eXpress

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Contents

Chapter 1

Class Index

1.1 Class Hierarchy

This inheritance list is sorted roughly, but not completely, alphabetically:

Chapter 2

Class Index

2.1 Class List

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

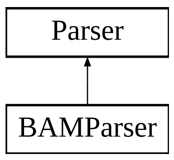
Chapter 3

Class Documentation

3.1 BAMParser Class Reference

`#include <mapparser.h>`

Inheritance diagram for BAMParser:



Public Member Functions

- BAMParser (BamTools::BamReader ∗reader)
- ∼BAMParser ()
- const std::string header () const
- const TransIndex & trans_index () const
- const TransIndex & trans_lengths () const
- bool next_fragment (Fragment &f)
- void reset ()

3.1.1 Detailed Description

The BAMParser class fills Fragment objects by parsing an input file in BAM format.

Author

Adam Roberts

Date

2011 Artistic License 2.0

Definition at line 102 of file mapparser.h.

3.1.2 Constructor & Destructor Documentation

3.1.2.1 BAMParser::BAMParser (BamTools::BamReader ∗ *reader*)

BAMParser constructor sets the reader

Definition at line 230 of file mapparser.cpp.

3.1.2.2 BAMParser::∼BAMParser ( ) `[inline]`

BAMParser destructor deletes the reader

Definition at line 140 of file mapparser.h.

3.1.3 Member Function Documentation

3.1.3.1 const std::string BAMParser::header ( ) const `[inline, virtual]`

a member function that returns a string version of the header

Returns

string version of the header

Implements Parser.

Definition at line 146 of file mapparser.h.

3.1.3.2 bool BAMParser::next_fragment (Fragment & *f*) `[virtual]`

a member function that loads all mappings of the next fragment

Parameters

f	the empty Fragment to add mappings to

Returns

true if more reads remain in the BAM file, false otherwise

Implements Parser.

Definition at line 253 of file mapparser.cpp.

3.1.3.3 void BAMParser::reset ( ) `[virtual]`

a member function that resets the parser and rewinds to the beginning of the BAM file

Implements Parser.

Definition at line 310 of file mapparser.cpp.

3.1.3.4 const TransIndex& BAMParser::trans_index ( ) const `[inline, virtual]`

a member function that returns the transcript-to-index map

Returns

the transcript-to-index map

Implements Parser.

Definition at line 152 of file mapparser.h.

3.1.3.5 const TransIndex& BAMParser::trans_lengths ( ) const `[inline, virtual]`

a member function that returns the transcript-to-length map

Returns

the transcript-to-length map

Implements Parser.

Definition at line 158 of file mapparser.h.

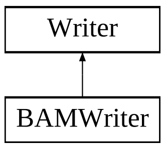
The documentation for this class was generated from the following files:

- src/mapparser.h
- src/mapparser.cpp

3.2 BAMWriter Class Reference

`#include <mapparser.h>`

Inheritance diagram for BAMWriter:



Public Member Functions

- BAMWriter (BamTools::BamWriter ∗writer, bool sample)
- ∼BAMWriter ()
- void write_fragment (Fragment &f)

3.2.1 Detailed Description

The BAMWriter class writes Fragment objects back to file (in BAM format) with per-mapping probabilistic assignments.

Author

Adam Roberts

Date

2011 Artistic License 2.0

Definition at line 179 of file mapparser.h.

3.2.2 Constructor & Destructor Documentation

3.2.2.1 BAMWriter::BAMWriter (BamTools::BamWriter ∗ *writer,* bool *sample*)

BAMWriter constructor stores a pointer to the BAM file

Parameters

writer	pointer to the BAM file object
sample	specifies if a single alignment should be sampled (true) or all output with their respective probabilities (false)

Definition at line 320 of file mapparser.cpp.

3.2.2.2 BAMWriter::∼BAMWriter ( )

BAMWriter destructor flushes and deletes the Bamtools::BamWriter

Definition at line 324 of file mapparser.cpp.

3.2.3 Member Function Documentation

3.2.3.1 void BAMWriter::write_fragment (Fragment & *f*) `[virtual]`

a member function that writes all mappings of the fragment to the ouptut file in BAM format along with their probabilities in the "XP" field

Parameters

f	the processed Fragment to output

Implements Writer.

Definition at line 330 of file mapparser.cpp.

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

- src/mapparser.h
- src/mapparser.cpp

3.3 BiasBoss Class Reference

```
#include <biascorrection.h>
```

Public Member Functions

- BiasBoss (double alpha)
- void **copy_observations** (const BiasBoss &other)
- void **copy_expectations** (const BiasBoss &other)
- void update_expectations (const Transcript &trans, double mass=0)
- void normalize_expectations ()
- void update_observed (const FragHit &hit, double mass)
- double get_transcript_bias (std::vector< float > &start_bias, std::vector< float > &end_bias, const Transcript &trans) const
- std::string to_string () const
- void append_output (std::ofstream &outfile) const

3.3.1 Detailed Description

The BiasBoss class keeps track of sequence-specific and positional bias. It allows for the bias associated with a given fragment end to be calculated, and for the bias parameters to be updated based on additional observations. All stored and returned values are in log space.

Author

Adam Roberts

Date

2011 Artistic License 2.0

Definition at line 224 of file biascorrection.h.

3.3.2 Constructor & Destructor Documentation

3.3.2.1 BiasBoss::BiasBoss (double *alpha*)

a private SeqWeightTable that stores the 5' sequence-specific bias parameters (logged) a private SeqWeightTable that stores the 3' sequence-specific bias parameters (logged) BiasBoss Constructor

Parameters

alpha	a double specifying the strength of the uniform prior (logged pseudo-counts for each parameter)

Definition at line 241 of file biascorrection.cpp.

3.3.3 Member Function Documentation

3.3.3.1 void BiasBoss::append_output (std::ofstream & *outfile*) const

a member function that outputs the positional and sequence-specific bias parameter matrices

Parameters

outfile	the file to append to

3.3.3.2 double BiasBoss::get_transcript_bias (std::vector< float > & *start_bias*, std::vector< float > & *end_bias*, const Transcript & *trans*) const

a member function that returns the 5' and 3' bias values at each position in a given transcript based on the current bias parameters

Parameters

start_bias	a vector containing the logged bias for each 5' start site in the transcript
end_bias	a vector containing the logged bias for each 3' end site in the transcript
trans	the transcript for which to calculate the logged bias

Returns

the product of the average 5' and 3' bias (logged)

Definition at line 312 of file biascorrection.cpp.

3.3.3.3 void BiasBoss::normalize_expectations ( )

a member function that normalizes the expected counts and converts them to the log scale

Definition at line 284 of file biascorrection.cpp.

3.3.3.4 string BiasBoss::to_string ( ) const

a member function that returns a string containing the observed positional nucleotide probabilities (non-logged) in column-major order (A,C,G,T)

Returns

the string representation of the observed probabilities

Definition at line 344 of file biascorrection.cpp.

3.3.3.5 void BiasBoss::update_expectations (const Transcript & *trans*, double *mass* = 0)

a member function that updates the expectation parameters (sequence-specific and positional) assuming uniform expression of and accross the transcript's sequence

Parameters

trans	the transcript to measure expected counts from

Definition at line 260 of file biascorrection.cpp.

3.3.3.6 void BiasBoss::update_observed (const FragHit & *hit*, double *mass*)

a member function that updates the observed parameters (sequence-specific and positional) given a fragment mapping to a transcript and its logged probabilistic assignment

Parameters

hit	the fragment hit (alignment)
mass	the logged probabality of the mapping, which is the amount to update the observed counts by

Definition at line 292 of file biascorrection.cpp.

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

- src/biascorrection.h
- src/biascorrection.cpp

3.4 Bundle Class Reference

`#include <bundles.h>`

Public Member Functions

- Bundle (Transcript ∗trans)

- void incr_counts (size_t incr_amt=1)
- size_t size () const
- std::vector< Transcript $*$ > & transcripts ()
- size_t counts () const

3.4.1 Detailed Description

The Bundle class keeps track of a group of transcripts that have shared ambiguous (multi-mapped) reads. Besides storing the transcript, it keeps track of the number of observed fragments, the total fragment mass, and the next fragment mass (which it also updates).

Author

Adam Roberts

Date

2011 Artistic License 2.0

Definition at line 71 of file bundles.h.

3.4.2 Constructor & Destructor Documentation

3.4.2.1 Bundle::Bundle (Transcript $*$ *trans*)

Bundle Constructor.

Parameters

trans	a pointer to the initial Transcript object in the bundle
fmt	a pointer to the (global) FragMassTable

Definition at line 42 of file bundles.cpp.

3.4.3 Member Function Documentation

3.4.3.1 size_t Bundle::counts ( ) const [inline]

a member function that returns the total number of observed fragments mapped to transcripts in the bundle

Returns

the total number of fragments mapped to transcripts in the bundle

Definition at line 115 of file bundles.h.

3.4.3.2 void Bundle::incr_counts (size_t *incr_amt* = `1`)

a member function that increases the total bundle observed fragment counts by a given amount

Parameters

incr_amt	the amount to increase the counts by

Definition at line 46 of file bundles.cpp.

3.4.3.3 size_t Bundle::size ( ) const `[inline]`

a member function that returns the number of transcripts in the bundle

Returns

the number of transcripts in the bundle

Definition at line 103 of file bundles.h.

3.4.3.4 std::vector<Transcript*>& Bundle::transcripts ( ) `[inline]`

a member function that returns a reference to the vector of pointers to transcripts in the bundle

Returns

reference to the vector pointing to bundle transcripts

Definition at line 109 of file bundles.h.

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

- src/bundles.h
- src/bundles.cpp

3.5 BundleTable Class Reference

```
#include <bundles.h>
```

Public Member Functions

- BundleTable ()
- ~BundleTable ()
- const BundleSet & bundles () const
- size_t size () const
- Bundle * create_bundle (Transcript *trans)
- Bundle * merge (Bundle *b1, Bundle *b2)

3.5.1 Detailed Description

The BundleTable class keeps track of the Bundle objects for a given run. It has the ability to create, delete, and merge bundles. It also keeps track of the transcript covariances, since these are related to bundles in that all covariances outside of a bundle are nonzero.

Author

Adam Roberts

Date

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Definition at line 129 of file bundles.h.

3.5.2 Constructor & Destructor Documentation

3.5.2.1 BundleTable::BundleTable ( ) `[inline]`

BundleTable constructor.

Definition at line 141 of file bundles.h.

3.5.2.2 BundleTable::∼BundleTable ( )

BundleTable deconstructor. Deletes all Bundle objects.

Definition at line 51 of file bundles.cpp.

3.5.3 Member Function Documentation

3.5.3.1 const BundleSet& BundleTable::bundles ( ) const `[inline]`

a member function that returns the set of current Bundle objects

Returns

a reference to the unordered_set containing all current Bundle objects

Definition at line 152 of file bundles.h.

3.5.3.2 Bundle ∗ BundleTable::create_bundle (Transcript ∗ *trans*)

a member function that creates a new bundle, initially with only the single given Transcript

Parameters

trans	a pointer to the only Transcript initially contained in the Bundle

Returns

a pointer to the new Bundle object

Definition at line 59 of file bundles.cpp.

3.5.3.3 Bundle ∗ BundleTable::merge (Bundle ∗ *b1*, Bundle ∗ *b2*)

a member function that merges two Bundle objects into one the Transcripts are all move to the larger bundles and the other is deleted

Parameters

b1	a pointer to one of the Bundle objects to merge
b2	a pointer to the other Bundle object to merge

Returns

a pointer to the merged Bundle object

Definition at line 66 of file bundles.cpp.

3.5.3.4 size_t BundleTable::size ( ) const [inline]

a member function that returns the size of the set of current Bundle objects, which is the current number of bundles

Returns

the current number of bundles

Definition at line 159 of file bundles.h.

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

- src/bundles.h
- src/bundles.cpp

3.6 CovarTable Class Reference

`#include <bundles.h>`

Public Member Functions

- void increment (TransID trans1, TransID trans2, double covar)

- double get (TransID trans1, TransID trans2)
- size_t size () const

3.6.1 Detailed Description

The CovarTable is a sparse matrix for storing and updating pairwise covariances between targets.

Author

Adam Roberts

Date

2011 Artistic License 2.0

Definition at line 26 of file bundles.h.

3.6.2 Member Function Documentation

3.6.2.1 double CovarTable::get (TransID *trans1*, TransID *trans2*)

a member function that returns the covariance between two transcripts these returned value will be the the negative of the true value (logged)

Parameters

trans1	one of the transcripts in the pair
trans2	the other transcript in the pair

Returns

the negative of the pair's covariance (logged)

Definition at line 29 of file bundles.cpp.

3.6.2.2 void CovarTable::increment (TransID *trans1*, TransID *trans2*, double *covar*)

a member function that increases the covariance between two transcripts by the specified amount (logged) these values are stored positive even though they are negative

Parameters

trans1	one of the transcripts in the pair
trans2	the other transcript in the pair
covar	a double specifying the amount to increase the pair's covariance by (logged)

Definition at line 15 of file bundles.cpp.

3.6.2.3 size_t CovarTable::size ( ) const `[inline]`

a member function that returns the number of pairs of transcripts with non-zero covariance

Returns

the number of transcript pairs with non-zero covariance

Definition at line 60 of file bundles.h.

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

- src/bundles.h
- src/bundles.cpp

3.7 FLD Class Reference

```
#include <fld.h>
```

Public Member Functions

- FLD (double alpha, size_t max_val, size_t mean, size_t std_dev)
- size_t max_val () const
- size_t **min_val** () const
- double mean () const
- void add_val (size_t len, double mass)
- double pdf (size_t len) const
- double tot_mass () const
- std::string to_string () const
- void append_output (std::ofstream &outfile) const

3.7.1 Detailed Description

The FLD class keeps track of the observed fragment length distribution. It starts with a Gaussian prior with parameters specified by the arguments. A small "Gaussian" kernel is added for each observation. All mass values and probabilities are stored and returned in log space (except in to_string).

Definition at line 21 of file fld.h.

3.7.2 Constructor & Destructor Documentation

3.7.2.1 FLD::FLD (double *alpha*, size_t *max_val*, size_t *mean*, size_t *std_dev*)

FLD Constructor

Parameters

alpha	double that sets the average pseudo-counts (logged)
max_val	an integer that sets the maximum allowable FragHit length
mean	a size_t for the mean of the prior gaussian dist
std_dev	a size_t for the std dev of the prior gaussian dist

Definition at line 21 of file fld.cpp.

3.7.3 Member Function Documentation

3.7.3.1 void FLD::add_val (size_t *len*, double *mass*)

a member function that updates the distribution based on a new FragHit observation

Parameters

len	an integer for the observed FragHit length
mass	a double for the mass (logged) of the observed FragHit

Definition at line 53 of file fld.cpp.

3.7.3.2 void FLD::append_output (std::ofstream & *outfile*) const

a member function that appends the FLD parameters to the end of the given file

Parameters

outfile	the file to append to

3.7.3.3 size_t FLD::max_val ( ) const

a member function that returns the maximum allowed FragHit length

Returns

max allowed FragHit length

Definition at line 41 of file fld.cpp.

3.7.3.4 double FLD::mean ( ) const

a member function that returns the mean FragHit length

Returns

mean observed FragHit length

Definition at line 84 of file fld.cpp.

3.7.3.5 double FLD::pdf (size_t *len*) const

a member function that returns the (logged) probability of a given FragHit length

Parameters

len	an integer for the FragHit length to return the probability of

Returns

(logged) probability of observing the given FragHit length

Definition at line 73 of file fld.cpp.

3.7.3.6 string FLD::to_string ( ) const

a member function that returns a string containing the current distribution

Returns

space-separated string of probabilities ordered from length 0 to max_val (non-logged)

Definition at line 89 of file fld.cpp.

3.7.3.7 double FLD::tot_mass ( ) const

a member function that returns the (logged) number of observed FragHits (including pseudo-counts)

Returns

number of observed fragments

Definition at line 79 of file fld.cpp.

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

- src/fld.h
- src/fld.cpp

3.8 FragHit Struct Reference

```
#include <fragments.h>
```

Public Member Functions

- size_t length () const
- PairStatus pair_status () const

Public Attributes

- std::string name
- TransID trans_id
- Transcript ∗ mapped_trans
- Sequence seq_l
- Sequence seq_r
- size_t left
- size_t right
- int mate_l
- bool left_first
- std::vector< Indel > inserts_l
- std::vector< Indel > deletes_l
- std::vector< Indel > inserts_r
- std::vector< Indel > deletes_r
- double **probability**
- BamTools::BamAlignment **bam_l**
- BamTools::BamAlignment **bam_r**
- std::string **sam_l**
- std::string **sam_r**

3.8.1 Detailed Description

The FragHit struct stores the information for a single (multi-)mapping of a fragment.

Author

Adam Roberts

Date

2011 Artistic License 2.0

Definition at line 62 of file fragments.h.

3.8.2 Member Function Documentation

3.8.2.1 size_t FragHit::length ( ) const [inline]

a member function returning the length of the fragment according to this mapping note, that this result will be invalid if the fragment is single-end

Returns

int length of fragment mapping

Definition at line 140 of file fragments.h.

3.8.2.2 PairStatus FragHit::pair_status ( ) const [inline]

a member function returning whether the mapping is PAIRED, LEFT_ONLY, or RIGHT_-ONLY LEFT_ONLY denotes that the single read is not reverse complemented => its left end is the left fragment end RIGHT_ONLY denotes that the single read is reverse complemented => its right end is the right fragment end

Returns

PairStatus the pair status of the mapping

Definition at line 152 of file fragments.h.

3.8.3 Member Data Documentation

3.8.3.1 std::vector<Indel> FragHit::deletes_l

a public vector of Indel objects storing all deletions from the reference in the left read (in order from left to right)

Definition at line 123 of file fragments.h.

3.8.3.2 std::vector<Indel> FragHit::deletes_r

a public vector of Indel objects storing all deletions from the reference in the left read (in order from right to left)

Definition at line 133 of file fragments.h.

3.8.3.3 std::vector<Indel> FragHit::inserts_l

a public vector of Indel objects storing all insertions to the reference in the left read (in order from left to right)

Definition at line 118 of file fragments.h.

3.8.3.4 std::vector<Indel> FragHit::inserts_r

a public vector of Indel objects storing all insertions to the reference in the right read (in order from right to left)

Definition at line 128 of file fragments.h.

3.8.3.5 size_t FragHit::left

a public size_t containing the 0-based leftmost coordinate mapped to in the transcript valid only if PairStatus is PAIRED or LEFT_ONLY

Definition at line 93 of file fragments.h.

3.8.3.6 bool FragHit::left_first

a public bool specifying that the "right" (second according to SAM flag) is reverse complemented when true and the "left" (first according to SAM flag) is reverse complemented when false in other words, the "left" read is truly left of the "right" read in transcript coordinate space when true

Definition at line 113 of file fragments.h.

3.8.3.7 Transcript* FragHit::mapped_trans

a public pointer to the transcript mapped to

Definition at line 77 of file fragments.h.

3.8.3.8 int FragHit::mate_l

a public int containing the left position for the mate of the first read read in from the SAM file 0 if single-end fragment this is temporarily used to help find the mate, but is not important later on

Definition at line 106 of file fragments.h.

3.8.3.9 std::string FragHit::name

a public string for the SAM "Query Template Name" (fragment name)

Definition at line 67 of file fragments.h.

3.8.3.10 size_t FragHit::right

a public size_t containing the position following the 0-based rightmost coordinate mapped to in the transcript valid only if PairStatus is PAIRED or RIGHT_ONLY

Definition at line 99 of file fragments.h.

3.8.3.11 Sequence FragHit::seq_l

a public string containing the "left" read sequence (first according to SAM flag)

Definition at line 82 of file fragments.h.

3.8.3.12 Sequence FragHit::seq_r

a public string containing the "right" read sequence (second according to SAM flag)

Definition at line 87 of file fragments.h.

3.8.3.13 TransID FragHit::trans_id

a public TransID for the transcript mapped to

Definition at line 72 of file fragments.h.

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

- src/fragments.h

3.9 Fragment Class Reference

```
#include <fragments.h>
```

Public Member Functions

- ∼Fragment ()
- bool add_map_end (FragHit ∗f)
- const std::string & name () const
- const size_t num_hits () const
- const std::vector< FragHit ∗ > & hits () const
- const FragHit ∗ sample_hit () const

3.9.1 Detailed Description

The Fragment class stores information for all multi-mappings of a single fragment. By design, only paired-end mappings of paired-end reads will be accepted. All mappings of single-end reads will be accepted.

Author

Adam Roberts

Date

2011 Artistic License 2.0

Definition at line 177 of file fragments.h.

3.9.2 Constructor & Destructor Documentation

3.9.2.1 Fragment::∼Fragment ( )

Fragment destructor deletes all FragHit objects pointed to by the Fragment

Definition at line 17 of file fragments.cpp.

3.9.3 Member Function Documentation

3.9.3.1 bool Fragment::add_map_end (FragHit $*$ *f*)

a member function that adds a new FragHit (single read at this point) to the Fragment if it is the first FragHit, it sets the Fragment name and is added to _open_mates, if the fragment is not paired, it is added to _frag_hits, otherwise, add_open_mate is called

Parameters

f	the FragHit to be added

Definition at line 30 of file fragments.cpp.

3.9.3.2 const std::vector<FragHit$*$>& Fragment::hits ( ) const `[inline]`

a member function that returns FragHit multi-mappings of the fragment

Returns

a vector containing pointers to the FragHit multi-mappings

Definition at line 234 of file fragments.h.

3.9.3.3 const std::string& Fragment::name ( ) const `[inline]`

a member function that returns the SAM "Query Template Name" (fragment name)

Returns

the string SAM "Query Template Name" (fragment name)

Definition at line 222 of file fragments.h.

3.9.3.4 const size_t Fragment::num_hits ( ) const `[inline]`

a member function that returns the number of multi-mappings for the fragment

Returns

number of multi-mappings for fragment

Definition at line 228 of file fragments.h.

3.9.3.5 const FragHit $*$ Fragment::sample_hit ( ) const

a member function that returns a single FragHit of the fragment sampled at random based on the probabalistic assignment

Returns

a randomly sampled FragHit

Definition at line 98 of file fragments.cpp.

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

- src/fragments.h
- src/fragments.cpp

3.10 FrequencyMatrix Class Reference

```
#include <frequencymatrix.h>
```

Public Member Functions

- FrequencyMatrix ()
- FrequencyMatrix (size_t m, size_t n, double alpha, bool logged=true)
- double operator() (size_t i, size_t j) const
- double operator() (size_t k) const
- void increment (size_t i, size_t j, double incr_amt)
- void increment (size_t k, double incr_amt)
- double arr (size_t k) const
- double row (size_t i) const
- void set_logged (bool logged)

3.10.1 Detailed Description

The FrequencyMatrix class keeps track of the frequency parameters in order to allow for constant-time probability look-ups and updates. The table is rectangular to allow for multiple distributions to be stored in one FrequencyMatrix. Rows are distributions. Values are in log space by default.

Author

Adam Roberts

Date

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Definition at line 24 of file frequencymatrix.h.

3.10.2 Constructor & Destructor Documentation

3.10.2.1 FrequencyMatrix::FrequencyMatrix ( ) `[inline]`

dummy constructor

Definition at line 56 of file frequencymatrix.h.

3.10.2.2 FrequencyMatrix::FrequencyMatrix (size_t *m*, size_t *n*, double *alpha*, bool *logged* = `true`)

FrequencyMatrix constructor initializes the matrix based on the log of the given pseudo-counts

Parameters

m	a size_t specifying the number of distributions (rows)
n	a size_t specifying the number of values in each distribution (columns)
alpha	a double specifying the intial psuedo-counts (un-logged)
logged	bool that specifies if the table is in log space

Definition at line 16 of file frequencymatrix.cpp.

3.10.3 Member Function Documentation

3.10.3.1 double FrequencyMatrix::arr (size_t *k*) const `[inline]`

a member function that returns the raw value stored at a given position of the flattened matrix

Parameters

k	the array position

Returns

a double specifying the raw value stored at the given position of the flattened matrix

Definition at line 102 of file frequencymatrix.h.

3.10.3.2 void FrequencyMatrix::increment (size_t *i*, size_t *j*, double *incr_amt*)

a member function to increase the mass of a given position in the matrix

Parameters

i	the distribution (row)
j	the value (column)
incr_amt	the amount to increase the mass by (logged if table is logged)

Definition at line 39 of file frequencymatrix.cpp.

3.10.3.3 void FrequencyMatrix::increment (size_t *k*, double *incr_amt*)

a member function to increase the mass of a given position in the flattened matrix (logged if table is logged)

Parameters

k	the array position
incr_amt	the amount to increase the mass by (logged if table is logged)

Definition at line 56 of file frequencymatrix.cpp.

3.10.3.4 double FrequencyMatrix::operator() (size_t *k*) const

a member function to extract the probability of a given position in the flattened matrix (logged if table is logged)

Parameters

k	the array position

Returns

a double specifying the probability of the given position in the flattened matrix (logged if table is logged)

Definition at line 33 of file frequencymatrix.cpp.

3.10.3.5 double FrequencyMatrix::operator() (size_t *i*, size_t *j*) const

a member function to extract the probability of a given position in the matrix (logged if table is logged)

Parameters

i	the distribution (row)
j	the value (column)

Returns

a double specifying the probability of the given value in the given distribution (logged if table is logged)

Definition at line 24 of file frequencymatrix.cpp.

3.10.3.6 double FrequencyMatrix::row (size_t *i*) const `[inline]`

a member function that returns the raw row sum

Parameters

i	the distribution (row)

Returns

a double specifying the raw row sum for the given distribution

Definition at line 109 of file frequencymatrix.h.

3.10.3.7 void FrequencyMatrix::set_logged (bool *logged*)

a member function that converts the table between log-space and non-log space

Parameters

logged	bool specifying if the table should be converted to logged or non-logged space

Definition at line 61 of file frequencymatrix.cpp.

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

- src/frequencymatrix.h
- src/frequencymatrix.cpp

3.11 Globals Struct Reference

`#include <main.h>`

Public Attributes

- FLD ∗ **fld**
- MismatchTable ∗ **mismatch_table**
- BiasBoss ∗ **bias_table**
- TranscriptTable ∗ **trans_table**

3.11.1 Detailed Description

a struct for holding pointers to the global parameter tables (bias_table, mismatch_table, fld)

Definition at line 29 of file main.h.

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

- src/main.h

3.12 Indel Struct Reference

`#include <fragments.h>`

Public Member Functions

- Indel (size_t p, size_t l)

Public Attributes

- size_t pos
- size_t len

3.12.1 Detailed Description

The Indel struct stores the information for a single insertion or deletion.

Author

Adam Roberts

Date

2012 Artistic License 2.0

Definition at line 38 of file fragments.h.

3.12.2 Constructor & Destructor Documentation

3.12.2.1 Indel::Indel (size_t *p*, size_t *l*) `[inline]`

Indel constructor

Definition at line 53 of file fragments.h.

3.12.3 Member Data Documentation

3.12.3.1 size_t Indel::len

a public size_t for the length of the Indel in the read

Definition at line 48 of file fragments.h.

3.12.3.2 size_t Indel::pos

a public size_t for the position of the Indel in the read

Definition at line 43 of file fragments.h.

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

- src/fragments.h

3.13 MarkovModel Class Reference

Public Member Functions

- **MarkovModel** (size_t order, size_t window_size, size_t num_pos, double alpha, bool logged=true)
- double **transition_prob** (size_t p, size_t cond, size_t curr) const
- double **seq_prob** (const Sequence &seq, int left) const
- double **marginal_prob** (size_t w, size_t nuc) const
- void **update** (const Sequence &seq, int left, double mass)
- void **fast_learn** (const Sequence &seq, double mass)
- void **calc_marginals** ()
- void **set_logged** (bool logged)

3.13.1 Detailed Description

Definition at line 18 of file markovmodel.h.

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

- src/markovmodel.h
- src/markovmodel.cpp

3.14 MismatchTable Class Reference

```
#include <mismatchmodel.h>
```

Public Member Functions

- MismatchTable (double alpha)
- void activate (bool active=true)
- double log_likelihood (const FragHit &f) const
- void update (const FragHit &, double mass)
- std::string to_string () const
- void append_output (std::ofstream &outfile) const

3.14.1 Detailed Description

The MismatchTable class is used to store and update mismatch (error) parameters using a first-order Markov model based on nucleotide and position in a ride and to return likelihoods of mismatches in given reads. All values are stored and returned in log space.

Author

Adam Roberts

Date

2011 Artistic License 2.0

Definition at line 24 of file mismatchmodel.h.

3.14.2 Constructor & Destructor Documentation

3.14.2.1 MismatchTable::MismatchTable (double *alpha*)

MismatchTable constructor initializes the model parameters using the specified (non-logged) pseudo-counts.

Parameters

alpha	a double containing the non-logged pseudo-counts for parameter initialization

Definition at line 19 of file mismatchmodel.cpp.

3.14.3 Member Function Documentation

3.14.3.1 void MismatchTable::activate (bool *active* = `true`) `[inline]`

member function that 'activates' the table to allow its values to be used in calculating log-likelihoods when it is sufficiently burned-in

Parameters

active	a boolean specifying whether to activate (true) or deactivate (false)

Definition at line 69 of file mismatchmodel.h.

3.14.3.2 void MismatchTable::append_output (std::ofstream & *outfile*) const

a member function that outputs the final model parameters in a tab-separated file the file has 1 row for each read position and the parameters are in columns indexed as (ref, prev, obs) in base 4 with A,C,G,T encoded as 0,1,2,3.

Parameters

file	stream to append to

Definition at line 70 of file biascorrection.cpp.

3.14.3.3 double MismatchTable::log_likelihood (const FragHit & *f*) const

member function returns the log likeihood of mismatches in the mapping given the current error model paremeters

Parameters

f	the fragment mapping to calculate the log likelihood for

Returns

the log likelihood of the mapping based on mismatches

Definition at line 28 of file mismatchmodel.cpp.

3.14.3.4 string MismatchTable::to_string ( ) const

member function that returns a string containing a collapsed confusion matrix based on the model parameters for the first read

Returns

a space-separated string for the flattened, collapsed confusion matrix in row-major format (observed value as rows)

Definition at line 251 of file mismatchmodel.cpp.

3.14.3.5 void MismatchTable::update (const FragHit & *f*, double *mass*)

member function that updates the error model parameters based on a mapping and its (logged) mass

Parameters

f	the fragment mapping
mass	the logged mass to increase the parameters by

Definition at line 144 of file mismatchmodel.cpp.

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

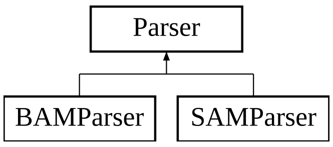
- src/mismatchmodel.h
- src/biascorrection.cpp
- src/fld.cpp

- src/mismatchmodel.cpp

3.15 Parser Class Reference

`#include <mapparser.h>`

Inheritance diagram for Parser:



Public Member Functions

- virtual const std::string header () const =0
- virtual const TransIndex & trans_index () const =0
- virtual const TransIndex & trans_lengths () const =0
- virtual bool next_fragment (Fragment &f)=0
- virtual void reset ()=0

3.15.1 Detailed Description

The Parser class is an abstract class that can be a SAMParser or BAMParser. It fills Fragment objects by parsing an input file in SAM/BAM format.

Author

Adam Roberts

Date

2011 Artistic License 2.0

Definition at line 33 of file mapparser.h.

3.15.2 Member Function Documentation

3.15.2.1 virtual const std::string Parser::header ( ) const `[pure virtual]`

a member function that returns a string version of the header

Returns

string version of the header

Implemented in BAMParser, and SAMParser.

3.15.2.2 virtual bool Parser::next_fragment (**Fragment & *f***) `[pure virtual]`

a member function that loads all mappings of the next fragment

Parameters

f	the empty Fragment to add mappings to

Returns

true if more reads remain in the SAM/BAM file/stream, false otherwise

Implemented in BAMParser, and SAMParser.

3.15.2.3 virtual void Parser::reset ( ) `[pure virtual]`

a member function that resets the parser and rewinds to the beginning of the input

Implemented in BAMParser.

3.15.2.4 virtual const TransIndex& Parser::trans_index ( ) const `[pure virtual]`

a member function that returns the transcript-to-index map

Returns

the transcript-to-index map

Implemented in BAMParser, and SAMParser.

3.15.2.5 virtual const TransIndex& Parser::trans_lengths ( ) const `[pure virtual]`

a member function that returns the transcript-to-length map

Returns

the transcript-to-length map

Implemented in BAMParser, and SAMParser.

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

- src/mapparser.h

3.16 ParseThreadSafety Struct Reference

```
#include <threadsafety.h>
```

Public Attributes

- Fragment ∗ next_frag
- boost::mutex mut
- boost::condition_variable cond
- bool frag_clean

3.16.1 Detailed Description

The ParseThreadSafety struct stores objects to allow for parsing to safely occur on a separate thread from processing.

Author

Adam Roberts

Date

2011 Artistic License 2.0

Definition at line 23 of file threadsafety.h.

3.16.2 Member Data Documentation

3.16.2.1 boost::condition_variable ParseThreadSafety::cond

a conditional variable where the processor waits for a new Fragment and the parser waits for the Fragment pointer to be copied by the processor

Definition at line 39 of file threadsafety.h.

3.16.2.2 bool ParseThreadSafety::frag_clean

a bool specifying the condition that the current next_frag pointer is clean, meaning that it hasn't been copied by the processor

Definition at line 45 of file threadsafety.h.

3.16.2.3 boost::mutex ParseThreadSafety::mut

a mutex for the conditional variable

Definition at line 33 of file threadsafety.h.

3.16.2.4 Fragment∗ ParseThreadSafety::next_frag

a pointer to the next Fragment to be processed by the main thread

Definition at line 28 of file threadsafety.h.

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

- src/threadsafety.h

3.17 PosWeightTable Class Reference

`#include <biascorrection.h>`

Public Member Functions

- PosWeightTable (const std::vector< size_t > &len_bins, const std::vector< double > &pos_bins, double alpha)
- const std::vector< size_t > & **len_bins** () const
- const std::vector< double > & **pos_bins** () const
- void increment_expected (size_t len, double pos)
- void increment_expected (size_t l, size_t p)
- void normalize_expected ()
- void increment_observed (size_t len, double pos, double normalized_mass)
- void increment_observed (size_t l, size_t p, double normalized_mass)
- double get_weight (size_t len, double pos) const
- double get_weight (size_t l, size_t p) const
- void append_output (std::ofstream &outfile) const

3.17.1 Detailed Description

The PosWeightTable class keeps track of fractional position bias parameters in log space. It allows for the bias associated with a given fractional position to be calculated, and for the bias parameters to be updated based on additional fragment observations.

Author

Adam Roberts

Date

2011 Artistic License 2.0

Definition at line 118 of file biascorrection.h.

3.17.2 Constructor & Destructor Documentation

3.17.2.1 PosWeightTable::PosWeightTable (const std::vector< size_t > & *len_bins*, const std::vector< double > & *pos_bins*, double *alpha*)

PosWeightTable Constructor

Parameters

len_bins	a vector of unsigned integers specifying the bin ranges for transcript lengths
pos_bins	a vector of doubles specifying the bin ranges for fractional positions
alpha	a double specifying the strength of the uniform prior (logged pseudo-counts for each parameter)

Definition at line 146 of file biascorrection.cpp.

3.17.3 Member Function Documentation

3.17.3.1 void PosWeightTable::append_output (std::ofstream & *outfile*) const

a member function that outputs the fractional position probabilities in matrix format with length bins as rows and fractional position bins as columns

Parameters

outfile	the file to append to

3.17.3.2 double PosWeightTable::get_weight (size_t *len,* double *pos*) const

a member function that return the bias weight (logged) of a fractional transcript position

Parameters

len	the transcript length
pos	the fractional transcript position

Returns

the logged bias weight for the fractional transcript position

Definition at line 182 of file biascorrection.cpp.

3.17.3.3 double PosWeightTable::get_weight (size_t *l,* size_t *p*) const

a member function that return the bias weight (logged) of a fractional transcript position bin

Parameters

l	the transcript length bin
p	the fractional transcript position bin

Returns

the logged bias weight for the fractional transcript position

Definition at line 189 of file biascorrection.cpp.

3.17.3.4 void PosWeightTable::increment_expected (size_t *l*, size_t *p*)

a member function that increments the expected counts for the given fractional position bin by 1 (logged)

Parameters

l	the transcript length bin
p	the fractional transcript position bin

Definition at line 160 of file biascorrection.cpp.

3.17.3.5 void PosWeightTable::increment_expected (size_t *len*, double *pos*)

a member function that increments the expected counts for the given fractional position by 1 (logged)

Parameters

len	the transcript length
pos	the fractional transcript position

Definition at line 153 of file biascorrection.cpp.

3.17.3.6 void PosWeightTable::increment_observed (size_t *l*, size_t *p*, double *normalized_mass*)

a member function that increments the observed counts for the given fragment position bin by some mass (logged)

Parameters

l	the transcript length bin
p	the fractional transcript position bin
normalized_-mass	the mass (logged probabilistic assignment) of the fragment normalized by its estimated expression

Definition at line 177 of file biascorrection.cpp.

3.17.3.7 void PosWeightTable::increment_observed (size_t *len*, double *pos*, double *normalized_mass*)

a member function that increments the observed counts for the given fragment position by some mass (logged)

Parameters

len	the transcript length

pos	the fractional transcript position
normalized_-mass	the mass (logged probabilistic assignment) of the fragment normalized by its estimated expression

Definition at line 170 of file biascorrection.cpp.

3.17.3.8 void PosWeightTable::normalize_expected ( )

a member function that normalizes the expected counts and converts them to the log scale

Definition at line 165 of file biascorrection.cpp.

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

- src/biascorrection.h
- src/biascorrection.cpp

3.18 RoundParams Struct Reference

```
#include <transcripts.h>
```

Public Member Functions

- RoundParams ()

Public Attributes

- double mass
- double ambig_mass
- double tot_ambig_mass
- double binom_var
- double samp_var
- double tot_unc

3.18.1 Detailed Description

The RoundParams struct stores the transcript parameters unique to a given round (iteration) of EM

Author

Adam Roberts

Date

2012 Artistic License 2.0

Definition at line 34 of file transcripts.h.

3.18.2 Constructor & Destructor Documentation

3.18.2.1 RoundParams::RoundParams ( ) `[inline]`

RoundParams constructor sets initial values for parameters

Definition at line 69 of file transcripts.h.

3.18.3 Member Data Documentation

3.18.3.1 double **RoundParams::ambig_mass**

a private double that stores the (logged) assigned mass derived from ambiguous fragments

Definition at line 44 of file transcripts.h.

3.18.3.2 double **RoundParams::binom_var**

a private double that stores the (logged) binomal variance of the mass

Definition at line 54 of file transcripts.h.

3.18.3.3 double **RoundParams::mass**

a private double that stores the (logged) assigned mass based on observed fragment mapping probabilities

Definition at line 39 of file transcripts.h.

3.18.3.4 double **RoundParams::samp_var**

a private double that stores the (logged) sampling variance of the mass

Definition at line 59 of file transcripts.h.

3.18.3.5 double **RoundParams::tot_ambig_mass**

a private double that stores the (logged) total mass of ambiguous fragments mapping to the transcript

Definition at line 49 of file transcripts.h.

3.18.3.6 double RoundParams::tot_unc

a private double that stores the (logged) variance due to uncertainty on p

Definition at line 64 of file transcripts.h.

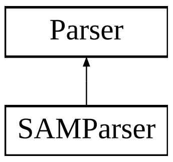
The documentation for this struct was generated from the following file:

- src/transcripts.h

3.19 SAMParser Class Reference

`#include <mapparser.h>`

Inheritance diagram for SAMParser:



Public Member Functions

- SAMParser (std::istream ∗in)
- const std::string header () const
- const TransIndex & trans_index () const
- const TransIndex & trans_lengths () const
- bool next_fragment (Fragment &f)

3.19.1 Detailed Description

The SAMParser class fills Fragment objects by parsing an input in SAM format. The input may come from a file or stdin.

Author

Adam Roberts

Date

2011 Artistic License 2.0

Definition at line 223 of file mapparser.h.

3.19.2 Constructor & Destructor Documentation

3.19.2.1 SAMParser::SAMParser (std::istream $*$ *in*)

SAMParser constructor removes the header, and parses the first line

Definition at line 350 of file mapparser.cpp.

3.19.3 Member Function Documentation

3.19.3.1 const std::string SAMParser::header ( ) const `[inline, virtual]`

a member function that returns a string version of the header

Returns

string version of the header

Implements Parser.

Definition at line 271 of file mapparser.h.

3.19.3.2 bool SAMParser::next_fragment (Fragment & *f*) `[virtual]`

a member function that loads all mappings of the next fragment when the next fragment is reached, the current alignment is left in the _frag_buff for the next call

Parameters

f	the empty Fragment to add mappings to

Returns

true if more reads remain in the SAM file, false otherwise

Implements Parser.

Definition at line 406 of file mapparser.cpp.

3.19.3.3 const TransIndex& SAMParser::trans_index ( ) const `[inline, virtual]`

a member function that returns the transcript-to-index map

Returns

the transcript-to-index map

Implements Parser.

Definition at line 277 of file mapparser.h.

3.19.3.4 const TransIndex& SAMParser::trans_lengths ( ) const `[inline, virtual]`

a member function that returns the transcript-to-length map

Returns

the transcript-to-length map

Implements Parser.

Definition at line 283 of file mapparser.h.

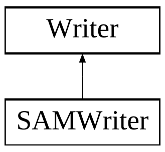
The documentation for this class was generated from the following files:

- src/mapparser.h
- src/mapparser.cpp

3.20 SAMWriter Class Reference

`#include <mapparser.h>`

Inheritance diagram for SAMWriter:



Public Member Functions

- SAMWriter (std::ostream ∗out, bool sample)
- ∼SAMWriter ()
- void write_fragment (Fragment &f)

3.20.1 Detailed Description

The SAMWriter class writes Fragment objects back to file (in SAM format) with per-mapping probabilistic assignments.

Author

Adam Roberts

Date

2011 Artistic License 2.0

Definition at line 301 of file mapparser.h.

3.20.2 Constructor & Destructor Documentation

3.20.2.1 SAMWriter::SAMWriter (std::ostream ∗ *out*, bool *sample*)

SAMWriter constructor stores a pointer to the output stream

Parameters

out	SAM output stream
sample	specifies if a single alignment should be sampled (true) or all output with their respective probabilities (false)

Definition at line 531 of file mapparser.cpp.

3.20.2.2 SAMWriter::∼SAMWriter ( )

SAMWriter destructor flushes and deletes output stream

Definition at line 535 of file mapparser.cpp.

3.20.3 Member Function Documentation

3.20.3.1 void SAMWriter::write_fragment (Fragment & *f*) `[virtual]`

a member function that writes all mappings of the fragment to the ouptut file in SAM format along with their probabilities in the "XP" field

Parameters

f	the processed Fragment to output

Implements Writer.

Definition at line 541 of file mapparser.cpp.

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

- src/mapparser.h
- src/mapparser.cpp

3.21 Sequence Class Reference

```
#include <sequence.h>
```

Public Member Functions

- Sequence ()
- Sequence (const std::string &seq, bool rev)

- Sequence (const Sequence &other)
- Sequence & operator= (const Sequence &other)
- ∼Sequence ()
- void set (const std::string &seq, bool rev)
- bool empty () const
- size_t operator[ ] (const size_t index) const
- size_t length () const

3.21.1 Detailed Description

The Sequence class is used to store and access encoded nucleotide sequences.

Author

Adam Roberts

Date

2012 Artistic License 2.0

Definition at line 20 of file sequence.h.

3.21.2 Constructor & Destructor Documentation

3.21.2.1 Sequence::Sequence ( )

dummy constructor

Definition at line 58 of file sequence.cpp.

3.21.2.2 Sequence::Sequence (const std::string & *seq*, bool *rev*)

Sequence constructor encodes and stores the given nucleotide sequence

Parameters

seq	the nucleotide sequence to encode and store
rev	a boolean if the sequence should be reverse complemented before encoding

Definition at line 60 of file sequence.cpp.

3.21.2.3 Sequence::Sequence (const Sequence & *other*)

Sequence copy constructor

Parameters

other	the Sequence object to copy

Definition at line 65 of file sequence.cpp.

3.21.2.4 Sequence::∼Sequence ( )

Sequence deconstructor. Deletes the char array.

Definition at line 88 of file sequence.cpp.

3.21.3 Member Function Documentation

3.21.3.1 bool Sequence::empty ( ) const `[inline]`

a member function that returns true iff the encoded sequence has zero length

Returns

true iff the encoded sequence has zero length

Definition at line 76 of file sequence.h.

3.21.3.2 size_t Sequence::length ( ) const `[inline]`

a member function that returns the length of the encoded sequence

Returns

the length of the encoded sequence

Definition at line 90 of file sequence.h.

3.21.3.3 Sequence & Sequence::operator= (const Sequence & *other*)

Sequence assignment constructor

Parameters

other	the Sequence object to copy

Definition at line 75 of file sequence.cpp.

3.21.3.4 size_t Sequence::operator[] (const size_t *index*) const

a member function that returns the encoded character at the given index

Parameters

index	the index of the encoded character to return (assumed to be < _len)

Returns

the encoded character at the given index

Definition at line 119 of file sequence.cpp.

3.21.3.5 void Sequence::set (const std::string & *seq*, bool *rev*)

a member function that encodes the given sequence and overwrites the current stored sequence with it

Parameters

seq	the nucleotide sequence to encode and store
rev	a boolean if the sequence should be reverse complemented before encoding

Definition at line 95 of file sequence.cpp.

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

- src/sequence.h
- src/sequence.cpp

3.22 SeqWeightTable Class Reference

```
#include <biascorrection.h>
```

Public Member Functions

- SeqWeightTable (size_t window_size, double alpha)
- void copy_observed (const SeqWeightTable &other)
- void copy_expected (const SeqWeightTable &other)
- void increment_expected (const Sequence &seq, double mass)
- void normalize_expected ()
- void increment_observed (const Sequence &seq, size_t i, double mass)
- double get_weight (const Sequence &seq, size_t i) const
- std::string to_string () const
- void append_output (std::ofstream &outfile) const

3.22.1 Detailed Description

The SeqWeightTable class keeps track of sequence-specific bias parameters. It allows for the bias associated with a given sequence to be calculated, and for the bias parameters to be updated based on additional observations. All values stored in log space.

Author

Adam Roberts

Date

2011 Artistic License 2.0

Definition at line 30 of file biascorrection.h.

3.22.2 Constructor & Destructor Documentation

3.22.2.1 SeqWeightTable::SeqWeightTable (size_t *window_size*, double *alpha*)

SeqWeightTable Constructor

Parameters

window_size	an unsigned integer specifying the size of the bias window surrounding fragment ends
alpha	a double specifying the strength of the uniform prior (logged pseudo-counts for each parameter)

Definition at line 31 of file biascorrection.cpp.

3.22.3 Member Function Documentation

3.22.3.1 void SeqWeightTable::append_output (std::ofstream & *outfile*) const

a member function that outputs the positional nucleotide probabilities in matrix format with nucleotides (A,C,G,T) as rows and window position as columns

Parameters

outfile	the file to append to

3.22.3.2 void SeqWeightTable::copy_expected (const SeqWeightTable & *other*)

a member function that overwrites the "expected" parameters with those from another SeqWeightTable

Parameters

other	another SeqWeightTable from which to copy the parameters

Definition at line 41 of file biascorrection.cpp.

3.22.3.3 void SeqWeightTable::copy_observed (const SeqWeightTable & *other*)

a member function that overwrites the "observed" parameters with those from another SeqWeightTable

Parameters

other	another SeqWeightTable from which to copy the parameters

Definition at line 36 of file biascorrection.cpp.

3.22.3.4 double SeqWeightTable::get_weight (const Sequence & *seq*, size_t *i*) const

a member function that calculates the bias weight (logged) of a bias window

Parameters

seq	the transcript sequence the fragment hits to
i	the fragment end point (the central point of the bias window)

Returns

the bias weight for the bias window which is the product of the individual nucleotide bias weights

Definition at line 63 of file biascorrection.cpp.

3.22.3.5 void SeqWeightTable::increment_expected (const Sequence & *seq*, double *mass*)

a member function that increments the expected counts for a sliding window through the given transcript sequence by some mass

Parameters

seq	the transcript sequence
mass	the amount of used to weight the transcript's sequence in the parameter table

Definition at line 46 of file biascorrection.cpp.

3.22.3.6 void SeqWeightTable::increment_observed (const Sequence & *seq*, size_t *i*, double *mass*)

a member function that increments the observed counts for the given fragment sequence by some mass (logged)

Parameters

seq	the transcript sequence (possibly reverse complemented) to which the fragment end maps
i	the index into the sequence at which to center the bias window (where the fragment starts/ends)
mass	the fragment's mass

Definition at line 57 of file biascorrection.cpp.

3.22.3.7 void SeqWeightTable::normalize_expected ( )

a member function that normalizes the expected counts and converts them to the log scale

Definition at line 51 of file biascorrection.cpp.

3.22.3.8 std::string SeqWeightTable::to_string ( ) const

a member function that returns a string containing the positional nucleotide probabilities in column-major order (A,C,G,T)

Returns

the string representation of the positional nucleotide probabilities

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

- src/biascorrection.h
- src/biascorrection.cpp

3.23 ThreadedMapParser Class Reference

```
#include <mapparser.h>
```

Public Member Functions

- ThreadedMapParser (std::string input_file, std::string output_file, bool write_-active)
- ∼ThreadedMapParser ()
- void threaded_parse (ParseThreadSafety ∗thread_safety, TranscriptTable ∗trans_-table)
- const TransIndex & trans_index ()
- const TransIndex & trans_lengths ()
- void write_active (bool b)
- void reset_reader ()

3.23.1 Detailed Description

The ThreadedMapParser class is meant to be run on as a separate thread from the main processing. Once started, this thread will read input from a file or stream in SAM/BAM format, parse, and collect read alignments into fragment alignments, and fragment alignments into fragments, which are placed on a buffer for the processing thread. Once the processing thread copies the fragment address from the buffer, the parser is unlocked to load the next fragment. The process stops when EOF is reached

Author

Adam Roberts

Date

2011 Artistic License 2.0

Definition at line 348 of file mapparser.h.

3.23.2 Constructor & Destructor Documentation

3.23.2.1 ThreadedMapParser::ThreadedMapParser (std::string *input_file*, std::string *output_file*, bool *write_active*)

ThreadedMapParser constructor determines what format the input is in and initializes the correct parser.

Parameters

input_file	string containing the path to the input SAM/BAM file
output_file	string containing the path the output file less its extension (empty if writing is to be disabled)

Definition at line 97 of file mapparser.cpp.

3.23.2.2 ThreadedMapParser::∼ThreadedMapParser ( )

ThreadedMapParser destructor deletes the parser and writer (if it exists).

Definition at line 161 of file mapparser.cpp.

3.23.3 Member Function Documentation

3.23.3.1 void ThreadedMapParser::reset_reader ( ) `[inline]`

a member function that resets the input parser

Definition at line 406 of file mapparser.h.

3.23.3.2 void ThreadedMapParser::threaded_parse (ParseThreadSafety ∗ *thread_safety*, TranscriptTable ∗ *trans_table*)

a member function that drives the parse thread when all valid mappings of a fragment have been parsed, its mapped transcripts are found and the information is passed in a Fragment object to the processing thread through the ParseThreadSafety struct

Parameters

thread_-safety	a pointer to the struct containing shared locks and data with the processing thread
trans_table	a pointer to the table of Transcript objects to lookup the mapped transcripts

Definition at line 168 of file mapparser.cpp.

3.23.3.3 const TransIndex& ThreadedMapParser::trans_index ( ) [inline]

a member function that returns the transcript-to-index map

Returns

the transcript-to-index map

Definition at line 388 of file mapparser.h.

3.23.3.4 const TransIndex& ThreadedMapParser::trans_lengths ( ) [inline]

a member function that returns the transcript-to-length map

Returns

the transcript-to-length map

Definition at line 394 of file mapparser.h.

3.23.3.5 void ThreadedMapParser::write_active (bool *b*) [inline]

a member function that sets the write-active status of the parser this specifies whether or not the alignments (sampled or with probs) sould be ouptut

Parameters

b	updated write-active status

Definition at line 401 of file mapparser.h.

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

- src/mapparser.h
- src/mapparser.cpp

3.24 Transcript Class Reference

```
#include <transcripts.h>
```

Public Member Functions

- Transcript (const size_t id, const std::string &name, const std::string &seq, double alpha, const Globals ∗globs)
- const std::string & name () const
- TransID id () const
- const Sequence & seq (bool rev) const
- size_t length () const
- double rho () const
- double mass (bool with_pseudo=true) const
- double ambig_mass () const
- double tot_ambig_mass () const
- double binom_var () const
- double samp_var () const
- double tot_uncertainty () const
- void round_reset ()
- size_t tot_counts () const
- size_t uniq_counts () const
- Bundle ∗ bundle ()
- void bundle (Bundle ∗b)
- void add_mass (double p, double v, double mass)
- void incr_counts (bool uniq, size_t incr_amt=1)
- double log_likelihood (const FragHit &frag, bool with_pseudo) const
- double est_effective_length (FLD ∗fld=NULL, bool with_bias=true) const
- double cached_effective_length (bool with_bias=true) const
- void update_transcript_bias (BiasBoss ∗bias_table=NULL, FLD ∗fld=NULL)

3.24.1 Detailed Description

The Transcript class is used to store objects for the transcripts being mapped to. Besides storing basic information about the object (id, length), it also stores a mass based on the number of fragments mapping to the object. To help with updating this number, it returns the likelihood that a given fragment originated from it. These values are stored and returned in log space.

Author

Adam Roberts

Date

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Definition at line 86 of file transcripts.h.

3.24.2 Constructor & Destructor Documentation

3.24.2.1 Transcript::Transcript (const size_t *id*, const std::string & *name*, const std::string & *seq*, double *alpha*, const Globals ∗ *globs*)

Transcript Constructor

Parameters

name	a string that stores the transcript name
seq	a string that stores the transcript sequence
alpha	a double that specifies the intial pseudo-counts (non-logged)
globs	a pointer to the struct containing pointers to the global parameter tables (bias_table, mismatch_table, fld)

Definition at line 23 of file transcripts.cpp.

3.24.3 Member Function Documentation

3.24.3.1 void Transcript::add_mass (double *p*, double *v*, double *mass*)

a member function that increases the expected fragment counts and variance by a given (logged) fragment mass

Parameters

p	a double for the (logged) probability that the fragment was generated by this transcript
v	a double for the (logged) approximate variance (uncertainty) on the probability
mass	a double specifying the (logged) mass of the fragment being mapped

Definition at line 48 of file transcripts.cpp.

3.24.3.2 double Transcript::ambig_mass ( ) const [inline]

a member function that returns the (logged) total mass derived from ambiguous fragments mapping to the transcript

Returns

the (logged) total mass derived from ambiguous fragments mapping to the transcript

Definition at line 233 of file transcripts.h.

3.24.3.3 double Transcript::binom_var ( ) const [inline]

a member function that returns the current (logged) binomial variance

Returns

logged binomial mass variance

Definition at line 245 of file transcripts.h.

3.24.3.4 void Transcript::bundle (Bundle * *b*) [inline]

a member function that set the Bundle this Transcript is a member of

Parameters

b	a pointer to the Bundle to set this Transcript as a member of

Definition at line 287 of file transcripts.h.

3.24.3.5 Bundle* Transcript::bundle ( ) [inline]

a member function that returns the Bundle this Transcript is a member of

Returns

a pointer to the Bundle this transcript is a member of

Definition at line 281 of file transcripts.h.

3.24.3.6 double Transcript::cached_effective_length (bool *with_bias* = true) const

a member function that returns the most recently estimated effective length (logged) as calculated by the bias updater thread

Returns

the cached effective length of the transcript calculated

Definition at line 146 of file transcripts.cpp.

3.24.3.7 double Transcript::est_effective_length (FLD * *fld* = NULL, bool *with_bias* = true) const

a member function that calcualtes and returns the estimated effective length of the transcript (logged) using the avg bias

Parameters

fld	an optional pointer to a different FLD than the global one, for thread-safety
with_bias	a boolean specifying whether or not the average bias should be used in the calculation

Returns

the estimated effective length of the transcript calculated as $\tilde{l} = \bar{bias} \sum_{l=1}^{L(t)} D(l)(L(t) - l + 1)$

Definition at line 123 of file transcripts.cpp.

3.24.3.8 TransID Transcript::id ( ) const [inline]

a member function that returns the transcript id

Returns

TransID transcript ID

Definition at line 203 of file transcripts.h.

3.24.3.9 void Transcript::incr_counts (bool *uniq*, size_t *incr_amt* = 1) [inline]

a member function that increases the count of fragments mapped to this transcript

Parameters

uniq	a bool specifying whether or not the fragment uniquely maps to this transcript
incr_amt	a size_t to increase the counts by

Definition at line 302 of file transcripts.h.

3.24.3.10 size_t Transcript::length ( ) const [inline]

a member function that returns the transcript length

Returns

transcript length

Definition at line 214 of file transcripts.h.

3.24.3.11 double Transcript::log_likelihood (const FragHit & *frag*, bool *with_pseudo*) const

a member function that returns (a value proportional to) the log likelihood the given fragment originated from this transcript

Parameters

frag	a FragHit to return the likelihood of being originated from this transcript
with_pseudo	a FragHit specifying whether or not pseudo-counts should be included in the calculation

Returns

(a value proportional to) the log likelihood the given fragment originated from this transcript

Definition at line 90 of file transcripts.cpp.

3.24.3.12 double Transcript::mass (bool *with_pseudo* = `true`) const

a member function that returns the current (logged) probabilistically assigned fragment mass

Parameters

with_pseudo	a boolean specifying whether pseudo-counts should be included in returned mass

Returns

logged mass

Definition at line 82 of file transcripts.cpp.

3.24.3.13 const std::string& Transcript::name ( ) const `[inline]`

a member function that returns the transcript name

Returns

string containing transcript name

Definition at line 197 of file transcripts.h.

3.24.3.14 double Transcript::rho ( ) const

a member function that returns the current estimated rho (logged, w/ pseudo-counts) for the transcript

Returns

the current estimated rho

Definition at line 73 of file transcripts.cpp.

3.24.3.15 void Transcript::round_reset ( )

a member function that readies the transcript object for the next round of batch EM

Definition at line 66 of file transcripts.cpp.

3.24.3.16 double Transcript::samp_var ( ) const [inline]

a member function that returns the (logged) sampling variance

Returns

the (logged) sampling variance

Definition at line 251 of file transcripts.h.

3.24.3.17 const Sequence& Transcript::seq (bool *rev*) const [inline]

a member function that returns the transcript sequence

Returns

string containing transcript sequence

Definition at line 208 of file transcripts.h.

3.24.3.18 double Transcript::tot_ambig_mass ( ) const [inline]

a member function that returns the (logged) total mass of ambiguous fragments mapping to the transcript

Returns

the (logged) total mass of ambiguous fragments mapping to the transcript

Definition at line 239 of file transcripts.h.

3.24.3.19 size_t Transcript::tot_counts ( ) const [inline]

a member function that returns the current count of fragments mapped to this transcript (uniquely or ambiguously)

Returns

total fragment count

Definition at line 269 of file transcripts.h.

3.24.3.20 double Transcript::tot_uncertainty ( ) const [inline]

a member function that returns the (logged) variance due to uncertainty on p

Returns

the (logged) variance due to uncertainty on p

Definition at line 258 of file transcripts.h.

3.24.3.21 size_t Transcript::uniq_counts ( ) const `[inline]`

a member function that returns the current count of fragments uniquely mapped to this transcript

Returns

unique fragment count

Definition at line 275 of file transcripts.h.

3.24.3.22 void Transcript::update_transcript_bias (BiasBoss ∗ *bias_table* = `NULL`, FLD ∗ *fld* = `NULL`)

a member function that causes the transcript bias to be re-calculated by the _bias_table based on curent parameters

Parameters

bias_table	an optional pointer to a different BiasBoss than the global one, for thread-safety
fld	an optional pointer to a different FLD than the global one, for thread-safety

Definition at line 155 of file transcripts.cpp.

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

- src/transcripts.h
- src/transcripts.cpp

3.25 TranscriptTable Class Reference

```
#include <transcripts.h>
```

Public Member Functions

- TranscriptTable (const std::string &trans_fasta_file, const TransIndex &trans_-index, const TransIndex &trans_lengths, double alpha, const AlphaMap ∗alpha_-map, Globals ∗globs)
- ∼TranscriptTable ()
- Transcript ∗ get_trans (TransID id)
- void round_reset ()
- size_t size () const
- double total_fpb () const
- void update_total_fpb (double incr_amt)
- void update_covar (TransID trans1, TransID trans2, double covar)
- double get_covar (TransID trans1, TransID trans2)

- size_t covar_size () const
- Bundle ∗ merge_bundles (Bundle ∗b1, Bundle ∗b2)
- size_t num_bundles ()
- void output_results (std::string output_dir, size_t tot_counts, bool output_varcov)
- void threaded_bias_update (boost::mutex ∗mut)

3.25.1 Detailed Description

The TranscriptTable class is used to keep track of the Transcript objects for a run. The constructor parses a fasta file to generate the Transcript objects and store them in a map that allows them to be looked up based on their string id.

Author

Adam Roberts

Date

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Definition at line 353 of file transcripts.h.

3.25.2 Constructor & Destructor Documentation

3.25.2.1 TranscriptTable::TranscriptTable (const std::string & *trans_fasta_file*, const TransIndex & *trans_index*, const TransIndex & *trans_lengths*, double *alpha*, const AlphaMap ∗ *alpha_map*, Globals ∗ *globs*)

TranscriptTable Constructor

Parameters

trans_fasta_file	a string storing the path to the fasta file from which to load transcripts
trans_index	the transcript-to-index map from the alignment file
trans_lengths	the transcript-to-length map from the alignment file
alpha	a double that specifies the intial pseudo-counts for each bp of the transcripts (non-logged)
alpha_map	an optional pointer to a map object that specifies proportional weights of pseudo-counts for each transcript
globs	a pointer to the struct containing pointers to the global parameter tables (bias_table, mismatch_table, fld)

Definition at line 176 of file transcripts.cpp.

3.25.2.2 TranscriptTable::∼TranscriptTable ( )

TranscriptTable Destructor deletes all of the transcript objects in the table

Definition at line 265 of file transcripts.cpp.

3.25.3 Member Function Documentation

3.25.3.1 size_t TranscriptTable::covar_size ( ) const `[inline]`

a member function that returns the number of pairs of transcripts with non-zero covariance

Returns

the number of transcript pairs with non-zero covariance

Definition at line 466 of file transcripts.h.

3.25.3.2 double TranscriptTable::get_covar (TransID *trans1*, TransID *trans2*) `[inline]`

a member function that returns the covariance between two transcripts these returned value will be the log of the negative of the true value

Parameters

trans1	one of the transcripts in the pair
trans2	the other transcript in the pair

Returns

the negative of the pair's covariance (logged)

Definition at line 460 of file transcripts.h.

3.25.3.3 Transcript ∗ TranscriptTable::get_trans (TransID *id*)

a member function that returns a pointer to the transcript with the given id

Parameters

id	of the transcript queried

Returns

pointer to the transcript wit the given id

Definition at line 295 of file transcripts.cpp.

3.25.3.4 Bundle ∗ TranscriptTable::merge_bundles (Bundle ∗ *b1*, Bundle ∗ *b2*)

a member function that merges the given Bundles

Parameters

b1	a pointer to the first Bundle to merge
b2	a pointer to the second Bundle to merge

Returns

a pointer to the merged Bundle

Definition at line 300 of file transcripts.cpp.

3.25.3.5 size_t TranscriptTable::num_bundles ( )

a member function that returns the number of bundles in the partition

Returns

the number of bundles in the partition

Definition at line 309 of file transcripts.cpp.

3.25.3.6 void TranscriptTable::output_results (std::string *output_dir*, size_t *tot_counts*, bool *output_varcov*)

a member function that outputs the final expression data in a file called 'results.xprs' and (optionally) the variance-covariance matrix in 'varcov.xprs' in the given output directory

Parameters

output_dir	the directory to output the expression file to
tot_counts	the total number of observed mapped fragments
output_-varcov	boolean specifying whether to also output the variance-covariance matrix

Definition at line 379 of file transcripts.cpp.

3.25.3.7 void TranscriptTable::round_reset ( )

a member function that readies all Transcript objects in the table for the next round of batch EM

Definition at line 314 of file transcripts.cpp.

3.25.3.8 size_t TranscriptTable::size ( ) const [inline]

a member function that returns the number of transcripts in the table

Returns

number of transcripts in the table

Definition at line 430 of file transcripts.h.

3.25.3.9 void TranscriptTable::threaded_bias_update (boost::mutex * *mut*)

a member function for driving a thread that continuously updates the transcript bias values

Definition at line 549 of file transcripts.cpp.

3.25.3.10 double TranscriptTable::total_fpb ( ) const

a member function that returns the (logged) total mass per base (including pseudo-counts)

Returns

the (logged) total mass per base (including pseudo-counts)

Definition at line 537 of file transcripts.cpp.

3.25.3.11 void TranscriptTable::update_covar (TransID *trans1*, TransID *trans2*, double *covar*) [inline]

a member function that increases the covariance between two transcripts by the specified amount these values are stored positive even though they are negative (logged)

Parameters

trans1	one of the transcripts in the pair
trans2	the other transcript in the pair
covar	a double specifying the amount to increase the pair's covariance by (logged)

Definition at line 451 of file transcripts.h.

3.25.3.12 void TranscriptTable::update_total_fpb (double *incr_amt*)

a member function that increments the (logged) total mass per base

Parameters

incr_amt	the (logged) amount to increment by

Definition at line 543 of file transcripts.cpp.

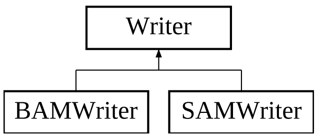
The documentation for this class was generated from the following files:

- src/transcripts.h
- src/transcripts.cpp

3.26 Writer Class Reference

`#include <mapparser.h>`

Inheritance diagram for Writer:



Public Member Functions

- virtual void write_fragment (Fragment &f)=0

3.26.1 Detailed Description

The Writer class is an abstract class than can be a SAMWriter or BAMWriter. It writes Fragment objects back to file (in SAM/BAM format) with per-mapping probabilistic assignments.

Author

Adam Roberts

Date

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Definition at line 76 of file mapparser.h.

3.26.2 Member Function Documentation

3.26.2.1 virtual void Writer::write_fragment (**Fragment & *f***) `[pure virtual]`

a member function that writes all mappings of the fragment to the ouptut file along with their probabilities in the "XP" field

Parameters

f	the processed Fragment to output

Implemented in BAMWriter, and SAMWriter.

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

- src/mapparser.h

Index