

# Package ‘CoSIA’

April 17, 2025

**Type** Package

**Title** An Investigation Across Different Species and Tissues

**Version** 1.9.0

**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), 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/>

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|              |                               |
|--------------|-------------------------------|
| CoSIAn-class | <i>CoSIAn Class S4 Object</i> |
|--------------|-------------------------------|

---

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. |

|                   |                                                                                                   |
|-------------------|---------------------------------------------------------------------------------------------------|
| 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 | <i>getConversion Generic</i> |
|---------------|------------------------------|

---

### 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 | <i>getGEx Generic</i> |
|--------|-----------------------|

---

**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 | <i>getGEx Method</i> |
|-----------------------|----------------------|

---

**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**

CoSIA object with gex slot filled

**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_gex <- getGEx(Kidney_gene_conversion)
```

---

getGExMetrics

getGExMetrics Generic

---

**Description**

getGExMetrics Generic

**Usage**

```
getGExMetrics(object)
```

**Arguments**

object                      CoSIA 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 <- 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)
```

---

```
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**

|                      |                                                                                      |
|----------------------|--------------------------------------------------------------------------------------|
| <code>species</code> | 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**

|                     |                                                                                                           |
|---------------------|-----------------------------------------------------------------------------------------------------------|
| <code>object</code> | 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 | <i>plotTissueGEx Generic</i> |
|---------------|------------------------------|

---

**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("ENSG000000008710", "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_gex <- getGEx(Kidney_gene_conversion)
plotTissueGEx(Kidney_gene_gex, "m_musculus", "ENSG000000008710")
```

---

|                              |                             |
|------------------------------|-----------------------------|
| plotTissueGEx, CoSIAn-method | <i>plotTissueGEx Method</i> |
|------------------------------|-----------------------------|

---

**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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