

Hamimc

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# Chapter 1

## Hierarchical Index

### 1.1 Class Hierarchy

This inheritance list is sorted roughly, but not completely, alphabetically:

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mh_rnd::default_rnd . . . . .	7
biostacs::Likelihood . . . . .	8
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## Chapter 2

# Class Index

### 2.1 Class List

Here are the classes, structs, unions and interfaces with brief descriptions:

<a href="#">biostacs_bmp::BITMATWRITE500</a>	7
<a href="#">mh_rnd::default_rnd</a>	
Default proposal: contains $\text{rnorm}(0,1)$ $\text{ruinf}(0,1)$	7
<a href="#">biostacs::Likelihood</a>	
Likelihood class <a href="#">Likelihood</a> calculation	8
<a href="#">biostacs::MetropolisMCMC</a>	
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<a href="#">mh_rnd::rnorm</a>	9





## Chapter 3

# File Index

### 3.1 File List

Here is a list of all documented files with brief descriptions:

D:/Git/MH/mh/src./ <b>bmp.h</b>	??
D:/Git/MH/mh/src./ <b>comm.h</b>	??
D:/Git/MH/mh/src./ <a href="#">MH_tm.h</a>	<a href="#">11</a>



## Chapter 4

# Class Documentation

### 4.1 biostacs\_bmp::BITMATWRITE500 Class Reference

#### Public Member Functions

- **BITMATWRITE500** (std::string filename\_, std::vector< int > xval\_, std::vector< int > yval\_)
- void [BITMAPCREATING\\_CT](#) ()

#### 4.1.1 Member Function Documentation

##### 4.1.1.1 void biostacs\_bmp::BITMATWRITE500::BITMAPCREATING\_CT ( )

FRAME

The documentation for this class was generated from the following file:

- D:/Git/MH/mh/src./bmp.h

### 4.2 mh\_rnd::default\_rnd Class Reference

Default proposal: contains rnorm(0,1) ruinf(0,1)

```
#include <comm.h>
```

#### Public Member Functions

- template<typename SeedSeq >  
  **default\_rnd** (SeedSeq &&seed)
- double **rproposal** ()
- double **runif** ()

#### Public Attributes

- std::mt19937 **eng** = make\_seeded\_engine()
- std::normal\_distribution **DefaultProposalDist** { 0, 1 }
- std::uniform\_real\_distribution **unif** { 0, 1 }

### 4.2.1 Detailed Description

Default proposal: contains  $\text{rnorm}(0,1)$   $\text{ruinf}(0,1)$

Author

Yifan Yang

The documentation for this class was generated from the following file:

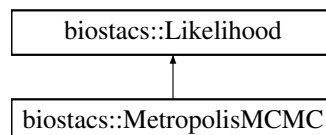
- D:/Git/MH/mh/src./comm.h

## 4.3 biostacs::Likelihood Class Reference

[Likelihood](#) class [Likelihood](#) calculation.

```
#include <MH_tm.h>
```

Inheritance diagram for biostacs::Likelihood:



### Public Member Functions

- **Likelihood** (vector< double > parameters, mat &data)

### 4.3.1 Detailed Description

[Likelihood](#) class [Likelihood](#) calculation.

Author

Yifan Yang

The documentation for this class was generated from the following file:

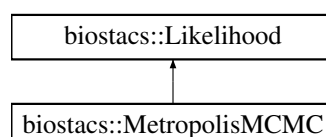
- D:/Git/MH/mh/src./[MH\\_tm.h](#)

## 4.4 biostacs::MetropolisMCMC Class Reference

MCMC class one chain MH MH calculation.

```
#include <MH_tm.h>
```

Inheritance diagram for biostacs::MetropolisMCMC:



## Public Member Functions

- double **priorlog** (double priorpdf(vector< double > param), vector< double > param)
- double **posterior** (double pdf(vector< double > param, mat x), double priorpdf(vector< double > param), vector< double > param)
- **MetropolisMCMC** (vector< double > parameters, mat &data, int MaxIterations, vector< double > starting-value)
- void **normal\_proposal** (vector< double > param)
- mat **MH\_MCMC** (double pdf(vector< double > param, mat x), double priorpdf(vector< double > param))

*Main HM Algorithm.*

### 4.4.1 Detailed Description

MCMC class one chain MH MH calculation.

#### Author

Yifan Yang

### 4.4.2 Member Function Documentation

4.4.2.1 mat biostacs::MetropolisMCMC::MH\_MCMC ( double *pdf*vector< double > *param*, mat *x*, double *priorpdf*vector< double > *param* ) [inline]

Main HM Algorithm.

Importance sampling

#### Parameters

in	<i>pdf</i>	index of a function with in put pdf(vector<double> param, mat x) mat = n * p, mat[i,j] is value of the i-th observation, j-th variable.
in	<i>priorpdf</i>	index of a function with in put priorpdf(vector<double> param)
out	<i>MonteCarloChain</i>	Monte Carlo Chain (double matrix)

#### Returns

the return matrix contain only one chain.

#### Warning

omp\_get\_thread\_num() fails on Windows

The documentation for this class was generated from the following file:

- D:/Git/MH/mh/src./MH\_tm.h

## 4.5 mh\_rnd::rnorm Struct Reference

### Public Member Functions

- template<typename SeedSeq >  
**rnorm** (SeedSeq &&seed)
- double **r** ()

### Public Attributes

- `std::mt19937 eng = make_seeded_engine()`
- `std::normal_distribution normal_01 { 0, 1 }`

The documentation for this struct was generated from the following file:

- `D:/Git/MH/mh/src./comm.h`

## Chapter 5

# File Documentation

### 5.1 D:/Git/MH/mh/src./MH\_tm.h File Reference

```
#include "comm.h"  
#include <omp.h>
```

#### Classes

- class [biostacs::Likelihood](#)  
*Likelihood class Likelihood calculation.*
- class [biostacs::MetropolisMCMC](#)  
*MCMC class one chain MH MH calculation.*

#### 5.1.1 Detailed Description

##### Author

Yifan Yang

##### Date

2016-04

1. Classical MH algorithm





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