# Package 'locuszoomr'

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**Title** Gene Locus Plot with Gene Annotations

**Version** 0.3.7

**BugReports** https://github.com/myles-lewis/locuszoomr/issues

**URL** https://github.com/myles-lewis/locuszoomr

**Description** Publication-ready regional gene locus plots similar to those produced by the web interface 'LocusZoom' <https://my.locuszoom.org>, but running locally in R. Genetic or genomic data with gene annotation tracks are plotted via R base graphics, 'ggplot2' or 'plotly', allowing flexibility and easy customisation including laying out multiple locus plots on the same page. It uses the 'LDlink' API <https://ldlink.nih.gov/?tab=apiaccess> to query linkage disequilibrium data from the 1000 Genomes Project and can overlay this on plots <doi:10.1093/bioadv/vbaf006>.

**Language** en-gb

**License** GPL (>= 3)

**Encoding** UTF-8

**Depends** R (>= 3.5)

**Imports** AnnotationFilter, BiocGenerics, cowplot, dplyr, ensembldb, GenomeInfoDb, GenomicRanges, gggrid, ggplot2, ggrepel, graphics, grDevices, grid, IRanges, LDlinkR, memoise, plotly, rlang, rtracklayer, zoo

**RoxygenNote** 7.3.2

**Suggests** AnnotationHub, EnsDb.Hsapiens.v75, knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** CRAN

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# Contents



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`eqtl_plot` *Locus eQTL plot*

---

## Description

Produces a plot of eQTL data embedded in a 'locus' class object. Intended for use with `set_layers()`.

## Usage

```
eqtl_plot(
  loc,
  tissue = "Whole Blood",
  eqtl_gene = loc$gene,
  scheme = "RdYlBu",
  col = NA,
  pcutoff = NULL,
  xlab = NULL,
  ylab = expression("-log"[10] ~ "P"),
  cex.axis = 0.9,
  xticks = TRUE,
  border = FALSE,
```

```
  add = FALSE,
  align = TRUE,
  legend_pos = "topright",
  ...
)
```

## Arguments

| | |
|---|---|
| loc | Object of class 'locus' to use for plot. See locus. |
| tissue | GTex tissue in which eQTL has been measured |
| eqtl_gene | Gene showing eQTL effect |
| scheme | Character string specifying palette for effect size showing up/downregulation eQTL using grDevices::hcl.colors. Alternatively a vector of 6 colours. |
| col | Outline point colour. NA for no outlines. |
| pcutoff | Cut-off for p value significance. Defaults to p = 5e-08. Set to NULL to disable. |
| xlab | x axis title. |
| ylab | y axis title. |
| cex.axis | Specifies font size for axis numbering. |
| xticks | Logical whether x axis numbers and axis title are plotted. |
| border | Logical whether a bounding box is plotted around upper and lower plots. |
| add | Logical whether to add points to an existing plot or generate a new plot. |
| align | Logical whether set par() to align the plot. |
| legend_pos | Character value specifying legend position. See legend(). |
| ... | Other arguments passed to plot() for the scatter plot. |

## Value

No return value. Produces a scatter plot using base graphics.

## See Also

locus() set_layers() scatter_plot()

---

genetracks *Plot gene tracks*

---

## Description

Plot gene annotation tracks from ensembldb data.

## Usage

```
genetracks(
  locus,
  filter_gene_name = NULL,
  filter_gene_biotype = NULL,
  border = FALSE,
  cex.axis = 0.9,
  cex.lab = 1,
  cex.text = 0.7,
  gene_col = ifelse(showExons, "blue4", "skyblue"),
  exon_col = "blue4",
  exon_border = "blue4",
  showExons = TRUE,
  maxrows = NULL,
  text_pos = "top",
  italics = FALSE,
  xticks = TRUE,
  xlab = NULL,
  highlight = NULL,
  highlight_col = "red",
  blanks = c("fill", "hide"),
  showRecomb = TRUE,
  align = TRUE
)
```

## Arguments

| | |
|---|---|
| locus | Object of class 'locus' generated by `locus()`. |
| filter_gene_name | Vector of gene names to display. |
| filter_gene_biotype | Vector of gene biotypes to be filtered. Use `ensembldb::listGenebiotypes()` to display possible biotypes. For example, `ensembldb::listGenebiotypes(EnsDb.Hsapiens.v75)` |
| border | Logical whether a bounding box is plotted. |
| cex.axis | Specifies font size for axis numbering. |
| cex.lab | Specifies font size for axis titles. |
| cex.text | Font size for gene text. |
| gene_col | Colour for gene lines. |
| exon_col | Fill colour for exons. |
| exon_border | Border line colour outlining exons (or genes if `showExons` is `FALSE`). Set to `NA` for no border. |
| showExons | Logical whether to show exons or simply show whole gene as a rectangle. If `showExons = FALSE` colours are specified by `exon_border` for rectangle border and `gene_col` for the fill colour. |
| maxrows | Specifies maximum number of rows to display in gene annotation panel. |

| | |
|---|---|
| text_pos | Character value of either 'top' or 'left' specifying placement of gene name labels. |
| italics | Logical whether gene text is in italics. |
| xticks | Logical whether x axis ticks and numbers are plotted. |
| xlab | Title for x axis. Defaults to chromosome seqname specified in locus. |
| highlight | Vector of genes to highlight. |
| highlight_col | Single colour or vector of colours for highlighted genes. |
| blanks | Controls handling of genes with blank names: "fill" replaces blank gene symbols with ensembl gene ids. "hide" hides genes which are missing gene symbols. |
| showRecomb | Logical controls alignment of right margin if recombination data present. |
| align | Logical whether to set par() to align the plot. |

## Details

This function is called by locus_plot(). It can be used to plot the gene annotation tracks on their own. It uses base graphics, so layout() can be used to position adjacent plots above or below.

gene_col, exon_col and exon_border set colours for all genes, while highlight and highlight_col can optionally be used together to highlight specific genes of interest. For full control over every single gene, users can add columns gene_col, exon_col and exon_border to the TX object within the 'locus' object. Columns added to TX override their equivalent arguments.

## Value

No return value.

## Examples

```
if(require(EnsDb.Hsapiens.v75)) {
data(SLE_gwas_sub)
loc <- locus(SLE_gwas_sub, gene = 'UBE2L3', flank = 1e5,
             ens_db = "EnsDb.Hsapiens.v75")
genetracks(loc)

## Limit the number of tracks
genetracks(loc, maxrows = 4)

## Filter by gene biotype
genetracks(loc, filter_gene_biotype = 'protein_coding')

## Customise colours
genetracks(loc, gene_col = 'grey', exon_col = 'orange',
           exon_border = 'darkgrey')
}
```

genetracks_grob *Create gene tracks grob*

## Description

Plot gene annotation tracks from ensembldb data using the grid package to create a grob.

## Usage

```
genetracks_grob(
  locus,
  filter_gene_name = NULL,
  filter_gene_biotype = NULL,
  border = FALSE,
  cex.text = 0.7,
  gene_col = ifelse(showExons, "blue4", "skyblue"),
  exon_col = "blue4",
  exon_border = "blue4",
  showExons = TRUE,
  maxrows = NULL,
  text_pos = "top",
  italics = FALSE,
  highlight = NULL,
  highlight_col = "red",
  blanks = c("fill", "hide")
)
```

## Arguments

| | |
|---|---|
| locus | Object of class 'locus' generated by locus(). |
| filter_gene_name | Vector of gene names to display. |
| filter_gene_biotype | Vector of gene biotypes to be filtered. Use ensembldb::listGenebiotypes() to display possible biotypes. For example, ensembldb::listGenebiotypes(EnsDb.Hsapiens.v75) |
| border | Logical whether a bounding box is plotted. |
| cex.text | Font size for gene text. |
| gene_col | Colour for gene lines. |
| exon_col | Fill colour for exons. |
| exon_border | Border line colour outlining exons (or genes if showExons is FALSE). Set to NA for no border. |
| showExons | Logical whether to show exons or simply show whole gene as a rectangle. If showExons = FALSE colours are specified by exon_border for rectangle border and gene_col for the fill colour. |

| | |
|---|---|
| maxrows | Specifies maximum number of rows to display in gene annotation panel. |
| text_pos | Character value of either 'top' or 'left' specifying placement of gene name labels. |
| italics | Logical whether gene text is in italics. |
| highlight | Vector of genes to highlight. |
| highlight_col | Single colour or vector of colours for highlighted genes. |
| blanks | Controls handling of genes with blank names: "fill" replaces blank gene symbols with ensembl gene ids. "hide" hides genes which are missing gene symbols. |

## Details

This function is called by gg_genetracks(). It can be used to generate a grob of the gene annotation tracks on their own.

## Value

A grob object.

## Examples

```
if(require(EnsDb.Hsapiens.v75)) {
data(SLE_gwas_sub)
loc <- locus(SLE_gwas_sub, gene = 'IRF5', flank = c(7e4, 2e5), LD = "r2",
             ens_db = "EnsDb.Hsapiens.v75")
g <- genetracks_grob(loc)
grid::grid.newpage()
grid::grid.draw(g)
}
```

---

# genetrack_ly *Gene tracks using 'plotly'*

---

## Description

Plot gene annotation tracks from ensembldb data using plotly.

## Usage

```
genetrack_ly(
  locus,
  filter_gene_name = NULL,
  filter_gene_biotype = NULL,
  cex.text = 0.7,
  italics = FALSE,
  gene_col = ifelse(showExons, "blue4", "skyblue"),
  exon_col = "blue4",
```

```
  exon_border = "blue4",
  showExons = TRUE,
  maxrows = 8,
  width = 600,
  xlab = NULL,
  blanks = c("fill", "hide", "show"),
  height = NULL,
  plot = TRUE
)
```

## Arguments

| | |
|---|---|
| locus | Object of class 'locus' generated by locus(). |
| filter_gene_name | Vector of gene names to display. |
| filter_gene_biotype | Vector of gene biotypes to be filtered. Use ensembldb::listGenebiotypes() to display possible biotypes. For example, ensembldb::listGenebiotypes(EnsDb.Hsapiens.v75) |
| cex.text | Font size for gene text. |
| italics | Logical whether gene text is in italics. |
| gene_col | Colour for gene lines. |
| exon_col | Fill colour for exons. |
| exon_border | Border line colour outlining exons (or genes if showExons is FALSE). Set to NA for no border. |
| showExons | Logical whether to show exons or simply show whole gene as a rectangle. If showExons = FALSE colours are specified by exon_border for rectangle border and gene_col for the fill colour. |
| maxrows | Specifies maximum number of rows to display in gene annotation panel. |
| width | Width of plotly plot in pixels which is purely used to prevent overlapping text for gene names. |
| xlab | Title for x axis. Defaults to chromosome seqname specified in locus. |
| blanks | Controls handling of genes with blank names: "fill" replaces blank gene symbols with ensembl gene ids. "hide" completely hides genes which are missing gene symbols. "show" shows gene lines but no label (hovertext is still available). |
| height | Height in pixels (optional, defaults to automatic sizing). |
| plot | Logical whether to produce plotly object or return plot coordinates. |

## Details

This function can used to plot gene annotation tracks on their own.

## Value

Either a 'plotly' plotting object showing gene tracks, or if plot = FALSE a list containing TX, a dataframe of coordinates for gene transcripts, and EX, a dataframe of coordinates for exons.

## Examples

```
if(require(EnsDb.Hsapiens.v75)) {
data(SLE_gwas_sub)
loc <- locus(SLE_gwas_sub, gene = 'UBE2L3', flank = 1e5,
             ens_db = "EnsDb.Hsapiens.v75")
genetrack_ly(loc)
}
```

---

gg_addgenes *Add gene tracks to a ggplot2 plot*

---

## Description

Adds gene tracks to an existing ggplot2 plot.

## Usage

```
gg_addgenes(p, loc, heights = c(3, 2), ...)
```

## Arguments

| | |
|---|---|
| p | ggplot2 plot object. This can be generated by gg_scatter() and then modified. |
| loc | Object of class 'locus' to use for plot. See locus(). |
| heights | Vector specifying ratio of heights of upper plot and lower gene track. |
| ... | Additional arguments passed to gg_genetracks() to control colours of gene tracks etc. |

## Value

A ggplot2 plotting object.

## See Also

gg_scatter() gg_genetracks()

## Examples

```
if(require(EnsDb.Hsapiens.v75)) {
data(SLE_gwas_sub)
loc <- locus(SLE_gwas_sub, gene = 'IRF5', flank = c(7e4, 2e5), LD = "r2",
             ens_db = "EnsDb.Hsapiens.v75")
p <- gg_scatter(loc)
gg_addgenes(p, loc)
}
```

gg_genetracks *Plot gene tracks*

## Description

Plot gene annotation tracks from ensembldb data using ggplot2 and grid.

## Usage

```
gg_genetracks(
  loc,
  filter_gene_name = NULL,
  filter_gene_biotype = NULL,
  border = FALSE,
  cex.axis = 1,
  cex.lab = 1,
  cex.text = 0.7,
  gene_col = ifelse(showExons, "blue4", "skyblue"),
  exon_col = "blue4",
  exon_border = "blue4",
  showExons = TRUE,
  maxrows = NULL,
  text_pos = "top",
  italics = FALSE,
  xticks = TRUE,
  xlab = NULL,
  highlight = NULL,
  highlight_col = "red",
  blanks = c("fill", "hide")
)
```

## Arguments

| | |
|---|---|
| loc | Object of class 'locus' generated by locus(). |
| filter_gene_name | Vector of gene names to display. |
| filter_gene_biotype | Vector of gene biotypes to be filtered. Use ensembldb::listGenebiotypes() to display possible biotypes. For example, ensembldb::listGenebiotypes(EnsDb.Hsapiens.v75) |
| border | Logical whether a bounding box is plotted. |
| cex.axis | Specifies font size for axis numbering. |
| cex.lab | Specifies font size for axis titles. |
| cex.text | Font size for gene text. |
| gene_col | Colour for gene lines. |
| exon_col | Fill colour for exons. |

| | |
|---|---|
| exon_border | Border line colour outlining exons (or genes if showExons is FALSE). Set to NA for no border. |
| showExons | Logical whether to show exons or simply show whole gene as a rectangle. If showExons = FALSE colours are specified by exon_border for rectangle border and gene_col for the fill colour. |
| maxrows | Specifies maximum number of rows to display in gene annotation panel. |
| text_pos | Character value of either 'top' or 'left' specifying placement of gene name labels. |
| italics | Logical whether gene text is in italics. |
| xticks | Logical whether x axis ticks and numbers are plotted. |
| xlab | Title for x axis. Defaults to chromosome seqname specified in locus. |
| highlight | Vector of genes to highlight. |
| highlight_col | Single colour or vector of colours for highlighted genes. |
| blanks | Controls handling of genes with blank names: "fill" replaces blank gene symbols with ensembl gene ids. "hide" hides genes which are missing gene symbols. |

## Details

This function is called by locus_ggplot(), and in turn it calls genetracks_grob(). It can be used to plot the gene annotation tracks on their own as a ggplot2 object.

gene_col, exon_col and exon_border set colours for all genes, while highlight and highlight_col can optionally be used together to highlight specific genes of interest. For full control over every single gene, users can add columns gene_col, exon_col and exon_border to the TX object within the 'locus' object. Columns added to TX override their equivalent arguments.

## Value

A ggplot2 object.

## See Also

locus_ggplot() genetracks_grob()

## Examples

```
if(require(EnsDb.Hsapiens.v75)) {
data(SLE_gwas_sub)
loc <- locus(SLE_gwas_sub, gene = 'IRF5', flank = c(7e4, 2e5), LD = "r2",
             ens_db = "EnsDb.Hsapiens.v75")
gg_genetracks(loc)
}
```

gg_scatter *Locus scatter plot using ggplot2*

## Description

Produces a scatter plot from a 'locus' class object (without gene tracks).

## Usage

```
gg_scatter(
  loc,
  index_snp = loc$index_snp,
  pcutoff = 5e-08,
  scheme = c("grey", "dodgerblue", "red"),
  size = 2,
  cex.axis = 1,
  cex.lab = 1,
  xlab = NULL,
  ylab = NULL,
  ylim = NULL,
  ylim2 = c(0, 100),
  yzero = (loc$yvar == "logP"),
  xticks = TRUE,
  border = FALSE,
  showLD = TRUE,
 LD_scheme = c("grey", "royalblue", "cyan2", "green3", "orange", "red", "purple"),
  recomb_col = "blue",
  recomb_offset = 0,
  legend_pos = "topleft",
  labels = NULL,
  eqtl_gene = NULL,
  beta = NULL,
  shape = NULL,
  shape_values = c(21, 24, 25),
  ...
)
```

## Arguments

| | |
|---|---|
| loc | Object of class 'locus' to use for plot. See locus. |
| index_snp | Specifies index SNP to be shown in a different colour and symbol. Defaults to the SNP with the lowest p-value. Set to NULL to not show this. |
| pcutoff | Cut-off for p value significance. Defaults to p = 5e-08. Set to NULL to disable. |
| scheme | Vector of 3 colours if LD is not shown: 1st = normal points, 2nd = colour for significant points, 3rd = index SNP. |
| size | Specifies size for points. |

| | |
|---|---|
| cex.axis | Specifies font size for axis numbering. |
| cex.lab | Specifies font size for axis titles. |
| xlab | x axis title. |
| ylab | y axis title. |
| ylim | y axis limits (y1, y2). |
| ylim2 | Secondary y axis limits for recombination line. |
| yzero | Logical whether to force y axis limit to include y=0. |
| xticks | Logical whether x axis numbers and axis title are plotted. |
| border | Logical whether a bounding box is plotted around the plot. |
| showLD | Logical whether to show LD with colours |
| LD_scheme | Vector of colours for plotting LD. The first colour is for SNPs which lack LD information. The next 5 colours are for r2 or D' LD results ranging from 0 to 1 in intervals of 0.2. The final colour is for the index SNP. |
| recomb_col | Colour for recombination rate line if recombination rate data is present. Set to NA to hide the line. See link_recomb() to add recombination rate data. |
| recomb_offset | Offset from 0-1 which shifts the scatter plot up and recombination line plot down. Recommended value 0.1. |
| legend_pos | Position of legend. Set to NULL to hide legend. |
| labels | Character vector of SNP or genomic feature IDs to label. The value "index" selects the highest point or index SNP as defined when locus() is called. Set to NULL to remove all labels. |
| eqtl_gene | Optional column name in loc$data for colouring eQTL genes. |
| beta | Optional column name for beta coefficient to display upward triangles for positive beta and downward triangles for negative beta (significant SNPs only). |
| shape | Optional column name in loc$data for controlling shapes. beta and shape cannot both be set. This column is expected to be a factor. |
| shape_values | Vector of shape values which match levels of the column specified by shape. This vector is passed to ggplot2::scale_shape_manual() as the argument values. See points() for a list of shapes and the numbers they map to. |
| ... | Optional arguments passed to geom_text_repel() to configure label drawing. |

## Details

If recombination rate data is included in the locus object following a call to link_recomb(), this is plotted as an additional line with a secondary y axis. In the base graphics version the line is placed under the scatter points, but this is not possible with ggplot2 as the secondary y axis data must be plotted on top of the primary scatter point data.

## Value

Returns a ggplot2 plot.

## See Also

locus() gg_addgenes()

## Examples

```
if(require(EnsDb.Hsapiens.v75)) {
data(SLE_gwas_sub)
loc <- locus(SLE_gwas_sub, gene = 'IRF5', flank = c(7e4, 2e5), LD = "r2",
             ens_db = "EnsDb.Hsapiens.v75")
gg_scatter(loc)
}
```

---

# line_plot *Locus line plot*

---

## Description

Produces a line plot from a 'locus' class object. Intended for use with set_layers().

## Usage

```
line_plot(
  loc,
  pcutoff = 5e-08,
  xlab = NULL,
  ylab = expression("-log"[10] ~ "P"),
  cex.axis = 1,
  xticks = FALSE,
  border = FALSE,
  align = TRUE,
  ...
)
```

## Arguments

| | |
|---|---|
| loc | Object of class 'locus' to use for plot. See locus. |
| pcutoff | Cut-off for p value significance. Defaults to p = 5e-08. Set to NULL to disable. |
| xlab | x axis title. |
| ylab | y axis title. |
| cex.axis | Specifies font size for axis numbering. |
| xticks | Logical whether x axis numbers and axis title are plotted. |
| border | Logical whether a bounding box is plotted around upper and lower plots. |
| align | Logical whether set par() to align the plot. |
| ... | Other arguments passed to plot() for the scatter plot. |

### Value

No return value. Produces a scatter plot using base graphics.

### See Also

`locus()` `set_layers()` `scatter_plot()`

---

`link_eqtl` *Obtain GTEx eQTL data via LDlinkR*

---

### Description

Adds eQTL (expression quantitative trait loci) information from GTEx (https://gtexportal.org/) to a 'locus' class object. It queries LDlink (https://ldlink.nci.nih.gov/) via the `LDlinkR` package to retrieve GTEx eQTL information on a reference SNP.

### Usage

```
link_eqtl(loc, pop = "CEU", r2d = "r2", token = "", ...)
```

### Arguments

| | |
|---|---|
| `loc` | Object of class 'locus' generated by `locus()` |
| `pop` | A 1000 Genomes Project population, (e.g. YRI or CEU), multiple allowed, default = "CEU". Passed to `LDlinkR::LDexpress()`. |
| `r2d` | Either "r2" for LD r^2 or "d" for LD D', default = "r2". Passed to `LDlinkR::LDexpress()`. |
| `token` | Personal access token for accessing 1000 Genomes LD data via LDlink API. See `LDlinkR` package documentation. |
| `...` | Optional arguments such as `genome_build` which are passed on to `LDlinkR::LDexpress()` |

### Details

The additional eQTL information obtained from LDlink web server can be displayed using `eqtl_plot()` which generates a scatter plot with gene tracks similar to a locus plot, or with `overlay_plot()` which tries to overlay the EQTL analysis over the original locus results (e.g. GWAS).

### Value

Returns an object of class 'locus' with an extra list element 'LDexp' containing a dataframe of information obtained via `LDexpress()`.

### See Also

`locus()` `eqtl_plot()` `overlay_plot()`

link_LD *Obtain LD at a locus from LDlink*

## Description

Adds LD information to a 'locus' class object. It queries LDlink (https://ldlink.nci.nih.gov/) via the LDlinkR package to retrieve linkage disequilibrium (LD) information on a reference SNP.

## Usage

```
link_LD(
  loc,
  pop = "CEU",
  r2d = "r2",
  token = "",
  method = c("proxy", "matrix"),
  genome_build = loc$genome,
  ...
)
```

## Arguments

| | |
|---|---|
| loc | Object of class 'locus' generated by locus() |
| pop | A 1000 Genomes Project population, (e.g. YRI or CEU), multiple allowed, default = "CEU". Passed to LDlinkR::LDmatrix(). |
| r2d | Either "r2" for LD r^2 or "d" for LD D', default = "r2". Passed to LDlinkR::LDmatrix() or LDproxy(). |
| token | Personal access token for accessing 1000 Genomes LD data via LDlink API. See LDlinkR package documentation. |
| method | Either "proxy" or "matrix". Controls whether to use LDproxy() or LDmatrix() to obtain LD data. |
| genome_build | Choose between one of the three options: 'grch37' for genome build GRCh37 (hg19), 'grch38' for GRCh38 (hg38), or 'grch38_high_coverage' for GRCh38 High Coverage (hg38) 1000 Genome Project data sets. Default is GRCh37 (hg19). |
| ... | Optional arguments which are passed on to LDlinkR::LDmatrix() or LDlinkR::LDproxy() |

## Details

The argument method controls which LDlinkR function is used to retrieve LD data. LDmatrix() is slower but usually more complete for small queries (<1000 SNPs). However, it has a limit of 1000 SNPs which can be queried. LDproxy() is faster but data on some SNPs may be absent.

Note, SNPs have to be correctly formatted as required by LDlinkR, either as rsID (works with either method) or chromosome coordinate e.g. "chr7:24966446" (works with LDproxy only). Default genome build is grch37, see LDproxy() or LDmatrix().

## Value

Returns a list object of class 'locus'. LD information is added as a column `ld` in list element `data`.

## See Also

`locus()`

---

`link_recomb` *Query UCSC for Recombination data*

---

## Description

Adds recombination data to a 'locus' object by querying UCSC genome browser.

## Usage

```
link_recomb(loc, genome = loc$genome, table = NULL, recomb = NULL)
```

## Arguments

| | |
|---|---|
| `loc` | Object of class 'locus' generated by `locus()` |
| `genome` | Either `"hg38"` or `"hg19"` |
| `table` | Optional character value specifying which recombination table to use. |
| `recomb` | Optional `GRanges` class object of recombination data. |

## Details

Uses the `rtracklayer` package to query UCSC genome browser for recombination rate data.

Possible options for `table` for hg19 are `"hapMapRelease24YRIRecombMap"`, `"hapMapRelease24CEURecombMap"`, `"hapMapRelease24CombinedRecombMap"` (the default). The only option for `table` for hg38 is `"recomb1000GAvg"` (the default).

If you are doing many queries, it may be much faster to download the entire recombination track data (around 30 MB for hg38) from the Recombination Rate Tracks page at UCSC genome browser. The link to the hg38 download folder is `http://hgdownload.soe.ucsc.edu/gbdb/hg38/recombRate/` and for hg19 is `http://hgdownload.soe.ucsc.edu/gbdb/hg19/decode/`. These .bw files can be converted to useable `GRanges` objects using `rtracklayer::import.bw()` (see the vignette).

Sometimes `rtracklayer` generates intermittent API errors or warnings: try calling `link_recomb()` again. If warnings persist restart your R session. Errors are handled gracefully using `try()` to allow users to wrap `link_recomb()` in a loop without quitting halfway. Error messages are still shown. Successful API calls are cached using `memoise` to reduce API requests.

## Value

A list object of class 'locus'. Recombination data is added as list element `recomb`.

locus *Create locus object for plotting*

## Description

Creates object of class 'locus' for genomic locus plot similar to `locuszoom`.

## Usage

```
locus(
  data = NULL,
  gene = NULL,
  xrange = NULL,
  seqname = NULL,
  flank = NULL,
  fix_window = NULL,
  ens_db,
  chrom = NULL,
  pos = NULL,
  p = NULL,
  yvar = NULL,
  labs = NULL,
  index_snp = NULL,
  LD = NULL,
  std_filter = TRUE
)
```

## Arguments

| | |
|---|---|
| `data` | Dataset (data.frame or data.table) to use for plot. If unspecified or `NULL`, gene track information alone is returned. |
| `gene` | Optional character value specifying which gene to view. Either `gene`, or `xrange` plus `seqname`, or `index_snp` must be specified. |
| `xrange` | Optional vector of genomic position range for the x axis. |
| `seqname` | Optional, specifies which chromosome to plot. |
| `flank` | Single value or vector with 2 values for how much flanking region left and right of the gene to show. Defaults to 100kb. |
| `fix_window` | Optional alternative to `flank`, which allows users to specify a fixed genomic window centred on the specified gene. Both `flank` and `fix_window` cannot be specified simultaneously. |
| `ens_db` | Either a character string which specifies which Ensembl database package (version 86 and earlier for Homo sapiens) to query for gene and exon positions (see `ensembldb` Bioconductor package). Or an `ensembldb` object which can be obtained from the AnnotationHub database. See the vignette and the `AnnotationHub` Bioconductor package for how to create this object. |

| | |
|---|---|
| chrom | Determines which column in data contains chromosome information. If NULL tries to autodetect the column. |
| pos | Determines which column in data contains position information. If NULL tries to autodetect the column. |
| p | Determines which column in data contains SNP p-values. If NULL tries to autodetect the column. |
| yvar | Specifies column in data for plotting on the y axis as an alternative to specifying p-values. Both p and yvar cannot be specified simultaneously. |
| labs | Determines which column in data contains SNP rs IDs. If NULL tries to autodetect the column. |
| index_snp | Specifies the index SNP. If not specified, the SNP with the lowest P value is selected. Can be used to specify locus region instead of specifying gene, or seqname and xrange. |
| LD | Optional character value to specify which column in data contains LD information. |
| std_filter | Logical, whether standard filters on chromosomes 1-22, X & Y, and filtering of genes to only those whose transcript ids start with "ENS" are applied. For users with novel genome assemblies, this probably needs to be set to FALSE. |

## Details

This is an R version of locuszoom (http://locuszoom.org) for generating publication ready Manhattan plots of gene loci. It references Ensembl databases using the ensembldb Bioconductor package framework for annotating genes and exons in the locus.

## Value

Returns a list object of class 'locus' ready for plotting, containing:

| | |
|---|---|
| seqname | chromosome value |
| xrange | vector of genomic position range |
| gene | gene name |
| ens_db | Ensembl or AnnotationHub database |
| ens_version | Ensembl database version |
| organism | Ensembl database organism |
| genome | Ensembl data genome build |
| chrom | column name in data containing chromosome information |
| pos | column name in data containing position |
| p | column name in data containing p-value |
| yvar | column name in data to be plotted on y axis as alternative to p |
| labs | column name in data containing SNP IDs |
| index_snp | id of the most significant SNP |
| data | the subset of GWAS data to be plotted |

| | |
|---|---|
| TX | dataframe of transcript annotations |
| EX | GRanges object of exon annotations |

If data is NULL when locus() is called then gene track information alone is returned.

## See Also

locus_plot() locus_ggplot() locus_plotly()

## Examples

```
## Bioconductor package EnsDb.Hsapiens.v75 is needed for these examples
if(require(EnsDb.Hsapiens.v75)) {
data(SLE_gwas_sub)
loc <- locus(SLE_gwas_sub, gene = 'UBE2L3', flank = 1e5,
             ens_db = "EnsDb.Hsapiens.v75")
summary(loc)
locus_plot(loc)
loc2 <- locus(SLE_gwas_sub, gene = 'STAT4', flank = 1e5,
              ens_db = "EnsDb.Hsapiens.v75")
locus_plot(loc2)
}
```

---

# locus_ggplot *Locus plot using ggplot2*

---

## Description

Genomic locus plot similar to locuszoom.

## Usage

```
locus_ggplot(
  loc,
  heights = c(3, 2),
  filter_gene_name = NULL,
  filter_gene_biotype = NULL,
  border = FALSE,
  cex.axis = 1,
  cex.lab = 1,
  cex.text = 0.7,
  gene_col = ifelse(showExons, "blue4", "skyblue"),
  exon_col = "blue4",
  exon_border = "blue4",
  showExons = TRUE,
  maxrows = 12,
  text_pos = "top",
  italics = FALSE,
```

```
  xticks = "top",
  xlab = NULL,
  highlight = NULL,
  highlight_col = "red",
  blanks = "fill",
  ...
)
```

## Arguments

| | |
|---|---|
| loc | Object of class 'locus' to use for plot. See locus(). |
| heights | Vector supplying the ratio of top to bottom plot. |
| filter_gene_name | Vector of gene names to display. |
| filter_gene_biotype | Vector of gene biotypes to be filtered. Use ensembldb::listGenebiotypes() to display possible biotypes. For example, ensembldb::listGenebiotypes(EnsDb.Hsapiens.v75) |
| border | Logical whether a bounding box is plotted. |
| cex.axis | Specifies font size for axis numbering. |
| cex.lab | Specifies font size for axis titles. |
| cex.text | Font size for gene text. |
| gene_col | Colour for gene lines. |
| exon_col | Fill colour for exons. |
| exon_border | Border line colour outlining exons (or genes if showExons is FALSE). Set to NA for no border. |
| showExons | Logical whether to show exons or simply show whole gene as a rectangle. If showExons = FALSE colours are specified by exon_border for rectangle border and gene_col for the fill colour. |
| maxrows | Specifies maximum number of rows to display in gene annotation panel. |
| text_pos | Character value of either 'top' or 'left' specifying placement of gene name labels. |
| italics | Logical whether gene text is in italics. |
| xticks | Logical whether x axis ticks and numbers are plotted. |
| xlab | Title for x axis. Defaults to chromosome seqname specified in locus. |
| highlight | Vector of genes to highlight. |
| highlight_col | Single colour or vector of colours for highlighted genes. |
| blanks | Controls handling of genes with blank names: "fill" replaces blank gene symbols with ensembl gene ids. "hide" hides genes which are missing gene symbols. |
| ... | Additional arguments passed to gg_scatter() to control the scatter plot, e.g. pcutoff, scheme, recomb_offset etc. |

## Details

Arguments to control plotting of the gene tracks are passed onto gg_genetracks() and for the scatter plot are passed via ... to gg_scatter(). See the documentation for each of these functions for details.

## Value

Returns a ggplot2 plot containing a scatter plot with genetracks underneath.

## See Also

gg_scatter() gg_genetracks()

## Examples

```
if(require(EnsDb.Hsapiens.v75)) {
data(SLE_gwas_sub)
loc <- locus(SLE_gwas_sub, gene = 'IRF5', flank = c(7e4, 2e5), LD = "r2",
             ens_db = "EnsDb.Hsapiens.v75")
locus_ggplot(loc)
}
```

---

# locus_plot *Locus plot*

---

## Description

Genomic locus plot similar to locuszoom.

## Usage

```
locus_plot(
  loc,
  filter_gene_name = NULL,
  filter_gene_biotype = NULL,
  xlab = NULL,
  cex = 1,
  cex.axis = 0.9,
  cex.lab = 1,
  cex.text = 0.7,
  use_layout = TRUE,
  heights = c(3, 2),
  showExons = TRUE,
  maxrows = 7,
  xticks = "bottom",
  border = FALSE,
  gene_col = ifelse(showExons, "blue4", "skyblue"),
```

```
  exon_col = "blue4",
  exon_border = "blue4",
  text_pos = "top",
  italics = FALSE,
  highlight = NULL,
  highlight_col = "red",
  blanks = "fill",
  recomb_col = "blue",
  ...
)
```

## Arguments

| | |
|---|---|
| loc | Object of class 'locus' to use for plot. See locus(). |
| filter_gene_name | Vector of gene names to display. |
| filter_gene_biotype | Vector of gene biotypes to be filtered. Use ensembldb::listGenebiotypes() to display possible biotypes. For example, ensembldb::listGenebiotypes(EnsDb.Hsapiens.v75) |
| xlab | x axis title. |
| cex | Specifies size for points. |
| cex.axis | Specifies font size for axis numbering. |
| cex.lab | Specifies font size for axis titles. |
| cex.text | Font size for gene text. |
| use_layout | Logical whether graphics::layout is called. Default TRUE is for a standard single plot. Set to FALSE if a more complex layout with multiple plots is required e.g. using multi_layout(). |
| heights | Ratio of top to bottom plot. See layout. |
| showExons | Logical whether to show exons or simply show whole gene as a rectangle |
| maxrows | Specifies maximum number of rows to display in gene annotation panel. |
| xticks | Character value of either 'top' or 'bottom' specifying whether x axis ticks and numbers are plotted on top or bottom plot window. |
| border | Logical whether a bounding box is plotted around upper and lower plots. |
| gene_col | Colour for gene lines. |
| exon_col | Fill colour for exons. |
| exon_border | Border line colour outlining exons (or genes if showExons is FALSE). Set to NA for no border. |
| text_pos | Character value of either 'top' or 'left' specifying placement of gene name labels. |
| italics | Logical whether gene text is in italics. |
| highlight | Vector of genes to highlight. |
| highlight_col | Single colour or vector of colours for highlighted genes. |

| | |
|---|---|
| blanks | Controls handling of genes with blank names: "fill" replaces blank gene symbols with ensembl gene ids. "hide" hides genes which are missing gene symbols. |
| recomb_col | Colour for recombination rate line if recombination rate data is present. Set to NA to hide the line. See link_recomb() to add recombination rate data. |
| ... | Other arguments passed to scatter_plot() e.g. index_snp, pcutoff, scheme, recomb_offset, etc, and arguments for plot() e.g. ylab, main, etc to control the scatter plot. |

## Details

This is an R version of locuszoom for generating publication ready Manhattan plots of gene loci. It references Ensembl databases for annotating genes and exons. Use locus() first to generate an object of class 'locus' for plotting. LDlink web server can be queried using function link_LD() to retrieve linkage disequilibrium (LD) information on the index SNP.

Arguments to control plotting of the gene tracks are passed onto genetracks() and for the scatter plot are passed via ... to scatter_plot(). See the documentation for each of these functions for details.

## Value

No return value.

## See Also

locus() scatter_plot() genetracks()

## Examples

```
if(require(EnsDb.Hsapiens.v75)) {
data(SLE_gwas_sub)
loc <- locus(SLE_gwas_sub, gene = 'UBE2L3', flank = 1e5,
             ens_db = "EnsDb.Hsapiens.v75")
locus_plot(loc)

## Use embedded LD information in column `r2`
loc2 <- locus(SLE_gwas_sub, gene = 'IRF5', flank = c(7e4, 2e5), LD = "r2",
              ens_db = "EnsDb.Hsapiens.v75")
## Add label for index SNP
locus_plot(loc2, labels = "index")
}
```

locus_plotly *Locus plotly*

## Description

Genomic locus plot similar to locuszoom, using plotly.

## Usage

```
locus_plotly(
  loc,
  heights = c(0.6, 0.4),
  filter_gene_name = NULL,
  filter_gene_biotype = NULL,
  cex.text = 0.7,
  italics = FALSE,
  gene_col = ifelse(showExons, "blue4", "skyblue"),
  exon_col = "blue4",
  exon_border = "blue4",
  showExons = TRUE,
  maxrows = 8,
  width = 600,
  xlab = NULL,
  blanks = "show",
  ...
)
```

## Arguments

| | |
|---|---|
| loc | Object of class 'locus' to use for plot. See locus(). |
| heights | Vector controlling relative height of each panel on 0-1 scale. Alternatively a vector of length 2 of height in pixels passed to scatter_plotly() and genetrack_ly(). |
| filter_gene_name | Vector of gene names to display. |
| filter_gene_biotype | Vector of gene biotypes to be filtered. Use ensembldb::listGenebiotypes() to display possible biotypes. For example, ensembldb::listGenebiotypes(EnsDb.Hsapiens.v75) |
| cex.text | Font size for gene text. |
| italics | Logical whether gene text is in italics. |
| gene_col | Colour for gene lines. |
| exon_col | Fill colour for exons. |
| exon_border | Border line colour outlining exons (or genes if showExons is FALSE). Set to NA for no border. |

| | |
|---|---|
| showExons | Logical whether to show exons or simply show whole gene as a rectangle. If showExons = FALSE colours are specified by exon_border for rectangle border and gene_col for the fill colour. |
| maxrows | Specifies maximum number of rows to display in gene annotation panel. |
| width | Width of plotly plot in pixels which is purely used to prevent overlapping text for gene names. |
| xlab | Title for x axis. Defaults to chromosome seqname specified in locus. |
| blanks | Controls handling of genes with blank names: "fill" replaces blank gene symbols with ensembl gene ids. "hide" completely hides genes which are missing gene symbols. "show" shows gene lines but no label (hovertext is still available). |
| ... | Optional arguments passed to scatter_plotly() to control the scatter plot. |

## Details

This is an R/plotly version of locuszoom for exploring regional Manhattan plots of gene loci. Use locus() first to generate an object of class 'locus' for plotting. This references a selected Ensembl database for annotating genes and exons. Hover over the points or gene tracks to reveal more information.

## Value

A 'plotly' plotting object showing a scatter plot above gene tracks.

## See Also

locus() genetrack_ly() scatter_plotly()

## Examples

```
if(require(EnsDb.Hsapiens.v75)) {
data(SLE_gwas_sub)
loc <- locus(SLE_gwas_sub, gene = "IRF5", flank = c(7e4, 2e5), LD = "r2",
             ens_db = "EnsDb.Hsapiens.v75")
locus_plotly(loc)
}
```

---

# multi_layout *Layout multiple locus plots*

---

## Description

Produces pages with multiple locus plots on.

## Usage

```
multi_layout(
  plots,
  nrow = 1,
  ncol = 1,
  heights = c(3, 2),
  legend_pos = "topleft",
  ...
)
```

## Arguments

| | |
|---|---|
| plots | Either an 'expression' to be evaluated which is a series of calls to locus_plot() or similar plotting functions, or a list of 'locus' class objects which are plotted in sequence. |
| nrow | Number of rows of plots |
| ncol | Number of columns of plots |
| heights | Vector of length 2 specifying height for plot and gene tracks |
| legend_pos | A keyword either "topleft" or "topright" or NULL to hide the legend. Not invoked if plots is an expression. The legend is only shown on one plot on each page. |
| ... | Optional arguments passed to locus_plot() if plots contains a list |

## Value

No return value.

## See Also

locus_plot()

## Examples

```
if(require(EnsDb.Hsapiens.v75)) {

data(SLE_gwas_sub)
genes <- c("STAT4", "UBE2L3", "IRF5")
loclist <- lapply(genes, locus,
                  data = SLE_gwas_sub,
                  ens_db = "EnsDb.Hsapiens.v75",
                  LD = "r2")
## produce 3 locus plots, one on each page
multi_layout(loclist)

## place 3 locus plots in a row on a single page
multi_layout(loclist, ncol = 3)

## full control
loc <- locus(SLE_gwas_sub, gene = 'STAT4', flank = 1e5, LD = "r2",
             ens_db = "EnsDb.Hsapiens.v75")
```

```
loc2 <- locus(SLE_gwas_sub, gene = 'IRF5', flank = c(7e4, 2e5), LD = "r2",
              ens_db = "EnsDb.Hsapiens.v75")
loc3 <- locus(SLE_gwas_sub, gene = 'UBE2L3', LD = "r2",
              ens_db = "EnsDb.Hsapiens.v75")
multi_layout(ncol = 3,
             plots = {
               locus_plot(loc, use_layout = FALSE, legend_pos = 'topleft')
               locus_plot(loc2, use_layout = FALSE, legend_pos = NULL)
               locus_plot(loc3, use_layout = FALSE, legend_pos = NULL)
             })

}
```

---

`overlay_plot` *Plot overlaying eQTL and GWAS data*

---

## Description

Experimental plotting function for overlaying eQTL data from GTEx on top of GWAS results. y axis shows the -log10 p-value for the GWAS result. Significant eQTL for the specified gene are overlaid using colours and symbols.

## Usage

```
overlay_plot(
  loc,
  base_col = "black",
  alpha = 0.5,
  scheme = "RdYlBu",
  tissue = "Whole Blood",
  eqtl_gene = loc$gene,
  legend_pos = "topright",
  ...
)
```

## Arguments

| | |
|---|---|
| `loc` | Object of class 'locus' to use for plot. See `locus()`. |
| `base_col` | Colour of points for SNPs which do not have eQTLs. |
| `alpha` | Alpha opacity for non-eQTL points |
| `scheme` | Character string specifying palette for effect size showing up/downregulation eQTL using grDevices::hcl.colors. Alternatively a vector of 6 colours. |
| `tissue` | GTex tissue in which eQTL has been measured |
| `eqtl_gene` | Gene showing eQTL effect |
| `legend_pos` | Character value specifying legend position. See `legend()`. |
| `...` | Other arguments passed to `locus_plot()` for the locus plot. |

## Value

No return value. Produces a plot using base graphics.

---

`quick_peak` *Fast peak finder in GWAS data*

---

## Description

Simple but fast function for finding peaks in genome-wide association study (GWAS) data based on setting a minimum distance between peaks.

## Usage

```
quick_peak(
  data,
  npeaks = NA,
  p_cutoff = 5e-08,
  span = 1e+06,
  min_points = 2,
  chrom = NULL,
  pos = NULL,
  p = NULL
)
```

## Arguments

| | |
|---|---|
| `data` | GWAS dataset (data.frame or data.table) |
| `npeaks` | Number of peaks to find. If set to `NA`, algorithm finds all distinct peaks separated from one another by region size specified by `span`. |
| `p_cutoff` | Specifies cut-off for p-value significance above which p-values are ignored. |
| `span` | Minimum genomic distance between peaks (default 1 Mb) |
| `min_points` | Minimum number of p-value significant points which must lie within the span of a peak. This removes peaks with single or only a few low p-value SNPs. To disable set `min_points` to 1 or less. |
| `chrom` | Determines which column in `data` contains chromosome information. If `NULL` tries to autodetect the column. |
| `pos` | Determines which column in `data` contains position information. If `NULL` tries to autodetect the column. |
| `p` | Determines which column in `data` contains SNP p-values. If `NULL` tries to autodetect the column. |

## Details

This function is designed for speed. SNP p-values are filtered to only those which are significant as specified by `p_cutoff`. Each peak is identified as the SNP with the lowest p-value and then SNPs in proximity to each peak within the distance specified by `span` are removed. Regions such as the HLA whose peaks may well be broader than `span` may produce multiple entries.

## Value

Vector of row indices

---

`scatter_plot` *Locus scatter plot*

---

## Description

Produces a base graphics scatter plot from a 'locus' class object. This function is called by `locus_plot()` to generate the scatter plot portion. Can be used manually with `set_layers()`.

## Usage

```
scatter_plot(
  loc,
  index_snp = loc$index_snp,
  pcutoff = 5e-08,
  scheme = c("grey", "dodgerblue", "red"),
  cex = 1,
  cex.axis = 0.9,
  cex.lab = 1,
  xlab = NULL,
  ylab = NULL,
  ylim = NULL,
  ylim2 = c(0, 100),
  yzero = (loc$yvar == "logP"),
  xticks = TRUE,
  border = FALSE,
  showLD = TRUE,
 LD_scheme = c("grey", "royalblue", "cyan2", "green3", "orange", "red", "purple"),
  recomb_col = "blue",
  recomb_offset = 0,
  legend_pos = "topleft",
  labels = NULL,
  label_x = 4,
  label_y = 4,
  eqtl_gene = NULL,
  beta = NULL,
  add = FALSE,
  align = TRUE,
  ...
)
```

## Arguments

| | |
|---|---|
| `loc` | Object of class 'locus' to use for plot. See locus. |

| | |
|---|---|
| index_snp | Specifies index SNP or a vector of SNPs to be shown in a different colour and symbol. Defaults to the SNP with the lowest p-value. Set to NULL to not show this. |
| pcutoff | Cut-off for p value significance. Defaults to p = 5e-08. Set to NULL to disable. |
| scheme | Vector of 3 colours if LD is not shown: 1st = normal points, 2nd = colour for significant points, 3rd = index SNP(s). |
| cex | Specifies size for points. |
| cex.axis | Specifies font size for axis numbering. |
| cex.lab | Specifies font size for axis titles. |
| xlab | x axis title. |
| ylab | y axis title. |
| ylim | y axis limits (y1, y2). |
| ylim2 | Secondary y axis limits for recombination line, if present. |
| yzero | Logical whether to force y axis limit to include y=0. |
| xticks | Logical whether x axis numbers and axis title are plotted. |
| border | Logical whether a bounding box is plotted around upper and lower plots. |
| showLD | Logical whether to show LD with colours |
| LD_scheme | Vector of colours for plotting LD. The first colour is for SNPs which lack LD information. The next 5 colours are for r2 or D' LD results ranging from 0 to 1 in intervals of 0.2. The final colour is for the index SNP. |
| recomb_col | Colour for recombination rate line if recombination rate data is present. Set to NA to hide the line. See link_recomb() to add recombination rate data. |
| recomb_offset | Offset from 0-1 which shifts the scatter plot up and recombination line plot down. Recommended value 0.1. |
| legend_pos | Position of legend. See legend(). Set to NULL to hide legend. |
| labels | Character vector of SNP or genomic feature IDs to label. The value "index" selects the highest point or index SNP as defined when locus() is called. Set to NULL to remove all labels. |
| label_x | Value or vector for position of label as percentage of x axis scale. |
| label_y | Value or vector for position of label as percentage of y axis scale. |
| eqtl_gene | Column name in loc$data for colouring eQTL genes. |
| beta | Optional column name for beta coefficient to display upward triangles for positive beta and downward triangles for negative beta (significant SNPs only). |
| add | Logical whether to add points to an existing plot or generate a new plot. |
| align | Logical whether to set par() to align the plot. |
| ... | Other arguments passed to plot() to control the scatter plot e.g. main, ylim etc. |

## Details

Advanced users familiar with base graphics can customise every single point on the scatter plot, by adding columns named bg, col, pch or cex directly to the dataframe stored in $data element of the 'locus' object. Setting these will overrule any default settings. These columns refer to their respective base graphics arguments, see graphics::points().

## Value

No return value. Produces a scatter plot using base graphics.

## See Also

locus() set_layers()

---

scatter_plotly *Locus scatter plotly*

---

## Description

Produces a scatter plot from a 'locus' class object using plotly.

## Usage

```
scatter_plotly(
  loc,
  index_snp = loc$index_snp,
  pcutoff = 5e-08,
  scheme = c("grey", "dodgerblue", "red"),
  xlab = NULL,
  ylab = NULL,
  yzero = (loc$yvar == "logP"),
  showLD = TRUE,
 LD_scheme = c("grey", "royalblue", "cyan2", "green3", "orange", "red", "purple"),
  marker_outline = "black",
  marker_size = 7,
  recomb_col = "blue",
  eqtl_gene = NULL,
  beta = NULL,
  add_hover = NULL,
  showlegend = TRUE,
  height = NULL,
  webGL = TRUE
)
```

## Arguments

| | |
|---|---|
| loc | Object of class 'locus' to use for plot. See locus. |
| index_snp | Specifies index SNP or a vector of SNPs to be shown in a different colour and symbol. Defaults to the SNP with the lowest p-value. Set to NULL to not show this. |
| pcutoff | Cut-off for p value significance. Defaults to p = 5e-08. Set to NULL to disable. |
| scheme | Vector of 3 colours if LD is not shown: 1st = normal points, 2nd = colour for significant points, 3rd = index SNP(s). |

| | |
|---|---|
| xlab | x axis title. |
| ylab | y axis title. |
| yzero | Logical whether to force y axis limit to include y=0. |
| showLD | Logical whether to show LD with colours |
| LD_scheme | Vector of colours for plotting LD. The first colour is for SNPs which lack LD information. The next 5 colours are for r^2 or D' LD results ranging from 0 to 1 in intervals of 0.2. The final colour is for the index SNP. |
| marker_outline | Specifies colour for outlining points. |
| marker_size | Value for size of markers in plotly units. |
| recomb_col | Colour for recombination rate line if recombination rate data is present. Set to NA to hide the line. See link_recomb() to add recombination rate data. |
| eqtl_gene | Column name in loc$data for eQTL genes. |
| beta | Optional column name for beta coefficient to display upward triangles for positive beta and downward triangles for negative beta (significant SNPs only). |
| add_hover | Optional vector of column names in loc$data to add to the plotly hover text for scatter points. |
| showlegend | Logical whether to show a legend for the scatter points. |
| height | Height in pixels (optional, defaults to automatic sizing). |
| webGL | Logical whether to use webGL or SVG for scatter plot. |

## Value

A plotly scatter plot.

## See Also

locus() locus_plotly()

---

# set_layers *Set up a column of multiple plots*

---

## Description

Uses layout() to set up multiple locus plots aligned in a column.

## Usage

```
set_layers(n = 1, heights = c(rep(3, n), 2), rev = FALSE)
```

## Arguments

| | |
|---|---|
| n | Number of plots (not including gene tracks on bottom) |
| heights | Vector of length nrow + 1 specifying height for plots with a gene track on the bottom |
| rev | Logical whether to reverse plotting order and plot from bottom to top |

## Value

Sets `layout()` to enable multiple plots aligned in a column. The gene track is assumed to be positioned on the bottom. Returns `par()` invisibly so that layout can be reset to default at the end of plotting.

## See Also

`layout()`

---

`SLE_gwas_sub` *SLE GWAS data subset*

---

## Description

Dataset of SNPs at 3 gene loci (UBE2L3, STAT4, IRF5) from GWAS on SLE (Bentham et al, 2015, Nature Genetics 47(12):1457-64, PMID: 26502338).

## Usage

```
data(SLE_gwas_sub)
```

## Format

Data frame with 1990 rows and 11 variables

## Source

https://www.ebi.ac.uk/gwas/studies/GCST003156

# Index