir | A character(1) vector, a path with write permission for storing InPAS analysis results. If it doesn't exist, it will be created. |
| chr2exclude | A character vector, NA or NULL, specifying chromosomes or scaffolds to be excluded for InPAS analysis. `chrM` and alternative scaffolds representing different haplotypes should be excluded. |
| lockfile | A character(1) vector, specifying a file name used for parallel writing to a SQLite database |

---

# setup_CPsSearch *prepare data for predicting cleavage and polyadenylation (CP) sites*

---

## Description

prepare data for predicting cleavage and polyadenylation (CP) sites

## Usage

```
setup_CPsSearch(
  sqlite_db,
  genome = getInPASGenome(),
  chr.utr3,
  seqname,
  background = c("same_as_long_coverage_threshold", "1K", "5K", "10K", "50K"),
  TxDb = getInPASTxDb(),
  hugeData = TRUE,
  outdir = getInPASOutputDirectory(),
  silence = FALSE,
  minZ = 2,
  cutStart = 10,
  MINSIZE = 10,
  coverage_threshold = 5
)
```

## Arguments

| | |
|---|---|
| sqlite_db | A path to the SQLite database for InPAS, i.e. the output of setup_sqlitedb(). |
| genome | An object of BSgenome::BSgenome |
| chr.utr3 | An object of GenomicRanges::GRanges, an element of the output of extract_UTR3Anno() |
| seqname | A character(1), the name of a chromosome/scaffold |
| background | A character(1) vector, the range for calculating cutoff threshold of local background. It can be "same_as_long_coverage_threshold", "1K", "5K","10K", or "50K". |
| TxDb | an object of GenomicFeatures::TxDb |
| hugeData | A logical(1) vector, indicating whether it is huge data |
| outdir | A character(1) vector, a path with write permission for storing InPAS analysis results. If it doesn't exist, it will be created. |
| silence | report progress or not. By default it doesn't report progress. |
| minZ | A numeric(1), a Z score cutoff value |
| cutStart | An integer(1) vector a numeric(1) vector. What percentage or how many nucleotides should be removed from 5' extremities before searching for CP sites? It can be a decimal between 0, and 1, or an integer greater than 1. 0.1 means 10 percent, 25 means cut first 25 bases |
| MINSIZE | A integer(1) vector, specifying the minimal length in bp of a short/proximal 3' UTR. Default, 10 |
| coverage_threshold | An integer(1) vector, specifying the cutoff threshold of coverage for first 100 nucleotides. If the coverage of first 100 nucleotides is lower than coverage_threshold, that transcript will be not considered for further analysis. Default, 5. |

## Value

A file storing a list as described below:

**background** The type of methods for background coverage calculation

**z2s** Z-score cutoff thresholds for each 3' UTRs

**depth.weight** A named vector containing depth weight

**chr.cov.merge** A matrix storing condition/sample-specific coverage for 3' UTR and next.exon.gap (if exist)

**conn_next_utr3** A logical vector, indicating whether a 3'UTR has a convergent 3' UTR of its downstream transcript

**chr.utr3** A GRangesList, storing extracted 3' UTR annotation of transcript on a given chr

## Author(s)

Jianhong Ou, Haibo Liu

## Examples

```
if (interactive()) {
  library(BSgenome.Mmusculus.UCSC.mm10)
  library("TxDb.Mmusculus.UCSC.mm10.knownGene")
  genome <- BSgenome.Mmusculus.UCSC.mm10
  TxDb <- TxDb.Mmusculus.UCSC.mm10.knownGene

  ## load UTR3 annotation and convert it into a GRangesList
  data(utr3.mm10)
  utr3 <- split(utr3.mm10, seqnames(utr3.mm10), drop = TRUE)

  bedgraphs <- system.file("extdata", c(
    "Baf3.extract.bedgraph",
    "UM15.extract.bedgraph"
  ),
  package = "InPAS"
  )
  tags <- c("Baf3", "UM15")
  metadata <- data.frame(
    tag = tags,
    condition = c("Baf3", "UM15"),
    bedgraph_file = bedgraphs
  )
  outdir <- tempdir()
  write.table(metadata,
    file = file.path(outdir, "metadata.txt"),
    sep = "\t", quote = FALSE, row.names = FALSE
  )

  sqlite_db <- setup_sqlitedb(
    metadata = file.path(
      outdir,
      "metadata.txt"
    ),
    outdir
  )
  addLockName(filename = tempfile())
  coverage <- list()
  for (i in seq_along(bedgraphs)) {
    coverage[[tags[i]]] <- get_ssRleCov(
      bedgraph = bedgraphs[i],
      tag = tags[i],
      genome = genome,
      sqlite_db = sqlite_db,
      outdir = outdir,
      chr2exclude = "chrM"
    )
  }
  data4CPsitesSearch <- setup_CPsSearch(sqlite_db,
    genome,
    chr.utr3 = utr3[["chr6"]],
    seqname = "chr6",
```

```
    background = "10K",
    TxDb = TxDb,
    hugeData = TRUE,
    outdir = outdir
  )
}
```

---

setup_GSEA *prepare files for GSEA analysis*

---

## Description

output the log2 transformed delta PDUI txt file, chip file, rank file and phynotype label file for GSEA analysis

## Usage

```
setup_GSEA(
  eset,
  groupList,
  outdir = getInPASOutputDirectory(),
  preranked = TRUE,
  rankBy = c("logFC", "P.value"),
  rnkFilename = "InPAS.rnk",
  chipFilename = "InPAS.chip",
  dataFilename = "dPDUI.txt",
  PhenFilename = "group.cls"
)
```

## Arguments

| | |
|---|---|
| eset | A UTR3eSet object, output of `test_dPDUI()` |
| groupList | A list of grouped sample tag names, with the group names as the list's name, such as list(groupA = c("sample_1", "sample_2", "sample_3"), groupB = c("sample_4", "sample_5", "sample_6")) |
| outdir | A character(1) vector, a path with write permission for storing InPAS analysis results. If it doesn't exist, it will be created. |
| preranked | A logical(1) vector, out preranked or not |
| rankBy | A character(1) vector, indicating how the gene list is ranked. It can be "logFC" or "P.value". |
| rnkFilename | A character(1) vector, specifying a filename for the preranked file |
| chipFilename | A character(1) vector, specifying a filename for the chip file |
| dataFilename | A character(1) vector, specifying a filename for the dataset file |
| PhenFilename | A character(1) vector, specifying a filename for the file containing samples' phenotype labels |

## Author(s)

Jianhong Ou, Haibo Liu

## See Also

data formats for GSEA. https://software.broadinstitute.org/cancer/software/gsea/wiki/index.php/Data_formats

## Examples

```
library(limma)
path <- system.file("extdata", package = "InPAS")
load(file.path(path, "eset.MAQC.rda"))
tags <- colnames(eset@PDUI)
g <- factor(gsub("\\..*$", "", tags))
design <- model.matrix(~ -1 + g)
colnames(design) <- c("Brain", "UHR")
contrast.matrix <- makeContrasts(
  contrasts = "Brain-UHR",
  levels = design
)
res <- test_dPDUI(
  eset = eset,
  method = "limma",
  normalize = "none",
  design = design,
  contrast.matrix = contrast.matrix
)
gp1 <- c("Brain.auto", "Brain.phiX")
gp2 <- c("UHR.auto", "UHR.phiX")
groupList <- list(Brain = gp1, UHR = gp2)
setup_GSEA(res,
  groupList = groupList,
  outdir = tempdir(),
  preranked = TRUE,
  rankBy = "P.value"
)
```

---

# setup_parCPsSearch *Prepare data for predicting cleavage and polyadenylation (CP) sites using parallel computing*

---

## Description

Prepare data for predicting cleavage and polyadenylation (CP) sites using parallel computing

## Usage

```
setup_parCPsSearch(
  sqlite_db,
  genome = getInPASGenome(),
  utr3,
  seqnames,
  background = c("same_as_long_coverage_threshold", "1K", "5K", "10K", "50K"),
  TxDb = getInPASTxDb(),
  future.chunk.size = 1,
  chr2exclude = getChr2Exclude(),
  hugeData = TRUE,
  outdir = getInPASOutputDirectory(),
  silence = FALSE,
  minZ = 2,
  cutStart = 10,
  MINSIZE = 10,
  coverage_threshold = 5
)
```

## Arguments

| | |
|---|---|
| sqlite_db | A path to the SQLite database for InPAS, i.e. the output of setup_sqlitedb(). |
| genome | An object of BSgenome::BSgenome |
| utr3 | An object of GenomicRanges::GRangesList, the output of extract_UTR3Anno() |
| seqnames | A character(1), the names of all chromosomes/scaffolds with both coverage and 3' UTR annotation. Users can get this by calling the get_chromosomes(). |
| background | A character(1) vector, the range for calculating cutoff threshold of local background. It can be "same_as_long_coverage_threshold", "1K", "5K","10K", or "50K". |
| TxDb | an object of GenomicFeatures::TxDb |
| future.chunk.size | The average number of elements per future ("chunk"). If Inf, then all elements are processed in a single future. If NULL, then argument future.scheduling = 1 is used by default. Users can set future.chunk.size = total number of elements/number of cores set for the backend. See the future.apply package for details. |
| chr2exclude | A character vector, NA or NULL, specifying chromosomes or scaffolds to be excluded for InPAS analysis. chrM and alternative scaffolds representing different haplotypes should be excluded. |
| hugeData | A logical(1) vector, indicating whether it is huge data |
| outdir | A character(1) vector, a path with write permission for storing InPAS analysis results. If it doesn't exist, it will be created. |
| silence | report progress or not. By default it doesn't report progress. |
| minZ | A numeric(1), a Z score cutoff value |

`cutStart` An integer(1) vector a numeric(1) vector. What percentage or how many nucleotides should be removed from 5' extremities before searching for CP sites? It can be a decimal between 0, and 1, or an integer greater than 1. 0.1 means 10 percent, 25 means cut first 25 bases

`MINSIZE` A integer(1) vector, specifying the minimal length in bp of a short/proximal 3' UTR. Default, 10

`coverage_threshold` An integer(1) vector, specifying the cutoff threshold of coverage for first 100 nucleotides. If the coverage of first 100 nucleotides is lower than coverage_threshold, that transcript will be not considered for further analysis. Default, 5.

## Value

A list of list as described below:

**background** The type of methods for background coverage calculation

**z2s** Z-score cutoff thresholds for each 3' UTRs

**depth.weight** A named vector containing depth weight

**chr.cov.merge** A list of matrice storing condition/sample- specific coverage for 3' UTR and next.exon.gap (if exist)

**conn_next_utr3** A logical vector, indicating whether a 3'UTR has a convergent 3' UTR of its downstream transcript

**chr.utr3** A GRangesList, storing extracted 3' UTR annotation of transcript on a given chr

## Author(s)

Jianhong Ou, Haibo Liu

---

# setup_sqlitedb *Create an SQLite database for storing metadata and paths to coverage files*

---

## Description

Create an SQLite database with five tables, "metadata","sample_coverage", "chromosome_coverage", "CPsites", and "utr3_coverage", for storing metadata (sample tag, condition, paths to bedgraph files, and sample total read coverage), sample-then-chromosome-oriented coverage files (sample tag, chromosome, paths to bedgraph files for each chromosome), and paths to chromosome-then-sample-oriented coverage files (chromosome, paths to bedgraph files for each chromosome), CP sites on each chromosome (chromosome, paths to cpsite files), read coverage for 3' UTR and last CDS regions on each chromosome (chromosome, paths to utr3 coverage file), respectively

## Usage

```
setup_sqlitedb(metadata, outdir = getInPASOutputDirectory())
```

### Arguments

| | |
|---|---|
| metadata | A path to a tab-delimited file, with columns "tag", "condition", and "bedgraph_file", storing a unique name tag for each sample, a condition name for each sample, such as "treatment" and "control", and a path to the bedgraph file for each sample |
| outdir | A character(1) vector, a path with write permission for storing InPAS analysis results. If it doesn't exist, it will be created. |

### Value

A character(1) vector, the path to the SQLite database

### Author(s)

Haibo Liu

### Examples

```
if (interactive()) {
  bedgraphs <- system.file("extdata", c(
    "Baf3.extract.bedgraph",
    "UM15.extract.bedgraph"
  ),
  package = "InPAS"
  )
  tags <- c("Baf3", "UM15")
  metadata <- data.frame(
    tag = tags,
    condition = c("Baf3", "UM15"),
    bedgraph_file = bedgraphs
  )
  outdir <- tempdir()
  write.table(metadata,
    file = file.path(outdir, "metadata.txt"),
    sep = "\t", quote = FALSE, row.names = FALSE
  )
  sqlite_db <- setup_sqlitedb(
    metadata =
      file.path(outdir, "metadata.txt"),
    outdir
  )
}
```

---

## test_dPDUI *do test for dPDUI*

---

### Description

do test for dPDUI

## Usage

```
test_dPDUI(
  eset,
  sqlite_db,
  outdir = getInPASOutputDirectory(),
  method = c("limma", "fisher.exact", "singleSample", "singleGroup"),
  normalize = c("none", "quantiles", "quantiles.robust", "mean", "median"),
  design,
  contrast.matrix,
  coef = 1,
  robust = FALSE,
  ...
)
```

## Arguments

| | |
|---|---|
| eset | An object of UTR3eSet. It is an output of `get_UTR3eSet()` |
| sqlite_db | A path to the SQLite database for InPAS, i.e. the output of setup_sqlitedb(). |
| outdir | A character(1) vector, a path with write permission for storing InPAS analysis results. If it doesn't exist, it will be created. |
| method | A character(1), indicating the method for testing dPDUI. It can be "limma", "fisher.exact", "singleSample", or "singleGroup" |
| normalize | A character(1), indicating the normalization method. It can be "none", "quantiles", "quantiles.robust", "mean", or "median" |
| design | a design matrix of the experiment, with rows corresponding to samples and columns to coefficients to be estimated. Defaults to the unit vector meaning that the samples are treated as replicates. see `stats::model.matrix()`. Required for limma-based analysis. |
| contrast.matrix | a numeric matrix with rows corresponding to coefficients in fit and columns containing contrasts. May be a vector if there is only one contrast. see `limma::makeContrasts()`. Required for limma-based analysis. |
| coef | column number or column name specifying which coefficient or contrast of the linear model is of interest. see more `limma::topTable()`. default value: 1 |
| robust | A logical(1) vector, indicating whether the estimation of the empirical Bayes prior parameters should be robustified against outlier sample variances. |
| ... | other arguments are passed to lmFit |

## Details

if method is "limma", design matrix and contrast is required. if method is "fisher.exact", gp1 and gp2 is required.

## Value

An object of UTR3eSet, with the last element `testRes` containing the test results in a matrix.

## Author(s)

Jianhong Ou, Haibo Liu

## See Also

run_singleSampleAnalysis(), run_singleGroupAnalysis(), run_fisherExactTest(), run_limmaAnalysis()

## Examples

```
library(limma)
path <- system.file("extdata", package = "InPAS")
load(file.path(path, "eset.MAQC.rda"))
tags <- colnames(eset@PDUI)
g <- factor(gsub("\\..*$", "", tags))
design <- model.matrix(~ -1 + g)
colnames(design) <- c("Brain", "UHR")
contrast.matrix <- makeContrasts(
  contrasts = "Brain-UHR",
  levels = design
)
res <- test_dPDUI(
  eset = eset,
  sqlite_db,
  method = "limma",
  normalize = "none",
  design = design,
  contrast.matrix = contrast.matrix
)
```

---

# utr3.mm10 *Annotation of 3' UTRs for mouse (mm10)*

---

## Description

A dataset containing the annotation of the 3' UTRs of the mouse

## Usage

```
utr3.mm10
```

## Format

An object of GenomicRanges::GRanges with 7 metadata columns

**feature** feature type, utr3, CDS, next.exon.gap

**annotatedProximalCP** candidate proximal CPsites

**exon** exon ID

**transcript** transcript ID

**gene** gene ID

**symbol** gene symbol

**truncated** whether the 3' UTR is trucated

---

`UTR3eSet-class` *UTR3eSet-class and its methods*

---

## Description

An object of class UTR3eSet representing the results of 3' UTR usage; methods for constructing, showing, getting and setting attributes of objects; methods for coercing object of other class to UTR3eSet objects.

## Objects from the Class

Objects can be created by calls of the form `new("UTR3eSet", ...)`

Objects can be created by calls of the form `new("UTR3eSet", ...)`.

## Slots

`usage` Object of class `"GRanges"`

`PDUI` Object of class `"matrix"`

`PDUI.log2` Object of class `"matrix"`

`short` Object of class `"matrix"`

`long` Object of class `"matrix"`

`signals` Object of class `"list"`

`testRes` Object of class `"matrix"`

## UTR3eSet-class methods

**$** `signature(x = "UTR3eSet")`: ...

**$<-** `signature(x = "UTR3eSet")`: ...

**coerce** `signature(from = "UTR3eSet", to = "ExpressionSet")`: ...

**coerce** `signature(from = "UTR3eSet", to = "GRanges")`: ...

**show** `signature(object = "UTR3eSet")`: ...

## Author(s)

Jianhong Ou

## See Also

`GRanges`

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