FragScanTibo

0.1

Gegenereerd door Doxygen 1.8.18

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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:

src/hmm.h																	 					13
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src/run_hmm.c																	 					31
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src/util_lib.c .																	 					39
src/util lib.h .																	 					49

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]

Gegenereerd door Doxygen

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:

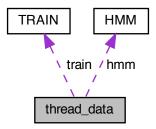
• src/hmm.h

8 Klassen Documentatie

3.2 thread_data Struct Referentie

#include <run_hmm.h>

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:

• src/run hmm.h

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:

• src/hmm.h

12 Klassen Documentatie

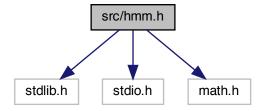
Hoofdstuk 4

Bestand Documentatie

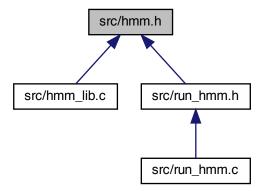
4.1 src/hmm.h Bestand Referentie

#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 I4_STATE 20
#define I5_STATE 21
#define I6_STATE 22
#define I1_STATE_1 23
#define I2_STATE_1 24

• #define I3_STATE 19

- #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 *mfilename, char *mfilename, char *sfilename, char *sfilename,
- 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 Gedetailleerde Beschrijving

This is the header file for the hmm datastructure.

4.1.2 Documentatie van macro's

4.1.2.1 A

#define A 0

4.1.2.2 C

#define C 1

4.1.2.3 **E_STATE**

#define E_STATE 1

4.1.2.4 E_STATE_1

#define E_STATE_1 4

4.1.2.5 G

#define G 2

4.1.2.6 I1_STATE

#define I1_STATE 17

4.1.2.7 I1_STATE_1

#define I1_STATE_1 23

4.1.2.8 I2_STATE

#define I2_STATE 18

4.1.2.9 I2_STATE_1

#define I2_STATE_1 24

4.1.2.10 I3_STATE

#define I3_STATE 19

4.1.2.11 I3_STATE_1

#define I3_STATE_1 25

4.1.2.12 I4_STATE

#define I4_STATE 20

4.1.2.13 I4_STATE_1

#define I4_STATE_1 26

4.1.2.14 I5_STATE

#define I5_STATE 21

#define I5_STATE_1 27

4.1.2.16 I6_STATE

#define I6_STATE 22

#define I6_STATE_1 28

4.1.2.18 M1_STATE

#define M1_STATE 5

4.1.2.19 M1_STATE_1

#define M1_STATE_1 11

4.1.2.20 M2_STATE

#define M2_STATE 6

4.1.2.21 M2_STATE_1

#define M2_STATE_1 12

4.1.2.22 M3_STATE

#define M3_STATE 7

4.1.2.23 M3_STATE_1

#define M3_STATE_1 13

4.1.2.24 M4_STATE

#define M4_STATE 8

4.1.2.25 M4_STATE_1

#define M4_STATE_1 14

4.1.2.26 M5_STATE

#define M5_STATE 9

4.1.2.27 M5_STATE_1

#define M5_STATE_1 15

4.1.2.28 M6_STATE

#define M6_STATE 10

4.1.2.29 M6_STATE_1

#define M6_STATE_1 16

4.1.2.30 NOSTATE

#define NOSTATE -1

4.1.2.31 NUM_STATE

#define NUM_STATE 29

Total number of states, mainly used in for loops.

4.1.2.32 R_STATE

#define R_STATE 2

4.1.2.33 S_STATE

#define S_STATE 0

4.1.2.34 S_STATE_1

#define S_STATE_1 3

4.1.2.35 T

#define T 3

4.1.2.36 TR_DD

#define TR_DD 5

4.1.2.37 TR_DM

#define TR_DM 6

4.1.2.38 TR_ER

#define TR_ER 9

4.1.2.39 TR_ES

#define TR_ES 12

4.1.2.40 TR_ES1

#define TR_ES1 13

4.1.2.41 TR_GE

#define TR_GE 7

4.1.2.42 TR_GG

#define TR_GG 8

4.1.2.43 TR_II

#define TR_II 3

4.1.2.44 TR_IM

#define TR_IM 4

4.1.2.45 TR_MD

#define TR_MD 2

4.1.2.46 TR_MI

#define TR_MI 1

4.1.2.47 TR_MM

#define TR_MM 0

4.1.2.48 TR_RR

#define TR_RR 11

4.1.2.49 TR_RS

#define TR_RS 10

4.1.3 Documentatie van functies

4.1.3.1 free_hmm()

```
void free_hmm ( _{\rm HMM} * _{hmm} )
```

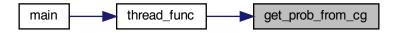
Hier is de call graaf voor deze functie:



4.1.3.2 get_corrected_dna()

4.1.3.3 get_prob_from_cg()

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



4.1.3.4 get_protein()

Get a protein of dna if Whole_genome equals to zero, then we want a short read and stop early. Hier is de caller graaf voor deze functie:



4.1.3.5 get_rc_dna()

copies dna to dna1 in reverse. and Hier is de call graaf voor deze functie:



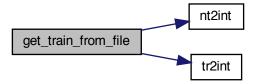


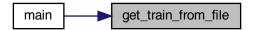
4.1.3.6 get_train_from_file()

Reads files.

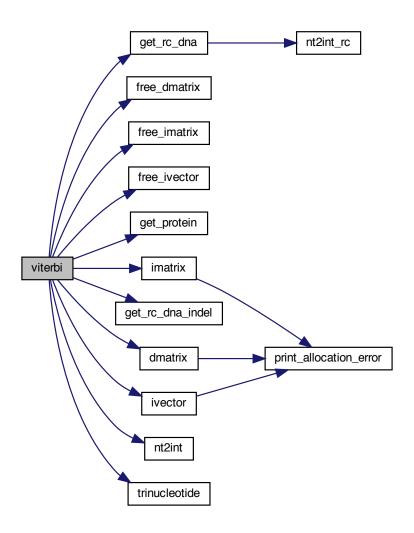
1. Reads trasition file and store in hmm datastructure

Hier is de call graaf voor deze functie:

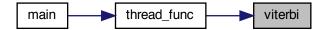




4.1.3.7 viterbi()



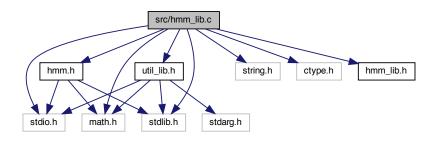
Hier is de caller graaf voor deze functie:



4.2 src/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 "hmm_lib.h"
```

Include afhankelijkheidsgraaf voor hmm_lib.c:



Functies

- 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 *sfilename, char *sfilename, char *sfilename, char *sfilename, char *filename, char *sfilename, char *sfilename,
- void free hmm (HMM *hmm ptr)
- void dump memory (void *p, int size)

4.2.1 Documentatie van functies

4.2.1.1 dump_memory()

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

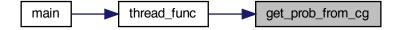
4.2.1.2 free_hmm()

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

Hier is de call graaf voor deze functie:



4.2.1.3 get_prob_from_cg()

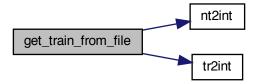


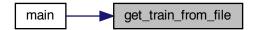
4.2.1.4 get_train_from_file()

Reads files.

1. Reads trasition file and store in hmm datastructure

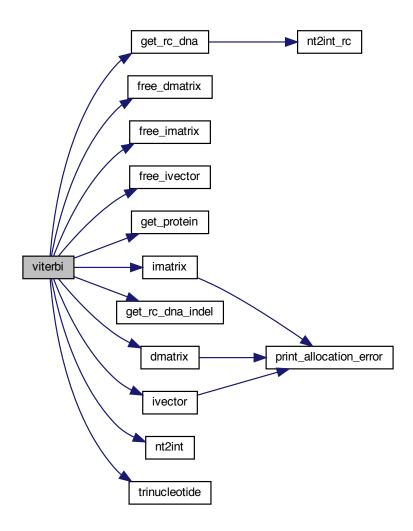
Hier is de call graaf voor deze functie:



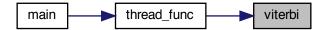


4.2.1.5 viterbi()

```
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 )
```

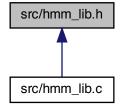


Hier is de caller graaf voor deze functie:



4.3 src/hmm_lib.h Bestand Referentie

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



Functies

- void dump_memory (void *p, int size)
- void get_rc_dna_indel (char dna_f[300000], char dna_f1[300000])

4.3.1 Documentatie van functies

4.3.1.1 dump_memory()

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

4.3.1.2 get_rc_dna_indel()

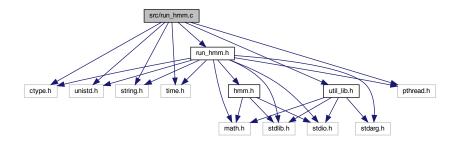
Hier is de caller graaf voor deze functie:



4.4 src/run hmm.c Bestand Referentie

```
#include <ctype.h>
#include <unistd.h>
#include <string.h>
#include <time.h>
#include "run_hmm.h"
#include "util_lib.h"
#include <pthread.h>
```

Include afhankelijkheidsgraaf voor run_hmm.c:



Macros

- #define ADD LEN 1024
- #define STRINGLEN 4096

Functies

- int main (int argc, char **argv)
- void * thread_func (void *threadarr)
- int appendSeq (char *input, char **seq, int input_max)
- void print_error (const char *error_message,...)
- void print_file_error (const char *error_message, char *file)

4.4.1 Documentatie van macro's

4.4.1.1 ADD_LEN

```
#define ADD_LEN 1024
```

4.4.1.2 STRINGLEN

```
#define STRINGLEN 4096
```

4.4.2 Documentatie van functies

4.4.2.1 appendSeq()

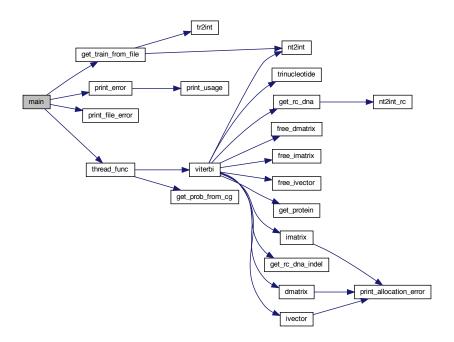
4.4.2.2 main()

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

Entry point of program

- 1. Initialization of variables and datatypes
- 2. Check File acessiblity

Hier is de call graaf voor deze functie:



4.4.2.3 print_error()

Error function:

- 1. Print error message
- 2. Call print_usage() from util_lib
- 3. EXIT program



Hier is de caller graaf voor deze functie:



4.4.2.4 print_file_error()

Error function:

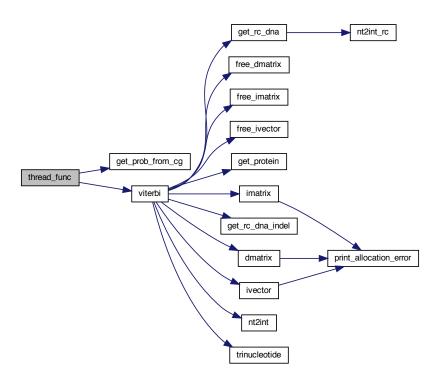
- 1. Print error message
- 2. EXIT program

Hier is de caller graaf voor deze functie:



4.4.2.5 thread_func()

Hier is de call graaf voor deze functie:



Hier is de caller graaf voor deze functie:

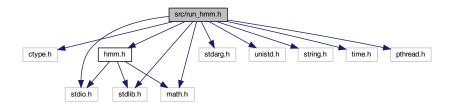


4.5 src/run_hmm.h Bestand Referentie

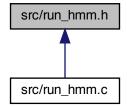
```
#include <ctype.h>
#include <stdio.h>
#include <stdlib.h>
#include <stdarg.h>
#include <math.h>
#include <unistd.h>
#include <string.h>
#include <time.h>
#include "hmm.h"
```

#include <pthread.h>

Include afhankelijkheidsgraaf voor run_hmm.h:



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



Klassen

• struct thread_data

Typedefs

• typedef struct thread_data thread_data

Functies

- void * thread func (void *threadarr)
- void print_error (const char *error_message,...)
- void print_file_error (const char *error_message, char *file)

4.5.1 Documentatie van typedefs

4.5.1.1 thread_data

```
typedef struct thread_data thread_data
```

4.5.2 Documentatie van functies

4.5.2.1 print_error()

Error function:

- 1. Print error message
- 2. Call print_usage() from util_lib
- 3. EXIT program

Hier is de call graaf voor deze functie:





4.5.2.2 print_file_error()

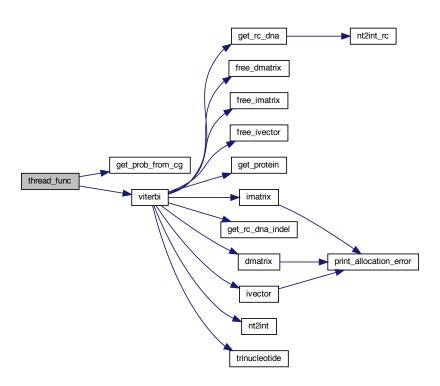
Error function:

- 1. Print error message
- 2. EXIT program

Hier is de caller graaf voor deze functie:



4.5.2.3 thread_func()



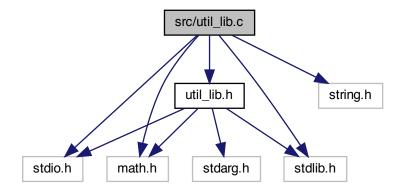
Hier is de caller graaf voor deze functie:



4.6 src/util_lib.c Bestand Referentie

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

Include afhankelijkheidsgraaf voor util_lib.c:



Macros

• #define TR_SIZE 14

Functies

- 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 ()
- void print_allocation_error (const char *format,...)

Variabelen

```
char * tr_list [TR_SIZE] = { "MM","MI","MD","II","IM","DD","DM","GE","GG","ER","RS","RR","ES","ES1" }
char codon5 [5] = { 'A', 'C', 'G', 'T', 'N' }
char codon11 [11] = { 'A', 'C', 'G', 'T', 'N', 'a', 'c', 'g', 't', 'n', 'x' }
char codon_code [65]
char anti_codon_code [65]
```

4.6.1 Documentatie van macro's

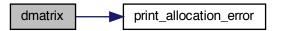
4.6.1.1 TR SIZE

```
#define TR_SIZE 14
```

4.6.2 Documentatie van functies

4.6.2.1 dmatrix()

Makes an matrix with datatype double. Elements are double pointers en matrix is a double double pointer (**pointer). Exits when allocation fails. Hier is de call graaf voor deze functie:



Hier is de caller graaf voor deze functie:



4.6.2.2 dvector()

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

Makes an vector (array) with datatype double. Elements are doubles en vector is a double pointer. Exits when allocation fails. Hier is de call graaf voor deze functie:



4.6.2.3 free_dmatrix()

Frees the memory allocation of an matrix with datatype double. Hier is de caller graaf voor deze functie:



4.6.2.4 free_dvector()

```
void free_dvector ( \mbox{double } * \ v \ )
```

Frees the memory allocation of an vector with datatype double. Hier is de caller graaf voor deze functie:



4.6.2.5 free_imatrix()

Frees the memory allocation of an matrix with datatype int. Hier is de caller graaf voor deze functie:



4.6.2.6 free_ivector()

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

Frees the memory allocation of an vector with datatype int. Hier is de caller graaf voor deze functie:



4.6.2.7 get_protein()

Get a protein of dna if Whole_genome equals to zero, then we want a short read and stop early. Hier is de call graaf voor deze functie:



Hier is de caller graaf voor deze functie:



4.6.2.8 get_rc_dna()

copies dna to dna1 in reverse. and Hier is de call graaf voor deze functie:



Hier is de caller graaf voor deze functie:



4.6.2.9 get_rc_dna_indel()

copies dna to dna1 in reverse. and Hier is de call graaf voor deze functie:



4.6.2.10 imatrix()

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

Makes an matrix with datatype int. Elements are int pointers en matrix is a double int pointer. Exits when allocation fails. Hier is de call graaf voor deze functie:



Hier is de caller graaf voor deze functie:



4.6.2.11 ivector()

Makes an vector array) with datatype int. Elements are ints en vector is a int pointer. Exits when allocation fails. Hier is de call graaf voor deze functie:

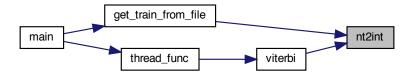


Hier is de caller graaf voor deze functie:



4.6.2.12 nt2int()

Hier is de caller graaf voor deze functie:



4.6.2.13 nt2int_rc()

Hier is de caller graaf voor deze functie:

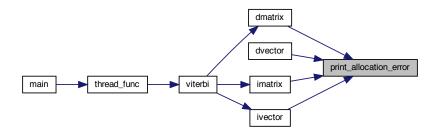


4.6.2.14 nt2int_rc_indel()



4.6.2.15 print_allocation_error()

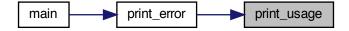
Custom error function to print allocation errors. Mostly called from matrix or vector functions. Hier is de caller graaf voor deze functie:



4.6.2.16 print_usage()

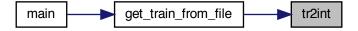
```
void print_usage ( )
```

Print how the program should be used. called mainly on help or error. Hier is de caller graaf voor deze functie:



4.6.2.17 tr2int()

Converts a given transition to int. Use for example as indexing. switch case not possible due the fact that strings are not constonant. Hier is de caller graaf voor deze functie:



4.6.2.18 trinucleotide()

```
int trinucleotide ( \label{eq:char_a,} \operatorname{char}\ b, \label{eq:char_c} \operatorname{char}\ c\ )
```

Hier is de caller graaf voor deze functie:



4.6.2.19 trinucleotide_pep()

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



4.6.3 Documentatie van variabelen

4.6.3.1 anti_codon_code

```
char anti_codon_code[65]
```

Initiële waarde:

```
= { 'F','V','L','I',

'C','G','R','S',

'S','A','P','T',

'Y','D','H','N',

'L','V','L','M',

'W','G','R','R',

'S','A','P','T',

'*','E','Q','K',

'F','V','L','I',

'C','G','R','S',

'S','A','P','T',

'Y','D','H','N',

'L','V','L','I',

'*','G','R','R',

'S','A','P','T',

'*','G','R','R',

'S','A','P','T',

'*','G','R','R',

'S','A','P','T',
```

4.6.3.2 codon11

```
char codon11[11] = { 'A', 'C', 'G', 'T', 'N', 'a', 'c', 'g', 't', 'n', 'x' }
```

4.6.3.3 codon5

```
char codon5[5] = { 'A', 'C', 'G', 'T', 'N' }
```

4.6.3.4 codon_code

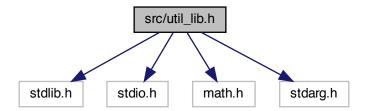
```
char codon_code[65]
```

Initiële waarde:

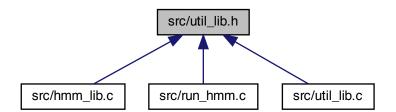
4.6.3.5 tr_list

4.7 src/util_lib.h Bestand Referentie

```
#include <stdlib.h>
#include <stdio.h>
#include <math.h>
#include <stdarg.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)
- void get_protein (char *dna, char *protein, int strand, int whole_genome)
- void print_usage ()
- void print allocation error (const char *format,...)

4.7.1 Documentatie van functies

4.7.1.1 dmatrix()

Makes an matrix with datatype double. Elements are double pointers en matrix is a double double pointer (**pointer). Exits when allocation fails. Hier is de call graaf voor deze functie:

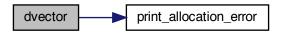




4.7.1.2 dvector()

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

Makes an vector (array) with datatype double. Elements are doubles en vector is a double pointer. Exits when allocation fails. Hier is de call graaf voor deze functie:



4.7.1.3 free_dmatrix()

Frees the memory allocation of an matrix with datatype double. Hier is de caller graaf voor deze functie:



4.7.1.4 free_dvector()

```
void free_dvector ( \mbox{double } * \ v \ )
```

Frees the memory allocation of an vector with datatype double. Hier is de caller graaf voor deze functie:



4.7.1.5 free_imatrix()

Frees the memory allocation of an matrix with datatype int. Hier is de caller graaf voor deze functie:



4.7.1.6 free_ivector()

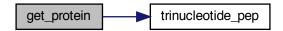
```
void free_ivector ( int \, * \, v \,)
```

Frees the memory allocation of an vector with datatype int. Hier is de caller graaf voor deze functie:



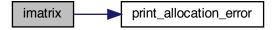
4.7.1.7 get_protein()

Get a protein of dna if Whole_genome equals to zero, then we want a short read and stop early. Hier is de call graaf voor deze functie:



4.7.1.8 imatrix()

Makes an matrix with datatype int. Elements are int pointers en matrix is a double int pointer. Exits when allocation fails. Hier is de call graaf voor deze functie:



Hier is de caller graaf voor deze functie:

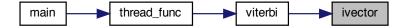


4.7.1.9 ivector()

Makes an vector array) with datatype int. Elements are ints en vector is a int pointer. Exits when allocation fails. Hier is de call graaf voor deze functie:

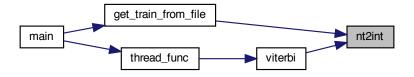


Hier is de caller graaf voor deze functie:



4.7.1.10 nt2int()

Hier is de caller graaf voor deze functie:

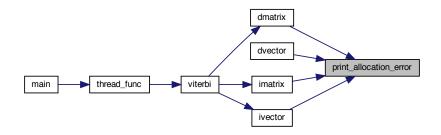


4.7.1.11 nt2int_rc()



4.7.1.12 print_allocation_error()

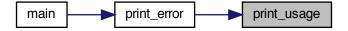
Custom error function to print allocation errors. Mostly called from matrix or vector functions. Hier is de caller graaf voor deze functie:



4.7.1.13 print_usage()

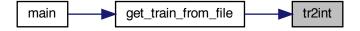
```
void print_usage ( )
```

Print how the program should be used. called mainly on help or error. Hier is de caller graaf voor deze functie:



4.7.1.14 tr2int()

Converts a given transition to int. Use for example as indexing. switch case not possible due the fact that strings are not constonant. Hier is de caller graaf voor deze functie:



4.7.1.15 trinucleotide()

