Package ‘DNAmotif’

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Type Package

Title DNA Sequence Motifs

Version 0.1.1

Description Motifs within biological sequences show a significant role. This package utilizes a user-defined threshold value (window size and similarity) to create consensus segments or motifs through local alignment of dynamic programming with gap and it calculates the frequency of each identified motif, offering a detailed view of their prevalence within the dataset. It allows for thorough exploration and understanding of sequence patterns and their biological importance.

License GPL-3

Encoding UTF-8

Imports stats, Biostrings, Rcpp

LinkingTo Rcpp

NeedsCompilation yes

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`DNAmotifs` *Generation of motifs from DNA sequences*

Description

Using a fasta file as input, the motifs and its corresponding frequencies are generated, considering threshold values (window size and similarity), by making consensus segments via local alignment with gap.

Usage

```
DNAmotifs(fasta_file, ws, cut_off)
```

Arguments

`fasta_file`	Sequence file path (.fasta format)
`ws`	Window size
`cut_off`	Minimum similarity percentage between the motifs for generating a consensus motif

Value

`final_results` A dataframe of motifs and their corresponding frequncies

Examples

```
example_fasta = system.file("exdata/sample.fasta", package = "DNAmotif")
DNAmotifs(fasta_file = example_fasta, ws = 15, cut_off = 0.75)
```

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