

# Package ‘SCATEData’

April 16, 2024

**Version** 1.12.0

**Title** Data for SCATE (Single-cell ATAC-seq Signal Extraction and Enhancement)

**Description** SCATEData is an ExperimentHub package for SCATE which is a software tool for extracting and enhancing the sparse and discrete Single-cell ATAC-seq Signal.

**BugReports** <https://github.com/Winnie09/SCATEData/issues>

**License** MIT + file LICENSE

**VignetteBuilder** knitr

**Encoding** UTF-8

**biocViews** ExperimentHub, ExperimentData

**Depends** ExperimentHub, GenomicAlignments, GenomicRanges, base

**Imports** utils

**Suggests** knitr, rmarkdown

**PackageStatus** Deprecated

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GSM1596831 .bam	<i>'GSM1596831.bam.Rd'</i> data
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**Description**

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

**Details**

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

**Examples**

```
library(GenomicAlignments)
f1 <- system.file("extdata", "GSM1596831.bam", package = "SCATEData")
a <- readGAlignments(f1)
```

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GSM1596840.bam	<i>'GSM1596840.bam.Rd'</i> data
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**Description**

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

**Details**

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

**Examples**

```
library(GenomicAlignments)
fl <- system.file("extdata", "GSM1596840.bam", package = "SCATEData")
a <- readGAlignments(fl)
```

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GSM1596874.bam	<i>'GSM1596874.bam.Rd'</i> data
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**Description**

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

**Details**

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

**Examples**

```
library(GenomicAlignments)
fl <- system.file("extdata", "GSM1596874.bam", package = "SCATEData")
a <- readGAlignments(fl)
```

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GSM1596881.bam	<i>'GSM1596881.bam.Rd'</i> data
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**Description**

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

**Details**

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

**Examples**

```
library(GenomicAlignments)
fl <- system.file("extdata", "GSM1596881.bam", package = "SCATData")
a <- readGAlignments(fl)
```

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GSM1596940.bam	<i>'GSM1596940.bam.Rd'</i> data
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**Description**

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

**Details**

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

**Examples**

```
library(GenomicAlignments)
fl <- system.file("extdata", "GSM1596940.bam", package = "SCATData")
a <- readGAlignments(fl)
```

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GSM1596942.bam	<i>'GSM1596942.bam.Rd'</i> data
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**Description**

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

**Details**

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

**Examples**

```
library(GenomicAlignments)
f1 <- system.file("extdata", "GSM1596942.bam", package = "SCATEData")
a <- readGAlignments(f1)
```

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GSM1596944.bam	<i>'GSM1596944.bam.Rd'</i> data
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**Description**

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

**Details**

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

**Examples**

```
library(GenomicAlignments)
f1 <- system.file("extdata", "GSM1596944.bam", package = "SCATEData")
a <- readGAlignments(f1)
```

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GSM1596961.bam	<i>'GSM1596961.bam.Rd'</i> data
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**Description**

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

**Details**

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

**Examples**

```
library(GenomicAlignments)
fl <- system.file("extdata", "GSM1596961.bam", package = "SCATData")
a <- readGAlignments(fl)
```

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GSM1597041.bam	<i>'GSM1597041.bam.Rd'</i> data
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**Description**

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

**Details**

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

**Examples**

```
library(GenomicAlignments)
fl <- system.file("extdata", "GSM1597041.bam", package = "SCATData")
a <- readGAlignments(fl)
```

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GSM1597096.bam	<i>'GSM1597096.bam.Rd' data</i>
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**Description**

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

**Details**

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

**Examples**

```
library(GenomicAlignments)
f1 <- system.file("extdata", "GSM1597096.bam", package = "SCATEData")
a <- readGAlignments(f1)
```

---

hg19.rds	<i>'hg19' dataset</i>
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**Description**

hg19 annotation file for SCATE

**Details**

This is a hg19 annotation file for SCATE package.

File sizes: 66 MB.

Source: <https://github.com/zji90/SCATE/tree/master/inst/extdata>

**Examples**

```
f1 <- system.file("extdata", "hg19.rds", package = "SCATEData")
a <- readRDS(f1)
```

---

mm10.rds	<i>'mm10' dataset</i>
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---

### Description

mm10 annotation file for SCATE

### Details

This is a mm10 annotation file for SCATE package.

File sizes: 58 MB.

Source: <https://github.com/zji90/SCATE/tree/master/inst/extdata>

### Examples

```
f1 <- system.file("extdata", "mm10.rds", package = "SCATEData")
a <- readRDS(f1)
```

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SCATEData	<i>Data package for SCATE to extract and enhance the sparse and discrete Single-cell ATAC-seq Signal</i>
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### Description

Data package for SCATE which is a software for extracting and enhancing the sparse and discrete Single-cell ATAC-seq Signal. This package contains data in the [GenomicRanges](#) format that SCATE needs for compiling examples or running the algorithm. It is hosted on Bioconductor ExperimentHub.

### Details

#### *Overview*

The 'SCATEData' is an extensive data resources containing the location of genomic regions bins, the mean and standard deviation of normalized bulk DNase-seq signals across ENCODE samples, and the clustering of the genomic bins based on bulk DNase-seq signals. These data have been formatted as 'GenomicRanges' Bioconductor objects and hosted on Bioconductor's 'ExperimentHub' platform.

'SCATEData' provides data resources for the package 'SCATE' to extract and enhance the sparse and discrete Single-cell ATAC-seq Signal.

#### *Datasets*

The package contains the following datasets, which can be used by 'SCATE' to extract and enhance the sparse Single-cell ATAC-seq signals. They are grouped into datasets useful for (i) running 'SCATE', and (ii) providing examples.

- Loaded by 'SCATE':



- hg19.rds
- mm10.rds

- scATAC-seq example files:

- GSM1596831.bam
- GSM1596940.bam
- GSM1597041.bam
- SRR1779856.bam
- SRR1779973.bam
- GSM1596840.bam
- GSM1596942.bam
- GSM1597096.bam
- SRR1779874.bam
- SRR1780018.bam
- GSM1596874.bam
- GSM1596944.bam
- SRR1779746.bam
- SRR1779956.bam
- SRR1780020.bam
- GSM1596881.bam
- GSM1596961.bam
- SRR1779805.bam
- SRR1779959.bam
- SRR1780054.bam
- GSM1596831.bam.bai
- GSM1596940.bam.bai
- GSM1597041.bam.bai
- SRR1779856.bam.bai
- SRR1779973.bam.bai
- GSM1596840.bam.bai
- GSM1596942.bam.bai
- GSM1597096.bam.bai
- SRR1779874.bam.bai
- SRR1780018.bam.bai
- GSM1596874.bam.bai
- GSM1596944.bam.bai
- SRR1779746.bam.bai
- SRR1779956.bam.bai

- SRR1780020.bam.bai
- GSM1596881.bam.bai
- GSM1596961.bam.bai
- SRR1779805.bam.bai
- SRR1779959.bam.bai
- SRR1780054.bam.bai

These ‘.bam’ files are Single-cell ATAC-seq reads and the corresponding ‘.bam.bai’ files are for indexing and searching for the reads in these files. For more extensive documentation, please refer to the metadata or help files for the objects.

#### *How to load data*

Please refer to [‘SCATE’ tutorial](<https://github.com/Winnie09/SCATE>) for the loading and use of the data.

#### *Citation*

If the ‘SCATEData’ package is useful in your work, please cite the following paper: - Zhicheng Ji, Weiqiang Zhou, Wenpin Hou, Hongkai Ji, [\*Single-cell ATAC-seq Signal Extraction and Enhancement with SCATE\*](<https://doi.org/10.1186/s13059-020-02075-3>), Genome Biol 21, 161 (2020).

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SRR1779746.bam	'SRR1779746.bam.Rd'data
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## **Description**

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

## **Details**

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

## **Examples**

```
library(GenomicAlignments)
fl <- system.file("extdata", "SRR1779746.bam", package = "SCATEData")
a <- readGAlignments(fl)
```

---

SRR1779805.bam	<i>'SRR1779805.bam.Rd'</i> data
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---

**Description**

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

**Details**

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

**Examples**

```
library(GenomicAlignments)
fl <- system.file("extdata", "SRR1779805.bam", package = "SCATData")
a <- readGAlignments(fl)
```

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SRR1779856.bam	<i>'SRR1779856.bam.Rd'</i> data
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**Description**

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

**Details**

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

**Examples**

```
library(GenomicAlignments)
fl <- system.file("extdata", "SRR1779856.bam", package = "SCATData")
a <- readGAlignments(fl)
```

---

SRR1779874.bam	<i>'SRR1779874.bam.Rd'</i> data
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---

**Description**

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

**Details**

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

**Examples**

```
library(GenomicAlignments)
f1 <- system.file("extdata", "SRR1779874.bam", package = "SCATData")
a <- readGAlignments(f1)
```

---

SRR1779956.bam	<i>'SRR1779956.bam.Rd'</i> data
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**Description**

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

**Details**

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

**Examples**

```
library(GenomicAlignments)
f1 <- system.file("extdata", "SRR1779956.bam", package = "SCATData")
a <- readGAlignments(f1)
```

---

SRR1779959.bam	<i>'SRR1779959.bam.Rd'data</i>
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**Description**

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

**Details**

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

**Examples**

```
library(GenomicAlignments)
fl <- system.file("extdata", "SRR1779959.bam", package = "SCATData")
a <- readGAlignments(fl)
```

---

SRR1779973.bam	<i>'SRR1779973.bam.Rd'data</i>
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---

**Description**

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

**Details**

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

**Examples**

```
library(GenomicAlignments)
fl <- system.file("extdata", "SRR1779973.bam", package = "SCATData")
a <- readGAlignments(fl)
```

---

SRR1780018.bam	<i>'SRR1780018.bam.Rd'</i> data
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### Description

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

### Details

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

### Examples

```
library(GenomicAlignments)
f1 <- system.file("extdata", "SRR1780018.bam", package = "SCATData")
a <- readGAlignments(f1)
```

---

SRR1780020.bam	<i>'SRR1780020.bam.Rd'</i> data
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### Description

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

### Details

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

### Examples

```
library(GenomicAlignments)
f1 <- system.file("extdata", "SRR1780020.bam", package = "SCATData")
a <- readGAlignments(f1)
```

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SRR1780054.bam	'SRR1780054.bam.Rd'data
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**Description**

Bam file for single-cell ATAC-seq data (GEO Accession GSE65360).

**Details**

Original .fastq files were downloaded and then alignments were performed to obtain these files

Source: <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65360>

**Examples**

```
library(GenomicAlignments)
f1 <- system.file("extdata", "SRR1780054.bam", package = "SCATData")
a <- readGAlignments(f1)
```

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