Package ‘CoSIA’

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Type Package

Title An Investigation Across Different Species and Tissues

Version 1.6.0

Description Cross-Species Investigation and Analysis (CoSIA) is a package that provides researchers with an alternative methodology for comparing across species and tissues using normal wild-type RNA-Seq Gene Expression data from Bgee. Using RNA-Seq Gene Expression data, CoSIA provides multiple visualization tools to explore the transcriptome diversity and variation across genes, tissues, and species. CoSIA uses the Coefficient of Variation and Shannon Entropy and Specificity to calculate transcriptome diversity and variation. CoSIA also provides additional conversion tools and utilities to provide a streamlined methodology for cross-species comparison.

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Encoding UTF-8

Depends R (>= 4.3.0), methods (>= 4.3.0), ExperimentHub (>= 2.7.0)

Imports dplyr (>= 1.0.7), magrittr (>= 2.0.1), RColorBrewer (>= 1.1-2), tidyr (>= 1.2.0), plotly (>= 4.10.0), stringr (>= 1.4.0), ggplot2 (>= 3.3.5), tibble (>= 3.1.7), org.Hs.eg.db (>= 3.12.0), org.Mm.eg.db (>= 3.12.0), org.Dr.eg.db (>= 3.12.0), org.Ce.eg.db (>= 3.12.0), org.Dm.eg.db (>= 3.12.0), org.Rn.eg.db (>= 3.12.0), AnnotationDbi (>= 1.52.0), biomaRt (>= 2.46.3), homologene (>= 1.4.68.19), annotationTools (>= 1.64.0), readr (>= 2.1.1), tidyselect (>= 1.1.2), stats (>= 4.1.2)

RoxygenNote 7.2.3

Suggests BiocStyle (>= 2.22.0), tidyverse (>= 1.3.1), knitr (>= 1.42), rmarkdown (>= 2.20), testthat (>= 3.1.6), qpdf (>= 1.3.0)

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BugReports `https://github.com/lasseignelab/CoSIA/issues`

URL `https://www.lasseigne.org/`

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Contents

`CoSIAn-class` *CoSIAn Class S4 Object*

Description

This Class is used to specify the information needed to conduct analysis using CoSIA's other methods. An object of this class will pass as an argument to other methods in CoSIA

Value

CoSIAn object

Slots

`gene_set` character. A singular gene or a list of genes.

`i_species` character. The species corresponding to gene_set.

`input_id` character. The type of id corresponding to gene_set.

`o_species` character. The singular or list of species that the gene set is being converted to.

`output_ids` character. The singular or list of id types that the gene set is being converted to.

`mapping_tool` character. The mapping tool, BiomaRt or annotationDBI, being used to map the conversion between IDs.

`ortholog_database` character. The ortholog database, HomoloGene or NCBIOrtho, being used to map the conversion between species.

`converted_id` data frame. Output of getConversion.

`map_tissues` character. A list of tissues being investigated.

`map_species` character. A list of species being investigated.

`gex` data frame. Output of gene expression data.

`metric_type` character. A list of possible metric the user wants to calculate.

`metric` data frame. Output of coefficient of variation of gene expression data.

`CoSIAn-Constructor Constructor for the CoSIAn Class`
Constructor for the CoSIAn Object

Description

The `CoSIAn` constructor creates a `CoSIAn` object from character vector(s).

Usage

```
CoSIAn(
  gene_set,
  i_species,
  input_id,
  o_species,
  output_ids,
  mapping_tool = "annotationDBI",
  ortholog_database = "HomoloGene",
  map_tissues,
  map_species,
  metric_type
)
```

Arguments

`gene_set`	A singular gene or a list of genes.
`i_species`	The species corresponding to gene_set.
`input_id`	The type of id corresponding to gene_set.
`o_species`	The singular or list of species that the gene set is being converted to.

`output_ids`	The singular or list of id types that the gene set is being converted to.
`mapping_tool`	The mapping tool, BiomaRt or annotationDBI, being used to map the conversion between IDs.
`ortholog_database`	The ortholog database, HomoloGene or NCBIOrtho, being used to map the conversion between species.
`map_tissues`	A list of tissues being investigated
`map_species`	A list of species being investigated
`metric_type`	A list of possible metric the user wants to calculate.

Value

An S4 `CoSIAn` object with character vector(s) as slots.

Examples

```
Kidney_Genes <- CoSIAn(
    gene_set = c(
        "ENSG00000008710", "ENSG00000118762",
        "ENSG00000152217"
    ), i_species = "h_sapiens", input_id = "Ensembl_id",
    o_species = c(
        "d_melanogaster", "m_musculus", "h_sapiens", "d_rerio",
        "c_elegans", "r_norvegicus"
    ), output_ids = c("Ensembl_id", "Symbol"),
    mapping_tool = "annotationDBI", ortholog_database = "HomoloGene",
    map_tissues = "heart", map_species = c("m_musculus"),
    metric_type = "DS_Gene"
)
```

`getConversion` *getConversion Generic*

Description

getConversion Generic

Usage

```
getConversion(object)
```

Arguments

`object`	CoSIAn object with all user accessible slots filled

Value

initializes a generic function for getConversion as preparation for defining the getConversion Method

Examples

```
Kidney_Genes <- CoSIAn(
    gene_set = c("ENSG00000008710", "ENSG00000118762", "ENSG00000152217"),
    i_species = "h_sapiens", input_id = "Ensembl_id",
    o_species = c(
        "d_melanogaster", "m_musculus", "h_sapiens", "d_rerio",
        "c_elegans", "r_norvegicus"
    ),
    output_ids = c("Ensembl_id", "Symbol"), mapping_tool = "annotationDBI",
    ortholog_database = "HomoloGene", map_tissues = "heart",
    map_species = c("m_musculus"), metric_type = "DS_Gene"
)
Kidney_gene_conversion <- CoSIA::getConversion(Kidney_Genes)
```

`getConversion,CoSIAn-method`

getConversion Method

Description

getConversion Method

Usage

```
## S4 method for signature 'CoSIAn'
getConversion(object)
```

Arguments

`object`	CoSIAn object with all user accessible slots filled

Value

CoSIAn object with converted_id slot filled

Examples

```
Kidney_Genes <- CoSIAn(
    gene_set = c("ENSG00000008710", "ENSG00000118762", "ENSG00000152217"),
    i_species = "h_sapiens", input_id = "Ensembl_id",
    o_species = c(
        "d_melanogaster", "m_musculus", "h_sapiens", "d_rerio",
        "c_elegans", "r_norvegicus"
    ),
    output_ids = c("Ensembl_id", "Symbol"), mapping_tool = "annotationDBI",
    ortholog_database = "HomoloGene", map_tissues = "heart",
    map_species = c("m_musculus"), metric_type = "DS_Gene"
)
Kidney_gene_conversion <- CoSIA::getConversion(Kidney_Genes)
```

`getGEx` *getGEx Generic*

Description

getGEx Generic

Usage

```
getGEx(object)
```

Arguments

`object`	CoSIAn object with all user accessible slots filled with converted_id slot filled

Value

initializes a generic function for getGEx as preparation for defining the getGEx Method

Examples

```
Kidney_Genes <- CoSIAn(
    gene_set = c("ENSG00000008710", "ENSG00000118762", "ENSG00000152217"),
    i_species = "h_sapiens", input_id = "Ensembl_id",
    o_species = c(
        "h_sapiens", "r_norvegicus"
    ), output_ids = c("Ensembl_id", "Symbol"),
    mapping_tool = "annotationDBI", ortholog_database = "HomoloGene",
    map_tissues = "heart", map_species = c("r_norvegicus"),
    metric_type = "DS_Gene"
)
Kidney_gene_conversion <- CoSIA::getConversion(Kidney_Genes)
Kidney_gene_gex <- getGEx(Kidney_gene_conversion)
```

`getGEx,CoSIAn-method` *getGEx Method*

Description

getGEx Method

Usage

```
## S4 method for signature 'CoSIAn'
getGEx(object)
```

Arguments

`object`	CoSIAn object with all user accessible slots filled with converted_id slot filled

Value

CoSIAn Object with gex slot filled

Examples

```
Kidney_Genes <- CoSIAn(
    gene_set = c("ENSG00000008710", "ENSG00000118762", "ENSG00000152217"),
    i_species = "h_sapiens", input_id = "Ensembl_id",
    o_species = c(
        "h_sapiens", "r_norvegicus"
    ), output_ids = c("Ensembl_id", "Symbol"),
    mapping_tool = "annotationDBI", ortholog_database = "HomoloGene",
    map_tissues = "heart", map_species = c("r_norvegicus"),
    metric_type = "DS_Gene"
)
Kidney_gene_conversion <- CoSIA::getConversion(Kidney_Genes)
Kidney_gene_gex <- getGEx(Kidney_gene_conversion)
```

`getGExMetrics` *getGExMetrics Generic*

Description

getGExMetrics Generic

Usage

```
getGExMetrics(object)
```

Arguments

`object`	CoSIAn object with all user accessible slots filled with converted_id slot filled

Value

initializes a generic function for getGExMetrics as preparation for defining the getGExMetrics Method

Examples

```
Kidney_Genes <- CoSIAn(
    gene_set = c("ENSG00000008710", "ENSG00000118762", "ENSG00000152217"),
    i_species = "h_sapiens", input_id = "Ensembl_id", o_species = c(
        "h_sapiens", "r_norvegicus"
    ), output_ids = c("Ensembl_id", "Symbol"),
    mapping_tool = "annotationDBI", ortholog_database = "HomoloGene",
    map_tissues = "heart", map_species = c("r_norvegicus"),
    metric_type = "DS_Gene"
)
Kidney_gene_conversion <- CoSIA::getConversion(Kidney_Genes)
Kidney_gene_metric <- getGExMetrics(Kidney_gene_conversion)
```

`getGExMetrics,CoSIAn-method` *getGExMetrics Method*

Description

getGExMetrics Method

Usage

```
## S4 method for signature 'CoSIAn'
getGExMetrics(object)
```

Arguments

`object`	CoSIAn object with all user accessible slots filled with converted_id slot filled

Value

CoSIAn Object with metric slot filled

References

Kohl M (2022). MKdescr: Descriptive Statistics. R package version 0.8, https://github.com/stamats/MKdescr.

Zhang JD, Hatje K, Sturm G, Broger C, Ebeling M, Burtin M, Terzi F, Pomposiello SI, Badi L (2017). “Detect tissue heterogeneity in gene expression data with BioQC.” BMC Genomics, 18(1), 277. http://accio.github.io/BioQC/.

Examples

```
Kidney_Genes <- CoSIAn(
    gene_set = c("ENSG00000008710", "ENSG00000118762", "ENSG00000152217"),
    i_species = "h_sapiens", input_id = "Ensembl_id", o_species = c(
        "h_sapiens", "r_norvegicus"
    ), output_ids = c("Ensembl_id", "Symbol"),
    mapping_tool = "annotationDBI", ortholog_database = "HomoloGene",
    map_tissues = "heart", map_species = c("r_norvegicus"),
    metric_type = "DS_Gene"
)
Kidney_gene_conversion <- CoSIA::getConversion(Kidney_Genes)
Kidney_gene_metric <- getGExMetrics(Kidney_gene_conversion)
```

`getTissues` *getTissues*

Description

getTissues

Usage

```
getTissues(species)
```

Arguments

`species`	name of a species or multiple species that you want to get available tissue list for

Value

list of tissues that are common/available among the species or multiple species inputted

Examples

```
tissue <- getTissues(c("m_musculus"))
```

`plotCVGEx` *plotCVGEx Generic*

Description

plotCVGEx Generic

Usage

```
plotCVGEx(object)
```

Arguments

`object`	CoSIAn object with all user accessible slots filled in as well as the converted_id and metric slot filled

Value

initializes a generic function for plotCVGEx as preparation for defining the plotCVGEx Method

Examples

```
Kidney_Genes <- CoSIAn(
    gene_set = c("ENSG00000008710", "ENSG00000118762", "ENSG00000152217"),
    i_species = "h_sapiens", input_id = "Ensembl_id", o_species = c(
        "h_sapiens", "r_norvegicus"
    ), output_ids = c("Ensembl_id", "Symbol"),
    mapping_tool = "annotationDBI", ortholog_database = "HomoloGene",
    map_tissues = c("adult mammalian kidney","heart"),
    map_species = c("h_sapiens", "r_norvegicus"),
    metric_type = "CV_Tissue"
)
Kidney_gene_conversion <- CoSIA::getConversion(Kidney_Genes)
Kidney_gene_metric <- getGExMetrics(Kidney_gene_conversion)
plot <- plotCVGEx(Kidney_gene_metric)
```

`plotCVGEx,CoSIAn-method`

plotCVGEx Method

Description

plotCVGEx Method

Usage

```
## S4 method for signature 'CoSIAn'
plotCVGEx(object)
```

Arguments

`object`	CoSIAn object with all user accessible slots filled in as well as the converted_id and metric slot filled

Value

plot object

References

Dot plot in R with the dotchart function [with examples]. R CODER. (2020, November 20). Retrieved from https://r-coder.com/dot-plot-r/

Examples

```
Kidney_Genes <- CoSIAn(
    gene_set = c("ENSG00000008710", "ENSG00000118762", "ENSG00000152217"),
    i_species = "h_sapiens", input_id = "Ensembl_id", o_species = c(
        "h_sapiens", "r_norvegicus"
    ), output_ids = c("Ensembl_id", "Symbol"),
    mapping_tool = "annotationDBI", ortholog_database = "HomoloGene",
    map_tissues = c("adult mammalian kidney","heart"),
    map_species = c("h_sapiens", "r_norvegicus"),
    metric_type = "CV_Tissue"
```

```
)
Kidney_gene_conversion <- CoSIA::getConversion(Kidney_Genes)
Kidney_gene_metric <- getGExMetrics(Kidney_gene_conversion)
plot <- plotCVGEx(Kidney_gene_metric)
```

`plotDSGEx` *plotDSGEx Generic*

Description

plotDSGEx Generic

Usage

```
plotDSGEx(object)
```

Arguments

`object`	CoSIAn object with all user accessible slots filled in as well as the converted_id and metric slot filled

Value

initializes a generic function for plotDSGEx as preparation for defining the plotDSGEx Method

Examples

```
Kidney_Genes <- CoSIAn(
    gene_set = c("ENSG00000008710", "ENSG00000118762", "ENSG00000152217"),
    i_species = "h_sapiens", input_id = "Ensembl_id", o_species = c(
        "d_melanogaster", "m_musculus",
        "h_sapiens", "d_rerio", "c_elegans", "r_norvegicus"
    ), output_ids = c("Ensembl_id", "Symbol"),
    mapping_tool = "annotationDBI", ortholog_database = "HomoloGene",
    map_tissues = "heart", map_species = c("m_musculus"),
    metric_type = "DS_Gene"
)
Kidney_gene_conversion <- CoSIA::getConversion(Kidney_Genes)
Kidney_gene_metric <- getGExMetrics(Kidney_gene_conversion)
plotDSGEx(Kidney_gene_metric)
```

`plotDSGEx,CoSIAn-method` *plotDSGEx Method*

Description

plotDSGEx Method

Usage

```
## S4 method for signature 'CoSIAn'
plotDSGEx(object)
```

Arguments

`object`	CoSIAn object with all user accessible slots filled in as well as the converted_id and metric slot filled

Value

plot object

Examples

```
Kidney_Genes <- CoSIAn(
    gene_set = c("ENSG00000008710", "ENSG00000118762", "ENSG00000152217"),
    i_species = "h_sapiens", input_id = "Ensembl_id", o_species = c(
        "d_melanogaster", "m_musculus",
        "h_sapiens", "d_rerio", "c_elegans", "r_norvegicus"
    ), output_ids = c("Ensembl_id", "Symbol"),
    mapping_tool = "annotationDBI", ortholog_database = "HomoloGene",
    map_tissues = "heart", map_species = c("m_musculus"),
    metric_type = "DS_Gene"
)
Kidney_gene_conversion <- CoSIA::getConversion(Kidney_Genes)
Kidney_gene_metric <- getGExMetrics(Kidney_gene_conversion)
plotDSGEx(Kidney_gene_metric)
```

`plotSpeciesGEx` *plotSpeciesGEx Generic*

Description

plotSpeciesGEx Generic

Usage

```
plotSpeciesGEx(object, single_tissue, single_gene)
```

Arguments

`object`	CoSIAn object with all user accessible slots filled in as well as the converted_id and gex slot filled
`single_tissue`	one tissue that the user wants to investigate across the mapped species
`single_gene`	one ensembl id that the user wants to investigate across the mapped species

Value

initializes a generic function for plotSpeciesGEx as preparation for defining the plotSpeciesGEx Method

Examples

```
Kidney_Genes <- CoSIAn(
    gene_set = c("ENSG00000008710", "ENSG00000118762", "ENSG00000152217"),
    i_species = "h_sapiens", input_id = "Ensembl_id", o_species = c(
        "d_melanogaster", "m_musculus",
        "h_sapiens", "d_rerio", "c_elegans", "r_norvegicus"
    ), output_ids = c("Ensembl_id", "Symbol"),
    mapping_tool = "annotationDBI", ortholog_database = "HomoloGene",
    map_tissues = "heart", map_species = c("m_musculus"),
    metric_type = "DS_Gene"
)
Kidney_gene_conversion <- CoSIA::getConversion(Kidney_Genes)
Kidney_gene_gex <- getGEx(Kidney_gene_conversion)
plotSpeciesGEx(Kidney_gene_gex, "liver", "ENSG00000008710")
```

`plotSpeciesGEx,CoSIAn-method`

plotSpeciesGEx Method

Description

plotSpeciesGEx Method

Usage

```
## S4 method for signature 'CoSIAn'
plotSpeciesGEx(object, single_tissue, single_gene)
```

Arguments

`object`	CoSIAn object with all user accessible slots filled in as well as the converted_id and gex slot filled
`single_tissue`	one tissue that the user wants to investigate across the mapped species
`single_gene`	one ensembl id that the user wants to investigate across the mapped species

Value

plot object

Examples

```
Kidney_Genes <- CoSIAn(
    gene_set = c("ENSG00000008710", "ENSG00000118762", "ENSG00000152217"),
    i_species = "h_sapiens", input_id = "Ensembl_id", o_species = c(
        "d_melanogaster", "m_musculus",
        "h_sapiens", "d_rerio", "c_elegans", "r_norvegicus"
    ), output_ids = c("Ensembl_id", "Symbol"),
    mapping_tool = "annotationDBI", ortholog_database = "HomoloGene",
    map_tissues = "heart", map_species = c("m_musculus"),
    metric_type = "DS_Gene"
)
Kidney_gene_conversion <- CoSIA::getConversion(Kidney_Genes)
Kidney_gene_gex <- getGEx(Kidney_gene_conversion)
plotSpeciesGEx(Kidney_gene_gex, "liver", "ENSG00000008710")
```

`plotTissueGEx` *plotTissueGEx Generic*

Description

plotTissueGEx Generic

Usage

```
plotTissueGEx(object, single_species, single_gene)
```

Arguments

`object`	CoSIAn object with all user accessible slots filled in as well as the converted_id and gex slot filled
`single_species`	one species that the user wants to investigate across the mapped tissues
`single_gene`	one ensembl id that the user wants to investigate across the mapped tissues

Value

initializes a generic function for plotTissueGEx as preparation for defining the plotTissueGEx Method

Examples

```
Kidney_Genes <- CoSIAn(
    gene_set = c("ENSG00000008710", "ENSG00000118762", "ENSG00000152217"),
    i_species = "h_sapiens", input_id = "Ensembl_id", o_species = c(
        "d_melanogaster", "m_musculus",
        "h_sapiens", "d_rerio", "c_elegans", "r_norvegicus"
    ), output_ids = c("Ensembl_id", "Symbol"),
    mapping_tool = "annotationDBI", ortholog_database = "HomoloGene",
    map_tissues = "heart",
    map_species = c("m_musculus"), metric_type = "DS_Gene"
)
Kidney_gene_conversion <- CoSIA::getConversion(Kidney_Genes)
Kidney_gene_gex <- getGEx(Kidney_gene_conversion)
plotTissueGEx(Kidney_gene_gex, "m_musculus", "ENSG00000008710")
```

`plotTissueGEx,CoSIAn-method`
plotTissueGEx Method

Description

plotTissueGEx Method

Usage

```
## S4 method for signature 'CoSIAn'
plotTissueGEx(object, single_species, single_gene)
```

Arguments

`object`	CoSIAn object with all user accessible slots filled in as well as the converted_id and gex slot filled
`single_species`	one species that the user wants to investigate across the mapped tissues
`single_gene`	one ensembl id that the user wants to investigate across the mapped tissues

Value

plot object

Examples

```
Kidney_Genes <- CoSIAn(
    gene_set = c("ENSG00000008710", "ENSG00000118762", "ENSG00000152217"),
    i_species = "h_sapiens", input_id = "Ensembl_id", o_species = c(
        "d_melanogaster", "m_musculus",
        "h_sapiens", "d_rerio", "c_elegans", "r_norvegicus"
    ), output_ids = c("Ensembl_id", "Symbol"),
    mapping_tool = "annotationDBI", ortholog_database = "HomoloGene",
    map_tissues = "heart", map_species = c("m_musculus"),
    metric_type = "DS_Gene"
)
Kidney_gene_conversion <- CoSIA::getConversion(Kidney_Genes)
Kidney_gene_gex <- getGEx(Kidney_gene_conversion)
plotTissueGEx(Kidney_gene_gex, "m_musculus", "ENSG00000008710")
```

`viewCoSIAn` *viewCoSIAn Generics*

Description

viewCoSIAn Generics

Usage

```
viewCoSIAn(object, slot_name)
```

Arguments

`object`	CoSIAn object with all user accessible slots filled
`slot_name`	name of output slots

Value

initializes a generic function for viewCoSIAn as preparation for defining the viewCoSIAn Method

Examples

```
Kidney_Genes <- CoSIAn(
    gene_set = c("ENSG00000008710", "ENSG00000152217"),
    i_species = "h_sapiens", input_id = "Ensembl_id",
    o_species = c(
        "d_melanogaster"
    ),
    output_ids = c("Ensembl_id", "Symbol"), mapping_tool = "annotationDBI",
    ortholog_database = "HomoloGene", map_tissues = "heart",
    map_species = c("d_melanogaster"), metric_type = "DS_Gene"
)
viewCoSIAn(Kidney_Genes, "converted_id")
```

`viewCoSIAn,CoSIAn-method` *viewCoSIAn*

Description

viewCoSIAn

Usage

```
## S4 method for signature 'CoSIAn'
viewCoSIAn(object, slot_name)
```

Arguments

`object`	CoSIAn object with all user accessible slots filled
`slot_name`	name of output slots

Value

slots in CoSIAn object

Examples

```
Kidney_Genes <- CoSIAn(
    gene_set = c("ENSG00000008710", "ENSG00000152217"),
    i_species = "h_sapiens", input_id = "Ensembl_id",
    o_species = c(
        "d_melanogaster"
    ),
    output_ids = c("Ensembl_id", "Symbol"), mapping_tool = "annotationDBI",
    ortholog_database = "HomoloGene", map_tissues = "heart",
    map_species = c("d_melanogaster"), metric_type = "DS_Gene"
)
viewCoSIAn(Kidney_Genes, "converted_id")
```

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