

# Package ‘tracktables’

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**Type** Package

**Title** Build IGV tracks and HTML reports

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**Author** Tom Carroll, Sanjay Khadayate, Anne Pajon, Ziwei Liang

**Maintainer** Tom Carroll <tc.infomatics@gmail.com>

**Description** Methods to create complex IGV genome browser sessions and dynamic IGV reports in HTML pages.

**biocViews** Sequencing, ReportWriting

**VignetteBuilder** knitr

**License** GPL (>= 3)

**LazyLoad** yes

**Depends** R (>= 3.0.0)

**Imports** IRanges, GenomicRanges, XVector, Rsamtools, XML, tractor.base, stringr, RColorBrewer, methods

**Suggests** knitr, BiocStyle

**Collate** 'tracktablesFunctions.R'

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igvParam	<i>Parameters for displaying bigwigs, bams and intervals in IGV</i>
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## Description

Use `igvParam( object)` to create a parameter object to control IGV display invoked from `make-tracktable()` report or from `makeIGVSession()` XML files. Parameters for bigwig, bam and intervals files may be provided. See IGV manual for a full description of options.

## Usage

```
igvParam(bigwig.altColor = "darkgrey", bigwig.color = "darkgrey",
  bigwig.autoScale = "true", bigwig.displayMode = "COLLAPSED",
  bigwig.featureVisibilityWindow = -1, bigwig.fontSize = 10,
  bigwig.normalize = "false", bigwig.renderer = "BAR_CHART",
  bigwig.sortable = "true", bigwig.visible = "true",
  bigwig.windowFunction = "mean", bigwig.baseline = 0,
  bigwig.drawBaseline = "true", bigwig.flipAxis = "false",
  bigwig.maximum = 50, bigwig.minimum = 0, bigwig.type = "LINEAR",
  interval.altColor = "darkgrey", interval.color = "darkgrey",
  interval.autoScale = "true", interval.displayMode = "character",
  interval.featureVisibilityWindow = -1, interval.fontSize = 10,
  interval.height = 40, interval.normalize = "false",
  interval.renderer = "BASIC_FEATURE", interval.sortable = "true",
  interval.visible = "true", interval.windowFunction = "count",
  bam.altColor = "darkgrey", bam.color = "darkgrey",
  bam.autoScale = "true", bam.displayMode = "EXPANDED",
  bam.featureVisibilityWindow = -1, bam.fontSize = 10,
  bam.showSpliceJunctions = "false", bam.colorByTag = "",
  bam.colorOption = "UNEXPECTED_PAIR", bam.flagUnmappedPairs = "false",
  bam.groupByTag = "", bam.maxInsertSize = 1000, bam.minInsertSize = 50,
  bam.shadeBasesOption = "QUALITY", bam.shadeCenters = "true",
  bam.showAllBases = "false", bam.sortByTag = "")
```

```
igvParam(bigwig.altColor = "darkgrey", bigwig.color = "darkgrey",
  bigwig.autoScale = "true", bigwig.displayMode = "COLLAPSED",
  bigwig.featureVisibilityWindow = -1, bigwig.fontSize = 10,
  bigwig.normalize = "false", bigwig.renderer = "BAR_CHART",
  bigwig.sortable = "true", bigwig.visible = "true",
  bigwig.windowFunction = "mean", bigwig.baseline = 0,
  bigwig.drawBaseline = "true", bigwig.flipAxis = "false",
```

```

bigwig.maximum = 50, bigwig.minimum = 0, bigwig.type = "LINEAR",
interval.altColor = "darkgrey", interval.color = "darkgrey",
interval.autoScale = "true", interval.displayMode = "character",
interval.featureVisibilityWindow = -1, interval.fontSize = 10,
interval.height = 40, interval.normalize = "false",
interval.renderer = "BASIC_FEATURE", interval.sortable = "true",
interval.visible = "true", interval.windowFunction = "count",
bam.altColor = "darkgrey", bam.color = "darkgrey",
bam.autoScale = "true", bam.displayMode = "EXPANDED",
bam.featureVisibilityWindow = -1, bam.fontSize = 10,
bam.showSpliceJunctions = "false", bam.colorByTag = "",
bam.colorOption = "UNEXPECTED_PAIR", bam.flagUnmappedPairs = "false",
bam.groupByTag = "", bam.maxInsertSize = 1000, bam.minInsertSize = 50,
bam.shadeBasesOption = "QUALITY", bam.shadeCenters = "true",
bam.showAllBases = "false", bam.sortByTag = "")

```

## Arguments

- bigwig.altColor**  
A character vector of alternate colour for bigwigs displayed in IGV.
- bigwig.color**  
A character vector of main colour for bigwigs displayed in IGV.
- bigwig.displayMode**  
A character vector of display mode for bigwigs displayed in IGV.
- bigwig.featureVisibilityWindow**  
A numeric vector of feature visibility window for bigwigs displayed in IGV (Default -1).
- bigwig.fontSize**  
A numeric vector of font size for bigwigs displayed in IGV.
- bigwig.autoScale**  
A character vector ("true"/"false") to indicate whether data is autoscaled for bigwigs displayed in IGV (Default "true").
- bigwig.normalize**  
A character vector ("true"/"false") to indicate whether data is normalised for bigwigs displayed in IGV (Default "false").
- bigwig.renderer**  
A character vector of renderer for bigwigs displayed in IGV (Default "BAR\_CHART").
- bigwig.sortable**  
A character vector ("true"/"false") to indicate whether data is sortable for bigwigs displayed in IGV (Default "true").
- bigwig.visible**  
A character vector ("true"/"false") to indicate whether data is visible for bigwigs displayed in IGV (Default "true").
- bigwig.windowFunction**  
A character vector ("true"/"false") of window function for bigwigs displayed in IGV (Default "mean").
- bigwig.baseline**  
A numeric vector of baseline bigwigs displayed in IGV.

<code>bigwig.drawBaseline</code>	A character vector ("true"/"false") of whether to draw baseline for bigwigs displayed in IGV (Default "true").
<code>bigwig.flipAxis</code>	A character vector ("true"/"false") to indicate whether to flip axis for bigwigs displayed in IGV (Default "false").
<code>bigwig.maximum</code>	A numeric vector of maximum value to display for bigwigs displayed in IGV (Default 50).
<code>bigwig.minimum</code>	A numeric vector of minimum value to display for bigwigs displayed in IGV (Default 0).
<code>bigwig.type</code>	A character vector of display type for bigwigs displayed in IGV (Default "LINEAR").
<code>interval.altColor</code>	A character vector of alternate colour for intervals displayed in IGV.
<code>interval.color</code>	A character vector of main colour for intervals displayed in IGV.
<code>interval.autoScale</code>	A character vector ("true"/"false") to indicate whether data is autoscaled for intervals displayed in IGV (Default "false").
<code>interval.displayMode</code>	A character vector of display mode for intervals displayed in IGV (Default "COLLAPSED").
<code>interval.featureVisibilityWindow</code>	A numeric vector of feature visibility window for intervals displayed in IGV (Default -1).
<code>interval.fontSize</code>	A numeric vector of font size for intervals displayed in IGV.
<code>interval.height</code>	A numeric vector of height for intervals displayed in IGV.
<code>interval.normalize</code>	A character vector ("true"/"false") to indicate whether data is normalised for intervals displayed in IGV (Default "false").
<code>interval.renderer</code>	A character vector of renderer for intervals displayed in IGV (Default "BASIC_FEATURE").
<code>interval.sortable</code>	A character vector ("true"/"false") to indicate whether data is sortable for intervals displayed in IGV (Default "true").
<code>interval.visible</code>	A character vector ("true"/"false") to indicate whether data is visible for intervals displayed in IGV (Default "true").
<code>interval.windowFunction</code>	A character vector ("true"/"false") of window function for intervals displayed in IGV (Default "count").
<code>bam.altColor</code>	A character vector of alternate colour for bam files displayed in IGV.
<code>bam.color</code>	A character vector of main colour for bam files displayed in IGV.

bam.autoScale	A character vector ("true"/"false") to indicate whether data is autoscaled for bam files displayed in IGV (Default "false").
bam.displayMode	A character vector of display mode for bam files displayed in IGV (Default "EXPANDED").
bam.featureVisibilityWindow	A numeric vector of feature visibility window for bam files displayed in IGV (Default -1).
bam.fontSize	A numeric vector of font size for intervals displayed in IGV.
bam.showSpliceJunctions	A character vector ("true"/"false") to indicate whether to show splice junctions for bam files displayed in IGV (Default "false").
bam.colorByTag	A character vector to indicate whether to colour reads by Tags for Bam files (Default = "").
bam.colorOption	A character vector of option to highlight Tags for Bam files (Default = "UNEXPECTED_PAIR").
bam.flagUnmappedPairs	A character vector ("true"/"false") to indicate whether to flaf unmapped pairs for bam files displayed in IGV (Default "false").
bam.groupByTag	A character vector ("true"/"false") to indicate how to groups reads by Tag for bam files displayed in IGV (Default "").
bam.maxInsertSize	A numeric vector of maximum insert size to display for Bam files.
bam.minInsertSize	A numeric vector of minimum insert size to display for Bam files.
bam.shadeBasesOption	A character vector of option to shade bases for Bam files (Default "QUALITY").
bam.shadeCenters	A character vector ("true"/"false") to indicate whether to shade centres for bam files displayed in IGV (Default "false").
bam.showAllBases	A character vector ("true"/"false") to indicate to show all bases for bam files displayed in IGV (Default "false").
bam.sortByTag	A character vector ("true"/"false") to indicate how to sort reads by Tag for bam files displayed in IGV (Default "").

**Value**

An igvParam class object to use with maketracktable, MakeIGVSession and makeIGVSessionMXL

**Author(s)**

Thomas Carroll

**Examples**

```
## Simple initialisation of an IGVParam object
igvDisplayParams <- igvParam()

## More custom initialisation of an IGVParam object .
igvDisplayParams <- igvParam(bigwig.color="red",bigwig.autoScale = "false",
bigwig.minimum = 10,bigwig.maximum = 100)

# See full parameters and IGV online manual for more details on customisations

## Use igvParams with maketracktables function to customise bigwig display colour and data range.
fileLocations <- system.file("extdata",package="tracktables")

bigwigs <- dir(fileLocations,pattern="*.bw",full.names=TRUE)

intervals <- dir(fileLocations,pattern="*.bed",full.names=TRUE)

bigWigMat <- cbind(gsub("_Example.bw","",basename(bigwigs)),
bigwigs)

intervalsMat <- cbind(gsub("_Peaks.bed","",basename(intervals)),
intervals)

fileSheet <- merge(bigWigMat,intervalsMat,all=TRUE)

fileSheet <- as.matrix(cbind(fileSheet,NA))

colnames(fileSheet) <- c("SampleName","bigwig","interval","bam")

SampleSheet <- cbind(as.vector(fileSheet["SampleName"]),
c("EBF","H3K4me3","H3K9ac","RNAPol2"),
c("ProB","ProB","ProB","ProB"))

colnames(SampleSheet) <- c("SampleName","Antibody","Species")
MakeIGVSession(SampleSheet,fileSheet,
igvdirectory=getwd(),"Example","mm9",
igvParams=igvDisplayParams)
```

---

Intervals

*Example genomic intervals*


---

**Description**

This dataset contains peaks from an in-house EBF1 ChIP-seq

**Usage**

```
data(Intervals)
```

**Details**

- Intervals GRanges object containing EBF1 peaks

**Value**

A GRanges object with two rows

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makebedtable	<i>Make HTML pages for interval files or GRanges.</i>
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**Description**

Creates HTML pages for interval files or GRanges (Tracktables Interval Report).

**Usage**

```
makebedtable(grangesObject, name, basedirectory)
```

**Arguments**

grangesObject A GRanges object.  
name Character of the name for Interval HTML report.  
basedirectory Character of the directory to which HTML report is written.

**Value**

A character of file location for the Tracktables HTML Report

**Author(s)**

Thomas Carroll

**Examples**

```
data(Intervals)  
htmlpage <- makebedtable(Intervals, "EBF_PeaksTable.html", getwd())
```





```

c("ProB", "ProB", "ProB", "ProB"))

colNames(SampleSheet) <- c("SampleName", "Antibody", "Species")
MakeIGVSampleMetadata(SampleSheet, fileSheet, igvdirectory=getwd())

```

---

MakeIGVSession

*Make IGV session XML and sample information file*


---

### Description

#' Creates IGV session XML and sample information file from a Samplesheet of metadata and FileSheet of file locations.

### Usage

```

MakeIGVSession(SampleSheet, fileSheet, igvdirectory, XMLname, genomeName,
  locusName = "All", colourBy = NULL, igvParams = igvParam())

```

### Arguments

SampleSheet	A data.frame object with metadata information for samples. First column must contain unique sample ids.
fileSheet	A data.frame of file locations. First column must contain the unique sample ids.
igvdirectory	A character of the directory to which sample metadata file is written.
XMLname	A character of the name for IGV session xml
genomeName	A character of genome for IGV (See IGV user guide for details)
locusName	A character of locus to display in igv on loading (See IGV user guide for details)
colourBy	Character defining which sample metadata to be used for colouring bigwig files
igvParams	An object of class igvParam containing display parameters for IGV. When providing a list, this list must be same length as number of samples and each element have two numeric values corresponding to minimum and maximum value to be used in setting data range. Currently only "autoscale" or a list of minimum and maximum values are accepted.

### Value

A character of file location for the IGV session XML

### Author(s)

Thomas Carroll

**Examples**

```

fileLocations <- system.file("extdata",package="tracktables")

bigwigs <- dir(fileLocations,pattern="*.bw",full.names=TRUE)

intervals <- dir(fileLocations,pattern="*.bed",full.names=TRUE)

bigWigMat <- cbind(gsub("_Example.bw","",basename(bigwigs)),
                  bigwigs)

intervalsMat <- cbind(gsub("_Peaks.bed","",basename(intervals)),
                    intervals)

fileSheet <- merge(bigWigMat,intervalsMat,all=TRUE)

fileSheet <- as.matrix(cbind(fileSheet,NA))

colnames(fileSheet) <- c("SampleName","bigwig","interval","bam")

SampleSheet <- cbind(as.vector(fileSheet[, "SampleName"]),
                    c("EBF","H3K4me3","H3K9ac","RNAPol2"),
                    c("ProB","ProB","ProB","ProB"))

colnames(SampleSheet) <- c("SampleName","Antibody","Species")
MakeIGVSession(SampleSheet,fileSheet,igvdirectory=getwd(),"Example","mm9")

```

---

 MakeIGVSessionXML

*Make IGV session XML*


---

**Description**

Creates session XML for IGV from a FileSheet of file locations.

**Usage**

```

MakeIGVSessionXML(fileSheet, igvdirectory, XMLname, genomeName,
                  locusName = "All", colourBy = NULL, igvParams = igvParam())

```

**Arguments**

fileSheet	A data.frame of file locations. First column must contain the unique sample ids.
igvdirectory	A character of the directory to which IGV XML session is written.
XMLname	A character of the name for IGV session xml
genomeName	A character of genome for IGV (See IGV user guide for details)
locusName	A character of locus to display in igv on loading (See IGV user guide for details)
colourBy	Character vector of RGB colours to use for colouring displayed BigWigs

`igvParams` An object of class `igvParam` containing display parameters for IGV. When providing a list, this list must be same length as number of samples and each element have two numeric values corresponding to minimum and maximum value to be used in setting data range. Currently only "autoscale" or a list of minimum and maximum values are accepted.

**Value**

A character of file location for the IGV session XML

**Author(s)**

Thomas Carroll

**Examples**

```
fileLocations <- system.file("extdata",package="tracktables")
bigwigs <- dir(fileLocations,pattern="*.bw",full.names=TRUE)
intervals <- dir(fileLocations,pattern="*.bed",full.names=TRUE)
bigWigMat <- cbind(gsub("_Example.bw","",basename(bigwigs)),
                  bigwigs)
intervalsMat <- cbind(gsub("_Peaks.bed","",basename(intervals)),
                    intervals)
fileSheet <- merge(bigWigMat,intervalsMat,all=TRUE)
fileSheet <- as.matrix(cbind(fileSheet,NA))
colnames(fileSheet) <- c("SampleName","bigwig","interval","bam")
MakeIGVSessionXML(fileSheet,igvdirectory=getwd(),"Example","mm9")
```

---

`maketracktable`

*Make HTML pages for IGV sessions (Tracktables Experiment Report)*

---

**Description**

Creates HTML table of sample metadata and all required files for interacting with IGV.

**Usage**

```
maketracktable(fileSheet, SampleSheet, filename, basedirectory, genome,
               colourBy = NULL, igvParams = igvParam())
```

**Arguments**

fileSheet	A data frame containing sample file locations (e.g. BigWig locations).
SampleSheet	A data frame containing sample metadata
filename	Character of name for tracktables HTML report. (.html prefix is added automatically)
basedirectory	Character of directory for tracktables HTML report, IGV sessions and any interval files
genome	Character of genome for IGV (See IGV user guide for details)
colourBy	Character defining which sample metadata to be used for colouring bigwig files
igvParams	An object of class igvParam containing display parameters for IGV. When providing a list, this list must be same length as number of samples and each element have two numeric values corresponding to minimum and maximum value to be used in setting data range. Currently only "autoscale" or a list of minimum and maximum values are accepted.

**Value**

An object containing XML document (HTMLInternalDocument,XMLInternalDocument,XMLAbstractDocument)

**Author(s)**

Thomas Carroll

**Examples**

```
fileLocations <- system.file("extdata",package="tracktables")

bigwigs <- dir(fileLocations,pattern="*.bw",full.names=TRUE)

intervals <- dir(fileLocations,pattern="*.bed",full.names=TRUE)

bigWigMat <- cbind(gsub("_Example.bw","",basename(bigwigs)),
                  bigwigs)

intervalsMat <- cbind(gsub("_Peaks.bed","",basename(intervals)),
                    intervals)

fileSheet <- merge(bigWigMat,intervalsMat,all=TRUE)

fileSheet <- as.matrix(cbind(fileSheet,NA))

colnames(fileSheet) <- c("SampleName","bigwig","interval","bam")

SampleSheet <- cbind(as.vector(fileSheet[, "SampleName"]),
                    c("EBF","H3K4me3","H3K9ac","RNAPol2"),
                    c("ProB","ProB","ProB","ProB"))

colnames(SampleSheet) <- c("SampleName","Antibody","Species")
HTMLreport <- maketracktable(fileSheet,SampleSheet,
```

```
"IGV_Example.html",  
basedirectory=getwd(),  
"mm9")
```

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