

dCME
1.0

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Chapter 1

Class Index

1.1 Class List

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

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Chapter 2

File Index

2.1 File List

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

dCME/All/buildStateSpace/ anyoption.cpp	??
dCME/All/buildStateSpace/ anyoption.h	??
dCME/All/buildStateSpace/ buildStateSpace_BFS.cpp	??
dCME/All/buildStateSpace/ buildStateSpace_DFS.cpp	??
dCME/All/expokit/ blas.f	??
dCME/All/expokit/ clock.f	??
dCME/All/expokit/ expokit.f	??
dCME/All/expokit/ lapack.f	??
dCME/All/expokit/ loadhb.f	??
dCME/All/expokit/ mataid.f	??
dCME/All/expokit/ mxexp.f	??
dCME/All/expokit/split/ dgchbv.f	??
dCME/All/expokit/split/ dgcncvr.f	??
dCME/All/expokit/split/ dgexpv.f	??
dCME/All/expokit/split/ dgmattv.f	??
dCME/All/expokit/split/ dgpadm.f	??
dCME/All/expokit/split/ dgphiv.f	??
dCME/All/expokit/split/ dmexpv.f	??
dCME/All/expokit/split/ dnchbv.f	??
dCME/All/expokit/split/ dschbv.f	??
dCME/All/expokit/split/ dsexpv.f	??
dCME/All/expokit/split/ dspadm.f	??
dCME/All/expokit/split/ dsphiv.f	??
dCME/All/expokit/split/ sample_b.f	??
dCME/All/expokit/split/ sample_d.f	??
dCME/All/expokit/split/ sample_g.f	??
dCME/All/expokit/split/ sample_m.f	??
dCME/All/expokit/split/ sample_p.f	??
dCME/All/expokit/split/ sample_z.f	??
dCME/All/expokit/split/ zgchbv.f	??
dCME/All/expokit/split/ zgcncvr.f	??
dCME/All/expokit/split/ zgexpv.f	??
dCME/All/expokit/split/ zgmattv.f	??
dCME/All/expokit/split/ zgpadm.f	??

dCME/All/expokit/split/zgphiv.f	??
dCME/All/expokit/split/zhexpv.f	??
dCME/All/expokit/split/zhpadm.f	??
dCME/All/expokit/split/zhphiv.f	??
dCME/All/expokit/split/znchbv.f	??
dCME/All/libBioModel/debug.h	??
dCME/All/libBioModel/DestinationSet.cpp	??
dCME/All/libBioModel/DestinationSet.h	??
dCME/All/libBioModel/GaussianRNG.cpp	??
dCME/All/libBioModel/GaussianRNG.h	??
dCME/All/libBioModel/HashTable.cpp	??
dCME/All/libBioModel/HashTable.h	??
dCME/All/libBioModel/HashTableS.cpp	??
dCME/All/libBioModel/HashTableS.h	??
dCME/All/libBioModel/InitialConds.cpp	??
dCME/All/libBioModel/InitialConds.h	??
dCME/All/libBioModel/MatrixElement.cpp	??
dCME/All/libBioModel/MatrixElement.h	??
dCME/All/libBioModel/Network.cpp	??
dCME/All/libBioModel/Network.h	??
dCME/All/libBioModel/Queue.cpp	??
dCME/All/libBioModel/Queue.h	??
dCME/All/libBioModel/Sampling.cpp	??
dCME/All/libBioModel/Sampling.h	??
dCME/All/libBioModel/SamplingState.cpp	??
dCME/All/libBioModel/SamplingState.h	??
dCME/All/libBioModel/SLinkedList.cpp	??
dCME/All/libBioModel/SLinkedList.h	??
dCME/All/libBioModel/SLinkedListS.cpp	??
dCME/All/libBioModel/SLinkedListS.h	??
dCME/All/libBioModel/SLinkedListT.cpp	??
dCME/All/libBioModel/SLinkedListT.h	??
dCME/All/libBioModel/SparseMatrix.cpp	??
dCME/All/libBioModel/SparseMatrix.h	??
dCME/All/libBioModel/Stack.cpp	??
dCME/All/libBioModel/Stack.h	??
dCME/All/libBioModel/State.cpp	??
dCME/All/libBioModel/State.h	??
dCME/All/libBioModel/StateSpace.cpp	??
dCME/All/libBioModel/StateSpace.h	??
dCME/All/libBioModel/StateType.h	??
dCME/All/libBioModel/Stoichiometry.cpp	??
dCME/All/libBioModel/Stoichiometry.h	??
dCME/All/net2matrix/anyoption.cpp	??
dCME/All/net2matrix/anyoption.h	??
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dCME/All/Sampling/anyoption.h	??
dCME/All/Sampling/directSSA.cpp	??
dCME/All/Sampling/dwSSA.cpp	??
dCME/All/Sampling/dwSSA_PE.cpp	??
dCME/All/Sampling/HLookaheadSSA_2P.cpp	??

Chapter 3

Class Documentation

3.1 AnyOption Class Reference

Public Member Functions

- **AnyOption** (int maxoptions)
- **AnyOption** (int maxoptions, int maxcharoptions)
- void **setCommandPrefixChar** (char _prefix)
- void **setCommandLongPrefix** (char *_prefix)
- void **setFileCommentChar** (char _comment)
- void **setFileDelimiterChar** (char _delimiter)
- void **useCommandArgs** (int _argc, char **_argv)
- void **useFileName** (const char *_filename)
- void **noPOSIX** ()
- void **setVerbose** ()
- void **setOption** (const char *opt_string)
- void **setOption** (char opt_char)
- void **setOption** (const char *opt_string, char opt_char)
- void **setFlag** (const char *opt_string)
- void **setFlag** (char opt_char)
- void **setFlag** (const char *opt_string, char opt_char)
- void **setCommandOption** (const char *opt_string)
- void **setCommandOption** (char opt_char)
- void **setCommandOption** (const char *opt_string, char opt_char)
- void **setCommandFlag** (const char *opt_string)
- void **setCommandFlag** (char opt_char)
- void **setCommandFlag** (const char *opt_string, char opt_char)
- void **setFileOption** (const char *opt_string)
- void **setFileOption** (char opt_char)
- void **setFileOption** (const char *opt_string, char opt_char)
- void **setFileFlag** (const char *opt_string)
- void **setFileFlag** (char opt_char)
- void **setFileFlag** (const char *opt_string, char opt_char)
- void **processOptions** ()
- void **processCommandArgs** ()
- void **processCommandArgs** (int max_args)

- bool **processFile** ()
- void **processCommandArgs** (int _argc, char **_argv)
- void **processCommandArgs** (int _argc, char **_argv, int max_args)
- bool **processFile** (const char *_filename)
- char * **getValue** (const char *_option)
- bool **getFlag** (const char *_option)
- char * **getValue** (char _optchar)
- bool **getFlag** (char _optchar)
- void **printUsage** ()
- void **printAutoUsage** ()
- void **addUsage** (const char *line)
- void **printHelp** ()
- void **autoUsagePrint** (bool flag)
- int **getArgc** ()
- char * **getArgv** (int index)
- bool **hasOptions** ()
- **AnyOption** (int maxoptions)
- **AnyOption** (int maxoptions, int maxcharoptions)
- void **setCommandPrefixChar** (char _prefix)
- void **setCommandLongPrefix** (char *_prefix)
- void **setFileCommentChar** (char _comment)
- void **setFileDelimiterChar** (char _delimiter)
- void **useCommandArgs** (int _argc, char **_argv)
- void **useFileName** (const char *_filename)
- void **noPOSIX** ()
- void **setVerbose** ()
- void **setOption** (const char *opt_string)
- void **setOption** (char opt_char)
- void **setOption** (const char *opt_string, char opt_char)
- void **setFlag** (const char *opt_string)
- void **setFlag** (char opt_char)
- void **setFlag** (const char *opt_string, char opt_char)
- void **setCommandOption** (const char *opt_string)
- void **setCommandOption** (char opt_char)
- void **setCommandOption** (const char *opt_string, char opt_char)
- void **setCommandFlag** (const char *opt_string)
- void **setCommandFlag** (char opt_char)
- void **setCommandFlag** (const char *opt_string, char opt_char)
- void **setFileOption** (const char *opt_string)
- void **setFileOption** (char opt_char)
- void **setFileOption** (const char *opt_string, char opt_char)
- void **setFileFlag** (const char *opt_string)
- void **setFileFlag** (char opt_char)
- void **setFileFlag** (const char *opt_string, char opt_char)
- void **processOptions** ()
- void **processCommandArgs** ()
- void **processCommandArgs** (int max_args)
- bool **processFile** ()
- void **processCommandArgs** (int _argc, char **_argv)
- void **processCommandArgs** (int _argc, char **_argv, int max_args)
- bool **processFile** (const char *_filename)

- char * **getValue** (const char * _option)
- bool **getFlag** (const char * _option)
- char * **getValue** (char _optchar)
- bool **getFlag** (char _optchar)
- void **printUsage** ()
- void **printAutoUsage** ()
- void **addUsage** (const char *line)
- void **printHelp** ()
- void **autoUsagePrint** (bool flag)
- int **getArgc** ()
- char * **getArgv** (int index)
- bool **hasOptions** ()
- **AnyOption** (int maxoptions)
- **AnyOption** (int maxoptions, int maxcharoptions)
- void **setCommandPrefixChar** (char _prefix)
- void **setCommandLongPrefix** (char *_prefix)
- void **setFileCommentChar** (char _comment)
- void **setFileDelimiterChar** (char _delimiter)
- void **useCommandArgs** (int _argc, char ** _argv)
- void **useFileName** (const char *_filename)
- void **noPOSIX** ()
- void **setVerbose** ()
- void **setOption** (const char *opt_string)
- void **setOption** (char opt_char)
- void **setOption** (const char *opt_string, char opt_char)
- void **setFlag** (const char *opt_string)
- void **setFlag** (char opt_char)
- void **setFlag** (const char *opt_string, char opt_char)
- void **setCommandOption** (const char *opt_string)
- void **setCommandOption** (char opt_char)
- void **setCommandOption** (const char *opt_string, char opt_char)
- void **setCommandFlag** (const char *opt_string)
- void **setCommandFlag** (char opt_char)
- void **setCommandFlag** (const char *opt_string, char opt_char)
- void **setFileOption** (const char *opt_string)
- void **setFileOption** (char opt_char)
- void **setFileOption** (const char *opt_string, char opt_char)
- void **setFileFlag** (const char *opt_string)
- void **setFileFlag** (char opt_char)
- void **setFileFlag** (const char *opt_string, char opt_char)
- void **processOptions** ()
- void **processCommandArgs** ()
- void **processCommandArgs** (int max_args)
- bool **processFile** ()
- void **processCommandArgs** (int _argc, char ** _argv)
- void **processCommandArgs** (int _argc, char ** _argv, int max_args)
- bool **processFile** (const char *_filename)
- char * **getValue** (const char *_option)
- bool **getFlag** (const char *_option)
- char * **getValue** (char _optchar)
- bool **getFlag** (char _optchar)

- void **printUsage** ()
- void **printAutoUsage** ()
- void **addUsage** (const char *line)
- void **printHelp** ()
- void **autoUsagePrint** (bool flag)
- int **getArgc** ()
- char * **getArgv** (int index)
- bool **hasOptions** ()

3.1.1 Detailed Description

Definition at line 33 of file anyoption.h.

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

- dCME/All/buildStateSpace/anyoption.h
- dCME/All/net2matrix/anyoption.h
- dCME/All/Sampling/anyoption.h
- dCME/All/buildStateSpace/anyoption.cpp
- dCME/All/net2matrix/anyoption.cpp
- dCME/All/Sampling/anyoption.cpp

3.2 DestinationSet Class Reference

Public Member Functions

- int **readDestinationSet** (char *destfile)
- double **getDistanceFromState** ([State](#) *astate)
- double **getDistanceBtwTwoStates** ([State](#) *astate, [State](#) *bstate)
- double **getDistanceFromState** ([SamplingState](#) *astate)
- double **getDistanceBtwTwoStates** ([SamplingState](#) *astate, [SamplingState](#) *bstate)
- int **getDistance2Edge** ([SamplingState](#) *astate)
- double **getDistanceFromPath** ([SLinkedListS](#) *path)
- double **getPathDistanceToDest** ([SamplingState](#) *astate, [SamplingState](#) **path, unsigned int length)
- double **getPathDistanceToBegin** ([SamplingState](#) *X0, [SamplingState](#) *astate, [SamplingState](#) **path, unsigned int length)
- vector< int > * **geteffspecies** ()

3.2.1 Detailed Description

Definition at line 13 of file DestinationSet.h.

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

- dCME/All/libBioModel/DestinationSet.h
- dCME/All/libBioModel/DestinationSet.cpp

3.3 Distance Struct Reference

Public Attributes

- int **index**
- double **distance**

3.3.1 Detailed Description

Definition at line 35 of file dwSSA_PE.cpp.

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

- dCME/All/Sampling/dwSSA_PE.cpp

3.4 HashTable Class Reference

Public Member Functions

- **HashTable** (unsigned long nbuckets)
- unsigned long **getNumTotalItems** ()
- unsigned long **getNumBuckets** ()
- unsigned int **getSizеofBucket** (unsigned long i)
- **State** * **getHeadofBucket** (unsigned int i)
- unsigned long **hashfunc** (**State** *key) const
- int **Insert** (**State** *item)
- int **Find** (**State** *item) const
- void **Delete** (**State** *item)

3.4.1 Detailed Description

Definition at line 17 of file HashTable.h.

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

- dCME/All/libBioModel/HashTable.h
- dCME/All/libBioModel/HashTable.cpp

3.5 HashTableS Class Reference

Public Member Functions

- **HashTableS** (vector< int > *effspecies)
- **HashTableS** (unsigned long nbuckets)
- unsigned long **getNumTotalItems** ()
- unsigned long **getNumBuckets** ()
- unsigned int **getSizеofBucket** (unsigned long i)
- **SamplingState** * **getHeadofBucket** (unsigned int i)

- unsigned long **hashfunc** ([SamplingState](#) *key) const
- unsigned long **hashfunc1** ([SamplingState](#) *key) const
- int **Insert** ([SamplingState](#) *item)
- [SamplingState](#) * **Find** ([SamplingState](#) *item) const
- vector< [SamplingState](#) * > * **BatchFind** ([SamplingState](#) *item) const
- void **Delete** ([SamplingState](#) *item)

3.5.1 Detailed Description

Definition at line 18 of file HashTableS.h.

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

- dCME/All/libBioModel/HashTableS.h
- dCME/All/libBioModel/HashTableS.cpp

3.6 InitialConds Class Reference

Public Member Functions

- int **readInitialConds** (char *pdvfile)
- unsigned int **getNumInitialstates** ()
- [State](#) * **getInitialState** (unsigned int i) const
- double **getInitialPdv** (unsigned int i)

3.6.1 Detailed Description

Definition at line 8 of file InitialConds.h.

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

- dCME/All/libBioModel/InitialConds.h
- dCME/All/libBioModel/InitialConds.cpp

3.7 MatrixElement Class Reference

Public Member Functions

- **MatrixElement** (unsigned int i, unsigned int j, VALUETYPE v)
- **MatrixElement** (unsigned int i, unsigned int j, VALUETYPE v, vector< unsigned int > &rv)
- unsigned int **SetValues** (unsigned int i, unsigned int j, VALUETYPE v, unsigned int k)
- unsigned long **getI** ()
- unsigned long **getJ** ()
- VALUETYPE **getValue** ()
- vector< unsigned int > * **getR** ()
- [MatrixElement](#) * **getNext** ()
- void **setNext** ([MatrixElement](#) *next)

3.7.1 Detailed Description

Definition at line 15 of file MatrixElement.h.

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

- dCME/All/libBioModel/MatrixElement.h
- dCME/All/libBioModel/MatrixElement.cpp

3.8 Network Class Reference

Public Member Functions

- int **initializeNetwork** (char *sbmlfile)
- int **getNumErrors** ()
- int **printErrors** ()
- Model * **getModel** ()
- int **getSpeciesIndex** (string Id)
- int **getCompartmentIndex** (string Id)
- int **getRateRuleIndex** (string Id)
- string **getSpeciesID** (unsigned int sindex)
- string **getReactionID** (unsigned int sindex)
- string **getRuleID** (unsigned int rindex)
- string **getParameterID** (unsigned int pindex)
- double **getReactionRate** (const KineticLaw *klaw, unsigned int sindex, [State](#) *curstate)
- double **getReactionRate** (const KineticLaw *klaw, unsigned int sindex, [SamplingState](#) *curstate)
- double **computeASTNodeValue** (const ASTNode *node, unsigned int sindex, [State](#) *curstate)
- double **getValueOfParameter** (const char *parameter_id, unsigned int rindex, [State](#) *curstate)
- int **isParameter** (const char *parameter_id, unsigned int rindex)
- double **getValueOfRateConstant** (unsigned int rindex)
- void **initializeRateArrays** ()
- [SparseMatrix](#) * **getTransitionMatrix** ()
- void **setTransitionMatrix** ([SparseMatrix](#) *tmatrix)
- [Stoichiometry](#) * **getStoichiometricMatrix** ()
- STATETYPE * **getStateSpace** ()
- unsigned int **getNumCompartments** ()
- unsigned int **getNumReactions** ()
- unsigned int **getNumStoiReactions** ()
- unsigned int **getNumSpecies** ()
- unsigned int **getNumRules** ()
- unsigned int **getNumParameters** ()
- unsigned int **getNumRealStates** ()
- unsigned int **getNumStates** ()
- void **setNumRealStates** (unsigned long num)
- void **setStateSpace** (STATETYPE *states)
- void **setNumStates** (unsigned long n_states)
- double **SSADirect_updateState** ([State](#) *astate)
- double **SSADirect_newState** ([State](#) *astate, [State](#) *destState)
- double **dwSSADirect_newState** ([State](#) *astate, [State](#) *destState, double *gamma, double &weight)
- double **dwSSADirect_updateState** ([State](#) *astate, double *gamma, double &weight)

- double **Lookahead_dwSSADirect_updateState** ([State](#) *astate, [State](#) *X0, [DestinationSet](#) *dest, double &weight, double bias)
- double **LookaheadSSAPathField3Steps_updateState** ([State](#) *astate, [State](#) *X0, [DestinationSet](#) *dest, double d_ab, double &weight, double bias)
- double **LookaheadSSAPathField4Steps_updateState** ([State](#) *astate, [State](#) *X0, [DestinationSet](#) *dest, double d_ab, double &weight, double lambda1, double lambda2, int V, long n_reoccurs[])
- double **LookaheadSSAPathField4StepsRepBack_updateState** ([State](#) *astate, [State](#) *X0, [DestinationSet](#) *dest, double d_ab, double &weight, double bias, int V, long n_reoccurs[])
- double **LookaheadSSAField_updateState** ([State](#) *astate, [State](#) *X0, [DestinationSet](#) *dest, double d_ab, double &weight, double bias)
- double **Lookahead_wSSADirect_updateState** ([State](#) *astate, [State](#) *X0, [DestinationSet](#) *dest, double &weight, double bias)

3.8.1 Detailed Description

Definition at line 27 of file Network.h.

3.8.2 Member Function Documentation

3.8.2.1 double Network::getValueOfParameter (const char * parameter_id, unsigned int rindex, State * curstate)

```
double v = stoichiometry->getValue(speciesIndex, sindex);
if (v < 0) /* for reactants

return -1 * v;

} else if ( stoichiometry->getReactionAttribute(sindex) < 0 ) /* for reverse reactions

    return v;
}

} else /* for products

return 0;

}
```

Definition at line 506 of file Network.cpp.

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

- dCME/All/libBioModel/Network.h
- dCME/All/libBioModel/Network.cpp

3.9 Queue Class Reference

Public Member Functions

- void **push** ([State](#) *astate)
- [State](#) * **pop** ()
- bool **isEmpty** ()
- void **setNumSpecies** (unsigned int n)
- void **removeDir** ()

3.9.1 Detailed Description

Definition at line 16 of file Queue.h.

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

- dCME/All/libBioModel/Queue.h
- dCME/All/libBioModel/Queue.cpp

3.10 Sampling Class Reference

Public Member Functions

- void **Initialize** ([Network](#) *nw, [DestinationSet](#) *dest, int V)
- [HashTableS](#) * **getHashTable** ()
- double **SSADirect_updateState** ([SamplingState](#) *astate)
- double **dwSSADirect_updateState** ([SamplingState](#) *astate, double *gamma, double &weight, long n_reoccurs[])
- double **dwSSADirectPE_updateState** ([SamplingState](#) *astate, double *gamma, double &weight, double n_reoccurs[], double n_reoccurs_SSA[])
- int **CalculateDirectSSA** ([SamplingState](#) *astate)
- double **LookaheadSSA_KSteps_updateState** (int K, [SamplingState](#) *astate, [SamplingState](#) *X0, double d_ab, double &weight, double lambda1, double lambda2, int V, long n_reoccurs[])
- double **LookaheadSSA_KSteps_updateState** (int K, [SamplingState](#) *astate, [SamplingState](#) *X0, double d_ab, double &weight, double lambda, int V, long n_reoccurs[])
- double **LookaheadSSA_KSteps2Stage_updateState** (int K, [SamplingState](#) *astate, [SamplingState](#) *X0, double d_ab, double &weight, double lambda1, double lambda2, int V, long n_reoccurs[])
- int **CalculateLookahead_2Steps** ([SamplingState](#) *astate, [SamplingState](#) *X0, double d_ab, double lambda1, double lambda2, int V)
- int **CalculateLookahead_3Steps** ([SamplingState](#) *astate, [SamplingState](#) *X0, double d_ab, double lambda1, double lambda2, int V)
- int **CalculateLookahead_4Steps** ([SamplingState](#) *astate, [SamplingState](#) *X0, double d_ab, double lambda1, double lambda2, int V)
- int **CalculateLookahead_5Steps** ([SamplingState](#) *astate, [SamplingState](#) *X0, double d_ab, double lambda1, double lambda2, int V)
- int **CalculateLookahead_6Steps** ([SamplingState](#) *astate, [SamplingState](#) *X0, double d_ab, double lambda1, double lambda2, int V)
- int **CalculateLookahead_3Steps2** ([SamplingState](#) *astate, [SamplingState](#) *X0, double d_ab, double lambda1, double lambda2, int V)
- int **CalculateLookahead_4Steps2** ([SamplingState](#) *astate, [SamplingState](#) *X0, double d_ab, double lambda1, double lambda2, int V)
- int **CalculateLookahead_3StepsOLD** ([SamplingState](#) *astate, [SamplingState](#) *X0, double d_ab, double lambda1, double lambda2, int V)
- int **CalculateLookahead_5StepsOLD** ([SamplingState](#) *astate, [SamplingState](#) *X0, double d_ab, double lambda1, double lambda2, int V)
- int **CalculateLookahead_2Steps** ([SamplingState](#) *astate, [SamplingState](#) *X0, double d_ab, double lambda, int V)
- int **CalculateLookahead_3Steps** ([SamplingState](#) *astate, [SamplingState](#) *X0, double d_ab, double lambda, int V)
- int **CalculateLookahead_4Steps** ([SamplingState](#) *astate, [SamplingState](#) *X0, double d_ab, double lambda, int V)
- int **CalculateLookahead_5Steps** ([SamplingState](#) *astate, [SamplingState](#) *X0, double d_ab, double lambda, int V)

- int **Bias_Average** ([SamplingState](#) *astate)
- double **Bias_Function** ([SamplingState](#) *astate, double lambda1, double lambda2, int *n_paths, int *m_forward, int *m_backward, double *la_probs, double *p_f, double *p_b, double *p_fn, double *p_bn)
- double **Bias_Function** ([SamplingState](#) *astate, double lambda1, double lambda2, int *n_paths, int *m_forward, int *m_backward, double *la_probs, double *p_f, double *p_b, double *p_fn, double *p_bn, double p_fA, double p_bA, double p_fAn, double p_bAn, double p_fB, double p_bB, double p_fBn, double p_bBn)
- double **Bias_Function** ([SamplingState](#) *astate, double lambda1, double lambda2, int *n_paths, int *m_forward, int *m_backward, double *la_probs, double *p_f, double *p_b, double *p_fn, double *p_bn, double *p_fpairs, double *p_bpairs, double *p_fnpairs, double *p_bnpairs)
- double **Bias_Function** ([SamplingState](#) *astate, double lambda1, double lambda2, double *nFiresForwardPaths, double *nFiresAllPaths)
- double **Bias_Function** ([SamplingState](#) *astate, double lambda, int *n_paths, int *m_forward, int *m_backward, double *la_probs, double *p_f, double *p_b, double *p_fn, double *p_bn)
- int **RollADie** ([SamplingState](#) *p, [SamplingState](#) *astate, double &dt, int &k, double &weight, int V)
- int **RollADie_DSSA** ([SamplingState](#) *p, [SamplingState](#) *astate, double &dt, int &k)
- unsigned long **getHTSize** ()

3.10.1 Detailed Description

Definition at line 19 of file Sampling.h.

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

- dCME/All/libBioModel/Sampling.h
- dCME/All/libBioModel/Sampling.cpp

3.11 SamplingState Class Reference

Public Member Functions

- **SamplingState** ([SamplingState](#) *astate)
- **SamplingState** ([SamplingState](#) *astate, unsigned int n_stoireactions)
- **SamplingState** ([State](#) *astate, unsigned int n_stoireactions)
- **SamplingState** (unsigned int n_species, unsigned int n_stoireactions)
- **SamplingState** (int *values, unsigned int n_species, unsigned int n_stoireactions)
- int **initialize** (unsigned int n_stoireactions)
- int **CopyfromState** ([SamplingState](#) *astate)
- int **CopyfromState** ([State](#) *astate, unsigned int n_stoireactions)
- int **PrintState** ()
- int **PrintState_Full** ()
- int **PrintState_Full** (ofstream &fout)
- int **PrintState_nonl** ()
- int **PrintState** (ofstream &fout)
- STATETYPE **getStateValue** (unsigned int i)
- unsigned int **getNumSpecies** ()
- int **setStateValue** (unsigned int i, STATETYPE value)
- int **setState** (STATETYPE *astate, unsigned int n_species)
- [SamplingState](#) * **getPrev** ()
- [SamplingState](#) * **getNext** ()
- int **setPrev** ([SamplingState](#) *pt)

- int **setNext** ([SamplingState](#) *pt)
- int **setSN** (unsigned long index)
- unsigned long **getSN** ()
- int **setRatesA** (int j, double v)
- int **setRatesB** (int j, double v)
- int **setGamma** (int j, double v)
- double **getRatesA** (int j)
- double **getRatesB** (int j)
- double **getGamma** (int j)
- double **geta0** ()
- int **seta0** (double v)
- int **calca0** ()
- double **getb0** ()
- int **setb0** (double v)
- int **setpFn** (unsigned int i, double v)
- int **setpBn** (unsigned int i, double v)
- double **getpFn** (unsigned int i)
- double **getpBn** (unsigned int i)
- unsigned long **getnVisits** ()
- int **setnVisits** (unsigned long v)
- int **increase1Visit** ()
- double **calcB0** ()
- unsigned int **getNumStoiReactions** ()
- int **setNumStoiReactions** (unsigned int n_stoireactions)
- [SamplingState](#) & **operator=** (const [SamplingState](#) &pt)
- bool **operator==** (const [SamplingState](#) &other)

3.11.1 Detailed Description

Definition at line 13 of file [SamplingState.h](#).

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

- [dCME/All/libBioModel/SamplingState.h](#)
- [dCME/All/libBioModel/SamplingState.cpp](#)

3.12 SLinkedList Class Reference

Public Member Functions

- [State](#) * **AddtoHead** ([State](#) *node)
- [State](#) * **AddtoTail** ([State](#) *node)
- [State](#) * **HeadDel** ()
- [State](#) * **TailDel** ()
- [State](#) * **Find** ([State](#) *item) const
- unsigned long **getSize** () const
- [State](#) * **getHead** () const
- [State](#) * **getTail** () const
- int **DeleteList** ()

- int **PrintPath** ()
- int **PrintLongPath** ()
- int **PrintList** ()
- int **WriteList** (char *filepath)
- int **WriteListQ** (char *filepath)
- int **WriteListA** (char *filepath)
- int **ReadList** (char *filepath, int n_species, unsigned int num_states)
- int **ReadListQ** (char *filepath, int n_species, unsigned int num_states)

3.12.1 Detailed Description

Definition at line 12 of file SLinkedList.h.

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

- dCME/All/libBioModel/SLinkedList.h
- dCME/All/libBioModel/SLinkedList.cpp

3.13 SLinkedListS Class Reference

Public Member Functions

- [SamplingState](#) * **AddtoHead** ([SamplingState](#) *node)
- [SamplingState](#) * **AddtoTail** ([SamplingState](#) *node)
- [SamplingState](#) * **HeadDel** ()
- [SamplingState](#) * **TailDel** ()
- [SamplingState](#) * **Find** ([SamplingState](#) *item) const
- unsigned long **getSize** () const
- [SamplingState](#) * **getHead** () const
- [SamplingState](#) * **getTail** () const
- double **CalcAllA0** ()
- int **DeleteList** ()
- int **PrintPath** ()
- int **PrintPathA0s** ()
- int **PrintLongPath** ()
- int **PrintList** ()
- int **WriteList** (char *filepath)
- int **WriteListQ** (char *filepath)
- int **WriteListA** (char *filepath)

3.13.1 Detailed Description

Definition at line 12 of file SLinkedListS.h.

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

- dCME/All/libBioModel/SLinkedListS.h
- dCME/All/libBioModel/SLinkedListS.cpp

3.14 SLinkedListT< T > Class Template Reference

Public Member Functions

- T * **AddtoHead** (T *node)
- T * **AddtoTail** (T *node)
- T * **HeadDel** ()
- T * **TailDel** ()
- T * **Find** (T *item) const
- unsigned long **getSize** () const
- T * **getHead** () const
- T * **getTail** () const
- int **PrintPath** ()
- int **PrintList** ()
- int **WriteList** (char *filepath)
- int **WriteListQ** (char *filepath)
- int **WriteListA** (char *filepath)
- int **ReadList** (char *filepath, int n_species, unsigned int num_states)
- int **ReadListQ** (char *filepath, int n_species, unsigned int num_states)

3.14.1 Detailed Description

```
template<class T>class SLinkedListT< T >
```

Definition at line 13 of file SLinkedListT.h.

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

- dCME/All/libBioModel/SLinkedListT.h
- dCME/All/libBioModel/SLinkedListT.cpp

3.15 SparseMatrix Class Reference

Public Member Functions

- **SparseMatrix** (unsigned int n_reactions)
- [MatrixElement](#) * **getHead** ()
- unsigned long **SetNumStates** (unsigned long num)
- unsigned long **Increment1NumNonZeroElements** ()
- [MatrixElement](#) * **SaveCurCol** (bool w_rlabels)
- [MatrixElement](#) * **Add** ([MatrixElement](#) *node)
- unsigned long **getSize** () const
- [MatrixElement](#) * **getHead** () const
- int **WriteMatrix** (char *filepath, bool w_rlabels)
- int **validateTransMatrix** ()

3.15.1 Detailed Description

Definition at line 14 of file SparseMatrix.h.

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

- dCME/All/libBioModel/SparseMatrix.h
- dCME/All/libBioModel/SparseMatrix.cpp

3.16 Stack Class Reference

Public Member Functions

- void **push** ([State](#) *astate)
- [State](#) * **pop** ()
- bool **isEmpty** ()
- void **setNumSpecies** (unsigned int n)
- void **removeDir** ()

3.16.1 Detailed Description

Definition at line 15 of file Stack.h.

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

- dCME/All/libBioModel/Stack.h
- dCME/All/libBioModel/Stack.cpp

3.17 State Class Reference

Public Member Functions

- **State** ([State](#) *astate)
- **State** ([SamplingState](#) *astate)
- **State** (unsigned int n_species)
- **State** (int *values, unsigned int n_species)
- int **CopyfromState** ([State](#) *astate)
- int **PrintState** ()
- int **PrintState_nonl** ()
- int **PrintState** (ofstream &f)
- STATETYPE **getStateValue** (unsigned int i)
- unsigned int **getNumSpecies** ()
- int **setStateValue** (unsigned int i, STATETYPE value)
- int **setState** (STATETYPE *astate, unsigned int n_species)
- [State](#) * **getPrev** ()
- [State](#) * **getNext** ()
- int **setPrev** ([State](#) *pt)
- int **setNext** ([State](#) *pt)
- int **setSN** (unsigned long index)

- unsigned long **getSN** ()
- int **initialize** ()
- **State** & **operator=** (const **State** &pt)
- bool **operator==** (const **State** &other)

3.17.1 Detailed Description

Definition at line 13 of file State.h.

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

- dCME/All/libBioModel/State.h
- dCME/All/libBioModel/State.cpp

3.18 StateSpace Class Reference

Public Member Functions

- int **readStateSpace** (char *ssfilename)
- int **writeStateSpace** (char *ssfilename)
- unsigned int **getValue** (unsigned int i, unsigned int j)
- **State** * **getState** (unsigned int i)
- **HashTable** * **getHashTable** ()
- unsigned int **getNumSpecies** ()
- int **setNumSpecies** (unsigned int n)
- unsigned long **getNumStates** ()
- int **setNumStates** (unsigned long n)
- string * **getSpeciesID** ()
- int **setSpeciesID** (string *speciesID, unsigned int n_species)
- const char * **getSpeciesIDValue** (unsigned int i)
- STATETYPE * **getStates** ()
- int **setStates** (STATETYPE *states)
- int **findState** (**State** *astate)

3.18.1 Detailed Description

Definition at line 13 of file StateSpace.h.

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

- dCME/All/libBioModel/StateSpace.h
- dCME/All/libBioModel/StateSpace.cpp

3.19 Stoichiometry Class Reference

Public Member Functions

- double **getValue** (unsigned int species_i, unsigned int reactions_j)

- unsigned int **getModifierValue** (unsigned int species_i, unsigned int reactions_j)
- unsigned int **getNumSpecies** ()
- int **setNumSpecies** (unsigned int n)
- int **getSpeciesIndex** (string Id)
- unsigned int **getNumReactions** ()
- int **setNumReactions** (unsigned int n)
- double * **getStoichiometricMatrix** ()
- int **setStoichiometricMatrix** (double *matrix)
- int **genStoichiometricMatrix** (class Model *m)
- KineticLaw * **getKineticLaw** (unsigned int i)
- int **getReactionAttribute** (unsigned int i)
- int **MapAllReversiblePairs** ()
- unsigned int **getNumReversiblePairs** ()
- int **getReversiblePairID** (unsigned int i_pair, unsigned int idx)
- [State](#) * **reactWithState** (unsigned int i_reaction, [State](#) *astate)
- int **reactWithState** (unsigned int i_reaction, [State](#) *astate, [State](#) *destState)
- int **updateStateWithReaction** (unsigned int i_reaction, [State](#) *curstate)
- int **updateNewStateWithReaction** (unsigned int i_reaction, [State](#) *before, [State](#) *after)
- int **canReact** (unsigned int i_reaction, [State](#) *curstate)
- [SamplingState](#) * **reactWithState** (unsigned int i_reaction, [SamplingState](#) *astate)
- int **reactWithState** (unsigned int i_reaction, [SamplingState](#) *astate, [SamplingState](#) *destState)
- int **updateStateWithReaction** (unsigned int i_reaction, [SamplingState](#) *curstate)
- int **updateNewStateWithReaction** (unsigned int i_reaction, [SamplingState](#) *before, [SamplingState](#) *after)
- int **canReact** (unsigned int i_reaction, [SamplingState](#) *curstate)
- double * **getStoichiometricVector** (unsigned int i_reaction, int withModifiers)
- int **printStoichiometricMatrix** ()

3.19.1 Detailed Description

Definition at line 14 of file Stoichiometry.h.

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

- dCME/All/libBioModel/Stoichiometry.h
- dCME/All/libBioModel/Stoichiometry.cpp

Chapter 4

File Documentation

4.1 dCME/All/net2matrix/net2matrix.cpp File Reference

compute a transition matrix from a biological network model.

```
#include "sbml/SBMLTypes.h"
#include "../libBioModel/SparseMatrix.h"
#include "../libBioModel/MatrixElement.h"
#include "../libBioModel/Network.h"
#include "../libBioModel/Stoichiometry.h"
#include "../libBioModel/StateSpace.h"
#include "../libBioModel/State.h"
#include "../libBioModel/Stack.h"
#include "../libBioModel/HashTable.h"
#include "anyoption.h"
#include <iostream>
#include <string>
#include <cmath>
#include <vector>
```

Macros

- #define **MAX_SCALE** 8e6
- #define **PRECISION** 10

Functions

- int **main** (int argc, char *argv[])

4.1.1 Detailed Description

compute a transition matrix from a biological network model.

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