

# Package ‘nuCpos’

September 23, 2026

**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

**biocViews** Genetics, Epigenetics, NucleosomePositioning

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## 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)

Hiroaki Kato and Takeshi Urano

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

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### 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 <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")
```

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|          |                                                                                               |
|----------|-----------------------------------------------------------------------------------------------|
| 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 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 <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")
```

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