

# Package ‘shiny.gosling’

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**Title** A Grammar-based Toolkit for Scalable and Interactive Genomics  
Data Visualization for R and Shiny

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**Description** A Grammar-based Toolkit for Scalable and Interactive Genomics Data Visualization. <http://gosling-lang.org/>. This R package is based on gosling.js. It uses R functions to create gosling plots that could be embedded onto R Shiny apps.

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---

`add_file_to_resource_path`*Track data object builder for local csv files*

---

**Description**

Get an object for using local csv to build plots

**Usage**

```
add_file_to_resource_path(file_path = NULL, object = NULL)
```

**Arguments**

<code>file_path</code>	A character. Specify the <code>file_path</code> to the local csv file.
<code>object</code>	A gr ranges object.

**Value**

list of data specs for a local csv file

---

`add_mark`*Visual marks*

---

**Description**

Visual marks (e.g., points, lines, and bars) are the basic graphical elements of a visualization.

**Usage**

```
add_mark(  
  x = NULL,  
  xe = NULL,  
  x1 = NULL,  
  x1e = NULL,  
  y = NULL,  
  strokeWidth = NULL,  
  opacity = NULL,  
  row = NULL,  
  size = NULL,  
  color = NULL,  
  stroke = NULL  
)
```

**Arguments**

x	An object returned by visual_channel_x().
xe	An object returned by visual_channel_x().
x1	An object returned by visual_channel_x().
x1e	An object returned by visual_channel_x().
y	An object returned by visual_channel_y().
strokeWidth	A number or an object returned by visual_channel_stroke_width().
opacity	A number or an object returned by visual_channel_opacity().
row	A factor data column Channel row is used with channel y to stratify a visualization with categorical values.
size	A number or an object returned by visual_channel_size().
color	A character or an object returned by visual_channel_color().
stroke	A number or an object returned by visual_channel_stroke().

**Details**

For info visit <http://gosling-lang.org/docs/mark>

**Value**

list of mark specifications

---

add\_multi\_tracks      *Combine single tracks.*

---

**Description**

Combine single tracks.

**Usage**

```
add_multi_tracks(...)
```

**Arguments**

...      Multiple tracks from add\_single\_track() function.

**Value**

json list.

**Examples**

```
if(interactive()) {
  library(shiny)
  library(shiny.gosling)

  track5_styles <- default_track_styles(
    legendTitle = "SV Class"
  )
  track5_data <- track_data(
    url = "https://s3.amazonaws.com/gosling-lang.org/data/cancer/rearrangement.PD35930a.csv",
    type = "csv",
    genomicFieldsToConvert = json_list(
      json_list(
        chromosomeField = "chr1",
        genomicFields = c("start1", "end1")
      ),
      json_list(
        chromosomeField = "chr2",
        genomicFields = c("start2", "end2")
      )
    )
  )
  track5_tracks <- add_multi_tracks(
    add_single_track(
      mark = "rect"
    ),
    add_single_track(
      mark = "withinLink", x = visual_channel_x(linkingId = "mid-scale"),
      strokeWidth = 0
    )
  )
  track5_color <- visual_channel_color(
    field = "svclass",
    type = "nominal",
    legend = TRUE,
    domain = json_list(
      "tandem-duplication", "translocation", "deletion", "inversion"
    ),
    range = json_list(
      "#569C4D", "#4C75A2", "#DA5456", "#EA8A2A"
    )
  )
  track5_stroke <- visual_channel_stroke(
    field = "svclass",
    type = "nominal",
    domain = json_list(
      "tandem-duplication", "translocation", "deletion", "inversion"
    ),
    range = json_list(
      "#569C4D", "#4C75A2", "#DA5456", "#EA8A2A"
    )
  )
}
```

```

track5_x <- visual_channel_x(field = "start1", type = "genomic")
track5_xe <- visual_channel_x(field = "end2", type = "genomic")
track5 <- add_single_track(
  id = "track5", title = "Structural Variant",
  data = track5_data, mark = "withinLink",
  x = track5_x, xe = track5_xe,
  color = track5_color, width = 500, height = 80, stroke = track5_stroke,
  strokeWidth = 1, opacity = 0.6, style = track5_styles
)

composed_track <- compose_view(
  multi = TRUE,
  tracks = add_multi_tracks(
    track5
  ),
  xOffset = 190, layout = "circular", spacing = 1
)

composed_views <- arrange_views(
  views = composed_track,
  arrangement = "vertical"
)

ui <- fluidPage(
  use_gosling(),
  fluidRow(
    column(6, goslingOutput("gosling_plot"))
  )
)

server <- function(input, output, session) {
  output$gosling_plot <- renderGosling({
    gosling(
      component_id = "component_2",
      composed_views, clean_braces = FALSE
    )
  })
}

shinyApp(ui, server)
}

```

---

add\_single\_track

*Add a single track*


---

### Description

Add a single track to the plot of a mark type ( plot type ). This function constructs a single track from the inputs. The inputs can be id, data, mark etc. Please check gosling.js documentation for

usage.

### Usage

```
add_single_track(
  id = NULL,
  data = NULL,
  mark = NULL,
  assembly = NULL,
  row = NULL,
  size = NULL,
  color = NULL,
  strokeWidth = NULL,
  opacity = NULL,
  x = NULL,
  xe = NULL,
  x1 = NULL,
  x1e = NULL,
  y = NULL,
  stroke = NULL,
  width = NULL,
  height = NULL,
  dataTransform = NULL,
  ...
)
```

### Arguments

id	Optional argument to assign an id to the track.
data	An object of from track_data() function.
mark	Type of plot. One of c("point", "line", "rect", "bar", "area", "link", "triangle", "text"). Each mark type has some supported visual channel. Different marks support different visual channels: <ul style="list-style-type: none"> <li>• point: x, y, row, size, color, strokeWidth, opacity</li> <li>• line: x, y, row, color, strokeWidth</li> <li>• rect: x, xe, row, color, strokeWidth, opacity</li> <li>• bar: x, y, row, color, strokeWidth, opacity</li> <li>• area: x, y, row, color, strokeWidth</li> <li>• link: x, xe, x1, x1e, color, opacity</li> <li>• triangle: x, xe, row, size, color, opacity</li> <li>• text: x, xe, row, color, opacity</li> </ul> For more info visit <a href="http://gosling-lang.org/tutorials/">http://gosling-lang.org/tutorials/</a>
assembly	Currently support "hg38", "hg19", "hg18", "hg17", "hg16", "mm10", "mm9". Defaults to "hg38".
row	An object of from visual_channel_row().
size	An object of from visual_channel_size() OR an atomic number.

color	An object of from <code>visual_channel_color()</code> OR and atomic character hex code of the form "#123456".
strokeWidth	An object of from <code>visual_channel_stroke_width()</code> OR an atomic number.
opacity	An object of from <code>visual_channel_opacity()</code> OR and atomic ratio from 0 to 1.
x	An object of from <code>visual_channel_x()</code> OR an atomic value.
xe	An object of from <code>visual_channel_x()</code> OR an atomic value.
x1	An object of from <code>visual_channel_x()</code> OR an atomic value.
x1e	An object of from <code>visual_channel_x()</code> OR an atomic value.
y	An object of from <code>visual_channel_y()</code> OR an atomic value.
stroke	An object of from <code>visual_channel_stroke()</code> function OR a character of hex color code like "#123456".
width	A number interpreted in units of pixel.
height	A number interpreted in units of pixel.
dataTransform	An object of from <code>track_data_transform()</code> function.
...	Any other arguments to be passed onto <code>gosling.js</code> .

**Value**

list object.

**Examples**

```
if(interactive()) {
  library(shiny)
  library(shiny.gosling)

  cistrome_data <-
    "https://server.gosling-lang.org/api/v1/tileset_info/?d=cistrome-multivec"

  single_track <- add_single_track(
    id = "track1",
    data = track_data(
      url = cistrome_data,
      type = "multivec",
      row = "sample",
      column = "position",
      value = "peak",
      categories = c("sample 1", "sample 2", "sample 3", "sample 4"),
      binSize = 4,
    ),
    mark = "rect",
    x = visual_channel_x(field = "start", type = "genomic", axis = "top"),
    xe = visual_channel_x(field = "end", type = "genomic"),
    row = visual_channel_row(
      field = "sample",
      type = "nominal",
      legend = TRUE
    )
  )
}
```

```

    ),
    color = visual_channel_color(
      field = "peak",
      type = "quantitative",
      legend = TRUE
    ),
    tooltip = visual_channel_tooltips(
      visual_channel_tooltip(field = "start", type = "genomic",
                             alt = "Start Position"),
      visual_channel_tooltip(field = "end", type = "genomic",
                             alt = "End Position"),
      visual_channel_tooltip(
        field = "peak",
        type = "quantitative",
        alt = "Value",
        format = "0.2"
      )
    ),
    width = 600,
    height = 130
  )

single_composed_track <- compose_view(
  tracks = single_track
)

single_composed_views <- arrange_views(
  title = "Single Track",
  subtitle = "This is the simplest single track visualization with a linear layout",
  layout = "circular", # "linear"
  views = single_composed_track,
  xDomain = list(
    chromosome = "chr1",
    interval = c(1, 3000500)
  )
)

ui <- fluidPage(
  use_gosling(),
  fluidRow(
    column(6, goslingOutput("gosling_plot")),
    column(
      1, br(), actionButton(
        "download_png",
        "PNG",
        icon = icon("cloud-arrow-down")
      )
    )
  )
)

server <- function(input, output, session) {

```

```

output$gosling_plot <- renderGosling({
  gosling(
    component_id = "component_1",
    single_composed_views,
    clean_braces = TRUE
  )
})

observeEvent(input$download_png, {
  export_png(component_id = "component_1")
})
}

shinyApp(ui, server)
}

```

---

arrange\_views

*Arrange views*


---

### Description

Arrange views from `compose_view()` function.

### Usage

```
arrange_views(layout = NULL, views = NULL, listify = TRUE, ...)
```

### Arguments

<code>layout</code>	One of "linear" or "circular".
<code>views</code>	An object from <code>compose_view()</code> function.
<code>listify</code>	A Boolean. Convert views to list..
<code>...</code>	More options passed to <code>gosling.js</code> .

### Value

list object.

### Examples

```

if(interactive()) {
  library(shiny)
  library(shiny.gosling)

  # View 2 Track 3----
  view2_track3_data <- track_data(
    url = "https://server.gosling-lang.org/api/v1/tileset_info/?d=NC_045512_2-multivec",
    type = "multivec",

```

```
    row = "base",
    column = "position",
    value = "count",
    categories = c("A", "T", "G", "C"),
    start = "start",
    end = "end"
  )

view2_track3a <- add_single_track(
  mark = "bar",
  y = visual_channel_y(
    field = "count", type = "quantitative", axis = "none"
  )
)

view2_track3b <- add_single_track(
  dataTransform = track_data_transform(
    type = "filter",
    field = "count",
    oneOf = list(0),
    not = TRUE
  ),
  mark = "text",
  x = visual_channel_x(
    field = "start", type = "genomic"
  ),
  xe = visual_channel_x(
    field = "end", type = "genomic"
  ),
  size = 24,
  color = "white",
  visibility = list(list(
    operation = "less-than",
    measure = "width",
    threshold = "|xe-x|",
    transitionPadding = 30,
    target = "mark"
  )),
  list(
    operation = "LT",
    measure = "zoomLevel",
    threshold = 40,
    target = "track"
  ))
)

view2_track3_x <- visual_channel_x(
  field = "position", type = "genomic"
)

view2_track3_color <- visual_channel_color(
  field = "base",
  type = "nominal",
```

```

    domain = c("A", "T", "G", "C"),
    legend = TRUE
  )

view2_track3_text <- visual_channel_text(
  field = "base", type = "nominal"
)

view2_track3_style <- default_track_styles(
  inlineLegend = TRUE
)

view2_track3 <- add_single_track(
  title = "NC_045512.2 Sequence",
  alignment = "overlay",
  data = view2_track3_data,
  tracks = add_multi_tracks(
    view2_track3a, view2_track3b
  ),
  x = view2_track3_x,
  color = view2_track3_color,
  text = view2_track3_text,
  style = view2_track3_style,
  width = 800, height = 40
)

view2 <- compose_view(
  multi = TRUE,
  centerRadius = 0,
  xDomain = list(interval = c(1, 29903)),
  linkingId = "detail",
  alignment = "stack",
  tracks = add_multi_tracks(
    view2_track3
  )
)

combined_view <- arrange_views(
  title = "SARS-CoV-2",
  subtitle = "Data Source: WashU Virus Genome Browser, NCBI, GISAID",
  assembly = list(list("NC_045512.2", 29903)),
  layout = "linear",
  spacing = 50,
  views = list(view2),
  listify = FALSE
)

ui <- fluidPage(
  use_gosling(),
  fluidRow(
    column(6, goslingOutput("gosling_plot"))
  )
)

```

```

server <- function(input, output, session) {
  output$gosling_plot <- renderGosling({
    gosling(
      component_id = "sars_cov2",
      combined_view
    )
  })
}

shinyApp(ui, server)
}

```

---

atomic\_values\_to\_list *atomic\_values\_to\_list*

---

### Description

atomic\_values\_to\_list

### Usage

```
atomic_values_to_list(property_list)
```

### Arguments

property\_list A character or number or another atomic value.

### Value

List.

---

brush\_styles *style of the brush mark*

---

### Description

Customize the style of the brush mark in the rangeSelect mouse event.

### Usage

```

brush_styles(
  strokeWidth = NULL,
  strokeOpacity = NULL,
  stroke = NULL,
  opacity = NULL,
  color = NULL
)

```

**Arguments**

strokeWidth	A number. stroke width of the marks when mouse events are triggered.
strokeOpacity	A number.
stroke	A character. Stroke color of the marks when mouse events are triggered.
opacity	A number. Opacity of the marks when mouse events are triggered.
color	A character. Color of the marks when mouse events are triggered.

**Details**

For more info visit <http://gosling-lang.org/docs/visual-channel/#type-brush>

**Value**

List object with brush styles.

---

 build\_json

*Build gosling spec from R list*


---

**Description**

Build gosling spec from R list

**Usage**

```
build_json(r_list, clean_braces = TRUE, pretty = TRUE, auto_unbox = TRUE)
```

**Arguments**

r_list	R list object built with other gosling functions
clean_braces	Whether to remove extra square brackets from the json string.
pretty	Whether to get json with indentation, line breaks etc.
auto_unbox	If TRUE will automatically unbox() all atomic vectors of length 1.

**Value**

json spec for the gosling output

---

component	<i>Create react component</i>
-----------	-------------------------------

---

**Description**

Create react component

**Usage**

component(name)

**Arguments**

name	name of the react component
------	-----------------------------

**Value**

function to create react element

---

compose_view	<i>Compose views</i>
--------------	----------------------

---

**Description**

Compose views from add\_single\_track() and add\_multi\_tracks() functions.

**Usage**

```
compose_view(
  multi = FALSE,
  layout = NULL,
  width = NULL,
  height = NULL,
  centerRadius = NULL,
  tracks,
  ...
)
```

**Arguments**

multi	Whether multiple tracks in the view.
layout	One of "linear" or "circular".
width	A number interpreted in units of pixel.
height	A number interpreted in units of pixel.

centerRadius	Specify the proportion of the radius of the center white space. A number between c(0,1), default=0.3
tracks	The tracks with add_multi_tracks() function.
...	More arguments passed along with view to gosling.js.

**Value**

list object.

**Examples**

```

if(interactive()) {
  library(shiny)
  library(shiny.gosling)

  # View 2 Track 3----
  view2_track3_data <- track_data(
    url = "https://server.gosling-lang.org/api/v1/tileset_info/?d=NC_045512_2-multivec",
    type = "multivec",
    row = "base",
    column = "position",
    value = "count",
    categories = c("A", "T", "G", "C"),
    start = "start",
    end = "end"
  )

  view2_track3a <- add_single_track(
    mark = "bar",
    y = visual_channel_y(
      field = "count", type = "quantitative", axis = "none"
    )
  )

  view2_track3b <- add_single_track(
    dataTransform = track_data_transform(
      type = "filter",
      field = "count",
      oneOf = list(),
      not = TRUE
    ),
    mark = "text",
    x = visual_channel_x(
      field = "start", type = "genomic"
    ),
    xe = visual_channel_x(
      field = "end", type = "genomic"
    ),
    size = 24,
    color = "white",
    visibility = list(list(
      operation = "less-than",

```

```
        measure = "width",
        threshold = "|xe-x|",
        transitionPadding = 30,
        target = "mark"
    ),
    list(
        operation = "LT",
        measure = "zoomLevel",
        threshold = 40,
        target = "track"
    ))
)

view2_track3_x <- visual_channel_x(
  field = "position", type = "genomic"
)

view2_track3_color <- visual_channel_color(
  field = "base",
  type = "nominal",
  domain = c("A", "T", "G", "C"),
  legend = TRUE
)

view2_track3_text <- visual_channel_text(
  field = "base", type = "nominal"
)

view2_track3_style <- default_track_styles(
  inlineLegend = TRUE
)

view2_track3 <- add_single_track(
  title = "NC_045512.2 Sequence",
  alignment = "overlay",
  data = view2_track3_data,
  tracks = add_multi_tracks(
    view2_track3a, view2_track3b
  ),
  x = view2_track3_x,
  color = view2_track3_color,
  text = view2_track3_text,
  style = view2_track3_style,
  width = 800, height = 40
)

view2 <- compose_view(
  multi = TRUE,
  centerRadius = 0,
  xDomain = list(interval = c(1, 29903)),
  linkingId = "detail",
  alignment = "stack",
  tracks = add_multi_tracks(
```

```

        view2_track3
      )
    )

    combined_view <- arrange_views(
      title = "SARS-CoV-2",
      subtitle = "Data Source: WashU Virus Genome Browser, NCBI, GISAID",
      assembly = list(list("NC_045512.2", 29903)),
      layout = "linear",
      spacing = 50,
      views = list(view2),
      listify = FALSE
    )

    ui <- fluidPage(
      use_gosling(),
      fluidRow(
        column(6, goslingOutput("gosling_plot"))
      )
    )

    server <- function(input, output, session) {
      output$gosling_plot <- renderGosling({
        gosling(
          component_id = "sars_cov2",
          combined_view
        )
      })
    }

    shinyApp(ui, server)
  }

```

---

default\_track\_styles *Default styles for tracks*

---

## Description

Default styles for tracks

## Usage

```

default_track_styles(
  textStrokeWidth = NULL,
  textStroke = NULL,
  textFontWeight = NULL,
  textFontSize = NULL,

```

```

    textAnchor = NULL,
    select = NULL,
    outlineWidth = NULL,
    outline = NULL,
    mouseOver = NULL,
    matrixExtent = NULL,
    linkStyle = NULL,
    linkMinHeight = NULL,
    linkConnectionType = NULL,
    linePattern = NULL,
    legendTitle = NULL,
    inlineLegend = NULL,
    enableSmoothPath = NULL,
    dy = NULL,
    dx = NULL,
    dashed = NULL,
    curve = NULL,
    brush = NULL,
    backgroundOpacity = NULL,
    background = NULL,
    align = NULL,
    ...
)

```

### Arguments

textStrokeWidth	A number. Specify the stroke width of text marks. Can also be specified using the strokeWidth channel option of text marks.
textStroke	A character. Specify the stroke of text marks. Can also be specified using the stroke channel option of text marks.
textFontWeight	A character. One of "bold", "normal". Specify the font weight of text marks.
textFontSize	A number. Specify the font size of text marks. Can also be specified using the size channel option of text marks.
textAnchor	A character. One of "start", "middle", "end". Specify the alignment of text marks to a given point.
select	An object returned by event_styles(). Customize visual effects of rangeSelect events on marks.
outlineWidth	A number.
outline	A character.
mouseOver	An object returned by event_styles(). Customize visual effects of mouseOver events on marks.
matrixExtent	A character. One of "full", "upper-right", "lower-left". Determine to show only one side of the diagonal in a HiGlass matrix. Default: "full".
linkStyle	A character. One of "elliptical", "circular", "straight", "experimentalEdgeBundling". The style of withinLink and betweenLink marks. Default: 'circular' 'elliptical' will be used as a default option.

linkMinHeight	A number. The minimum height of withinLink and betweenLink marks. Unit is a percentage Default: 0.5.
linkConnectionType	A character. One of "straight", "curve", "corner". Specify the connection type of betweenLink marks. Default: "corner".
linePattern	A list of the form list(size="number",type="string"). One of "triangleLeft", "triangleRight".) Specify the pattern of dashes and gaps for rule marks.
legendTitle	A character. If defined, show legend title on the top or left.
inlineLegend	A Boolean. Specify whether to show legend in a single horizontal line?
enableSmoothPath	A Boolean. Whether to enable smooth paths when drawing curves. Default: FALSE.
dy	A number. Offset the position of marks in y direction. This property is currently only supported for text marks.
dx	A number. Offset the position of marks in x direction. This property is currently only supported for text marks.
dashed	An vector of number like c(1, 2). Specify the pattern of dashes and gaps for rule marks.
curve	A character. One of "top", "bottom", "left", "right". Specify the curve of rule marks.
brush	An object returned by brush_styles(). Customize the style of the brush mark in the rangeSelect mouse event.
backgroundOpacity	A number.
background	A character.
align	A character. One of "left", "right". Specify the alignment of marks. This property is currently only supported for triangle marks.
...	Any other styles to be passed to gosling.js.

### Details

For more info visit <http://gosling-lang.org/docs/visual-channel/#style-related-properties>

### Value

List object with default styles.

### Examples

```
if(interactive()) {
  library(shiny)
  library(shiny.gosling)

  track5_styles <- default_track_styles(
    legendTitle = "SV Class"
  )
}
```

```

track5_data <- track_data(
  url = "https://s3.amazonaws.com/gosling-lang.org/data/cancer/rearrangement.PD35930a.csv",
  type = "csv",
  genomicFieldsToConvert = json_list(
    json_list(
      chromosomeField = "chr1",
      genomicFields = c("start1", "end1")
    ),
    json_list(
      chromosomeField = "chr2",
      genomicFields = c("start2", "end2")
    )
  )
)
track5_tracks <- add_multi_tracks(
  add_single_track(
    mark = "rect"
  ),
  add_single_track(
    mark = "withinLink", x = visual_channel_x(linkingId = "mid-scale"),
    strokeWidth = 0
  )
)
track5_color <- visual_channel_color(
  field = "svclass",
  type = "nominal",
  legend = TRUE,
  domain = json_list(
    "tandem-duplication", "translocation", "deletion", "inversion"
  ),
  range = json_list(
    "#569C4D", "#4C75A2", "#DA5456", "#EA8A2A"
  )
)
track5_stroke <- visual_channel_stroke(
  field = "svclass",
  type = "nominal",
  domain = json_list(
    "tandem-duplication", "translocation", "deletion", "inversion"
  ),
  range = json_list(
    "#569C4D", "#4C75A2", "#DA5456", "#EA8A2A"
  )
)
track5_x <- visual_channel_x(field = "start1", type = "genomic")
track5_xe <- visual_channel_x(field = "end2", type = "genomic")
track5 <- add_single_track(
  id = "track5", title = "Structural Variant",
  data = track5_data, mark = "withinLink",
  x = track5_x, xe = track5_xe,
  color = track5_color, width = 500, height = 80, stroke = track5_stroke,
  strokeWidth = 1, opacity = 0.6, style = track5_styles
)

```

```

composed_track <- compose_view(
  multi = TRUE,
  tracks = add_multi_tracks(
    track5
  ),
  xOffset = 190, layout = "circular", spacing = 1
)

composed_views <- arrange_views(
  views = composed_track,
  arrangement = "vertical"
)

ui <- fluidPage(
  use_gosling(),
  fluidRow(
    column(6, goslingOutput("gosling_plot"))
  )
)

server <- function(input, output, session) {
  output$gosling_plot <- renderGosling({
    gosling(
      component_id = "component_2",
      composed_views, clean_braces = FALSE
    )
  })
}

shinyApp(ui, server)
}

```

---

event\_styles

*Mouse event styles*


---

### Description

The styles defined here will be applied to the targets of mouse events, such as a point mark after user click mouse.

### Usage

```

event_styles(
  strokeWidth = NULL,
  strokeOpacity = NULL,
  stroke = NULL,
  opacity = NULL,

```

```

    color = NULL,
    arrange = NULL
  )

```

### Arguments

strokeWidth	A number. stroke width of the marks when mouse events are triggered.
strokeOpacity	A number.
stroke	A character. Stroke color of the marks when mouse events are triggered.
opacity	A number. Opacity of the marks when mouse events are triggered.
color	A character. Color of the marks when mouse events are triggered.
arrange	A character. One of "behind", "front". Show event effects behind or in front of marks.

### Details

For more info visit <http://gosling-lang.org/docs/visual-channel/#type-eventstyle>

### Value

List object with event styles.

---

export\_pdf

*Export PDF*

---

### Description

Exports PDF

### Usage

```

export_pdf(
  component_id,
  transparent_background = FALSE,
  session = getDefaultReactiveDomain()
)

```

### Arguments

component_id	A character. The id of the component_id prop passed to the GoslingComponent function.
transparent_background	A Boolean. Determine if the background should be transparent or not (Default: false).
session	A shiny session object.

**Value**

None.

**Examples**

```
if(interactive()) {
  library(shiny)
  library(shiny.gosling)

  cistrome_data <-
    "https://server.gosling-lang.org/api/v1/tileset_info/?d=cistrome-multivec"

  single_track <- add_single_track(
    id = "track1",
    data = track_data(
      url = cistrome_data,
      type = "multivec",
      row = "sample",
      column = "position",
      value = "peak",
      categories = c("sample 1", "sample 2", "sample 3", "sample 4"),
      binSize = 4,
    ),
    mark = "rect",
    x = visual_channel_x(field = "start", type = "genomic", axis = "top"),
    xe = visual_channel_x(field = "end", type = "genomic"),
    row = visual_channel_row(
      field = "sample",
      type = "nominal",
      legend = TRUE
    ),
    color = visual_channel_color(
      field = "peak",
      type = "quantitative",
      legend = TRUE
    ),
    tooltip = visual_channel_tooltips(
      visual_channel_tooltip(field = "start", type = "genomic",
                            alt = "Start Position"),
      visual_channel_tooltip(field = "end", type = "genomic",
                            alt = "End Position"),
      visual_channel_tooltip(
        field = "peak",
        type = "quantitative",
        alt = "Value",
        format = "0.2"
      )
    ),
    width = 600,
    height = 130
  )
}
```

```
single_composed_track <- compose_view(  
  tracks = single_track  
)  
  
single_composed_views <- arrange_views(  
  title = "Single Track",  
  subtitle = "This is the simplest single track visualization with a linear layout",  
  layout = "circular", #"linear"  
  views = single_composed_track,  
  xDomain = list(  
    chromosome = "chr1",  
    interval = c(1, 3000500)  
  )  
)  
  
ui <- fluidPage(  
  use_gosling(),  
  fluidRow(  
    column(6, goslingOutput("gosling_plot")),  
    column(  
      1, br(), actionButton(  
        "download_pdf",  
        "PDF",  
        icon = icon("cloud-arrow-down")  
      )  
    )  
  )  
)  
  
server <- function(input, output, session) {  
  output$gosling_plot <- renderGosling({  
    gosling(  
      component_id = "component_1",  
      single_composed_views,  
      clean_braces = TRUE  
    )  
  })  
  
  observeEvent(input$download_pdf, {  
    export_pdf(component_id = "component_1")  
  })  
}  
  
shinyApp(ui, server)  
}
```

**Description**

Exports PNG

**Usage**

```
export_png(  
  component_id,  
  transparent_background = FALSE,  
  session = getDefaultReactiveDomain()  
)
```

**Arguments**

`component_id` A character. The id of the `component_id` prop passed to the `GoslingComponent` function.

`transparent_background` A Boolean. Determine if the background should be transparent or not (Default: `false`).

`session` A shiny session object.

**Value**

None.

**Examples**

```
if(interactive()) {  
  library(shiny)  
  library(shiny.gosling)  
  
  cistrome_data <-  
    "https://server.gosling-lang.org/api/v1/tileset_info/?d=cistrome-multivec"  
  
  single_track <- add_single_track(  
    id = "track1",  
    data = track_data(  
      url = cistrome_data,  
      type = "multivec",  
      row = "sample",  
      column = "position",  
      value = "peak",  
      categories = c("sample 1", "sample 2", "sample 3", "sample 4"),  
      binSize = 4,  
    ),  
    mark = "rect",  
    x = visual_channel_x(field = "start", type = "genomic", axis = "top"),  
    xe = visual_channel_x(field = "end", type = "genomic"),  
    row = visual_channel_row(  
      field = "sample",  
      type = "nominal",  
      legend = TRUE
```

```

    ),
    color = visual_channel_color(
      field = "peak",
      type = "quantitative",
      legend = TRUE
    ),
    tooltip = visual_channel_tooltips(
      visual_channel_tooltip(field = "start", type = "genomic",
        alt = "Start Position"),
      visual_channel_tooltip(field = "end", type = "genomic",
        alt = "End Position"),
      visual_channel_tooltip(
        field = "peak",
        type = "quantitative",
        alt = "Value",
        format = "0.2"
      )
    ),
    width = 600,
    height = 130
  )

single_composed_track <- compose_view(
  tracks = single_track
)

single_composed_views <- arrange_views(
  title = "Single Track",
  subtitle = "This is the simplest single track visualization with a linear layout",
  layout = "circular", # "linear"
  views = single_composed_track,
  xDomain = list(
    chromosome = "chr1",
    interval = c(1, 3000500)
  )
)

ui <- fluidPage(
  use_gosling(),
  fluidRow(
    column(6, goslingOutput("gosling_plot")),
    column(
      1, br(), actionButton(
        "download_png",
        "PNG",
        icon = icon("cloud-arrow-down")
      )
    )
  )
)

server <- function(input, output, session) {

```

```

output$gosling_plot <- renderGosling({
  gosling(
    component_id = "component_1",
    single_composed_views,
    clean_braces = TRUE
  )
})

observeEvent(input$download_png, {
  export_png(component_id = "component_1")
})
}

shinyApp(ui, server)
}

```

---

get\_file\_track\_data    *Track data object builder for local csv files*

---

## Description

Get an object for using local csv to build plots

## Usage

```

get_file_track_data(
  file_name,
  chromosomeField = NULL,
  genomicFields = NULL,
  separator = ",",
  sampleLength = 1000,
  headerNames = NULL,
  ...
)

```

## Arguments

file_name	A character. Specify the file_name.
chromosomeField	A character. Specify the name of chromosome data fields.
genomicFields	A character vector. Specify the name of genomic data fields.
separator	A character. Specify file separator, Default: ','
sampleLength	A number. Specify the number of rows loaded from the URL. Default: 1000
headerNames	A character vector. Specify the names of data fields if a CSV file does not have header row.
...	Any other parameters passed to json data object.

**Value**

list of data specs for a local csv file

---

gosling	<i>Build gosling plot object</i>
---------	----------------------------------

---

**Description**

Build gosling plot object

**Usage**

```
gosling(component_id, composed_views, clean_braces = TRUE)
```

**Arguments**

`component_id` Assign a component id to use other api like zoom.  
`composed_views` The views composed with `arrange_views`.  
`clean_braces` Whether to remove extra square brackets from the json string.

**Value**

Gosling component for rendering on R shiny apps

**Examples**

```
if (interactive()) {
  library(shiny)
  library(shiny.gosling)

  # Circular track 1 ----
  circular_track1_data <- track_data(
    url = "https://server.gosling-lang.org/api/v1/tileset_info/?d=cistrome-multivec",
    type = "multivec",
    row = "sample",
    column = "position",
    value = "peak",
    categories = c("sample 1", "sample 2", "sample 3", "sample 4"),
    binSize = 4
  )

  circular_track1_x <- visual_channel_x(field = "start", type = "genomic")
  circular_track1_xe <- visual_channel_x(field = "end", type = "genomic")

  circular_track1_y <- visual_channel_y(field = "peak", type = "quantitative")

  circular_track1_row <- visual_channel_row(
    field = "sample", type = "nominal"
  )
}
```

```

)

circular_track1_color <- visual_channel_color(
  field = "sample", type = "nominal"
)

circular_track1_tracks <- add_multi_tracks(
  add_single_track(
    mark = "bar"
  ),
  add_single_track(
    mark = "brush",
    x = visual_channel_x(linkingId = "detail-1"),
    color = "blue"
  ),
  add_single_track(
    mark = "brush",
    x = visual_channel_x(linkingId = "detail-2"),
    color = "red"
  )
)

circular_track1_styles <- default_track_styles(
  outlineWidth = 0
)

circular_track1 <- add_single_track(
  id = "circular_track1", alignment = "overlay", data = circular_track1_data,
  x = circular_track1_x, xe = circular_track1_xe,
  y = circular_track1_y, row = circular_track1_row,
  color = circular_track1_color,
  stroke = "black", strokeWidth = 0.3,
  tracks = circular_track1_tracks,
  style = circular_track1_styles,
  width = 500, height = 100
)

# Compose Circular track ----
circular_composed_view <- compose_view(
  multi = TRUE,
  tracks = add_multi_tracks(
    circular_track1
  ),
  static = TRUE, layout = "circular", alignment = "stack"
)

# Arrange final view
circular_linear_view <- arrange_views(
  arrangement = "horizontal",
  views = list(circular_composed_view)
)

```

```
ui <- fluidPage(  
  use_gosling(),  
  fluidRow(  
    column(6, goslingOutput("gosling_plot"))  
  )  
)  
  
server <- function(input, output, session) {  
  output$gosling_plot <- renderGosling({  
    gosling(  
      component_id = "circular_component",  
      circular_linear_view, clean_braces = FALSE  
    )  
  })  
}  
  
shinyApp(ui, server)  
}
```

---

GoslingComponent	<i>Create Gosling component</i>
------------------	---------------------------------

---

### Description

Create Gosling component

### Usage

```
GoslingComponent(...)
```

### Arguments

...                   Name of component.

### Value

A function to create the gosling component.

---

goslingDependency	<i>Setup gosling dependencies</i>
-------------------	-----------------------------------

---

**Description**

Setup gosling dependencies

**Usage**

```
goslingDependency()
```

**Value**

list of dependencies for Gosling

---

goslingOutput	<i>gosling output function</i>
---------------	--------------------------------

---

**Description**

gosling output function for shiny use. Must use this function instead of shiny output functions.

**Usage**

```
goslingOutput(outputId)
```

**Arguments**

outputId	ID of the output element
----------	--------------------------

**Value**

reactOutput HTML for UI render

**Examples**

```
if(interactive()) {
  library(shiny)
  library(shiny.gosling)

  track5_styles <- default_track_styles(
    legendTitle = "SV Class"
  )
  track5_data <- track_data(
    url = "https://s3.amazonaws.com/gosling-lang.org/data/cancer/rearrangement.PD35930a.csv",
    type = "csv",
    genomicFieldsToConvert = json_list(
```

```

    json_list(
      chromosomeField = "chr1",
      genomicFields = c("start1", "end1")
    ),
    json_list(
      chromosomeField = "chr2",
      genomicFields = c("start2", "end2")
    )
  )
)
)
track5_tracks <- add_multi_tracks(
  add_single_track(
    mark = "rect"
  ),
  add_single_track(
    mark = "withinLink", x = visual_channel_x(linkingId = "mid-scale"),
    strokeWidth = 0
  )
)
)
track5_color <- visual_channel_color(
  field = "svclass",
  type = "nominal",
  legend = TRUE,
  domain = json_list(
    "tandem-duplication", "translocation", "deletion", "inversion"
  ),
  range = json_list(
    "#569C4D", "#4C75A2", "#DA5456", "#EA8A2A"
  )
)
)
track5_stroke <- visual_channel_stroke(
  field = "svclass",
  type = "nominal",
  domain = json_list(
    "tandem-duplication", "translocation", "deletion", "inversion"
  ),
  range = json_list(
    "#569C4D", "#4C75A2", "#DA5456", "#EA8A2A"
  )
)
)
track5_x <- visual_channel_x(field = "start1", type = "genomic")
track5_xe <- visual_channel_x(field = "end2", type = "genomic")
track5 <- add_single_track(
  id = "track5", title = "Structural Variant",
  data = track5_data, mark = "withinLink",
  x = track5_x, xe = track5_xe,
  color = track5_color, width = 500, height = 80, stroke = track5_stroke,
  strokeWidth = 1, opacity = 0.6, style = track5_styles
)
)
composed_track <- compose_view(
  multi = TRUE,
  tracks = add_multi_tracks(

```

```
      track5
    ),
    xOffset = 190, layout = "circular", spacing = 1
  )

  composed_views <- arrange_views(
    views = composed_track,
    arrangement = "vertical"
  )

  ui <- fluidPage(
    use_gosling(),
    fluidRow(
      column(6, goslingOutput("gosling_plot"))
    )
  )

  server <- function(input, output, session) {
    output$gosling_plot <- renderGosling({
      gosling(
        component_id = "component_2",
        composed_views, clean_braces = FALSE
      )
    })
  }

  shinyApp(ui, server)
}
```

---

`is_atomic_field`

*is\_atomic\_field*

---

### **Description**

`is_atomic_field`

### **Usage**

```
is_atomic_field(field_name)
```

### **Arguments**

`field_name`      A character or number or another atomic value.

### **Value**

List.

---

`json_list`*Create list*

---

**Description**

Create list

**Usage**`json_list(...)`**Arguments**`...` Items to be put in a list**Value**

list of items

**Examples**

```
if (interactive()) {
  library(shiny)
  library(shiny.gosling)

  track5_styles <- default_track_styles(
    legendTitle = "SV Class"
  )
  track5_data <- track_data(
    url = "https://s3.amazonaws.com/gosling-lang.org/data/cancer/rearrangement.PD35930a.csv",
    type = "csv",
    genomicFieldsToConvert = json_list(
      json_list(
        chromosomeField = "chr1",
        genomicFields = c("start1", "end1")
      ),
      json_list(
        chromosomeField = "chr2",
        genomicFields = c("start2", "end2")
      )
    )
  )
  track5_tracks <- add_multi_tracks(
    add_single_track(
      mark = "rect"
    ),
    add_single_track(
      mark = "withinLink", x = visual_channel_x(linkingId = "mid-scale"),
      strokeWidth = 0
    )
  )
}
```

```

)
track5_color <- visual_channel_color(
  field = "svclass",
  type = "nominal",
  legend = TRUE,
  domain = json_list(
    "tandem-duplication", "translocation", "deletion", "inversion"
  ),
  range = json_list(
    "#569C4D", "#4C75A2", "#DA5456", "#EA8A2A"
  )
)
track5_stroke <- visual_channel_stroke(
  field = "svclass",
  type = "nominal",
  domain = json_list(
    "tandem-duplication", "translocation", "deletion", "inversion"
  ),
  range = json_list(
    "#569C4D", "#4C75A2", "#DA5456", "#EA8A2A"
  )
)
track5_x <- visual_channel_x(field = "start1", type = "genomic")
track5_xe <- visual_channel_x(field = "end2", type = "genomic")
track5 <- add_single_track(
  id = "track5", title = "Structural Variant",
  data = track5_data, mark = "withinLink",
  x = track5_x, xe = track5_xe,
  color = track5_color, width = 500, height = 80, stroke = track5_stroke,
  strokeWidth = 1, opacity = 0.6, style = track5_styles
)

composed_track <- compose_view(
  multi = TRUE,
  tracks = add_multi_tracks(
    track5
  ),
  xOffset = 190, layout = "circular", spacing = 1
)

composed_views <- arrange_views(
  views = composed_track,
  arrangement = "vertical"
)

ui <- fluidPage(
  use_gosling(),
  fluidRow(
    column(6, goslingOutput("gosling_plot"))
  )
)

```

```

server <- function(input, output, session) {
  output$gosling_plot <- renderGosling({
    gosling(
      component_id = "component_2",
      composed_views, clean_braces = FALSE
    )
  })
}

shinyApp(ui, server)
}

```

---

list_rm_null	<i>Remove null from list</i>
--------------	------------------------------

---

**Description**

Remove null from list

**Usage**

```
list_rm_null(r_list)
```

**Arguments**

r\_list            An r list with NULL values

**Value**

r list without NULL values

---

print.gosling	<i>Print method for the gosling component</i>
---------------	---

---

**Description**

Print method for the gosling component

**Usage**

```
## S3 method for class 'gosling'
print(x, ...)
```

**Arguments**

x                    A gosling object  
 ...                  further arguments passed to or from other methods.

**Value**

r list without NULL values

---

renderGosling	<i>gosling render function</i>
---------------	--------------------------------

---

**Description**

gosling render function for shiny use

**Usage**

```
renderGosling(expr, env = parent.frame(), quoted = FALSE)
```

**Arguments**

expr	Expression returning the HTML / 'React' to render.
env	Environment in which to evaluate expr.
quoted	Is expr a quoted expression?

**Value**

A function which can be assigned to an output in a Shiny server function.

**Examples**

```
if(interactive()) {
  library(shiny)
  library(shiny.gosling)

  track5_styles <- default_track_styles(
    legendTitle = "SV Class"
  )
  track5_data <- track_data(
    url = "https://s3.amazonaws.com/gosling-lang.org/data/cancer/rearrangement.PD35930a.csv",
    type = "csv",
    genomicFieldsToConvert = json_list(
      json_list(
        chromosomeField = "chr1",
        genomicFields = c("start1", "end1")
      ),
      json_list(
        chromosomeField = "chr2",
        genomicFields = c("start2", "end2")
      )
    )
  )
  track5_tracks <- add_multi_tracks(
```

```

    add_single_track(
      mark = "rect"
    ),
    add_single_track(
      mark = "withinLink", x = visual_channel_x(linkingId = "mid-scale"),
      strokeWidth = 0
    )
  )
)
track5_color <- visual_channel_color(
  field = "svclass",
  type = "nominal",
  legend = TRUE,
  domain = json_list(
    "tandem-duplication", "translocation", "deletion", "inversion"
  ),
  range = json_list(
    "#569C4D", "#4C75A2", "#DA5456", "#EA8A2A"
  )
)
)
track5_stroke <- visual_channel_stroke(
  field = "svclass",
  type = "nominal",
  domain = json_list(
    "tandem-duplication", "translocation", "deletion", "inversion"
  ),
  range = json_list(
    "#569C4D", "#4C75A2", "#DA5456", "#EA8A2A"
  )
)
)
track5_x <- visual_channel_x(field = "start1", type = "genomic")
track5_xe <- visual_channel_x(field = "end2", type = "genomic")
track5 <- add_single_track(
  id = "track5", title = "Structural Variant",
  data = track5_data, mark = "withinLink",
  x = track5_x, xe = track5_xe,
  color = track5_color, width = 500, height = 80, stroke = track5_stroke,
  strokeWidth = 1, opacity = 0.6, style = track5_styles
)
)

composed_track <- compose_view(
  multi = TRUE,
  tracks = add_multi_tracks(
    track5
  ),
  xOffset = 190, layout = "circular", spacing = 1
)
)

composed_views <- arrange_views(
  views = composed_track,
  arrangement = "vertical"
)
)

ui <- fluidPage(

```

```
    use_gosling(),
    fluidRow(
      column(6, goslingOutput("gosling_plot"))
    )
  )

server <- function(input, output, session) {
  output$gosling_plot <- renderGosling({
    gosling(
      component_id = "component_2",
      composed_views, clean_braces = FALSE
    )
  })
}

shinyApp(ui, server)
}
```

---

run\_example

*Runs a shiny.gosling example*

---

### **Description**

Runs a shiny.gosling example

### **Usage**

```
run_example(example = NA)
```

### **Arguments**

example            A character indicating a valid example.

### **Value**

A Shiny App is launched.

### **Examples**

```
if (interactive()) {
  run_example("circularLinearWithBrush")
}
```

---

track_data	<i>Data object builder</i>
------------	----------------------------

---

## Description

Build the data object for gosling plots

## Usage

```
track_data(  
  url = NULL,  
  type,  
  separator = NULL,  
  sampleLength = NULL,  
  headerNames = NULL,  
  genomicFields = NULL,  
  chromosomeField = NULL,  
  genomicFieldsToConvert = NULL,  
  ...  
)
```

## Arguments

url	A character. Specify the URL address of the data file.
type	A character. Type of data. One of "csv", "json", "bigwig", "bam", "vcf", "vector", "multivec" and "beddb". For usage refer to <a href="http://gosling-lang.org/docs/data#supported-data-formats">http://gosling-lang.org/docs/data#supported-data-formats</a> .
separator	A character. Specify file separator, Default: ','
sampleLength	A number. Specify the number of rows loaded from the URL. Default: 1000
headerNames	A character vector. Specify the names of data fields if a CSV file does not have header row.
genomicFields	A character vector. Specify the name of genomic data fields.
chromosomeField	A character. Specify the name of chromosome data fields.
genomicFieldsToConvert	Define the genomic fields from the data in list format. Experimental Property. Each object follows the format "chromosomeField":"string","genomicFields":"string[]" ( )
...	Any other parameters passed to json data object.

## Details

For info visit <http://gosling-lang.org/docs/data>. Check the various supported data formats and their parameters. All of them can be constructed using this function.

**Value**

list of data specs

**Examples**

```

if (interactive()) {
  library(shiny)
  library(shiny.gosling)

  # View 2 Track 3----
  view2_track3_data <- track_data(
    url = "https://server.gosling-lang.org/api/v1/tileset_info/?d=NC_045512_2-multivec",
    type = "multivec",
    row = "base",
    column = "position",
    value = "count",
    categories = c("A", "T", "G", "C"),
    start = "start",
    end = "end"
  )

  view2_track3a <- add_single_track(
    mark = "bar",
    y = visual_channel_y(
      field = "count", type = "quantitative", axis = "none"
    )
  )

  view2_track3b <- add_single_track(
    dataTransform = track_data_transform(
      type = "filter",
      field = "count",
      oneOf = list(0),
      not = TRUE
    ),
    mark = "text",
    x = visual_channel_x(
      field = "start", type = "genomic"
    ),
    xe = visual_channel_x(
      field = "end", type = "genomic"
    ),
    size = 24,
    color = "white",
    visibility = list(
      list(
        operation = "less-than",
        measure = "width",
        threshold = "|xe-x|",
        transitionPadding = 30,
        target = "mark"
      )
    )
  ),

```

```

    list(
      operation = "LT",
      measure = "zoomLevel",
      threshold = 40,
      target = "track"
    )
  )
)

view2_track3_x <- visual_channel_x(
  field = "position", type = "genomic"
)

view2_track3_color <- visual_channel_color(
  field = "base",
  type = "nominal",
  domain = c("A", "T", "G", "C"),
  legend = TRUE
)

view2_track3_text <- visual_channel_text(
  field = "base", type = "nominal"
)

view2_track3_style <- default_track_styles(
  inlineLegend = TRUE
)

view2_track3 <- add_single_track(
  title = "NC_045512.2 Sequence",
  alignment = "overlay",
  data = view2_track3_data,
  tracks = add_multi_tracks(
    view2_track3a, view2_track3b
  ),
  x = view2_track3_x,
  color = view2_track3_color,
  text = view2_track3_text,
  style = view2_track3_style,
  width = 800, height = 40
)

view2 <- compose_view(
  multi = TRUE,
  centerRadius = 0,
  xDomain = list(interval = c(1, 29903)),
  linkingId = "detail",
  alignment = "stack",
  tracks = add_multi_tracks(
    view2_track3
  )
)

```

```
combined_view <- arrange_views(  
  title = "SARS-CoV-2",  
  subtitle = "Data Source: WashU Virus Genome Browser, NCBI, GISAID",  
  assembly = list(list("NC_045512.2", 29903)),  
  layout = "linear",  
  spacing = 50,  
  views = list(view2),  
  listify = FALSE  
)  
  
ui <- fluidPage(  
  use_gosling(),  
  fluidRow(  
    column(6, goslingOutput("gosling_plot"))  
  )  
)  
  
server <- function(input, output, session) {  
  output$gosling_plot <- renderGosling({  
    gosling(  
      component_id = "sars_cov2",  
      combined_view  
    )  
  })  
}  
  
shinyApp(ui, server)  
}
```

---

track\_data\_csv

*Data object builder for a csv file*

---

## Description

Build the data object for gosling plots

## Usage

```
track_data_csv(  
  file,  
  genomicFields = NULL,  
  chromosomeField = NULL,  
  separator = ",",  
  sampleLength = 1000,  
  headerNames = NULL,  
  ...  
)
```

**Arguments**

file	A character. Specify the URL address or local file name in the www directory of the data file.
genomicFields	A character vector. Specify the name of genomic data fields.
chromosomeField	A character. Specify the name of chromosome data fields.
separator	A character. Specify file separator, Default: ','
sampleLength	A number. Specify the number of rows loaded from the URL. Default: 1000
headerNames	A character vector. Specify the names of data fields if a CSV file does not have header row.
...	Any other parameters passed to json data object.

**Value**

list of data specs for a csv file

**Examples**

```

if (interactive()) {
  library(shiny.gosling)
  library(shiny)
  library(GenomicRanges)

  url <- "https://rb.gy/7y3fx"
  temp_file <- file.path(tempdir(), "GSM1295076_CBX6_BF_ChipSeq_mergedReps_peaks.bed.gz")
  download.file(url, destfile = temp_file)
  df <- read.delim(
    temp_file,
    header = FALSE,
    comment.char = "#"
  )
  gr <- GRanges(
    seqnames = df$V1,
    ranges = IRanges(df$V2, df$V3)
  )

  if (!dir.exists("data")) {
    dir.create("data")
  }
  utils::write.csv(gr, "data/ChipSeqPeaks.csv", row.names = FALSE)

  ui <- fluidPage(
    use_gosling(clear_files = FALSE),
    goslingOutput("gosling_plot")
  )

  track_1 <- add_single_track(
    width = 800,
    height = 180,

```

```

data = track_data_csv(
  "data/ChipSeqPeaks.csv", chromosomeField = "seqnames",
  genomicFields = c("start", "end")
),
mark = "bar",
x = visual_channel_x(
  field = "start", type = "genomic", axis = "bottom"
),
xe = visual_channel_x(field = "end", type = "genomic"),
y = visual_channel_y(
  field = "width", type = "quantitative", axis = "right"
),
size = list(value = 5)
)

composed_view <- compose_view(
  layout = "linear",
  tracks = track_1
)

arranged_view <- arrange_views(
  title = "Basic Marks: bar",
  subtitle = "Tutorial Examples",
  views = composed_view
)

server <- function(input, output, session) {
  output$gosling_plot <- renderGosling({
    gosling(
      component_id = "component_1",
      arranged_view
    )
  })
}

shiny::shinyApp(ui, server)
}

```

---

track\_data\_gr

*Data object builder for a GRanges object by locally saving it*


---

### Description

Build the data object for gosling plots

### Usage

```

track_data_gr(
  granges,

```

```

    chromosomeField = NULL,
    genomicFields = NULL,
    separator = ",",
    sampleLength = 1000,
    headerNames = NULL,
    ...
  )

```

## Arguments

granges	A GRanges object from the GenomicRanges package with seqnames and ranges
chromosomeField	A character. Specify the name of chromosome data fields.
genomicFields	A character vector. Specify the name of genomic data fields.
separator	A character. Specify file separator, Default: ','
sampleLength	A number. Specify the number of rows loaded from the URL. Default: 1000
headerNames	A character vector. Specify the names of data fields if a CSV file does not have header row.
...	Any other parameters passed to json data object.

## Value

list of data specs for a csv file

## Examples

```

if (interactive()) {
  library(shiny.gosling)
  library(shiny)
  library(GenomicRanges)

  url <- "https://rb.gy/7y3fx"
  temp_file <- file.path(tempdir(), "GSM1295076_CBX6_BF_ChipSeq_mergedReps_peaks.bed.gz")
  download.file(url, destfile = temp_file)
  df <- read.delim(
    temp_file,
    header = FALSE,
    comment.char = "#"
  )
  gr <- GRanges(
    seqnames = df$V1,
    ranges = IRanges(df$V2, df$V3)
  )

  ui <- fluidPage(
    use_gosling(clear_files = FALSE),
    goslingOutput("gosling_plot")
  )
}

```

```
track_1 <- add_single_track(  
  width = 800,  
  height = 180,  
  data = track_data_gr(  
    gr, chromosomeField = "seqnames",  
    genomicFields = c("start", "end")  
  ),  
  mark = "bar",  
  x = visual_channel_x(  
    field = "start", type = "genomic", axis = "bottom"  
  ),  
  xe = visual_channel_x(field = "end", type = "genomic"),  
  y = visual_channel_y(  
    field = "width", type = "quantitative", axis = "right"  
  ),  
  size = list(value = 5)  
)  
  
composed_view <- compose_view(  
  layout = "linear",  
  tracks = track_1  
)  
  
arranged_view <- arrange_views(  
  title = "Basic Marks: bar",  
  subtitle = "Tutorial Examples",  
  views = composed_view  
)  
  
server <- function(input, output, session) {  
  output$gosling_plot <- renderGosling({  
    gosling(  
      component_id = "component_1",  
      arranged_view  
    )  
  })  
}  
  
shiny::shinyApp(ui, server)  
}
```

---

track\_data\_transform *Data transformer*

---

## Description

Do data transformations

**Usage**

```
track_data_transform(type = NULL, field = NULL, oneOf = NULL, not = NULL, ...)
```

**Arguments**

type	A character. One of "filter", "concat", "replace", "log", "displace", "exonSplit", "coverage", "genomicLength", "svType" and "subjson". Check usage details at <a href="http://gosling-lang.org/docs/data/#data-transform">http://gosling-lang.org/docs/data/#data-transform</a> .
field	A character. filter is applied based on the values of the specified data field.
oneOf	A vector of characters or numbers. Check whether the value is an element in the provided list.
not	A Boolean. When "not": true, apply a NOT logical operation to the filter. Default: false.
...	Any other parameters to pass to gosling.js.

**Details**

For info visit <http://gosling-lang.org/docs/data#data-transform> There are multiple ways to transform data. Check documentation for details of usage.

**Value**

list of data transformations specs

**Examples**

```
if (interactive()) {
  library(shiny)
  library(shiny.gosling)

  # View 2 Track 3----
  view2_track3_data <- track_data(
    url = "https://server.gosling-lang.org/api/v1/tileset_info/?d=NC_045512_2-multivec",
    type = "multivec",
    row = "base",
    column = "position",
    value = "count",
    categories = c("A", "T", "G", "C"),
    start = "start",
    end = "end"
  )

  view2_track3a <- add_single_track(
    mark = "bar",
    y = visual_channel_y(
      field = "count", type = "quantitative", axis = "none"
    )
  )

  view2_track3b <- add_single_track(
```

```
dataTransform = track_data_transform(  
  type = "filter",  
  field = "count",  
  oneOf = list(0),  
  not = TRUE  
)  
mark = "text",  
x = visual_channel_x(  
  field = "start", type = "genomic"  
)  
xe = visual_channel_x(  
  field = "end", type = "genomic"  
)  
size = 24,  
color = "white",  
visibility = list(  
  list(  
    operation = "less-than",  
    measure = "width",  
    threshold = "|xe-x|",  
    transitionPadding = 30,  
    target = "mark"  
  ),  
  list(  
    operation = "LT",  
    measure = "zoomLevel",  
    threshold = 40,  
    target = "track"  
  )  
)  
)  
  
view2_track3_x <- visual_channel_x(  
  field = "position", type = "genomic"  
)  
  
view2_track3_color <- visual_channel_color(  
  field = "base",  
  type = "nominal",  
  domain = c("A", "T", "G", "C"),  
  legend = TRUE  
)  
  
view2_track3_text <- visual_channel_text(  
  field = "base", type = "nominal"  
)  
  
view2_track3_style <- default_track_styles(  
  inlineLegend = TRUE  
)  
  
view2_track3 <- add_single_track(  
  title = "NC_045512.2 Sequence",
```

```
alignment = "overlay",
data = view2_track3_data,
tracks = add_multi_tracks(
  view2_track3a, view2_track3b
),
x = view2_track3_x,
color = view2_track3_color,
text = view2_track3_text,
style = view2_track3_style,
width = 800, height = 40
)

view2 <- compose_view(
  multi = TRUE,
  centerRadius = 0,
  xDomain = list(interval = c(1, 29903)),
  linkingId = "detail",
  alignment = "stack",
  tracks = add_multi_tracks(
    view2_track3
  )
)

combined_view <- arrange_views(
  title = "SARS-CoV-2",
  subtitle = "Data Source: WashU Virus Genome Browser, NCBI, GISAID",
  assembly = list(list("NC_045512.2", 29903)),
  layout = "linear",
  spacing = 50,
  views = list(view2),
  listify = FALSE
)

ui <- fluidPage(
  use_gosling(),
  fluidRow(
    column(6, goslingOutput("gosling_plot"))
  )
)

server <- function(input, output, session) {
  output$gosling_plot <- renderGosling({
    gosling(
      component_id = "sars_cov2",
      combined_view
    )
  })
}

shinyApp(ui, server)
}
```

---

`track_data_transforms` *Combine multiple data transforms*

---

**Description**

Combine multiple data transforms

**Usage**

```
track_data_transforms(...)
```

**Arguments**

... Multiple data transform specs separated by comma.

**Value**

list of multiple data transform specs

---

`use_gosling` *Initiate gosling*

---

**Description**

Add this function at the beginning of ui. This is needed for gosling to work in shiny plots.

**Usage**

```
use_gosling(clear_files = TRUE)
```

**Arguments**

`clear_files` default FALSE. To clear the locally stored csv files created by gosling or not.

**Value**

Gosling initiator HTML.

**Examples**

```
if (interactive()) {
  library(shiny)
  library(shiny.gosling)

  track5_styles <- default_track_styles(
    legendTitle = "SV Class"
  )
  track5_data <- track_data(
    url = "https://s3.amazonaws.com/gosling-lang.org/data/cancer/rearrangement.PD35930a.csv",
    type = "csv",
    genomicFieldsToConvert = json_list(
      json_list(
        chromosomeField = "chr1",
        genomicFields = c("start1", "end1")
      ),
      json_list(
        chromosomeField = "chr2",
        genomicFields = c("start2", "end2")
      )
    )
  )
  track5_tracks <- add_multi_tracks(
    add_single_track(
      mark = "rect"
    ),
    add_single_track(
      mark = "withinLink", x = visual_channel_x(linkingId = "mid-scale"),
      strokeWidth = 0
    )
  )
  track5_color <- visual_channel_color(
    field = "svclass",
    type = "nominal",
    legend = TRUE,
    domain = json_list(
      "tandem-duplication", "translocation", "deletion", "inversion"
    ),
    range = json_list(
      "#569C4D", "#4C75A2", "#DA5456", "#EA8A2A"
    )
  )
  track5_stroke <- visual_channel_stroke(
    field = "svclass",
    type = "nominal",
    domain = json_list(
      "tandem-duplication", "translocation", "deletion", "inversion"
    ),
    range = json_list(
      "#569C4D", "#4C75A2", "#DA5456", "#EA8A2A"
    )
  )
}
```

```

track5_x <- visual_channel_x(field = "start1", type = "genomic")
track5_xe <- visual_channel_x(field = "end2", type = "genomic")
track5 <- add_single_track(
  id = "track5", title = "Structural Variant",
  data = track5_data, mark = "withinLink",
  x = track5_x, xe = track5_xe,
  color = track5_color, width = 500, height = 80, stroke = track5_stroke,
  strokeWidth = 1, opacity = 0.6, style = track5_styles
)

composed_track <- compose_view(
  multi = TRUE,
  tracks = add_multi_tracks(
    track5
  ),
  xOffset = 190, layout = "circular", spacing = 1
)

composed_views <- arrange_views(
  views = composed_track,
  arrangement = "vertical"
)

ui <- fluidPage(
  use_gosling(),
  fluidRow(
    column(6, goslingOutput("gosling_plot"))
  )
)

server <- function(input, output, session) {
  output$gosling_plot <- renderGosling({
    gosling(
      component_id = "component_2",
      composed_views, clean_braces = FALSE
    )
  })
}

shinyApp(ui, server)
}

```

---

visual\_channel

*Generic visual channel builder*


---

### Description

Generic visual channel builder

**Usage**

```
visual_channel(field = NULL, type = NULL, range = NULL, domain = NULL, ...)
```

**Arguments**

field	A character. Name of the data field.
type	A character. Must be "genomic". Specify the data type.
range	A vector of characters or numbers. Values of the visual channel.
domain	A vector of characters or numbers. Values of the data.
...	Any other parameters to pass to gosling.js.

**Details**

For more info visit <http://gosling-lang.org/docs/visual-channel#encode-a-visual-channel>

**Value**

List object.

---

visual\_channel\_color *color visual channel*

---

**Description**

color visual channel

**Usage**

```
visual_channel_color(  
  field = NULL,  
  title = NULL,  
  type = NULL,  
  scaleOffset = NULL,  
  scale = NULL,  
  legend = NULL,  
  grid = NULL,  
  axis = NULL,  
  aggregate = NULL,  
  ...  
)
```

**Arguments**

field	A character. Name of the data field.
title	A character. Title of the legend. Default: undefined.
type	A character. Must be "genomic". Specify the data type.
scaleOffset	A number vector of the form $c(1, 2)$ . Whether to use offset of the domain proportionally. This is bound to brushes on the color legend. Default: $c(0, 1)$ .
scale	A character. One of "linear", "log".
legend	A Boolean. Whether to display legend. Default: FALSE.
grid	A Boolean. Whether to display grid. Default: FALSE.
axis	A character. One of "none", "top", "bottom", "left", "right". Specify where should the axis be put.
aggregate	A character. One of "max", "min", "mean", "bin", "count". Specify how to aggregate data. Default: undefined.
...	Any other parameters to pass to gosling.js.

**Details**

For more info visit <http://gosling-lang.org/docs/visual-channel#color>

**Value**

List object.

**Examples**

```
if(interactive()) {
  library(shiny)
  library(shiny.gosling)

  # View 2 Track 3----
  view2_track3_data <- track_data(
    url = "https://server.gosling-lang.org/api/v1/tileset_info/?d=NC_045512_2-multivec",
    type = "multivec",
    row = "base",
    column = "position",
    value = "count",
    categories = c("A", "T", "G", "C"),
    start = "start",
    end = "end"
  )

  view2_track3a <- add_single_track(
    mark = "bar",
    y = visual_channel_y(
      field = "count", type = "quantitative", axis = "none"
    )
  )
}
```

```
view2_track3b <- add_single_track(  
  dataTransform = track_data_transform(  
    type = "filter",  
    field = "count",  
    oneOf = list(0),  
    not = TRUE  
  ),  
  mark = "text",  
  x = visual_channel_x(  
    field = "start", type = "genomic"  
  ),  
  xe = visual_channel_x(  
    field = "end", type = "genomic"  
  ),  
  size = 24,  
  color = "white",  
  visibility = list(list(  
    operation = "less-than",  
    measure = "width",  
    threshold = "|xe-x|",  
    transitionPadding = 30,  
    target = "mark"  
  )),  
  list(  
    operation = "LT",  
    measure = "zoomLevel",  
    threshold = 40,  
    target = "track"  
  ))  
)  
  
view2_track3_x <- visual_channel_x(  
  field = "position", type = "genomic"  
)  
  
view2_track3_color <- visual_channel_color(  
  field = "base",  
  type = "nominal",  
  domain = c("A", "T", "G", "C"),  
  legend = TRUE  
)  
  
view2_track3_text <- visual_channel_text(  
  field = "base", type = "nominal"  
)  
  
view2_track3_style <- default_track_styles(  
  inlineLegend = TRUE  
)  
  
view2_track3 <- add_single_track(  
  title = "NC_045512.2 Sequence",  
  alignment = "overlay",
```

```

    data = view2_track3_data,
    tracks = add_multi_tracks(
      view2_track3a, view2_track3b
    ),
    x = view2_track3_x,
    color = view2_track3_color,
    text = view2_track3_text,
    style = view2_track3_style,
    width = 800, height = 40
  )

view2 <- compose_view(
  multi = TRUE,
  centerRadius = 0,
  xDomain = list(interval = c(1, 29903)),
  linkingId = "detail",
  alignment = "stack",
  tracks = add_multi_tracks(
    view2_track3
  )
)

combined_view <- arrange_views(
  title = "SARS-CoV-2",
  subtitle = "Data Source: WashU Virus Genome Browser, NCBI, GISAID",
  assembly = list(list("NC_045512.2", 29903)),
  layout = "linear",
  spacing = 50,
  views = list(view2),
  listify = FALSE
)

ui <- fluidPage(
  use_gosling(),
  fluidRow(
    column(6, goslingOutput("gosling_plot"))
  )
)

server <- function(input, output, session) {
  output$gosling_plot <- renderGosling({
    gosling(
      component_id = "sars_cov2",
      combined_view
    )
  })
}

shinyApp(ui, server)
}

```

---

```
visual_channel_opacity
      opacity visual channel
```

---

**Description**

opacity visual channel

**Usage**

```
visual_channel_opacity(
  field = NULL,
  type = NULL,
  range = NULL,
  domain = NULL,
  ...
)
```

**Arguments**

field	A character. Name of the data field.
type	A character. Must be "genomic". Specify the data type.
range	A vector of characters or numbers. Values of the visual channel.
domain	A vector of characters or numbers. Values of the data.
...	Any other parameters to pass to gosling.js.

**Details**

For more info visit <http://gosling-lang.org/docs/visual-channel#opacity>

**Value**

List object.

---

```
visual_channel_row      row visual channel
```

---

**Description**

row visual channel

**Usage**

```
visual_channel_row(
  field = NULL,
  type = NULL,
  padding = NULL,
  legend = NULL,
  grid = NULL,
  clip = NULL,
  axis = NULL,
  aggregate = NULL,
  ...
)
```

**Arguments**

field	A character. Name of the data field.
type	A character. Must be "genomic". Specify the data type.
padding	A number. Determines the size of inner white spaces on the top and bottom of individual rows. Default: 0.
legend	A Boolean. Whether to display legend. Default: FALSE.
grid	A Boolean. Whether to display grid. Default: FALSE.
clip	A Boolean. Clip row when the actual y value exceeds the max value of the y scale. Used only for bar marks at the moment. Default: TRUE.
axis	A character. One of "none", "top", "bottom", "left", "right". Specify where should the axis be put.
aggregate	A character. One of "max", "min", "mean", "bin", "count". Specify how to aggregate data. Default: undefined.
...	Any other parameters to pass to gosling.js.

**Details**

For more info visit <http://gosling-lang.org/docs/visual-channel#row>

**Value**

List object.

**Examples**

```
if(interactive()) {
  library(shiny)
  library(shiny.gosling)

  # Circular track 1 ----
  circular_track1_data <- track_data(
    url = "https://server.gosling-lang.org/api/v1/tileset_info/?d=cistrome-multivec",
    type = "multivec",
```

```

    row = "sample",
    column = "position",
    value = "peak",
    categories = c("sample 1", "sample 2", "sample 3", "sample 4"),
    binSize = 4
  )

circular_track1_x <- visual_channel_x(field = "start", type = "genomic")
circular_track1_xe <- visual_channel_x(field = "end", type = "genomic")

circular_track1_y <- visual_channel_y(field = "peak", type = "quantitative")

circular_track1_row <- visual_channel_row(
  field = "sample", type = "nominal"
)

circular_track1_color <- visual_channel_color(
  field = "sample", type = "nominal"
)

circular_track1_tracks <- add_multi_tracks(
  add_single_track(
    mark = "bar"
  ),
  add_single_track(
    mark = "brush",
    x = visual_channel_x(linkingId = "detail-1"),
    color = "blue"
  ),
  add_single_track(
    mark = "brush",
    x = visual_channel_x(linkingId = "detail-2"),
    color = "red"
  )
)

circular_track1_styles <- default_track_styles(
  outlineWidth = 0
)

circular_track1 <- add_single_track(
  id = "circular_track1", alignment = "overlay", data = circular_track1_data,
  x = circular_track1_x, xe = circular_track1_xe,
  y = circular_track1_y, row = circular_track1_row,
  color = circular_track1_color,
  stroke = "black", strokeWidth = 0.3,
  tracks = circular_track1_tracks,
  style = circular_track1_styles,
  width = 500, height = 100
)

# Compose Circular track ----
circular_composed_view <- compose_view(

```

```

    multi = TRUE,
    tracks = add_multi_tracks(
      circular_track1
    ),
    static = TRUE, layout = "circular", alignment = "stack"
  )

# Arrange final view
circular_linear_view <- arrange_views(
  arrangement = "horizontal",
  views = list(circular_composed_view)
)

ui <- fluidPage(
  use_gosling(),
  fluidRow(
    column(6, goslingOutput("gosling_plot"))
  )
)

server <- function(input, output, session) {
  output$gosling_plot <- renderGosling({
    gosling(
      component_id = "circular_component",
      circular_linear_view, clean_braces = FALSE
    )
  })
}

shinyApp(ui, server)
}

```

---

visual\_channel\_size    *size visual channel*

---

### Description

size visual channel

### Usage

```

visual_channel_size(
  field = NULL,
  type = NULL,

```

```

    range = NULL,
    domain = NULL,
    ...
)

```

### Arguments

field	A character. Name of the data field.
type	A character. Must be "genomic". Specify the data type.
range	A vector of characters or numbers. Values of the visual channel. Range to be specified like range = c(min_size, max_size)
domain	A vector of characters or numbers. Values of the data.
...	Any other parameters to pass to gosling.js.

### Details

For more info visit <http://gosling-lang.org/docs/visual-channel#size>

### Value

List object.

---

visual\_channel\_stroke *stroke visual channel*

---

### Description

stroke visual channel

### Usage

```

visual_channel_stroke(
  field = NULL,
  title = NULL,
  type = NULL,
  scaleOffset = NULL,
  legend = NULL,
  grid = NULL,
  axis = NULL,
  aggregate = NULL,
  ...
)

```

**Arguments**

field	A character. Name of the data field.
title	A character. Title of the legend. Default: undefined.
type	A character. Must be "genomic". Specify the data type.
scaleOffset	A number vector of the form c(1, 2). Whether to use offset of the domain proportionally. This is bound to brushes on the color legend. Default: c(0, 1).
legend	A Boolean. Whether to display legend. Default: FALSE.
grid	A Boolean. Whether to display grid. Default: FALSE.
axis	A character. One of "none", "top", "bottom", "left", "right". Specify where should the axis be put.
aggregate	A character. One of "max", "min", "mean", "bin", "count". Specify how to aggregate data. Default: undefined.
...	Any other parameters to pass to gosling.js.

**Details**

For more info visit <http://gosling-lang.org/docs/visual-channel#stroke>

**Value**

List object.

**Examples**

```
if(interactive()) {
  library(shiny)
  library(shiny.gosling)

  track5_styles <- default_track_styles(
    legendTitle = "SV Class"
  )
  track5_data <- track_data(
    url = "https://s3.amazonaws.com/gosling-lang.org/data/cancer/rearrangement.PD35930a.csv",
    type = "csv",
    genomicFieldsToConvert = json_list(
      json_list(
        chromosomeField = "chr1",
        genomicFields = c("start1", "end1")
      ),
      json_list(
        chromosomeField = "chr2",
        genomicFields = c("start2", "end2")
      )
    )
  )
  track5_tracks <- add_multi_tracks(
    add_single_track(
      mark = "rect"
    )
  )
}
```

```

    ),
    add_single_track(
      mark = "withinLink", x = visual_channel_x(linkingId = "mid-scale"),
      strokeWidth = 0
    )
  )
  track5_color <- visual_channel_color(
    field = "svclass",
    type = "nominal",
    legend = TRUE,
    domain = json_list(
      "tandem-duplication", "translocation", "deletion", "inversion"
    ),
    range = json_list(
      "#569C4D", "#4C75A2", "#DA5456", "#EA8A2A"
    )
  )
  track5_stroke <- visual_channel_stroke(
    field = "svclass",
    type = "nominal",
    domain = json_list(
      "tandem-duplication", "translocation", "deletion", "inversion"
    ),
    range = json_list(
      "#569C4D", "#4C75A2", "#DA5456", "#EA8A2A"
    )
  )
  track5_x <- visual_channel_x(field = "start1", type = "genomic")
  track5_xe <- visual_channel_x(field = "end2", type = "genomic")
  track5 <- add_single_track(
    id = "track5", title = "Structural Variant",
    data = track5_data, mark = "withinLink",
    x = track5_x, xe = track5_xe,
    color = track5_color, width = 500, height = 80, stroke = track5_stroke,
    strokeWidth = 1, opacity = 0.6, style = track5_styles
  )

  composed_track <- compose_view(
    multi = TRUE,
    tracks = add_multi_tracks(
      track5
    ),
    xOffset = 190, layout = "circular", spacing = 1
  )

  composed_views <- arrange_views(
    views = composed_track,
    arrangement = "vertical"
  )

  ui <- fluidPage(
    use_gosling(),
    fluidRow(

```

```

      column(6, goslingOutput("gosling_plot"))
    )
  )

  server <- function(input, output, session) {
    output$gosling_plot <- renderGosling({
      gosling(
        component_id = "component_2",
        composed_views, clean_braces = FALSE
      )
    })
  }

  shinyApp(ui, server)
}

```

---

visual\_channel\_stroke\_width

*stroke width visual channel*

---

## Description

stroke width visual channel

## Usage

```

visual_channel_stroke_width(
  field = NULL,
  type = NULL,
  range = NULL,
  domain = NULL,
  ...
)

```

## Arguments

field	A character. Name of the data field.
type	A character. Must be "genomic". Specify the data type.
range	A vector of characters or numbers. Values of the visual channel.
domain	A vector of characters or numbers. Values of the data.
...	Any other parameters to pass to gosling.js.

## Details

For more info visit <http://gosling-lang.org/docs/visual-channel#strokewidth>

**Value**

List object.

---

```
visual_channel_text  text visual channel
```

---

**Description**

text visual channel

**Usage**

```
visual_channel_text(  
  field = NULL,  
  type = NULL,  
  range = NULL,  
  domain = NULL,  
  ...  
)
```

**Arguments**

field	A character. Name of the data field.
type	A character. Must be "genomic". Specify the data type.
range	A vector of characters or numbers. Values of the visual channel.
domain	A vector of characters or numbers. Values of the data.
...	Any other parameters to pass to gosling.js.

**Details**

For more info visit <http://gosling-lang.org/docs/visual-channel#text>

**Value**

List object.

**Examples**

```
if(interactive()) {  
  library(shiny)  
  library(shiny.gosling)  
  
  # View 2 Track 3----  
  view2_track3_data <- track_data(  
    url = "https://server.gosling-lang.org/api/v1/tileset_info/?d=NC_045512_2-multivec",  
    type = "multivec",  
    row = "base",
```

```

    column = "position",
    value = "count",
    categories = c("A", "T", "G", "C"),
    start = "start",
    end = "end"
  )

view2_track3a <- add_single_track(
  mark = "bar",
  y = visual_channel_y(
    field = "count", type = "quantitative", axis = "none"
  )
)

view2_track3b <- add_single_track(
  dataTransform = track_data_transform(
    type = "filter",
    field = "count",
    oneOf = list(),
    not = TRUE
  ),
  mark = "text",
  x = visual_channel_x(
    field = "start", type = "genomic"
  ),
  xe = visual_channel_x(
    field = "end", type = "genomic"
  ),
  size = 24,
  color = "white",
  visibility = list(list(
    operation = "less-than",
    measure = "width",
    threshold = "|xe-x|",
    transitionPadding = 30,
    target = "mark"
  )),
  list(
    operation = "LT",
    measure = "zoomLevel",
    threshold = 40,
    target = "track"
  ))
)

view2_track3_x <- visual_channel_x(
  field = "position", type = "genomic"
)

view2_track3_color <- visual_channel_color(
  field = "base",
  type = "nominal",
  domain = c("A", "T", "G", "C"),

```

```
    legend = TRUE
  )

view2_track3_text <- visual_channel_text(
  field = "base", type = "nominal"
)

view2_track3_style <- default_track_styles(
  inlineLegend = TRUE
)

view2_track3 <- add_single_track(
  title = "NC_045512.2 Sequence",
  alignment = "overlay",
  data = view2_track3_data,
  tracks = add_multi_tracks(
    view2_track3a, view2_track3b
  ),
  x = view2_track3_x,
  color = view2_track3_color,
  text = view2_track3_text,
  style = view2_track3_style,
  width = 800, height = 40
)

view2 <- compose_view(
  multi = TRUE,
  centerRadius = 0,
  xDomain = list(interval = c(1, 29903)),
  linkingId = "detail",
  alignment = "stack",
  tracks = add_multi_tracks(
    view2_track3
  )
)

combined_view <- arrange_views(
  title = "SARS-CoV-2",
  subtitle = "Data Source: WashU Virus Genome Browser, NCBI, GISAID",
  assembly = list(list("NC_045512.2", 29903)),
  layout = "linear",
  spacing = 50,
  views = list(view2),
  listify = FALSE
)

ui <- fluidPage(
  use_gosling(),
  fluidRow(
    column(6, goslingOutput("gosling_plot"))
  )
)
```

```
server <- function(input, output, session) {  
  output$gosling_plot <- renderGosling({  
    gosling(  
      component_id = "sars_cov2",  
      combined_view  
    )  
  })  
}  
  
shinyApp(ui, server)  
}
```

---

visual\_channel\_tooltip

*tooltip visual channel*

---

### Description

tooltip visual channel

### Usage

```
visual_channel_tooltip(field = NULL, type = NULL, alt = NULL, ...)
```

### Arguments

field	A character. Name of the data field.
type	A character. Must be "genomic". Specify the data type.
alt	A character.
...	Any other parameters to pass to gosling.js.

### Details

For more info visit <https://gosling.js.org/> and check for tooltip implementation

### Value

List object. list object with tooltip list object

**Examples**

```
if(interactive()) {
  library(shiny)
  library(shiny.gosling)

  cistrome_data <-
    "https://server.gosling-lang.org/api/v1/tileset_info/?d=cistrome-multivec"

  single_track <- add_single_track(
    id = "track1",
    data = track_data(
      url = cistrome_data,
      type = "multivec",
      row = "sample",
      column = "position",
      value = "peak",
      categories = c("sample 1", "sample 2", "sample 3", "sample 4"),
      binSize = 4,
    ),
    mark = "rect",
    x = visual_channel_x(field = "start", type = "genomic", axis = "top"),
    xe = visual_channel_x(field = "end", type = "genomic"),
    row = visual_channel_row(
      field = "sample",
      type = "nominal",
      legend = TRUE
    ),
    color = visual_channel_color(
      field = "peak",
      type = "quantitative",
      legend = TRUE
    ),
    tooltip = visual_channel_tooltips(
      visual_channel_tooltip(field = "start", type = "genomic",
        alt = "Start Position"),
      visual_channel_tooltip(field = "end", type = "genomic",
        alt = "End Position"),
      visual_channel_tooltip(
        field = "peak",
        type = "quantitative",
        alt = "Value",
        format = "0.2"
      )
    ),
    width = 600,
    height = 130
  )

  single_composed_track <- compose_view(
    tracks = single_track
  )
}
```

```

single_composed_views <- arrange_views(
  title = "Single Track",
  subtitle = "This is the simplest single track visualization with a linear layout",
  layout = "circular", #"linear"
  views = single_composed_track,
  xDomain = list(
    chromosome = "chr1",
    interval = c(1, 3000500)
  )
)

ui <- fluidPage(
  use_gosling(),
  fluidRow(
    column(6, goslingOutput("gosling_plot")),
    column(
      1, br(), actionButton(
        "download_pdf",
        "PDF",
        icon = icon("cloud-arrow-down")
      )
    )
  )
)

server <- function(input, output, session) {
  output$gosling_plot <- renderGosling({
    gosling(
      component_id = "component_1",
      single_composed_views,
      clean_braces = TRUE
    )
  })

  observeEvent(input$download_pdf, {
    export_pdf(component_id = "component_1")
  })
}

shinyApp(ui, server)
}

```

**Description**

Combine tooltips into a list

**Usage**

```
visual_channel_tooltips(...)
```

**Arguments**

... Any other parameters to pass to gosling.js.

**Value**

List object. json list with tooltips combined into a single spec

**Examples**

```
if(interactive()) {
  library(shiny)
  library(shiny.gosling)

  cistrome_data <-
    "https://server.gosling-lang.org/api/v1/tileset_info/?d=cistrome-multivec"

  single_track <- add_single_track(
    id = "track1",
    data = track_data(
      url = cistrome_data,
      type = "multivec",
      row = "sample",
      column = "position",
      value = "peak",
      categories = c("sample 1", "sample 2", "sample 3", "sample 4"),
      binSize = 4,
    ),
    mark = "rect",
    x = visual_channel_x(field = "start", type = "genomic", axis = "top"),
    xe = visual_channel_x(field = "end", type = "genomic"),
    row = visual_channel_row(
      field = "sample",
      type = "nominal",
      legend = TRUE
    ),
    color = visual_channel_color(
      field = "peak",
      type = "quantitative",
      legend = TRUE
    ),
    tooltip = visual_channel_tooltips(
      visual_channel_tooltip(field = "start", type = "genomic",
        alt = "Start Position"),
      visual_channel_tooltip(field = "end", type = "genomic",
```

```

        alt = "End Position"),
  visual_channel_tooltip(
    field = "peak",
    type = "quantitative",
    alt = "Value",
    format = "0.2"
  )
),
width = 600,
height = 130
)

single_composed_track <- compose_view(
  tracks = single_track
)

single_composed_views <- arrange_views(
  title = "Single Track",
  subtitle = "This is the simplest single track visualization with a linear layout",
  layout = "circular", #"linear"
  views = single_composed_track,
  xDomain = list(
    chromosome = "chr1",
    interval = c(1, 3000500)
  )
)

ui <- fluidPage(
  use_gosling(),
  fluidRow(
    column(6, goslingOutput("gosling_plot")),
    column(
      1, br(), actionButton(
        "download_pdf",
        "PDF",
        icon = icon("cloud-arrow-down")
      )
    )
  )
)

server <- function(input, output, session) {
  output$gosling_plot <- renderGosling({
    gosling(
      component_id = "component_1",
      single_composed_views,
      clean_braces = TRUE
    )
  })
}

observeEvent(input$download_pdf, {
  export_pdf(component_id = "component_1")
})

```

```

    })
  }

  shinyApp(ui, server)
}

```

---

visual\_channel\_x      *x and xe axis visual channel*

---

### Description

x and xe axis visual channel

### Usage

```

visual_channel_x(
  field = NULL,
  type = NULL,
  legend = NULL,
  grid = NULL,
  axis = NULL,
  aggregate = NULL,
  ...
)

```

### Arguments

field	A character. Name of the data field.
type	A character. Must be "genomic". Specify the data type.
legend	A Boolean. Whether to display legend. Default: FALSE.
grid	A Boolean. Whether to display grid. Default: FALSE.
axis	A character. One of "none", "top", "bottom", "left", "right". Specify where should the axis be put.
aggregate	A character. One of "max", "min", "mean", "bin", "count". Specify how to aggregate data. Default: undefined.
...	Any other parameters to pass to gosling.js.

### Details

For more info visit <http://gosling-lang.org/docs/visual-channel#x-xe>

### Value

List object.

**Examples**

```

if(interactive()) {
  library(shiny)
  library(shiny.gosling)

  cistrome_data <-
    "https://server.gosling-lang.org/api/v1/tileset_info/?d=cistrome-multivec"

  single_track <- add_single_track(
    id = "track1",
    data = track_data(
      url = cistrome_data,
      type = "multivec",
      row = "sample",
      column = "position",
      value = "peak",
      categories = c("sample 1", "sample 2", "sample 3", "sample 4"),
      binSize = 4,
    ),
    mark = "rect",
    x = visual_channel_x(field = "start", type = "genomic", axis = "top"),
    xe = visual_channel_x(field = "end", type = "genomic"),
    row = visual_channel_row(
      field = "sample",
      type = "nominal",
      legend = TRUE
    ),
    color = visual_channel_color(
      field = "peak",
      type = "quantitative",
      legend = TRUE
    ),
    tooltip = visual_channel_tooltips(
      visual_channel_tooltip(field = "start", type = "genomic",
        alt = "Start Position"),
      visual_channel_tooltip(field = "end", type = "genomic",
        alt = "End Position"),
      visual_channel_tooltip(
        field = "peak",
        type = "quantitative",
        alt = "Value",
        format = "0.2"
      )
    ),
    width = 600,
    height = 130
  )

  single_composed_track <- compose_view(
    tracks = single_track
  )
}

```

```

single_composed_views <- arrange_views(
  title = "Single Track",
  subtitle = "This is the simplest single track visualization with a linear layout",
  layout = "circular", #"linear"
  views = single_composed_track,
  xDomain = list(
    chromosome = "chr1",
    interval = c(1, 3000500)
  )
)

ui <- fluidPage(
  use_gosling(),
  fluidRow(
    column(6, goslingOutput("gosling_plot")),
    column(
      1, br(), actionButton(
        "download_pdf",
        "PDF",
        icon = icon("cloud-arrow-down")
      )
    )
  )
)

server <- function(input, output, session) {
  output$gosling_plot <- renderGosling({
    gosling(
      component_id = "component_1",
      single_composed_views,
      clean_braces = TRUE
    )
  })

  observeEvent(input$download_pdf, {
    export_pdf(component_id = "component_1")
  })
}

shinyApp(ui, server)
}

```

---

visual\_channel\_y      *y and ye axis visual channel*

---

### Description

y and ye axis visual channel

**Usage**

```
visual_channel_y(
  field = NULL,
  zeroBaseline = NULL,
  type = NULL,
  legend = NULL,
  grid = NULL,
  flip = NULL,
  baseline = NULL,
  axis = NULL,
  aggregate = NULL,
  ...
)
```

**Arguments**

field	A character. Name of the data field.
zeroBaseline	A Boolean. Specify whether to use zero baseline. Default: TRUE.
type	A character. Must be "genomic". Specify the data type.
legend	A Boolean. Whether to display legend. Default: FALSE.
grid	A Boolean. Whether to display grid. Default: FALSE.
flip	A Boolean. Whether to flip the y-axis. This is done by inverting the range property. Default: FALSE.
baseline	A character or number. Custom baseline of the y-axis. Default: 0.
axis	A character. One of "none", "top", "bottom", "left", "right". Specify where should the axis be put.
aggregate	A character. One of "max", "min", "mean", "bin", "count". Specify how to aggregate data. Default: undefined.
...	Any other parameters to pass to gosling.js.

**Details**

For more info visit <http://gosling-lang.org/docs/visual-channel#y-ye>

**Value**

List object.

**Examples**

```
if(interactive()) {
  library(shiny)
  library(shiny.gosling)

  # Circular track 1 ----
  circular_track1_data <- track_data(
    url = "https://server.gosling-lang.org/api/v1/tileset_info/?d=cistrome-multivec",
```

```

    type = "multivec",
    row = "sample",
    column = "position",
    value = "peak",
    categories = c("sample 1", "sample 2", "sample 3", "sample 4"),
    binSize = 4
  )

circular_track1_x <- visual_channel_x(field = "start", type = "genomic")
circular_track1_xe <- visual_channel_x(field = "end", type = "genomic")

circular_track1_y <- visual_channel_y(field = "peak", type = "quantitative")

circular_track1_row <- visual_channel_row(
  field = "sample", type = "nominal"
)

circular_track1_color <- visual_channel_color(
  field = "sample", type = "nominal"
)

circular_track1_tracks <- add_multi_tracks(
  add_single_track(
    mark = "bar"
  ),
  add_single_track(
    mark = "brush",
    x = visual_channel_x(linkingId = "detail-1"),
    color = "blue"
  ),
  add_single_track(
    mark = "brush",
    x = visual_channel_x(linkingId = "detail-2"),
    color = "red"
  )
)

circular_track1_styles <- default_track_styles(
  outlineWidth = 0
)

circular_track1 <- add_single_track(
  id = "circular_track1", alignment = "overlay", data = circular_track1_data,
  x = circular_track1_x, xe = circular_track1_xe,
  y = circular_track1_y, row = circular_track1_row,
  color = circular_track1_color,
  stroke = "black", strokeWidth = 0.3,
  tracks = circular_track1_tracks,
  style = circular_track1_styles,
  width = 500, height = 100
)

# Compose Circular track ----

```

```
circular_composed_view <- compose_view(  
  multi = TRUE,  
  tracks = add_multi_tracks(  
    circular_track1  
  ),  
  static = TRUE, layout = "circular", alignment = "stack"  
)  
  
# Arrange final view  
circular_linear_view <- arrange_views(  
  arrangement = "horizontal",  
  views = list(circular_composed_view)  
)  
  
ui <- fluidPage(  
  use_gosling(),  
  fluidRow(  
    column(6, goslingOutput("gosling_plot"))  
  )  
)  
  
server <- function(input, output, session) {  
  output$gosling_plot <- renderGosling({  
    gosling(  
      component_id = "circular_component",  
      circular_linear_view, clean_braces = FALSE  
    )  
  })  
}  
  
shinyApp(ui, server)  
}
```

---

zoom\_to

*Zoom to*

---

### Description

Zooms to a specific genomic position with the animated transition.

### Usage

```
zoom_to(  
  
```

```

    component_id,
    view_id,
    position,
    padding = 0,
    duration = 1000,
    session = getDefaultReactiveDomain()
  )

```

### Arguments

component_id	A character. The id of the component_id prop passed to the GoslingComponent function.
view_id	A character. The ID of a view that you want to control. This ID is consistent to what you specify as track.id in your spec.
position	A character. The genomic position that your view should be navigated to. You can either specify chromosome (e.g., chr1) or a chromosome and range pair (e.g., chr1:1-10000).
padding	A numeric. This determines the padding around the specified position. The unit of this number is a base pair (Default: 0).
duration	A numeric. A duration of the animated transition in ms (Default: 1000).
session	A shiny session object.

### Value

None.

### Examples

```

if(interactive()) {
  library(shiny)
  library(shiny.gosling)

  chromosome_options <- c(
    "Chr 1" = "chr1",
    "Chr 2" = "chr2",
    "Chr X" = "chrX",
    "Chr Y" = "chrY"
  )

  cistrome_data <-
    "https://server.gosling-lang.org/api/v1/tileset_info/?d=cistrome-multivec"

  single_track <- add_single_track(
    id = "track1",
    data = track_data(
      url = cistrome_data,
      type = "multivec",
      row = "sample",
      column = "position",

```

```

    value = "peak",
    categories = c("sample 1", "sample 2", "sample 3", "sample 4"),
    binSize = 4,
  ),
  mark = "rect",
  x = visual_channel_x(field = "start", type = "genomic", axis = "top"),
  xe = visual_channel_x(field = "end", type = "genomic"),
  row = visual_channel_row(
    field = "sample",
    type = "nominal",
    legend = TRUE
  ),
  color = visual_channel_color(
    field = "peak",
    type = "quantitative",
    legend = TRUE
  ),
  tooltip = visual_channel_tooltips(
    visual_channel_tooltip(field = "start", type = "genomic",
                          alt = "Start Position"),
    visual_channel_tooltip(field = "end", type = "genomic",
                          alt = "End Position"),
    visual_channel_tooltip(
      field = "peak",
      type = "quantitative",
      alt = "Value",
      format = "0.2"
    )
  ),
  width = 600,
  height = 130
)

single_composed_track <- compose_view(
  tracks = single_track
)

single_composed_views <- arrange_views(
  title = "Single Track",
  subtitle = "This is the simplest single track visualization with a linear layout",
  layout = "circular", #"linear"
  views = single_composed_track,
  xDomain = list(
    chromosome = "chr1",
    interval = c(1, 3000500)
  )
)

ui <- fluidPage(
  use_gosling(),
  fluidRow(
    column(6, goslingOutput("gosling_plot")),
    column(

```

```

      1, br(), actionButton(
        "zoom_out",
        "Zoom To"
      )
    ),
    column(
      2,
      selectInput(
        "chromosomes",
        "Chromosome",
        selected = "chr1",
        choices = chromosome_options
      )
    )
  )
)
)

server <- function(input, output, session) {
  output$gosling_plot <- renderGosling({
    gosling(
      component_id = "component_1",
      single_composed_views,
      clean_braces = TRUE
    )
  })

  observeEvent(input$zoom_out, {
    zoom_to(
      component_id = "component_1",
      view_id = "track1",
      position = input$chromosomes
    )
  })
}

shinyApp(ui, server)
}

```

---

 zoom\_to\_extent

*Zoom to extent*


---

### Description

Zooms out to see the entire view\_id passed to this function.

**Usage**

```
zoom_to_extent(
  component_id,
  view_id,
  duration = 1000,
  session = getDefaultReactiveDomain()
)
```

**Arguments**

<code>component_id</code>	A character. The id of the <code>component_id</code> prop passed to the <code>GoslingComponent</code> function.
<code>view_id</code>	A character. The ID of a view that you want to control. This ID is consistent to what you specify as <code>track.id</code> in your spec.
<code>duration</code>	A numeric. A duration of the animated transition in ms (Default: 1000).
<code>session</code>	A shiny session object.

**Value**

None.

**Examples**

```
if(interactive()) {
  library(shiny)
  library(shiny.gosling)

  cistrome_data <-
    "https://server.gosling-lang.org/api/v1/tileset_info/?d=cistrome-multivec"

  single_track <- add_single_track(
    id = "track1",
    data = track_data(
      url = cistrome_data,
      type = "multivec",
      row = "sample",
      column = "position",
      value = "peak",
      categories = c("sample 1", "sample 2", "sample 3", "sample 4"),
      binSize = 4,
    ),
    mark = "rect",
    x = visual_channel_x(field = "start", type = "genomic", axis = "top"),
    xe = visual_channel_x(field = "end", type = "genomic"),
    row = visual_channel_row(
      field = "sample",
      type = "nominal",
      legend = TRUE
    ),
    color = visual_channel_color(
```

```

        field = "peak",
        type = "quantitative",
        legend = TRUE
    ),
    tooltip = visual_channel_tooltips(
        visual_channel_tooltip(field = "start", type = "genomic",
                               alt = "Start Position"),
        visual_channel_tooltip(field = "end", type = "genomic",
                               alt = "End Position"),
        visual_channel_tooltip(
            field = "peak",
            type = "quantitative",
            alt = "Value",
            format = "0.2"
        )
    ),
    width = 600,
    height = 130
)

single_composed_track <- compose_view(
  tracks = single_track
)

single_composed_views <- arrange_views(
  title = "Single Track",
  subtitle = "This is the simplest single track visualization with a linear layout",
  layout = "circular", #"linear"
  views = single_composed_track,
  xDomain = list(
    chromosome = "chr1",
    interval = c(1, 3000500)
  )
)

ui <- fluidPage(
  use_gosling(),
  fluidRow(
    column(6, goslingOutput("gosling_plot")),
    column(
      1, br(), actionButton(
        "zoom_out",
        "Zoom Out"
      )
    )
  )
)

server <- function(input, output, session) {
  output$gosling_plot <- renderGosling({
    gosling(
      component_id = "component_1",

```

```
        single_composed_views,  
        clean_braces = TRUE  
      )  
    })  
  
    observeEvent(input$zoom_out, {  
      zoom_to_extent(  
        component_id = "component_1",  
        view_id = "track1"  
      )  
    })  
  }  
  
  shinyApp(ui, server)  
}
```

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