

# Package ‘ICAMS’

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**Type** Package

**Title** In-depth Characterization and Analysis of Mutational Signatures

**Version** 2.0.0.9000

**Author** Steve Rozen, Nanhai Jiang, Arnoud Boot, Mo Liu

**Maintainer** Steve Rozen <steverozen@gmail.com>

**Description** Analysis and visualization of experimentally elucidated mutational signatures -- the kind of analysis and visualization in Boot et al., "In-depth characterization of the cisplatin mutational signature in human cell lines and in esophageal and liver tumors", 2018, <https://genome.cshlp.org/content/28/5/654.short>. ICAMS has functions to read in variant call files (VCFs) and to collate the corresponding catalogs of mutational spectra and to analyze and plot catalogs of mutational spectra and signatures. Handles both "counts-based" and "density-based" catalogs of mutational spectra or signatures.

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BSgenome,  
BSgenome.Hsapiens.1000genomes.hs37d5,  
BSgenome.Hsapiens.UCSC.hg38,  
data.table,  
dplyr,  
GenomeInfoDb,  
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stringi,  
utils

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## R topics documented:

as.catalog	2
CatalogRowOrder	3
CollapseCatalog	3
FindDelMH	4
GetVAF	6
ICAMS	6
MutectVCFFilesToCatalog	9
MutectVCFFilesToCatalogAndPlotToPdf	10
PlotCatalog	11
PlotCatalogToPdf	12
ReadAndSplitMutectVCFs	13
ReadAndSplitStrelkaSBSVCFs	13
ReadCatalog	14
ReadStrelkaIDVCFs	15
revc	15
StrelkaIDVCFFilesToCatalog	16
StrelkaIDVCFFilesToCatalogAndPlotToPdf	16
StrelkaSBSVCFFilesToCatalog	17
StrelkaSBSVCFFilesToCatalogAndPlotToPdf	18
TranscriptRanges	19
TransformCatalog	20
VCFsToDBSCatalogs	21
VCFsToIDCatalogs	21
VCFsToSBSCatalogs	22
WriteCatalog	22
<b>Index</b>	<b>24</b>

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as.catalog	<i>Create a catalog from a numeric matrix or numeric data frame</i>
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### Description

Create a catalog from a numeric matrix or numeric data frame

### Usage

```
as.catalog(object, ref.genome, region, catalog.type, abundance)
```

### Arguments

object	A numeric matrix or numeric data frame. This object must have rownames to denote the mutation types. See <a href="#">CatalogRowOrder</a> for more details.
ref.genome	A ref.genome argument as described in <a href="#">ICAMS</a> .
region	A character string acting as a region identifier, one of "genome", "exome", or "transcript".
catalog.type	One of "counts", "density", "counts.signature", "density.signature".
abundance	Optional, only needed when ref.genome does not belong to the two human reference genomes supported by ICAMS. The abundance should contain the counts of different source sequences for mutations. See <code>ICAMS::abundance.3bp.exome.unstranded.GRCh37</code> for an example.

**Value**

A catalog as described in [ICAMS](#).

---

CatalogRowOrder	<i>Standard order of row names in a catalog.</i>
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---

**Description**

This data is designed for those who need to create their own catalogs from formats not supported by this package. The rownames denote the mutation types. For example, for SBS96 catalogs, the rowname AGAT represents a mutation from AGA > ATA.

**Usage**

```
catalog.row.order
```

**Format**

A list of character vectors indicating the standard orders of row names in catalogs.

**Note**

In ID (insertion and deletion) catalogs, deletion repeat sizes range from 0 to 5+, but for plotting and end-user documentation deletion repeat sizes range from 1 to 6+.

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CollapseCatalog	<i>"Collapse" a catalog.</i>
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**Description**

1. Take a mutational spectrum or signature catalog that is based on a fined-grained set of features (for example, single-nucleotide substitutions in the context of the preceding and following 2 bases).
2. Collapse it to a catalog based on a coarser-grained set of features (for example, single-nucleotide substitutions in the context of the immediately preceding and following bases).

Collapse192CatalogTo96 Collapse an SBS 192 catalog to an SBS 96 catalog.

Collapse1536CatalogTo96 Collapse an SBS 1536 catalog to an SBS 96 catalog.

Collapse144CatalogTo78 Collapse a DBS 144 catalog to a DBS 78 catalog.

**Usage**

```
Collapse192CatalogTo96(catalog)
```

```
Collapse1536CatalogTo96(catalog)
```

```
Collapse144CatalogTo78(catalog)
```

**Arguments**

catalog            A catalog as defined in [ICAMS](#).

**Value**

A catalog as defined in [ICAMS](#).

---

FindDelMH

---

*Return the length of microhomology at a deletion.*


---

**Description**

Return the length of microhomology at a deletion.

**Usage**

```
FindDelMH(context, deleted.seq, pos, trace = 0)
```

**Arguments**

context            The deleted sequence plus ample surrounding sequence on each side (at least as long as del.sequence).

deleted.seq        The deleted sequence in context.

pos                The position of del.sequence in context.

trace              If > 0, cat various messages.

**Details**

This function is primarily for internal use, but we export it to document the underlying logic.

Example:

GGCTAGTT aligned to GGCTAGAACTAGTT with a deletion represented as:

```
GGCTAGAACTAGTT
GG-----CTAGTT  GGCTAGTT  GG[CTAGAA]CTAGTT
                        ----  ----
```

Presumed repair mechanism leading to this:

```
....
GGCTAGAACTAGTT
CCGATCTTGATCAA
```

=>

```
....
GGCTAG      TT
CC      GATCAA
....
```

=>

```
GGCTAGTT
CCGATCAA
```

Variant-caller software can represent the same deletion in several different, but completely equivalent, ways.

```
GGC-----TAGTT  GGCTAGTT  GGC[TAGAAC]TAGTT
                      *  ---  *  ---
```

```
GGCT-----AGTT  GGCTAGTT  GGCT[AGAACT]AGTT
                      **  --  **  --
```

```
GGCTA-----GTT  GGCTAGTT  GGCTA[GAACTA]GTT
                      ***  -  ***  -
```

```
GGCTAG-----TT  GGCTAGTT  GGCTAG[AACTAG]TT
                      *****  *****
```

A deletion in a *repeat* can also be represented in several different ways. A deletion in a repeat is abstractly equivalent to microhomology that spans the entire deleted sequence. For example;

```
GACTAGCTAGTT
GACTA----GTT  GACTAGTT  GACTA[GCTA]GTT
                      ***  -***  -
```

is really a repeat

```
GACTAG----TT  GACTAGTT  GACTAG[CTAG]TT
                      *****  ----
```

```
GACT----AGTT  GACTAGTT  GACT[AGCT]AGTT
                      **  -***  --
```

**This function only flags this case with a -1 return; it does not figure out the repeat extent.**

This function finds:

1. The maximum match of undeleted sequence to the left of the deletion that is identical to the right end of the deleted sequence, and
2. The maximum match of undeleted sequence to the right of the deletion that is identical to the left end of the deleted sequence.

The microhomology sequence is the concatenation of items (1) and (2).

## Value

The length of the maximum microhomology of `del` . sequence in context.

---

GetVAF

---

*Extract the VAFs (variant allele frequencies) from a VCF file.*


---

### Description

Extract the VAFs (variant allele frequencies) from a VCF file.

### Usage

```
GetStrelkaVAF(vcf)
```

```
GetMutectVAF(vcf)
```

### Arguments

vcf                      Said VCF as a data.frame.

### Value

A vector of VAFs, one for each row of vcf.

---

ICAMS

---

*ICAMS: In-depth Characterization and Analysis of Mutational Signatures*


---

### Description

Analysis and visualization of experimentally elucidated mutational "In-depth characterization of the cisplatin mutational signature in human cell lines and in esophageal and liver tumors", *Genome Research* 2018, <https://genome.cshlp.org/content/28/5/654.short>. ICAMS has functions to read in variant call files (VCFs) and to collate the corresponding catalogs of mutational spectra and to analyze and plot catalogs of mutational spectra and signatures. Handles both "counts-based" and "density-based" catalogs of mutational spectra or signatures. ICAMS can read in VCFs generated by Strelka or Mutect, and collate the mutations into "catalogs" of mutational spectra. ICAMS can create and plot catalogs of mutational spectra or signatures for single base substitutions (SBS), double base substitutions (DBS), and small insertions and deletions (ID). It can also read and write these catalogs.

### Catalogs

A key data type in ICAMS is a "catalog" of mutation counts, of mutation densities, or of mutational signatures.

Catalogs are R S3 objects of class `matrix` and one of several additional classes that specify the types of the mutations represented in the catalog (e.g. `SBS96`, `ID`, etc, ...). The possible additional classes are one of `SBS96Catalog`, `SBS192Catalog`, `SBS1536Catalog`, `DBS78Catalog`, `DBS144Catalog`, `DBS136Catalog`, `IndelCatalog`.

Conceptually, a catalog has one of the following types, which are indicated in the attribute `catalog.type`:

1. Matrix of mutation counts (one column per sample), representing (counts-based) mutational spectra (`catalog.type = "counts"`).

2. Matrix of mutation densities, i.e. mutations per occurrences of source sequences (one column per sample), representing (density-based) mutational spectra (`catalog.type = "density"`).
3. Matrix of mutational signatures, which are similar to spectra. However where spectra consist of counts or densities of mutations in each mutation class (e.g. `ACA > AAA`, `ACA > AGA`, `ACA > ATA`, `ACC > AAC`, ...), signatures consist of the proportions of mutations in each class (with all the proportions summing to 1). A mutational signature can be based on either:
  - mutation counts (a "counts-based mutational signature", `catalog.type = "counts.signature"`), or
  - mutation densities (a "density-based mutational signature", `catalog.type = "density.signature"`).

Catalogs also have the attribute `abundance`, which contains the counts of different source sequences for mutations. For example, for SBSs in trinucleotide context, the abundances would be the counts of each trinucleotide in the human genome, exome, or in the transcribed region of the genome. See below under [TransformCatalog](#) for more information.

TODO(Nanhai): I think the following is no longer true, correct? Many functions take the argument `catalog.type`, with possible values `"counts"`, `"density"`, `"counts.signature"`, or `"density.signature"`, corresponding to the types of catalogs in items 1, 2, 3.1, and 3.2, above.

If you need to create a catalog from a source other than this package (i.e. other than with [ReadCatalog](#) or [StrelkaSBSVCFFilesToCatalog](#), [MutectVCFFilesToCatalog](#), etc.), then use `as.catalog`.

### Creating catalogs from variant call files (VCF files)

1. [StrelkaSBSVCFFilesToCatalog](#) creates 3 SBS catalogs (96, 192, 1536) and 3 DBS catalogs (78, 136, 144) from the Strelka SBS VCFs.
2. [StrelkaIDVCFFilesToCatalog](#) creates ID (indel) catalog from the Strelka ID VCFs.
3. [MutectVCFFilesToCatalog](#) creates 3 SBS catalogs (96, 192, 1536), 3 DBS catalogs (78, 136, 144) and ID (indel) catalog from the Mutect VCFs.

### Plotting catalogs

The [PlotCatalog](#) functions plot mutational spectra for **one** sample or plot **one** mutational signature.

The [PlotCatalogToPdf](#) functions plot catalogs of mutational spectra or of mutational signatures to a PDF file.

### Wrapper functions to create catalogs from VCFs and plot the catalogs to PDF files

1. [StrelkaSBSVCFFilesToCatalogAndPlotToPdf](#) creates all type of SBS and DBS catalogs from Strelka SBS VCFs and plots the catalogs.
2. [StrelkaIDVCFFilesToCatalog](#) creates an ID (indel) catalog from Strelka ID VCFs and plot it.
3. [MutectVCFFilesToCatalog](#) creates all types of SBS, DBS, and ID catalogs from Mutect VCFs and plots the catalogs.

### The `ref.genome` (reference genome) argument

Many functions take the argument `ref.genome`.

In order to create a mutational spectrum catalog, ICAMS needs to know the sequence context of the mutations in the VCF file. For this, ICAMS needs the reference genome sequence that matches the VCF file. The `ref.genome` argument provides this.

`ref.genome` can be either

1. A variable from the Bioconductor `BSgenome` package that contains a particular reference genome, for example `BSgenome.Hsapiens.1000genomes.hs37d5`.
2. The strings "hg38" or "GRCh38" are shorthand for `BSgenome.Hsapiens.UCSC.hg38`, and the strings "hg19" or "GRCh37" are shorthand for `BSgenome.Hsapiens.1000genomes.hs37d5`.

The Bioconductor `BSgenome` package and two human genomes from `BSgenome` are "imported" by ICAMS and therefore should be installed when ICAMS is installed. The two genomes that are installed as dependencies are:

- `BSgenome.Hsapiens.1000genomes.hs37d5`
- `BSgenome.Hsapiens.UCSC.hg38`

Any other needed reference genomes must be installed separately by the user. Use `available.genomes()` to get the list of available genomes. Further instructions are at <https://bioconductor.org/packages/release/bioc/html/BSgenome.html>.

Use of ICAMS with other reference genomes is restricted to `catalog.type` of counts or `counts.signature` unless the user also creates the necessary abundance vectors.

See `ICAMS::abundance.3bp.exome.unstranded.GRCh37` for an example.

### Writing catalogs to files

The `WriteCatalog` functions write a catalog to a file.

### Reading catalogs

The `ReadCatalog` functions read a file that contains a catalog in standardized format.

### Transforming catalogs

The `TransformCatalog` function transforms catalogs of mutational spectra or signatures to account for differing abundances of the source sequence of the mutations in the genome.

For example, mutations from ACG are much rarer in the human genome than mutations from ACC simply because CG dinucleotides are rare in the genome. Consequently, there are two possible representations of mutational spectra or signatures. One representation is based on mutation counts as observed in a given genome or exome, and this approach is widely used, as, for example, at <https://cancer.sanger.ac.uk/cosmic/signatures>, which presents signatures based on observed mutation counts in the human genome. We call these "counts-based spectra" or "counts-based signatures".

Alternatively, mutational spectra or signatures can be represented as mutations per source sequence, for example the number of ACT > AGT mutations occurring at all ACT 3-mers in a genome. We call these "density-based spectra" or "density-based signatures".

This function can also transform spectra based on observed genome-wide counts to "density"-based catalogs. In density-based catalogs mutations are expressed as mutations per source sequences. For example, a density-based catalog represents the proportion of ACCs mutated to ATCs, the proportion of ACGs mutated to ATGs, etc. This is different from counts-based mutational spectra catalogs, which contain the number of ACC > ATC mutations, the number of ACG > ATG mutations, etc.

This function can also transform observed-count based spectra or signatures from genome to exome based counts, or between different species (since the abundances of source sequences vary between genome and exome and between species).



## Collapsing catalogs

The [CollapseCatalog](#) functions

1. Take a mutational spectrum or signature catalog that is based on a fined-grained set of features (for example, single-nucleotide substitutions in the context of the preceding and following 2 bases).
2. Collapse it to a catalog based on a coarser-grained set of features (for example, single-nucleotide substitutions in the context of the immediately preceding and following bases).

## Data

1. [CatalogRowOrder](#) Standard order of rownames in a catalog. The rownames of encode the type of each mutation. The rownames denote the mutation types. For example, for SBS96 catalogs, the rowname AGAT represents a mutation from AGA > ATA.
2. [TranscriptRanges](#) Transcript ranges and strand information for a particular reference genome.

---

MutectVCFFilesToCatalog

*Create SBS, DBS and Indel catalogs from Mutect VCF files*

---

## Description

Create 3 SBS catalogs (96, 192, 1536), 3 DBS catalogs (78, 136, 144) and Indel catalog from the Mutect VCFs specified by files

## Usage

```
MutectVCFFilesToCatalog(files, ref.genome, trans.ranges, region)
```

## Arguments

files	Character vector of file paths to the Mutect VCF files.
ref.genome	A ref.genome argument as described in <a href="#">ICAMS</a> .
trans.ranges	a <a href="#">data.table</a> which contains transcript range and strand information. Please refer to <a href="#">TranscriptRanges</a> for more details.
region	A character string acting as a region identifier, one of "genome", "exome".

## Details

This function calls [VCFsToSBSCatalogs](#), [VCFsToDBSCatalogs](#) and [VCFsToIDCatalogs](#)

## Value

A list of 3 SBS catalogs (one each for 96, 192, and 1536), 3 DBS catalogs (one each for 78, 136, and 144) and ID catalog. Each catalog has attributes added. See [as.catalog](#) for more details.

## Note

SBS 192 and DBS 144 catalogs include only mutations in transcribed regions.

---

MutectVCFFilesToCatalogAndPlotToPdf

*Create SBS, DBS and Indel catalogs from Mutect VCF files and plot them to PDF*

---

## Description

Create 3 SBS catalogs (96, 192, 1536), 3 DBS catalogs (78, 136, 144) and Indel catalog from the Mutect VCFs specified by files and plot them to PDF

## Usage

```
MutectVCFFilesToCatalogAndPlotToPdf(files, ref.genome, trans.ranges,
  region, file, no.context)
```

## Arguments

files	Character vector of file paths to the Mutect VCF files.
ref.genome	A ref.genome argument as described in <a href="#">ICAMS</a> .
trans.ranges	a <a href="#">data.table</a> which contains transcript range and strand information. Please refer to <a href="#">TranscriptRanges</a> for more details.
region	A character string acting as a region identifier, one of "genome", "exome".
file	The name of the PDF file to be produced.
no.context	A logical value indicating whether there is preceding and following base context for the plot. Only implemented for SBS192Catalog.

## Details

This function calls [MutectVCFFilesToCatalog](#) and [PlotCatalogToPdf](#)

## Value

A list of 3 SBS catalogs (one each for 96, 192, and 1536), 3 DBS catalogs (one each for 78, 136, and 144), Indel catalog and their graphs plotted to PDF with specified file name. Each catalog has attributes added. See [as.catalog](#) for more details.

## Note

SBS 192 and DBS 144 catalogs include only mutations in transcribed regions.

---

PlotCatalog	<i>Plot <b>one</b> spectrum or signature.</i>
-------------	---

---

## Description

Plot the spectrum of **one** sample or plot **one** signature. The type of graph is based on one attribute("catalog.type") of the input catalog. You can first use [TransformCatalog](#) to get different types of catalog and then do the plotting.

## Usage

```
PlotCatalog(catalog, no.context, cex, grid, upper, xlabel)
```

## Arguments

catalog	A catalog as defined in <a href="#">ICAMS</a> with attributes added. See <a href="#">as.catalog</a> for more details.
no.context	A logical value indicating whether there is preceding and following base context for the plot. Only implemented for SBS192Catalog.
cex	A numerical value giving the amount by which mutation class labels, mutation counts(if it exists), y axis and its labels, x axis labels and its annotations(if it exists), sample name and legend(if it exists) should be magnified relative to the default. Only implemented for SBS96Catalog, SBS192Catalog and DBS144Catalog.
grid	A logical value indicating whether to draw grid lines. Only implemented for SBS96Catalog.
upper	A logical value indicating whether to draw horizontal lines and the names of major mutation class on top of graph. Only implemented for SBS96Catalog.
xlabels	A logical value indicating whether to draw x axis labels. Only implemented for SBS96Catalog.

## Value

```
invisible(TRUE)
```

## Note

The sizes of repeats involved in deletions range from 0 to 5+ in the mutational-spectra and signature catalog rownames, but for plotting and end-user documentation they range from 1 to 6+.

---

PlotCatalogToPdf	<i>Plot catalog to a PDF file.</i>
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---

### Description

Plot catalog to a PDF file. The type of graph is based on one attribute("catalog.type") of the input catalog. You can first use [TransformCatalog](#) to get different types of catalog and then do the plotting.

### Usage

```
PlotCatalogToPdf(catalog, file, no.context, cex, grid, upper, xlabel)
```

### Arguments

catalog	A catalog as defined in <a href="#">ICAMS</a> with attributes added. See <a href="#">as.catalog</a> for more details.
file	The name of the PDF file to be produced.
no.context	A logical value indicating whether there is preceding and following base context for the plot. Only implemented for SBS192Catalog.
cex	A numerical value giving the amount by which mutation class labels, mutation counts(if it exists), y axis and its labels, x axis labels and its annotations(if it exists), sample name and legend(if it exists) should be magnified relative to the default. Only implemented for SBS96Catalog, SBS192Catalog and DBS144Catalog.
grid	A logical value indicating whether to draw grid lines. Only implemented for SBS96Catalog.
upper	A logical value indicating whether to draw horizontal lines and the names of major mutation class on top of graph. Only implemented for SBS96Catalog.
xlabels	A logical value indicating whether to draw x axis labels. Only implemented for SBS96Catalog.

### Value

```
invisible(TRUE)
```

### Note

The sizes of repeats involved in deletions range from 0 to 5+ in the mutational-spectra and signature catalog rownames, but for plotting and end-user documentation they range from 1 to 6+.

---

`ReadAndSplitMutectVCFs`*Read and split Mutect VCF files.*

---

**Description**

Read and split Mutect VCF files.

**Usage**

```
ReadAndSplitMutectVCFs(files)
```

**Arguments**

`files`                      Character vector of file paths to the Mutect VCF files.

**Value**

A list with 3 in-memory VCFs and two left-over VCF-like data frames with rows that were not incorporated into the first 3 VCFs, as follows:

1. SBS VCF with only single base substitutions.
2. DBS VCF with only doublet base substitutions as called by Mutect.
3. ID VCF with only small insertions and deletions.
4. `other.subs` VCF like `data.frame` with rows for coordinate substitutions involving 3 or more nucleotides, e.g. `ACT > TGA` or `AACT > GGTA`.
5. `multiple.alternative.alleles` VCF like `data.frame` with rows for variants with multiple alternative alleles, for example `ACT` mutated to both `AGT` and `ACT` at the same position.

**See Also**

[MutectVCFFilesToCatalog](#)

---

`ReadAndSplitStrelkaSBSVCFs`*Read and split Strelka SBS VCF files.*

---

**Description**

Read and split Strelka SBS VCF files.

**Usage**

```
ReadAndSplitStrelkaSBSVCFs(files)
```

**Arguments**

`files`                      Character vector of file paths to the Strelka SBS VCF files.

**Value**

A list of 3 in-memory objects as follows:

1. `SBS.vcfs` List of data.frames of pure SBS mutations – no DBS or 3+BS mutations.
2. `DBS.vcfs` List of data.frames of pure DBS mutations – no SBS or 3+BS mutations.
3. `ThreePlus` List of data.tables with the key `CHROM`, `LOW.POS`, `HIGH.POS`. containing rows that that in the input that did not represent SBSs or DBSs.

**See Also**

[StrelkaSBSVCFFilesToCatalog](#)

---

ReadCatalog	<i>Read catalog.</i>
-------------	----------------------

---

**Description**

Read a catalog in standardized format from path.

**Usage**

```
ReadCatalog(file, ref.genome, region, catalog.type, strict = TRUE)
```

**Arguments**

<code>file</code>	Path to a catalog on disk in the standardized format.
<code>ref.genome</code>	A <code>ref.genome</code> argument as described in <a href="#">ICAMS</a> .
<code>region</code>	One of "genome", "exome".
<code>catalog.type</code>	One of "counts", "density", "counts.signature", "density.signature".
<code>strict</code>	If TRUE, do additional checks on the input, and stop if the checks fail.

**Details**

See also [WriteCatalog](#)

**Value**

A catalog in standard in-memory format with attributes added. See [as.catalog](#) for more details.

**Note**

In ID (insertion and deletion) catalogs, deletion repeat sizes range from 0 to 5+, but for plotting and end-user documentation deletion repeat sizes range from 1 to 6+.

---

ReadStrelkaIDVCFs	<i>Read Strelka ID (insertion and deletion) VCF files.</i>
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---

**Description**

Read Strelka ID (insertion and deletion) VCF files.

**Usage**

```
ReadStrelkaIDVCFs(files)
```

**Arguments**

files	Character vector of file paths to the VCF files.
-------	--

**Value**

A list of vcfs from files.

**Note**

In ID (insertion and deletion) catalogs, deletion repeat sizes range from 0 to 5+, but for plotting and end-user documentation deletion repeat sizes range from 1 to 6+.

**See Also**

[StrelkaIDVCFFilesToCatalog](#)

---

revc	<i>Reverse complement every string in string.vec.</i>
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---

**Description**

Reverse complement every string in string.vec.

**Usage**

```
revc(string.vec)
```

**Arguments**

string.vec	a vector of type character.
------------	-----------------------------

**Value**

A vector of type characters with the reverse complement of every string in string.vec.

---

**StrelkaIDVCFFilesToCatalog***Create ID (indel) catalog from Strelka ID VCF files*

---

**Description**

Create ID (indel) catalog from the Strelka ID VCFs specified by files

**Usage**

```
StrelkaIDVCFFilesToCatalog(files, ref.genome, region)
```

**Arguments**

files	Character vector of file paths to the Strelka ID VCF files.
ref.genome	A ref.genome argument as described in <a href="#">ICAMS</a> .
region	A character string acting as a region identifier, one of "genome", "exome".

**Details**

This function calls [VCFsToIDCatalogs](#)

**Value**

An ID (indel) catalog with attributes added. See [as.catalog](#) for more details.

**Note**

In ID (insertion and deletion) catalogs, deletion repeat sizes range from 0 to 5+, but for plotting and end-user documentation deletion repeat sizes range from 1 to 6+.

---

**StrelkaIDVCFFilesToCatalogAndPlotToPdf***Create ID (indel) catalog from Strelka ID VCF files and plot them to PDF*

---

**Description**

Create ID (indel) catalog from the Strelka ID VCFs specified by files and plot them to PDF

**Usage**

```
StrelkaIDVCFFilesToCatalogAndPlotToPdf(files, ref.genome, region, file)
```

**Arguments**

files	Character vector of file paths to the Strelka ID VCF files.
ref.genome	A ref.genome argument as described in <a href="#">ICAMS</a> .
region	A character string acting as a region identifier, one of "genome", "exome".
file	The name of the PDF file to be produced.



**Details**

This function calls [VCFsToIDCatalogs](#) and [PlotCatalogToPdf](#)

**Value**

An ID (indel) catalog and its graph plotted to PDF with specified file name. The ID (indel) catalog has attributes added. See [as.catalog](#) for more details.

**Note**

In ID (insertion and deletion) catalogs, deletion repeat sizes range from 0 to 5+, but for plotting and end-user documentation deletion repeat sizes range from 1 to 6+.

---

StrelkaSBSVCFFilesToCatalog

*Create SBS and DBS catalogs from Strelka SBS VCF files.*

---

**Description**

Create 3 SBS catalogs (96, 192, 1536) and 3 DBS catalogs (78, 136, 144) from the Strelka SBS VCFs specified by files

**Usage**

```
StrelkaSBSVCFFilesToCatalog(files, ref.genome, trans.ranges, region)
```

**Arguments**

files	Character vector of file paths to the Strelka SBS VCF files.
ref.genome	A ref.genome argument as described in <a href="#">ICAMS</a> .
trans.ranges	a <a href="#">data.table</a> which contains transcript range and strand information. Please refer to <a href="#">TranscriptRanges</a> for more details.
region	A character string acting as a region identifier, one of "genome", "exome".

**Details**

This function calls [VCFsToSBSCatalogs](#) and [VCFsToDBSCatalogs](#).

**Value**

A list of 3 SBS catalogs (one each for 96, 192, and 1536) and 3 DBS catalogs (one each for 78, 136, and 144). Each catalog has attributes added. See [as.catalog](#) for more details.

**Note**

SBS 192 and DBS 144 catalog only contains mutations in transcribed regions.

---

StrelkaSBSVCFFilesToCatalogAndPlotToPdf

*Create SBS and DBS catalogs from Strelka SBS VCF files and plot them to PDF*

---

## Description

Create 3 SBS catalogs (96, 192, 1536) and 3 DBS catalogs (78, 136, 144) from the Strelka SBS VCFs specified by files and plot them to PDF

## Usage

```
StrelkaSBSVCFFilesToCatalogAndPlotToPdf(files, ref.genome, trans.ranges,
  region, file, no.context)
```

## Arguments

files	Character vector of file paths to the Strelka SBS VCF files.
ref.genome	A ref.genome argument as described in <a href="#">ICAMS</a> .
trans.ranges	a <a href="#">data.table</a> which contains transcript range and strand information. Please refer to <a href="#">TranscriptRanges</a> for more details.
region	A character string acting as a region identifier, one of "genome", "exome".
file	The name of the PDF file to be produced.
no.context	A logical value indicating whether there is preceding and following base context for the plot. Only implemented for SBS192Catalog.

## Details

This function calls [StrelkaSBSVCFFilesToCatalog](#) and [PlotCatalogToPdf](#)

## Value

A list of 3 SBS catalogs (one each for 96, 192, and 1536), 3 DBS catalogs (one each for 78, 136, and 144) and their graphs plotted to PDF with specified file name. Each catalog has attributes added. See [as.catalog](#) for more details.

## Note

SBS 192 and DBS 144 catalogs include only mutations in transcribed regions.

---

TranscriptRanges	<i>Transcript ranges data</i>
------------------	-------------------------------

---

## Description

Transcript ranges and strand information for a particular reference genome.

## Usage

`trans.ranges.GRCh37`

`trans.ranges.GRCh38`

## Format

A [data.table](#) which contains transcript range and strand information for a particular reference genome. It contains chromosome name, start, end position, strand information and gene name and is keyed by `chrom`, `chromStart`, and `chromEnd`. It uses one-based coordinate system.

## Details

`trans.ranges.GRCh37` A [data.table](#) which contains transcript range and strand information for **Human** GRCh37. It is derived from a raw **GFF3** format file ([ftp://ftp.ebi.ac.uk/pub/databases/gencode/Gencode\\_human/release\\_30/GRCh37\\_mapping/gencode.v30lift37.annotation.gff3.gz](ftp://ftp.ebi.ac.uk/pub/databases/gencode/Gencode_human/release_30/GRCh37_mapping/gencode.v30lift37.annotation.gff3.gz)), only genes that are associated with a CCDS ID are kept for transcriptional strand bias analysis. Needed for [StrelkaSBSCFFFilesToCatalog](#), [StrelkaSBSCFFFilesToCatalogAndPlotToPdf](#), [MutectVCFFilesToCatalog](#), [MutectVCFFilesToCatalogAndPlotToPdf](#), [VCFsToSBSCatalogs](#) and [VCFsToDBSCatalogs](#).

`trans.ranges.GRCh38` A [data.table](#) which contains transcript range and strand information for **Human** GRCh38. It is derived from a raw **GFF3** format file ([ftp://ftp.ebi.ac.uk/pub/databases/gencode/Gencode\\_human/release\\_30/gencode.v30.annotation.gff3.gz](ftp://ftp.ebi.ac.uk/pub/databases/gencode/Gencode_human/release_30/gencode.v30.annotation.gff3.gz)), only genes that are associated with a CCDS ID are kept for transcriptional strand bias analysis. Needed for [StrelkaSBSCFFFilesToCatalog](#), [StrelkaSBSCFFFilesToCatalogAndPlotToPdf](#), [MutectVCFFilesToCatalog](#), [MutectVCFFilesToCatalogAndPlotToPdf](#), [VCFsToSBSCatalogs](#) and [VCFsToDBSCatalogs](#).

## Source

[ftp://ftp.ebi.ac.uk/pub/databases/gencode/Gencode\\_human/release\\_30/GRCh37\\_mapping/gencode.v30lift37.annotation.gff3.gz](ftp://ftp.ebi.ac.uk/pub/databases/gencode/Gencode_human/release_30/GRCh37_mapping/gencode.v30lift37.annotation.gff3.gz)

[ftp://ftp.ebi.ac.uk/pub/databases/gencode/Gencode\\_human/release\\_30/gencode.v30.annotation.gff3.gz](ftp://ftp.ebi.ac.uk/pub/databases/gencode/Gencode_human/release_30/gencode.v30.annotation.gff3.gz)

---

TransformCatalog	<i>Transform between counts and density spectrum catalogs and counts and density signature catalogs.</i>
------------------	--

---

## Description

Transform between counts and density spectrum catalogs and counts and density signature catalogs.

## Usage

```
TransformCatalog(catalog, target.ref.genome, target.region,
                 target.catalog.type)
```

## Arguments

catalog	An SBS or DBS catalog as described in <a href="#">ICAMS</a> ; must <b>not</b> be an ID (indel) catalog.
target.ref.genome	A ref.genome argument as described in <a href="#">ICAMS</a> .
target.region	One of "genome", "exome"; see <a href="#">as.catalog</a> .
target.catalog.type	A character string acting as a catalog type identifier, one of "counts", "density", "counts.signature", "density.signature"; see <a href="#">as.catalog</a> .

## Details

Only the following transformations are legal:

1. counts -> counts (used to transform between target.ref.genome and/or target.region)
2. counts -> density
3. counts -> (counts.signature, density.signature)
4. density -> counts (the semantics are to infer the genome-wide or exome-wide counts based on the densities)
5. density -> (counts.signature, density.signature)
6. counts.signature -> (counts.signature, density.signature)
7. density.signature -> counts.signature
8. density.signature -> density.signature (a null operation)
9. density -> density (a null operation)

## Value

A catalog as defined in [ICAMS](#).

---

VCFsToDBSCatalogs	<i>Create DBS catalogs from VCFs</i>
-------------------	--------------------------------------

---

**Description**

Create a list of 3 catalogs (one each for DBS78, DBS144 and DBS136) out of the contents in `list.of.DBS.vcfs`. The VCFs must not contain any type of mutation other than DBSs.

**Usage**

```
VCFsToDBSCatalogs(list.of.DBS.vcfs, ref.genome, trans.ranges, region)
```

**Arguments**

<code>list.of.DBS.vcfs</code>	List of in-memory data frames of pure DBS mutations – no SBS or 3+BS mutations. The list names will be the sample ids in the output catalog.
<code>ref.genome</code>	A <code>ref.genome</code> argument as described in <a href="#">ICAMS</a> .
<code>trans.ranges</code>	a <a href="#">data.table</a> which contains transcript range and strand information. Please refer to <a href="#">TranscriptRanges</a> for more details.
<code>region</code>	A character string acting as a region identifier, one of "genome", "exome".

**Value**

A list of 3 DBS catalogs, one each for 78, 144, 136: `catDBS78 catDBS144 catDBS136`. Each catalog has attributes added. See [as.catalog](#) for more details.

**Note**

DBS 144 catalog only contains mutations in transcribed regions.

---

VCFsToIDCatalogs	<i>Create ID (insertion and deletion) catalog from ID VCFs</i>
------------------	--

---

**Description**

Create ID (insertion and deletion) catalog from ID VCFs

**Usage**

```
VCFsToIDCatalogs(list.of.vcfs, ref.genome, region)
```

**Arguments**

<code>list.of.vcfs</code>	List of in-memory VCFs. The list names will be the sample ids in the output catalog.
<code>ref.genome</code>	A <code>ref.genome</code> argument as described in <a href="#">ICAMS</a> .
<code>region</code>	A character string acting as a region identifier, one of "genome", "exome".

**Value**

An S3 object containing an ID (indel) catalog with class "catalog". See [as.catalog](#) for more details.

---

VCFsToSBSCatalogs	<i>Create SBS catalogs from SBS VCFs</i>
-------------------	--

---

**Description**

Create a list of 3 catalogs (one each for 96, 192, 1536) out of the contents in `list.of.SBS.vcfs`. The SBS VCFs must not contain DBSs, indels, or other types of mutations.

**Usage**

```
VCFsToSBSCatalogs(list.of.SBS.vcfs, ref.genome, trans.ranges, region)
```

**Arguments**

<code>list.of.SBS.vcfs</code>	List of in-memory data frames of pure SBS mutations – no DBS or 3+BS mutations. The list names will be the sample ids in the output catalog.
<code>ref.genome</code>	A <code>ref.genome</code> argument as described in <a href="#">ICAMS</a> .
<code>trans.ranges</code>	a <a href="#">data.table</a> which contains transcript range and strand information. Please refer to <a href="#">TranscriptRanges</a> for more details.
<code>region</code>	A character string acting as a region identifier, one of "genome", "exome".

**Value**

A list of 3 SBS catalogs, one each for 96, 192, 1536: `catSBS96` `catSBS192` `catSBS1536`. Each catalog has attributes added. See [as.catalog](#) for more details.

**Note**

SBS 192 catalog only contains mutations in transcribed regions.

---

WriteCatalog	<i>Write a catalog</i>
--------------	------------------------

---

**Description**

Write a catalog to a file.

**Usage**

```
WriteCatalog(catalog, file, strict = TRUE)
```

**Arguments**

<code>catalog</code>	A catalog as defined in <a href="#">ICAMS</a> ; see also <a href="#">as.catalog</a> .
<code>file</code>	The path to the file to be created.
<code>strict</code>	If TRUE, do additional checks on the input, and stop if the checks fail.

**Details**

See also [ReadCatalog](#).

**Note**

In ID (insertion and deletion) catalogs, deletion repeat sizes range from 0 to 5+, but for plotting and end-user documentation deletion repeat sizes range from 1 to 6+.

# Index

## \*Topic **datasets**

- CatalogRowOrder, [3](#)
- TranscriptRanges, [19](#)
- as.catalog, [2](#), [7](#), [9–12](#), [14](#), [16–18](#), [20–23](#)
- available.genomes, [8](#)
- BSgenome, [8](#)
- BSgenome.Hsapiens.1000genomes.hs37d5, [8](#)
- BSgenome.Hsapiens.UCSC.hg38, [8](#)
- catalog.row.order (CatalogRowOrder), [3](#)
- CatalogRowOrder, [2](#), [3](#), [9](#)
- Collapse144CatalogTo78 (CollapseCatalog), [3](#)
- Collapse1536CatalogTo96 (CollapseCatalog), [3](#)
- Collapse192CatalogTo96 (CollapseCatalog), [3](#)
- CollapseCatalog, [3](#), [9](#)
- data.table, [9](#), [10](#), [17–19](#), [21](#), [22](#)
- FindDelMH, [4](#)
- GetMutectVAF (GetVAF), [6](#)
- GetStrelkaVAF (GetVAF), [6](#)
- GetVAF, [6](#)
- ICAMS, [2–4](#), [6](#), [9–12](#), [14](#), [16–18](#), [20–23](#)
- ICAMS-package (ICAMS), [6](#)
- MutectVCFFilesToCatalog, [7](#), [9](#), [10](#), [13](#), [19](#)
- MutectVCFFilesToCatalogAndPlotToPdf, [10](#), [19](#)
- PlotCatalog, [7](#), [11](#)
- PlotCatalogToPdf, [7](#), [10](#), [12](#), [17](#), [18](#)
- ReadAndSplitMutectVCFs, [13](#)
- ReadAndSplitStrelkaSBSVCFs, [13](#)
- ReadCatalog, [7](#), [8](#), [14](#), [23](#)
- ReadStrelkaIDVCFs, [15](#)
- revc, [15](#)
- StrelkaIDVCFFilesToCatalog, [7](#), [15](#), [16](#)
- StrelkaIDVCFFilesToCatalogAndPlotToPdf, [16](#)
- StrelkaSBSVCFFilesToCatalog, [7](#), [14](#), [17](#), [18](#), [19](#)
- StrelkaSBSVCFFilesToCatalogAndPlotToPdf, [7](#), [18](#), [19](#)
- trans.ranges.GRCh37 (TranscriptRanges), [19](#)
- trans.ranges.GRCh38 (TranscriptRanges), [19](#)
- TranscriptRanges, [9](#), [10](#), [17](#), [18](#), [19](#), [21](#), [22](#)
- TransformCatalog, [7](#), [8](#), [11](#), [12](#), [20](#)
- VCFsToDBSCatalogs, [9](#), [17](#), [19](#), [21](#)
- VCFsToIDCatalogs, [9](#), [16](#), [17](#), [21](#)
- VCFsToSBCatalogs, [9](#), [17](#), [19](#), [22](#)
- WriteCatalog, [8](#), [14](#), [22](#)