

# Package ‘ICAMS.shiny’

November 4, 2020

**Title** An Amazing Shiny App

**Version** 0.0.2

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**Description** What the package does (one paragraph).

**License** GPL-3 | file LICENSE

**Encoding** UTF-8

**LazyData** true

**Language** en-US

**biocViews**

**Imports** BSgenome.Hsapiens.1000genomes.hs37d5,  
BSgenome.Hsapiens.UCSC.hg38,  
BSgenome.Mmusculus.UCSC.mm10,  
config,  
data.table,  
GenSA,  
golem,  
htmltools,  
ICAMS,  
ICAMSxtra,  
PCAWG7,  
pkgload,  
quadprog,  
shiny,  
stringi,  
zip

**Remotes** github::steverozen/PCAWG7,  
github::steverozen/ICAMSxtra

**RoxygenNote** 7.1.1

**Suggests** testthat (>= 2.1.0),  
shinytest

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CancerTypeToSigSubset	<i>Get the subset of signatures for a specified cancer type from a specified tumor cohort</i>
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## Description

Get the subset of signatures for a specified cancer type from a specified tumor cohort

## Usage

```
CancerTypeToSigSubset(
  cancer.type,
  tumor.cohort = "PCAWG",
  sig.type = "SBS96",
  region = "genome"
)
```

## Arguments

cancer.type	Cancer type of the tumor, e.g. "Biliary-AdenoCA".
tumor.cohort	The cohort of tumors to get information from package PCAWG7. Can be "PCAWG", "TCGA", "other.genome", "other.exome".
sig.type	Type of the signature, e.g. "SBS96".
region	A character string designating a genomic region; see <a href="#">as.catalog</a> and <a href="#">ICAMS</a> .

## Value

The set of signatures found present in the specified cancer.type from the specified tumor.cohort.

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GetExposureAndPlotToPdf	<i>Get signature exposure for one sample and plot to Pdf</i>
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## Description

Get signature exposure for one sample and plot to Pdf

**Usage**

```

GetExposureAndPlotToPdf(
  catalog,
  file,
  sig.universe,
  num.of.bootstrap.replicates = 1000,
  method = decomposeQP,
  conf.int = 0.95,
  ...
)

```

**Arguments**

catalog	A <b>counts</b> catalog as defined in <a href="#">ICAMS</a> . It can only has <b>one</b> column.
file	The name of the PDF file to be produced.
sig.universe	The universe of signatures used to do signature attribution.
num.of.bootstrap.replicates	The number of bootstrap replicates.
method	Method used to get the optimal solution for signature attribution.
conf.int	A number specifying the required confidence interval.
...	Optional arguments passed to <code>ICAMStextra::PlotExposureToPdf</code>

**Value**

A matrix showing the signature exposure results for catalog with lower and upper bound of the specified confidence interval.

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GetExposureWithConfidence

*Get signature exposure for one sample with confidence interval*

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**Description**

Get signature exposure for one sample with confidence interval

**Usage**

```

GetExposureWithConfidence(
  catalog,
  sig.universe,
  num.of.bootstrap.replicates = 1000,
  method = decomposeQP,
  conf.int = 0.95
)

```

**Arguments**

catalog	A <b>counts</b> catalog as defined in <a href="#">ICAMS</a> . It can only has <b>one</b> column.
sig.universe	The universe of signatures used to do signature attribution.
num.of.bootstrap.replicates	The number of bootstrap replicates.
method	Method used to get the optimal solution for signature attribution.
conf.int	A number specifying the required confidence interval.

**Value**

A matrix showing the signature exposure results for catalog with lower and upper bound of the specified confidence interval.

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run_app	<i>Run the Shiny Application</i>
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**Description**

Run the Shiny Application

**Usage**

```
run_app(...)
```

**Arguments**

... Further arguments to be passed to the function.

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