Package ‘nuCpos’

May 2, 2024

Title  An R package for prediction of nucleosome positions

Version  1.22.0

Description  nuCpos, a derivative of NuPoP, is an R package for prediction of nucleosome positions. nuCpos calculates local and whole nucleosomal histone binding affinity (HBA) scores for a given 147-bp sequence. Note: This package was designed to demonstrate the use of chemical maps in prediction. As the parental package NuPoP now provides chemical-map-based prediction, the function for dHMM-based prediction was removed from this package. nuCpos continues to provide functions for HBA calculation.

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License  GPL-2

Depends  R (>= 4.2.0)

Imports  graphics, methods

Suggests  NuPoP, Biostrings, testthat

biocViews  Genetics, Epigenetics, NucleosomePositioning

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nuCpos-package

An R package for nucleosome positioning prediction

Description

nuCpos, a derivative of NuPoP, is an R package for prediction of nucleosome positions. nuCpos calculates local and whole nucleosomal histone binding affinity (HBA) scores for a given 147-bp sequence. Note: This package was designed to demonstrate the use of chemical maps in prediction. As the parental package NuPoP now provides chemical-map-based prediction, the function for dHMM-based prediction was removed from this package. Please refer to Xi et al. (2010) and Wang et al. (2008) for technical details of NuPoP. nuCpos continues to provide functions for HBA calculation. The models are based on chemical maps of nucleosomes from budding yeast (Brogaard et al. (2012)), fission yeast (Moyle-Heyrman et al. (2012)), or mouse embryonic stem cells (Voong et al. (2016)).

Details

Package: nuCpos
Type: Package
Version: 1.17.4
Date: 2023-02-16
License: GPL-2

HBA: R function for calculation of the histone binding affinity score of a whole nucleosome.
localHBA: R function for calculation of the local histone binding affinity.

Author(s)

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References


Examples

```r
load(system.file("extdata","inseq.RData",package="nuCpos"))
HBA(inseq, species = "sc")
localHBA(inseq, species = "sc")
```

**HBA**

*R function for calculating the histone binding affinity score of a given 147-bp sequence.*

**Description**

This function calculates the histone binding score for a given 147-bp sequence. Nucleosomal and linker models built upon the chemical maps are used for the calculation.

**Usage**

```
HBA(inseq, species = "mm", silent = FALSE)
```

**Arguments**

- `inseq`: a character or DNAString object. The length of the character string must be 147 bp.
- `species`: a character = mm, sc or sp; "mm" for mouse, "sc" for *S. cerevisiae* and "sp" for *S. pombe*.
- `silent`: a logical value indicating whether messages are printed in the console.

**Value**

HBA outputs one numeric value: histone binding affinity for a whole nucleosome.

**Examples**

```
load(system.file("extdata","inseq.RData",package="nuCpos"))
HBA(inseq, species = "sc")
```
localHBA

R function for calculating the local histone binding score of a given 147-bp sequence.

**Description**

This function calculates local histone binding scores for 13 nucleosomal subsegments. Nucleosomal and linker models built upon the chemical maps are used for the calculation.

**Usage**

`localHBA(inseq, species = "mm", silent = FALSE)`

**Arguments**

- `inseq`: a character or DNAString object. The length of the character string must be 147 bp.
- `species`: a character = mm, sc or sp; "mm" for mouse, "sc" for *S. cerevisiae* and "sp" for *S. pombe*.
- `silent`: a logical value indicating whether messages are printed in the console.

**Value**

`localHBA` outputs a numeric vector of length 13: local histone binding affinity scores for specific regions in a nucleosome.

**Examples**

```r
load(system.file("extdata","inseq.RData",package="nuCpos"))
localHBA(inseq, species = "sc")
```
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