

# Package ‘ggchord’

July 22, 2025

**Title** Multi-Sequence 'BLAST' Alignment Chord Diagram Visualization Tool

**Version** 0.2.0

**Description**

A function built on 'ggplot2' that visualizes pairwise 'BLAST' alignment results as chord diagrams, intuitively displaying homologous regions between query and subject sequences.

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**Depends** R (>= 3.6.0)

**Imports** ggplot2 (>= 3.3.0), ggnewscale (>= 0.5.0), RColorBrewer, grDevices, grid

**VignetteBuilder** knitr

**Suggests** knitr, rmarkdown, qpdf, dplyr, testthat (>= 3.0.0)

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.3.2

**Config/testthat/edition** 3

**URL** <https://github.com/DangJem/ggchord>

**BugReports** <https://github.com/DangJem/ggchord/issues>

**NeedsCompilation** no

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**Repository** CRAN

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gene_data_example	<i>Example gene annotation data</i>
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**Description**

Gene annotation data for ggchord demonstration (short genes have been filtered out)

**Usage**

```
gene_data_example
```

**Format**

A data frame containing the following columns:

- seq\_id: Sequence ID
- start: Gene start position
- end: Gene end position
- strand: Strand direction (+/-)
- anno: Gene annotation category

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ggchord	<i>ggchord: A ggplot2-based tool for multi-sequence alignment chord plots</i>
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**Description**

ggchord is used to draw chord plots containing multiple sequences, which can display alignment relationships between sequences and gene annotation information. ggchord supports customizing various parameters such as sequence arrangement, colors, ribbon styles, and gene arrow styles, making it suitable for genome alignment visualization.

**Usage**

```
ggchord(  
  seq_data,  
  ribbon_data = NULL,  
  gene_data = NULL,  
  title = NULL,  
  seq_order = NULL,  
  seq_labels = NULL,  
  seq_orientation = NULL,  
  seq_gap = 0.03,  
)
```

```

seq_radius = 1,
seq_colors = NULL,
seq_curvature = 1,
gene_offset = 0.1,
gene_width = 0.05,
gene_label_show = FALSE,
gene_label_rotation = 0,
gene_label_size = 2.5,
gene_label_radial_offset = 0,
gene_label_circum_offset = 0,
gene_label_circum_limit = TRUE,
gene_color_scheme = c("strand", "manual"),
gene_colors = NULL,
gene_order = NULL,
ribbon_color_scheme = c("pident", "query", "single"),
ribbon_colors = NULL,
ribbon_alpha = 0.35,
ribbon_ctrl_point = c(0, 0),
ribbon_gap = 0.15,
axis_gap = 0.04,
axis_tick_major_number = 5,
axis_tick_major_length = 0.02,
axis_tick_minor_number = 4,
axis_tick_minor_length = 0.01,
axis_label_size = 3,
axis_label_offset = 1.5,
axis_label_orientation = "horizontal",
rotation = 45,
panel_margin = 0,
show_legend = TRUE,
show_axis = TRUE,
debug = FALSE
)

```

## Arguments

seq_data	data.frame/tibble, required. A data frame containing basic sequence information, must include columns: - seq_id: Unique sequence identifier (character) - length: Sequence length (numeric, > 0)
ribbon_data	data.frame/tibble, optional. BLAST alignment result data frame, must include columns: - qaccver: Query sequence ID (matching seq_id) - saccver: Subject sequence ID (matching seq_id) - length: Alignment length - pident: Percentage of sequence identity (0-100) - qstart/qend: Start/end positions of the query sequence in the alignment - sstart/send: Start/end positions of the subject sequence in the alignment
gene_data	data.frame/tibble, optional. Gene annotation data frame, must include columns: - seq_id: ID of the associated sequence (matching seq_id) - start/end: Gene start/end positions (numeric) - strand: Strand direction (only "+" or "-") - anno:

	Gene annotation name (character)
title	Character. Main title of the plot, default NULL (no title displayed)
seq_order	Character vector, optional. Specifies the drawing order of sequences (must be a subset of seq_id), default follows the order in seq_data
seq_labels	Character vector/named vector, optional. Sequence labels (length matching the number of sequences or named to match seq_id), default uses seq_id
seq_orientation	Numeric (1 or -1), optional. Sequence direction (1 = forward, -1 = reverse), supports single value/vector/named vector, default 1
seq_gap	Numeric ( $0 \leq x < 0.5$ ), optional. Proportion of gap between sequences, supports single value/vector/named vector, default 0.03
seq_radius	Numeric ( $> 0$ ), optional. Radius of sequence arcs, supports single value/vector/named vector, default 1.0
seq_colors	Color vector/named vector, optional. Colors of sequence arcs, default auto-generated based on RColorBrewer Set1
seq_curvature	Numeric, optional. Curvature of sequence arcs (0 = straight line, 1 = standard arc, $> 1$ = more curved), default 1.0
gene_offset	Numeric/vector/list, optional. Radial offset of gene arrows from sequences (positive values outward, negative values inward), supports: - single value: shared by all sequences/strands - vector: length matching the number of sequences (assigned by sequence) - list: named list (elements are single values or vectors with "+"/"-" to distinguish strands), default 0.1
gene_width	Numeric/vector/list, optional. Width of gene arrows, format same as gene_offset, default 0.05
gene_label_show	Logical. Whether to display gene labels, default FALSE
gene_label_rotation	Numeric/vector/list, optional. Rotation angle (degrees) of gene labels, format same as gene_offset, default 0
gene_label_size	Numeric. Font size of gene labels, default 2.5
gene_label_radial_offset	Numeric/vector/list, optional. Radial offset of gene labels relative to arrows, format same as gene_offset, default 0
gene_label_circum_offset	Numeric/vector/list, optional. Circumferential offset proportion of gene labels along sequences, format same as gene_offset, default 0
gene_label_circum_limit	Logical/vector/list, optional. Whether to limit circumferential offset to half the gene length, format same as gene_offset, default TRUE
gene_color_scheme	Character. Color scheme for genes, optional "strand" (by strand direction) or "manual" (by annotation), default "strand"

gene_colors	Color vector, optional. Fill colors for gene arrows, format depends on gene_color_scheme: - "strand": named vector ("+"/"-"), unnamed vector of length 1/2 - "manual": named vector (matching anno), unnamed vector (recycled), default auto-generated
gene_order	Character vector, optional. Display order of genes in the legend (matching anno), default follows the order in data
ribbon_color_scheme	Character. Color scheme for ribbons, optional "pident" (gradient by identity), "query" (by query sequence), "single" (uniform color), default "pident"
ribbon_colors	Color vector, optional. Color parameters for ribbons: - "single": uniform color - "query": color vector matching seq_id - "pident": color gradient (at least 2 colors), default blue-to-yellow gradient
ribbon_alpha	Numeric (0-1). Transparency of ribbons, default 0.35
ribbon_ctrl_point	Vector/list, optional. Control points for Bézier curves (adjust ribbon shape): - vector: length 2 (single control point) or 4 (c1x,c1y,c2x,c2y for two control points) - list: each element is a sublist with 1-2 control points, default c(0,0)
ribbon_gap	Numeric/vector/named vector, optional. Radial distance between sequences and ribbons, default 0.15
axis_gap	Numeric/vector/named vector, optional. Radial distance between sequences and axes, default 0.04
axis_tick_major_number	Integer/vector/named vector, optional. Number of major ticks, default 5
axis_tick_major_length	Numeric/vector/named vector, optional. Length proportion of major ticks, default 0.02
axis_tick_minor_number	Integer/vector/named vector, optional. Number of minor ticks per major tick, default 4
axis_tick_minor_length	Numeric/vector/named vector, optional. Length proportion of minor ticks, default 0.01
axis_label_size	Numeric/vector/named vector, optional. Font size of axis labels, default 3
axis_label_offset	Numeric/vector/named vector, optional. Offset proportion of labels relative to ticks, default 1.5
axis_label_orientation	Character/numeric/vector, optional. Orientation of axis labels: - "horizontal": horizontal - numeric: rotation angle (degrees) - vector: length matching the number of sequences or named vector (matching seq_id), default "horizontal"
rotation	Numeric. Overall rotation angle of the plot (degrees), default 45
panel_margin	Numeric/list, optional. Margin around the plot panel (t=top, r=right, b=bottom, l=left): - single value: same margin for all sides - list: named list (e.g., list(t=1,r=1)), default 0
show_legend	Logical. Whether to display legends, default TRUE

show\_axis      Logical. Whether to display axes and ticks, default TRUE  
 debug          Logical. Whether to output debugging information (e.g., number of valid ribbons), default FALSE

**Value**

A ggplot2 graph object, which can be further adjusted with ggplot2 functions

**Examples**

```
# Example code
p <- ggchord(
  seq_data = seq_data_example,
  ribbon_data = ribbon_data_example,
  gene_data = gene_data_example
)
print(p)
```

---

ribbon\_data\_example      *Example alignment data*

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**Description**

BLAST alignment data for ggchord demonstration (length >= 100)

**Usage**

ribbon\_data\_example

**Format**

A data frame containing standard BLAST columns (qaccver, saccver, pident, etc.)

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seq\_data\_example          *Example sequence data*

---

**Description**

Sequence length data for ggchord demonstration

**Usage**

seq\_data\_example

**Format**

A data frame containing columns: seq\_id, length

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