

# Package ‘DNAcycP2’

July 29, 2025

**Title** DNA Cyclizability Prediction

**Version** 1.1.0

**Description** This package performs prediction of intrinsic cyclizability of every 50-bp subsequence in a DNA sequence. The input could be a file either in FASTA or text format. The output will be the C-score, the estimated intrinsic cyclizability score for each 50 bp sequences in each entry of the sequence set.

**Depends** R (>= 4.4.0)

**Imports** basilisk, reticulate

**License** Artistic-2.0

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2

**StagedInstall** yes

**BinaryFiles** inst/extdata/irlstm/saved\_model.pb,  
inst/extdata/irlstm\_smooth/saved\_model.pb

**biocViews** NeuralNetwork, StructuralPrediction

**VignetteBuilder** knitr

**Suggests** knitr, rmarkdown, BiocGenerics, RUnit, tinytest, BiocStyle,  
Biostrings

**LazyData** false

**URL** <https://github.com/jipingw/DNAcycP2>

**BugReports** <https://github.com/jipingw/DNAcycP2>

**git\_url** <https://git.bioconductor.org/packages/DNAcycP2>

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|       |                              |
|-------|------------------------------|
| cycle | <i>Predict Cyclizability</i> |
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## Description

This predicts cyclizability for a set of sequences.

## Usage

```
cycle(sequences, smooth, save_path_prefix = "")
```

## Arguments

|                  |                                                                                                       |
|------------------|-------------------------------------------------------------------------------------------------------|
| sequences        | A list or vector of sequences                                                                         |
| smooth           | Whether to predict smoothed C0 (DNAcycP2) or original C0 (DNAcycP)                                    |
| save_path_prefix | Base path for output files. If it is an empty string, the output files will not be saved (default="") |

## Details

Optionally, saves output files (use argument 'save\_path\_prefix')

## Value

A list of predictions for each input sequence.

## Examples

```
# Example usage of cycle
cycle(c("ACTGCTAGTCACTGCTAGTCACTGCTAGTCACTGCTAGTCACTGCTAGTC"), smooth=TRUE)
# where sequences is a list/vector of sequences
```

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|             |                              |
|-------------|------------------------------|
| cycle_fasta | <i>Predict Cyclizability</i> |
|-------------|------------------------------|

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## Description

This predicts cyclizability for all subsequences of length 50bp from a .fasta input file.

## Usage

```
cycle_fasta(
  file_path,
  smooth,
  n_cores = 1,
  chunk_length = 1e+05,
  save_path_prefix = ""
)
```

## Arguments

|                  |                                                                                                       |
|------------------|-------------------------------------------------------------------------------------------------------|
| file_path        | .fasta input file path                                                                                |
| smooth           | Whether to predict smoothed C0 (DNAcycP2) or original C0 (DNAcycP)                                    |
| n_cores          | Number of cores to use for parallel processing (default=1)                                            |
| chunk_length     | Length of sequence that each core will predict on at a given time. (default=100000)                   |
| save_path_prefix | Base path for output files. If it is an empty string, the output files will not be saved (default="") |

## Details

Optionally, saves output files (use argument 'save\_path\_prefix')

## Value

A list of predictions for each ID in the .fasta file.

Each list item has the following columns: position, c\_score\_norm ( predictions on a normalized scale), and c\_score\_unnorm (predictions on an unnormalized scale).

Each list item is named "cycle\_\$id\$" corresponding to the fasta id

## Examples

```
# Create a temporary file
temp_file <- tempfile(fileext = ".fasta")
writelines(">1", temp_file)
writelines("ACTGCTAGTCACTGCTAGTCACTGCTAGTCACTGCTAGTCACTGCTAGTC", temp_file)

# Example usage of cycle_fasta
cycle_fasta(temp_file, smooth=TRUE)

# Cleanup
unlink(temp_file)
```

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