Package 'nuCpos'

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Title An R package for prediction of nucleosome positions

Version 1.30.0

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

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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

1. Wang JP, Fondufe-Mittendorf Y, Xi L, Tsai GF, Segal E and Widom J (2008). Preferentially quantized linker DNA lengths in *Saccharomyces cerevisiae*. *PLoS Computational Biology*, 4(9):e1000175.
2. Xi L, Fondufe-Mittendorf Y, Xia L, Flatow J, Widom J and Wang JP (2010). Predicting nucleosome positioning using a duration hidden markov model. *BMC Bioinformatics*, 11:346
3. Brogaard K, Xi L, and Widom J (2012). A map of nucleosome positions in yeast at base-pair resolution. *Nature*, 486(7404):496-501.
4. Moyle-Heyrman G, Zaichuk T, Xi L, Zhang Q, Uhlenbeck OC, Holmgren R, Widom J and Wang JP (2013). Chemical map of *Schizosaccharomyces pombe* reveals species-specific features in nucleosome positioning. *Proc. Natl. Acad. Sci. U. S. A.*, 110(50):20158-63.

5. Ichikawa Y, Morohoshi K, Nishimura Y, Kurumizaka H and Shimizu M (2014). Telomeric repeats act as nucleosome-disfavouring sequences in vivo. *Nucleic Acids Res.*, 42(3):1541-1552.
6. Voong LN, Xi L, Sebeson AC, Xiong B, Wang JP and Wang X (2016). Insights into Nucleosome Organization in Mouse Embryonic Stem Cells through Chemical Mapping. *Cell*, 167(6):1555-1570.
7. Fuse T, Katsumata K, Morohoshi K, Mukai Y, Ichikawa Y, Kurumizaka H, Yanagida A, Urano T, Kato H, and Shimizu M (2017). Parallel mapping with site-directed hydroxyl radicals and micrococcal nuclease reveals structural features of positioned nucleosomes in vivo. *Plos One*, 12(10):e0186974.

Examples

```
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

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

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