# Package: fourSynergy (via r-universe)

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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, r.4cker 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

**Depends** R (>= 4.5.0), GenomicRanges

**Imports** magrittr, dplyr, ggplot2, tibble, org.Hs.eg.db, org.Mm.eg.db, reshape2, tidyr, methods, jsonlite, karyoploteR, TxDb.Mmusculus.UCSC.mm10.knownGene, TxDb.Hsapiens.UCSC.hg19.knownGene, bamsignals, DESeq2, GenomeInfoDb, graphics, stringr, yaml

**VignetteBuilder** knitr

**Suggests** testthat (>= 3.0.0), knitr, rmarkdown, BiocStyle

**biocViews** Sequencing, Software, DifferentialPeakCalling

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

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

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.3

**Config/pak/sysreqs** cmake make libbz2-dev libicu-dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

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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, r.4cker 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 *checkConfig*

## 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 *consensusIa*

## 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)
```

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, fourSig, 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-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).

## 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

| | |
|---|---|
| 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.lab | character expansion for y labels. |
| cex.y.track | character expansion y axis track. |

| | |
|---|---|
| cex.vp | character expansion viewpoint label. |
| cex.leg | character expansion for legend. |
| highlight_regions | regions to highlight in the plot. |
| plot_spider | plotting connections from VP to interactions. |
| 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)
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

| | |
|---|---|
| ia | fourSynergy object with interactions from all base tools (peakC, r3c-seq, fourSig, r4cker) and more 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.y.lab | character expansion for y labels. |
| cex.ideo | character expansion base numbers of ideogram. |

| | |
|---|---|
| cex.y.track | character expansion y axis track. |
| cex.vp | character expansion viewpoint label. |
| cex.leg | character expansion for legend. |
| plot_spider | plotting connections from VP to interactions |
| highlight_regions | regions to highlight in the plot |
| gene.name.cex | 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)
```

---

# plotIaIndiviualTools *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

```
plotIaIndiviualTools(
  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)
plotIaIndiviualTools(ia = sia)
```

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