# Package: SMTrackR (via r-universe)

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**Type** Package

**Title** SMTrackR: an R/Bioconductor package for mapping protein binding at individual DNA molecules

**Version** 1.1.0

**Date** 2024-12-31

**Description** The package uses exogenous enzyme imprinted information to map protein-DNA binding on individual sequenced DNA molecules. For example, GpC methyltransferase, CpG methyltransferase, and Adenine methyltransferases. Public datasets from such assays are compiled into tracks, and hosted at public servers like Galaxy for their seamless access by this package.

**biocViews** NucleosomePositioning, Visualization, GeneTarget, GenomeAssembly

**Imports** jsonlite, GenomicRanges, rtracklayer, stringr, BiocFileCache, S4Vectors

**License** MIT + file LICENSE

**Suggests** knitr, rmarkdown, BiocStyle

**VignetteBuilder** knitr

**Encoding** UTF-8

**RoxygenNote** 7.3.2

**Depends** R (>= 4.5)

**URL** https://www.raolab.in

**BugReports** https://github.com/satyanarayan-rao/SMTrackR

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**Config/pak/sysreqs** make libbz2-dev libicu-dev liblzma-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

**Repository** https://bioc.r-universe.dev

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**RemoteRef** HEAD

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`generateGvizCodeforSMF` *Visualize Single Molecule Footprint Patterns with Ideogram and Gene Tracks*

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## Description

Generates Gviz-compatible R code that puts SMF footprints below ideogram and genetracks. This call assumes that you have already ran ‘plotFootprints‘ function. Designed for Drosophila melanogaster analysis with expandable parameters for other organisms.

## Usage

```
generateGvizCodeforSMF(
  organism = "demlanogaster",
  model = "S2",
  condition = "WT",
  genome_assembly = "dm6",
  type = "dSMF",
  chromosome = "chr2L",
  start = 480290,
  end = 480320,
  tr = "fp_and_mvec",
  label = "peak229",
  span_left = 150,
  span_right = 150,
  remove_dup = FALSE,
  fp_cap = 50,
  gviz_left = 1000,
  gviz_right = 1000,
  target_dir = ""
)
```

## Arguments

| | |
|---|---|
| `organism` | Organism code (default: "dmelanogaster") |
| `model` | Biological model/system (default: "S2" cells) |

| | |
|---|---|
| condition | Experimental condition (default: "WT") |
| genome_assembly | Genome version (default: "dm6") |
| type | Data type ("dSMF" = dual enzyme Single Molecule Footprinting) |
| chromosome | Chromosome ID (e.g., "chr2L") |
| start | Genomic start position (numeric/character) |
| end | Genomic end position (numeric/character) |
| tr | Track name for BigBed file resource (default: "fp_and_mvec") |
| label | Plot title annotation |
| span_left | Upstream window size from region (default: 150) |
| span_right | Downstream window size from region (default: 150) |
| remove_dup | Remove duplicate reads? (default: FALSE) |
| fp_cap | Maximum footprint value for y-axis scaling (default: 50) |
| gviz_left | left zoom (bases) from the start |
| gviz_right | right zoom (bases) from the end |
| target_dir | destination directory (must be the same used in ‘plotFootprints‘ function) |

## Details

This function generates a R code running which one can get ideogram, genetracks and SMF heatmap altogether in one plot.

## Value

Saves a heatmap in pdf, png, and eps file formats.

## Examples

```
# Basic usage with default parameters
generateGvizCodeforSMF(organism = "mmusculus", model = "16cell",
                         condition = "WT", genome_assembly = "mm10",
                         type = "SMF", chromosome = "chr1",start = 191718250,
                         end = 191718280, tr = "16cell", label = "tss",
                         fp_cap = 50, remove_dup = FALSE, gviz_left = 500,
                         gviz_right = 500, target_dir = "")
```

`listTracks` *Discover Available Single Molecule Data Tracks*

## Description

Retrieves track metadata from a centralized Google Sheet containing organism-specific single-molecule datasets and experimental conditions.

## Usage

```
listTracks()
```

## Value

A tibble containing track metadata with columns:

- organism: Species identifier (e.g. "dmelanogaster")
- genome_assembly: Reference genome version
- condition: Experimental condition
- model: Biological model/system
- track_name: Identifier for ‘tr‘ parameter in ‘plotFootprints‘
- data_type: NOME-seq protocol variant
- bigbed_url: Cloud-hosted data location

## See Also

‘plotFootprints()‘: Use track names from this list to visualize specific datasets

## Examples

```
# List all available tracks from default repository
listTracks()
```

plotFootprints *Visualize Single Molecule Footprint Patterns*

## Description

Generates footprint plots from NOME-seq data within specified genomic regions. Designed for Drosophila melanogaster analysis with expandable parameters for other organisms.

## Usage

```
plotFootprints(
  organism = "dmelanogaster",
  model = "S2",
  condition = "WT",
  genome_assembly = "dm6",
  type = "dSMF",
  chromosome = "chr2L",
  start = 480290,
  end = 480320,
  tr = "fp_and_mvec",
  label = "peak229",
  span_left = 150,
  span_right = 150,
  remove_dup = FALSE,
  fp_cap = 50,
  target_dir = ""
)
```

## Arguments

| | |
|---|---|
| organism | Organism code (default: "dmelanogaster") |
| model | Biological model/system (default: "S2" cells) |
| condition | Experimental condition (default: "WT") |
| genome_assembly | Genome version (default: "dm6") |
| type | Data type ("dSMF" = dual enzyme Single Molecule Footprinting) |
| chromosome | Chromosome ID (e.g., "chr2L") |
| start | Genomic start position (numeric/character) |
| end | Genomic end position (numeric/character) |
| tr | Track name for BigBed file resource (default: "fp_and_mvec") |
| label | Plot title annotation |
| span_left | Upstream window size from region (default: 150) |
| span_right | Downstream window size from region (default: 150) |

| | |
|---|---|
| remove_dup | Remove duplicate reads? (default: FALSE) |
| fp_cap | Maximum footprint value for y-axis scaling (default: 50) |
| target_dir | destination directory where outputs will be stored |

## Details

This function retrieves and visualizes DNA accessibility patterns from single-molecule data: - Integrates with UCSC-style track hubs via 'tr' parameter - Automatically handles coordinate conversion for dm6 genome - Implements dynamic y-axis scaling using 'fp_cap'

## Value

Saves a heatmap in pdf, png, and eps file formats. Also, occupancies are saved in a tsv file

## Examples

```
# Basic usage with default parameters
plotFootprints()

# Custom genomic region analysis
plotFootprints(
  chromosome = "chr2L", start = 480290, end = 480320, label = "peak229")
```

---

# plotFootprintsUsingLocalBigBed

*Visualize Single Molecule Footprint Patterns using Local BigBed file*

---

## Description

Generates footprint plots from SMF/dSMF data within specified genomic regions. Designed for Drosophila melanogaster analysis with expandable parameters for other organisms.

## Usage

```
plotFootprintsUsingLocalBigBed(
  bigBed = "",
  organism = "dmelanogaster",
  model = "S2",
  condition = "WT",
  genome_assembly = "dm3",
  chromosome = "chr2L",
  start = 480290,
  end = 480320,
  label = "peak229",
  span_left = 150,
  span_right = 150,
```

```
  remove_dup = FALSE,
  fp_cap = 50,
  target_dir = ""
)
```

## Arguments

| | |
|---|---|
| bigBed | BigBed file path (e.g., "demo.bb") |
| organism | Organism code (default: "dmelanogaster") |
| model | Biological model/system (default: "S2" cells) |
| condition | Experimental condition (default: "WT") |
| genome_assembly | Genome version (default: "dm6") |
| chromosome | Chromosome ID (e.g., "chr2L") |
| start | Genomic start position (numeric/character) |
| end | Genomic end position (numeric/character) |
| label | Plot title annotation |
| span_left | Upstream window size from region (default: 150) |
| span_right | Downstream window size from region (default: 150) |
| remove_dup | Remove duplicate reads? (default: FALSE) |
| fp_cap | Maximum footprint value for y-axis scaling (default: 50) |
| target_dir | destination directory where outputs will be stored |

## Details

This function uses local SMF/dSMF bigBed file and plot heatmap

## Value

Saves a heatmap in pdf, png, and eps file formats. Also, occupancies are saved in a tsv file

## Examples

```
# Basic usage with default parameters
plotFootprintsUsingLocalBigBed()

# Custom genomic region analysis
plotFootprintsUsingLocalBigBed(
  bigBed = "inst/extdata/demo.bb", organism = "dmelanogaster",
  model = "S2", condition = "WT", genome_assembly = "dm3",
  chromosome = "chr2L", start = 480290, end = 480320, label = "peak229")
```

`plotMethylationCallsNanopore` *Visualize Single Molecule Footprint Patterns*

## Description

Generates footprint plots from NOME-seq data within specified genomic regions. Designed for Drosophila melanogaster analysis with expandable parameters for other organisms.

## Usage

```
plotMethylationCallsNanopore(
  organism = "scerevisiae",
  model = "BY4741 strain",
  condition = "WT",
  genome_assembly = "sacCer3",
  type = "SMF",
  chromosome = "chrIII",
  start = 114300,
  end = 114600,
  tr = "nanopore_meth_calls",
  label = "smac_seq",
  span_left = 1000,
  span_right = 1000,
  stride = 5,
  target_dir = ""
)
```

## Arguments

| | |
|---|---|
| `organism` | Organism code (default: "scerevisiae") |
| `model` | Biological model/system (default: "BY4741 strain") |
| `condition` | Experimental condition (default: "WT") |
| `genome_assembly` | Genome version (default: "sacCer3") |
| `type` | Data type ("Nanopore" = dual enzyme Single Molecule Footprinting) |
| `chromosome` | Chromosome ID (e.g., "chrIII") |
| `start` | Genomic start position (numeric/character) |
| `end` | Genomic end position (numeric/character) |
| `tr` | Track name for BigBed file resource (default: "nanopore_meth_calls") |
| `label` | Plot title annotation (default: "smac_seq") |
| `span_left` | Upstream window size from region (default: 1000) |
| `span_right` | Downstream window size from region (default: 1000) |
| `stride` | sliding window used for singal aggregation |
| `target_dir` | destination directory where outputs will be stored |

## Details

This function retrieves and visualizes DNA accessibility patterns from single-molecule data: - Integrates with UCSC-style track hubs via 'tr' parameter - Automatically handles coordinate conversion for dm6 genome - Implements dynamic y-axis scaling using 'fp_cap'

## Value

Saves a heatmap in pdf, png, and eps file formats. Also, occupancies are saved in a tsv file

## Examples

```
# Basic usage with default parameters
plotMethylationCallsNanopore()

# Custom genomic region analysis

plotMethylationCallsNanopore (
        organism = "scerevisiae", model = "BY4741 strain",
        condition = "WT", genome_assembly = "sacCer3",
        type = "SMF", chromosome = "chrIII",
        start = 114300, end = 114600,
        tr = "nanopore_meth_calls", label = "smac_seq",
        span_left = 1000, span_right = 1000, stride = 5, target_dir = "")
```

---

# plotMethylationCallsNanoporeUsingLocalBigBed

*Visualize aggregate methylation calls from ONT sequencing data*

---

## Description

Generates heatmap of methylation calls from likes of SMAC-seq datasets. currently has data from Yeast (sacCer3)

## Usage

```
plotMethylationCallsNanoporeUsingLocalBigBed(
  bigBed = "",
  chromosome = "chrIII",
  start = 114300,
  end = 114600,
  label = "smac_seq",
  span_left = 1000,
  span_right = 1000,
  remove_dup = FALSE,
  stride = 5,
  target_dir = ""
)
```

## Arguments

| | |
|---|---|
| bigBed | BigBed file path (e.g., "demo.bb") |
| chromosome | Chromosome ID (e.g., "chr2L") |
| start | Genomic start position (numeric/character) |
| end | Genomic end position (numeric/character) |
| label | Plot title annotation |
| span_left | Upstream window size from region (default: 150) |
| span_right | Downstream window size from region (default: 150) |
| remove_dup | Remove duplicate reads? (default: FALSE) |
| stride | a window size used for averaging the methylation call values |
| target_dir | destination directory where outputs will be stored |

## Details

This function uses local SMF/dSMF bigBed file and plot heatmap

## Value

Saves a methylation calls (binary) heatmap in pdf, png, and eps file formats.

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