

Package ‘nuCpos’

April 10, 2023

Title An R package for prediction of nucleosome positions

Version 1.16.3

Description nuCpos, a derivative of NuPoP, is an R package for prediction of nucleosome positions. In nuCpos, a duration hidden Markov model is trained with a chemical map of nucleosomes either from budding yeast, fission yeast, or mouse embryonic stem cells. nuCpos outputs the Viterbi (most probable) path of nucleosome-linker states, predicted nucleosome occupancy scores and histone binding affinity (HBA) scores as NuPoP does. nuCpos can also calculate local and whole nucleosomal 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 provide chemical-map-based prediction, users are strongly encouraged to use it for dHMM-based prediction.

Author Hiroaki Kato, Takeshi Urano

License GPL-2

Depends R (>= 4.2.0)

Imports graphics, methods

Suggests NuPoP, Biostrings, testthat

biocViews Genetics, Epigenetics, NucleosomePositioning, HiddenMarkovModel, ImmunoOncology

Date 2022-08-10

NeedsCompilation yes

git_url <https://git.bioconductor.org/packages/nuCpos>

git_branch RELEASE_3_16

git_last_commit d7c5314

git_last_commit_date 2023-01-19

Date/Publication 2023-04-10

Maintainer Hiroaki Kato <hkato@med.shimane-u.ac.jp>

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nuCpos-package	<i>An R package for nucleosome positioning prediction</i>
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Description

nuCpos, a derivative of **NuPoP**, is an R package for prediction of nucleosome positions. In **nuCpos**, a duration hidden Markov model is trained with a chemical map of nucleosomes either from budding yeast (Brogaard et al. (2012)), fission yeast (Moyle-Heyrman et al. (2012)), or mouse embryonic stem cells (Voong et al. (2016)). **nuCpos** outputs the Viterbi (most probable) path of nucleosome-linker states, predicted nucleosome occupancy scores and histone binding affinity (HBA) scores as **NuPoP** does. **nuCpos** can also calculate local and whole nucleosomal 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 provide chemical-map-based prediction, users are strongly encouraged to use it for dHMM-based prediction. Please refer to Xi et al. (2010) and Wang et al. (2008) for technical details of **NuPoP**.

Details

Package:	nuCpos
Type:	Package
Version:	1.15.3
Date:	2022-08-10
License:	GPL-2

[predNuCpos](#): R function for prediction of nucleosome positioning, nucleosome occupancy and HBA scores.

[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)

Hiroaki Kato and Takeshi Urano

Maintainer: Hiroaki Kato<hkato@med.shimane-u.ac.jp>

References

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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.
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Examples

```
predNuCpos(file = system.file("extdata", "TRP1ARS1x1.fasta",
  package = "nuCpos"), species = "sc",
  ActLikePredNuPoP = TRUE)
```

```
## The prediction results are stored in the working directory.
```

HBA	<i>R</i> function for calculating the histone binding affinity score of a given 147-bp sequence.
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Description

This function invokes a Fortran subroutine to calculate histone binding score. 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 DNAStrng object. The length of the character string must be 147 bp.
species	a character = mm, sc or sp; "mm" for mouse, "sc" for <i>S. cerevisiae</i> and "sp" for <i>S. pombe</i> .
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	<i>R function for calculating the local histone binding score of a given 147-bp sequence.</i>
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Description

This function invokes a Fortran subroutine to calculate local histone binding score. 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 <i>S. cerevisiae</i> and "sp" for <i>S. pombe</i> .
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")
```

 predNuCpos

R function for prediction of nucleosome positioning

Description

Like the predNuPoP function of the parental package **NuPoP** does, this function invokes Fortran codes to compute the Viterbi prediction of nucleosome positioning, nucleosome occupancy score and histone binding affinity score. Nucleosomal and linker models built upon the chemical maps are used for the calculation.

When ActLikePredNuPoP is TRUE, this function acts like the predNuPoP function of **NuPoP**: the function receives the path to a file containing a DNA sequence (specified by file) and save a text file containing the prediction results in the working directory. Nucleosome positioning throughout a long chromosome containing 'N' can be predicted.

When ActLikePredNuPoP is FALSE (dafault), this function directly receives a DNA sequence as an R object (inseq) and returns the prediction results as a data frame. 'N' must not be in the sequence.

Usage

```
predNuCpos(file, inseq, species="mm", smoothHBA=FALSE,
           std=FALSE, ActLikePredNuPoP = FALSE)
```

Arguments

file	The file path to the FASTA file to be tested. The FASTA must be in a single FASTA format. This will be ignored when ActLikePredNuPoP = FALSE.
inseq	a character or DNASTring object. The length of the character string must be over 1 kb. This will be ignored when ActLikePredNuPoP = TRUE.
species	a character = mm, sc or sp; "mm" for mouse, "sc" for <i>S. cerevisiae</i> and "sp" for <i>S. pombe</i> .
smoothHBA	a logical value indicating whether smoothing of histone binding affinity should be applied as in the predNuPoP function of the parental package NuPoP .
std	a logical value indicating whether standardization should be applied to the histone binding affinity score.
ActLikePredNuPoP	a logical value indicating whether the function acts like the predNuPoP function in the parental package NuPoP .

Value

When the ActLikePredNuPoP argument is set as TRUE, predNuCpos outputs the prediction results into the working directory, in the same format as that generated by the predNuPoP function of **NuPoP**. Thus, it can be handled by the **NuPoP** functions readNuPoP and plotNuPoP. The output file is named after the input file with an extension "_Prediction4.txt". The output file has five columns:

Position	position in the input DNA sequence
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P-start	probability that a nucleosome starts at
Occup	nucleosome occupancy score
N/L	Viterbi path (1 and 0 for the nucleosome and linker states, respectively)
Affinity	histone binding affinity score

When the `ActLikePredNuPoP` argument is set as `FALSE`, `predNuCpos` outputs the prediction results as a data frame object with five columns, on which the `plotNuPoP` function of **NuPoP** can be applied:

<code>pos</code>	position in the input DNA sequence
<code>pstart</code>	probability that a nucleosome starts at
<code>nucoccup</code>	nucleosome occupancy score
<code>viterbi</code>	Viterbi path (1 and 0 for the nucleosome and linker states, respectively)
<code>affinity</code>	histone binding affinity score

Examples

```
predNuCpos(file = system.file("extdata", "TRP1ARS1x1.fasta",
  package="nuCpos"), species="sc", smoothHBA=FALSE,
  std=FALSE, ActLikePredNuPoP = TRUE)
library(NuPoP)
results.TRP1ARS1.1 <- readNuPoP("TRP1ARS1x1.fasta_Prediction4.txt",
  startPos = 1, endPos = 1465)
results.TRP1ARS1.1[72:76,]
plotNuPoP(results.TRP1ARS1.1)
TRP1ARS1 <- paste(scan(file =
  system.file("extdata", "TRP1ARS1x1.fasta", package = "nuCpos"),
  what = character(), skip = 1), sep = "", collapse = "")
results.TRP1ARS1.2 <-
  predNuCpos(inseq = TRP1ARS1, species = "sc", smoothHBA = FALSE,
  ActLikePredNuPoP = FALSE)
results.TRP1ARS1.2[72:76,]
plotNuPoP(results.TRP1ARS1.2)
## The DNA sequence TRP1ARS1 is from Fuse et al. (2017).
```

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