

# Package ‘Ularcirc’

April 16, 2019

**Type** Package

**Title** Shiny app for canonical and back splicing analysis (i.e. circular and mRNA analysis)

**Version** 1.0.0

**Description** Ularcirc reads in STAR aligned splice junction files and provides visualisation and analysis tools for splicing analysis. Users can assess backsplice junctions and forward canonical junctions.

**biocViews** DataRepresentation, Visualization, Genetics, Sequencing, Annotation, Coverage, AlternativeSplicing, DifferentialSplicing

**License** file LICENSE

**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 3.5.0)

**Imports** data.table (>= 1.9.4), shiny, shinyFiles, gsubfn, Biostrings, GenomicFeatures, GenomeInfoDb, GenomeInfoDbData, Sushi, moments, DT, yaml, AnnotationHub, BSgenome, httpuv, mirbase.db

**RoxygenNote** 6.0.1

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**git\_url** <https://git.bioconductor.org/packages/Ularcirc>

**git\_branch** RELEASE\_3\_8

**git\_last\_commit** 95e51c5

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Compatible\_Annotation\_DBs

*Compatible\_Annotation\_DBs*

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### Description

Interrogates Bioconductor databases and identifies those that are compatible with Ularcirc. Builds a list of commands that the user can copy to install the required database on their local computer. Once installed the databases are immediately available to Ularcirc upon re-starting the shiny app. This function requires connection to the internet.

### Usage

```
Compatible_Annotation_DBs(search_term = "")
```

### Arguments

`search_term` : character string of a full or part name of a database. Will return only those entries that contain this search term. Not case sensitive.

### Value

Returns a list of compatible annotation databases

### Examples

```
# Get all Bioconductor annotation databases that are compatible with Ularcirc
library('BSgenome')
library('httpuv')
library('AnnotationHub')
# Prepare a dataframe of all compatible annotation databases
compatible_DBs <- Compatible_Annotation_DBs()
comatible_DBs_human <- Compatible_Annotation_DBs("Hsapiens")

# Example of how to find a relevant database and load the relevant databases:
# This example find hg38 databases
idx <- grep(pattern="hg38", x= compatible_DBs[, "genome"])
if (!requireNamespace("BiocManager", quietly=TRUE))
  install.packages("BiocManager")
BiocManager::install(c(compatible_DBs[idx, ]))
```

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Ularcirc

*Ularcirc*

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### Description

When the function is invoked the Ularcirc shiny app is started. The starting screen has quickstart instructions on how to use the software. Please refer to the Ularcirc vignette for a more detailed workflow.

**Usage**

```
Ularcirc()
```

**Value**

Does not return anything

**Examples**

```
# The following commands will load the shiny app either through an RStudio session or  
# through your internet browser
```

```
library("Ularcirc")  
Ularcirc()
```

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