

FragScanTibo

0.1

Gegenereerd door Doxygen 1.8.18

1 Klasse Index	1
1.1 Klasse Lijst	1
2 Bestand Index	3
2.1 Bestandslijst	3
3 Klassen Documentatie	5
3.1 HMM Struct Referentie	5
3.1.1 Documentatie van data members	5
3.1.1.1 E1_dist	5
3.1.1.2 E_dist	6
3.1.1.3 e_M	6
3.1.1.4 e_M_1	6
3.1.1.5 N	6
3.1.1.6 pi	6
3.1.1.7 S1_dist	6
3.1.1.8 S_dist	6
3.1.1.9 tr	6
3.1.1.10 tr_E	7
3.1.1.11 tr_E_1	7
3.1.1.12 tr_I_I	7
3.1.1.13 tr_M_I	7
3.1.1.14 tr_R_R	7
3.1.1.15 tr_S	7
3.1.1.16 tr_S_1	7
3.2 thread_data Struct Referentie	8
3.2.1 Documentatie van data members	8
3.2.1.1 aa	8
3.2.1.2 cg	8
3.2.1.3 dna	8
3.2.1.4 format	8
3.2.1.5 hmm	9
3.2.1.6 obs_head	9
3.2.1.7 obs_seq	9
3.2.1.8 out	9
3.2.1.9 train	9
3.2.1.10 wholegenome	9
3.3 TRAIN Struct Referentie	9
3.3.1 Documentatie van data members	10
3.3.1.1 E1_dist	10
3.3.1.2 E_dist	10
3.3.1.3 noncoding	10
3.3.1.4 rtrans	10

3.3.1.5 S1_dist	10
3.3.1.6 S_dist	11
3.3.1.7 start	11
3.3.1.8 start1	11
3.3.1.9 stop	11
3.3.1.10 stop1	11
3.3.1.11 trans	11
4 Bestand Documentatie	13
4.1 hmm.h Bestand Referentie	13
4.1.1 Documentatie van macro's	14
4.1.1.1 A	14
4.1.1.2 C	15
4.1.1.3 E_STATE	15
4.1.1.4 E_STATE_1	15
4.1.1.5 G	15
4.1.1.6 I1_STATE	15
4.1.1.7 I1_STATE_1	15
4.1.1.8 I2_STATE	15
4.1.1.9 I2_STATE_1	15
4.1.1.10 I3_STATE	16
4.1.1.11 I3_STATE_1	16
4.1.1.12 I4_STATE	16
4.1.1.13 I4_STATE_1	16
4.1.1.14 I5_STATE	16
4.1.1.15 I5_STATE_1	16
4.1.1.16 I6_STATE	16
4.1.1.17 I6_STATE_1	16
4.1.1.18 M1_STATE	17
4.1.1.19 M1_STATE_1	17
4.1.1.20 M2_STATE	17
4.1.1.21 M2_STATE_1	17
4.1.1.22 M3_STATE	17
4.1.1.23 M3_STATE_1	17
4.1.1.24 M4_STATE	17
4.1.1.25 M4_STATE_1	17
4.1.1.26 M5_STATE	18
4.1.1.27 M5_STATE_1	18
4.1.1.28 M6_STATE	18
4.1.1.29 M6_STATE_1	18
4.1.1.30 NOSTATE	18
4.1.1.31 NUM_STATE	18

4.1.1.32 R_STATE	18
4.1.1.33 S_STATE	18
4.1.1.34 S_STATE_1	19
4.1.1.35 T	19
4.1.1.36 TR_DD	19
4.1.1.37 TR_DM	19
4.1.1.38 TR_ER	19
4.1.1.39 TR_ES	19
4.1.1.40 TR_ES1	19
4.1.1.41 TR_GE	19
4.1.1.42 TR_GG	20
4.1.1.43 TR_II	20
4.1.1.44 TR_IM	20
4.1.1.45 TR_MD	20
4.1.1.46 TR_MI	20
4.1.1.47 TR_MM	20
4.1.1.48 TR_RR	20
4.1.1.49 TR_RS	20
4.1.2 Documentatie van functies	21
4.1.2.1 free_hmm()	21
4.1.2.2 get_corrected_dna()	21
4.1.2.3 get_prob_from_cg()	21
4.1.2.4 get_protein()	21
4.1.2.5 get_rc_dna()	21
4.1.2.6 get_train_from_file()	22
4.1.2.7 viterbi()	22
4.2 hmm_lib.c Bestand Referentie	22
4.2.1 Documentatie van functies	23
4.2.1.1 dump_memory()	23
4.2.1.2 free_hmm()	23
4.2.1.3 get_prob_from_cg()	23
4.2.1.4 get_train_from_file()	23
4.2.1.5 viterbi()	24
4.3 run_hmm.c Bestand Referentie	24
4.3.1 Documentatie van macro's	25
4.3.1.1 ADD_LEN	25
4.3.1.2 STRINGLEN	25
4.3.2 Documentatie van typedefs	25
4.3.2.1 thread_data	25
4.3.3 Documentatie van functies	25
4.3.3.1 appendSeq()	25
4.3.3.2 main()	25

4.3.3.3 thread_func()	26
4.4 util_lib.c Bestand Referentie	26
4.4.1 Documentatie van functies	26
4.4.1.1 dmatrix()	26
4.4.1.2 dvector()	27
4.4.1.3 free_dmatrix()	27
4.4.1.4 free_dvector()	27
4.4.1.5 free_imatrix()	27
4.4.1.6 free_ivector()	27
4.4.1.7 get_protein()	27
4.4.1.8 get_rc_dna()	28
4.4.1.9 get_rc_dna_indel()	28
4.4.1.10 imatrix()	28
4.4.1.11 iverector()	28
4.4.1.12 log2()	28
4.4.1.13 nt2int()	28
4.4.1.14 nt2int_rc()	29
4.4.1.15 nt2int_rc_indel()	29
4.4.1.16 print_usage()	29
4.4.1.17 tr2int()	29
4.4.1.18 trinucleotide()	29
4.4.1.19 trinucleotide_pep()	29
4.5 util_lib.h Bestand Referentie	30
4.5.1 Documentatie van functies	30
4.5.1.1 dmatrix()	30
4.5.1.2 dvector()	30
4.5.1.3 free_dmatrix()	31
4.5.1.4 free_dvector()	31
4.5.1.5 free_imatrix()	31
4.5.1.6 free_iverector()	31
4.5.1.7 get_protein()	31
4.5.1.8 imatrix()	31
4.5.1.9 iverector()	32
4.5.1.10 log2()	32
4.5.1.11 nt2int()	32
4.5.1.12 nt2int_rc()	32
4.5.1.13 print_usage()	32
4.5.1.14 tr2int()	32
4.5.1.15 trinucleotide()	32

Hoofdstuk 1

Klasse Index

1.1 Klasse Lijst

Hieronder volgen de klassen, structs en unions met voor elk een korte beschrijving:

HMM	5
thread_data	8
TRAIN	9

Hoofdstuk 2

Bestand Index

2.1 Bestandslijst

Hieronder volgt de lijst met alle bestanden, elk met een korte beschrijving:

hmm.h	13
hmm_lib.c	22
run_hmm.c	24
util_lib.c	26
util_lib.h	30

Hoofdstuk 3

Klassen Documentatie

3.1 HMM Struct Referentie

```
#include <hmm.h>
```

Public Attributen

- double [pi](#) [29]
- int [N](#)
- double [tr](#) [14]
- double [e_M_1](#) [6][16][4]
- double [e_M](#) [6][16][4]
- double [tr_R_R](#) [4][4]
- double [tr_I_I](#) [4][4]
- double [tr_M_I](#) [4][4]
- double [tr_S](#) [61][64]
- double [tr_E](#) [61][64]
- double [tr_S_1](#) [61][64]
- double [tr_E_1](#) [61][64]
- double [S_dist](#) [6]
- double [E_dist](#) [6]
- double [S1_dist](#) [6]
- double [E1_dist](#) [6]

3.1.1 Documentatie van data members

3.1.1.1 E1_dist

```
double E1_dist[6]
```

3.1.1.2 E_dist

```
double E_dist[6]
```

3.1.1.3 e_M

```
double e_M[6][16][4]
```

3.1.1.4 e_M_1

```
double e_M_1[6][16][4]
```

3.1.1.5 N

```
int N
```

3.1.1.6 pi

```
double pi[29]
```

3.1.1.7 S1_dist

```
double S1_dist[6]
```

3.1.1.8 S_dist

```
double S_dist[6]
```

3.1.1.9 tr

```
double tr[14]
```

3.1.1.10 tr_E

```
double tr_E[61][64]
```

3.1.1.11 tr_E_1

```
double tr_E_1[61][64]
```

3.1.1.12 tr_I_I

```
double tr_I_I[4][4]
```

3.1.1.13 tr_M_I

```
double tr_M_I[4][4]
```

3.1.1.14 tr_R_R

```
double tr_R_R[4][4]
```

3.1.1.15 tr_S

```
double tr_S[61][64]
```

3.1.1.16 tr_S_1

```
double tr_S_1[61][64]
```

De documentatie voor deze struct is gegenereerd op grond van het volgende bestand:

- [hmm.h](#)

3.2 thread_data Struct Referentie

Collaboratie diagram voor thread_data:

Public Attributen

- FILE * [out](#)
- FILE * [aa](#)
- FILE * [dna](#)
- char * [obs_head](#)
- char * [obs_seq](#)
- int [wholegenome](#)
- int [cg](#)
- int [format](#)
- HMM * [hmm](#)
- TRAIN * [train](#)

3.2.1 Documentatie van data members

3.2.1.1 aa

```
FILE* aa
```

3.2.1.2 cg

```
int cg
```

3.2.1.3 dna

```
FILE* dna
```

3.2.1.4 format

```
int format
```

3.2.1.5 hmm

[HMM*](#) hmm

3.2.1.6 obs_head

char* obs_head

3.2.1.7 obs_seq

char* obs_seq

3.2.1.8 out

FILE* out

3.2.1.9 train

[TRAIN*](#) train

3.2.1.10 wholegenome

int wholegenome

De documentatie voor deze struct is gegenereerd op grond van het volgende bestand:

- [run_hmm.c](#)

3.3 TRAIN Struct Referentie

```
#include <hmm.h>
```

Public Attributen

- double [trans](#) [44][6][16][4]
- double [rtrans](#) [44][6][16][4]
- double [noncoding](#) [44][4][4]
- double [start](#) [44][61][64]
- double [stop](#) [44][61][64]
- double [start1](#) [44][61][64]
- double [stop1](#) [44][61][64]
- double [S_dist](#) [44][6]
- double [E_dist](#) [44][6]
- double [S1_dist](#) [44][6]
- double [E1_dist](#) [44][6]

3.3.1 Documentatie van data members

3.3.1.1 E1_dist

```
double E1_dist[44][6]
```

3.3.1.2 E_dist

```
double E_dist[44][6]
```

3.3.1.3 noncoding

```
double noncoding[44][4][4]
```

3.3.1.4 rtrans

```
double rtrans[44][6][16][4]
```

3.3.1.5 S1_dist

```
double S1_dist[44][6]
```


3.3.1.6 S_dist

```
double S_dist[44][6]
```

3.3.1.7 start

```
double start[44][61][64]
```

3.3.1.8 start1

```
double start1[44][61][64]
```

3.3.1.9 stop

```
double stop[44][61][64]
```

3.3.1.10 stop1

```
double stop1[44][61][64]
```

3.3.1.11 trans

```
double trans[44][6][16][4]
```

De documentatie voor deze struct is gegenereerd op grond van het volgende bestand:

- [hmm.h](#)

Hoofdstuk 4

Bestand Documentatie

4.1 hmm.h Bestand Referentie

```
#include <stdlib.h>
#include <stdio.h>
#include <math.h>
```

Include afhankelijkheidsgraaf voor hmm.h: Deze graaf geeft aan welke bestanden direct of indirect afhankelijk zijn van dit bestand:

Klassen

- struct [HMM](#)
- struct [TRAIN](#)

Macros

- #define [A](#) 0
- #define [C](#) 1
- #define [G](#) 2
- #define [T](#) 3
- #define [NUM_STATE](#) 29
- #define [NOSTATE](#) -1
- #define [S_STATE](#) 0
- #define [E_STATE](#) 1
- #define [R_STATE](#) 2
- #define [S_STATE_1](#) 3
- #define [E_STATE_1](#) 4
- #define [M1_STATE](#) 5
- #define [M2_STATE](#) 6
- #define [M3_STATE](#) 7
- #define [M4_STATE](#) 8
- #define [M5_STATE](#) 9
- #define [M6_STATE](#) 10
- #define [M1_STATE_1](#) 11
- #define [M2_STATE_1](#) 12
- #define [M3_STATE_1](#) 13

- #define M4_STATE_1 14
- #define M5_STATE_1 15
- #define M6_STATE_1 16
- #define I1_STATE 17
- #define I2_STATE 18
- #define I3_STATE 19
- #define I4_STATE 20
- #define I5_STATE 21
- #define I6_STATE 22
- #define I1_STATE_1 23
- #define I2_STATE_1 24
- #define I3_STATE_1 25
- #define I4_STATE_1 26
- #define I5_STATE_1 27
- #define I6_STATE_1 28
- #define TR_MM 0
- #define TR_MI 1
- #define TR_MD 2
- #define TR_II 3
- #define TR_IM 4
- #define TR_DD 5
- #define TR_DM 6
- #define TR_GE 7
- #define TR_GG 8
- #define TR_ER 9
- #define TR_RS 10
- #define TR_RR 11
- #define TR_ES 12
- #define TR_ES1 13

Funcities

- int `get_prob_from_cg` (HMM *hmm, TRAIN *train, char *O)
- void `get_train_from_file` (char *filename, HMM *hmm_ptr, char *mfilename, char *mfilename1, char *nfilename, char *sfilename, char *pfilename, char *s1filename, char *p1filename, char *dfilename, TRAIN *train_ptr)
- void `viterbi` (HMM *hmm_ptr, TRAIN *train_ptr, char *O, FILE *out_filename, FILE *log_filename, FILE *dna_filename, char *head, int metagene, int cg, int format)
- void `free_hmm` (HMM *hmm)
- void `get_protein` (char *dna, char *protein, int strand, int whole_genome)
- void `get_rc_dna` (char *dna, char *dna1)
- void `get_corrected_dna` (char *dna, char *dna_f)

4.1.1 Documentatie van macro's

4.1.1.1 A

```
#define A 0
```

4.1.1.2 C

```
#define C 1
```

4.1.1.3 E_STATE

```
#define E_STATE 1
```

4.1.1.4 E_STATE_1

```
#define E_STATE_1 4
```

4.1.1.5 G

```
#define G 2
```

4.1.1.6 I1_STATE

```
#define I1_STATE 17
```

4.1.1.7 I1_STATE_1

```
#define I1_STATE_1 23
```

4.1.1.8 I2_STATE

```
#define I2_STATE 18
```

4.1.1.9 I2_STATE_1

```
#define I2_STATE_1 24
```

4.1.1.10 I3_STATE

```
#define I3_STATE 19
```

4.1.1.11 I3_STATE_1

```
#define I3_STATE_1 25
```

4.1.1.12 I4_STATE

```
#define I4_STATE 20
```

4.1.1.13 I4_STATE_1

```
#define I4_STATE_1 26
```

4.1.1.14 I5_STATE

```
#define I5_STATE 21
```

4.1.1.15 I5_STATE_1

```
#define I5_STATE_1 27
```

4.1.1.16 I6_STATE

```
#define I6_STATE 22
```

4.1.1.17 I6_STATE_1

```
#define I6_STATE_1 28
```

4.1.1.18 M1_STATE

```
#define M1_STATE 5
```

4.1.1.19 M1_STATE_1

```
#define M1_STATE_1 11
```

4.1.1.20 M2_STATE

```
#define M2_STATE 6
```

4.1.1.21 M2_STATE_1

```
#define M2_STATE_1 12
```

4.1.1.22 M3_STATE

```
#define M3_STATE 7
```

4.1.1.23 M3_STATE_1

```
#define M3_STATE_1 13
```

4.1.1.24 M4_STATE

```
#define M4_STATE 8
```

4.1.1.25 M4_STATE_1

```
#define M4_STATE_1 14
```

4.1.1.26 M5_STATE

```
#define M5_STATE 9
```

4.1.1.27 M5_STATE_1

```
#define M5_STATE_1 15
```

4.1.1.28 M6_STATE

```
#define M6_STATE 10
```

4.1.1.29 M6_STATE_1

```
#define M6_STATE_1 16
```

4.1.1.30 NOSTATE

```
#define NOSTATE -1
```

4.1.1.31 NUM_STATE

```
#define NUM_STATE 29
```

4.1.1.32 R_STATE

```
#define R_STATE 2
```

4.1.1.33 S_STATE

```
#define S_STATE 0
```


4.1.1.34 S_STATE_1

```
#define S_STATE_1 3
```

4.1.1.35 T

```
#define T 3
```

4.1.1.36 TR_DD

```
#define TR_DD 5
```

4.1.1.37 TR_DM

```
#define TR_DM 6
```

4.1.1.38 TR_ER

```
#define TR_ER 9
```

4.1.1.39 TR_ES

```
#define TR_ES 12
```

4.1.1.40 TR_ES1

```
#define TR_ES1 13
```

4.1.1.41 TR_GE

```
#define TR_GE 7
```

4.1.1.42 TR_GG

```
#define TR_GG 8
```

4.1.1.43 TR_II

```
#define TR_II 3
```

4.1.1.44 TR_IM

```
#define TR_IM 4
```

4.1.1.45 TR_MD

```
#define TR_MD 2
```

4.1.1.46 TR_MI

```
#define TR_MI 1
```

4.1.1.47 TR_MM

```
#define TR_MM 0
```

4.1.1.48 TR_RR

```
#define TR_RR 11
```

4.1.1.49 TR_RS

```
#define TR_RS 10
```

4.1.2 Documentatie van functies

4.1.2.1 free_hmm()

```
void free_hmm (
    HMM * hmm )
```

Hier is de call graaf voor deze functie:

4.1.2.2 get_corrected_dna()

```
void get_corrected_dna (
    char * dna,
    char * dna_f )
```

4.1.2.3 get_prob_from_cg()

```
int get_prob_from_cg (
    HMM * hmm,
    TRAIN * train,
    char * O )
```

Hier is de caller graaf voor deze functie:

4.1.2.4 get_protein()

```
void get_protein (
    char * dna,
    char * protein,
    int strand,
    int whole_genome )
```

Hier is de caller graaf voor deze functie:

4.1.2.5 get_rc_dna()

```
void get_rc_dna (
    char * dna,
    char * dna1 )
```

Hier is de call graaf voor deze functie: Hier is de caller graaf voor deze functie:

4.1.2.6 get_train_from_file()

```
void get_train_from_file (
    char * filename,
    HMM * hmm_ptr,
    char * mfilename,
    char * mfilename1,
    char * nfilename,
    char * sfilename,
    char * pfilename,
    char * s1filename,
    char * p1filename,
    char * dfilename,
    TRAIN * train_ptr )
```

Hier is de call graaf voor deze functie: Hier is de caller graaf voor deze functie:

4.1.2.7 viterbi()

```
void viterbi (
    HMM * hmm_ptr,
    TRAIN * train_ptr,
    char * O,
    FILE * out_filename,
    FILE * log_filename,
    FILE * dna_filename,
    char * head,
    int metagene,
    int cg,
    int format )
```

Hier is de call graaf voor deze functie: Hier is de caller graaf voor deze functie:

4.2 hmm_lib.c Bestand Referentie

```
#include <stdio.h>
#include <math.h>
#include <string.h>
#include <stdlib.h>
#include <ctype.h>
#include "hmm.h"
#include "util_lib.h"
```

Include afhankelijkheidsgraaf voor hmm_lib.c:

Functies

- void [dump_memory](#) (void *p, int size)
- void [viterbi](#) (HMM *hmm_ptr, TRAIN *train_ptr, char *O, FILE *fp_out, FILE *fp_aa, FILE *fp_dna, char *head, int whole_genome, int cg, int format)
- int [get_prob_from_cg](#) (HMM *hmm_ptr, TRAIN *train_ptr, char *O)
- void [get_train_from_file](#) (char *filename, HMM *hmm_ptr, char *mfilename, char *mfilename1, char *nfilename, char *sfilename, char *pfilename, char *s1filename, char *p1filename, char *dfilename, TRAIN *train_ptr)
- void [free_hmm](#) (HMM *hmm_ptr)

4.2.1 Documentatie van functies

4.2.1.1 dump_memory()

```
void dump_memory (
    void * p,
    int size )
```

4.2.1.2 free_hmm()

```
void free_hmm (
    HMM * hmm_ptr )
```

Hier is de call graaf voor deze functie:

4.2.1.3 get_prob_from_cg()

```
int get_prob_from_cg (
    HMM * hmm_ptr,
    TRAIN * train_ptr,
    char * O )
```

Hier is de caller graaf voor deze functie:

4.2.1.4 get_train_from_file()

```
void get_train_from_file (
    char * filename,
    HMM * hmm_ptr,
    char * mfilename,
    char * mfilename1,
    char * nfilename,
    char * sfilename,
    char * pfilename,
    char * slfilename,
    char * plfilename,
    char * dfilename,
    TRAIN * train_ptr )
```

Hier is de call graaf voor deze functie: Hier is de caller graaf voor deze functie:

4.2.1.5 viterbi()

```
void viterbi (
    HMM * hmm_ptr,
    TRAIN * train_ptr,
    char * O,
    FILE * fp_out,
    FILE * fp_aa,
    FILE * fp_dna,
    char * head,
    int whole_genome,
    int cg,
    int format )
```

Hier is de call graaf voor deze functie: Hier is de caller graaf voor deze functie:

4.3 run_hmm.c Bestand Referentie

```
#include <ctype.h>
#include <stdio.h>
#include <stdlib.h>
#include <math.h>
#include <unistd.h>
#include <string.h>
#include <time.h>
#include "hmm.h"
#include <pthread.h>
Include afhankelijkheidsgraaf voor run_hmm.c:
```

Klassen

- struct [thread_data](#)

Macros

- #define [ADD_LEN](#) 1024
- #define [STRINGLEN](#) 4096

Typedefs

- typedef struct [thread_data](#) [thread_data](#)

Functies

- void * [thread_func](#) (void *threadarr)
- int [main](#) (int argc, char **argv)
- int [appendSeq](#) (char *input, char **seq, int input_max)

4.3.1 Documentatie van macro's

4.3.1.1 ADD_LEN

```
#define ADD_LEN 1024
```

4.3.1.2 STRINGLEN

```
#define STRINGLEN 4096
```

4.3.2 Documentatie van typedefs

4.3.2.1 thread_data

```
typedef struct thread_data thread_data
```

4.3.3 Documentatie van functies

4.3.3.1 appendSeq()

```
int appendSeq (
    char * input,
    char ** seq,
    int input_max )
```

4.3.3.2 main()

```
int main (
    int argc,
    char ** argv )
```

Hier is de call graaf voor deze functie:

4.3.3.3 thread_func()

```
void * thread_func (
    void * threadarr )
```

Hier is de call graaf voor deze functie: Hier is de caller graaf voor deze functie:

4.4 util_lib.c Bestand Referentie

```
#include <stdio.h>
#include <math.h>
#include <stdlib.h>
#include <string.h>
Include afhankelijkheidsgraaf voor util_lib.c:
```

Functies

- double [log2](#) (double a)
- double ** [dmatrix](#) (int num_row, int num_col)
- int ** [imatrix](#) (int num_row, int num_col)
- double * [dvector](#) (int nh)
- int * [ivector](#) (int nh)
- void [free_dvector](#) (double *v)
- void [free_ivector](#) (int *v)
- void [free_dmatrix](#) (double **m, int num_row)
- void [free_imatrix](#) (int **m, int num_row)
- int [tr2int](#) (char *tr)
- int [nt2int](#) (char nt)
- int [nt2int_rc](#) (char nt)
- int [nt2int_rc_indel](#) (char nt)
- int [trinucleotide](#) (char a, char b, char c)
- int [trinucleotide_pep](#) (char a, char b, char c)
- void [get_rc_dna](#) (char *dna, char *dna1)
- void [get_rc_dna_indel](#) (char *dna, char *dna1)
- void [get_protein](#) (char *dna, char *protein, int strand, int whole_genome)
- void [print_usage](#) ()

4.4.1 Documentatie van functies

4.4.1.1 dmatrix()

```
double** dmatrix (
    int num_row,
    int num_col )
```

Hier is de caller graaf voor deze functie:

4.4.1.2 dvector()

```
double* dvector (
    int nh )
```

4.4.1.3 free_dmatrix()

```
void free_dmatrix (
    double ** m,
    int num_row )
```

Hier is de caller graaf voor deze functie:

4.4.1.4 free_dvector()

```
void free_dvector (
    double * v )
```

Hier is de caller graaf voor deze functie:

4.4.1.5 free_imatrix()

```
void free_imatrix (
    int ** m,
    int num_row )
```

Hier is de caller graaf voor deze functie:

4.4.1.6 free_ivector()

```
void free_ivector (
    int * v )
```

Hier is de caller graaf voor deze functie:

4.4.1.7 get_protein()

```
void get_protein (
    char * dna,
    char * protein,
    int strand,
    int whole_genome )
```

Hier is de call graaf voor deze functie: Hier is de caller graaf voor deze functie:

4.4.1.8 get_rc_dna()

```
void get_rc_dna (
    char * dna,
    char * dna1 )
```

Hier is de call graaf voor deze functie: Hier is de caller graaf voor deze functie:

4.4.1.9 get_rc_dna_indel()

```
void get_rc_dna_indel (
    char * dna,
    char * dna1 )
```

Hier is de call graaf voor deze functie: Hier is de caller graaf voor deze functie:

4.4.1.10 imatrix()

```
int** imatrix (
    int num_row,
    int num_col )
```

Hier is de caller graaf voor deze functie:

4.4.1.11 ivector()

```
int* ivector (
    int nh )
```

Hier is de caller graaf voor deze functie:

4.4.1.12 log2()

```
double log2 (
    double a )
```

4.4.1.13 nt2int()

```
int nt2int (
    char nt )
```

Hier is de caller graaf voor deze functie:

4.4.1.14 nt2int_rc()

```
int nt2int_rc (
    char nt )
```

Hier is de caller graaf voor deze functie:

4.4.1.15 nt2int_rc_indel()

```
int nt2int_rc_indel (
    char nt )
```

Hier is de caller graaf voor deze functie:

4.4.1.16 print_usage()

```
void print_usage ( )
```

Hier is de caller graaf voor deze functie:

4.4.1.17 tr2int()

```
int tr2int (
    char * tr )
```

Hier is de caller graaf voor deze functie:

4.4.1.18 trinucleotide()

```
int trinucleotide (
    char a,
    char b,
    char c )
```

Hier is de caller graaf voor deze functie:

4.4.1.19 trinucleotide_pep()

```
int trinucleotide_pep (
    char a,
    char b,
    char c )
```

Hier is de caller graaf voor deze functie:

4.5 util_lib.h Bestand Referentie

```
#include <stdlib.h>
#include <stdio.h>
#include <math.h>
```

Include afhankelijkheidsgraaf voor util_lib.h: Deze graaf geeft aan welke bestanden direct of indirect afhankelijk zijn van dit bestand:

Functies

- double ** [dmatrix](#) (int num_row, int num_col)
- double * [dvector](#) (int nh)
- int ** [imatrix](#) (int num_row, int num_col)
- int * [ivector](#) (int nh)
- void [free_dvector](#) (double *v)
- void [free_dmatrix](#) (double **m, int num_row)
- void [free_ivector](#) (int *v)
- void [free_imatrix](#) (int **m, int num_row)
- int [tr2int](#) (char *nt)
- int [nt2int](#) (char nt)
- int [nt2int_rc](#) (char nt)
- int [trinucleotide](#) (char a, char b, char c)
- double [log2](#) (double a)
- void [get_protein](#) (char *dna, char *protein, int strand, int whole_genome)
- void [print_usage](#) ()

4.5.1 Documentatie van functies

4.5.1.1 [dmatrix\(\)](#)

```
double** dmatrix (
    int num_row,
    int num_col )
```

Hier is de caller graaf voor deze functie:

4.5.1.2 [dvector\(\)](#)

```
double* dvector (
    int nh )
```

4.5.1.3 free_dmatrix()

```
void free_dmatrix (
    double ** m,
    int num_row )
```

Hier is de caller graaf voor deze functie:

4.5.1.4 free_dvector()

```
void free_dvector (
    double * v )
```

Hier is de caller graaf voor deze functie:

4.5.1.5 free_imatrix()

```
void free_imatrix (
    int ** m,
    int num_row )
```

Hier is de caller graaf voor deze functie:

4.5.1.6 free_ivector()

```
void free_ivector (
    int * v )
```

Hier is de caller graaf voor deze functie:

4.5.1.7 get_protein()

```
void get_protein (
    char * dna,
    char * protein,
    int strand,
    int whole_genome )
```

Hier is de call graaf voor deze functie:

4.5.1.8 imatrix()

```
int** imatrix (
    int num_row,
    int num_col )
```

Hier is de caller graaf voor deze functie:

4.5.1.9 ivector()

```
int* ivector (
    int nh )
```

Hier is de caller graaf voor deze functie:

4.5.1.10 log2()

```
double log2 (
    double a )
```

4.5.1.11 nt2int()

```
int nt2int (
    char nt )
```

Hier is de caller graaf voor deze functie:

4.5.1.12 nt2int_rc()

```
int nt2int_rc (
    char nt )
```

Hier is de caller graaf voor deze functie:

4.5.1.13 print_usage()

```
void print_usage ( )
```

Hier is de caller graaf voor deze functie:

4.5.1.14 tr2int()

```
int tr2int (
    char * nt )
```

Hier is de caller graaf voor deze functie:

4.5.1.15 trinucleotide()

```
int trinucleotide (
    char a,
    char b,
    char c )
```

Hier is de caller graaf voor deze functie:

Index

A

hmm.h, [14](#)

aa

thread_data, [8](#)

ADD_LEN

run_hmm.c, [25](#)

appendSeq

run_hmm.c, [25](#)

C

hmm.h, [14](#)

cg

thread_data, [8](#)

dmatrix

util_lib.c, [26](#)

util_lib.h, [30](#)

dna

thread_data, [8](#)

dump_memory

hmm_lib.c, [23](#)

dvector

util_lib.c, [26](#)

util_lib.h, [30](#)

E1_dist

HMM, [5](#)

TRAIN, [10](#)

E_dist

HMM, [5](#)

TRAIN, [10](#)

e_M

HMM, [6](#)

e_M_1

HMM, [6](#)

E_STATE

hmm.h, [15](#)

E_STATE_1

hmm.h, [15](#)

format

thread_data, [8](#)

free_dmatrix

util_lib.c, [27](#)

util_lib.h, [30](#)

free_dvector

util_lib.c, [27](#)

util_lib.h, [31](#)

free_hmm

hmm.h, [21](#)

hmm_lib.c, [23](#)

free_imatrix

util_lib.c, [27](#)

util_lib.h, [31](#)

free_ivector

util_lib.c, [27](#)

util_lib.h, [31](#)

G

hmm.h, [15](#)

get_corrected_dna

hmm.h, [21](#)

get_prob_from_cg

hmm.h, [21](#)

hmm_lib.c, [23](#)

get_protein

hmm.h, [21](#)

util_lib.c, [27](#)

util_lib.h, [31](#)

get_rc_dna

hmm.h, [21](#)

util_lib.c, [27](#)

get_rc_dna_indel

util_lib.c, [28](#)

get_train_from_file

hmm.h, [21](#)

hmm_lib.c, [23](#)

HMM, [5](#)

E1_dist, [5](#)

E_dist, [5](#)

e_M, [6](#)

e_M_1, [6](#)

N, [6](#)

pi, [6](#)

S1_dist, [6](#)

S_dist, [6](#)

tr, [6](#)

tr_E, [6](#)

tr_E_1, [7](#)

tr_I_I, [7](#)

tr_M_I, [7](#)

tr_R_R, [7](#)

tr_S, [7](#)

tr_S_1, [7](#)

hmm

thread_data, [8](#)

hmm.h, [13](#)

A, [14](#)

C, [14](#)

- E_STATE, 15
- E_STATE_1, 15
- free_hmm, 21
- G, 15
- get_corrected_dna, 21
- get_prob_from_cg, 21
- get_protein, 21
- get_rc_dna, 21
- get_train_from_file, 21
- I1_STATE, 15
- I1_STATE_1, 15
- I2_STATE, 15
- I2_STATE_1, 15
- I3_STATE, 15
- I3_STATE_1, 16
- I4_STATE, 16
- I4_STATE_1, 16
- I5_STATE, 16
- I5_STATE_1, 16
- I6_STATE, 16
- I6_STATE_1, 16
- M1_STATE, 16
- M1_STATE_1, 17
- M2_STATE, 17
- M2_STATE_1, 17
- M3_STATE, 17
- M3_STATE_1, 17
- M4_STATE, 17
- M4_STATE_1, 17
- M5_STATE, 17
- M5_STATE_1, 18
- M6_STATE, 18
- M6_STATE_1, 18
- NOSTATE, 18
- NUM_STATE, 18
- R_STATE, 18
- S_STATE, 18
- S_STATE_1, 18
- T, 19
- TR_DD, 19
- TR_DM, 19
- TR_ER, 19
- TR_ES, 19
- TR_ES1, 19
- TR_GE, 19
- TR_GG, 19
- TR_II, 20
- TR_IM, 20
- TR_MD, 20
- TR_MI, 20
- TR_MM, 20
- TR_RR, 20
- TR_RS, 20
- viterbi, 22
- hmm_lib.c, 22
 - dump_memory, 23
 - free_hmm, 23
 - get_prob_from_cg, 23
 - get_train_from_file, 23
 - viterbi, 23
- I1_STATE
 - hmm.h, 15
- I1_STATE_1
 - hmm.h, 15
- I2_STATE
 - hmm.h, 15
- I2_STATE_1
 - hmm.h, 15
- I3_STATE
 - hmm.h, 15
- I3_STATE_1
 - hmm.h, 16
- I4_STATE
 - hmm.h, 16
- I4_STATE_1
 - hmm.h, 16
- I5_STATE
 - hmm.h, 16
- I5_STATE_1
 - hmm.h, 16
- I6_STATE
 - hmm.h, 16
- I6_STATE_1
 - hmm.h, 16
- imatrix
 - util_lib.c, 28
 - util_lib.h, 31
- ivector
 - util_lib.c, 28
 - util_lib.h, 31
- log2
 - util_lib.c, 28
 - util_lib.h, 32
- M1_STATE
 - hmm.h, 16
- M1_STATE_1
 - hmm.h, 17
- M2_STATE
 - hmm.h, 17
- M2_STATE_1
 - hmm.h, 17
- M3_STATE
 - hmm.h, 17
- M3_STATE_1
 - hmm.h, 17
- M4_STATE
 - hmm.h, 17
- M4_STATE_1
 - hmm.h, 17
- M5_STATE
 - hmm.h, 17
- M5_STATE_1
 - hmm.h, 18
- M6_STATE

- hmm.h, 18
- M6_STATE_1
 - hmm.h, 18
- main
 - run_hmm.c, 25
- N
 - HMM, 6
- noncoding
 - TRAIN, 10
- NOSTATE
 - hmm.h, 18
- nt2int
 - util_lib.c, 28
 - util_lib.h, 32
- nt2int_rc
 - util_lib.c, 28
 - util_lib.h, 32
- nt2int_rc_indel
 - util_lib.c, 29
- NUM_STATE
 - hmm.h, 18
- obs_head
 - thread_data, 9
- obs_seq
 - thread_data, 9
- out
 - thread_data, 9
- pi
 - HMM, 6
- print_usage
 - util_lib.c, 29
 - util_lib.h, 32
- R_STATE
 - hmm.h, 18
- rtrans
 - TRAIN, 10
- run_hmm.c, 24
 - ADD_LEN, 25
 - appendSeq, 25
 - main, 25
 - STRINGLEN, 25
 - thread_data, 25
 - thread_func, 25
- S1_dist
 - HMM, 6
 - TRAIN, 10
- S_dist
 - HMM, 6
 - TRAIN, 10
- S_STATE
 - hmm.h, 18
- S_STATE_1
 - hmm.h, 18
- start
 - TRAIN, 11
- start1
 - TRAIN, 11
- stop
 - TRAIN, 11
- stop1
 - TRAIN, 11
- STRINGLEN
 - run_hmm.c, 25
- T
 - hmm.h, 19
- thread_data, 8
 - aa, 8
 - cg, 8
 - dna, 8
 - format, 8
 - hmm, 8
 - obs_head, 9
 - obs_seq, 9
 - out, 9
 - run_hmm.c, 25
 - train, 9
 - wholegenome, 9
- thread_func
 - run_hmm.c, 25
- tr
 - HMM, 6
- tr2int
 - util_lib.c, 29
 - util_lib.h, 32
- TR_DD
 - hmm.h, 19
- TR_DM
 - hmm.h, 19
- tr_E
 - HMM, 6
- tr_E_1
 - HMM, 7
- TR_ER
 - hmm.h, 19
- TR_ES
 - hmm.h, 19
- TR_ES1
 - hmm.h, 19
- TR_GE
 - hmm.h, 19
- TR_GG
 - hmm.h, 19
- tr_I_I
 - HMM, 7
- TR_II
 - hmm.h, 20
- TR_IM
 - hmm.h, 20
- tr_M_I
 - HMM, 7
- TR_MD
 - hmm.h, 20

- TR_MI
 - hmm.h, [20](#)
- TR_MM
 - hmm.h, [20](#)
- tr_R_R
 - HMM, [7](#)
- TR_RR
 - hmm.h, [20](#)
- TR_RS
 - hmm.h, [20](#)
- tr_S
 - HMM, [7](#)
- tr_S_1
 - HMM, [7](#)
- TRAIN, [9](#)
 - E1_dist, [10](#)
 - E_dist, [10](#)
 - noncoding, [10](#)
 - rtrans, [10](#)
 - S1_dist, [10](#)
 - S_dist, [10](#)
 - start, [11](#)
 - start1, [11](#)
 - stop, [11](#)
 - stop1, [11](#)
 - trans, [11](#)
- train
 - thread_data, [9](#)
- trans
 - TRAIN, [11](#)
- trinucleotide
 - util_lib.c, [29](#)
 - util_lib.h, [32](#)
- trinucleotide_pep
 - util_lib.c, [29](#)
- util_lib.c, [26](#)
 - dmatrix, [26](#)
 - dvector, [26](#)
 - free_dmatrix, [27](#)
 - free_dvector, [27](#)
 - free_imatrix, [27](#)
 - free_ivecator, [27](#)
 - get_protein, [27](#)
 - get_rc_dna, [27](#)
 - get_rc_dna_indel, [28](#)
 - imatrix, [28](#)
 - ivecator, [28](#)
 - log2, [28](#)
 - nt2int, [28](#)
 - nt2int_rc, [28](#)
 - nt2int_rc_indel, [29](#)
 - print_usage, [29](#)
 - tr2int, [29](#)
 - trinucleotide, [29](#)
 - trinucleotide_pep, [29](#)
- util_lib.h, [30](#)
 - dmatrix, [30](#)
 - dvector, [30](#)
 - free_dmatrix, [30](#)
 - free_dvector, [31](#)
 - free_imatrix, [31](#)
 - free_ivecator, [31](#)
 - get_protein, [31](#)
 - imatrix, [31](#)
 - ivecator, [31](#)
 - log2, [32](#)
 - nt2int, [32](#)
 - nt2int_rc, [32](#)
 - print_usage, [32](#)
 - tr2int, [32](#)
 - trinucleotide, [32](#)
- viterbi
 - hmm.h, [22](#)
 - hmm_lib.c, [23](#)
- wholegenome
 - thread_data, [9](#)