Package 'HilbertCurve'

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Type Package

Title Making 2D Hilbert Curve

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VignetteBuilder knitr

Description Hilbert curve is a type of space-filling curves that fold one dimensional axis into a two dimensional space, but with still preserves the locality. This package aims to provide an easy and flexible way to visualize data through Hilbert curve.

biocViews Software, Visualization, Sequencing, Coverage, GenomeAnnotation

URL https://github.com/jokergoo/HilbertCurve

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Contents

`default_overlay` *Default color overlay for adding new layers*

Description

Default color overlay for adding new layers

Usage

```
default_overlay(r0, g0, b0, r, g, b, alpha = 1)
```

Arguments

`r0`	red channel for the layers that are already in the plot.
`g0`	green channel for the layers that are already in the plot.
`b0`	blue channel for the layers that are already in the plot.
`r`	red channel for the new layer
`g`	green channel for the new layer
`b`	blue channel for the new layer
`alpha`	alpha channel for the new layer

Details

The default overlay is (take red channel for example) `r*alpha + r0*(1-alpha)`.

Value

A list which contains overlayed RGB colors (values between 0 and 1).

Author(s)

Zuguang Gu <z.gu@dkfz.de>

See Also

Color overlay function is always used in `hc_layer,HilbertCurve-method` or `hc_layer,GenomicHilbertCurve-method`.

Examples

```
# red (1, 0, 0) overlay to the grey (0.5, 0.5, 0.5) with 0.5 transparency
default_overlay(1, 0, 0, 0.5, 0.5, 0.5, 0.5)
```

GenomicHilbertCurve *Initialize a Hilbert curve specifically for genomic data*

Description

Initialize a Hilbert curve specifically for genomic data

Usage

```
GenomicHilbertCurve(chr = paste0("chr", c(1:22, "X", "Y")), species = "hg19",
    background = NULL, ...)
```

Arguments

chr	a vector of chromosome names. Note it should have 'chr' prefix. This argument will be ignored when background is set.
species	abbreviation of species, e.g. 'hg19' or 'mm10'. read.chromInfo is used to retrieve the chromosome information.
background	the background can be provided as a GRanges object. Chromosomes should be unique across rows. Or more generally, the 'seqnames' should be different.
...	common arguments in HilbertCurve can be used here.

Details

Multiple chromosomes can be visualized in a same Hilbert curve. All chromosomes are concatenated on after the other based on the order which is specified.

Since chromosomes will have irregular shapes on the curve, under 'pixel' mode, users can set border option in hc_map,GenomicHilbertCurve-method to highlight borders of chromosomes to identify their locations on the curve.

Value

A GenomicHilbertCurve-class object

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
require(circlize)
require(GenomicRanges)
bed = generateRandomBed()
gr = GRanges(seqnames = bed[[1]], ranges = IRanges(bed[[2]], bed[[3]]))
hc = GenomicHilbertCurve()
hc_points(hc, gr)
```

```
hc = GenomicHilbertCurve(chr = c("chr1", "chr2"))
hc_points(hc, gr)

bg = GRanges(seqnames = c("chr1", "chr2"),
    ranges = IRanges(c(1,10000000), c(10000000,20000000)))
hc = GenomicHilbertCurve(background = bg, level = 6)
hc_points(hc, gr, gp = gpar(fill = rand_color(length(gr))))
hc_map(hc, fill = NA, border = "grey", add = TRUE)
```

GenomicHilbertCurve-class

The GenomicHilbertCurve class

Description

The GenomicHilbertCurve class

Details

The GenomicHilbertCurve-class is inherited from the HilbertCurve-class. Basically the structure of this class is almost the same as the HilbertCurve-class but with several additional slots added to facilitate visualizing genomic data.

Methods

The GenomicHilbertCurve-class provides following methods:

- GenomicHilbertCurve: constructor method;
- hc_points,GenomicHilbertCurve-method: add points;
- hc_segments,GenomicHilbertCurve-method: add lines;
- hc_rect,GenomicHilbertCurve-method: add rectangles;
- hc_polygon,GenomicHilbertCurve-method: add poygons;
- hc_text,GenomicHilbertCurve-method: add text;
- hc_layer,GenomicHilbertCurve-method: add layers undel "pixel" mode;
- hc_map,GenomicHilbertCurve-method: show the map of different categories on the curve. Works both for "normal" and "pixel" mode

The usage of above functions are almost same as those functions for the HilbertCurve-class except that the second argument which specifies the intervals should be a GRanges object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
NULL
```

hc_centered_text-HilbertCurve-method *Add text to the center of the block*

Description

Add text to the center of the block

Usage

```
## S4 method for signature 'HilbertCurve'
hc_centered_text(object, ir = NULL, labels, x1 = NULL, x2 = NULL, gp = gpar(), ...)
```

Arguments

object	A HilbertCurve-class object.
ir	an IRanges object that contains positions which correspond to text. The middle points of the intervals will be the positions of the text.
labels	text corresponding to intervals in ir.
x1	if start positions are not integers, they can be set by x1.
x2	if end positions are not integers, they can be set by x2.
gp	graphic parameters for text. It should be specified by gpar.
...	pass to grid.text. E.g. you can set text justification by just here.

Details

If the interval is long enough that it represents as a block in the 2D space, the corresponding label is put approximately at center (or at least inside) of the block.

Please use hc_text,HilbertCurve-method directly.

Value

NULL

Author(s)

Zuguang Gu <z.gu@dkfz.de>

See Also

It is used in hc_map,GenomicHilbertCurve-method to put chromosome names in the center of chromosomes.

Examples

```
hc = HilbertCurve(1, 10)
hc_rect(hc, x1 = c(1, 3, 7), x2 = c(3, 7, 10), gp = gpar(fill = 2:5))
hc_centered_text(hc, x1 = 1, x2 = 3, labels = "A")
hc_centered_text(hc, x1 = 3, x2 = 7, labels = "B")
hc_centered_text(hc, x1 = 7, x2 = 10, labels = "C")
```

---

hc_layer-dispatch *Method dispatch page for hc_layer*

Description

Method dispatch page for hc_layer.

Dispatch

hc_layer can be dispatched on following classes:

- hc_layer,GenomicHilbertCurve-method, GenomicHilbertCurve-class class method
- hc_layer,HilbertCurve-method, HilbertCurve-class class method

Examples

```
# no example
NULL
```

---

hc_layer-GenomicHilbertCurve-method *Add a new layer to the Hilbert curve*

Description

Add a new layer to the Hilbert curve

Usage

```
## S4 method for signature 'GenomicHilbertCurve'
hc_layer(object, gr, col = "red", border = NA,
    mean_mode = c("w0", "absolute", "weighted", "max_freq"), grid_line = 0,
    grid_line_col = "black", overlay = default_overlay)
```

Arguments

object	a GenomicHilbertCurve-class object
gr	a GRanges object which contains the genomic regions to be mapped to the curve
col	a scalar or a vector of colors which correspond to regions in gr, pass to hc_layer,HilbertCurve-method
border	a scalar or a vector of colors which correspond to the borders of regions. Set it to NA if borders are suppressed.
mean_mode	Under 'pixel' mode, each pixel represents a small window. This argument provides methods to summarize value for the small window if the input genomic regions can not completely overlap with the window, pass to hc_layer,HilbertCurve-method
grid_line	whether add grid lines to show blocks of the Hilber curve, pass to hc_layer,HilbertCurve-method
grid_line_col	color for the grid lines, pass to hc_layer,HilbertCurve-method
overlay	a self-defined function which defines how to overlay new layer to the plot, pass to hc_layer,HilbertCurve-method

Details

It is basically a wrapper of hc_layer,HilbertCurve-method.

Value

Refer to hc_layer,HilbertCurve-method

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
require(circlize)
require(GenomicRanges)
bed = generateRandomBed()
gr = GRanges(seqnames = bed[[1]], ranges = IRanges(bed[[2]], bed[[3]]))
hc = GenomicHilbertCurve(mode = "pixel", level = 9)
hc_layer(hc, gr, col = rand_color(length(gr)))
```

---

hc_layer-HilbertCurve-method

Add a new layer to the Hilbert curve

Description

Add a new layer to the Hilbert curve

Usage

```
## S4 method for signature 'HilbertCurve'
hc_layer(object, ir = NULL, x1 = NULL, x2 = x1, col = "red", border = NA,
    mean_mode = c("w0", "absolute", "weighted", "max_freq"), grid_line = 0,
    grid_line_col = "black", overlay = default_overlay)
```

Arguments

object	A HilbertCurve-class object.
ir	an IRanges object which specifies the input intervals.
x1	if start positions are not integers, they can be set by x1.
x2	if end positions are not integers, they can be set by x2.
col	a scalar or a vector of colors which correspond to intervals in ir (or x1 and x2).
border	a scalar or a vector of colors for the borders of intervals. Set it to NA if borders are suppressed.
mean_mode	Under 'pixel' mode, each pixel represents a small window. This argument provides methods to summarize value for the small window if the input intervals can not completely overlap with the window. See explanation in hc_points,HilbertCurve-method.
grid_line	whether add grid lines to show blocks of the Hilber curve. It should be an integer number and there will be 2^(grid_line-1)-1 horizontal and vertical grid lines.
grid_line_col	color for the grid lines
overlay	a self-defined function which defines how to overlay new layer to the plot. By default it is default_overlay. Let's assume the red channel for the layers which are already in the plot is r0, the red channel for the new layer is r and the alpha channel is alpha, the overlayed color is calculated as r*alpha + r0*(1-alpha). This self-defined function should accept 7 arguments which are: vectors of r, g, b channels which correspond to the layers that are already in the plot, and r, g, b, alpha channels which corresponds to the new layer. All the values passed into are between 0 to 1. The returned value for this function should be a list which contains r, g, b channels which correspond to the overlayed colors. Note that these 7 arguments only correspond to the pixels which are covered by the new layer.

Details

This function only works under 'pixel' mode.

Under "pixel" mode, color is the only graphic representation of values in the input intervals. To make a more precise and robust color mapping, users may consider colorRamp2 to create a color mapping function.

If you want to add more than one layers to the curve, remember to set colors with transparency.

overlay argument is useful for changing color themes for the overlapped areas, please refer to the vignette to see examples of how to swith color themes in easy ways.

Value

No value is returned.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
hc = HilbertCurve(1, 100, level = 9, mode = "pixel")

x = sort(sample(100, 20))
s = x[1:10*2 - 1]
e = x[1:10*2]
require(IRanges)
ir = IRanges(s, e)

hc_layer(hc, ir)

hc = HilbertCurve(1, 100, level = 9, mode = "pixel")
hc_layer(hc, ir, grid_line = 3)

hc = HilbertCurve(1, 100, level = 9, mode = "pixel")
hc_layer(hc, ir, border = "black")
```

---

hc_level-HilbertCurve-method

Level of the Hilbert curve

Description

Level of the Hilbert curve

Usage

```
## S4 method for signature 'HilbertCurve'
hc_level(object)
```

Arguments

object	A HilbertCurve-class object.

Value

The level of the Hilbert curve.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
hc = HilbertCurve(1, 100)
hc_level(hc)

hc = HilbertCurve(1, 100, level = 5)
hc_level(hc)
```

`hc_map-GenomicHilbertCurve-method` *Draw a map which represents positions of different chromosomes on the curve*

Description

Draw a map which represents positions of different chromosomes on the curve

Usage

```
## S4 method for signature 'GenomicHilbertCurve'
hc_map(object, level = 7,
    fill = rand_color(length(background), transparency = 0.5), border = NA,
    labels = names(object@background), show_labels = TRUE, labels_gp = gpar(),
    add = FALSE, ...)
```

Arguments

`object`	a `GenomicHilbertCurve-class` object
`level`	Since a map does not need to have high resolution, a value of around 7 would be enough. If `add` is set to `TRUE`, `level` will be enforced to have the same level in the current Hilbert curve.
`fill`	colors for different chromosomes, or more generally, for different 'seqnames'.
`border`	colors for the borders of chromosomes. Set it to `NA` if borders are suppressed.
`labels`	label for each chromosome, or more generally, for different 'sequences'
`show_labels`	whether show text labels
`labels_gp`	graphic settings for labels
`add`	whether add the map to the current curve or draw it in a new graphic device. Notice if `add` is set to `TRUE`, you should set `fill` with transparency so that it will not hide your original plot.
`...`	pass to `GenomicHilbertCurve`. It is only used if you want the map to be plotted in a new graphic device.

Details

When multiple genomic categories (e.g. chromosomes) are drawn into one single Hilbert curve, a map which shows the positions of categories on the curve is necessary to distinguish different genomic categories.

Under "pixel" mode, if the map is directly added to the Hilbert curve, no chromosome name is drawn. The chromosome names are only drawn if the map is plotted in a new graphic device or added to the Hilbert curve under "normal" mode.

Just be careful if you directly overlay the map to the curve that the color of the map does not affect the original plot too much.

Value

A GenomicHilbertCurve-class object

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
require(circlize)
require(GenomicRanges)
bed = generateRandomBed(nr = 100)
gr = GRanges(seqnames = bed[[1]], ranges = IRanges(bed[[2]], bed[[3]]))
hc = GenomicHilbertCurve()
hc_points(hc, gr, gp = gpar(fill = rand_color(length(gr))))
# add it in the same graphic device
hc_map(hc, fill = rand_color(24, transparency = 0.5), add = TRUE)

# add the map only with borders
hc = GenomicHilbertCurve()
hc_points(hc, gr, gp = gpar(fill = rand_color(length(gr))))
hc_map(hc, fill = NA, border = "grey", add = TRUE)

# or open a new graphic device
hc_map(hc, fill = rand_color(24))
```

---

hc_normal_points-HilbertCurve-method

Add points to the Hilbert curve

Description

Add points to the Hilbert curve

Usage

```
## S4 method for signature 'HilbertCurve'
hc_normal_points(object, ir = NULL, x1 = NULL, x2 = x1, gp = gpar(),
    pch = 1, size = unit(1, "char"))
```

Arguments

object	A HilbertCurve-class object.
ir	an IRanges object which specifies the input intervals.
x1	if start positions are not integers, they can be set by x1.
x2	if end positions are not integers, they can be set by x2.
size	size of the points. It should be a unit object, pass to grid.points.
pch	shape of points, pass to grid.points.
gp	graphic parameters for points. It should be specified by gpar.

Details

Points are added at the middle of the intervals in ir (or x1 and x2), so there is only one point for each interval.

This function is used internally. Please use hc_points,HilbertCurve-method instead.

Value

A data frame which contains coordinates (in the 2D space) of points.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

See Also

hc_points,HilbertCurve-method

Examples

```
# see documentation of hc_points
NULL
```

`hc_offset-HilbertCurve-method` *Adjust positions*

Description

Adjust positions

Usage

```
## S4 method for signature 'HilbertCurve'
hc_offset(object, x)
```

Arguments

`object`	A `HilbertCurve-class` object.
`x`	positions.

Details

Since internally positions are transformed to positive integers, if input positions are specified as negative values when initializing the Hilbert curve, a shift will be recorded internally and positions are transformed to positive value automatically.

Value

A positive numeric value.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
hc = HilbertCurve(-100, 100)
hc_offset(hc, c(-100, -50, 0, 50, 100))
```

hc_png-HilbertCurve-method *Save Hilbert curve as a PNG figure*

Description

Save Hilbert curve as a PNG figure

Usage

```
## S4 method for signature 'HilbertCurve'
hc_png(object, file = "HilbertCurve.png")
```

Arguments

object	A HilbertCurve-class object.
file	file name. If the suffix of the file name is not .png, it will be added automatically no matter you like it or not.

Details

A PNG figure with resolution of 2^level x 2^level is generated.

Only the body of the Hilbert curve will be written to PNG file.

This function only works under 'pixel' mode.

Value

No value is returned.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
hc = HilbertCurve(1, 100, level = 9, mode = "pixel")

x = sort(sample(100, 20))
s = x[1:10*2 - 1]
e = x[1:10*2]
require(IRanges)
ir = IRanges(s, e)

hc_layer(hc, ir)
hc_png(hc, file = "test.png")
```

---

hc_points-dispatch *Method dispatch page for hc_points*

Description

Method dispatch page for hc_points.

Dispatch

hc_points can be dispatched on following classes:

- hc_points,HilbertCurve-method, HilbertCurve-class class method
- hc_points,GenomicHilbertCurve-method, GenomicHilbertCurve-class class method

Examples

```
# no example
NULL
```

---

hc_points-GenomicHilbertCurve-method
Add points to the Hilbert curve

Description

Add points to the Hilbert curve

Usage

```
## S4 method for signature 'GenomicHilbertCurve'
hc_points(object, gr,
    np = max(c(2, 10 - hc_level(object))), size = unit(1, "char"),
   pch = 1, gp = gpar(), mean_mode = c("w0", "absolute", "weighted", "max_freq"),
    shape = "circle")
```

Arguments

object	a GenomicHilbertCurve-class object
gr	a GRanges object which contains the genomic regions to be mapped to the curve
np	pass to hc_points,HilbertCurve-method
size	size of points when np <= 1, pass to hc_points,HilbertCurve-method
pch	shape of the points when np <= 1, pass to hc_points,HilbertCurve-method
gp	graphic parameters of the points when np <= 1, pass to hc_points,HilbertCurve-method
mean_mode	pass to hc_points,HilbertCurve-method
shape	shape of the points when np >= 2, pass to hc_points,HilbertCurve-method

Details

It is basically a wrapper of hc_points,HilbertCurve-method.

Value

Refer to hc_points,HilbertCurve-method

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
require(circlize)
require(GenomicRanges)
bed = generateRandomBed(nr = 100)
gr = GRanges(seqnames = bed[[1]], ranges = IRanges(bed[[2]], bed[[3]]))
hc = GenomicHilbertCurve()
hc_points(hc, gr, gp = gpar(fill = rand_color(length(gr))))
```

---

hc_points-HilbertCurve-method

Add points to the Hilbert curve

Description

Add points to the Hilbert curve

Usage

```
## S4 method for signature 'HilbertCurve'
hc_points(object, ir = NULL, x1 = NULL, x2 = x1,
    np = max(c(2, 10 - hc_level(object))), size = unit(1, "char"),
   pch = 1, gp = gpar(), mean_mode = c("w0", "absolute", "weighted", "max_freq"),
    shape = "circle")
```

Arguments

object	A HilbertCurve-class object.
ir	an IRanges object which specifies the input intervals.
x1	if start positions are not integers, they can be set by x1.
x2	if end positions are not integers, they can be set by x2.
np	number of points (a circle or a square, ...) that are put in a segment. np controls the mode of how to add the points to the curve. See 'Details' section.
size	size of the points. It should be a unit object. Only works if np <= 1
pch	shape of points, used for points if np <= 1.

gp	graphic parameters for points. It should be specified by gpar.
mean_mode	when np >= 2, each segment on the curve is split into np windows and each window actually represents an small interval in the axis. When overlapping input intervals to the windows on the curve and when the window can not completely cover the input intervals, some averaging method should be applied to get a more accurate estimation for the value in the window. Here the HilbertCurve package provides four modes: "w0", "weighted", "absolute" and "max_freq" which calculate the mean value in the window with respect to different scenarios. See 'Details' section and the vignette for more informative explanation.
shape	shape of points, used for points if np >= 2. Possible values are "circle", "square", "triangle", "hexagon", "star".

Details

If np is set to 1 or NULL, points will be added in the middle for each interval in ir (or x1, x2).

If np is set to a value larger or equal to 2, every segment on the curve is split by np points (e.g. circles). In this case, each point actually represent a window on the curve and when the window is not fully covered by the input intervals, there are three different metrics to average the values in the window.

Following illustrates different settings for mean_mode:

```
   100    80     60    values in ir
++++++   +++   +++++   ir
  ================     window (width = 16)
    4     3     3      overlap

absolute: (100 + 80 + 60)/3
weighted: (100*4 + 80*3 + 60*3)/(4 + 3 + 3)
w0:       (100*4 + 80*3 + 60*3 + 0*6)/16
```

So which mode to use depends on specific scenario. If the background is not of interest, absolute and weighted modes may be proper and if the value also needs to be averaged with background, w0 is the proper choice. Section "Averaging models" in the vignette gives a more detailed explanation for this argument.

There is one more value for mean_mode which is max_freq. max_freq is mainly for discrete signals and in a segment, value with the highest frequency (or with the highest length) is selected for this segment

If np >= 2, the value of np also controls the size of points.

Graphic parameters is always represented as numeric values (e.g. colors can be converted into numeric RGB values) and they will be averaged according to above rules.

Internally, it will depatch to hc_normal_points,HilbertCurve-method or hc_segmented_points,HilbertCurve-method depending on the value of np.

Value

A data frame which contains coordinates (in the 2D space) of points.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
hc = HilbertCurve(1, 100, level = 4, reference = TRUE)

x = sort(sample(100, 20))
s = x[1:10*2 - 1]
e = x[1:10*2]
require(IRanges)
ir = IRanges(s, e)

hc_points(hc, ir)

hc = HilbertCurve(1, 100, level = 4, reference = TRUE)
hc_points(hc, x1 = c(1.5, 50.5), x2 = c(10.5, 60.5))

require(circlize)
value = runif(length(ir))
col_fun = colorRamp2(range(value), c("white", "red"))
hc = HilbertCurve(1, 100, level = 4, reference = TRUE)
hc_points(hc, ir, np = 3, shape = "star", gp = gpar(fill = col_fun(value)))

hc = HilbertCurve(1, 100, level = 4, reference = TRUE)
hc_points(hc, ir, np = 0)

hc = HilbertCurve(1, 100, level = 4, reference = TRUE)
hc_points(hc, np = 0, x1 = c(1.5, 50.5), x2 = c(10.5, 60.5))
hc_points(hc, np = 0, x1 = 70.5, gp = gpar(col = "red"))
```

---

hc_polygon-dispatch *Method dispatch page for hc_polygon*

Description

Method dispatch page for hc_polygon.

Dispatch

hc_polygon can be dispatched on following classes:

- hc_polygon,GenomicHilbertCurve-method, GenomicHilbertCurve-class class method
- hc_polygon,HilbertCurve-method, HilbertCurve-class class method

Examples

```
# no example
NULL
```

---

hc_polygon-GenomicHilbertCurve-method
Add text to Hilbert curve

Description

Add text to Hilbert curve

Usage

```
## S4 method for signature 'GenomicHilbertCurve'
hc_polygon(object, gr, gp = gpar(),
    end_type = c("average", "expanding", "shrinking"))
```

Arguments

object	a GenomicHilbertCurve-class object
gr	a GRanges object which contains the genomic regions to be mapped to the curve
gp	pass to hc_polygon,HilbertCurve-method
end_type	pass to hc_polygon,HilbertCurve-method

Details

It is basically a wrapper of hc_polygon,HilbertCurve-method.

Value

Refer to hc_polygon,HilbertCurve-method

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
require(circlize)
require(GenomicRanges)
bed = generateRandomBed(nr = 20)
gr = GRanges(seqnames = bed[[1]], ranges = IRanges(bed[[2]], bed[[3]]))
hc = GenomicHilbertCurve()
hc_polygon(hc, gr)
```

hc_polygon-HilbertCurve-method *Add polygons to Hilbert curve*

Description

Add polygons to Hilbert curve

Usage

```
## S4 method for signature 'HilbertCurve'
hc_polygon(object, ir = NULL, x1 = NULL, x2 = NULL,
    gp = gpar(), end_type = c("expanding", "average", "shrinking"))
```

Arguments

object	a HilbertCurve-class object.
ir	an IRanges object which specifies the input intervals.
x1	if start positions are not integers, they can be set by x1.
x2	if end positions are not integers, they can be set by x2.
gp	graphic parameters. It should be specified by gpar.
end_type	since two ends of a continuous interval do not necessarily completely overlap with the Hilbert curve segments, this argument controls how to determine the ends of the interval which will be presented on the curve. average: if the end covers more than half of the segment, the whole segment is included and if the end covers less than half of the segment, the segment is removed; expanding: segments are included as long as they are overlapped; shrinking: segments are removed if they are not completely covered.

Details

Drawing polygons are quite visually similar as drawing rectangles. The major differences are: 1) for rectangles, colors for the ends of the interval can change if they are not completely covered by the Hilbert curve segments, and 2) polygons can have borders.

Normally polygons are used to mark areas in the Hilbert curve.

Value

No value is returned.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
require(IRanges)
ir = IRanges(10, 40)

hc = HilbertCurve(0, 100, level = 4, reference = TRUE)
hc_segments(hc, ir)
hc_text(hc, x1 = 10:40, labels = 10:40)
hc_polygon(hc, ir, gp = gpar(fill = "#FF000080", col = 1))
```

`hc_rect-dispatch` *Method dispatch page for hc_rect*

Description

Method dispatch page for `hc_rect`.

Dispatch

`hc_rect` can be dispatched on following classes:

- `hc_rect,GenomicHilbertCurve-method`, `GenomicHilbertCurve-class` class method
- `hc_rect,HilbertCurve-method`, `HilbertCurve-class` class method

Examples

```
# no example
NULL
```

`hc_rect-GenomicHilbertCurve-method`
Add rectangles on Hilbert curve

Description

Add rectangles on Hilbert curve

Usage

```
## S4 method for signature 'GenomicHilbertCurve'
hc_rect(object, gr, gp = gpar(fill = "red", col = "red"),
    mean_mode = c("w0", "absolute", "weighted", "max_freq"))
```

Arguments

object	a GenomicHilbertCurve-class object
gr	a GRanges object which contains the genomic regions to be mapped to the curve
gp	pass to hc_rect,HilbertCurve-method
mean_mode	pass to hc_rect,HilbertCurve-method

Details

It is basically a wrapper of hc_rect,HilbertCurve-method.

Value

Refer to hc_rect,HilbertCurve-method

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
require(circlize)
require(GenomicRanges)
bed = generateRandomBed(nr = 100)
gr = GRanges(seqnames = bed[[1]], ranges = IRanges(bed[[2]], bed[[3]]))
hc = GenomicHilbertCurve()
hc_rect(hc, gr, gp = gpar(fill = rand_color(length(gr))))
```

---

hc_rect-HilbertCurve-method

Add rectangles on Hilbert curve

Description

Add rectangles on Hilbert curve

Usage

```
## S4 method for signature 'HilbertCurve'
hc_rect(object, ir = NULL, x1 = NULL, x2 = NULL,
    gp = gpar(fill = "red"),
    mean_mode = c("w0", "absolute", "weighted", "max_freq"))
```

Arguments

object	A HilbertCurve-class object.
ir	an IRanges object which specifies the input intervals.
x1	if start positions are not integers, they can be set by x1.
x2	if end positions are not integers, they can be set by x2.
gp	graphic parameters for rectangles. It should be specified by gpar. Note you cannot set linejoin and lineend.
mean_mode	when a segment in the curve can not be overlapped with intervals in ir, how to calculate the mean values for this segment. See explanation in hc_points,HilbertCurve-method.

Details

Rectangles are put if a segment in the Hilbert curve overlaps with the input intervals. You cannot set the width or height of the rectangles. It is always fixed (actually it is a square).

It can be thought as the low-resolution version of hc_layer,HilbertCurve-method.

Value

A data frame which contains coordinates (in the 2D space) of rectangles.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
hc = HilbertCurve(1, 100, level = 4, reference = TRUE)

x = sort(sample(100, 20))
s = x[1:10*2 - 1]
e = x[1:10*2]
require(IRanges)
ir = IRanges(s, e)
hc_rect(hc, ir)
```

---

hc_segmented_points-HilbertCurve-method

Add points to the Hilbert curve

Description

Add points to the Hilbert curve

Usage

```
## S4 method for signature 'HilbertCurve'
hc_segmented_points(object, ir = NULL, x1 = NULL, x2 = NULL, gp = gpar(),
    np = max(c(2, 10 - hc_level(object))),
    mean_mode = c("w0", "absolute", "weighted", "max_freq"),
    shape = "circle")
```

Arguments

object	A HilbertCurve-class object.
ir	an IRanges object which specifies the input intervals.
x1	if start positions are not integers, they can be set by x1.
x2	if end positions are not integers, they can be set by x2.
np	number of points (a circle or a square, ...) that are put in a segment.
gp	graphic parameters for points. It should be specified by gpar. The size of the points can be set here because the size of points are determined by np argument.
mean_mode	when a segment in the curve overlaps with intervals in ir, how to calculate the mean values for this segment. See explanation in hc_points.
shape	shape of points. Possible values are "circle", "square", "triangle", "hexagon", "star".

Details

Every segment on the curve is split by np points.

This function is used internally, please use hc_points,HilbertCurve-method directly.

Value

A data frame which contains coordinates (in the 2D space) of points.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
# see documentation of hc_points
NULL
```

hc_segments-dispatch *Method dispatch page for hc_segments*

Description

Method dispatch page for hc_segments.

Dispatch

hc_segments can be dispatched on following classes:

- hc_segments,GenomicHilbertCurve-method, GenomicHilbertCurve-class class method
- hc_segments,HilbertCurve-method, HilbertCurve-class class method

Examples

```
# no example
NULL
```

hc_segments-GenomicHilbertCurve-method *Add line segments to Hilbert curve*

Description

Add line segments to Hilbert curve

Usage

```
## S4 method for signature 'GenomicHilbertCurve'
hc_segments(object, gr, gp = gpar(lty = 1, lwd = 1, col = 1))
```

Arguments

object	a GenomicHilbertCurve-class object
gr	a GRanges object which contains the genomic regions to be mapped to the curve
gp	pass to hc_segments,HilbertCurve-method

Details

It is basically a wrapper of hc_segments,HilbertCurve-method.

Value

Refer to hc_segments,HilbertCurve-method

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
require(circlize)
require(GenomicRanges)
bed = generateRandomBed(nr = 100)
gr = GRanges(seqnames = bed[[1]], ranges = IRanges(bed[[2]], bed[[3]]))
hc = GenomicHilbertCurve()
hc_segments(hc, gr, gp = gpar(col = rand_color(length(gr))))
```

---

hc_segments-HilbertCurve-method

Add line segments to Hilbert curve

Description

Add line segments to Hilbert curve

Usage

```
## S4 method for signature 'HilbertCurve'
hc_segments(object, ir = NULL, x1 = NULL, x2 = NULL,
    gp = gpar(lty = 1, lwd = 1, col = 1))
```

Arguments

object	A HilbertCurve-class object.
ir	an IRanges object which specifies the input intervals.
x1	if start positions are not integers, they can be set by x1.
x2	if end positions are not integers, they can be set by x2.
gp	graphic parameters for lines. It should be specified by gpar. Note you cannot set linejoin and lineend.

Value

A data frame which contains coordinates (in the 2D space) of segments.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
hc = HilbertCurve(1, 100, level = 4, reference = TRUE)

x = sort(sample(100, 20))
s = x[1:10*2 - 1]
e = x[1:10*2]
require(IRanges)
ir = IRanges(s, e)

hc_segments(hc, ir)
```

`hc_text-dispatch` *Method dispatch page for hc_text*

Description

Method dispatch page for `hc_text`.

Dispatch

`hc_text` can be dispatched on following classes:

- `hc_text,HilbertCurve-method`, `HilbertCurve-class` class method
- `hc_text,GenomicHilbertCurve-method`, `GenomicHilbertCurve-class` class method

Examples

```
# no example
NULL
```

`hc_text-GenomicHilbertCurve-method`
Add text to Hilbert curve

Description

Add text to Hilbert curve

Usage

```
## S4 method for signature 'GenomicHilbertCurve'
hc_text(object, gr, labels, gp = gpar(),
    centered_by = c("interval", "polygon"), ...)
```

Arguments

object	a GenomicHilbertCurve-class object
gr	a GRanges object which contains the genomic regions to be mapped to the curve
labels	pass to hc_text,HilbertCurve-method
gp	pass to hc_text,HilbertCurve-method
centered_by	how to define the "center" of the interval represented in Hilbert curve. Pass to hc_text,HilbertCurve-method.
...	pass to hc_text,HilbertCurve-method

Details

It is basically a wrapper of hc_text,HilbertCurve-method.

Value

Refer to hc_text,HilbertCurve-method

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
require(circlize)
require(GenomicRanges)
bed = generateRandomBed(nr = 20)
gr = GRanges(seqnames = bed[[1]], ranges = IRanges(bed[[2]], bed[[3]]))
hc = GenomicHilbertCurve()
hc_text(hc, gr, labels = sample(letters, nrow(bed), replace = TRUE))
```

---

hc_text-HilbertCurve-method

Add text to Hilbert curve

Description

Add text to Hilbert curve

Usage

```
## S4 method for signature 'HilbertCurve'
hc_text(object, ir = NULL, labels, x1 = NULL, x2 = x1, gp = gpar(),
    centered_by = c("interval", "polygon"), ...)
```

Arguments

object	A HilbertCurve-class object.
ir	an IRanges object that contains positions which correspond to text. The middle point of the interval will be the position of the text.
labels	text corresponding to intervals in ir.
x1	if start positions are not integers, they can be set by x1.
x2	if end positions are not integers, they can be set by x2.
gp	graphic parameters for text. It should be specified by gpar.
centered_by	how to define the "center" of the interval represented in Hilbert curve. See Details section.
...	pass to grid.text. E.g. you can set text justification by just here.

Details

If centered_by == "interval", the text is added correspoding to the middle of each interval in ir, while if centered_by == "polygon", the text is put in the visual center of the polygon of the interval in the Hilbert curve.

Value

A data frame which contains coordinates (in the 2D space) of text.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
hc = HilbertCurve(1, 100, level = 4, reference = TRUE)

x = sort(sample(100, 20))
s = x[1:10*2 - 1]
e = x[1:10*2]
require(IRanges)
ir = IRanges(s, e)

labels = sample(letters, length(ir), replace = TRUE)
hc_text(hc, ir, labels = labels)
```

hc_which-dispatch *Method dispatch page for hc_which*

Description

Method dispatch page for hc_which.

Dispatch

hc_which can be dispatched on following classes:

- hc_which,HilbertCurve-method, HilbertCurve-class class method
- hc_which,GenomicHilbertCurve-method, GenomicHilbertCurve-class class method

Examples

```
# no example
NULL
```

hc_which-GenomicHilbertCurve-method *Query regions*

Description

Query regions

Usage

```
## S4 method for signature 'GenomicHilbertCurve'
hc_which(object, ix, iy)
```

Arguments

object	a GenomicHilbertCurve-class object
ix	A single position on x-axis.
iy	A single position on y-axis.

Details

Values of ix and iy should be integers and take values in [1, 2^level].

Value

A data frame with three columns `chr`, `start` and `end`. The value corresponds to the genomic ranges.

Examples

```
# There is no example
NULL
```

`hc_which-HilbertCurve-method`
Query regions

Description

Query regions

Usage

```
## S4 method for signature 'HilbertCurve'
hc_which(object, ix, iy)
```

Arguments

`object`	A `HilbertCurve-class` object.
`ix`	A single position on x-axis.
`iy`	A single position on y-axis.

Details

Values of `ix` and `iy` should be integers and take values in [1, 2^level].

Value

A data frame with two columns `start` and `end`. The value corresponds to the range in data.

Examples

```
# There is no example
NULL
```

`HilbertCurve` *Initialize a Hilbert curve*

Description

Initialize a Hilbert curve

Usage

```
HilbertCurve(s, e, level = 4, mode = c("normal", "pixel"),
    reference = FALSE, reference_gp = gpar(lty = 3, col = "#999999"),
    arrow = TRUE, zoom = NULL, newpage = TRUE,
    background_col = "transparent", background_border = NA,
    title = NULL, title_gp = gpar(fontsize = 16),
    start_from = c("bottomleft", "topleft", "bottomright", "topright"),
    first_seg = c("horizontal", "vertical"), legend = list(),
    padding = unit(2, "mm"))
```

Arguments

`s`	position that will be mapped as the start of the Hilbert curve. The value should a single numeric value. If it is a vector, the minimum is used.
`e`	position that will be mapped as the end of the Hilbert curve. The value should a single numeric value. If it is a vector, the maximum is used.
`level`	iteration level of the Hilbert curve. There will by `4^level - 1` segments in the curve.
`mode`	"normal" mode is used for low `level` value and "pixel" mode is always used for high `level` value, so the "normal" mode is always for low-resolution visualization while "pixel" mode is used for high-resolution visualization. See 'details' for explanation.
`reference`	whether add reference lines on the plot. Only works under 'normal' mode. The reference line is only used for illustrating how the curve folds.
`reference_gp`	graphic settings for the reference lines. It should be specified by `gpar`.
`arrow`	whether add arrows on the reference line. Only works under 'normal' mode.
`zoom`	Internally, position are stored as integer values. To better map the data to the Hilbert curve, the original positions are zoomed according to the range and the level of Hilbert curve. E.g. if the curve visualizes data ranging from 1 to 2 but level of the curve is set to 4, the positions will be zoomed by ~x2000 so that values like 1.5, 1.555 can be mapped to the curve with more accuracy. You don't need to care the zooming thing, proper zooming factor is calculated automatically.
`newpage`	whether call `grid.newpage` to draw on a new graphic device.
`background_col`	background color.

background_border	background border border.
title	title of the plot.
title_gp	graphic parameters for the title. It should be specified by gpar.
start_from	which corner on the plot should the curve starts?
first_seg	the orientation of the first segment.
legend	a grob object, a Legends-class object, or a list of them.
padding	padding around the Hilbert curve.

Details

This funciton initializes a Hilbert curve with level level which corresponds to the range between s and e.

Under 'normal' mode, there is a visible Hilbert curve which plays like a folded axis and different low-level graphics can be added afterwards according to the coordinates. It works nice if the level of the Hilbert curve is small (say less than 6).

When the level is high (e.g. > 10), the whole 2D space will be almost completely filled by the curve and it is impossible to add or visualize e.g. points on the curve. In this case, the 'pixel' mode visualizes each tiny 'segment' as a pixel and maps values to colors. Internally, the whole plot is represented as an RGB matrix and every time a new layer is added to the plot, the RGB matrix will be updated according to the color overlay. When all the layers are added, normally a PNG figure is generated directly from the RGB matrix. So the Hilbert curve with level 11 will generate a PNG figure with 2048x2048 resolution. This is extremely useful for visualize genomic data. E.g. If we make a Hilbert curve for human chromosome 1 with level 11, then each pixel can represent 60bp (249250621/2048/2048) which is of very high resolution.

Under 'pixel' mode, if the current device is an interactive deivce, every time a new layer is added, the image will be add to the interactive device as a rastered image. But still you can use hc_png,HilbertCurve-method to export the plot as PNG file.

To make it short and clear, under "normal" mode, you can use following low-level graphic functions:

- hc_points,HilbertCurve-method
- hc_segments,HilbertCurve-method
- hc_rect,HilbertCurve-method
- hc_polygon,HilbertCurve-method
- hc_text,HilbertCurve-method

And under "pixel" mode, you can use following functions:

- hc_layer,HilbertCurve-method
- hc_png,HilbertCurve-method
- hc_polygon,HilbertCurve-method
- hc_text,HilbertCurve-method

Notice, s and e are not necessarily to be integers, it can be any values (e.g. numeric or even negative values).

Value

A HilbertCurve-class object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
HilbertCurve(1, 100, reference = TRUE)
HilbertCurve(1, 100, level = 5, reference = TRUE)
HilbertCurve(1, 100, title = "title", reference = TRUE)
HilbertCurve(1, 100, start_from = "topleft", reference = TRUE)

# plot with one legend
require(ComplexHeatmap)
legend = Legend(labels = c("a", "b"), title = "foo",
    legend_gp = gpar(fill = c("red", "blue")))
hc = HilbertCurve(1, 100, title = "title", legend = legend)
hc_segments(hc, x1 = 20, x2 = 40)

# plot with more than one legend
require(circlize)
legend1 = Legend(labels = c("a", "b"), title = "foo",
    legend_gp = gpar(fill = c("red", "blue")))
col_fun = colorRamp2(c(-1, 0, 1), c("green", "white", "red"))
legend2 = Legend(col_fun = col_fun, title = "bar")
hc = HilbertCurve(1, 100, title = "title", legend = list(legend1, legend2))
hc_segments(hc, x1 = 20, x2 = 40)
```

HilbertCurve-class *The HilbertCurve class*

Description

The HilbertCurve class

Details

Hilbert curve (https://en.wikipedia.org/wiki/Hilbert_curve) is a type of space-filling curves that folds one-dimensional axis into a two-dimensional space, but still keeps the locality. It has advantages to visualize data with long axis with high resolution.

This package aims to provide an easy and flexible way to visualize data through Hilbert curve. The implementation and example figures are based on following sources:

- http://mkweb.bcgsc.ca/hilbert/
- http://corte.si/posts/code/hilbert/portrait/index.html
- http://bioconductor.org/packages/devel/bioc/html/HilbertVis.html

Methods

The HilbertCurve-class provides following methods:

- HilbertCurve: constructor method;
- hc_points,HilbertCurve-method: add points;
- hc_segments,HilbertCurve-method: add lines;
- hc_rect,HilbertCurve-method: add rectangles;
- hc_polygon,HilbertCurve-method: add polygons;
- hc_text,HilbertCurve-method: add text;
- hc_layer,HilbertCurve-method: add layers, works under "pixel" mode;
- hc_png,HilbertCurve-method: save plot as PNG format, works under "pixel" mode.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

See Also

The GenomicHilbertCurve-class inherits HilbertCurve-class and is designed specifically for handling genomic data.

Examples

```
NULL
```

---

is_white *Whether the color is white*

Description

Whether the color is white

Usage

```
is_white(r, g, b, maxColorValue = 1)
```

Arguments

r	Red channel.
g	Green channel.
b	Blue channel.
maxColorValue	1 or 255.

Examples

```
# There is no example
NULL
```

show-HilbertCurve-method

Print the HilbertCurve object

Description

Print the HilbertCurve object

Usage

```
## S4 method for signature 'HilbertCurve'
show(object)
```

Arguments

object	A HilbertCurve-class object.

Value

No value is returned.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
HilbertCurve(1, 100)
```

unzoom-HilbertCurve-method

Transform zoomed positions to their original values

Description

Transform zoomed positions to their original values

Usage

```
## S4 method for signature 'HilbertCurve'
unzoom(object, x)
```

Arguments

object	A HilbertCurve-class object.
x	positions.

Details

This is a reverse function of zoom,HilbertCurve-method.

The function is used internally.

Value

A numeric vector of original positions.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
hc = HilbertCurve(1, 2)
z = zoom(hc, 1.5)
unzoom(hc, z)
```

---

zoom-HilbertCurve-method

Zoom original positions

Description

Zoom original positions

Usage

```
## S4 method for signature 'HilbertCurve'
zoom(object, x)
```

Arguments

object	A HilbertCurve-class object.
x	original positions.

Details

Internally, position are stored as integer values. To better map the data to the Hilbert curve, the original positions are zoomed according to the range and the level of Hilbert curve. E.g. if the curve visualizes data ranging from 1 to 2 but level of the curve is set to 4, the positions will be zoomed by ~x2000 so that values like 1.5, 1.555 can be mapped to the curve with more accuracy.

The function is used internally.

Value

A numeric vector which is zoomed positions.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
hc = HilbertCurve(1, 2)
zoom(hc, 1.5)
```

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