

# Package ‘spiky’

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**Type** Package

**Title** Spike-in calibration for cell-free MeDIP

**Description**

spiky implements methods and model generation for cfMeDIP (cell-free methylated DNA immunoprecipitation) with spike-in controls. CfMeDIP is an enrichment protocol which avoids destructive conversion of scarce template, making it ideal as a “liquid biopsy,” but creating certain challenges in comparing results across specimens, subjects, and experiments. The use of synthetic spike-in standard oligos allows diagnostics performed with cfMeDIP to quantitatively compare samples across subjects, experiments, and time points in both relative and absolute terms.

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**URL** <https://github.com/trichelab/spiky>

**BugReports** <https://github.com/trichelab/spiky/issues>

**License** GPL-2

**Depends** Rsamtools, GenomicRanges, R (>= 3.6.0)

**Imports** stats, scales, bamIseq, methods, tools, IRanges, Biostrings, GenomicAlignments, BlandAltmanLeh, GenomeInfoDb, BSgenome, S4Vectors, graphics, ggplot2, utils

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---

<code>add_frag_info</code>	<i>decode fragment identifiers for spike-in standards</i>
----------------------------	---

---

**Description**

given a vector of fragment identifiers like 160\_2\_35 or 80b\_1C\_35G-2, encoded typically as length-InBp\_numberOfCpGs\_GCpercent, and optionally a database of spike-in sequences corresponding to those fragments, add those columns to the source data (along with, if present in the database, other metadata such as standard concentrations, GC fraction, etc.) and return i an updated DataFrame.

**Usage**

```
add_frag_info(x, frag_grp = "frag_grp", spike = NULL)
```

**Arguments**

- `x` data.frame with a column of spike information (see above)
- `frag_grp` column name for the spike contig information (frag\_grp)
- `spike` optional database of spike-in properties (none)

**Value**

the data.frame `x`, augmented with metadata columns

**Examples**

```
data(spike_cram_counts)
data(spike, package="spiky")
spike <- subset(spike, methylated == 1)
add_frag_info(spike_cram_counts, spike=spike)
```

---

<code>bam_to_bins</code>	<i>create a tiled representation of a genome from the BAM/CRAM file</i>
--------------------------	---

---

**Description**

This function replaces a bedtools call: `bedtools intersect -wao -a fragments.bed -b hg38_300bp_windows.bed > data.bed`

**Usage**

```
bam_to_bins(x, width = 300, param = NULL, which = IRangesList(), ...)
```

**Arguments**

x	a BAM or CRAM filename (or a BamFile object)
width	the width of the bins to tile (default is 300)
param	optional ScanBamParam (whence we attempt to extract which)
which	an optional GRanges restricting the bins to certain locations
...	additional arguments to pass on to seqinfo_from_header

**Details**

The idea is to skip the BED creation step for most runs, and just do it once. In order to count reads in bins, we need bins. In order to have bins, we need to know how long the chromosomes are. In order to have a BAM or CRAM file, we need to have those same lengths. This function takes advantage of all of the above to create binned ranges. Note that a very recent branch of Rsamtools is required for CRAM file bins.

**Value**

a GRangesList with y-base-pair-wide bins tiled across it

**See Also**

seqinfo\_from\_header

**Examples**

```
library(Rsamtools)
fl <- system.file("extdata", "ex1.bam", package="Rsamtools", mustWork=TRUE)
bam_to_bins(fl)
```

---

bin\_pmol

*Binned estimation of picomoles of DNA present in cfMeDIP assays*


---

**Description**

Given the results of model\_glm\_pmol and predict\_pmol, adjust the predictions to reflect picomoles of captured DNA overlapping a given bin in the genome.

**Usage**

```
bin_pmol(x)
```

**Arguments**

x	results from predict_pmol (a data.frame or GRanges)
---	---

**Value**

the same object, but with a column `adjusted_pred_con`

**See Also**

model\_glm\_pmol  
 predict\_pmol

**Examples**

```
data(spike, package="spiky")
data(spike_res, package="spiky")
data(genomic_res, package="spiky")
fit <- model_glm_pmol(covg_to_df(spike_res, spike=spike), spike=spike)
pred <- predict_pmol(fit, genomic_res, ret="df")
bin_pmol(pred)
```

---

convertPairedGRtoGR      *Convert Pairs to GRanges*

---

**Description**

Convert Pairs to GRanges

**Usage**

```
convertPairedGRtoGR(pairs)
```

**Arguments**

pairs                      the Pairs object

**Value**

a GRanges

---

covg\_to\_df                      *reshape scan\_spiked\_bam results into data.frames for model\_glm\_pmol*

---

**Description**

reshape scan\_spiked\_bam results into data.frames for model\_glm\_pmol

**Usage**

```
covg_to_df(spike_gr, spike, meth = TRUE, ID = NULL)
```

**Arguments**

spike_gr	GRanges of spike contigs (e.g. output object from scan_spiked_bam, scan_spike_contigs, or scan_spike_bedpe)
spike	spike database (as from data(spike, package="spiky"))
meth	only keep methylated spike reads? (TRUE; if FALSE, sum both)
ID	an identifier for this sample, if running several (autogenerate)

**Value**

a data.frame with columns 'frag\_grp', 'id', and 'read\_count'

**See Also**

scan\_spiked\_bam

**Examples**

```
data(spike, package="spiky")
data(spike_res, package="spiky")
subsetting <- covg_to_df(spike_res, spike=spike, meth=TRUE)
summed <- covg_to_df(spike_res, spike=spike, meth=FALSE)
round((summed$read_count - subsetting$read_count) / summed$read_count, 3)
```

---

dedup

*spike-in counts for two samples, as a wide data.frame*

---

**Description**

A data.frame with spike-in results from control samples in the manuscript. This maps 1:1 onto spike\_read\_counts using reshape2::melt.

**Usage**

```
data(dedup)
```

**Format**

A data.frame object with

**frag\_grp** the encoded spike contig name: basepairs\_CpGs\_GCpercent

**read\_count\_6547** read coverage for this spike in sample 6547

**read\_count\_6548** read coverage for this spike in sample 6548

**Source**

This data was created using inst/script/loadDedup.R

---

find\_spike\_contigs     *find spike-in seqlevels in an object x, where !is.null(seqinfo(x))*

---

### Description

Find the spike-like contigs in a BAM with both natural and spiked contigs. This started out as glue in some other functions and got refactored out.

### Usage

```
find_spike_contigs(x, spike)
```

### Arguments

x	something with seqlevels
spike	a DataFrame with spike-in information

### Details

The indices have an attribute "mappings", which is a character vector such that `attr(find_spike_contigs(x), "mappings") ==` standardized for all contig names in the CRAM/BAM/whatever, and standardized is the rowname in spike that corresponds to the original contig name.

### Value

indices of which contigs in `seqlevels(x)` are spike-in contigs

### See Also

`get_base_name`  
`rename_spike_seqlevels`

### Examples

```
sb <- system.file("extdata", "example.spike.bam", package="spiky",
                  mustWork=TRUE)
si <- seqinfo_from_header(sb)
data(spike, package="spiky")
find_spike_contigs(si, spike=spike)
```

---

genbank_mito	<i>various mitochondrial genomes sometimes used as endogenous spike-ins</i>
--------------	---

---

### Description

A DataFrame with species, genome, accession, and sequence for GenBank mitochondrial genome depositions. No concentration provided; add if needed.

### Usage

```
data(genbank_mito)
```

### Format

A DataFrame object with

**species** the species whence the record came, as a character string  
**genome** the genome assembly whence the mtDNA, as a character string  
**accession** the genbank accession, as a character string  
**sequence** genome sequence, as a DNASTringSet

### Source

[www.ncbi.nlm.nih.gov/genbank/](http://www.ncbi.nlm.nih.gov/genbank/)

---

generate_spike_fasta	<i>for CRAM files, a FASTA reference is required to decode; this builds that</i>
----------------------	--

---

### Description

A FASTA reference is *not* always needed, so long as .crai indices are available for all contigs in the CRAM. See spike\_counts for a fast and convenient alternative that extracts spike coverage from index stats. However, spike\_counts has its own issues, and it's better to use fragments.

### Usage

```
generate_spike_fasta(bam, spike, assembly = NULL, fa = "spike_contigs.fa")
```

### Arguments

bam	a BAM or CRAM file, hopefully with an index
spike	the spike contig database (mandatory as of 0.9.99)
assembly	optional BSgenome or seqinfo with reference contigs (NULL)
fa	the filename for the resulting FASTA ("spikes.fa")

## Details

If the contigs in a CRAM have even slightly different names from those in the reference, decoding will fail. In some cases there are multiple names for a given contig (which raises the question of whether to condense them), and thus the same reference sequence decodes multiple contig names.

This function generates an appropriate spike reference for a BAM or CRAM, using BAM/CRAM headers to figure out which references are used for which.

At the moment, CRAM support in Rsamtools only exists in the GitHub branch:

```
BiocManager::install("Bioconductor/Rsamtools@cram")
```

Using other versions of Rsamtools will yield an error on CRAM files.

Note that for merged genomic + spike reference BAMs/CRAMs, this function will only attempt to generate a FASTA for the spike contigs, not reference. If your reference contigs are screwed up, talk to your sequencing people, and keep better track of the FASTA reference against which you compress!

## Value

invisibly, a DNASTringSet as exported to `fa`

## See Also

rename\_contigs

## Examples

```
library(GenomicRanges)
data(spike, package="spiky")
sb <- system.file("extdata", "example.spike.bam", package="spiky",
                 mustWork=TRUE)
outFasta <- paste(system.file("extdata", package="spiky", mustWork=TRUE), "/spike_contigs.fasta", sep="")
show(generate_spike_fasta(sb, spike=spike, fa=outFasta))
```

---

genomic\_res

*A Granges object with genomic coverage from chr21q22, binned every 300bp for the genomic contigs then averaged across the bin. (In other words, the default output of scan\_genomic\_contigs or scan\_genomic\_bedpe, restricted to a small enough set of genomic regions to be practical for examples.) This represents what most users will want to generate from their own genomic BAMs or BEDPEs, and is used repeatedly in downstream examples throughout the package.*

---

## Description

A Granges object with genomic coverage from chr21q22, binned every 300bp for the genomic contigs then averaged across the bin. (In other words, the default output of scan\_genomic\_contigs or scan\_genomic\_bedpe, restricted to a small enough set of genomic regions to be practical for examples.) This represents what most users will want to generate from their own genomic BAMs or BEDPEs, and is used repeatedly in downstream examples throughout the package.

**Usage**

```
data(genomic_res)
```

**Format**

A GRanges of coverage results with one metadata column, coverage

**Source**

Generated using scan\_genomic\_bedpe or scan\_genomic\_contigs on an example bedpe or bam containing chr21q22 contigs.

---

get_base_name	<i>refactored out of rename_spikes and rename_spike_seqlevels</i>
---------------	---

---

**Description**

A common task between generate\_spike\_fasta, rename\_spikes, and rename\_spike\_seqlevels is to determine what the largest common subset of characters between existing contig names and stored standardized contigs might be. This function eases that task.

**Usage**

```
get_base_name(contig_names, sep = "_")
```

**Arguments**

contig_names	the names of contigs
sep	separator character in contig names ("_")

**Value**

a vector of elements 1:3 from each contig name

**Examples**

```
sb <- system.file("extdata", "example.spike.bam", package="spiky",
                  mustWork=TRUE)
bh <- scanBamHeader(BamFile(sb))
orig_contigs <- names(bh$targets)
get_base_name(orig_contigs)
```

---

get\_binned\_coverage    *tabulate read coverage in predefined bins*

---

## Description

refactored out of scan\_spiked\_bam

## Usage

```
get_binned_coverage(bins, covg)
```

## Arguments

bins	the GRanges with bins
covg	the coverage result (an RleList)

## Value

a GRanges of summarized coverage

## See Also

get\_spiked\_coverage

scan\_spiked\_bam

## Examples

```
sb <- system.file("extdata", "example.spike.bam", package="spiky",
                  mustWork=TRUE)
data(spike, package="spiky")
si <- seqinfo_from_header(sb)
genome(si) <- "spike"
mgr <- get_merged_gr(si, spike=spike)
fl <- scanBamFlag(isDuplicate=FALSE, isPaired=TRUE, isProperPair=TRUE)
bp <- ScanBamParam(flag=fl)
bamMapqFilter(bp) <- 20

covg <- get_spiked_coverage(sb, bp=bp, gr=mgr)
get_binned_coverage(bins=GRanges(), covg=covg)
```

---

get_merged_gr	<i>get a GRanges of (by default, standard) chromosomes from seqinfo</i>
---------------	---

---

### Description

refactored from scan\_spiked\_bam to clarify information flow

### Usage

```
get_merged_gr(si, spike, standard = TRUE)
```

### Arguments

si	seqinfo, usually from a BAM/CRAM file with spike contigs
spike	database of spike-in standard sequence features (spike)
standard	trim to standard chromosomes? (TRUE)

### Details

By default, get\_merged\_gr will return a GRanges with "standardized" genomic and spike contig names (i.e. genomic chr1-22, X, Y, M, and the canonical spike names in data(spike, package="spiky")).

The constraint to "standard" chromosomes on genomic contigs can be removed by setting standard to FALSE in the function arguments.

### Value

GRanges with two genomes: the organism assembly and "spike"

### Examples

```
sb <- system.file("extdata", "example.spike.bam", package="spiky",
                  mustWork=TRUE)
si <- seqinfo_from_header(sb)
genome(si) <- "spike" # no genomic contigs
data(spike, package="spiky")
get_merged_gr(si, spike=spike) # note canonicalized spikes
```

---

get_spiked_coverage	<i>tabulate coverage across assembly and spike contig subset in natural order</i>
---------------------	---

---

### Description

FIXME: this is wicked slow, ask Herve if a faster version exists

### Usage

```
get_spiked_coverage(bf, bp, gr)
```

**Arguments**

bf                the BamFile object  
 bp                the ScanBamParam object  
 gr                the GRanges with sorted seqlevels

**Details**

Refactored from scan\_spiked\_bam, this is a very simple wrapper

**Value**

a list of Rles

**See Also**

scan\_spiked\_bam  
 coverage

**Examples**

```
sb <- system.file("extdata", "example.spike.bam", package="spiky",
                 mustWork=TRUE)
si <- seqinfo_from_header(sb)
genome(si) <- "spike"
data(spike, package="spiky")
mgr <- get_merged_gr(si, spike=spike) # note canonicalized spikes

fl <- scanBamFlag(isDuplicate=FALSE, isPaired=TRUE, isProperPair=TRUE)
bp <- ScanBamParam(flag=fl)
bamMapqFilter(bp) <- 20
get_spiked_coverage(sb, bp=bp, gr=mgr)
```

---

get_spike_depth	<i>get the (max, median, or mean) coverage for spike-in contigs from a BAM/CRAM</i>
-----------------	---

---

**Description**

get the (max, median, or mean) coverage for spike-in contigs from a BAM/CRAM

**Usage**

```
get_spike_depth(covg, spike_gr = NULL, spike = NULL, how = c("max", "mean"))
```

**Arguments**

covg             the coverage RleList  
 spike\_gr        the spike-in GRanges (default: figure out from seqinfo)  
 spike           information about the spikes (default: load spike)  
 how             how to summarize the per-spike coverage (max)

**Value**

a GRanges with summarized coverage and features for each

**Examples**

```
sb <- system.file("extdata", "example.spike.bam", package="spiky",
                 mustWork=TRUE)
data(spike, package="spiky")
si <- seqinfo_from_header(sb)
genome(si) <- "spike"
mgr <- get_merged_gr(si, spike=spike)

fl <- scanBamFlag(isDuplicate=FALSE, isPaired=TRUE, isProperPair=TRUE)
bp <- ScanBamParam(flag=fl)
bamMapqFilter(bp) <- 20

covg <- get_spiked_coverage(sb, bp=bp, gr=mgr)
get_spike_depth(covg, spike_gr=mgr, spike=spike)
```

---

kmax

*simple contig kmer comparisons*


---

**Description**

simple contig kmer comparisons

**Usage**

```
kmax(km, normalize = TRUE)
```

**Arguments**

km	kmer summary
normalize	normalize (divide by row sums)? (TRUE)

**Value**

the most common kmers for each contig, across all contigs

**Examples**

```
data(genbank_mito, package="spiky")
mtk6 <- kmers(genbank_mito, k=6)
rownames(mtk6) <- paste0(rownames(mtk6), "_MT")
kmax(mtk6)

data(phage, package="spiky")
phk6 <- kmers(phage, k=6)
kmax(phk6, normalize=FALSE)

stopifnot(identical(colnames(phk6), colnames(mtk6)))
```

```
k6 <- rbind(mtk6, phk6)
kmax(k6)
```

---

kmers	<i>oligonucleotideFrequency, but less letters and more convenient.</i>
-------	--

---

### Description

*oligonucleotideFrequency*, but less letters and more convenient.

### Usage

```
kmers(x, k = 6)
```

### Arguments

x	BSgenome, DFrame with sequence column, or DNASTringSet
k	the length of the kmers (default is 6)

### Details

The companion `kmax` function finds the maximum frequency kmer for each contig and plots all of them together for comparison purposes.

### Value

a matrix of contigs (rows) by kmer frequencies (columns)

### See Also

`kmax`

### Examples

```
data(genbank_mito, package="spiky")
mtk6 <- kmers(genbank_mito, k=6)
kmax(mtk6)
```

```
data(phage, package="spiky")
phk6 <- kmers(phage, k=6)
kmax(phk6)
```

---

```
methylation_specificity
```

```
compute methylation specificity for spike-in standards
```

---

### Description

In a cfMeDIP experiment, the yield of methylated fragments should be >95% (ideally 98-99%) due to the nature of the assay.

### Usage

```
methylation_specificity(spike_gr, spike)
```

### Arguments

spike_gr	GRanges of spike contigs (e.g. output object from scan_spiked_bam, scan_spike_contigs, or scan_spike_bedpe)
spike	spike contig database, if needed (e.g. data(spike))

### Value

list with median and mean coverage across spike contigs

### Examples

```
data(genomic_res)
data(spike_res)
data(spike, package="spiky")
methylation_specificity(spike_res, spike=spike)
```

---

```
model_bam_standards Build a Bayesian additive model from spike-ins to correct bias in *-seq
```

---

### Description

Build a Bayesian additive model from spike-ins to correct bias in \*-seq

### Usage

```
model_bam_standards(x, conc = NULL, fm = NULL, ...)
```

### Arguments

x	data with assorted feature information (GCfrac, CpGs, etc)
conc	concentration for each spike (must be provided!)
fm	model formula (conc ~ read_count + fraglen + GCfrac + CpGs_3)
...	other arguments to pass to bam1ss

**Value**

the model fit for the data

**Examples**

```
library(bamlss)
data(spike_cram_counts, package="spiky")
data(spike, package="spiky")
scc <- add_frag_info(spike_cram_counts, spike=spike)
scc$conc <- scc$conc * 0.9 # adjust for dilution
scc$CpGs_3 <- scc$CpGs ^ (1/3)
fit0 <- model_bam_standards(scc,
                           fm=conc ~ read_count + fraglen)
fit1 <- model_bam_standards(scc,
                           fm=conc ~ read_count + fraglen + GCfrac + CpGs_3)
DIC(fit0, fit1)
```

---

model_glm_pmol	<i>Build a generalized linear model from spike-ins to correct bias in cfMeDIP</i>
----------------	---

---

**Description**

formerly '2020\_model\_glm\_fmol'. Note that everything in `x` can be had from a BAM/CRAM with spike contigs named as `frag_grp (len_CpGs_GC)` in the index and in fact that is what `scan_spiked_bam` now does.

**Usage**

```
model_glm_pmol(x, spike, conc = NULL, ...)
```

**Arguments**

<code>x</code>	data w/frag_grp, id, and read_count; or scan_spiked_bam result
<code>spike</code>	spike database, e.g. <code>data(spike, package='spiky')</code>
<code>conc</code>	concentration for each spike (will be referenced if NULL)
<code>...</code>	other arguments to pass to <code>glm</code> (e.g. family)

**Value**

the model fit for the data

**Examples**

```
data(spike, package="spiky")

data(spike_read_counts, package="spiky")
fit1 <- model_glm_pmol(spike_read_counts, spike=spike)

data(spike_res) # scan_spiked_bam result
fit2 <- model_glm_pmol(spike_res, spike=spike)
```

---

parse_spike_UMI	<i>parse out the forward and reverse UMIs and contig for a BED/BAM</i>
-----------------	--

---

**Description**

parse out the forward and reverse UMIs and contig for a BED/BAM

**Usage**

```
parse_spike_UMI(UMI, pos = NULL, seqs = NULL)
```

**Arguments**

UMI	a vector of UMIs
pos	optional vector of positions (else all are set to 1)
seqs	optional vector of read sequences (else widths default to 96)

**Value**

a GRanges

---

phage	<i>lambda and phiX phage sequences, sometimes used as spike-ins</i>
-------	---

---

**Description**

A DataFrame with sequence, methylated, CpGs, GCfrac, and OECpG for phages

**Usage**

```
data(phage)
```

**Format**

A DataFrame object with

<b>sequence</b>	genome sequence, as a DNASTringSet
<b>methylated</b>	whether CpGs are methylated, as an integer
<b>CpGs</b>	the number of CpGs in the phage genome, as an integer
<b>GCfrac</b>	the GC fraction of the phage genome, as a numeric
<b>OECpG</b>	the observed / expected CpG fraction, as a numeric

**Source**

[www.ncbi.nlm.nih.gov/genbank/](http://www.ncbi.nlm.nih.gov/genbank/)

---

predict_pmol	<i>predict picomoles of DNA from a fit and read counts (coverage)</i>
--------------	---

---

### Description

FIXME: this could be made MUCH faster by precomputing CpG/GC stats per bin

### Usage

```
predict_pmol(  
  fit,  
  genomic_gr,  
  bsgenome = NULL,  
  ret = c("gr", "df"),  
  slide = FALSE  
)
```

### Arguments

fit	result of model_glm_pmol
genomic_gr	the genomic data / new data
bsgenome	BSgenome name (if null, will guess from genomic_gr)
ret	return a data.frame ("df") or GRanges ("gr")? ("gr")
slide	compute a sliding window estimate for GCfrac (1/3 width)?

### Details

Using GRanges as the return value is (perhaps counterintuitively) *much* faster than the data.frame, since the sequence of the bins gets converted from a BSgenome representation to characters in the latter (it is implied by the bin start, stop, and genome when left as a GRanges).

### Value

object with read count, fraglen, GC%, CpG\*\*(1/3), and concentration

### Examples

```
data(spike_res)  
data(genomic_res)  
data(spike, package="spiky")  
fit <- model_glm_pmol(covg_to_df(spike_res, spike=spike), spike=spike)  
preddf <- predict_pmol(fit, genomic_res, ret="df")  
pred <- predict_pmol(fit, genomic_res, ret="gr")  
bin_pmol(pred)
```

---

`process_spikes`*QC, QA, and processing for a new spike database*

---

### Description

Sequence feature verification: never trust anyone, least of all yourself.

### Usage

```
process_spikes(fasta, methylated = 0, ...)
```

### Arguments

<code>fasta</code>	fasta file (or GRanges or DataFrame) w/spike sequences
<code>methylated</code>	whether CpGs in each are methylated (0 or 1, default 0)
<code>...</code>	additional arguments, e.g. kernels (currently unused)

### Details

GCfrac is the GC content of spikes as a proportion instead of a percent. OECpG is (observed/expected) CpGs (expectation is 25% of GC dinucleotides).

### Value

a DataFrame suitable for downstream processing

### See Also

`kmers`

### Examples

```
data(spike)
spikes <- system.file("extdata", "spikes.fa", package="spiky", mustWork=TRUE)
spikemeth <- spike$methylated
process_spikes(spikes, spikemeth)
```

```
data(phage)
phages <- system.file("extdata", "phages.fa", package="spiky", mustWork=TRUE)
identical(process_spikes(phage), phage)
identical(phage, process_spikes(phage))
```

```
data(genbank_mito)
(mt <- process_spikes(genbank_mito)) # see also genbank_mito.R
gb_mito <- system.file("extdata", "genbank_mito.R", package="spiky")
```

---

read_bedpe	<i>read a BEDPE file into Pairs of GRanges (as if a GAlignmentPairs or similar)</i>
------------	---

---

### Description

read a BEDPE file into Pairs of GRanges (as if a GAlignmentPairs or similar)

### Usage

```
read_bedpe(
  x,
  ...,
  stranded = FALSE,
  fraglen = TRUE,
  optional = FALSE,
  keep = FALSE
)
```

### Arguments

x	a Tabixed BEDPE file, or a TabixFile of one
...	additional arguments to pass to scanTabix internally
stranded	Is the data stranded? (FALSE)
fraglen	compute the fragment length? (TRUE)
optional	scan the optional columns (name, score, strand1)? (FALSE)
keep	keep additional columns? (FALSE)

### Details

BEDPE import in R is a shambles. This is a bandaid on a GSW.

See the [\href{https://bedtools.readthedocs.io/en/latest/content/general-usage.html#bedpe}](https://bedtools.readthedocs.io/en/latest/content/general-usage.html#bedpe)

In short, for a pair of ranges 1 and 2, we have fields chrom1, start1, end1, chrom2, start2, end2, and (optionally) name, score, strand1, strand2, plus any other user defined fields that may be included (these are not yet supported by read\_bedpe). For example, two valid BEDPE lines are:

```
chr1 100 200 chr5 5000 5100 bedpe_example1 30
chr9 900 5000 chr9 3000 3800 bedpe_example2 99 + -
```

### Value

a Pairs of GRanges, perhaps with \$score or \$fraglen

### See Also

bedpe\_covg

**Examples**

```
## Not run:
bedpe <- "GSM5067076_2020_A64_bedpe.bed.gz"
WT1_hg38 <- GRanges("chr11", IRanges(32387775, 32435564), "-")
read_bedpe(bedpe, param=WT1_hg38)

## End(Not run)
```

---

rename_spikes	<i>for BAM/CRAM files with renamed contigs, we need to rename spike rows</i>
---------------	--

---

**Description**

This function does that.

**Usage**

```
rename_spikes(x, spike)
```

**Arguments**

`x` a BAM/CRAM file, hopefully with an index  
`spike` a DataFrame where `spike$sequence` is a DNASTringSet

**Value**

a DataFrame with renamed contigs (rows)

**See Also**

`generate_spike_fasta`

---

rename_spike_seqlevels	<i>for spike-in contigs in GRanges, match to standardized spike seqlevels</i>
------------------------	---

---

**Description**

This function is essentially the opposite of `rename_spikes`, except that it works well on `GRanges/GAlignments` from or for merged genome+spike BAMs. If spike contigs are found, it will assign `genome='spike'` to those, while changing the `seqlevels` to standardized names that match `rownames(spike)`.

**Usage**

```
rename_spike_seqlevels(x, spike = NULL)
```

**Arguments**

x something with seqlevels (GRanges, GAlignments, Seqinfo...)  
 spike a DataFrame where spike\$sequence is a DNASTringSet (or NULL)

**Value**

x, but with standardized spike seqlevels and genomes

**See Also**

rename\_spikes

---

scan\_genomic\_bedpe *Scan genomic BEDPE*

---

**Description**

Scan genomic BEDPE

**Usage**

```
scan_genomic_bedpe(
  bedpe,
  bin = TRUE,
  binwidth = 300L,
  bins = NULL,
  standard = TRUE,
  genome = "hg38"
)
```

**Arguments**

bedpe the BEDPE file path, or output from read\_bedpe()  
 bin Bin reads? (TRUE)  
 binwidth width of the bins for chromosomal tiling (300)  
 bins a pre-tiled GRanges for binning coverage (NULL)  
 standard restrict non-spike contigs to "standard" chromosomes? (TRUE)  
 genome Name of genome (default hg38)

**Value**

a GRanges with coverage

**Examples**

```
f1 <- system.file("extdata", "example_chr21_bedpe.bed.gz", package="spiky", mustWork=TRUE)
scan_genomic_bedpe(f1) # will warn user about spike contigs
```

---

scan\_genomic\_contigs *scan genomic contigs in a BAM/CRAM file*

---

## Description

The default workflow for spiky is roughly as follows:

## Usage

```
scan_genomic_contigs(
  bam,
  spike,
  param = NULL,
  bin = TRUE,
  binwidth = 300L,
  bins = NULL,
  standard = TRUE,
  genome = "hg38",
  ...
)
```

## Arguments

bam	the BAM or CRAM filename, or a vector of them
spike	the spike-in reference database (e.g. data(spike))
param	a ScanBamParam object specifying which reads to count (NULL)
bin	Bin reads? (TRUE)
binwidth	width of the bins for chromosomal tiling (300)
bins	a pre-tiled GRanges for binning coverage (NULL)
standard	restrict non-spike contigs to "standard" chromosomes? (TRUE)
genome	Name of genome (default hg38)
...	additional arguments to pass to scanBamFlag()

## Details

1. Identify and quantify the spike-in contigs in an experiment.
2. Fit a model for sequence-based abundance artifacts using the spike-ins.
3. Quantify raw fragment abundance on genomic contigs, and adjust per step 2.

scan\_genomic\_contigs addresses the first half of step 3. The assumption is that anything which isn't a spike contig, is a genomic contig. This isn't necessarily true, so the user can also supply a ScanBamParam object for the param argument and restrict scanning to whatever contigs they wish, which also allows for non-default MAPQ, pairing, and quality filters.

If multiple BAM or CRAM filenames are provided, all indices will be checked before attempting to run through any of the files.

## Value

a CompressedGRangesList with bin- and spike-level coverage

**See Also**

Rsamtools::ScanBamParam

**Examples**

```
library(Rsamtools)
data(spike, package="spiky")

fl <- system.file("extdata", "ex1.bam", package="Rsamtools",
                 mustWork=TRUE)
scan_genomic_contigs(fl, spike=spike, standard=FALSE) # will warn user about spike contigs

sb <- system.file("extdata", "example_chr21.bam", package="spiky",
                 mustWork=TRUE)
scan_genomic_contigs(sb, spike=spike) # will warn user about genomic contigs
```

---

scan\_methylation\_specificity

*tabulate methylation specificity for multiple spike-in BAM/CRAM files*

---

**Description**

Methylation specificity is here defined as methylated\_spike\_covg/spike\_covg

**Usage**

```
scan_methylation_specificity(files, spike, sep = "_")
```

**Arguments**

files	a vector of BAM/CRAM file names
spike	a spike-in database
sep	the separator for spike-in contig names ("_")

**Value**

a matrix with columns "mean" and "median"

**Examples**

```
data(spike)
library(GenomicRanges)
sb <- system.file("extdata", "example.spike.bam", package="spiky",
                 mustWork=TRUE)
scan_methylation_specificity(sb, spike=spike)
```

---

scan_spiked_bam	<i>pretty much what it says: scan standard chroms + spike contigs from a BAM</i>
-----------------	--

---

### Description

Note: behind the scenes, this is being refactored into scan\_spike\_contigs and scan\_genomic\_contigs. Once that is done, perhaps before release, the default workflow will switch to

### Usage

```
scan_spiked_bam(
  bam,
  spike,
  mapq = 20,
  binwidth = 300L,
  bins = NULL,
  how = c("max", "mean"),
  dupe = FALSE,
  paired = TRUE,
  standard = TRUE,
  ...
)
```

### Arguments

bam	the BAM file
spike	the spike-in reference database (e.g. data(spike))
mapq	minimum mapq value to count a pair (20)
binwidth	width of the bins for chromosomal tiling (300)
bins	a pre-tiled GRanges for binning coverage (NULL)
how	how to record spike read coverage (max or mean)? (max)
dupe	unique (FALSE), duplicate (TRUE), or all (NA) reads? (FALSE)
paired	restrict coverage to that from properly paired reads? (TRUE)
standard	restrict non-spike contigs to "standard" chromosomes? (TRUE)
...	additional arguments to pass to scanBamFlag()

### Details

1. scan spike contigs and count fragments per contig or per bin.
2. fit the appropriate model for adjusting genomic contigs based on spikes.
3. scan and adjust binned fragment tallies along genomic contigs per above.

This approach decouples binning schemes from model generation (using spikes) and model-based adjustment (using genomic fragment counts), decreasing code complexity while increasing the opportunities for caching & parallelization.

For a more realistic example (not run), one might do something like:

```
data(spike, package="spiky"); bam <- "2021_ctl.hg38_withSpikes.bam"; ssb_res <- scan_spiked_bam(bam,
mapq=20, spike=spike);
```

An extract from the resulting `ssb_res` object is available via

```
data(ssb_res, package="spiky");
```

The full `ssb_res` is a `GRangesList` object with 300bp-binned coverage on the standard (chr1-22, chrX, chrY, chrM) chromosomes (as determined by the `GenomeInfoDb::standardChromosomes()` function against the assembly defined in the BAM or CRAM file, by default; if desired, a user can scan all genomic contigs by setting `standard=FALSE` when calling the function). By default, the mean base-level coverage of genomic bins is reported, and the maximum spike-level coverage is reported, though this can also be adjusted as needed. The results then inform the reliability of measurements from replicate samples in multiple labs, as well as the adjusted quantitative coverage in each bin once the absolute quantity of captured cell-free methylated DNA has been fit by `model_glm_pmol` and `predict_pmol`. In some sense, this function converts BAMs/CRAMs into usable data structures for high-throughput standardized cfMeDIP experiments.

The data extract used in other examples is the same as the full version, with the sole difference being that genomic bins are limited to chr22.

### Value

a `CompressedGRangesList` with bin- and spike-level coverage

### See Also

`GenomeInfoDb::keepStandardChromosomes`

`Rsamtools::ScanBamParam`

### Examples

```
library(GenomicRanges)
data(spike, package="spiky")
sb <- system.file("extdata", "example.spike.bam", package="spiky",
                 mustWork=TRUE)
res <- scan_spiked_bam(sb, spike=spike, bins=GRanges())
summary(res$spikes$coverage)
```

---

scan_spike_bedpe	<i>Scan spikes BEDPE</i>
------------------	--------------------------

---

### Description

Scan spikes BEDPE

### Usage

```
scan_spike_bedpe(bedpe, spike, how = "max")
```

**Arguments**

bedpe	the BEDPE file path, or output from read_bedpe()
spike	information about the spikes (default: load spike)
how	how to summarize the per-spike coverage (max)

**Value**

a GRanges with coverage

**Examples**

```
data(spike, package="spiky")
fl <- system.file("extdata", "example_spike_bedpe.bed.gz", package="spiky", mustWork=TRUE)
scan_spike_bedpe(fl, spike=spike) # will warn user about spike contigs
```

---

scan\_spike\_contigs      *pretty much what it says: scan spike contigs from a BAM or CRAM file*

---

**Description**

default workflow is

**Usage**

```
scan_spike_contigs(bam, spike, how = "max", param = NULL, mc.cores = 16, ...)
```

**Arguments**

bam	the BAM or CRAM filename, or a vector of such filenames
spike	the spike-in reference database (e.g. data(spike))
how	how to summarize the per-spike coverage (max)
param	a ScanBamParam object, or NULL (will default to MAPQ=20 etc)
mc.cores	Number of cores to run on (default 16)
...	additional arguments to pass to scanBamFlag()

**Details**

1. scan spike contigs and count fragments per contig or per bin.
2. fit the appropriate model for adjusting genomic contigs based on spikes.
3. scan and adjust binned fragment tallies along genomic contigs per above.

scan\_spike\_contigs implements step 1.

If multiple BAM or CRAM filenames are provided, all indices will be checked before attempting to run through any of the files.

**Value**

a CompressedGRangesList with bin- and spike-level coverage

**See Also**

Rsamtools::ScanBamParam

**Examples**

```
library(GenomicRanges)
data(spike, package="spiky")
sb <- system.file("extdata", "example.spike.bam", package="spiky",
                  mustWork=TRUE) # switch to a CRAM
res <- scan_spike_contigs(sb, spike=spike) # use default ScanBamParam
summary(res)
```

---

scan\_spike\_counts      *run spike\_counts on BAM/CRAM files and shape the results for model\_glm\_pmol*

---

**Description**

Typically one will want to fit a correction model to multiple samples. This function eases this task by merging the output of spike\_counts into a data.frame that model\_glm\_pmol can directly fit.

**Usage**

```
scan_spike_counts(files, spike, methylated = 1, sep = "_")
```

**Arguments**

files	a vector of BAM/CRAM file names
spike	a spike-in database
methylated	a logical (0/1) to include only methylated fragments
sep	the separator for spike-in contig names ("_")

**Value**

a data.frame with columns "frag\_grp", "id", and "read\_count"

**Examples**

```
data(spike)
library(GenomicRanges)
sb <- system.file("extdata", "example.spike.bam", package="spiky",
                  mustWork=TRUE)
scan_spike_counts(sb, spike=spike)
fit <- model_glm_pmol(scan_spike_counts(sb, spike=spike), spike=spike)
```

---

```
seqinfo_from_header    create seqinfo (and thus a standard chromosome filter) from a BAM header
```

---

### Description

create seqinfo (and thus a standard chromosome filter) from a BAM header

### Usage

```
seqinfo_from_header(x, gen = NA, std = FALSE, ret = c("si", "gr"))
```

### Arguments

x	the BAM file or its header
gen	genome of the BAM file, if known (NULL; autodetect)
std	standard chromosomes only? (FALSE; will be empty if spikes)
ret	return Seqinfo ("si", the default) or GRanges ("gr")? ("si")

### Details

Setting std=TRUE on a spike-in BAM will produce an empty result.

### Value

Seqinfo object or GRanges (or ``as(seqinfo, "GRanges")``)

### Examples

```
library(Rsamtools)
fl <- system.file("extdata", "ex1.bam", package="Rsamtools", mustWork=TRUE)

hdr <- scanBamHeader(BamFile(fl))
si <- seqinfo_from_header(hdr)
gr <- seqinfo_from_header(fl, ret="gr")
stopifnot(identical(gr, as(si, "GRanges")))

std_si <- seqinfo_from_header(fl, std=TRUE)
seqlevels(std_si)

# for comparison with below
data(spike, package="spiky")
spike

sp <- system.file("extdata", "example.spike.bam", package="spiky")
sp_gr <- seqinfo_from_header(sp, ret="gr")
sp_gr
```

---

`spike`*spike-in contig properties for Sam's cfMeDIP spikes*

---

**Description**

A DataFrame with sequence, concentration, and other properties of Sam's synthetic cfMeDIP spike-in controls. The row names redundantly encode some of these properties, such as the number of CpGs in the spike-in sequence.

**Usage**`data(spike)`**Format**

A DataFrame object with

**sequence** contig sequence, as a DNASTringSet

**methyated** are the CpGs in this spike-in methylated? 0 or 1

**CpGs** number of CpG dinucleotides in the spike, from 1 to 16

**fmol** femtomolar concentration of the spike-in for standard mix

**molmass** molar mass of spike-in sequence

**Source**

<https://doi.org/10.1101/2021.02.12.430289>

---

`spike_bland_altman_plot`*Bland-Altman plot for cfMeDIP spike standards*

---

**Description**

Bland-Altman plot for cfMeDIP spike standards

**Usage**`spike_bland_altman_plot(fit)`**Arguments**

`fit` a model fit, from `predict_pmol` (?)

**Value**

a `ggplot2` object

**Examples**

```
data(spike_res)
data(spike, package="spiky")
fit <- model_glm_pmol(covg_to_df(spike_res, spike=spike),spike=spike)
ba_plot <- spike_bland_altman_plot(fit)
```

---

spike\_counts

*use the index of a spiked BAM/CRAM file for spike contig coverage*


---

**Description**

It dawned on me one day that we don't even have to bother reading the file if we have an index for a spiked BAM/CRAM result, since any fragments that map properly to the spike contigs are generated from synthetic templates. This function takes an index and a spike database (usually a DataFrame) as inputs and provides a rough coverage estimate over "rehabilitated" contig names (i.e., canonicalized contigs mapping to the database) as its output.

**Usage**

```
spike_counts(
  bam,
  spike,
  sep = "_",
  ref = "spike",
  verbose = FALSE,
  dump_idx = FALSE
)
```

**Arguments**

bam	the BAM or CRAM file (MUST HAVE AN INDEX)
spike	a data.frame, DataFrame, or similar with spikes
sep	separator character in contig names ("_")
ref	reference name for spike genome ("spike")
verbose	be verbose? (FALSE)
dump_idx	dump the renamed idxstats to aggregate? (FALSE)

**Details**

The argument spike has no default since we are attempting to refactor the spike-in databases into their own data packages and allow more general use.

**Value**

a GRanges of spike-in contig read counts

**Examples**

```
data(spike, package="spiky")
sb <- system.file("extdata", "example.spike.bam", package="spiky",
                  mustWork=TRUE)
spike_counts(sb, spike=spike)
```

---

spike\_cram\_counts      *spike-in counts, as a long data.frame*

---

**Description**

A data.frame with spike-in results from CRAM files (generated from scan\_spike\_counts(CRAMs, spike=spike))

**Usage**

```
data(spike_cram_counts)
```

**Format**

A data.frame object with

**frag\_grp** the encoded spike contig name: basepairs\_CpGs\_GCpercent

**id** subject from whom cfMeDIP spike reads (column 3) were counted

**read\_count** read coverage for this spike in this subject (column 2)

**Source**

Generated from scan\_spike\_counts(CRAMs, spike=spike) using example CRAMs containing spike contigs

---

spike\_read\_counts      *spike-in counts, as a long data.frame*

---

**Description**

A data.frame with spike-in results from control samples in the manuscript. This maps 1:1 onto dedup using reshape2::melt.

**Usage**

```
data(spike_read_counts)
```

**Format**

A data.frame object with

**frag\_grp** the encoded spike contig name: basepairs\_CpGs\_GCpercent

**id** subject from whom cfMeDIP spike reads (column 3) were counted

**read\_count** read coverage for this spike in this subject (column 2)

**Source**

This data was created using `inst/script/loadDedup.R`

---

spike_res	<i>A Granges object with spike-in sequence coverage, and summarized for each spike contig as (the default) max coverage. (In other words, the default output of <code>scan_spike_contigs</code> or <code>scan_spike_bedpe</code>) This represents what most users will want to generate from their own spike-in BAMs or BEDPEs, and is used repeatedly in downstream examples throughout the package.</i>
-----------	---

---

**Description**

A Granges object with spike-in sequence coverage, and summarized for each spike contig as (the default) max coverage. (In other words, the default output of `scan_spike_contigs` or `scan_spike_bedpe`) This represents what most users will want to generate from their own spike-in BAMs or BEDPEs, and is used repeatedly in downstream examples throughout the package.

**Usage**

```
data(spike_res)
```

**Format**

A GRanges of coverage results with one metadata column, coverage

**Source**

Generated using `scan_spike_bedpe` or `scan_spike_contigs` on an example bedpe or bam containing spike contigs.

---

spiky-methods	<i>A handful of methods that I've always felt were missing</i>
---------------	--

---

**Description**

Particularly, simple methods to plot coverage results.

**Usage**

```
## S4 method for signature 'Rle,ANY'
plot(x, y, ...)

## S4 method for signature 'SimpleRleList,ANY'
plot(x, y, ...)
```

**Arguments**

x                    an Rle or RleList, usually  
 y                    not used an Rle or RleList, usually  
 ...                  other params such as ylim passed to barplot

**Details**

selectMethod("plot", "Rle") and also selectMethod("plot", "RleList") too.

**Value**

invisibly, the plot details

---

ssb_res	<i>scan_spiked_bam results from a merged cfMeDIP CRAM file (chr22 and spikes)</i>
---------	---

---

**Description**

A CompressedGRangesList object with genomic (chr22) and spikes coverage, binned every 300bp for the genomic contigs then averaged across the bin, and summarized for each spike contig as (the default) max coverage. (In other words, the default output of scan\_spiked\_bam, restricted to a small enough set of genomic regions to be practical for examples.) This represents what most users will want to generate from their own merged BAMs or CRAMs, and is used repeatedly in downstream examples throughout the package.

**Usage**

```
data(ssb_res)
```

**Format**

A CompressedGRangesList of coverage results, containing

**genomic** a GRanges with one metadata column, coverage

**spikes** a GRanges with one metadata column, coverage

**Source**

Generated using scan\_spiked\_bam on an example bam containing chr22 and spike contigs.

---

testGR	<i>a test GRanges with UMI'ed genomic sequences used as controls</i>
--------	--

---

**Description**

Sources and overlap widths of various read sequences in a test CRAM.

**Usage**

```
data(testGR)
```

**Format**

A GRanges object with an mcols() DataFrame containing

**UMI1** the unique molecular identifier on the forward read

**UMI2** the unique molecular identifier on the reverse read

**seq** the sequence of the fragment

**name** the name of the fragment

**score** whether the fragment passes filters (always 1)

**Source**

Generated using inst/script/loadTest.R

---

tile_bins	<i>Tile the assembly-based contigs of a merged assembly/spike GRanges.</i>
-----------	--

---

**Description**

refactored out of scan\_spiked\_bam for more explicit information flow

**Usage**

```
tile_bins(gr, binwidth = 300L)
```

**Arguments**

gr                    the GRanges

binwidth            bin width to tile (default is 300)

**Value**

a GRanges of bins

**Examples**

```
bam <- system.file("extdata", "ex1.bam", package="Rsamtools",
                  mustWork=TRUE)
gr <- as(seqinfo_from_header(bam), "GRanges")
genome(gr) <- "notspike"
tile_bins(gr)
```

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