FragScanTibo

0.1

Gegenereerd door Doxygen 1.8.18

Hoofdstuk 1

Klasse Index

1.1 Klasse Lijst

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

Hoofdstuk 2

Bestand Index

2.1 Bestandslijst

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

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

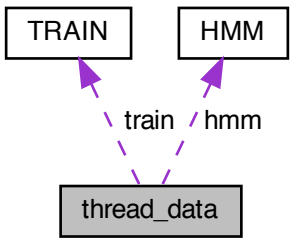
```
double tr_S_1[61][64]
```

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

- FragGeneScan1.31/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:

- FragGeneScan1.31/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:

- FragGeneScan1.31/hmm.h

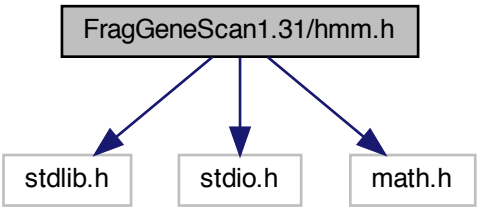
Hoofdstuk 4

Bestand Documentatie

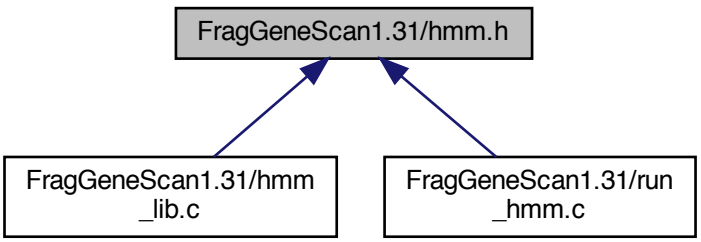
4.1 FragGeneScan1.31/hmm.h Bestand Referentie

```
#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 *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

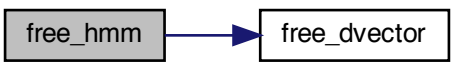
```
#define TR_RS 10
```

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:



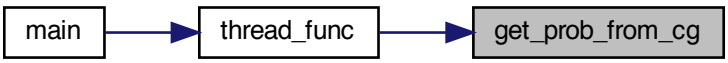
4.1.2.2 get_corrected_dna()

```
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 )
```

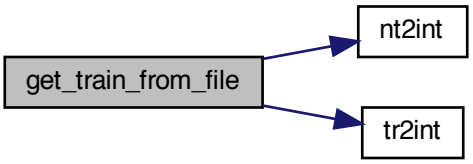
Hier is de call graaf voor deze functie:

Hier is de caller graaf voor deze functie:

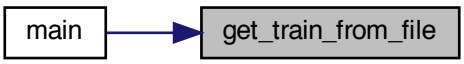
4.1.2.6 get_train_from_file()

```
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:



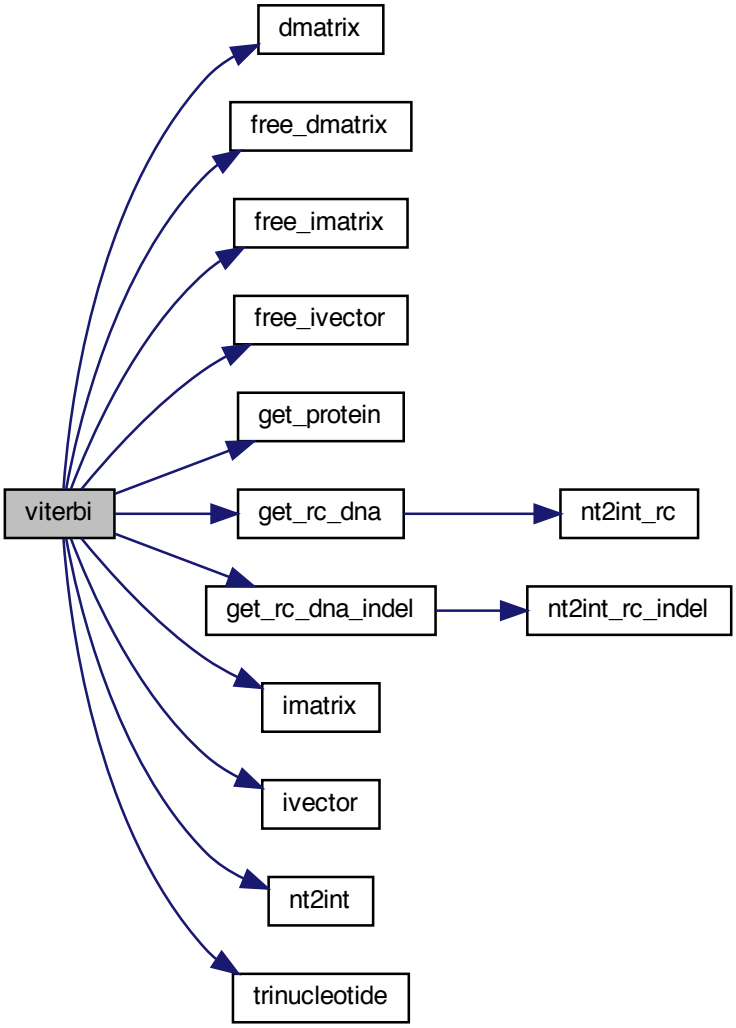
Hier is de caller graaf voor deze functie:



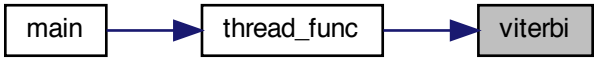
4.1.2.7 viterbi()

```
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:



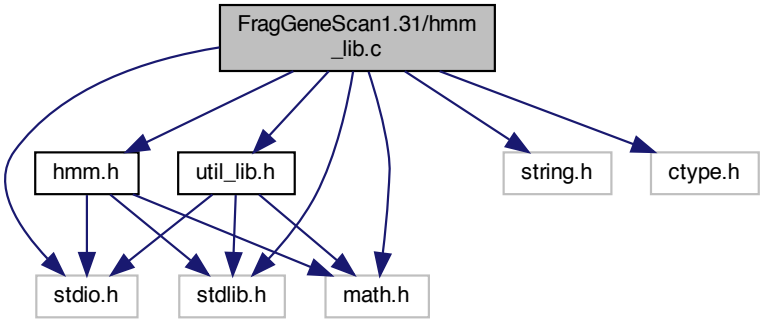
Hier is de caller graaf voor deze functie:



4.2 FragGeneScan1.31/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()

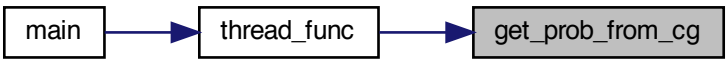
```
void free_hmm (
            HMM * hmm_ptr )
```

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:

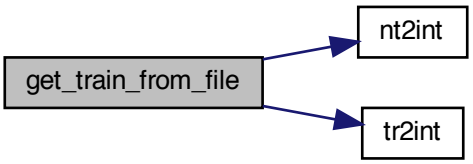


4.2.1.4 get_train_from_file()

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

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

Hier is de call graaf voor deze functie:

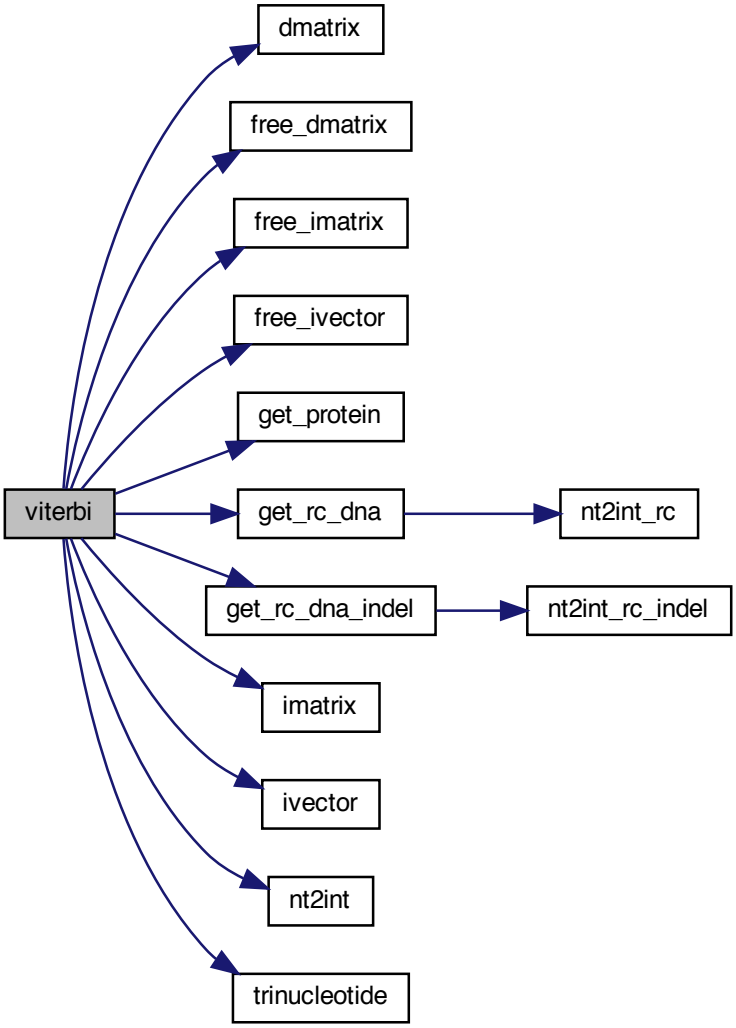


Hier is de caller graaf voor deze functie:

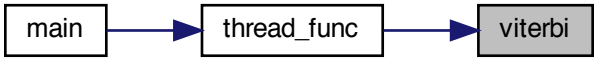
4.2.1.5 viterbi()

```
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:



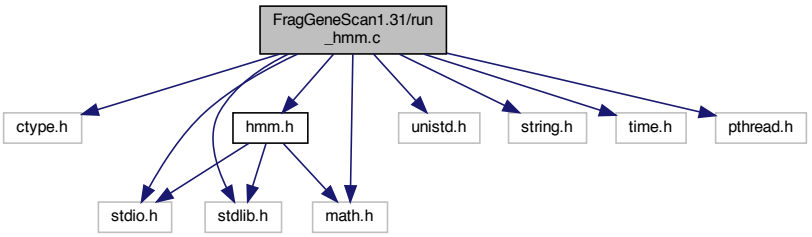
Hier is de caller graaf voor deze functie:



4.3 FragGeneScan1.31/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

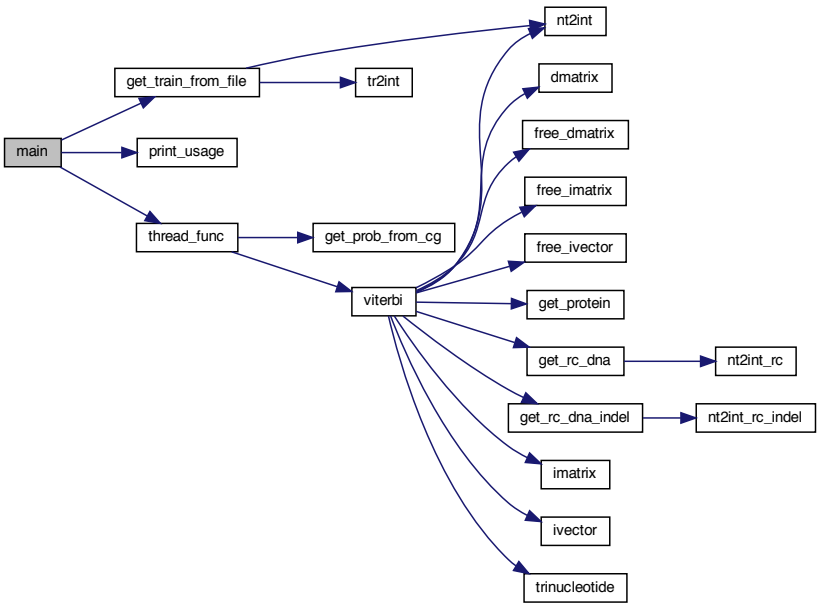
4.3.3.1 appendSeq()

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

4.3.3.2 main()

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

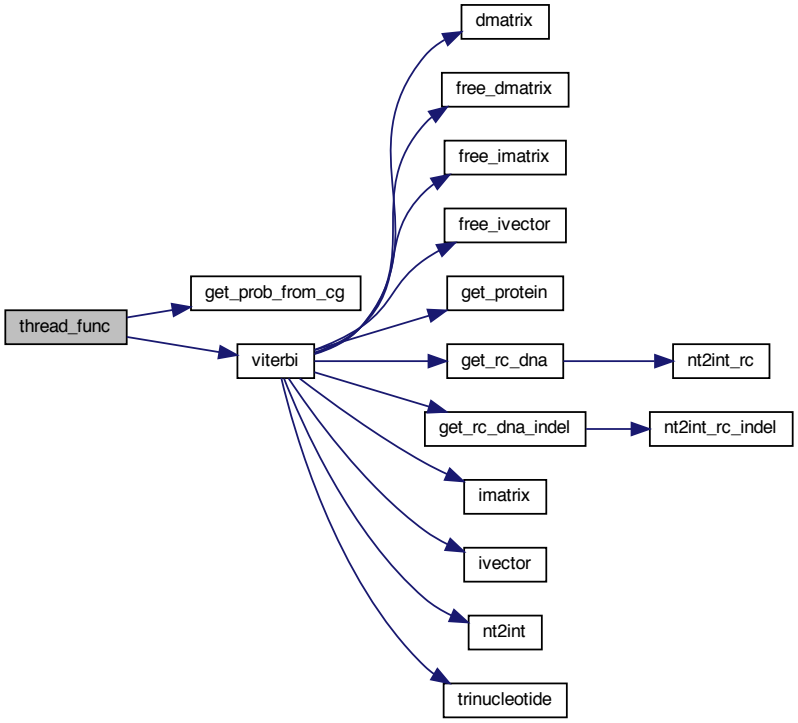
Hier is de call graaf voor deze functie:



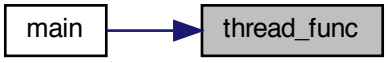
4.3.3.3 thread_func()

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

Hier is de call graaf voor deze functie:



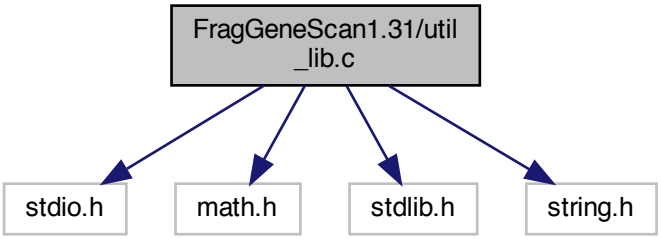
Hier is de caller graaf voor deze functie:



4.4 FragGeneScan1.31/util_lib.c Bestand Referentie

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

Include afhankelijkheidsgraaf voor util_lib.c:



Functies

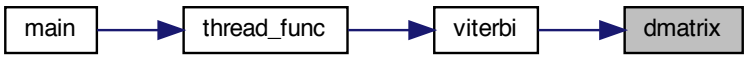
- double log2 (double a)
- double ∗∗ dmatrix (int num_row, int num_col)
- int ∗∗ imatrix (int num_row, int num_col)
- double ∗ dvector (int nh)
- int ∗ ivector (int nh)
- void free_dvector (double ∗v)
- void free_ivector (int ∗v)
- void free_dmatrix (double ∗∗m, int num_row)
- void free_imatrix (int ∗∗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()

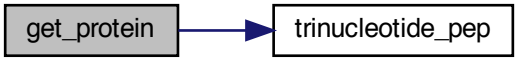
```
void free_ivector (
            int * v )
```

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:

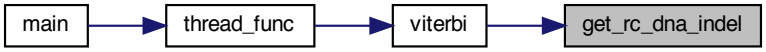
Hier is de caller graaf voor deze functie:

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:

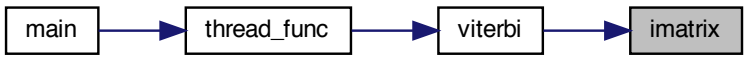
Hier is de caller graaf voor deze functie:



4.4.1.10 imatrix()

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

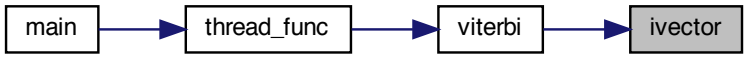
Hier is de caller graaf voor deze functie:



4.4.1.11 ivector()

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

Hier is de caller graaf voor deze functie:



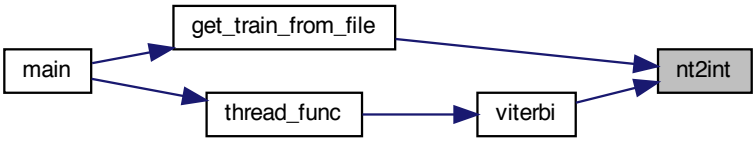
4.4.1.12 log2()

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

4.4.1.13 nt2int()

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

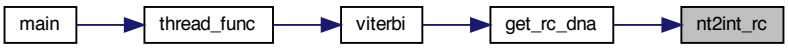
Hier is de caller graaf voor deze functie:



4.4.1.14 nt2int_rc()

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

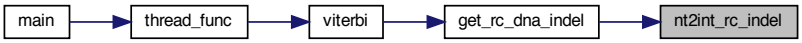
Hier is de caller graaf voor deze functie:



4.4.1.15 nt2int_rc_indel()

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

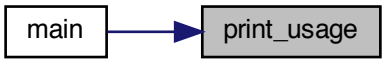
Hier is de caller graaf voor deze functie:



4.4.1.16 print_usage()

```
void print_usage ( )
```

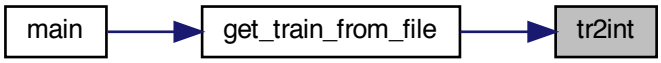
Hier is de caller graaf voor deze functie:



4.4.1.17 tr2int()

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

Hier is de caller graaf voor deze functie:



4.4.1.18 trinucleotide()

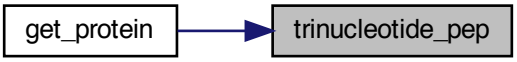
```
int trinucleotide (
             char a,
             char b,
             char c )
```

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:

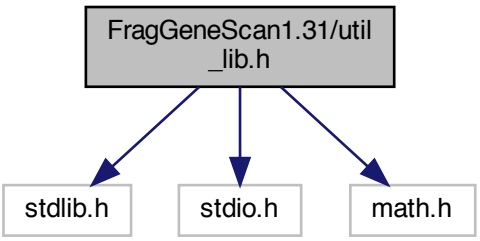


4.5 FragGeneScan1.31/util_lib.h Bestand Referentie

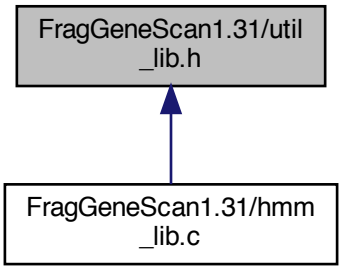
```
#include <stdlib.h>
#include <stdio.h>
```

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

Include afhankelijkheidsgraaf voor util_lib.h:



Deze graaf geeft aan welke bestanden direct of indirect afhankelijk zijn van dit bestand:



Functies

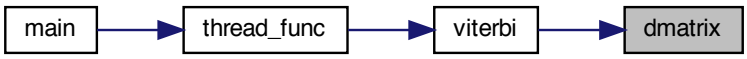
- double ∗∗ dmatrix (int num_row, int num_col)
- double ∗ dvector (int nh)
- int ∗∗ imatrix (int num_row, int num_col)
- int ∗ ivector (int nh)
- void free_dvector (double ∗v)
- void free_dmatrix (double ∗∗m, int num_row)
- void free_ivector (int ∗v)
- void free_imatrix (int ∗∗m, int num_row)
- int tr2int (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()

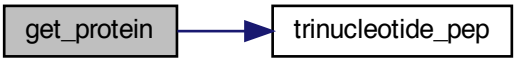
```
void free_ivector (
            int * v )
```

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 )
```

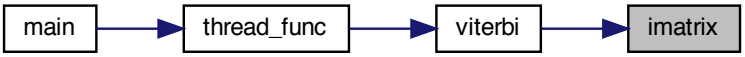
Hier is de call graaf voor deze functie:



4.5.1.8 imatrix()

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

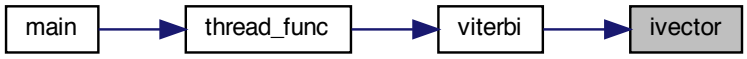
Hier is de caller graaf voor deze functie:



4.5.1.9 ivector()

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

Hier is de caller graaf voor deze functie:



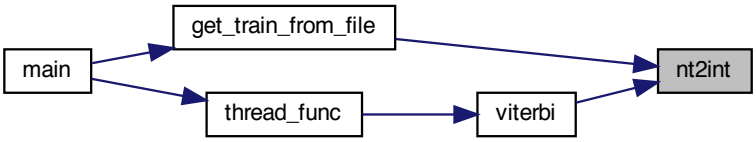
4.5.1.10 log2()

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

4.5.1.11 nt2int()

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

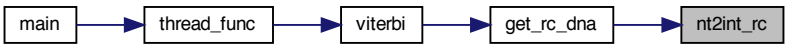
Hier is de caller graaf voor deze functie:



4.5.1.12 nt2int_rc()

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

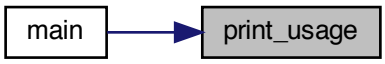
Hier is de caller graaf voor deze functie:



4.5.1.13 print_usage()

```
void print_usage ( )
```

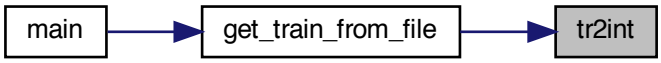
Hier is de caller graaf voor deze functie:



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: