# Package: ggseqalign (via r-universe)

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**Type** Package

**Title** Minimal Visualization of Sequence Alignments

**Version** 1.7.0

**Description** Simple visualizations of alignments of DNA or AA sequences as well as arbitrary strings. Compatible with Biostrings and ggplot2. The plots are fully customizable using ggplot2 modifiers such as theme().

**License** Artistic-2.0

**Encoding** UTF-8

**RoxygenNote** 7.3.1

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**biocViews** Alignment, MultipleSequenceAlignment, Software, Visualization

**Depends** R (>= 4.4.0)

**Imports** pwalign, dplyr, ggplot2

**Suggests** Biostrings, BiocStyle, knitr, rmarkdown, testthat (>= 3.0.0)

**URL** https://github.com/simeross/ggseqalign

**BugReports** https://github.com/simeross/ggseqalign/issues

**VignetteBuilder** knitr

**Config/testthat/edition** 3

**Config/pak/sysreqs** zlib1g-dev

**Repository** https://bioc.r-universe.dev

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`alignment_table` *Alignment Table*

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## Description

Generate a table of mismatches and indels between one or many query sequences and a subject sequence.

## Usage

```
alignment_table(query = XStringSet, subject = XStringSet, ...)
```

## Arguments

| | |
|---|---|
| `query` | A string or vector of strings or object of class XStringSet containing the query sequences/strings. |
| `subject` | A string or object of class XStringSet containing the subject sequence/strin. Must be of length 1. |
| `...` | Any additional parameters are passed on to `pwalign::pairwiseAlignment()`. This allows for adjusting alignment algorithm and parameters. |

## Value

A list containing tibbles with information on mismatches and indels.

## Examples

```
query_seq <- Biostrings::DNAStringSet(c("ACCGTACCTGG", "ACCTTGG"))
subject_seq <- Biostrings::DNAStringSet("ACCGTACCGGG")
alignment_table(query_seq, subject_seq)

# Works with any string
query_string <- c("boo", "fizzbuzz")
subject_string <- "boofizz"
alignment_table(query_string, subject_string)
```

plot_sequence_alignment *Plot sequence alignment*

## Description

This function generates a sequence alignment plot using ggplot2 based on the input alignment table.

## Usage

```
plot_sequence_alignment(
  alignment_tbl = alignment_table(query, subject),
  insertion_color = "#21918c",
  hide_mismatches = FALSE
)
```

## Arguments

| | |
|---|---|
| alignment_tbl | An alignment table containing query and subject information for sequence alignment. Generated with alignment_table(). |
| insertion_color | The color to use for indicating insertions in the alignment. Default is '#21918c'. Can be any output of colors() or hex code. |
| hide_mismatches | A logical value indicating whether to hide mismatches in the alignment plot. Default is FALSE. |

## Value

A ggplot object of the sequence alignment plot.

## Examples

```
q <- (c("boo", "fibububuzz", "bozz", "baofuzz"))
s <- "boofizz"

alignment <- alignment_table(q, s)
pl1 <- plot_sequence_alignment(alignment_tbl = alignment)
pl1

# Provide names for (some) query and subject elements to label the y-axis
names(q) <- c("Seq1", NA, "Seq3")
names(s) <- "reference"
pl2 <- plot_sequence_alignment(alignment_table(q, s))
pl2

# Compatible with StringSets from Biostrings
library(Biostrings)
```

```
dna <- readDNAStringSet(system.file("extdata", "dm3_upstream2000.fa.gz",
    package = "Biostrings"
))
# The entries dna[2:5] are identical
q <- dna[2:4]
s <- dna[5]
pl3 <- plot_sequence_alignment(alignment_table(q, s))
pl3

# Let's introduce some SNPs, insertions and deletions
q[1] <- as(
    replaceLetterAt(q[[1]], c(5, 200, 400), "AGC"),
    "DNAStringSet"
)
q[2] <- as(
    c(substr(q[[2]], 300, 1500), substr(q[[2]], 1800, 2000)),
    "DNAStringSet"
)
q[3] <- as(
    replaceAt(
        q[[3]], 1500,
        paste(rep("A", 1000), collapse = "")
    ),
    "DNAStringSet"
)
names(q) <- c("mismatches", "deletions", "insertion")
names(s) <- substr(names(s)[1], 1, 34)

pl4 <- plot_sequence_alignment(alignment_table(q, s))
pl4

# Compatible with ggplot2 theming
library(ggplot2)

pl4 +
    ylab("Sequence variants") +
    xlab("Length in bp") +
    scale_color_viridis_d() +
    theme(
        axis.text.x = element_text(angle = 90, vjust = 0.5, hjust = 1),
        axis.title = element_text()
    )
```

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