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_l_l	7
3.1.1.13 tr_M_l	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	
3.2.1.3 dna	9
3.2.1.4 format	9
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	
3.2.1.9 train	9
3.2.1.10 wholegenome	10
3.3 TRAIN Struct Referentie	
3.3.1 Documentatie van data members	
3.3.1.1 E1 dist	
3.3.1.2 E_dist	
3.3.1.3 noncoding	
3.3.1.4 rtrans	
	· ·

3.3.1.5 S1_dist	11
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	15
4.1.1.1 A	15
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	16
4.1.1.7 I1_STATE_1	16
4.1.1.8 I2_STATE	16
4.1.1.9 I2_STATE_1	16
4.1.1.10 3_STATE	16
4.1.1.11 3_STATE_1	16
4.1.1.12 I4_STATE	16
4.1.1.13 I4_STATE_1	16
4.1.1.14 I5_STATE	17
4.1.1.15 I5_STATE_1	17
4.1.1.16 l6_STATE	17
4.1.1.17 6_STATE_1	17
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	18
4.1.1.23 M3_STATE_1	18
4.1.1.24 M4_STATE	
4.1.1.25 M4_STATE_1	18
4.1.1.26 M5_STATE	18
4.1.1.27 M5_STATE_1	
4.1.1.28 M6_STATE	
4.1.1.29 M6_STATE_1	
4.1.1.30 NOSTATE	
4.1.1.31 NUM_STATE	19

4.1.1.32 R_STATE	1	9
4.1.1.33 S_STATE	1	9
4.1.1.34 S_STATE_1	1	9
4.1.1.35 T	1	9
4.1.1.36 TR_DD	1	9
4.1.1.37 TR_DM	1	9
4.1.1.38 TR_ER	2	20
4.1.1.39 TR_ES	2	20
4.1.1.40 TR_ES1	2	20
4.1.1.41 TR_GE	2	20
4.1.1.42 TR_GG	2	20
4.1.1.43 TR_II	2	20
4.1.1.44 TR_IM	2	20
4.1.1.45 TR_MD	2	20
4.1.1.46 TR_MI	2	1:
4.1.1.47 TR_MM	2	1:
4.1.1.48 TR_RR	2	1:
4.1.1.49 TR_RS	2	1:
4.1.2 Documentatie van functies	2	1:
4.1.2.1 free_hmm()	2	1:
4.1.2.2 get_corrected_dna()	2	2
4.1.2.3 get_prob_from_cg()	2	2
4.1.2.4 get_protein()	2	2
4.1.2.5 get_rc_dna()	2	23
4.1.2.6 get_train_from_file()	2	23
4.1.2.7 viterbi()	2	24
4.2 hmm_lib.c Bestand Referentie	2	26
4.2.1 Documentatie van functies	2	26
4.2.1.1 dump_memory()	2	26
4.2.1.2 free_hmm()	2	?7
4.2.1.3 get_prob_from_cg()	2	27
4.2.1.4 get_train_from_file()	2	?7
4.2.1.5 viterbi()	2	28
4.3 run_hmm.c Bestand Referentie	3	0
4.3.1 Documentatie van macro's	3	0
4.3.1.1 ADD_LEN	3	1
4.3.1.2 STRINGLEN	3	1
4.3.2 Documentatie van typedefs	3	1
4.3.2.1 thread_data	3	1
4.3.3 Documentatie van functies	3	1
4.3.3.1 appendSeq()	3	1
4.3.3.2 main()	3	12

4.3.3.3 thread_tunc()	32
4.4 util_lib.c Bestand Referentie	33
4.4.1 Documentatie van functies	34
4.4.1.1 dmatrix()	34
4.4.1.2 dvector()	35
4.4.1.3 free_dmatrix()	35
4.4.1.4 free_dvector()	35
4.4.1.5 free_imatrix()	36
4.4.1.6 free_ivector()	36
4.4.1.7 get_protein()	36
4.4.1.8 get_rc_dna()	37
4.4.1.9 get_rc_dna_indel()	37
4.4.1.10 imatrix()	38
4.4.1.11 ivector()	38
4.4.1.12 log2()	39
4.4.1.13 nt2int()	39
4.4.1.14 nt2int_rc()	39
4.4.1.15 nt2int_rc_indel()	40
4.4.1.16 print_usage()	40
4.4.1.17 tr2int()	40
4.4.1.18 trinucleotide()	41
4.4.1.19 trinucleotide_pep()	41
4.5 util_lib.h Bestand Referentie	41
4.5.1 Documentatie van functies	43
4.5.1.1 dmatrix()	43
4.5.1.2 dvector()	43
4.5.1.3 free_dmatrix()	43
4.5.1.4 free_dvector()	44
4.5.1.5 free_imatrix()	44
4.5.1.6 free_ivector()	44
4.5.1.7 get_protein()	45
4.5.1.8 imatrix()	45
4.5.1.9 ivector()	45
4.5.1.10 log2()	46
4.5.1.11 nt2int()	46
4.5.1.12 nt2int_rc()	46
4.5.1.13 print_usage()	47
4.5.1.14 tr2int()	47
4.5.1.15 trinucleotide()	47
Index	49

Hoofdstuk 1

Klasse Index

1.1 Klasse Lijst

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

HMM																							5
thread	_dat	a																					8
TRAIN																							10

2 Klasse Index

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 \ \ldots $	26
run_hmm.c	30
util_lib.c	33
util lib.h	41

4 Bestand Index

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]
```

6 Klassen Documentatie

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 HMM Struct Referentie 7

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_l_l

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]

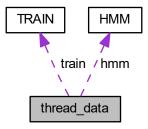
De documentatie voor deze struct is gegenereerd op grond van het volgende bestand:

• hmm.h

8 Klassen Documentatie

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

10 Klassen Documentatie

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 TRAIN Struct Referentie

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

12 Klassen Documentatie

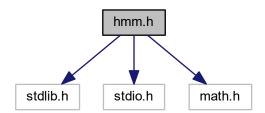
Hoofdstuk 4

Bestand Documentatie

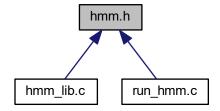
4.1 hmm.h Bestand Referentie

#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

Functies

- 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 *sfilename, char *sfilename, char *sfilename, char *sfilename, char *sfilename, 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

#define I4_STATE_1 26

4.1.1.14 I5_STATE

#define I5_STATE 21

#define I5_STATE_1 27

4.1.1.16 I6_STATE

#define I6_STATE 22

#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 ( {\tt HMM} \; * \; \mathit{hmm} \; )
```

Hier is de call graaf voor deze functie:

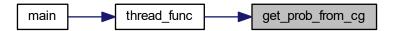


4.1.2.2 get_corrected_dna()

4.1.2.3 get_prob_from_cg()

```
int get_prob_from_cg (
    HMM * hmm,
    TRAIN * train,
    char * 0 )
```

Hier is de caller graaf voor deze functie:



4.1.2.4 get_protein()

Hier is de caller graaf voor deze functie:



4.1.2.5 get_rc_dna()

Hier is de call graaf voor deze functie:

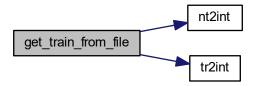


Hier is de caller graaf voor deze functie:



4.1.2.6 get_train_from_file()

Hier is de call graaf voor deze functie:

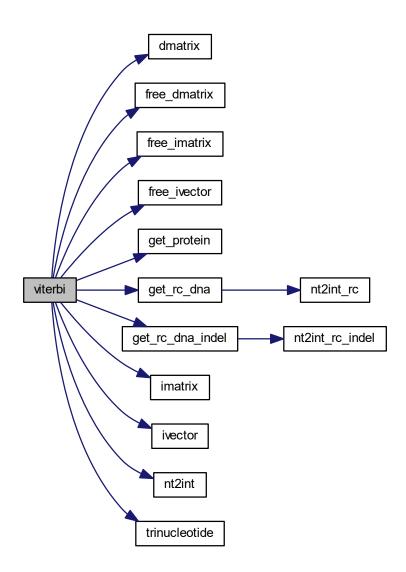


Hier is de caller graaf voor deze functie:

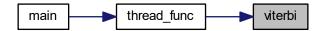


4.1.2.7 viterbi()

Hier is de call graaf voor deze functie:



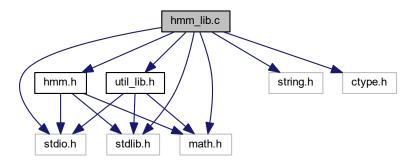
Hier is de caller graaf voor deze functie:



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 *mfilename, char *mfilename, char *filename, char *sfilename, char *sfilename, char *sfilename, char *filename, char *filename, char *dfilename, ch
- void free_hmm (HMM *hmm_ptr)

4.2.1 Documentatie van functies

4.2.1.1 dump_memory()

```
void dump_memory ( \label{eq:condition} \mbox{void} \, * \, p, \\ \mbox{int } size \; )
```

4.2.1.2 free_hmm()

```
void free_hmm ( {\tt HMM} \, * \, \mathit{hmm\_ptr} \, )
```

Hier is de call graaf voor deze functie:



4.2.1.3 get_prob_from_cg()

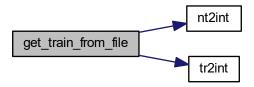
Hier is de caller graaf voor deze functie:



4.2.1.4 get_train_from_file()

```
char * dfilename,
TRAIN * train_ptr )
```

Hier is de call graaf voor deze functie:



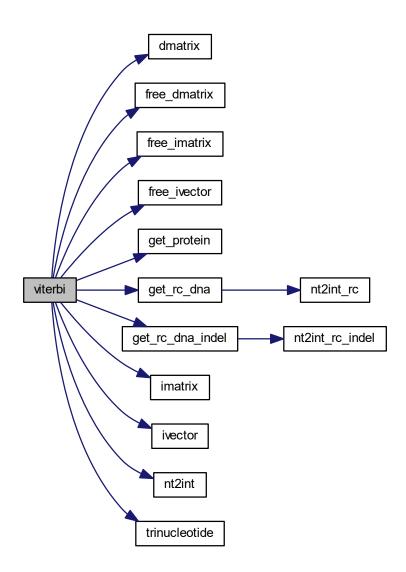
Hier is de caller graaf voor deze functie:



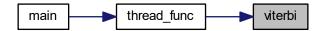
4.2.1.5 viterbi()

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

Hier is de call graaf voor deze functie:



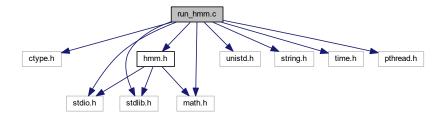
Hier is de caller graaf voor deze functie:



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
```

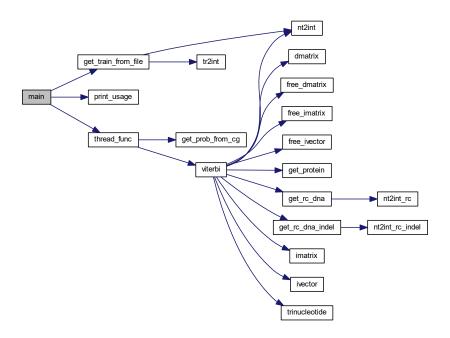
4.3.3 Documentatie van functies

4.3.3.1 appendSeq()

4.3.3.2 main()

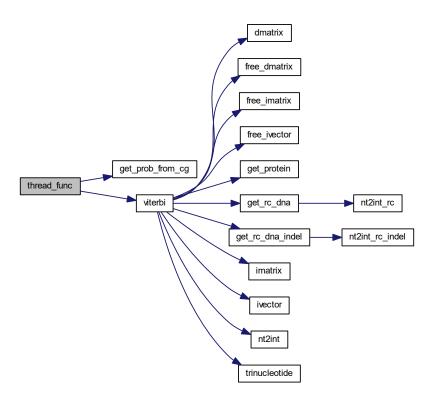
```
int main (  \mbox{int $argc$,} \\ \mbox{char $**$ $argv$ )}
```

Hier is de call graaf voor deze functie:



4.3.3.3 thread_func()

Hier is de call graaf voor deze functie:



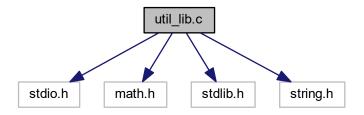
Hier is de caller graaf voor deze functie:



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

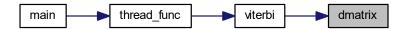
```
• double log2 (double a)
```

- 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()

Hier is de caller graaf voor deze functie:



4.4.1.2 dvector()

```
double* dvector ( \inf \ nh \ )
```

4.4.1.3 free_dmatrix()

Hier is de caller graaf voor deze functie:



4.4.1.4 free_dvector()

```
void free_dvector ( \mbox{double * $v$ )} \label{eq:condition}
```



4.4.1.5 free_imatrix()

Hier is de caller graaf voor deze functie:



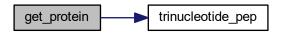
4.4.1.6 free_ivector()

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

Hier is de caller graaf voor deze functie:



4.4.1.7 get_protein()



Hier is de caller graaf voor deze functie:



4.4.1.8 get_rc_dna()

Hier is de call graaf voor deze functie:



Hier is de caller graaf voor deze functie:

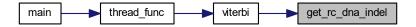


4.4.1.9 get_rc_dna_indel()

Hier is de call graaf voor deze functie:



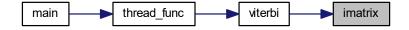
Hier is de caller graaf voor deze functie:



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:



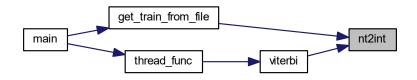
4.4.1.12 log2()

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

4.4.1.13 nt2int()

```
int nt2int ( {\tt char} \ {\it nt} \ )
```

Hier is de caller graaf voor deze functie:



4.4.1.14 nt2int_rc()



4.4.1.15 nt2int_rc_indel()

Hier is de caller graaf voor deze functie:



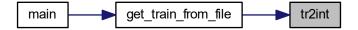
4.4.1.16 print_usage()

```
void print_usage ( )
```

Hier is de caller graaf voor deze functie:



4.4.1.17 tr2int()



4.4.1.18 trinucleotide()

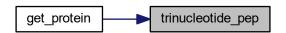
Hier is de caller graaf voor deze functie:



4.4.1.19 trinucleotide_pep()

```
int trinucleotide_pep (  \begin{array}{ccc} \text{char $a$,} \\ \text{char $b$,} \\ \text{char $c$} \end{array} )
```

Hier is de caller graaf voor deze functie:

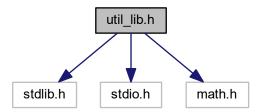


4.5 util_lib.h Bestand Referentie

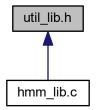
```
#include <stdlib.h>
#include <stdio.h>
```

#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()

Hier is de caller graaf voor deze functie:



4.5.1.2 dvector()

```
double* dvector ( \inf \ nh \ )
```

4.5.1.3 free_dmatrix()



4.5.1.4 free_dvector()

```
void free_dvector ( \mbox{double * $v$ )} \label{eq:condition}
```

Hier is de caller graaf voor deze functie:



4.5.1.5 free_imatrix()

Hier is de caller graaf voor deze functie:



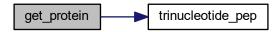
4.5.1.6 free_ivector()

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



4.5.1.7 get_protein()

Hier is de call graaf voor deze functie:



4.5.1.8 imatrix()

Hier is de caller graaf voor deze functie:



4.5.1.9 ivector()

Hier is de caller graaf voor deze functie:



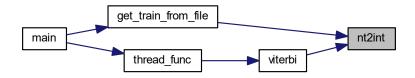
4.5.1.10 log2()

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

4.5.1.11 nt2int()

```
int nt2int ( {\tt char} \ {\it nt} \ )
```

Hier is de caller graaf voor deze functie:



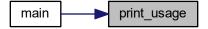
4.5.1.12 nt2int_rc()



4.5.1.13 print_usage()

```
void print_usage ( )
```

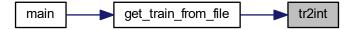
Hier is de caller graaf voor deze functie:



4.5.1.14 tr2int()

```
int tr2int ( {\tt char} \ * \ nt \ )
```

Hier is de caller graaf voor deze functie:



4.5.1.15 trinucleotide()



Index

A	hmm_lib.c, 26
hmm.h, 15 aa	free_imatrix util_lib.c, 35
thread_data, 8	util_lib.h, 44
ADD_LEN run_hmm.c, 30	free_ivector util_lib.c, 36
appendSeq	util_lib.h, 44
run_hmm.c, 31	
	G
C hmm.h, 15	hmm.h, 15 get_corrected_dna
cg	hmm.h, 21
thread_data, 8	get_prob_from_cg
	hmm.h, 22
dmatrix	hmm_lib.c, 27
util_lib.c, 34 util_lib.h, 43	get_protein hmm.h, 22
dna	util_lib.c, 36
thread_data, 8	util_lib.h, 44
dump_memory	get_rc_dna
hmm_lib.c, 26	hmm.h, 22
dvector	util_lib.c, 37
util_lib.c, 35	get_rc_dna_indel
util_lib.h, 43	util_lib.c, 37 get_train_from_file
E1 dist	hmm.h, 23
HMM, 5	hmm lib.c, 27
TRAIN, 10	
E_dist	HMM, 5
HMM, 5	E1_dist, 5
TRAIN, 10 e M	E_dist, 5 e_M, 6
HMM, 6	e_M_1, 6
e_M_1	N, 6
HMM, 6	pi, 6
E_STATE	S1_dist, 6
hmm.h, 15	S_dist, 6
E_STATE_1 hmm.h, 15	tr, 6 tr E, 6
111111.11, 13	tr_E_1, 7
format	tr_l_l, 7
thread_data, 9	tr_M_I, 7
free_dmatrix	tr_R_R, 7
util_lib.c, 35	tr_S, 7
util_lib.h, 43 free dvector	tr_S_1, 7 hmm
util_lib.c, 35	thread_data, 9
util_lib.h, 43	hmm.h, 13
free_hmm	A, 15
hmm.h, 21	C, 15

50 INDEX

E_STATE, 15	get_train_from_file, 27
E_STATE_1, 15	viterbi, 28
free_hmm, 21	
G, 15	I1_STATE
get_corrected_dna, 21	hmm.h, 15
get_prob_from_cg, 22	I1_STATE_1
get_protein, 22	hmm.h, 16
get_rc_dna, <mark>22</mark>	I2_STATE
get_train_from_file, 23	hmm.h, 16
I1_STATE, 15	I2_STATE_1
I1 STATE 1, 16	hmm.h, 16
I2 STATE, 16	I3_STATE
I2_STATE_1, 16	hmm.h, 16
I3 STATE, 16	I3_STATE_1
I3_STATE_1, 16	hmm.h, 16
14 STATE, 16	I4_STATE
I4_STATE_1, 16	hmm.h, 16
I5 STATE, 16	I4_STATE_1
15_STATE_1, 17	hmm.h, 16
16 STATE, 17	I5 STATE
- '	_ hmm.h, 16
16_STATE_1, 17	I5 STATE 1
M1_STATE, 17	hmm.h, 17
M1_STATE_1, 17	I6 STATE
M2_STATE, 17	hmm.h, 17
M2_STATE_1, 17	I6 STATE 1
M3_STATE, 17	hmm.h, 17
M3_STATE_1, 18	imatrix
M4_STATE, 18	util lib.c, 38
M4_STATE_1, 18	util_lib.h, 45
M5_STATE, 18	ivector
M5_STATE_1, 18	util lib.c, 38
M6_STATE, 18	<u> </u>
M6_STATE_1, 18	util_lib.h, 45
NOSTATE, 18	log2
NUM_STATE, 19	util_lib.c, 39
R_STATE, 19	util_lib.h, 46
S_STATE, 19	utii_iio.ii, 40
S_STATE_1, 19	M1 STATE
T, 19	hmm.h, 17
TR_DD, 19	M1_STATE_1
TR_DM, 19	hmm.h, 17
TR ER, 19	M2 STATE
TR ES, 20	hmm.h, 17
TR ES1, 20	M2 STATE 1
TR GE, 20	hmm.h, 17
TR GG, 20	M3 STATE
TR II, 20	hmm.h, 17
TR IM, 20	M3 STATE 1
TR MD, 20	hmm.h, 18
TR MI, 20	M4 STATE
TR MM, 21	hmm.h, 18
TR RR, 21	M4 STATE 1
TR RS, 21	
viterbi, 24	hmm.h, 18
hmm lib.c, 26	M5_STATE
_	hmm.h, 18
dump_memory, 26	M5_STATE_1
free_hmm, 26	hmm.h, 18
get_prob_from_cg, 27	M6_STATE

INDEX 51

hmm.h, 18	TRAIN, 11
M6_STATE_1	start1
hmm.h, 18	TRAIN, 11
main	stop
run_hmm.c, 31	TRAIN, 11
Tun_mm.c, 01	stop1
N	•
	TRAIN, 11
HMM, 6	STRINGLEN
noncoding	run_hmm.c, 31
TRAIN, 10	_
NOSTATE	T
hmm.h, 18	hmm.h, 19
nt2int	thread_data, 8
util_lib.c, 39	aa, <mark>8</mark>
util lib.h, 46	cg, 8
nt2int rc	dna, 8
-	format, 9
util_lib.c, 39	hmm, 9
util_lib.h, 46	
nt2int_rc_indel	obs_head, 9
util_lib.c, 39	obs_seq, 9
NUM_STATE	out, 9
hmm.h, 19	run_hmm.c, 31
,	train, 9
obs_head	wholegenome, 9
thread_data, 9	thread func
obs_seq	run_hmm.c, 32
	tr
thread_data, 9	HMM, 6
out	
thread_data, 9	tr2int
	util_lib.c, 40
pi	util_lib.h, 47
HMM, 6	TR_DD
print usage	hmm.h, 19
util_lib.c, 40	TR DM
util lib.h, 46	_ hmm.h, 19
atii_iis.ii, 10	tr_E
R_STATE	HMM, 6
	tr_E_1
hmm.h, 19	
rtrans	HMM, 7
TRAIN, 10	TR_ER
run_hmm.c, 30	hmm.h, 19
ADD_LEN, 30	TR_ES
appendSeq, 31	hmm.h, 20
main, 31	TR ES1
STRINGLEN, 31	_ hmm.h, 20
thread data, 31	TR_GE
- · · ·	hmm.h, 20
thread_func, 32	
O4 aliak	TR_GG
S1_dist	hmm.h, 20
HMM, 6	tr_l_l
TRAIN, 11	HMM, 7
S_dist	TR_II
HMM, 6	hmm.h, 20
TRAIN, 11	TR_IM
S STATE	_ hmm.h, 20
hmm.h, 19	tr M I
S_STATE_1	HMM, 7
hmm.h, 19	TR_MD
start	hmm.h, 20

52 INDEX

TR MI	free_dmatrix, 43
 hmm.h, 20	free_dvector, 43
TR_MM	free_imatrix, 44
hmm.h, 21	free_ivector, 44
tr_R_R	get_protein, 44
HMM, 7	imatrix, 45
TR_RR	ivector, 45
hmm.h, 21	log2, 46
TR_RS	nt2int, 46
hmm.h, 21	nt2int_rc, 46
tr_S	print_usage, 46
HMM, 7	tr2int, 47
tr_S_1	trinucleotide, 47
HMM, 7	
TRAIN, 10	viterbi
E1_dist, 10	hmm.h, 24
E_dist, 10	hmm_lib.c, 28
noncoding, 10	wholegenome
rtrans, 10	thread_data, 9
S1_dist, 11	iiiieau_uaia, 9
S_dist, 11	
start, 11	
start1, 11	
stop, 11	
stop1, 11	
trans, 11	
train	
thread_data, 9	
trans	
TRAIN, 11	
trinucleotide	
util_lib.c, 40	
util_lib.h, 47	
trinucleotide_pep	
util_lib.c, 41	
util_lib.c, 33	
dmatrix, 34	
dvector, 35	
free dmatrix, 35	
free_dvector, 35	
free_imatrix, 35	
free_ivector, 36	
get_protein, 36	
get_rc_dna, 37	
get_rc_dna_indel, 37	
imatrix, 38	
ivector, 38	
log2, 39	
nt2int, 39	
nt2int_rc, 39	
nt2int_rc_indel, 39	
print_usage, 40	
tr2int, 40	
trinucleotide, 40	
trinucleotide_pep, 41	
util_lib.h, 41	
dmatrix, 43	
dvector, 43	