mapgd

2.2

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Contents

Chapter 1

Data Structure Index

1.1 Data Structures

Here are the data structures with brief descriptions:

Chapter 2

Data Structure Documentation

2.1   allele_stat Class Reference

Public Member Functions

- allele_stat & **operator=** (const allele_stat &)

Data Fields

- bool **pooled**
- char **delim**
- std::string **id0**
- count_t **id1**
- count_t **excluded**
- float_t **freq**
- count_t **minor**
- count_t **major**
- float_t **error**
- float_t **null_error**
- float_t **coverage**
- float_t **ll**
- float_t **monoll**
- float_t **hwell**
- float_t **MM**
- float_t **Mm**
- float_t **mm**
- float_t **N**
- float_t **f**
- float_t **h**
- float_t **gof**
- float_t **efc**

Friends

- std::ostream & **operator**$<<$ (std::ostream &, const allele_stat &)

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

- stable/Likelihood.h
- stable/Likelihood.cpp

2.2   arg_t Class Reference

Public Member Functions

- **arg_t** (char opt_, char *lopt_, void *parm_, int(*func_)(int, char **, void *), char *emsg_, char *umsg_)

Data Fields

- bool **set**
- char **opt**
- char * **lopt**
- void * **parm**
- int(* **func**)(int, char **, void *)
- char * **emsg**
- char * **umsg**

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

- stable/interface.h

2.3   Args Struct Reference

Data Fields

- float_t **pvalue**
- int **min**
- bool **pro**
- bool **binary**

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

- stable/proview.h

2.4   com_t Class Reference

Public Member Functions

- **com_t** (char opt_, char *lopt_, int(*func_)(int, char **), char *emsg_, char *umsg_)

Data Fields

- bool **set**
- char **opt**
- char * **lopt**
- int(* **func**)(int, char **)
- char * **emsg**
- char * **umsg**

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

- stable/interface.h

2.5   env_t Class Reference

Public Member Functions

- void **setname** (const char ∗c)
- void **setver** (const char ∗c)
- void **setauthor** (const char ∗c)
- void **setdescription** (const char ∗c)
- void **optional_arg** (char opt_, char ∗lopt_, void ∗parm_, int(∗func_)(int, char ∗∗, void ∗), char ∗emsg_, char ∗umsg_)
- void **required_arg** (char opt_, char ∗lopt_, void ∗parm_, int(∗func_)(int, char ∗∗, void ∗), char ∗emsg_, char ∗umsg_)
- void **command** (char opt_, char ∗lopt_, int(∗func_)(int, char ∗∗), char ∗emsg_, char ∗umsg_)
- void **flag** (char opt_, char ∗lopt_, void ∗parm_, int(∗func_)(void ∗), char ∗emsg_, char ∗umsg_)
- bool **required_set** (void)
- void **close** (void)

Data Fields

- const char ∗ **name**
- const char ∗ **version**
- const char ∗ **author**
- const char ∗ **description**
- std::list< flag_t > **flags**
- std::list< arg_t > **args**
- std::list< com_t > **commands**
- std::list< arg_t ∗ > **required_args**
- std::list< com_t ∗ > **required_coms**

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

- stable/interface.h
- stable/interface.cpp

2.6   flag_t Class Reference

Public Member Functions

- **flag_t** (char opt_, char ∗lopt_, void ∗parm_, int(∗func_)(void ∗), char ∗emsg_, char ∗umsg_)

Data Fields

- bool **set**
- char **opt**
- char ∗ **lopt**
- void ∗ **parm**
- int(∗ **func**)(void ∗)
- char ∗ **emsg**
- char ∗ **umsg**

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

- stable/interface.h

2.7 genotype Class Reference

Data Fields

- float_t **g** [3]
- float_t ∗ **MM**
- float_t ∗ **Mm**
- float_t ∗ **mm**
- float_t **G** [10]
- float_t ∗ **AA**
- float_t ∗ **AC**
- float_t ∗ **AG**
- float_t ∗ **AT**
- float_t ∗ **CC**
- float_t ∗ **CG**
- float_t ∗ **CT**
- float_t ∗ **GG**
- float_t ∗ **GT**
- float_t ∗ **TT**

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

- stable/Likelihood.h

2.8 Inmultinomial Class Reference

Public Member Functions

- **Inmultinomial** (float_t ∗, const count_t &)
- **Inmultinomial** (const count_t &)
- void **set** (float_t ∗)
- void **set** (float_t, float_t, float_t, float_t)
- void **set** (void(∗)(const allele_stat &, float_t ∗), const allele_stat &)
- float_t **lnprob** (const count_t ∗)
- float_t **lnprob_approx** (const count_t ∗)
- float_t **lnfact** (const count_t &)
- float_t **lnmultinomcoef** (const count_t ∗)

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

- stable/Likelihood.h
- stable/Likelihood.cpp

2.9 mapfile Class Reference

Public Member Functions

- **profile** ()
- profile ∗ **open** (const char ∗, const char ∗)
- profile ∗ **open** (const char ∗)
- bool **is_open** (void) const
- int **copy** (const profile &)

- int **read** ()
- int **read** (int)
- int **write** ()
- int **seek** (const std::streampos)
- int **seek** (std::string, std::string)
- void **close** (void)
- int **copyheader** (const profile &)
- int **readheader** ()
- int **writeheader** ()
- void **set_delim_column** (const char &)
- void **set_delim_genotype** (const char &)
- int **setsamples** (count_t)
- int **setcolumns** (count_t)
- int **setcolumn_name** (const count_t &, const std::string &)
- int **setsample_name** (const count_t &, const std::string &)
- const std::string **getsample_name** (const count_t &) const
- const count_t **encodeid0** (const std::string &)
- const uint64_t **encodeid1** (const std::string &)
- const count_t **encodeextraid** (const char &, const count_t &)
- const std::string **decodeid0** (const count_t &)
- const std::string **decodeid1** (const uint64_t &)
- const std::string **decodeextraid** (const count_t &, const count_t &)
- count_t **size** (void) const
- const count_t **getindex** (count_t) const
- const count_t ∗ **getquartet** (count_t) const
- std::string **getids** (void)
- bool **noheader** (void)
- const count_t **getlinenumber** (void) const
- const count_t **getid0** (void) const
- const uint64_t **getid1** (void) const
- const count_t **getextraid** (const count_t &) const
- void **setid0** (const count_t &)
- void **setid1** (const uint64_t &)
- void **setextraid** (const count_t &, const count_t &)

Static Public Member Functions

- static void **merge** (std::list< profile ∗ >)

Friends

- void **mapfile_header::init** (mapfile ∗)

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

- stable/mapFile.h

2.10 mapfile_header Class Reference

Public Member Functions

- **profile_header** ()
- **profile_header** (profile ∗)
- void **init** (profile ∗)
- const count_t **encodeid0** (const std::string &)
- const uint64_t **encodeid1** (const std::string &)
- const count_t **encodeextraid** (const char &, const count_t &)
- const std::string **decodeid0** (const count_t &)
- const std::string **decodeid1** (const uint64_t &)
- const std::string **decodeextraid** (const count_t &, const count_t &)
- int **readheader** (std::istream ∗)
- int **readtailer** (std::istream ∗)
- int **writeheader** (std::ostream ∗)
- int **writetailer** (std::ostream ∗)
- void **set_delim_column** (const char &)
- void **set_delim_quartet** (const char &)
- int **setsamples** (const count_t &)
- int **setcolumns** (const count_t &)
- int **setcolumn_name** (const count_t &, const std::string &)
- const std::string **getcolumn_name** (const count_t &) const
- profile_header & **operator=** (const profile_header &)

Data Fields

- char **control**

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

- stable/mapFile.h

2.11 models Class Reference

Public Member Functions

- float_t **loglikelihood** (const site_t &, const allele_stat &, const count_t &)
- float_t **lnP** (const count_t ∗, const allele_stat &)
- float_t **genotypelikelihood** (const quartet_t &, const allele_stat &, const count_t &)

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

- stable/indLikelihood.h
- stable/indLikelihood.cpp

2.12 profile Class Reference

Public Member Functions

- const float_t **getsample_property** (const count_t &) const
- profile ∗ open (const char ∗, const char ∗)

    opens a .pro file in the modes "r" or "w".

- profile ∗ **open** (const char ∗)
- bool **is_open** (void) const
- int **copy** (const profile &)
- int **read** ()
- int **read** (site_t &)
- int **write** ()
- int **write** (site_t const &)
- int **seek** (const std::streampos)
- int **seek** (std::string, std::string)
- void close (void)

    closes a .pro file and unsets members. return value

- int **copyheader** (const profile &)
- int **readheader** ()
- int **writeheader** ()
- int **writetailer** ()
- void **set_delim_column** (const char &)
- void **set_delim_quartet** (const char &)
- int **setsamples** (count_t)
- int **setcolumns** (count_t)
- int **setcolumn_name** (const count_t &, const std::string &)
- int **setsample_name** (const count_t &, const std::string &)
- const std::string **getsample_name** (const count_t &) const
- const count_t **encodeid0** (const std::string &)
- const uint64_t **encodeid1** (const std::string &)
- const count_t **encodeextraid** (const char &, const count_t &)
- const std::string **decodeid0** (const count_t &)
- const std::string **decodeid1** (const uint64_t &)
- const std::string **decodeextraid** (const count_t &, const count_t &)
- count_t **size** (void) const
- uint64_t **length** (void) const
- void **setbasecount** (const count_t &, const count_t &, const count_t &)
- void **mpileup** (void)
- bool **noheader** (void)
- const uint64_t **getlinenumber** (void) const
- const count_t **getid0** (void) const
- const uint64_t **getid1** (void) const
- const count_t **getextraid** (const count_t &) const
- void **setid0** (const count_t &)
- void **setid1** (const uint64_t &)
- void **setextraid** (const count_t &, const count_t &)
- std::string **getids** (const site_t &)
- std::string **getids** (void)
- void **maskall** (void)
- void **unmask** (count_t)
- void **unmask** (quartet ∗)
- void **mask** (quartet ∗)
- void **mask** (count_t)

- void **sort** (void)
- site_t **getsite** (void)
- std::vector< quartet_t >::iterator **begin** (void)
- std::vector< quartet_t >::iterator **end** (void)

Static Public Member Functions

- static void **merge** (std::list< profile ∗ >)

Static Public Attributes

- static const std::string names_ ="ACGT∗"

  Read a .pro file in the five column format.

Friends

- void **profile_header::init** (profile ∗)

2.12.1 Member Function Documentation

2.12.1.1 profile ∗ profile::open (const char ∗ *filename,* const char ∗ *mode*)

opens a .pro file in the modes "r" or "w".

Returns

a pointer to the profile

2.12.2 Field Documentation

2.12.2.1 const std::string profile::names_ ="ACGT∗" `[static]`

Read a .pro file in the five column format.

Returns

0 iff successful

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

- stable/proFile.h
- stable/proFile.cpp

2.13 profile_header Class Reference

Public Member Functions

- const float_t **getsample_property** (const count_t &) const
- const std::string **getsample_name** (const count_t &) const
- **profile_header** (profile ∗)
- void **init** (profile ∗)
- const count_t **encodeid0** (const std::string &)

- const uint64_t **encodeid1** (const std::string &)
- const count_t **encodeextraid** (const char &, const count_t &)
- const std::string **decodeid0** (const count_t &)
- const std::string **decodeid1** (const uint64_t &)
- const std::string **decodeextraid** (const count_t &, const count_t &)
- int **readheader** (std::istream ∗)
- int **readtailer** (std::istream ∗)
- int **writeheader** (std::ostream ∗)
- int **writetailer** (std::ostream ∗)
- void **set_delim_column** (const char &)
- void **set_delim_quartet** (const char &)
- int **setsamples** (const count_t &)
- int **setcolumns** (const count_t &)
- int **setcolumn_name** (const count_t &, const std::string &)
- const std::string **getcolumn_name** (const count_t &) const
- profile_header & **operator=** (const profile_header &)

Data Fields

- char **control**

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

- stable/proFile.h
- stable/proFile.cpp

2.14 quartet Struct Reference

Public Member Functions

- **quartet** (const count_t &A, const count_t &C, const count_t &G, const count_t &T, const count_t &N)
- quartet & **operator+=** (const quartet &x)
- quartet **operator+** (const quartet &x) const
- quartet & **operator=** (const count_t &x)

Data Fields

- count_t **base** [5]
- bool **masked**

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

- stable/proFile.h

2.15 site_t Class Reference

Public Member Functions

- **site_t** (count_t)
- site_t & **operator=** (const site_t &)
- const count_t **getindex** (count_t) const

- count_t **getcoverage** (count_t) const
- count_t **getcoverage** (void) const
- count_t **getcount** (count_t) const
- count_t **getcount** (count_t, count_t) const
- name_t **getname** (count_t) const
- name_t **getname_gt** (count_t) const
- void **swap** (count_t, count_t)
- void **sort** (count_t)
- void **sort** (void)
- count_t **maskedcount** (void) const
- const count_t ∗ **getquartet** (count_t) const
- void **maskall** (void)
- void **unmaskall** (void)
- void **unmask** (count_t)
- void **unmask** (quartet ∗)
- void **mask** (quartet ∗)
- void **mask** (count_t)

Data Fields

- count_t **sorted_** [5]
- std::vector< quartet_t > **sample**
- count_t **samples_**
- count_t **id0**
- uint64_t **id1**
- std::vector< count_t > **extraid**

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

- stable/proFile.h
- stable/proFile.cpp

2.16 sort_second Struct Reference

Public Member Functions

- bool **operator()** (const std::pair< count_t, float_t > &left, const std::pair< count_t, float_t > &right)
- bool **operator()** (const std::pair< count_t, count_t > &left, const std::pair< count_t, count_t > &right)

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

- stable/Likelihood.cpp

Index