Package ‘SomaticCancerAlterations’

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SomaticCancerAlterations-package

Description

A collection of studies with somatic cancer alterations.

Details

The 'SomaticCancerAlterations' package provides a collection of the mutational calls for different cancer studies, aiming for a tight integration with R and Bioconductor. At the moment, this covers somatic single nucleotide variants (SNVs) and indels for several TCGA studies. Over time, this collection will be updated to include additional studies.

The Cancer Genome Atlas (TCGA) is a consortium effort to analyze a variety of tumor types at multiple levels, including gene expression, methylation, copy number alterations and somatic mutations [http://cancergenome.nih.gov]. Most of this data is publically available, and offers a rich resource in understanding cancer-related data sets and experiments [https://wiki.nci.nih.gov/display/TCGA/TCGA+Home].

Author(s)

Julian Gehring, with suggestions and contributions from Bernd Fischer

Maintainer: Julian Gehring

References

https://tcga-data.nci.nih.gov/tcga/
https://tcga-data.nci.nih.gov/docs/publications/

See Also

SomaticCancerAlterations-functions
SomaticCancerAlterations-data

SomaticCancerAlterations-data

Description

Data sets with studies of somatic cancer alterations.
Details

Currently, the data sets include somatic mutations (SNVs and indels) of the publically available TCGA studies. Further studies will be included in the future.

For details on the TCGA mutation calls, please see the TCGA documentation https://wiki.nci.nih.gov/display/TCGA/TCGA+Data+Primer. Please note that the mutational calling was performed by different centers. The original '*.maf' files can be obtained from the TCGA data portal https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/.

After importing, the data is automatically processed to improve consistency across studies and remove common artifacts in the annotation. The most obvious changes are:

- Only studies cleared for unrestricted usage are included (see http://cancergenome.nih.gov/publications/publicationguidelines).
- Only studies processed by the Broad Instutite are considered at the moment.
- All variants located on the mitochondrium are mapped to the sequence identifier 'MT' (note that the original files contain both 'MT' and 'M' mixed).
- All locations are now consistent with the 1000genomes reference sequence (NCBI37 coordinates).

About the TCGA data:

“All data generated by The Cancer Genome Atlas (TCGA) Research Network are made open to the public through the Data Coordinating Center and the TCGA Data Portal.” For details on the usage of the data, please have a look at http://cancergenome.nih.gov/abouttcga/policies/publicationguidelines.

Value

A ‘GRanges’ object for each study. Each row corresponds to a somatic variant reported in the respective study, with the coordinates refering to the location on the reference genome.

References

https://tcga-data.nci.nih.gov/tcga/

See Also

SomaticCancerAlterations-functions
SomaticCancerAlterations-package

Examples

all_datasets = scaListDatasets()
grl = scaLoadDatasets(all_datasets[1])
SomaticCancerAlterations-functions

SomaticCancerAlterations functions

Description
Functions to interact with the 'SomaticCancerAlterations' datasets.

Usage
scaMetadata()
scaListDatasets()
scaLoadDatasets(names, merge = FALSE)

Arguments
names Character vector with data set name(s) to load. The names are the same as returned from 'scaListDatasets'.
merge Logical. Should the results be a merged 'GRanges' object with data of all studies (TRUE), or a 'GRangesList' with one list element per dataset (FALSE [default]).

Details
The 'sca_load_dataset' function makes it easy to load the data of a study directly into a variable.

Value
scaMetadata A data frame summarizing the available data sets, with rows corresponding to data sets.
scaListDatasets A character vector with all available study names.
sca_load_dataset A GRangesList or GRanges objects, depending on the 'merge' argument.

References
https://tcga-data.nci.nih.gov/tcga/
https://wiki.nci.nih.gov/display/TCGA/TCGA+Data+Primer
https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftputers/anonymous/tumor/

See Also
SomaticCancerAlterations-data
Examples

```r
meta_data = scaMetadata()
head(meta_data)

all_datasets = scaListDatasets()
head(all_datasets)

g1 = scaLoadDatasets(all_datasets[1], merge = FALSE)
gr = scaLoadDatasets(all_datasets[1], merge = TRUE)
```

Description

Functions to help with common analysis tasks.

Usage

```r
ncbi2hg(x)

hg2ncbi(x)

seqchr(x)
```

Arguments

- `x` A GRanges object

Details

These functions provide useful wrappers for converting between genomic coordinate systems and classes.

Value

- `ncbi2hg`, `hg2ncbi`
  A GRanges object.

- `seqchr`
  A character vector with the ‘seqnames’.
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