Package 'COSMIC.67'

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Type Package

Title COSMIC.67

Version 1.46.0

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Imports GenomicRanges, SummarizedExperiment, VariantAnnotation

Depends R (>= 3.0.2)

Suggests testthat, BiocStyle, knitr

VignetteBuilder knitr

Description COSMIC: Catalogue Of Somatic Mutations In Cancer, version 67 (2013-10-24)

License GPL-3

Encoding UTF-8

LazyLoad yes

biocViews ExperimentData, Genome, CancerData

git_url https://git.bioconductor.org/packages/COSMIC.67

git_branch RELEASE_3_22

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git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

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COSMIC.67-package *COSMIC.67 package*

Description

Mutations of the 'Catalogue Of Somatic Mutations In Cancer'(COSMIC), version 67 (2013-10-24).

Details

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) a single object of class 'CollapsedVCF' and (b) a bgzipped and tabix-index 'VCF' file. Additionally, the package contains the cancer gene census, a list of genes causally linked to cancer.

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/.

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 all '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'.

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'.

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.

Author(s)

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References

http://cancer.sanger.ac.uk/cancergenome/projects/cosmic/

http://nar.oxfordjournalls.org/content/39/suppl_1/D945.long

ftp://ftp.sanger.ac.uk/pub/CGP/cosmic/GUIDELINES_ON_THE_USE_OF_THIS_DATA.txt

See Also

VCF-class

Examples

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

library(VariantAnnotation)
library(GenomicRanges)

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

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