

Package ‘DNAcycP2’

July 9, 2025

Title DNA Cyclizability Prediction

Version 1.0.0

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>
1	0.0000
2	0.0000
3	0.0000
4	0.0000
5	0.0000
6	0.0000
7	0.0000
8	0.0000
9	0.0000
10	0.0000
11	0.0000
12	0.0000
13	0.0000
14	0.0000
15	0.0000
16	0.0000
17	0.0000
18	0.0000
19	0.0000
20	0.0000
21	0.0000
22	0.0000
23	0.0000
24	0.0000
25	0.0000
26	0.0000
27	0.0000
28	0.0000
29	0.0000
30	0.0000
31	0.0000
32	0.0000
33	0.0000
34	0.0000
35	0.0000
36	0.0000
37	0.0000
38	0.0000
39	0.0000
40	0.0000
41	0.0000
42	0.0000
43	0.0000
44	0.0000
45	0.0000
46	0.0000
47	0.0000
48	0.0000
49	0.0000
50	0.0000
51	0.0000
52	0.0000
53	0.0000
54	0.0000
55	0.0000
56	0.0000
57	0.0000
58	0.0000
59	0.0000
60	0.0000
61	0.0000
62	0.0000
63	0.0000
64	0.0000
65	0.0000
66	0.0000
67	0.0000
68	0.0000
69	0.0000
70	0.0000
71	0.0000
72	0.0000
73	0.0000
74	0.0000
75	0.0000
76	0.0000
77	0.0000
78	0.0000
79	0.0000
80	0.0000
81	0.0000
82	0.0000
83	0.0000
84	0.0000
85	0.0000
86	0.0000
87	0.0000
88	0.0000
89	0.0000
90	0.0000
91	0.0000
92	0.0000
93	0.0000
94	0.0000
95	0.0000
96	0.0000
97	0.0000
98	0.0000
99	0.0000
100	0.0000

This predicts cyclizability for a set of sequences.

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

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="")

Optionally, saves output files (use argument 'save_path_prefix')

A list of predictions for each input sequence.

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

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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