

# Package ‘fourSynergy’

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**Type** Package

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

**Version** 1.0.0

**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

**BugReports** <https://github.com/sophiewind/fourSynergy/issues>

**URL** <https://github.com/sophiewind/fourSynergy>

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fourSynergy-package    *fourSynergy: Ensemble based interaction calling in 4C-seq data*

---

## 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>

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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      *Internal function to create karyoplot*

---

### 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      *differentialAnalysis*

---

### 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        *fourSynergy Class*

---

### 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     *fourSynergy setters*

---

### 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     *plotBaseTracks*

---

### 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`      *plotConsensusIa*

---

**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)

```

---

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

---

**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**

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

**genes\_of\_interest** Vector with genes of interest. Set to all if you want to plot all genes in this area.

**cex.chr** character expansion of chromosome label.

**cex.ideo** character expansion base numbers of ideogram.

**cex.y.track** character expansion y axis track.

**cex.y.lab** character expansion y lab.

**cex.vp** character expansion viewpoint label.

**cex.leg** character expansion for legend.

**highlight\_regions** regions to highlight in the plot

**gene.name.cex** 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

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