

# Package ‘MouseFM’

December 9, 2025

**Type** Package

**Title** In-silico methods for genetic finemapping in inbred mice

**Version** 1.21.0

**Description** This package provides methods for genetic finemapping in inbred mice by taking advantage of their very high homozygosity rate (>95%).

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**LazyData** false

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**Depends** R (>= 4.0.0)

**License** GPL-3

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|                       |                                   |
|-----------------------|-----------------------------------|
| annotate_consequences | <i>Annotate with consequences</i> |
|-----------------------|-----------------------------------|

---

Description

Request variant consequences from Variant Effect Predictor (VEP) via Ensembl Rest Service. Not recommended for large queries.

Usage

```
annotate_consequences(geno, species)
```

Arguments

|         |                                                                               |
|---------|-------------------------------------------------------------------------------|
| geno    | Data frame or GenomicRanges::GRanges object including columns rsid, ref, alt. |
| species | Species name, e.g. mouse (GRCm38) or human (GRCh38).                          |

Value

Data frame.

## Examples

```

geno = finemap("chr1",
  start = 5000000, end = 6000000,
  strain1 = c("C57BL_6J"), strain2 = c("AKR_J", "A_J", "BALB_cJ")
)

df = annotate_consequences(geno[seq_len(10), ], "mouse")

geno.granges = finemap("chr1",
  start = 5000000, end = 6000000,
  strain1 = c("C57BL_6J"), strain2 = c("AKR_J", "A_J", "BALB_cJ"),
  return_obj = "granges"
)

df2 = annotate_consequences(geno.granges[seq_len(10), ], "mouse")

```

---

annotate\_mouse\_genes    *Annotate with genes*

---

## Description

Request mouse genes from Ensembl Biomart.

## Usage

```
annotate_mouse_genes(geno, flanking = NULL)
```

## Arguments

|          |                                                                         |
|----------|-------------------------------------------------------------------------|
| geno     | Data frame or GenomicRanges::GRanges object including columns chr, pos. |
| flanking | Size of flanking sequence to be included.                               |

## Value

Data frame.

## Examples

```

geno = finemap("chr1",
  start = 5000000, end = 6000000,
  strain1 = c("C57BL_6J"), strain2 = c("AKR_J", "A_J", "BALB_cJ")
)

genes = annotate_mouse_genes(geno, 50000)

```

---

|                   |                              |
|-------------------|------------------------------|
| avail_chromosomes | <i>Available chromosomes</i> |
|-------------------|------------------------------|

---

**Description**

Available mouse chromosomes.

**Usage**

```
avail_chromosomes()
```

**Value**

Data frame

**Examples**

```
avail_chromosomes()
```

---

|                    |                               |
|--------------------|-------------------------------|
| avail_consequences | <i>Available consequences</i> |
|--------------------|-------------------------------|

---

**Description**

Available consequence and impact types.

**Usage**

```
avail_consequences()
```

**Value**

Data frame.

**Examples**

```
avail_consequences()$consequence  
  
unique(avail_consequences()$impact)
```

---

|               |                          |
|---------------|--------------------------|
| avail_strains | <i>Available strains</i> |
|---------------|--------------------------|

---

**Description**

There are 37 strains available.

**Usage**

```
avail_strains()
```

**Value**

Data frame.

**Examples**

```
avail_strains()
```

---

|                 |                                            |
|-----------------|--------------------------------------------|
| backend_request | <i>Send HTTP request to backend server</i> |
|-----------------|--------------------------------------------|

---

**Description**

Send HTTP request to backend server

**Usage**

```
backend_request(q, n.tries = 2, method = "GET")
```

**Arguments**

|         |                    |
|---------|--------------------|
| q       | Query string       |
| n.tries | Number of tries    |
| method  | HTTP method to use |

**Value**

Data frame.

---

|      |                                   |
|------|-----------------------------------|
| comb | <i>Strain combination builder</i> |
|------|-----------------------------------|

---

### Description

Generate strain sets and calculate reduction factors

### Usage

```
comb(geno, min_strain_benef = 0.1, max_set_size = 3)
```

### Arguments

|                  |                                                                    |
|------------------|--------------------------------------------------------------------|
| geno             | Data frame of genotypes for additional strains.                    |
| min_strain_benef | Minimum reduction factor (min) of a single strain. Default is 0.1. |
| max_set_size     | Maximum set of strains. Default is 3.                              |

### Value

Data frame

---

|            |                                                    |
|------------|----------------------------------------------------|
| df2GRanges | <i>Data frame to GenomicRanges::GRanges object</i> |
|------------|----------------------------------------------------|

---

### Description

Wrapper for GenomicRanges::makeGRangesFromDataFrame().

### Usage

```
df2GRanges(
  geno,
  chr_name = "chr",
  start_name = "pos",
  end_name = "pos",
  strand_name = NULL,
  ref_version = ref_genome(),
  seq_lengths = NULL,
  is_circular = FALSE
)
```

**Arguments**

|             |                                                                      |
|-------------|----------------------------------------------------------------------|
| geno        | Data frame.                                                          |
| chr_name    | Name of chromosome column. Default is 'chr'.                         |
| start_name  | Name of start position column. Default is 'pos.'                     |
| end_name    | Name of end position column. Default is 'pos'                        |
| strand_name | Name of end position column. Default is NULL.                        |
| ref_version | Reference genome version. Default is 'ref_genome()'.                 |
| seq_lengths | List of sequence lengths with sequence name as key. Default is NULL. |
| is_circular | Whether genome is circular. Default is FALSE.                        |

**Value**

GenomicRanges::GRanges object.

**Examples**

```

geno = finemap("chr1",
  start = 5000000, end = 6000000,
  strain1 = c("C57BL_6J"), strain2 = c("AKR_J", "A_J", "BALB_cJ")
)

geno$strand = "+"
seq_lengths = stats::setNames(
  as.list(avail_chromosomes()$length),
  avail_chromosomes()$chr
)
geno.granges = df2GRanges(geno,
  strand_name = "strand",
  seq_lengths = seq_lengths
)

```

df\_split

*Splits data frame df into subsets with maximum n rows***Description**

Splits data frame df into subsets with maximum n rows

**Usage**

```
df_split(df, n)
```

**Arguments**

|    |                                |
|----|--------------------------------|
| df | Data frame.                    |
| n  | Max number of rows per subset. |

**Value**

List of data frames.

---

|                  |                                                                                                  |
|------------------|--------------------------------------------------------------------------------------------------|
| ensembl_rest_vep | <i>Request variant consequences from Variant Effect Predictor (VEP) via Ensembl Rest Service</i> |
|------------------|--------------------------------------------------------------------------------------------------|

---

**Description**

Request variant consequences from Variant Effect Predictor (VEP) via Ensembl Rest Service

**Usage**

```
ensembl_rest_vep(geno, species)
```

**Arguments**

- geno                Data frame including columns rsid, ref, alt.
- species            Species name, e.g. mouse or human.

**Value**

Data frame.

---

|       |              |
|-------|--------------|
| fetch | <i>Fetch</i> |
|-------|--------------|

---

**Description**

Fetch homozygous genotypes for a specified chromosomal region in 37 inbred mouse strains.

**Usage**

```
fetch(  
  chr,  
  start = NULL,  
  end = NULL,  
  consequence = NULL,  
  impact = NULL,  
  return_obj = "dataframe"  
)
```

**Arguments**

|             |                                                                                                                                                                   |
|-------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| chr         | Vector of chromosome names.                                                                                                                                       |
| start       | Optional vector of chromosomal start positions of target regions (GRCm38).                                                                                        |
| end         | Optional vector of chromosomal end positions of target regions (GRCm38).                                                                                          |
| consequence | Optional vector of consequence types.                                                                                                                             |
| impact      | Optional vector of impact types.                                                                                                                                  |
| return_obj  | The user can choose to get the result to be returned as data frame ("dataframe") or as a GenomicRanges::GRanges ("granges") object. Default value is "dataframe". |

**Value**

Data frame or GenomicRanges::GRanges object containing result data.

**Examples**

```
geno = fetch("chr7", start = 5000000, end = 6000000)
comment(geno)
```

---

finemap

*Finemapping of genetic regions*


---

**Description**

Finemapping of genetic regions in 37 inbred mice by taking advantage of their very high homozygosity rate (>95 chromosomal regions (GRCm38), this method extracts homozygous SNVs for which the allele differs between two sets of strains (e.g. case vs controls) and outputs respective causal SNV/gene candidates.

**Usage**

```
finemap(
  chr,
  start = NULL,
  end = NULL,
  strain1,
  strain2,
  consequence = NULL,
  impact = NULL,
  thr1 = 0,
  thr2 = 0,
  return_obj = "dataframe"
)
```

**Arguments**

|             |                                                                                                                                                                   |
|-------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| chr         | Vector of chromosome names.                                                                                                                                       |
| start       | Optional vector of chromosomal start positions of target regions (GRCm38).                                                                                        |
| end         | Optional vector of chromosomal end positions of target regions (GRCm38).                                                                                          |
| strain1     | First strain set with strains from avail_strains().                                                                                                               |
| strain2     | Second strain set with strains from avail_strains().                                                                                                              |
| consequence | Optional vector of consequence types.                                                                                                                             |
| impact      | Optional vector of impact types.                                                                                                                                  |
| thr1        | Number discordant strains in strain1. Between 0 and length(strain1)-1. 0 by default.                                                                              |
| thr2        | Number discordant strains in strain2. Between 0 and length(strain2)-1. 0 by default.                                                                              |
| return_obj  | The user can choose to get the result to be returned as data frame ("dataframe") or as a GenomicRanges::GRanges ("granges") object. Default value is "dataframe". |

**Value**

Data frame or GenomicRanges::GRanges object containing result data.

**Examples**

```
geno = finemap("chr1",
  start = 5000000, end = 6000000,
  strain1 = c("C57BL_6J"), strain2 = c(
    "129S1_SvImJ", "129S5SvEvBrd",
    "AKR_J"
  )
)

comment(geno)
```

---

finemap\_query

*Finemap query builder*


---

**Description**

Finemap query builder

**Usage**

```
finemap_query(
  chr,
  start = NULL,
  end = NULL,
  strain1 = NULL,
```

```

    strain2 = NULL,
    consequence = NULL,
    impact = NULL,
    thr1 = 0,
    thr2 = 0
)

```

### Arguments

|             |                                                                                      |
|-------------|--------------------------------------------------------------------------------------|
| chr         | Vector of chromosome names.                                                          |
| start       | Optional vector of chromosomal start positions of target regions (GRCm38).           |
| end         | Optional vector of chromosomal end positions of target regions (GRCm38).             |
| strain1     | First strain set with strains from avail_strains().                                  |
| strain2     | Second strain set with strains from avail_strains().                                 |
| consequence | Optional vector of consequence types.                                                |
| impact      | Optional vector of impact types.                                                     |
| thr1        | Number discordant strains in strain1. Between 0 and length(strain1)-1. 0 by default. |
| thr2        | Number discordant strains in strain2. Between 0 and length(strain2)-1. 0 by default. |

### Value

Query string.

---

|        |                                |
|--------|--------------------------------|
| getUrl | <i>Get backend service url</i> |
|--------|--------------------------------|

---

### Description

Get backend service URL. Default: <http://45.85.146.64:9000/rest/finemap/>

### Usage

```
getUrl()
```

### Value

URL string.

### Examples

```
getUrl()
```

---

|         |                                 |
|---------|---------------------------------|
| get_top | <i>Best strain combinations</i> |
|---------|---------------------------------|

---

**Description**

Get best strain combinations

**Usage**

```
get_top(red, n_top)
```

**Arguments**

|       |                                        |
|-------|----------------------------------------|
| red   | Reduction factors data frame.          |
| n_top | Number of combinations to be returned. |

**Value**

Data frame

**Examples**

```
l = prio("chr1",
  start = 5000000, end = 6000000,
  strain1 = "C57BL_6J", strain2 = "AKR_J"
)

get_top(l$reduction, 3)
```

---

|            |                                                    |
|------------|----------------------------------------------------|
| GRanges2df | <i>GenomicRanges::GRanges object to data frame</i> |
|------------|----------------------------------------------------|

---

**Description**

Wrapper for as.data.frame().

**Usage**

```
GRanges2df(granges)
```

**Arguments**

|         |                               |
|---------|-------------------------------|
| granges | GenomicRanges::GRanges object |
|---------|-------------------------------|

**Value**

Data frame.

## Examples

```

geno.granges = finemap("chr1",
  start = 5000000, end = 6000000,
  strain1 = c("C57BL_6J"), strain2 = c("AKR_J", "A_J", "BALB_cJ"),
  return_obj = "granges"
)

geno = GRanges2df(geno.granges)

```

---

prio

---

*Prioritization of inbred mouse strains for refining genetic regions*


---

## Description

This method allows to select strain combinations which best refine a specified genetic region (GRCm38). E.g. if a crossing experiment with two inbred mouse strains 'strain1' and 'strain2' resulted in a QTL, the outputted strain combinations can be used to refine the respective region in further crossing experiments.

## Usage

```

prio(
  chr,
  start = NULL,
  end = NULL,
  strain1 = NULL,
  strain2 = NULL,
  consequence = NULL,
  impact = NULL,
  min_strain_benef = 0.1,
  max_set_size = 3,
  return_obj = "dataframe"
)

```

## Arguments

|                  |                                                                            |
|------------------|----------------------------------------------------------------------------|
| chr              | Vector of chromosome names.                                                |
| start            | Optional vector of chromosomal start positions of target regions (GRCm38). |
| end              | Optional vector of chromosomal end positions of target regions (GRCm38).   |
| strain1          | First strain set with strains from avail_strains().                        |
| strain2          | Second strain set with strains from avail_strains().                       |
| consequence      | Optional vector of consequence types.                                      |
| impact           | Optional vector of impact types.                                           |
| min_strain_benef | Minimum reduction factor (min) of a single strain.                         |

max\_set\_size      Maximum set of strains.

return\_obj        The user can choose to get the result to be returned as data frame ("dataframe") or as a GenomicRanges::GRanges ("granges") object. Default value is "data frame".

**Value**

Data frame

**Examples**

```
res = prio("chr1",
  start = 5000000, end = 6000000, strain1 = "C57BL_6J",
  strain2 = "AKR_J"
)

comment(res$genotypes)
```

---

|           |                                     |
|-----------|-------------------------------------|
| reduction | <i>Reduction factor calculation</i> |
|-----------|-------------------------------------|

---

**Description**

Generate strain sets and calculate reduction factors

**Usage**

```
reduction(combs, geno)
```

**Arguments**

combs             Data frame of strain sets.

geno              Data frame of genotypes for additional strains.

**Value**

Data frame

---

|            |                                 |
|------------|---------------------------------|
| ref_genome | <i>Reference genome version</i> |
|------------|---------------------------------|

---

**Description**

Returns version of reference genome used in package MouseFM.

**Usage**

```
ref_genome()
```

**Value**

Vector.

**Examples**

```
ref_genome()
```

---

|        |                                |
|--------|--------------------------------|
| setURL | <i>Set backend service url</i> |
|--------|--------------------------------|

---

**Description**

Set backend service URL. Default: `http://45.85.146.64:9000/rest/finemap/`

**Usage**

```
setURL(url)
```

**Arguments**

|     |                                                    |
|-----|----------------------------------------------------|
| url | URL of backend service. With backslash at the end. |
|-----|----------------------------------------------------|

**Value**

No return value.

**Examples**

```
setURL("http://45.85.146.64:9000/rest/finemap/")
```

---

`vis_reduction_factors` *Visualize*

---

**Description**

Visualize reduction factors

**Usage**

```
vis_reduction_factors(geno, red, n_top)
```

**Arguments**

|                    |                                                       |
|--------------------|-------------------------------------------------------|
| <code>geno</code>  | Genotype data frame or GenomicRanges::GRanges object. |
| <code>red</code>   | Reduction factor data frame.                          |
| <code>n_top</code> | Number of combinations to be returned.                |

**Value**

Data frame

**Examples**

```
l = prio(c("chr1", "chr2"),
  start = c(5000000, 5000000),
  end = c(6000000, 6000000), strain1 = c("C3H_HeH"), strain2 = "AKR_J"
)

plots = vis_reduction_factors(l$genotypes, l$reduction, 2)

plots[[1]]
plots[[2]]
```

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