

# Package ‘bedr’

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**Type** Package

**Title** Genomic Region Processing using Tools Such as 'BEDTools', 'BEDOPS' and 'Tabix'

**Version** 1.1.5

**Description** Genomic regions processing using open-source command line tools such as 'BEDTools', 'BEDOPS' and 'Tabix'. These tools offer scalable and efficient utilities to perform genome arithmetic e.g indexing, formatting and merging. bedr API enhances access to these tools as well as offers additional utilities for genomic regions processing.

**Depends** R (>= 3.0)

**SystemRequirements** Preferred genomic operations engine: 'BEDTools', 'BEDOPS' and 'Tabix (>= 1.3)'.

**Suggests** knitr (>= 1.4), rmarkdown (>= 0.9.5)

**VignetteBuilder** knitr

**License** GPL-2

**URL** <https://github.com/theboutroslab/package-bedr>

**BugReports** <https://github.com/theboutroslab/package-bedr/issues>

**Imports** testthat (>= 3.0.0), VennDiagram (>= 1.6.4), data.table (>= 1.8.11), R.utils (>= 2.0.2), yaml (>= 2.1.10), parallel, grid

**Config/testthat/edition** 3

**NeedsCompilation** no

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---

`adjust.coordinates`      *adjust coordinates for a BEDPE file*

---

### Description

Adjust coordinates for a breakpoint in dataframe using confidence intervals specified an INFO field in the VCF file, if it exists. Used in the ‘vcf2bedpe’ function.

### Usage

```
adjust.coordinates(df, info_tag, start, end)
```

### Arguments

<code>df</code>	a dataframe object obtained from a VCF file
<code>info_tag</code>	an info tag from the dataframe/VCF file, e.g. ‘CIPOS’ or ‘CIEND’
<code>start</code>	VCF column containing the start coordinate
<code>end</code>	VCF column containing the end coordinate

### Value

a named list of the adjusted start and end coordinates of a breakpoint.

### Author(s)

Helena Winata

### Examples

```
## Not run:  
coordsA <- adjust.coordinates(x, 'CIPOS', x$POS, x$POS);  
coordsB <- adjust.coordinates(x, 'CIEND', x$END, x$END)  
  
## End(Not run)
```

---

bed2index	<i>bed dataframe to index string</i>
-----------	--------------------------------------

---

**Description**

convert a dataframe in bed format to an index string

**Usage**

```
bed2index(x, sort = TRUE)
```

**Arguments**

x	a object region object or index
sort	should the index be sorted

**Value**

Returns a vector of string based genomic regions

**Author(s)**

Daryl Waggott

**Examples**

```
test.regions <- get.random.regions(10);
bed2index(test.regions);
```

---

bed2vcf	<i>convert bed to vcf</i>
---------	---------------------------

---

**Description**

convert bed to vcf

**Usage**

```
bed2vcf(x, filename = NULL, zero.based = TRUE, header = NULL, fasta = NULL)
```

**Arguments**

x	the input bed object
filename	a filename to write to.
zero.based	is the file zero based i.e. bed format. defaults to true.
header	a list of things to put in the header. repeated elements such as INFO, FILTER, FORMAT can be put in data.frames.
fasta	build of the genome in fasta format

**Author(s)**

Daryl Waggott

**Examples**

```
## Not run:
  bed2vcf(x)

## End(Not run)
```

---

bedr	<i>Main bedtools wrapper function.</i>
------	--

---

**Description**

Main bedtools wrapper function.

**Usage**

```
bedr(engine = "bedtools",
      params = NULL,
      input = list(),
      method = NULL,
      tmpDir = NULL,
      deleteTmpDir = TRUE,
      outputDir = NULL,
      outputFile = NULL,
      check.chr = TRUE,
      check.zero.based = TRUE,
      check.valid = TRUE,
      check.sort = TRUE,
      check.merge = TRUE,
      verbose = TRUE
    );
```

**Arguments**

engine	What analytical engine to use i.e. bedtools, bedops, tabix, unix
params	A string that includes all the extra parameters and arguments to the bedtools command. For example if you wanted to do a left outer join you would specify method as intersect and use params = c("-loj -header"). If you leave input and method as defaults then this is this string represents the full command.
input	A list of input items to be used by bedtools. Each item should be named by its parameter name in bedtools for example input = list(a=xxx, b=yyy, i=zzz). Items can be R objects or external files. R objects need to be in bed format i.e. have chr, start, stop as the first three columns, or, have an position index as the first column or rowname i.e. chr1:100-1000.

method	What bedtools method. This can be intersect, sort, merge etc. See bedtools documentation for specifics.
tmpDir	The directory to be used for writing files
deleteTmpDir	Should tmp files be deleted. helpful for diagnostics.
outputDir	The output directory. Only used if outputFile is specified. It defaults to the current working directory.
outputFile	The name of the output file. If this is specified the output will be sent to a file not an R object
check.chr	check for chr prefix
check.zero.based	check for zero based coordinates
check.valid	do all region integrity checks
check.sort	check if region is sorted
check.merge	check if region is merged
verbose	Should messages be printed to screen.

**Value**

The output of command with some parsing to keep it consistent with the input.

**Author(s)**

Daryl Waggon

**See Also**

iranges

**Examples**

```
if (check.binary("bedtools")) {
  set.seed(666)

  index <- get.example.regions();
  a <- index[[1]];
  b <- index[[2]];

  ### check
  is.a.valid <- is.valid.region(a);
  is.b.valid <- is.valid.region(b);
  a <- a[is.a.valid];
  b <- b[is.b.valid];

  ### sort
  is.sorted <- is.sorted.region(a);
  a.sort1 <- bedr(engine = "bedtools", input = list(i = a), method = "sort", params = "");
  b.sort1 <- bedr(engine = "bedtools", input = list(i = b), method = "sort", params = "");
  a.sort2 <- bedr(engine = "bedops", input = list(i = a), method = "sort", params = "");
```

```

a.sort3 <- bedr.sort.region(a);
a.sort4 <- bedr.sort.region(a, engine = "unix", method = "natural");
a.sort5 <- bedr.sort.region(a, engine = "R", method = "natural");

### merge
is.merged <- is.merged.region(a.sort1);
a.merge1 <- bedr(engine = "bedtools", input = list(i = a.sort1), method = "merge", params = "");
b.merge1 <- bedr(engine = "bedtools", input = list(i = b.sort1), method = "merge", params = "");
a.merge2 <- bedr(engine = "bedops", input = list(i = a.sort1), method = "merge", params = "");
# a.merge3 <- bedr.merge.region(a); this will throw an error b/c region is not sorted

### subtract
a.sub1 <- bedr(input = list(a = a.merge1, b = b.merge1), method = "subtract", params="");
a.sub2 <- bedr.subtract.region(a.merge1, b.merge1);

### in.region
is.region <- in.region(a.merge1, b.merge1);
#is.region <- a.merge1 %in.region% b.merge1
### intersect
# note for bedtools its recommended to bedr.sort.regions before intersect for faster processing
# also if regions are not merged this can cause unexpected behaviour
a.int1 <- bedr(input = list(a = a.sort1, b = b.sort1), method = "intersect", params = "-loj");
a.int1 <- bedr(input = list(a = a.sort1, b = b.sort1), method="intersect",params="-loj -sorted");
a.int2 <- bedr(input = list(a = a.merge1, b = b.merge1), method="intersect",params="-loj -sorted");
a.int3 <- bedr.join.region(a.merge1, b.merge1);

### multiple join
d <- get.random.regions(100, chr="chr1", sort = TRUE);
a.mult <- bedr.join.multiple.region(x = list(a.merge1,b.merge1,bedr.sort.region(d)));

## Not run:
### groupby
# note the "g" column number is based on bed format i.e. first three columns chr, start, stop
# note the use of first, first, last on the region columns i.e. the union of the regions
# note currently missing values are not dealt with in bedtools. also the 5th column is
# assumed to be "score" and gets a default "-1" not a "."
cnv.gene <- bedr(
  input = list(i=cnv.gene), method = "groupby", params = paste(
    "-g 16 -c ",
    paste(1:15, collapse = ","),
    " -o ", "first,first,last, ",
    paste(rep("sum",12), collapse = ","),
    sep = ""
  )
);

### example 1
### workflow adding gene names to exome sequencing target file
# download refseq genes from ucsc or query biomart for ensemble gene names.
# format them in basic bed format.
# sort, merge target
# sort, merge -nms target. Overlapping genes/features get merged.

```

```

# this may not be ideal if there are some really big features.
# intersect -loj target, genes.
# alternatively, do not merge the target and apply the merge after the intersect.
# this will provide precision at the level of the exon.

## End(Not run)
}

```

---

```

bedr.join.multiple.region
      join multiple region objects

```

---

## Description

join multiple objects

## Usage

```

bedr.join.multiple.region(
  x = list(),
  fraction.overlap = 1/1e9,
  empty = FALSE,
  missing.values = ".",
  cluster = FALSE,
  species = "human",
  build = "hg19",
  check.zero.based = TRUE,
  check.chr = TRUE,
  check.valid = TRUE,
  check.sort = TRUE,
  check.merge = TRUE,
  verbose = TRUE
)

```

## Arguments

x	list of region objects
fraction.overlap	proportion of bases to be considered an overlap
empty	print rows if no match
missing.values	missing value character
cluster	TRUE/FALSE for clustering
species	species i.e. human or mouse
build	genome build to use for empty regions
check.zero.based	should 0 based coordinates be checked

check.chr	should chr prefix be checked
check.valid	check if region is valid
check.sort	check if region is sorted
check.merge	check if overlapping regions are merged
verbose	messages and checks

**Author(s)**

Daryl Waggett

**References**

<http://bedtools.readthedocs.io/en/latest/content/tools/multiinter.html>

**Examples**

```
if (check.binary("bedtools")) {
  index <- get.example.regions();

  a <- index[[1]];
  b <- index[[2]];

  a.sort <- bedr.sort.region(a);
  b.sort <- bedr.sort.region(b);
  d <- get.random.regions(100, chr="chr1", sort = TRUE);

  a.mult <- bedr.join.multiple.region(x = list(a.sort,b.sort,bedr.sort.region(d)));
}
```

---

bedr.join.region      *join two region objects using a left outer join*

---

**Description**

join two region objects using a left outer join

**Usage**

```
bedr.join.region(
  x,
  y,
  fraction.overlap = 1/1e9,
  reciporical = FALSE,
  report.n.overlap = FALSE,
  check.zero.based = TRUE,
  check.chr = TRUE,
```

```
check.valid = TRUE,  
check.sort = TRUE,  
check.merge = TRUE,  
verbose = TRUE  
)
```

### Arguments

x	object a
y	object b
fraction.overlap	proportion of overlap to be considered a match
report.n.overlap	should the number of overlapping bases be reported
reciporical	should the fraction overlap be applied to object b as well
check.zero.based	should 0 based coordinates be checked
check.chr	should chr prefix be checked
check.valid	check if region is valid
check.sort	check if region is sorted
check.merge	check if overlapping regions are merged
verbose	messages and checks

### Author(s)

Daryl Waggott

### References

<http://bedtools.readthedocs.io/en/latest/content/tools/intersect.html>

### Examples

```
if (check.binary("bedtools")) {  
  
  index <- get.example.regions();  
  
  a <- index[[1]];  
  b <- index[[2]];  
  
  a.sort <- bedr.sort.region(a);  
  b.sort <- bedr.sort.region(b);  
  
  d <- bedr.join.region(a.sort, b.sort);  
}
```

---

bedr.merge.region      *merge i.e. collapse overlaping regions*

---

### Description

merge i.e. collapse overlaping regions

### Usage

```
bedr.merge.region(  
  x,  
  distance = 0,  
  list.names = TRUE,  
  number = FALSE,  
  stratify.by = NULL,  
  check.zero.based = TRUE,  
  check.chr = TRUE,  
  check.valid = TRUE,  
  check.sort = TRUE,  
  verbose = TRUE  
);
```

### Arguments

x	input
distance	maximum distance between regions to be merged. defaults to 0 which means overlapping or bookended features. note that you can use negative distances to enforce a minimum overlap.
list.names	output list of names for merged items
number	output number of merged items
stratify.by	a column name indicating the groups to stratify merging within i.e. gene name. merging will not happen between groups.
check.zero.based	should 0 based coordinates be checked
check.chr	should chr prefix be checked
check.valid	should the region be checked for integrity
check.sort	should the sort order be checked
verbose	should log messages and checking take place

### Author(s)

Daryl Waggott

### References

<http://bedtools.readthedocs.io/en/latest/content/tools/merge.html>

**Examples**

```

if (check.binary("bedtools")) {

index <- get.example.regions();

a <- index[[1]];

a.sort <- bedr.sort.region(a);
a.merged <- bedr.merge.region(a.sort);

}

```

---

bedr.plot.region      *Visualize regions or intervals*

---

**Description**

Visualize regions or intervals. e.g. VennDiagrams of intersections of distinct intervals, base pairs and genes.

**Usage**

```

bedr.plot.region(
input,
filename = NULL,
type = "venn",
feature = "interval",
fraction.overlap = 0.000000001,
group = NULL,
params = list(),
verbose = TRUE
)

```

**Arguments**

input	A list of input regions or indices
filename	The name of the output image file
type	The type of plot. only 'venn' is supported for intersections at the moment.
feature	How should the regions be intersected. By unique "interval", "gene", "size" or "other" to use the features in the first item in the input list.
fraction.overlap	Minimum overlap required as a fraction of A. Default is 1E-9 (i.e. 1bp).
group	A grouping parameter for barplots. Possible values include "input", "chr", or a categorical vector of length equal to the sum of the input.
params	Additional parameters for plotting or intersecting. See <a href="#">venn.diagram</a> function for possible options.
verbose	Include text messages.

**Details**

By default a venn diagram is output. If a single input is used then the plot shows the number of unique and collapsed regions after applying a merge.

**Value**

Plots!

**Author(s)**

Daryl Waggott

**Examples**

```
## Not run:
if (check.binary("bedtools")) {
# example data
a <- get.random.regions(n = 1000, chr = "chr22", size.mean = 10)
b <- get.random.regions(n = 1000, chr = "chr22", size.mean = 10)
d <- get.random.regions(n = 1000, chr = "chr22", size.mean = 10)
e <- get.random.regions(n = 1000, chr = "chr22", size.mean = 10)
f <- get.random.regions(n = 1000, chr = "chr22", size.mean = 10)

pdf("bedr.plot.region.ex.pdf")

# basic venn diagrams
bedr.plot.region(input = list(a=a,b=b))
bedr.plot.region(input = list(a=a,b=b,d=d))
#bedr.plot.region(input = list(a=a,b=b,d=d,e=e))
#bedr.plot.region(input = list(a=a,b=b,d=d,e=e,f=f))

### change venn parameters
bedr.plot.region(
input = list(a=a,b=b,d=d),
params = list(lty = 2, label.col = "black", main = "Region Overlap")
)

### try with different
#bedr.plot.region(input = list(a=a,b=b), feature = "gene")
#bedr.plot.region(input = list(a=a,b=b), feature = "reference")
#bedr.plot.region(input = list(a=a,b=b), feature = "interval")
#bedr.plot.region(input = list(a=a,b=b), feature = "cluster")
#bedr.plot.region(input = list(a=a,b=b), feature = "bp")

dev.off()
}

## End(Not run)
```

---

bedr.setup	<i>Initialize some config settings for bedr</i>
------------	---

---

### Description

Initialize some config settings for bedr. This includes downloading useful datasets if requested.

### Usage

```
bedr.setup(datasets = "all", data.dir = paste0(Sys.getenv("HOME"), "/bedr/data"))
```

### Arguments

datasets	A list of datasets to download. Defaults to "all" i.e. c("refgene", "hg19", "b37", "hugo", "cosmic", "clinvar")
data.dir	A directory to put the data. Defaults to ~/bedr/data

### Details

The default config file is at ~/bedr/config.yml. It's in yaml format.

### Author(s)

Daryl Waggott

### Examples

```
## Not run:  
bedr.setup()  
  
## End(Not run)
```

---

bedr.snm.region	<i>sort a region file</i>
-----------------	---------------------------

---

### Description

Sort and merge regions object in one step

**Usage**

```
bedr.snm.region(  
  x,  
  method = "lexicographical",  
  distance = 0,  
  list.names = TRUE,  
  number = FALSE,  
  check.zero.based = TRUE,  
  check.chr = TRUE,  
  check.valid = TRUE,  
  verbose = TRUE  
)
```

**Arguments**

x	a object region object or index
method	natural or lexicographic
distance	distance between regions to be merged
list.names	output list of names for merged items
number	output number of merged items
check.zero.based	should 0 based coordinates be checked
check.chr	should chr prefix be checked
check.valid	should the region be checked for integrity
verbose	should log messages and checking take place

**Value**

Sorted and merged regions object

**Author(s)**

Daryl Waggott

**Examples**

```
if (check.binary("bedtools")) {  
  index <- get.example.regions();  
  a <- index[[1]];  
  b <- bedr.snm.region(a);  
}
```

---

bedr.sort.region      *sort a region file*

---

### Description

sort a region file

### Usage

```
bedr.sort.region(  
  x,  
  method = "lexicographical",  
  engine = "R",  
  chr.to.num = c("X" = 23, "Y" = 24, "M" = 25),  
  check.zero.based = TRUE,  
  check.chr = TRUE,  
  check.valid = TRUE,  
  check.merge = TRUE,  
  verbose = TRUE  
)
```

### Arguments

x	a region object or index
method	natural or lexicographic
engine	what analytical engine to use for sorting i.e. bedtools, bedops, gnu unix
chr.to.num	chromosome letter names to numbers map. Defaults to Homo sapiens i.e c("X" = 23, "Y" = 24, "M" = 25)
check.zero.based	should 0 based coordinates be checked
check.chr	should chr prefix be checked
check.valid	should the region be checked for integrity
check.merge	should overlapping regions be checked
verbose	should log messages and checking take place

### Author(s)

Daryl Waggott

### References

<http://bedtools.readthedocs.io/en/latest/content/tools/sort.html>

**Examples**

```

if (check.binary("bedtools")) {

  index <- get.example.regions();
  a <- index[[1]];
  b <- bedr.sort.region(a);

}

```

---

bedr.subtract.region    *subtracts features or ranges in object b from object a*

---

**Description**

subtracts features or ranges in object b from object a

**Usage**

```

bedr.subtract.region(
  x,
  y,
  fraction.overlap = 1/1e9,
  remove.whole.feature = TRUE,
  check.zero.based = TRUE,
  check.chr = TRUE,
  check.valid = TRUE,
  check.sort = TRUE,
  check.merge = TRUE,
  verbose = TRUE
)

```

**Arguments**

x	item a
y	item b
fraction.overlap	what portion of A to be considered an overlap
remove.whole.feature	should whole feature be removed
check.zero.based	should 0 based coordinates be checked
check.chr	should chr prefix be checked
check.valid	should the region be checked for integrity
check.sort	check if region is sorted
check.merge	check if overlapping regions are merged
verbose	messages and checks

**Value**

Regions exclusive to one object of regions.

**Author(s)**

Daryl Waggott

**References**

<http://bedtools.readthedocs.io/en/latest/content/tools/subtract.html>

**Examples**

```
if (check.binary("bedtools")) {
  index <- get.example.regions();

  a <- index[[1]];
  b <- index[[2]];
  a <- bedr(engine = "bedtools", input = list(i = a), method = "sort", params = "");
  b <- bedr(engine = "bedtools", input = list(i = b), method = "sort", params = "");
  d <- bedr.subtract.region(a,b);
}
```

---

catv

*outputs text if verbose flag is set*

---

**Description**

outputs text if verbose flag is set

**Usage**

```
catv(x)
```

**Arguments**

x                   some text string

**Value**

Prints the text string

**Author(s)**

Daryl Waggott

**Examples**

```
verbose <- TRUE;
catv("Hello Universe!");
verbose <- FALSE;
catv("Goodbye Universe!")
```

---

check.binary	<i>checks if binary is in the path</i>
--------------	--

---

**Description**

check if a binary is in the path. Specifically used for bedtools, bedops and tabix.

**Usage**

```
check.binary(x = "bedtools", verbose = TRUE)
```

**Arguments**

x	a string referring to a binary/executable i.e. bedtools, bedops, tabix
verbose	print log

**Details**

Used internally to determine functionality selection options.

**Value**

TRUE or FALSE

**Author(s)**

Daryl Waggott

**Examples**

```
check.binary("bedtools")
```

---

cluster.region	<i>cluster intervals</i>
----------------	--------------------------

---

## Description

cluster intervals

## Usage

```
cluster.region(  
  x,  
  distance = 0,  
  check.zero.based = TRUE,  
  check.chr = TRUE,  
  check.valid = TRUE,  
  check.sort = TRUE,  
  verbose = TRUE  
)
```

## Arguments

x	The region
distance	maximum distance between regions to be merged. defaults to 0 which means overlapping or bookended features. note that you can use negative distances to enforce a minimum overlap.
check.zero.based	should 0 based coordinates be checked
check.chr	should chr prefix be checked
check.valid	should the region be checked for integrity
check.sort	should regions be checked for sort order
verbose	should log messages and checking take place

## Details

clusters adjacent features of a specified distance.

## Value

A data.frame in bed format

## Author(s)

Daryl Waggott

## References

<http://bedtools.readthedocs.io/en/latest/content/tools/cluster.html>

**See Also**[bedr.merge.region](#)**Examples**

```

if (check.binary("bedtools")) {

  index <- get.example.regions();

  a <- index[[1]];

  b <- cluster.region(a, distance = 0);
  d <- cluster.region(a, distance = 100);

}

```

---

 convert2bed

*convert object to bed format*


---

**Description**

checks if an object can be converted into a bed style data.frame then does the conversion.

**Usage**

```

convert2bed(
  x,
  set.type = TRUE,
  check.zero.based = TRUE,
  check.chr = TRUE,
  check.valid = TRUE,
  check.sort = TRUE,
  check.merge = TRUE,
  verbose = TRUE
)

```

**Arguments**

x	A region index (i.e. chr1:10-100, ...) either as a vector or row.names/first column of a data.frame. Or a data.frame with the first three columns "chr", "start", "end"
set.type	should the attribute input.type be set. Sometimes it is desirable to avoid setting it when applying intermediate conversion
check.zero.based	should 0 based coordinates be checked
check.chr	should chr prefix be checked
check.valid	should the region be checked for integrity

check.sort	should the region be checked to see if it is sorted
check.merge	should the region be checked for overlapping regions
verbose	messages and text

**Details**

Very useful to convert data before using other bedr functions

**Value**

Returns x converted to bedformat, as a data frame

**Author(s)**

Daryl Waggott

**Examples**

```
## Not run:  
a.bed <- convert.to.bed(a)  
  
## End(Not run)
```

---

create.tmp.bed.file    *output R objects as tmpfiles*

---

**Description**

output R objects as tmpfiles

**Usage**

```
create.tmp.bed.file(x, name = "bedr", tmpDir = NULL)
```

**Arguments**

x	region object
name	a prefix for the tmp file.
tmpDir	where should the temp files be put

**Author(s)**

Daryl Waggott

**Examples**

```
# create tmp file
```

---

determine.input	<i>Determine input format</i>
-----------------	-------------------------------

---

**Description**

Determine input format whether its tabular or bed

**Usage**

```
determine.input(x, check.chr = FALSE, verbose = TRUE)
```

**Arguments**

x	input vector, matrix or dataframe
check.chr	check whether the coordinates are in chromosomal format with chr prefix
verbose	messages and checks

**Value**

integer value. index format (0), bed (1), index in first column (2), rownames are index (3), unrecognized(4)

**Author(s)**

Daryl Waggott

**Examples**

```
if (check.binary("bedtools")) {  
  
  index <- get.example.regions();  
  a <- index[[1]];  
  bedr:::determine.input(a);  
}
```

---

df2list	<i>Data frame to list conversion</i>
---------	--------------------------------------

---

**Description**

Take data frame and return a list of rownames where column value is not 0 i.e. missing

**Usage**

```
df2list(x, start.col = 1)
```

**Arguments**

x                    data frame  
start.col            offset from first column to ignore certain columns

**Value**

returns a list following cleanup and change of data structure

**Author(s)**

Daryl Waggott

**Examples**

```
## Not run:  
df2list(data.frame(a = 1:10, b = 11:20));  
  
## End(Not run)
```

---

download.datasets      *Download some useful datasets*

---

**Description**

Download some useful datasets. Some functions such as plotting and fasta querying require additional data.

**Usage**

```
download.datasets(datasets = "all", data.dir = paste0(Sys.getenv("HOME"), "~/bedr/data"))
```

**Arguments**

datasets            A list of datasets to download. Defaults to "all" i.e. c("refgene","hg19","b37","hugo",  
"cosmic","clinvar")  
data.dir            A directory to put the data. Defaults to ~/bedr/data

**Details**

External datasets are required for some bedr functionality. For example, plotting intersections based on genes, get.fasta, bed2vcf and validate.gene.names. If these datasets already exist you can simply place symlinks in a directory and use bedr.setup() to define the data.dir.

**Value**

some datasets.

**Author(s)**

Daryl Waggott

**Examples**

```
## Not run:  
  download.datasets("cosmic");  
  
## End(Not run)
```

---

`flank.region`*Get adjacent flanks from regions*

---

**Description**

Get adjacent flanks from regions

**Usage**

```
flank.region(  
  x,  
  n.add = NULL,  
  start.add = NULL,  
  end.add = NULL,  
  species = "human",  
  build = "hg19",  
  check.zero.based = TRUE,  
  check.chr = TRUE,  
  check.valid = TRUE,  
  check.sort = TRUE,  
  check.merge = TRUE,  
  verbose = TRUE  
)
```

**Arguments**

<code>x</code>	a object region object or index
<code>n.add</code>	the number of bases to be selected from each side of a region
<code>start.add</code>	the number of based to be selected from the start of a region
<code>end.add</code>	the number of based to be selected from the end of a region
<code>species</code>	the species i.e. human or mouse
<code>build</code>	the genome build i.e. hg19 or mm10
<code>check.zero.based</code>	should 0 based coordinates be checked

check.chr	should chr prefix be checked
check.valid	should the region be checked for integrity
check.sort	should regions be checked for sort order
check.merge	should overlapping regions be checked
verbose	should log messages and checking take place

**Author(s)**

Daryl Waggott

**References**

<http://bedtools.readthedocs.io/en/latest/content/tools/flank.html>

**Examples**

```
if (check.binary("bedtools")) {
  index <- get.example.regions();

  a <- index[[1]];
  a <- bedr(engine = "bedtools", input = list(i = a), method = "sort", params = "");
  b <- flank.region(a, n.add = 20);
}
```

---

get.bedpe.id	<i>get BEDPE ID from VCF ID</i>
--------------	---------------------------------

---

**Description**

Get IDs for each breakpoint pair from the VCF file. Used in the 'vcf2bedpe' function.

**Usage**

```
get.bedpe.id(df)
```

**Arguments**

df                    a dataframe object from a VCF file

**Value**

A column vector of names assigned to each Structural Variant in the BEDPE file

**Author(s)**

Helena Winata

### Examples

```
## Not run:  
name <- get.bedpe.id(x.vcf)  
  
## End(Not run)
```

---

get.chr.length	<i>gets the length of each chromosome for a species/build</i>
----------------	---

---

### Description

Gets the length of each chromosome for a species/build. Choices are human (hg18, hg19, hg38), mouse(mm9, mm10)

### Usage

```
get.chr.length(chr = NULL, species = "human", build = "hg19")
```

### Arguments

chr	a vector of chromosomes to query. defaults to all.
species	species
build	build

### Value

A dataframe with chromosome annotations

### Author(s)

Daryl Waggott

### Examples

```
size <- get.chr.length();
```

get.example.regions     *return a set of regions for the examples and unit testing*

---

**Description**

return a set of regions for the examples and unit testing

**Usage**

```
get.example.regions()
```

**Value**

A list with three example regions

**Author(s)**

Daryl Waggott

**Examples**

```
index <- get.example.regions()
```

---

get.fasta                     *Query fasta sequence*

---

**Description**

Query fasta sequence using bedtools get.fasta

**Usage**

```
get.fasta(  
  x,  
  fasta = NULL,  
  bed12 = FALSE,  
  strand = FALSE,  
  output.fasta = FALSE,  
  use.name.field = FALSE,  
  check.zero.based = TRUE,  
  check.chr = TRUE,  
  check.valid = TRUE,  
  check.sort = TRUE,  
  check.merge = TRUE,  
  verbose = TRUE  
)
```

**Arguments**

x	region or index
fasta	a fasta file defaults to mini example hg19 human
bed12	should bed12 format be used
strand	strand specific i.e. reverse complement negative
output.fasta	output a fasta defaults to a data.frame for easier parsing
use.name.field	should the name field be used for
check.zero.based	check for zero based region
check.chr	check for "chr" prefix
check.valid	check for valid regions i.e. start < end
check.sort	check if region is sorted
check.merge	check if region is merged
verbose	print progress

**Details**

Uses bedtools getFasta to query a fasta file and load into R as a data.frame for easy parsing.

Note that the hg19 reference genome fasta is large and requires on the order of 4 GB RAM to avoid a segfault happens.

**Value**

A data.frame or fasta. The data.frame has is two columns corresponding to the region and the sequence.

**Author(s)**

Daryl Waggott, Syed Haider

**References**

<http://bedtools.readthedocs.io/en/latest/content/tools/getfasta.html>

**Examples**

```
if (check.binary("bedtools")) {  
  
## Not run:  
  
# get the sequence for a set of regions as a data.frame  
index <- get.example.regions();  
a <- index[[1]];  
b <- get.fasta(bedr.sort.region(a));
```

```

# this time output a fasta
d <- get.fasta(b, output.fasta = TRUE);
writeLines(d[[1]], con = "test.fasta");

# get the region adjacent to a set of mutations in a vcf
clinvar.vcf.example <- system.file(
  "extdata/clinvar_dbSNP138_example.vcf.gz",
  package = "bedr"
);
clinvar <- read.vcf(clinvar.vcf.example);

# note that clinvar uses ncbi fasta which does not use "chr" and codes chrM as MT
clinvar.bed <- data.frame(
  chr = paste0("chr", gsub("MT", "M", clinvar$vcf$CHROM)),
  start = clinvar$vcf$POS - 2,
  end = clinvar$vcf$POS + 1,
  stringsAsFactors = FALSE
);

# get trinucleotide sequences of variants on chr M only
mutation.triplet <- get.fasta(
  clinvar.bed[which(clinvar.bed$chr == "chrM"), ],
  fasta = system.file("extdata/ucsc.hg19.chrM.fasta", package = "bedr"),
  check.chr = FALSE
);

## End(Not run)
}

```

---

get.random.regions      *generates a set of random regions*

---

## Description

generates a set of random regions for a specific species/build. Choices are human (hg18, hg19), mouse(mm9, mm10). regions are sampled from a log-normal distribution.

## Usage

```

get.random.regions(
  n = 10,
  chr = NULL,
  species = "human",
  build = "hg19",
  size.mean = 10,
  size.sd = 0.25,
  mask.gaps = FALSE,
  mask.repeats = FALSE,
  sort.output = TRUE,

```

```
verbose = TRUE  
)
```

**Arguments**

<code>n</code>	number of regions
<code>chr</code>	the chr or region
<code>species</code>	species
<code>build</code>	build
<code>size.mean</code>	region mean in log space
<code>size.sd</code>	region sd in log space
<code>mask.gaps</code>	should the gaps (Ns) in the human reference be ignored as potential start points. This dramatically increases memory and run time but is more appropriate in almost all settings. By default it's off.
<code>mask.repeats</code>	should the repeats from repeatMasker be ignored as potential start points. This dramatically increases memory and run time but is more appropriate in almost all settings. By default it's off.
<code>sort.output</code>	return a sorted index
<code>verbose</code>	words

**Author(s)**

Daryl Waggott

**Examples**

```
test.regions <- get.random.regions(100)
```

---

<code>get.strand</code>	<i>get BEDPE ID from VCF ID</i>
-------------------------	---------------------------------

---

**Description**

Get strand information for each breakpoint from the VCF file (ALT or STRAND column). Used in the 'vcf2bedpe' function.

**Usage**

```
get.strand(df)
```

**Arguments**

<code>df</code>	a dataframe object from a VCF file
-----------------	------------------------------------

**Value**

A column vector of strand information for each breakpoints

**Author(s)**

Helena Winata

**Examples**

```
## Not run:
  name <- get.strand(x.vcf)

## End(Not run)
```

---

grow.region

*Get adjacent flanks from regions*

---

**Description**

Get adjacent flanks from regions

**Usage**

```
grow.region(
  x,
  n.add = NULL,
  start.add = NULL,
  end.add = NULL,
  species = "human",
  build = "hg19",
  check.zero.based = TRUE,
  check.chr = TRUE,
  check.valid = TRUE,
  check.sort = TRUE,
  check.merge = TRUE,
  verbose = TRUE
)
```

**Arguments**

x	a object region object or index
n.add	the number of bases to be selected from each side of a region
start.add	the number of based to be selected from the start of a region
end.add	the number of based to be selected from the end of a region
species	the species i.e. human or mouse

build	the genome build i.e. hg19 or mm10
check.zero.based	should 0 based coordinates be checked
check.chr	should chr prefix be checked
check.valid	should the region be checked for integrity
check.sort	should regions be checked for sort order
check.merge	should overlapping regions be checked
verbose	should log messages and checking take place

**Author(s)**

Daryl Waggott

**References**

<http://bedtools.readthedocs.io/en/latest/content/tools/slop.html>

**Examples**

```

if (check.binary("bedtools")) {
  index <- get.example.regions();

  a <- index[[1]];
  a <- bedr(engine = "bedtools", input = list(i = a), method = "sort", params = "");
  b <- grow.region(a, n.add = 20);

}

```

---

in.region	<i>checks if regions in object a are found in object b</i>
-----------	--

---

**Description**

checks if regions in object a are found in object b

**Usage**

```

in.region(
  x,
  y,
  proportion.overlap = 1e-09,
  method = "natural",
  reciprocal.overlap = FALSE,
  check.zero.based = TRUE,
  check.chr = TRUE,
  check.valid = TRUE,

```

```

check.sort = TRUE,
check.merge = TRUE,
verbose = FALSE
)

```

### Arguments

<code>x</code>	first region index in the form chr:start-stop. regions in this index will be checked for intersection in the values of the second index.
<code>y</code>	second region index.
<code>proportion.overlap</code>	Defaults 1e-9 which is 1 bp. See details below for the different interpretation between 0 and 1 based overlap
<code>method</code>	Sorting method ("natural" by default)
<code>reciprocal.overlap</code>	Should the <code>proportion.overlap</code> be reciprocal
<code>check.zero.based</code>	should 0 based coordinates be checked
<code>check.chr</code>	should chr prefix be checked
<code>check.valid</code>	check if region is valid
<code>check.sort</code>	check if region is sorted
<code>check.merge</code>	check if overlapping regions are merged
<code>verbose</code>	prints some debugging information. currently it just checks if the input regions are overlapping

### Details

The function can also be called using syntax similar to the `%in%` operator, for example "region1 `%in.region%` region2"

The default is to report TRUE if there is 1bp overlap in zero based bed format. That means that region chr1:10-20 and chr1:20-30 would not overlap. To switch to one based intuitive interpretation set `proportion.overlap = 0`.

### Value

Returns a logical vector the length of `x`.

### Author(s)

Daryl Waggott

### References

<http://bedtools.readthedocs.io/en/latest/content/tools/intersect.html>

**Examples**

```
if (check.binary("bedtools")) {  
  
  index <- get.example.regions();  
  
  a <- index[[1]];  
  b <- index[[2]];  
  a <- bedr(engine = "bedtools", input = list(i = a), method = "sort", params = "");  
  b <- bedr(engine = "bedtools", input = list(i = b), method = "sort", params = "");  
  
  d <- in.region(a,b);  
  
  # alternative calling  
  d <- a %in.region% b  
  
}
```

---

index2bed

*convert a region index into a bed file dataframe*

---

**Description**

convert a region index into a bed file dataframe

**Usage**

```
index2bed(x, set.type = TRUE)
```

**Arguments**

x	an index
set.type	should the attribute input.type be set. Sometimes it is desirable to avoid setting it when applying intermediate conversion

**Author(s)**

Daryl Waggott

**Examples**

```
if (check.binary("bedtools")) {  
  
  index <- get.example.regions();  
  a <- index[[1]];  
  a.bed <- index2bed(a);  
}
```

---

is.merged.region	<i>checks if region file is merged</i>
------------------	--

---

**Description**

checks if region file is merged

**Usage**

```
is.merged.region(  
  x,  
  check.zero.based = TRUE,  
  check.chr = TRUE,  
  check.valid = TRUE,  
  check.sort = TRUE,  
  verbose = FALSE  
)
```

**Arguments**

x	region or index
check.zero.based	should 0 based coordinates be checked
check.chr	should chr prefix be checked
check.valid	check if region is valid
check.sort	check if region is sorted
verbose	more words

**Author(s)**

Daryl Waggott

**Examples**

```
if (check.binary("bedtools")) {  
  index <- get.example.regions();  
  a <- index[[1]];  
  b <- is.merged.region(a);  
}
```

---

is.sorted.region      *checks if region file is sorted*

---

### Description

checks if region file is sorted

### Usage

```
is.sorted.region(  
  x,  
  method = "lex",  
  engine = "unix",  
  check.zero.based = TRUE,  
  check.chr = TRUE,  
  check.valid = TRUE,  
  check.merge = TRUE,  
  verbose = FALSE  
)
```

### Arguments

x	The region index, bed file, or bed formatted object
method	lexicographical or natural, lex is required for many operations but natural is better for interpretation
engine	what analytical engine to use for sorting i.e. bedtools, bedops, gnu unix
check.zero.based	should 0 based coordinates be checked
check.chr	should chr prefix be checked
check.valid	check if region is valid
check.merge	check if region is merged
verbose	more words

### Author(s)

Daryl Waggott

### Examples

```
if (check.binary("bedtools")) {  
  index <- get.example.regions();  
  
  a <- index[[1]];  
  
  b <- is.sorted.region(a);  
}
```

---

is.valid.ref                      *verifies the reference sequence in a vcf*

---

### **Description**

verifies the reference sequence in a vcf

### **Usage**

```
is.valid.ref(  
  x,  
  fasta = NULL,  
  strand = FALSE,  
  check.zero.based = TRUE,  
  check.chr = TRUE,  
  check.valid = TRUE,  
  check.sort = TRUE,  
  check.merge = TRUE,  
  verbose = TRUE  
)
```

### **Arguments**

x	input bed object
fasta	a reference build in fasta format
strand	should strand be used. if reverse then the sequence will be reverse complemented
check.zero.based	should 0 based coordinates be checked
check.chr	should chr prefix be checked
check.valid	should the region be checked for integrity
check.sort	should regions be checked for sort order
check.merge	should overlapping regions be checked
verbose	should log messages and checking take place

### **Value**

a logical vector the length of the input

### **Author(s)**

Daryl Waggott

**Examples**

```
## Not run:
vcf.path <- system.file("data/callerA.vcf.gz", package = "bedr");
vcf.data <- read.vcf(vcf.path, split.info = TRUE);
vcf.data$vcf <- vcf.data$vcf[,
c("CHROM", "POS", "END",
setdiff(colnames(vcf.data$vcf),
c("CHROM", "POS", "END"))
];
vcf.data$vcf$CHROM <- paste("chr", vcf.data$vcf$CHROM, sep = "");

# need reference sequence FASTA and index file to run this, as 'fasta' parameter
is.valid.ref(vcf.data);

## End(Not run)
```

---

is.valid.region	<i>checks if region/index is valid</i>
-----------------	--

---

**Description**

checks if region/index is valid

**Usage**

```
is.valid.region(
x,
check.zero.based = TRUE,
check.chr = TRUE,
throw.error = FALSE,
verbose = TRUE
)
```

**Arguments**

x	The region index, bed file, or bed formatted object
check.zero.based	should basic test for zero based coordinates be checked
check.chr	should the algorithm check for the "chr" prefix
throw.error	should an error be thrown. The default is to report a logical vector of inconsistencies.
verbose	should diagnostic messages be printed

**Author(s)**

Daryl Waggott

**Examples**

```

index <- get.example.regions();

a <- index[[1]];
is.valid <- is.valid.region(a);
a.valid <- a[is.valid];

```

---

is.valid.seq	<i>verifies that sequences are correct given coordinates and a reference</i>
--------------	--

---

**Description**

verifies that sequences are correct given coordinates and a reference

**Usage**

```

is.valid.seq(
  x,
  querySeq,
  fasta = NULL,
  strand = FALSE,
  check.zero.based = TRUE,
  check.chr = TRUE,
  check.valid = TRUE,
  check.sort = TRUE,
  check.merge = TRUE,
  verbose = TRUE
)

```

**Arguments**

x	input bed object
querySeq	a vector of sequences the same length as x
fasta	a reference build in fasta format
strand	should strand be used. if reverse then the sequence will be reverse complemented
check.zero.based	should 0 based coordinates be checked
check.chr	should chr prefix be checked
check.valid	should the region be checked for integrity
check.sort	should regions be checked for sort order
check.merge	should overlapping regions be checked
verbose	should log messages and checking take place

**Value**

a logical vector the length of the input querySeq

**Author(s)**

Daryl Waggott, Syed Haider

**Examples**

```
if (check.binary("bedtools")) {
  index <- get.example.regions();
  a <- index[[1]];
  a <- get.fasta(bedr.sort.region(a));
  is.valid.seq(x = a, querySeq = a$sequence);
}
```

---

jaccard

*calculate the jaccard distance between sets of intervals*


---

**Description**

calculate the jaccard distance between sets of intervals

**Usage**

```
jaccard(
  x,
  y,
  proportion.overlap = 1e-09,
  reciprocal.overlap = FALSE,
  check.zero.based = TRUE,
  check.chr = TRUE,
  check.valid = TRUE,
  check.sort = TRUE,
  check.merge = TRUE,
  verbose = TRUE
)
```

**Arguments**

x                    first region to be compared

y                    second region to be compared

proportion.overlap  
                     Defaults 1e-9 which is 1 bp. See details below for the different interpretation  
                     between 0 and 1 based overlap

reciprocal.overlap  
                     Should the proportion.overlap be reciprocal

<code>check.zero.based</code>	should 0 based coordinates be checked
<code>check.chr</code>	should chr prefix be checked
<code>check.valid</code>	should the region be checked for integrity
<code>check.sort</code>	should regions be checked for sort order
<code>check.merge</code>	should overlapping regions be checked
<code>verbose</code>	should log messages and checking take place

### Details

The Jaccard metric is the ratio of intersections to unions. The process can be tweaked by changing the proportion of overlap and even growing the regions.

### Value

A short vector.

### Author(s)

Daryl Waggott

### References

<http://bedtools.readthedocs.io/en/latest/content/tools/jaccard.html>

### See Also

`reldist`

### Examples

```
if (check.binary("bedtools")) {  
  
  index <- get.example.regions();  
  
  a <- index[[1]];  
  b <- index[[2]];  
  a <- bedr(engine = "bedtools", input = list(i = a), method = "sort", params = "");  
  b <- bedr(engine = "bedtools", input = list(i = b), method = "sort", params = "");  
  jaccard(a,b);  
  
}
```

---

modifyList2	<i>Interface to R's modifyList</i>
-------------	------------------------------------

---

**Description**

Interface to R's modifyList

**Usage**

```
modifyList2(x, val)
```

**Arguments**

x	a named list
val	a named list with components to be updated using x

**Value**

modified version of x

**Author(s)**

Daryl Waggott

**See Also**

modifyList

---

order.region	<i>Gets the sort order of a region index similar to the order command</i>
--------------	---

---

**Description**

Helps if you don't want to use sort region on a huge dataset

**Usage**

```
order.region(  
  x,  
  method = "lex",  
  check.zero.based = TRUE,  
  check.chr = TRUE,  
  check.valid = TRUE,  
  check.merge = TRUE  
)
```

**Arguments**

x	index or bed style data.frame
method	natural or lexicographical (lex)
check.zero.based	should 0 based coordinates be checked
check.chr	should chr prefix be checked
check.valid	check if region is valid
check.merge	check if region is sorted and merged

**Author(s)**

Daryl Waggott

**References**

<http://bedtools.readthedocs.io/en/latest/content/tools/intersect.html>

**Examples**

```
if (check.binary("bedtools")) {
  index <- get.example.regions();

  a <- index[[1]];
  a <- bedr(engine = "bedtools", input = list(i = a), method = "sort", params = "");
  a.order <- order.region(a)

  b <- a[a.order];
}
```

---

permute.region	<i>permute a set of regions</i>
----------------	---------------------------------

---

**Description**

permute a set of regions

**Usage**

```
permute.region(
  x,
  stratify.by.chr = FALSE,
  species = "human",
  build = "hg19",
  chr.names = paste0("chr", c(1:22, "X", "Y", "M")),
```

```

mask.gaps = FALSE,
gaps.file = NULL,
mask.repeats = FALSE,
repeats.file = NULL,
sort.output = TRUE,
is.checked = FALSE,
check.zero.based = TRUE,
check.chr = TRUE,
check.valid = TRUE,
verbose = TRUE
)

```

### Arguments

x	regions to permute
stratify.by.chr	Should the permutation be happen separately for each chromosome. That is are chromosomes exchangeable.
species	species
build	the build of the reference
chr.names	names of the chromosomes to use
mask.gaps	should the gaps (Ns) in the human reference be ignored as potential start points. This dramatically increases memory and run time but is more appropriate in almost all settings. It defaults to off
gaps.file	database file of gaps. Defaults to Homo sapiens Hg19 gap.txt.gz file available through UCSC
mask.repeats	should the repeats from repeatMasker be ignored as potential start points. This dramatically increases memory and run time but is more appropriate in almost all settings. By default it's off
repeats.file	database file of repeats as supplied by UCSC containing RepMasker data e.g rnsk.txt.gz
sort.output	should the output be sorted
is.checked	Has the input data already be tested for validity. This is often done once before multiple permutations.
check.zero.based	should 0 based coordinates be checked
check.chr	should chr prefix be checked
check.valid	should the region be checked for integrity
verbose	should log messages and checking take place

### Details

1. Sampling with replacement on region length.
  2. Sampling with replacement on start positions. Positions that contain Ns in the reference are set to 0 weight during sampling.
- Regions that overlap the end of a chromosome or gap are trimmed.
- Steps 1 and 2 are done within chromosomes if stratify.by.chr is set to true.

**Value**

A region object with randomized start positions.

**Author(s)**

Daryl Waggott

**Examples**

```
if (check.binary("bedtools")) {

  index <- get.example.regions();
  a <- index[[1]];
  a <- bedr(engine = "bedtools", input = list(i = a), method = "sort", params = "");
  a.perm <- permute.region(a);

}
```

---

process.input

*process.input*

---

**Description**

process.input

**Usage**

```
process.input(
  input,
  tmpDir = NULL,
  include.names = TRUE,
  check.zero.based = TRUE,
  check.chr = TRUE,
  check.valid = TRUE,
  check.sort = TRUE,
  check.merge = TRUE,
  verbose = TRUE
)
```

**Arguments**

input	regions input or a file in one of the standard formats. these are bed, vcf, gff, bam, sam, csv, tsv, txt
tmpDir	The directory to be used for writing files
include.names	should the names of the input files be included in the output
check.zero.based	should 0 based coordinates be checked

check.chr	should chr prefix be checked
check.valid	should the region be checked for integrity
check.sort	should the region sorting be checked
check.merge	should overlapping regions be checked
verbose	messages and checks

**Value**

list of input files

**Author(s)**

Daryl Waggott

**Examples**

```
if (check.binary("bedtools")) {  
  
  index <- get.example.regions();  
  a <- index[[1]];  
  a <- bedr(engine = "bedtools", input = list(i = a), method = "sort", params = "");  
  a.processed <- process.input(a, verbose = FALSE)  
  
}
```

---

query.ucsc	<i>read a ucsc table into R</i>
------------	---------------------------------

---

**Description**

read a ucsc table into R

**Usage**

```
query.ucsc(  
  x,  
  mirror = "http://hgdownload.soe.ucsc.edu/goldenPath/hg19/database",  
  download = TRUE,  
  overwrite.local = FALSE,  
  columns.keep = NULL,  
  verbose = TRUE  
)
```

**Arguments**

x	a ucsc data table. Include the full path including "txt.gz" extension to load from a local file. Note that \$HOME/bedr/data will be checked first before downloading.
mirror	the ucsc mirror
download	should the data be downloaded to \$HOME/bedr/data/
overwrite.local	should the local version be overwritten if it exists
columns.keep	what columns to load. this can help with very large tables where you only want 'chr,start,end'. defaults to all. you may have to check the sql for the actual column names.
verbose	more words

**Details**

tables can be found at <http://hgdownload.soe.ucsc.edu/goldenPath/hg19/database/>

**Value**

A data.frame

**Author(s)**

Daryl Wagott

**Examples**

```
## Not run:
  query.ucsc("refGene");

## End(Not run)
```

---

read.vcf

*Read a vcf into R*

---

**Description**

Read a vcf into R and parse it for downstream analysis

**Usage**

```
read.vcf(x, split.info = FALSE, split.samples = FALSE, nrows = -1, verbose = TRUE)
```

## Arguments

x	A vcf
split.info	Split the info into columns
split.samples	Split the sample into columns. If multiple samples then a list matrices will be created, one matrix for each element in the FORMAT tag.
nrows	The the number of rows to be read. Set to 0 to parse the header.
verbose	print progress

## Details

The function can be slow for splitting the INFO, FORMAT for large VCFs.

## Value

VCF representation in R as a list. The first element in the list is the header, the second the body of the VCF. Every repeating tag in the header i.e. INFO, FORMAT is structured as matrix. If reading a multi-sample VCF and the split.sample = TRUE, then a matrix is added to the list for every tag in the FORMAT string.

Note that by default the vcf is returned as a data.table not a data.frame. Therefore there are some quirks i.e. subsetting via named columns a\$vcf[,"CHROM", with = FALSE]. If in doubt just caset to data.frame.

## Author(s)

Daryl Waggott

## Examples

```
clinVar.vcf.example <- system.file("extdata/clinvar_dbSNP138_example.vcf.gz", package = "bedr")
singleSample.vcf.example <- system.file("extdata/singleSampleOICR_example.vcf.gz", package = "bedr")
multiSample.vcf.example <- system.file("extdata/multiSampleOICR_example.vcf.gz", package = "bedr")

# read a subset of NCBI clinVar vcf. Note this has no samples.
vcf1.a <- read.vcf(clinVar.vcf.example)
vcf1.b <- read.vcf(clinVar.vcf.example, split.info = TRUE)

## Not run:

# same as above but split multiple samples
vcf1.c <- read.vcf(clinVar.vcf.example, split.info = TRUE, split.sample = TRUE)

# read a single-sample VCF
system.time(
  vcf2.a <- read.vcf(singleSample.vcf.example, split.info = TRUE, split.sample = TRUE)
)

# read a multi-sample VCF
vcf3.a <- read.vcf(multiSample.vcf.example, split.info = FALSE, split.sample = TRUE);
```

```
# multi core example
options("cores"=9);
vcf2.a <- read.vcf(singleSample.vcf.example, split.info = TRUE, split.sample = TRUE)
options("cores"=1);

## End(Not run)
```

---

reldist

---

*Calculate the relative distance between two sets of intervals*


---

### Description

Calculate the relative distance between two sets of intervals

### Usage

```
reldist(
  x,
  y,
  detail = FALSE,
  check.zero.based = TRUE,
  check.chr = TRUE,
  check.valid = TRUE,
  check.sort = TRUE,
  check.merge = TRUE,
  verbose = TRUE
)
```

### Arguments

x	firt region to be compared
y	second region to be compared
detail	should the relative distance be printed for every region
check.zero.based	should 0 based coordinates be checked
check.chr	should chr prefix be checked
check.valid	should the region be checked for integrity
check.sort	should regions be checked for sort order
check.merge	should overlapping regions be checked
verbose	should log messages and checking take place

### Details

The frequency of relative distances in bins spanning 0 to 0.5

**Author(s)**

Daryl Waggott

**References**

<https://bedtools.readthedocs.io/en/latest/content/tools/reldist.html>

**See Also**

jaccard

**Examples**

```
if (check.binary("bedtools")) {  
  
  index <- get.example.regions();  
  
  a <- index[[1]];  
  b <- index[[2]];  
  a <- bedr(engine = "bedtools", input = list(i = a), method = "sort", params = "");  
  b <- bedr(engine = "bedtools", input = list(i = b), method = "sort", params = "");  
  reldist(a,b);  
  
}
```

---

size.region

*Get region size*

---

**Description**

Get region size

**Usage**

```
size.region(  
  x,  
  zero.based = TRUE,  
  check.zero.based = TRUE,  
  check.chr = TRUE,  
  check.valid = TRUE,  
  verbose = TRUE  
)
```

**Arguments**

x	region in vector, matrix or dataframe format
zero.based	whether the coordinates are zero-based or 1
check.zero.based	should 0 based coordinates be checked
check.chr	should chr prefix be checked
check.valid	should the region be checked for integrity
verbose	messages and checks

**Value**

size/length of the region

**Author(s)**

Daryl Waggott

**See Also**

convert2bed

**Examples**

```
if (check.binary("bedtools")) {  
  index <- get.example.regions();  
  a <- index[[1]];  
  a.sizes <- bedr:::size.region(a);  
}
```

---

strsplit2matrix      *split a vector of strings into tabular data*

---

**Description**

split a vector of strings into tabular data

**Usage**

```
strsplit2matrix(x, split, fixed = FALSE, perl = FALSE)
```

**Arguments**

x	a character vector
split	the character or regex to split on
fixed	fixed i.e. no regex
perl	perl style

**Author(s)**

Daryl Waggott

**Examples**

```
## Not run:  
a.bed <- strSplitToMatrix(x);  
  
## End(Not run)
```

---

tabix

*Main bedtools wrapper function.*

---

**Description**

Main bedtools wrapper function.

**Usage**

```
tabix(  
  region,  
  file.name,  
  params = NULL,  
  tmpDir = NULL,  
  deleteTmpDir = TRUE,  
  outputDir = NULL,  
  outputFile = NULL,  
  check.zero.based = TRUE,  
  check.chr = TRUE,  
  check.valid = TRUE,  
  check.sort = TRUE,  
  check.merge = TRUE,  
  verbose = TRUE  
)
```

**Arguments**

region	The regions to query the tabix'd file
file.name	The name of the bziped/indexed tabix file to query
params	A string that includes all the extra parameters and arguments to the bedtools command. For example if you wanted to do a left outer join you would specify method as intersect and use params = c("-loj -header"). If you leave input and method as defaults then this is this string represents the full command.
tmpDir	The directory to be used for writing files
deleteTmpDir	Should tmp files be deleted. helpful for diagnostics.
outputDir	The output directory. Only used if outputFile is specified. It defaults to the current working directory.
outputFile	The name of the output file. If this is specified the output will be sent to a file not an R object
check.chr	check for chr prefix
check.zero.based	check for zero based coordinates
check.valid	do all region integrity checks
check.sort	check if region is sorted
check.merge	check if region is merged
verbose	Should messages be printed to screen.

**Value**

The output of command with some parsing to keep it consistent with the input.

**Author(s)**

Daryl Waggott

**See Also**

genomicRanges

**Examples**

```
if (check.binary("tabix")) {
  query.regions <- c("1:1000-100000", "1:1000000-1100000")
  cosmic.vcf.example <- system.file(
    "extdata/CosmicCodingMuts_v66_20130725_ex.vcf.gz",
    package = "bedr"
  )
  cosmic.query <- tabix(query.regions, cosmic.vcf.example, check.chr = FALSE)
}
```

---

table2venn	<i>Plot venn diagram</i>
------------	--------------------------

---

**Description**

Plot venn diagram of regions intersect

**Usage**

```
table2venn(x, var.names)
```

**Arguments**

x	intersect table of regions
var.names	names of the overlapping regions

**Value**

venn diagram input list

**Author(s)**

Daryl Waggott

**See Also**

bedr.plot.region

---

test.region.similarity	<i>Compare sets of regions via jaccard and relative distance using permutation</i>
------------------------	--

---

**Description**

Compare sets of regions via jaccard and relative distance using permutation to get an empirical p-value.

**Usage**

```

test.region.similarity(
  x,
  y,
  n = 1000,
  stratify.by.chr = FALSE,
  species = "human",
  build = "hg19",
  mask.gaps = FALSE,
  mask.repeats = FALSE,
  gaps.file = NULL,
  repeats.file = NULL,
  check.zero.based = TRUE,
  check.chr = TRUE,
  check.valid = TRUE,
  verbose = TRUE
)

```

**Arguments**

x	first region to be compared. this is the region that is permuted
y	second region to be compared
n	the number of iterations to permute
stratify.by.chr	Should the permutation be happen separately for each chromosome. That is are chromosomes exchangeable.
species	species
build	the build of the reference
mask.gaps	should the gaps (Ns) in the human reference be ignored as potential start points. This dramatically increases memory and run time but is more appropriate in almost all settings. By default it's off.
mask.repeats	should the repeats from repeatMasker be ignored as potential start points. This dramatically increases memory and run time but is more appropriate in almost all settings. By default it's off.
gaps.file	database file of gaps. Defaults to Homo sapiens Hg19 gap.txt.gz file available through UCSC
repeats.file	database file of repeats as supplied by UCSC containing RepMasker data e.g rnsk.txt.gz
check.zero.based	should 0 based coordinates be checked
check.chr	should chr prefix be checked
check.valid	should the region be checked for integrity
verbose	should log messages and checking take place

**Details**

Iteratively permutes intervals and recalculates jaccard and reldist statistics.

**Value**

A list of results

**Author(s)**

Daryl Waggott

**Examples**

```
if (check.binary("bedtools")) {  
  
  index <- get.example.regions();  
  
  a <- index[[1]];  
  b <- index[[2]];  
  a <- bedr(engine = "bedtools", input = list(i = a), method = "sort", params = "");  
  b <- bedr(engine = "bedtools", input = list(i = b), method = "sort", params = "");  
  
  # a simple example  
  test.region.similarity(a, b, n = 8)  
  
  # note you can set the cores available to parallelize  
  options(cores = 4);  
  system.time(test.region.similarity(a, b, n = 8));  
  
  # a real example comparing the distribution of mRNA vs ncRNA genes in RefSeq  
  ## Not run:  
  
  # more core  
  options(cores = 8);  
  
  # load refgene  
  refgene <- query.ucsc("refGene")  
  refgene <- refgene[,c("chrom", "txStart", "txEnd", "name", "name2", "strand")]  
  
  # only include canonical chr  
  chr <- paste0("chr", c(1:22, "X", "Y"));  
  refgene <- refgene[refgene$chrom %in% chr,]  
  
  # remove genes with multiple positions  
  duplicated.gene <- duplicated(refgene$name2) | duplicated(rev(refgene$name2));  
  refgene <- refgene[!duplicated.gene,];  
  
  # only select pr coding genes  
  refgene.nm <- refgene[grepl("^NM", refgene$name),];  
  # only select non protein coding rna genes  
  refgene.nr <- refgene[grepl("^NR", refgene$name),];
```

```

# sort and merge
refgene.nm <- bedr.snm.region(refgene.nm,check.chr = FALSE);
refgene.nr <- bedr.snm.region(refgene.nr,check.chr = FALSE);

test.region.similarity(refgene.nm, refgene.nr, mask.unmapped = TRUE );

option(core = 1)

## End(Not run)

}

```

---

vcf2bed

*convert a vcf to a bed file*


---

### Description

Convert a vcf to a bed file. Currently, it needs to read into R via read.vcf

### Usage

```
vcf2bed(x, filename = NULL, header = FALSE, other = NULL, verbose = TRUE)
```

### Arguments

x	a vcf object
filename	the name of file if you want it exported
header	indicate if the bed file has header or not when exported
other	fields to include apart from chr, start, end.
verbose	more words

### Value

A bed styled R object or an external file

### Author(s)

Daryl Waggott

### Examples

```

clinVar.vcf.example <- system.file("extdata/clinvar_dbSNP138_example.vcf.gz", package = "bedr")
x <- read.vcf(clinVar.vcf.example)
x.bed <- vcf2bed(x)

```

---

vcf2bedpe	<i>convert a vcf to a bedpe file</i>
-----------	--------------------------------------

---

**Description**

Convert a vcf to a bedpe file. Currently, it needs to read into R via read.vcf

**Usage**

```
vcf2bedpe(x, filename = NULL, header = FALSE, verbose = TRUE)
```

**Arguments**

x	a vcf object
filename	the name of the output bedpe file, if NULL then bedpe is not exported
header	indicate if the bed file has header or not when exported
verbose	detailed messages

**Value**

A bedpe styled R object or an external file

**Author(s)**

Helena Winata

**Examples**

```
gridss.vcf.example <- system.file("extdata/gridssSV.vcf.gz", package = "bedr")
x <- read.vcf(gridss.vcf.example, split.info = TRUE)
x.bedpe <- vcf2bedpe(x)
```

---

write.vcf	<i>write a vcf object</i>
-----------	---------------------------

---

**Description**

write a vcf object

**Usage**

```
write.vcf(x, filename = NULL, verbose = TRUE)
```

**Arguments**

x	a vcf object
filename	a filename
verbose	more words

**Details**

The input needs to be a vcf object. This

**Value**

A vcf file

**Author(s)**

Daryl Waggott

**References**

vcf format specifications

**Examples**

```
vcf <- read.vcf(system.file("extdata/clinvar_dbSNP138_example.vcf.gz", package = "bedr"));
vcf$header <- c(vcf$header, NOTE="vcf processed by bedr")

## Not run:
write.vcf(vcf, filename = paste(tempdir(), "/bedr.example.vcf", sep = ""));

## End(Not run)
```

---

<i>%in.region%</i>	<i>checks if regions in object a are found in object b</i>
--------------------	--

---

**Description**

checks if regions in object a are found in object b

**Usage**

```
x %in.region% y
```

**Arguments**

x	first region index in the form chr:start-stop. regions in this index will be checked for intersection in the values of the second index.
y	second region index.

**Details**

The function can also be called using syntax similar to the `%in%` operator, for example `"region1 %in.region% region2"`

**Value**

Returns a logical vector the length of `x`.

**Author(s)**

Daryl Waggott

**Examples**

```
if (check.binary("bedtools")) {  
  
  index <- get.example.regions();  
  
  a <- index[[1]];  
  b <- index[[2]];  
  a <- bedr.sort.region(a);  
  b <- bedr.sort.region(b);  
  
  d <- a %in.region% b  
  
}
```

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