Package '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, r.4cker 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 *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)
```

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 fourSynergy 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

ia	fourSynergy object with interactions from all base tools (peakC, r3c-seq, fourSig, 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, four-Sig, 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, fourSig, 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)
```

plotpreTracks *plotpreTracks*

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 *Internal function to highlight regions in karyoplot.*

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, fourSig, r4cker) and other relevant information.
kp	karyoplot.
highlight_regions	regions to highlight in the plot.

Value

karyoplot base

plotTracks *Internal function to plot tracks*

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 *readAndTag*

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` *Internal function to read bedGraphs*

Description

Internal function to read bedGraphs

Usage

```
readBedGraph(ia)
```

Arguments

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

Value

GrangesList of bedGraph content

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