

Package ‘DNAcycP2’

March 30, 2025

Title DNA Cyclizability Prediction

Version 0.99.7

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>

git_branch devel

git_last_commit 5c1bc33

git_last_commit_date 2025-03-25

Repository Bioconductor 3.21

Date/Publication 2025-03-30


```
cycle_fasta(temp_file, smooth=TRUE)  
  
# Cleanup  
unlink(temp_file)
```

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