

# Package ‘DNAcycP2’

March 18, 2025

**Title** DNA Cyclizability Prediction

**Version** 0.99.4

**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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**Repository** Bioconductor 3.21

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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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