Package ‘CoSIA’

November 13, 2023

Type   Package
Title  An Investigation Across Different Species and Tissues
Version 1.2.0

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.

License  MIT + file LICENSE
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), markdown (>= 2.20), testthat (>= 3.1.6), qpdf (>= 1.3.0)

biocViews  Software, BiologicalQuestion, GeneExpression, MultipleComparison, ThirdPartyClient, DataImport, GUI

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

URL https://www.lasseigne.org/

VignetteBuilder knitr
CoSIAn-class

### 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.

**Description**

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

**Usage**

```r
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)
getConversion, CoSIAn-method

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

```r
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")
)
Kidney_gene_conversion <- CoSIA::getConversion(Kidney_Genes)
```

---

getConversion, CoSIAn-method

getConversion Method

Description

getConversion Method

Usage

```r
## 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

```r
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)
```

---

**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**

```r
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**

```r
## 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**

```r
Kidney_Genes <- CoSIAn(
    gene_set = c("ENSG000000008710", "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**

```r
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("ENSG000000008710", "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)

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

getTissues

Examples

Kidney_Genes <- CoSIA::
  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)

tissue <- getTissues(c("m_musculus"))
plotCVGEx, CoSIAn-method

---

### plotCVGEx

**Description**

plotCVGEx Generic

**Usage**

```r
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**

```r
Kidney_Genes <- CoSIAn(
gene_set = c("ENSG0000008710", "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

**Description**

plotCVGEx Method

**Usage**

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

### 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

```r
Kidney_Genes <- CoSIAn(
  gene_set = c("ENSG0000008710", "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)
```

---

---

### 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**

```r
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)
```

---

**Description**

plotDSGEx Method

**Usage**

```r
## 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**

```r
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"
)
```
plotSpeciesGEx

Kidney_gene_conversion <- CoSIA::getConversion(Kidney_Genes)
Kidney_gene_metric <- getGExMetrics(Kidney_gene_conversion)
plotDSGEx(Kidney_gene_metric)

---

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", "ENSG000000118762", "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")
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

```r
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")
```
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")
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")
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")

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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