

Package: fourSynergy (via r-universe)

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Type Package

Title Ensemble algorithm for 4C-seq data

Version 1.1.0

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.

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Depends R (>= 4.5.0), GenomicRanges

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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>

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

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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>
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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>
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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

<code>ia</code>	fourSynergy object with interactions from all base tools (peakC, r3c-seq, four-Sig, r4cker) and other relevant information.
<code>fitType</code>	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	<i>fourSynergy Class</i>
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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	<i>plotBaseTracks</i>
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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>
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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 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.lab</code>	character expansion for y labels.
<code>cex.y.track</code>	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

<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 all 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.

`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)

```

`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

<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)

```

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