

# Package ‘fourSynergy’

March 25, 2026

**Type** Package

**Title** Ensemble algorithm for 4C-seq data

**Version** 0.99.12

**Description** fourSynergy is an ensemble algorithm leveraging synergies among the existing 4C-seq algorithms r3C-seq, peakC, r4cker and fourSig. It uses a weighted voting approach to perform improved interaction calling. fourSynergy supports also differential interaction calling.

**License** LGPL-3

**Encoding** UTF-8

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**biocViews** Sequencing, Software, DifferentialPeakCalling

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## Contents

|                                 |           |
|---------------------------------|-----------|
| fourSynergy-package . . . . .   | 2         |
| checkConfig . . . . .           | 3         |
| consensusIa . . . . .           | 3         |
| createIa . . . . .              | 4         |
| createKaryoplot . . . . .       | 5         |
| differentialAnalysis . . . . .  | 5         |
| fourSynergy-accessors . . . . . | 6         |
| fourSynergy-class . . . . .     | 7         |
| fourSynergy-setters . . . . .   | 8         |
| plotBaseTracks . . . . .        | 8         |
| plotConsensusIa . . . . .       | 9         |
| plotConsensusTracks . . . . .   | 10        |
| plotDiffIa . . . . .            | 11        |
| plotIaIndividualTools . . . . . | 12        |
| plotpreTracks . . . . .         | 14        |
| plotRegions . . . . .           | 14        |
| plotTracks . . . . .            | 15        |
| readAndTag . . . . .            | 15        |
| readBedGraph . . . . .          | 16        |
| <b>Index</b>                    | <b>17</b> |

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|                     |                                                                       |
|---------------------|-----------------------------------------------------------------------|
| fourSynergy-package | <i>fourSynergy: Ensemble based interaction calling in 4C-seq data</i> |
|---------------------|-----------------------------------------------------------------------|

---

## Description

fourSynergy is an ensemble algorithm leveraging synergies among the existing 4C-seq algorithms r3C-seq, peakC, r4cker and fourSig. It uses a weighted voting approach to perform improved interaction calling. fourSynergy supports also differential interaction calling.

## Author(s)

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## See Also

Useful links:

- <https://github.com/sophiewind/fourSynergy>
- Report bugs at <https://github.com/sophiewind/fourSynergy/issues>

---

|             |                    |
|-------------|--------------------|
| checkConfig | <i>checkConfig</i> |
|-------------|--------------------|

---

**Description**

checkConfig

**Usage**

checkConfig(config)

**Arguments**

config                config file with path.

**Value**

TRUE if config is valid.

**Examples**

```
config <- system.file("extdata", "Datasets", "Demo", "info.yaml",
  package = "fourSynergy")
checkConfig(config)
```

---

|             |                    |
|-------------|--------------------|
| consensusIa | <i>consensusIa</i> |
|-------------|--------------------|

---

**Description**

This function performs an optimized weighted voting of 4C-seq tools.

**Usage**

consensusIa(ia, model = "F1")

**Arguments**

ia                    fourSynergy object with interactions from all base tools (peakC, r3c-seq, four-Sig, r4cker) and other relevant information.

model                Selected optimization model. Either 'F1' or 'AUPRC'.

**Value**

fourSynergy object with interactions from all base tools and weighted voting results.

## Examples

```
config <- system.file("extdata", "Datasets", "Demo", "info.yaml",
  package = "fourSynergy"
)
res_path <- system.file("extdata", "results", "Demo",
  package = "fourSynergy"
)
tracks <- system.file("extdata", "results", "Demo", "alignment",
  package = "fourSynergy"
)
sia <- createIa(res_path = res_path, config = config, tracks = tracks)
sia <- consensusIa(ia = sia, model = "AUPRC")
```

---

createIa

*createIa*

---

## Description

This function reads the interaction bed files created by the pipeline and transfers this information into an GrangesList.

## Usage

```
createIa(res_path = character(), config = list(), tracks = "")
```

## Arguments

|          |                                                                                                       |
|----------|-------------------------------------------------------------------------------------------------------|
| res_path | Path to results created by the pipeline. Typically stored in the results/[dataset]/nearbait_area.bed. |
| config   | Path of config file.                                                                                  |
| tracks   | Path to alignment files.                                                                              |

## Value

fourSynergy object with interactions from all base tools.

## Examples

```
config <- system.file("extdata", "Datasets", "Demo", "info.yaml",
  package = "fourSynergy"
)
res_path <- system.file("extdata", "results", "Demo",
  package = "fourSynergy"
)
tracks <- system.file("extdata", "results", "Demo", "alignment",
  package = "fourSynergy"
)
ia <- createIa(res_path = res_path, config = config, tracks = tracks)
```

---

|                 |                                              |
|-----------------|----------------------------------------------|
| createKaryoplot | <i>Internal function to create karyoplot</i> |
|-----------------|----------------------------------------------|

---

**Description**

Internal function to create karyoplot

**Usage**

```
createKaryoplot(ia, type = 1, cex = 1, cex.axis = 1, cex.lab = 1, cex.main = 1)
```

**Arguments**

|          |                                                                                                                             |
|----------|-----------------------------------------------------------------------------------------------------------------------------|
| ia       | fourSynergy object with interactions from all base tools (peakC, r3c-seq, four-Sig, r4cker) and other relevant information. |
| type     | Plottype.                                                                                                                   |
| cex      | character expansion                                                                                                         |
| cex.axis | character expansion axis                                                                                                    |
| cex.lab  | character expansion labels                                                                                                  |
| cex.main | character expansion main                                                                                                    |

**Value**

karyoplot base

---

|                      |                             |
|----------------------|-----------------------------|
| differentialAnalysis | <i>differentialAnalysis</i> |
|----------------------|-----------------------------|

---

**Description**

This function performs differential analysis to identify differential interacting regions using DESeq2.

**Usage**

```
differentialAnalysis(ia, fitType = "local")
```

**Arguments**

|         |                                                                                                                                                                           |
|---------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ia      | fourSynergy object with interactions from all base tools (peakC, r3c-seq, four-Sig, r4cker) and other relevant information.                                               |
| fitType | Parameter for DESeq2s estimateDispersions(). Should be either "parametric", "local", "mean", or "glmGamPoi" for the type of fitting of dispersions to the mean intensity. |

**Value**

sia object with GRanges of DESeq results in the diff slot.

**References**

<https://doi.org/10.1186/s13059-014-0550-8>

**Examples**

```
config <- system.file("extdata", "Datasets", "Demo", "info.yaml",
  package = "fourSynergy"
)
res_path <- system.file("extdata", "results", "Demo",
  package = "fourSynergy"
)
tracks <- system.file("extdata", "results", "Demo", "alignment",
  package = "fourSynergy"
)
sia <- createIa(res_path = res_path, config = config, tracks = tracks)
sia <- consensusIa(ia = sia, model = "AUPRC")
sia <- differentialAnalysis(ia = sia, fitType = "mean")
```

---

fourSynergy-accessors *fourSynergy* accessors

---

**Description**

Standard getter methods for [fourSynergy](#) object slots.

**Usage**

```
getMetadata(object)

getExpInteractions(object)

getCtrlInteractions(object)

getExpConsensus(object)

getCtrlConsensus(object)

getViewpoint(object)

getVirtualFragmentLibrary(object)

getTracks(object)

getDifferential(object)
```

getDDS(object)

### Arguments

object            A [fourSynergy](#) object

### Value

Various slots of the object (see individual methods)

### Functions

- getMetadata(): Get metadata
- getExpInteractions(): Get experimental interactions
- getCtrlInteractions(): Get control interactions
- getExpConsensus(): Get experimental consensus
- getCtrlConsensus(): Get control consensus
- getViewpoint(): Get viewpoint
- getVirtualFragmentLibrary(): Get virtual fragment library
- getTracks(): Get tracks
- getDifferential(): Get differential expression
- getDDS(): Get DESeq results

---

|                   |                          |
|-------------------|--------------------------|
| fourSynergy-class | <i>fourSynergy Class</i> |
|-------------------|--------------------------|

---

### Description

S4 class storing data collected from 4C-seq analyses.

### Slots

metadata   Experimental metadata from config file.  
expInteractions   Base tool interactions found in the experiment.  
ctrlInteractions   Base tool interactions found in the control.  
expConsensus   Consensus interactions found in the experiment.  
ctrlConsensus   Consensus interactions found in the control.  
vp   Viewpoint position.  
vfl   Virtual fragment library.  
tracks   Path to the alignment files.  
differential   Results of differential interaction calling (res).  
dds   Results of differential interaction calling (dds).

---

|                     |                            |
|---------------------|----------------------------|
| fourSynergy-setters | <i>fourSynergy setters</i> |
|---------------------|----------------------------|

---

**Description**

Standard setter methods for [fourSynergy](#) object slots.

**Usage**

```
setDifferential(object, value)

setDds(object, value)

setExpConsensus(object, value)

setctrlConsensus(object, value)
```

**Arguments**

|        |                                           |
|--------|-------------------------------------------|
| object | A <a href="#">fourSynergy</a> object      |
| value  | Replacement value for the respective slot |

**Value**

Updated fourSynergy object (invisibly)

**Functions**

- `setDifferential()`: Set `setDifferential` slot
- `setDds()`: Set `setDds` slot
- `setExpConsensus()`: Set `setExpConsensus` slot
- `setctrlConsensus()`: Set `setCtrlConsensus` slot

---

|                |                       |
|----------------|-----------------------|
| plotBaseTracks | <i>plotBaseTracks</i> |
|----------------|-----------------------|

---

**Description**

plotBaseTracks

**Usage**

```
plotBaseTracks(ia, highlight_regions = NULL, max_range = 3000)
```

**Arguments**

ia                    fourSynergy object with interactions from all base tools

highlight\_regions                    regions to highlight in the plot

max\_range            maximum plotting range

**Value**

Track-plots for all treatments with interactions from base tools

**Examples**

```
config <- system.file("extdata", "Datasets", "Demo", "info.yaml",
  package = "fourSynergy"
)
res_path <- system.file("extdata", "results", "Demo",
  package = "fourSynergy"
)
tracks <- system.file("extdata", "results", "Demo", "alignment",
  package = "fourSynergy"
)
sia <- createIa(res_path = res_path, config = config, tracks = tracks)
plotBaseTracks(sia)
```

---

|                 |                        |
|-----------------|------------------------|
| plotConsensusIa | <i>plotConsensusIa</i> |
|-----------------|------------------------|

---

**Description**

This function creates a karyotype plot displaying the interaction calls from the consensus approach.

**Usage**

```
plotConsensusIa(
  ia = GRangesList(),
  genes_of_interest = NULL,
  cex.chr = 1,
  cex.ideo = 0.6,
  cex.y.lab = 0.6,
  cex.y.track = 0.6,
  cex.vp = 1,
  cex.leg = 0.6,
  highlight_regions = NULL,
  plot_spider = FALSE,
  gene.name.cex = 1
)
```

**Arguments**

|                                |                                                                                                                             |
|--------------------------------|-----------------------------------------------------------------------------------------------------------------------------|
| <code>ia</code>                | fourSynergy object with interactions from all base tools (peakC, r3c-seq, four-Sig, r4cker) and other relevant information. |
| <code>genes_of_interest</code> | Vector with genes of interest. Set to <code>all</code> if you want to plot all genes in this area.                          |
| <code>cex.chr</code>           | character expansion of chromosome label.                                                                                    |
| <code>cex.ideo</code>          | character expansion base numbers of ideogram.                                                                               |
| <code>cex.y.lab</code>         | character expansion for y labels.                                                                                           |
| <code>cex.y.track</code>       | character expansion y axis track.                                                                                           |
| <code>cex.vp</code>            | character expansion viewpoint label.                                                                                        |
| <code>cex.leg</code>           | character expansion for legend.                                                                                             |
| <code>highlight_regions</code> | regions to highlight in the plot.                                                                                           |
| <code>plot_spider</code>       | plotting connections from VP to interactions.                                                                               |
| <code>gene.name.cex</code>     | character expansion for gene names.                                                                                         |

**Value**

karyoplot with calling results.

**Examples**

```

config <- system.file("extdata", "Datasets", "Demo", "info.yaml",
  package = "fourSynergy"
)
res_path <- system.file("extdata", "results", "Demo",
  package = "fourSynergy"
)
tracks <- system.file("extdata", "results", "Demo", "alignment",
  package = "fourSynergy"
)
sia <- createIa(res_path = res_path, config = config, tracks = tracks)
sia <- consensusIa(ia = sia, model = "AUPRC")
plotConsensusIa(ia = sia)

```

---

`plotConsensusTracks`     *plotConsensusTracks*

---

**Description**

`plotConsensusTracks`

**Usage**

```
plotConsensusTracks(ia, highlight_regions = NULL, max_range = 3000)
```

**Arguments**

ia                    fourSynergy object with interactions from all base tools  
highlight\_regions        regions to highlight in the plot  
max\_range            maximum plotting range

**Value**

Track-plots for all treatments with interactions from consensus tool

**Examples**

```
config <- system.file("extdata", "Datasets", "Demo", "info.yaml",
  package = "fourSynergy"
)
res_path <- system.file("extdata", "results", "Demo",
  package = "fourSynergy"
)
tracks <- system.file("extdata", "results", "Demo", "alignment",
  package = "fourSynergy"
)
sia <- createIa(res_path = res_path, config = config, tracks = tracks)
sia <- consensusIa(sia, model = "AUPRC")
plotConsensusTracks(sia)
```

---

plotDiffIa

*plotDiffIa*


---

**Description**

This function creates a karyoplot with the differential interactions calls.

**Usage**

```
plotDiffIa(
  ia,
  genes_of_interest = NULL,
  cex.chr = 1,
  cex.y.lab = 0.6,
  cex.ideo = 0.6,
  cex.y.track = 0.6,
  cex.vp = 1,
  cex.leg = 0.6,
  plot_spider = FALSE,
  highlight_regions = NULL,
  gene.name.cex = 1
)
```

**Arguments**

|                                |                                                                                                                            |
|--------------------------------|----------------------------------------------------------------------------------------------------------------------------|
| <code>ia</code>                | fourSynergy object with interactions from all base tools (peakC, r3c-seq, four-Sig, r4cker) and more relevant information. |
| <code>genes_of_interest</code> | Vector with genes of interest. Set to <code>all</code> if you want to plot all genes in this area.                         |
| <code>cex.chr</code>           | character expansion of chromosome label.                                                                                   |
| <code>cex.y.lab</code>         | character expansion for y labels.                                                                                          |
| <code>cex.ideo</code>          | character expansion base numbers of ideogram.                                                                              |
| <code>cex.y.track</code>       | character expansion y axis track.                                                                                          |
| <code>cex.vp</code>            | character expansion viewpoint label.                                                                                       |
| <code>cex.leg</code>           | character expansion for legend.                                                                                            |
| <code>plot_spider</code>       | plotting connections from VP to interactions                                                                               |
| <code>highlight_regions</code> | regions to highlight in the plot                                                                                           |
| <code>gene.name.cex</code>     | character expansion for gene names.                                                                                        |

**Value**

DESeq2 results of differential interaction calling.

**Examples**

```

config <- system.file("extdata", "Datasets", "Demo", "info.yaml",
  package = "fourSynergy"
)
res_path <- system.file("extdata", "results", "Demo",
  package = "fourSynergy"
)
tracks <- system.file("extdata", "results", "Demo", "alignment",
  package = "fourSynergy"
)
sia <- createIa(res_path = res_path, config = config, tracks = tracks)
sia <- consensusIa(ia = sia, model = "AUPRC")
sia <- differentialAnalysis(ia = sia, fitType = "mean")
plotDiffIa(ia = sia)

```

---

|                                    |                                                                                               |
|------------------------------------|-----------------------------------------------------------------------------------------------|
| <code>plotIaIndividualTools</code> | <i>This function creates a karyoplot with the interactions calls of the individual tools.</i> |
|------------------------------------|-----------------------------------------------------------------------------------------------|

---

**Description**

This function creates a karyoplot with the interactions calls of the individual tools.

**Usage**

```
plotIaIndividualTools(
  ia,
  genes_of_interest = NULL,
  cex.chr = 1,
  cex.ideo = 0.6,
  cex.y.track = 0.6,
  cex.y.lab = 0.6,
  cex.vp = 1,
  cex.leg = 0.6,
  highlight_regions = NULL,
  gene.name.cex = 1
)
```

**Arguments**

|                                |                                                                                                                             |
|--------------------------------|-----------------------------------------------------------------------------------------------------------------------------|
| <code>ia</code>                | fourSynergy object with interactions from all base tools (peakC, r3c-seq, four-Sig, r4cker) and other relevant information. |
| <code>genes_of_interest</code> | Vector with genes of interest. Set to all if you want to plot all genes in this area.                                       |
| <code>cex.chr</code>           | character expansion of chromosome label.                                                                                    |
| <code>cex.ideo</code>          | character expansion base numbers of ideogram.                                                                               |
| <code>cex.y.track</code>       | character expansion y axis track.                                                                                           |
| <code>cex.y.lab</code>         | character expansion y lab.                                                                                                  |
| <code>cex.vp</code>            | character expansion viewpoint label.                                                                                        |
| <code>cex.leg</code>           | character expansion for legend.                                                                                             |
| <code>highlight_regions</code> | regions to highlight in the plot                                                                                            |
| <code>gene.name.cex</code>     | character expansion for gene names.                                                                                         |

**Value**

karyoplot with calling results.

**Examples**

```
config <- system.file("extdata", "Datasets", "Demo", "info.yaml",
  package = "fourSynergy"
)
res_path <- system.file("extdata", "results", "Demo",
  package = "fourSynergy"
)
tracks <- system.file("extdata", "results", "Demo", "alignment",
  package = "fourSynergy"
)
sia <- createIa(res_path = res_path, config = config, tracks = tracks)
plotIaIndividualTools(ia = sia)
```

---

|               |                      |
|---------------|----------------------|
| plotpreTracks | <i>plotpreTracks</i> |
|---------------|----------------------|

---

**Description**

plotpreTracks

**Usage**

```
plotpreTracks(ia, highlight_regions = NULL)
```

**Arguments**

ia                      fourSynergy object with interactions from all base tools.  
highlight\_regions      regions to highlight in the plot.

**Value**

list with read counts and Granges of bedfiles

---

|             |                                                             |
|-------------|-------------------------------------------------------------|
| plotRegions | <i>Internal function to highlight regions in karyoplot.</i> |
|-------------|-------------------------------------------------------------|

---

**Description**

Internal function to highlight regions in karyoplot.

**Usage**

```
plotRegions(ia, kp, highlight_regions)
```

**Arguments**

ia                      fourSynergy object with interactions from all base tools (peakC, r3c-seq, four-Sig, r4cker) and other relevant information.  
kp                      karyoplot.  
highlight\_regions      regions to highlight in the plot.

**Value**

karyoplot base

---

|            |                                         |
|------------|-----------------------------------------|
| plotTracks | <i>Internal function to plot tracks</i> |
|------------|-----------------------------------------|

---

**Description**

Internal function to plot tracks

**Usage**

```
plotTracks(ia, kp, bgs, r0 = 0, r1 = 1, cex.vp = 1, cex.y.track = 0.6)
```

**Arguments**

|     |                                                                                                                             |
|-----|-----------------------------------------------------------------------------------------------------------------------------|
| ia  | fourSynergy object with interactions from all base tools (peakC, r3c-seq, four-Sig, r4cker) and other relevant information. |
| kp  | Kayroplot object.                                                                                                           |
| bgs | GrangesList of bedGraphs.                                                                                                   |
| r0  | r0 defines the vertical range of the data panel.                                                                            |
| r1  | r1 defines the vertical range of the data panel.                                                                            |

**Value**

karyoplot with tracks

---

|            |                   |
|------------|-------------------|
| readAndTag | <i>readAndTag</i> |
|------------|-------------------|

---

**Description**

Internal function to read base tools solutions in FourSynergy format.

**Usage**

```
readAndTag(file_path, tag, org)
```

**Arguments**

|           |                                                               |
|-----------|---------------------------------------------------------------|
| file_path | Path to the .bed files (results/[dataset]/nearbait_area.bed). |
| tag       | tool name.                                                    |
| org       | organism.                                                     |

**Value**

GRanges with interaction calls and tool name as mcol.

---

|              |                                            |
|--------------|--------------------------------------------|
| readBedGraph | <i>Internal function to read bedGraphs</i> |
|--------------|--------------------------------------------|

---

**Description**

Internal function to read bedGraphs

**Usage**

```
readBedGraph(ia)
```

**Arguments**

|    |                                                                                                                              |
|----|------------------------------------------------------------------------------------------------------------------------------|
| ia | fourSynergy object with interactions from all base tools. (peakC, r3c-seq, four-Sig, r4cker) and other relevant information. |
|----|------------------------------------------------------------------------------------------------------------------------------|

**Value**

GrangesList of bedGraph content

# Index

## \* internal

- createKaryoplot, [5](#)
- fourSynergy-accessors, [6](#)
- fourSynergy-setters, [8](#)
- plotpreTracks, [14](#)
- plotRegions, [14](#)
- plotTracks, [15](#)
- readAndTag, [15](#)
- readBedGraph, [16](#)

checkConfig, [3](#)  
consensusIa, [3](#)  
createIa, [4](#)  
createKaryoplot, [5](#)

differentialAnalysis, [5](#)

fourSynergy, [6–8](#)  
fourSynergy (fourSynergy-package), [2](#)  
fourSynergy-accessors, [6](#)  
fourSynergy-class, [7](#)  
fourSynergy-package, [2](#)  
fourSynergy-setters, [8](#)

getCtrlConsensus  
    (fourSynergy-accessors), [6](#)  
getCtrlInteractions  
    (fourSynergy-accessors), [6](#)  
getDDS (fourSynergy-accessors), [6](#)  
getDifferential  
    (fourSynergy-accessors), [6](#)  
getExpConsensus  
    (fourSynergy-accessors), [6](#)  
getExpInteractions  
    (fourSynergy-accessors), [6](#)  
getMetadata (fourSynergy-accessors), [6](#)  
getTracks (fourSynergy-accessors), [6](#)  
getViewpoint (fourSynergy-accessors), [6](#)  
getVirtualFragmentLibrary  
    (fourSynergy-accessors), [6](#)

plotBaseTracks, [8](#)  
plotConsensusIa, [9](#)  
plotConsensusTracks, [10](#)  
plotDiffIa, [11](#)  
plotIaIndividualTools, [12](#)  
plotpreTracks, [14](#)  
plotRegions, [14](#)  
plotTracks, [15](#)

readAndTag, [15](#)  
readBedGraph, [16](#)

setCtrlConsensus (fourSynergy-setters),  
    [8](#)  
setctrlConsensus (fourSynergy-setters),  
    [8](#)  
setDDS (fourSynergy-setters), [8](#)  
setDds (fourSynergy-setters), [8](#)  
setDifferential (fourSynergy-setters), [8](#)  
setExpConsensus (fourSynergy-setters), [8](#)