

Package ‘CoSIA’

September 22, 2026

Type Package

Title An Investigation Across Different Species and Tissues

Version 1.12.1

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 7.3.3

Suggests BiocStyle (>= 2.22.0), tidyverse (>= 1.3.1), knitr (>= 1.42), rmarkdown (>= 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

Config/testthat/edition 3**git_url** <https://git.bioconductor.org/packages/CoSIA>**git_branch** RELEASE_3_23**git_last_commit** e6987fd**git_last_commit_date** 2026-07-02**Repository** Bioconductor 3.23**Date/Publication** 2026-09-22

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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

<code>gene_set</code>	A singular gene or a list of genes.
<code>i_species</code>	The species corresponding to <code>gene_set</code> .
<code>input_id</code>	The type of id corresponding to <code>gene_set</code> .
<code>o_species</code>	The singular or list of species that the gene set is being converted to.
<code>output_ids</code>	The singular or list of id types that the gene set is being converted to.
<code>mapping_tool</code>	The mapping tool, BiomaRt or annotationDBI, being used to map the conversion between IDs.
<code>ortholog_database</code>	The ortholog database, HomoloGene or NCBIOrtho, being used to map the conversion between species.
<code>map_tissues</code>	A list of tissues being investigated
<code>map_species</code>	A list of species being investigated
<code>metric_type</code>	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	<i>getConversion Generic</i>
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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	<i>getConversion Method</i>
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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	<i>getGExMetrics Generic</i>
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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", "ENSG000000118762", "ENSG000000152217"),
  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	<i>getGExMetrics Method</i>
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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", "ENSG000000118762", "ENSG000000152217"),
  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", "ENSG000000118762", "ENSG000000152217"),
  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	<i>plotSpeciesGEx Generic</i>
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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	<i>plotTissueGEx Generic</i>
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Description

plotTissueGEx Generic

Usage

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

Arguments

object	CoSIA 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 <- CoSIA(
  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	
<pre>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")</pre>	
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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