

COSMIC 67

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1 Introduction

The *COSMIC.67* package provides the curated mutations published with the COSMIC release version 67 (2013-10-24). Both variants found in coding and non-coding regions are included and offered as a single object of class 'CollapsedVCF' and a bgzipped and tabix-index 'VCF' file.

Additionally, the package contains the Cancer Gene Census, a list of genes causally linked to cancer.

2 Accessing and Using the Data

```
library(VariantAnnotation)
```

```
Loading required package: BiocGenerics
```

```
Loading required package: parallel
```

```
Attaching package: 'BiocGenerics'
```

```
The following objects are masked from 'package:parallel':
```

```
  clusterApply, clusterApplyLB, clusterCall,  
  clusterEvalQ, clusterExport, clusterMap, parApply,  
  parCapply, parLapply, parLapplyLB, parRapply,  
  parSapply, parSapplyLB
```

```
The following objects are masked from 'package:stats':
```

IQR, mad, xtabs

The following objects are masked from 'package:base':

Filter, Find, Map, Position, Reduce, anyDuplicated, append, as.data.frame, as.vector, cbind, colnames, do.call, duplicated, eval, evalq, get, grep, grepl, intersect, is.unsorted, lapply, lengths, mapply, match, mget, order, paste, pmax, pmax.int, pmin, pmin.int, rank, rbind, rownames, sapply, setdiff, sort, table, tapply, union, unique, unlist, unsplit

Loading required package: *GenomeInfoDb*

Loading required package: *stats4*

Loading required package: *S4Vectors*

Loading required package: *IRanges*

Loading required package: *GenomicRanges*

Loading required package: *SummarizedExperiment*

Loading required package: *Biobase*

Welcome to Bioconductor

Vignettes contain introductory material; view with 'browseVignettes()'. To cite Bioconductor, see 'citation("Biobase")', and for packages 'citation("pkgname")'.

Loading required package: *Rsamtools*

Loading required package: *XVector*

Loading required package: *Biostrings*

Attaching package: *'VariantAnnotation'*

The following object is masked from 'package:base':

tabulate

```
library(GenomicRanges)
```

```
data(package = "COSMIC.67")
```

```
data(cosmic_67, package = "COSMIC.67")
```

```
tp53_range = GRanges("17", IRanges(7565097, 7590856))
```

```
vcf_path = system.file("vcf", "cosmic_67.vcf.gz", package = "COSMIC.67")
```

```
cosmic_tp53 = readVcf(vcf_path, genome = "GRCh37", ScanVcfParam(which = tp53_range))
```

```
cosmic_tp53
```

```
class: CollapsedVCF
```

```
dim: 5892 0
```

```
rowRanges(vcf):
```

```
GRanges with 5 metadata columns: paramRangeID, REF, ALT, QUAL, FILTER
```

```
info(vcf):
```

```
DataFrame with 5 columns: GENE, STRAND, CDS, AA, CNT
```

```
info(header(vcf)):
```

	Number	Type	Description
GENE	1	String	Gene name
STRAND	1	String	Gene strand
CDS	1	String	CDS annotation
AA	1	String	Peptide annotation
CNT	1	Integer	How many samples have this mutation

```

geno(vcf):
  SimpleList of length 0:

data(cgc_67, package = "COSMIC.67")
head(cgc_67)

  SYMBOL ENTREZID      ENSEMBL
1  ABI1    10006  ENSG00000136754
2  ABL1      25  ENSG00000097007
3  ABL2      27  ENSG00000143322
4  ACSL3    2181  ENSG00000123983
5  CASC5    57082  ENSG00000137812
6  MLLT11   10962  ENSG00000213190

```

For details on the collection and curation of the original data, please see the webpage of the COSMIC project: <http://cancer.sanger.ac.uk/cancergenome/projects/cosmic/>.

3 Data Provenance

3.1 COSMIC Mutations

The following steps are performed for importing and processing of the VCF data:

1. Downloading of the VCF files 'CosmicCodingMuts_v67_20131024.vcf.gz' and 'CosmicNonCodingVariants_v67_20131024.vcf.gz' from 'ftp://ngs.sanger.ac.uk/production/cosmic/' to 'inst/raw/'.
2. Importing of both files to R using 'readVcf'.
3. Sorting of the seqlevels and adding 'seqinfo' data for the toplevel chromosomes of 'GRCh37'.
4. Merging of both objects, sorting according to genomic position.
5. Converting the object to class `VariantAnnotation::VRanges`.
6. Converting the 'character' columns to 'factors'.
7. Saving the merged object to 'data/cosmic_v67_vcf.rda'.
8. Exporting the merged object as a bgzipped and tabix-indexed 'VCF' to 'inst/vcf/cosmic_v67.vcf.gz'.

3.2 Cancer Gene Census

The following steps are performed for importing and processing of the Cancer Gene Census data:

1. Downloading of the 'cancer_gene_census.tsv' file from ftp://ftp.sanger.ac.uk/pub/CGP/cosmic/data_export to 'inst/raw'.
2. Import of the files as a data frame.
3. Annotation of the 'HGNC' and 'ENSEMBLID' identifiers, using the 'ENTREZ gene ID' as query with the 'org.Hs.eg.db' object.
4. Saving the object to 'data/cgc_67.rda'.

4 Data Source

The mutation data was obtained from the Sanger Institute Catalogue Of Somatic Mutations In Cancer web site, <http://www.sanger.ac.uk/cosmic>

Bamford et al (2004):

The COSMIC (Catalogue of Somatic Mutations in Cancer) database and website.

Br J Cancer, 91,355-358.

For details on the usage and redistribution of the data, please see ftp://ftp.sanger.ac.uk/pub/CGP/cosmic/GUIDELINES_ON_THE_USE_OF_THIS_DATA.txt.

5 References

- <http://cancer.sanger.ac.uk/cancergenome/projects/cosmic/>
- http://nar.oxfordjournals.org/content/39/suppl_1/D945.long
- ftp://ftp.sanger.ac.uk/pub/CGP/cosmic/GUIDELINES_ON_THE_USE_OF_THIS_DATA.txt

6 Session Info

R version 3.2.2 (2015-08-14)

Platform: x86_64-pc-linux-gnu (64-bit)

Running under: Ubuntu 14.04.3 LTS

locale:

```
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8      LC_COLLATE=C
[5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8     LC_NAME=C
[9] LC_ADDRESS=C             LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

attached base packages:

```
[1] stats4    parallel  stats      graphics  grDevices  utils
[7] datasets  methods  base
```

other attached packages:

```
[1] VariantAnnotation_1.16.0  Rsamtools_1.22.0
[3] Biostrings_2.38.0        XVector_0.10.0
[5] SummarizedExperiment_1.0.0 Biobase_2.30.0
[7] GenomicRanges_1.22.0     GenomeInfoDb_1.6.0
[9] IRanges_2.4.0            S4Vectors_0.8.0
[11] BiocGenerics_0.16.0      knitr_1.11
```

loaded via a namespace (and not attached):

```
[1] AnnotationDbi_1.32.0     magrittr_1.5
[3] GenomicAlignments_1.6.0 zlibbioc_1.16.0
[5] BiocParallel_1.4.0      BSgenome_1.38.0
[7] highr_0.5.1             stringr_1.0.0
[9] tools_3.2.2             DBI_0.3.1
[11] lambda.r_1.1.7          futile.logger_1.4.1
[13] rtracklayer_1.30.0      formatR_1.2.1
[15] futile.options_1.0.0    bitops_1.0-6
[17] biomaRt_2.26.0         RCurl_1.95-4.7
[19] evaluate_0.8           RSQLite_1.0.0
[21] stringi_0.5-5          GenomicFeatures_1.22.0
[23] XML_3.98-1.3           BiocStyle_1.8.0
```