

# Package ‘scPloidy’

May 9, 2026

**Type** Package

**Title** Infer Ploidy of Single Cells

**Version** 0.6.2

**Description** Compute ploidy of single cells (or nuclei)  
based on single-cell (or single-nucleus)  
ATAC-seq (Assay for Transposase-Accessible Chromatin using sequencing)  
data <<https://github.com/fumi-github/scPloidy>>.

**BugReports** <https://github.com/fumi-github/scPloidy/issues>

**Depends** R (>= 3.5.0)

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.3.1

**Imports** dplyr, GenomicRanges, magrittr, MASS, matrixStats, mixtools,  
nimble, rlang, Rsamtools, tibble, tidyr, utils

**Suggests** gplots, IRanges, knitr, readr, rmarkdown, testthat (>= 3.0.0)

**Config/testthat/edition** 3

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** CRAN

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cnv	<i>Infer Copy Number Variations (CNVs) in Cancer Cells from ATAC-seq Fragment Overlap</i>
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## Description

Infer Copy Number Variations (CNVs) in Cancer Cells from ATAC-seq Fragment Overlap

## Usage

```
cnv(
  fragmentoverlap,
  windowcovariates,
  levels = c(2, 4),
  nfragspercellmin = 5000,
  nfragspercellmax = 10^5.5,
  deltaBICthreshold = 0
)
```

## Arguments

**fragmentoverlap**  
Frequency of fragment overlap in each cell-window computed by the function `fragmentoverlapcount`. barcode should be named as `AAACGAAAGATTGACA-1.window_1`, which represents cell `AAACGAAAGATTGACA-1` and window `window_1`. The format is "cell barcode", ".window\_" and integer.

**windowcovariates**  
Chromosomal windows for which copy number gain/loss are initially inferred. Required columns are `chr`, `start`, `end`, `window` (for example, `window_1`) and `peaks`. `peaks` is a numeric column representing chromatin accessibility.

**levels**  
Possible values of ploidy. For example, `c(2, 4)` if the cells can be diploids or tetraploids. The values must be larger than one.

**nfragspercellmin**  
Minimum number of fragments for a cell-window to be eligible.

**nfragspercellmax**  
Maximum number of fragments for a cell-window to be eligible.

**deltaBICthreshold**  
Only the CNVs with `deltaBIC` smaller than this threshold are adopted.

**Value**

A list with two elements. CNV is a data frame of the CNVs identified in the dataset. cellwindowCNV is a data frame indicating the ploidy for each cell and the inferred standardized copy number for each cell-window.

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fragmentoverlapcount    *Count Overlap of ATAC-seq Fragments*

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**Description**

Count Overlap of ATAC-seq Fragments

**Usage**

```
fragmentoverlapcount(
  file,
  targetregions,
  excluderegions = NULL,
  targetbarcodes = NULL,
  Tn5offset = c(1, 0),
  barcodesuffix = NULL,
  dobptonext = FALSE
)
```

**Arguments**

file	Filename of the file for ATAC-seq fragments. The file must be block gzipped (using the bgzip command) and accompanied with the index file (made using the tabix command). The uncompressed file must be a tab delimited file, where each row represents one fragment. The first four columns are chromosome name, start position, end position, and barcode (i.e., name) of the cell including the fragment. The remaining columns are ignored. See vignette for details.
targetregions	GRanges object for the regions where overlaps are counted. Usually all of the autosomes. If there is memory problem, split a chromosome into smaller chunks, for example by 10 Mb. The function loads each element of targetregions sequentially, and smaller elements require less memory.
excluderegions	GRanges object for the regions to be excluded. Simple repeats in the genome should be listed here, because repeats can cause false overlaps. A fragment is discarded if its 5' or 3' end is located in excluderegions. If NULL, fragments are not excluded by this criterion.
targetbarcodes	Character vector for the barcodes of cells to be analyzed, such as those passing quality control. If NULL, all barcodes in the input file are analyzed.

Tn5offset	Numeric vector of length two. The enzyme for ATAC-seq is a homodimer of Tn5. The transposition sites of two Tn5 proteins are 9 bp apart, and the (representative) site of accessibility is in between. If the start and end position of your input file is taken from BAM file, set the parameter to <code>c(4, -5)</code> to adjust the offset. Alternatively, values such as <code>c(0, -9)</code> could generate similar results; what matters the most is the difference between the two numbers. The fragments.tsv.gz file generated by 10x Cell Ranger already adjusts the shift but is recorded as a BED file. In this case, use <code>c(1, 0)</code> (default value). If unsure, set to "guess", in which case the program returns a guess.
barcodesuffix	Add suffix to barcodes per targetregions.
dobptonext	(experimental feature) Whether to compute smoothed distance to the next fragment (irrelevant to BC) as <code>bptonext</code> , which is the inverse of chromatin accessibility, and append as 9th to 14th columns.

### Value

A tibble with each row corresponding to a cell. For each cell, its barcode, the total count of the fragments `nfrag`, and the count distinguished by overlap depth are given.

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GSE129785\_SU008\_Tumor\_Pre

*Basal cell carcinoma sample SU008\_Tumor\_Pre*

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### Description

The dataset includes 788 nuclei obtained from basal cell carcinoma sample SU008\_Tumor\_Pre. Overlapping of single-nucleus ATAC-seq fragments was computed with the `fragmentoverlapcount` function.

### Usage

```
data(GSE129785_SU008_Tumor_Pre)
```

```
SU008_Tumor_Pre_windowcovariates
```

```
rescnv
```

### Format

`SU008_Tumor_Pre_fragmentoverlap` is a dataframe of `fragmentoverlap`.

`SU008_Tumor_Pre_windowcovariates` is a dataframe of windows and peaks.

`rescnv` is a list containing the output of `cnv` function.

### Source

[GEO, GSE129785](#)

## References

Satpathy et al. (2019) Nature Biotechnology 37:925 doi:10.1038/s415870190206z

## Examples

```
## Not run:
data(GSE129785_SU008_Tumor_Pre)
levels = c(2, 4)
result = cnv(SU008_Tumor_Pre_fragmentoverlap,
             SU008_Tumor_Pre_windowcovariates,
             levels = levels,
             deltaBICthreshold = -600)

## End(Not run)
```

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ploidy

*Infer Ploidy from ATAC-seq Fragment Overlap*

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## Description

Infer Ploidy from ATAC-seq Fragment Overlap

## Usage

```
ploidy(
  fragmentoverlap,
  levels,
  s = 100,
  epsilon = 1e-08,
  subsamplesize = NULL,
  dobayes = FALSE,
  prop = 0.9
)
```

## Arguments

fragmentoverlap	Frequency of fragment overlap in each cell computed by the function fragmentoverlapcount.
levels	Possible values of ploidy. For example, c(2, 4) if the cells can be diploids or tetraploids. The values must be larger than one.
s	Seed for random numbers used in EM algorithm.
epsilon	Convergence criterion for the EM algorithm.
subsamplesize	EM algorithm becomes difficult to converge when the number of cells is very large. By setting the parameter (e.g. to 1e4), we can run EM algorithm iteratively, first for subsamplesize randomly sampled cells, next for twice the number of cells in repetition. The inferred lambda/theta parameters are used as the initial value in the next repetition.

dobayes	(experimental feature) Whether to perform Bayesian inference, which takes long computation time.
prop	Proportion of peaks that can be fitted with binomial distribution in ploidy.bayes. The rest of peaks are allowed to have depth larger than the ploidy.

**Value**

A data.frame with each row corresponding to a cell. For each cell, its barcode, ploidy inferred by 1) moment method, 2) the same with additional K-means clustering, 3) EM algorithm of mixture, and, optionally, 4) Bayesian inference are given. I recommend using `ploidy.moment` or `ploidy.em`. When `fragmentoverlapcount` was computed with `dobptonext=TRUE`, we only use the chromosomal sites with chromatin accessibility in top 10. This requires longer computation time.

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SHR\_m154211

*Liver Cells from a Rat*


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**Description**

The dataset includes 3572 nuclei obtained from the liver of a 16 weeks old male rat, which was fed normal diet. Overlapping of single-nucleus ATAC-seq fragments was computed with the `fragmentoverlapcount` function and saved as `fragmentoverlap`. The cell type of the nuclei are saved in the data.frame `cells`. The data for rat SHR\_m154211 was taken from the publication cited below.

**Usage**

```
data(SHR_m154211)
```

**Format**

An object of class `list` of length 2.

**Source**

Takeuchi et al. (2022) bioRxiv [doi:10.1101/2022.07.12.499681](https://doi.org/10.1101/2022.07.12.499681)

**Examples**

```
data(SHR_m154211)
fragmentoverlap = SHR_m154211$fragmentoverlap
p = ploidy(fragmentoverlap, c(2, 4, 8))
head(p)
cells = SHR_m154211$cells
table(cells$celltype, p$ploidy.moment[match(cells$barcode, p$barcode)])
```

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