seqpp Reference Manual

4.0.0

Generated by Doxygen 1.3.9.1

Sun Apr 3 14:16:10 2005

Contents

Chapter 1

Welcome to seq++

The seq++ package offers

- a C++ object-oriented **Library**(p. 93) for developers
- a reference set of **Programs**(p. 94) for biologists working on sequences and statistics

seq++ modularity enables the study of genomic data at abstract levels, as well as any biological process which can be seen as a succession of states taken in a finite ensemble:

The genericity of seq++ is ensured by the possibility of storing and working with **any kind of sequence** based on any alphabet (DNA, proteins, codons, others...).

seq++ enables sequences modeling with **Markov, Variable Length Markov and newly developped Parsimonious Markov** models and **Mixture Transition Distributions** models. All these models can be phased.

Simulation modules are implemented so that developers can perform Monte Carlo methods.

- see section **Library**(p. 93) to use the library for your developments.
- see section **Programs**(p. 94) to use estimation and simulation programs.
- see section **References**(p. 101) for information on mathematical background.
- see section **Download and Installation**(p. 99) for operating instructions.
- see section **Bug and Feedback**(p. 97) for your comments on seq++.
- see section **What's new**(p. 96) and **ToDo**(p. 98) for updated releases.
- see section **Licence**(p. 100).

Contact: Vincent Miele `name@genopole.cnrs.fr` [anti-spam: please replace "name" by the corresponding name "miele"]

Chapter 2

seqpp Hierarchical Index

2.1 seqpp Class Hierarchy

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

Chapter 3

seqpp Class Index

3.1 seqpp Class List

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

Chapter 4

seqpp File Index

4.1 seqpp File List

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

Chapter 5

seqpp Page Index

5.1 seqpp Related Pages

Here is a list of all related documentation pages:

Chapter 6

seqpp Class Documentation

6.1 Coder Class Reference

Coded abstract representation of a word.

`#include <Coder.h>`

Public Member Functions

- **Coder** (short order, short size)

  constructor with the markovian order+1 == length of words and the size of the alphabet

- **Coder** (short order, short size, long first_code, short sizeword)
- **Coder** ()

  empty constructor

- **Coder** (const **Coder** &c)

  copy constructor

- ∼**Coder** ()

  destructor

- void **init** (long code, short sizeword)

  intial code is an initial word of size sizeword

- void **init** (long code)

  intial code is an initial word. The size sizeword is computed.

- void **init** (const vector< short > &X)

  initial by coding the word X, using only the last _order+1

- void **init** (const short ∗X)

  initial by coding the word "X(-_order)...X(-1)X(0)"

- void **restrict_init** (const short ∗X, short pseudo_order) *initial by coding the word "X(-pseudo_order)...X(1)X(0)"*

- void **clear** ()

  put code down to -1

- void **push_back** (short i)

  add a letter at the end of the coded-word

- long **virtual_push_back** (short i) const

  return the code obtained by adding a letter at the end of the coded-word but don't touch _code

- void **push_front** (short i)

  add a letter at the beginning of the coded-word

- long **virtual_push_front** (short i) const

  return the code obtained by adding a letter at the beginning of the coded-word but don't touch _code

- void **erase_back** ()

  erase the last letter

- short **pop_back** ()

  erase the last letter of the coded-word and return it

- void **erase_front** ()

  erase the first letter of the coded-word

- short **pop_front** ()

  erase the first letter and return it

- bool **empty** () const

  checks if coder is empty (no word coded)

- short **length** () const

  length of the current coded word

- long **tell_nbvalue** () const

  return nb of possible codes == words from a singleton to a order+1-word

- long **tell_jump** (short i) const

  return the ith jump to codes of word of i (and more than i) letters

- long **tell_jump** () const

  return the ith jump to codes of word of _order+1 letters

- long ∗ **get_jump** () const

  allows a const access to the vector jump

- vector< long > & **list_suffixed** (short sizeprefix)

  returns the vector of the code of words suffixed by the current _code with prefixes of size sizeprefix

- vector< long > & **list_suffixed** ()

  returns the vector of the code of words suffixed by the current _code with prefixes adapted to (_order+1)-words

- vector< long > & **bound_prefixed** (short sizesuffix)

  returns in a vect the 2 bound-codes between them all (including both of them) codes are prefixed by the current _code with suffixes of size sizesuffix

- vector< long > & **bound_prefixed** ()

  returns in a vect the 2 bound-codes between them all (including both of them) codes are prefixed by the current _code with suffixes adapted to (_order+1)-words

Public Attributes

- long **_code**

  code

- short **_sizeword**

  size of the coded word

6.1.1 Detailed Description

Coded abstract representation of a word.

Management of a code related to a word

6.1.2 Constructor & Destructor Documentation

6.1.2.1 Coder::Coder (short *order*, short *size*, long *first_code*, short *sizeword*)

constructor with the markovian order+1 == length of words and the size of the alphabet first_-code is an initial word of size sizeword

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

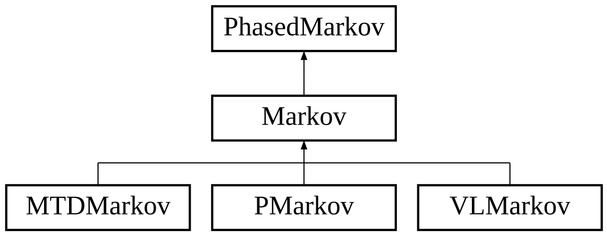
- **Coder.h**
- Coder.cc

6.2 Markov Class Reference

Markov modelling, estimation and simulation.

`#include <seqpp/Markov.h>`

Inheritance diagram for Markov::



Public Member Functions

- **Markov** (const char ∗ConfFile, bool calc_rank=false)

  Constructor 1 : read a configuration file.

- **Markov** (const **SequenceSet** &seqset, bool calc_rank=false)

  Constructor 2 : Estimate the transition matrices on the sequences of seqset.

- **Markov** (const **Sequence** &seq, bool calc_rank=false)

  Constructor 3 : Estimate the transition matrices on the sequence seq.

- **Markov** (const **Markov** &)

  Constructor 4 : Copy constructor.

- **Markov** ()

  Constructor 5 : Default constructor.

- **Markov** (short size, short order)

  Constructor 6 : Minimal Constructor.

- **Markov** (const **Markov** &M1, const **Markov** &M2, const float p)

  Constructor 7 : Creation of a "mixed" Markov chain M = p∗M1 + (1-p)∗M2 ∗/.

- **Markov** (const gsl_rng ∗r, short size, short order, bool calc_rank=false)

  Constructor 8 : random markov matrices.

- **Markov** (unsigned long ∗count, short size, short order, bool calc_rank=false)

  Constructor 9 : Estimate the transition matrices on a word-count.

- virtual ∼**Markov** ()

  Destructor.

- template<class TSeq> void **estimate** (const TSeq &tseq, unsigned long beg, unsigned long end, bool calc_rank)

Estimate the transition matrices on the sequence/sequenceset tseq.

- const double ∗ **markov_matrix** () const

  access to the markov matrix

- void **draw_markov_matrix** (const gsl_rng ∗r)

  draw at random the markov matrix

- void **free_markov_matrix** ()

  free the memory allocated for markov matrix

- void **compute_stat_law** (bool force)

  Compute the stationnary laws.

- void **free_stat_law** ()

  free the memory allocated for stationnary law

- const double ∗ **stat_law** () const

  access to the stationnary distrib

- virtual int **compute_rank** ()

  Computes the rank of convergence of the Markov Chain.

- void **compute_power** ()

  Initialisation the _rank powers of the markov matrix.

- int **free_power** ()

  free the memory allocated for the power

- double **proba_step** (long w1, long w2, int step)

  transition from word w1 to word w2 in step steps

- bool **isPi** () const
- bool **isPow** () const
- bool **isMu** () const
- double & **operator()** (int i)

  () operator for Markov matrix Pi elements

- double **Mu** (int i) const

  Access to stationnary vector Mu elements.

Protected Attributes

- double ∗ **_Pi**

  "Matrix" (in a vector format) of transition probabilities (=_Pis[0])

- double ∗ **_Mu**

  Vector of stationnary probabilities (=_Mus[0]).

- double *** **_PowPi**

  Power of the _Pi matrix.

6.2.1 Detailed Description

Markov modelling, estimation and simulation.

This is a special case of a phased Markov [**PhasedMarkov**(p. 24)] model when only one phase is considered.

6.2.2 Constructor & Destructor Documentation

6.2.2.1 Markov::Markov (const SequenceSet & *seqset*, bool *calc_rank* = `false`)

Constructor 2 : Estimate the transition matrices on the sequences of seqset.

Parameters:

seqset set of sequences for estimation

calc_rank calculus of the convergence rank if true

6.2.2.2 Markov::Markov (const Sequence & *seq*, bool *calc_rank* = `false`)

Constructor 3 : Estimate the transition matrices on the sequence seq.

Parameters:

seq sequence for estimation

calc_rank calculus of the convergence rank if true

6.2.2.3 Markov::Markov (short *size*, short *order*) `[inline]`

Constructor 6 : Minimal Constructor.

Initialises the constants of the model but not the matrix nor the stat law

Parameters:

size alphabet size

order markovian order

6.2.2.4 Markov::Markov (const Markov & *M1*, const Markov & *M2*, const float *p*)

Constructor 7 : Creation of a "mixed" Markov chain M = p*M1 + (1-p)*M2 */.

Parameters:

M1 first Markov chain object

M2 second Markov chain object

p weight of M1 in the resulting M(with 0<=p<=1)

6.2.2.5 Markov::Markov (const gsl_rng ∗ *r*, short *size*, short *order*, bool *calc_rank* = false) [inline]

Constructor 8 : random markov matrices.

Parameters:

r gsl random generator

size alphabet size

order markovian order

calc_rank calculus of the convergence rank if true

GSL use exple:

```
const gsl_rng_type * T;
// Choice a default generator and seed
// from environment variables
gsl_rng_env_setup();
// New created instance of the generator
T = gsl_rng_default;
gsl_rng * r = gsl_rng_alloc (T);
// Initialize/Seeds the random number generator
gsl_rng_set( r, (long)(time( NULL )) );
```

6.2.2.6 Markov::Markov (unsigned long ∗ *count*, short *size*, short *order*, bool *calc_rank* = false)

Constructor 9 : Estimate the transition matrices on a word-count.

Parameters:

count count of all the coded word(base size) of size order+1 for estimation

size alphabet size

order markovian order

calc_rank calculus of the convergence rank if true

6.2.3 Member Function Documentation

6.2.3.1 void Markov::draw_markov_matrix (const gsl_rng ∗ *r*) [inline]

draw at random the markov matrix

Parameters:

r gsl random generator

GSL use exple:

```
const gsl_rng_type * T;
// Choice a default generator and seed
// from environment variables
gsl_rng_env_setup();
// New created instance of the generator
T = gsl_rng_default;
gsl_rng * r = gsl_rng_alloc (T);
// Initialize/Seeds the random number generator
gsl_rng_set( r, (long)(time( NULL )) );
...
...
gsl_rng_free( r );
```

6.2.3.2 template<class TSeq> void Markov::estimate (const TSeq & *tseq*, unsigned long *beg*, unsigned long *end*, bool *calc_ rank*) `[inline]`

Estimate the transition matrices on the sequence/sequenceset tseq.

Parameters:

tseq sequence/sequenceset for estimation

beg begin position in sequence(s) if subsequences

end end position in sequence(s) if subsequences

calc_ rank calculus of the convergence rank if true

6.2.3.3 bool Markov::isMu () const `[inline]`

_Mu == NULL ?

6.2.3.4 bool Markov::isPi () const `[inline]`

_Pi == NULL ?

6.2.3.5 bool Markov::isPow () const `[inline]`

_PowPi == NULL ?

6.2.3.6 double Markov::Mu (int *i*) const `[inline]`

Access to stationnary vector Mu elements.

Parameters:

i index of the word

6.2.3.7 double& Markov::operator() (int *i*) `[inline]`

() operator for Markov matrix Pi elements

Parameters:

i index of the word

6.2.3.8 double Markov::proba_step (long *w1*, long *w2*, int *step*) `[inline]`

transition from word w1 to word w2 in step steps

if step > _rank, give stat_law(w2). You must have w1-jump, w2-jump < _nMu

Parameters:

w1 first word (of length order) as a Sequence-coded-like integer (see **Sequence**(p. 59))

w2 second word (of length order) as a Sequence-coded-like integer (see **Sequence**(p. 59))

step number of steps between w1 and w2

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

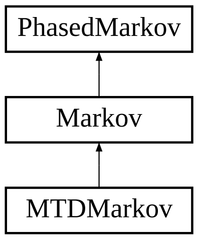
- **Markov.h**
- Markov.cc

6.3 MTDMarkov Class Reference

Mixture Transition Distribution **Markov**(p. 14) modelling, estimation and simulation.

`#include <seqpp/MTDMarkov.h>`

Inheritance diagram for MTDMarkov::



Public Member Functions

- template<class TSeq> **MTDMarkov** (const TSeq &tseq, short mkv_order, short nbseed=NBSEED, int nbiter_max=NBITERMAX, double eps=EPS, bool log=false)

  Constructor 1 from a **SequenceSet**(p. 62) *or a* **Sequence**(p. 59).

- **MTDMarkov** (unsigned long **count, short size, short mtd_order, short mkv_order, short nbseed=NBSEED, int nbiter_max=NBITERMAX, double eps=EPS, bool log=false)

  Constructor 2 from a coded-word count.

- void **estimate** (unsigned long **count, bool decal_required, short mkv_order, short nbseed, int nbiter_max, double eps, bool log)

  performs the estimation [used by each constructor]

- ~**MTDMarkov** ()

  Destructor.

Protected Attributes

- mtd_core * **_mtdcore**

  Parcimonious Context Trees.

6.3.1 Detailed Description

Mixture Transition Distribution **Markov**(p. 14) modelling, estimation and simulation.

MTDMarkov is a **Markov**(p. 14) object with a different estimation step. This object performs the estimation with the Mixture Transition Distribution algorithm and then transfoms, once per phase, the MTD model in a markovian matrix.

6.3.2 Constructor & Destructor Documentation

6.3.2.1 template<class TSeq> MTDMarkov::MTDMarkov (const TSeq & *tseq*, short *mkv_order*, short *nbseed* = `NBSEED`, int *nbiter_max* = `NBITERMAX`, double *eps* = `EPS`, bool *log* = `false`) `[inline]`

Constructor 1 from a **SequenceSet**(p. 62) or a **Sequence**(p. 59).

Parameters:

tseq a set of sequences or a sequence for estimation

mkv_order markovian order on the markovian matrix of the MTD

nbseed number of seeds for the EM algorithm

nbiter_max maximum iterations number of the EM algorithm

eps value of the epsilon of the EM algorithm

log true to log the successive likelihood values

6.3.2.2 MTDMarkov::MTDMarkov (unsigned long ** *count*, short *size*, short *mtd_order*, short *mkv_order*, short *nbseed* = `NBSEED`, int *nbiter_max* = `NBITERMAX`, double *eps* = `EPS`, bool *log* = `false`) `[inline]`

Constructor 2 from a coded-word count.

Parameters:

count count of all the coded word(base size) of size order+1 for each phase, for estimation

size alphabet size

mtd_order markovian order for the resulting model

mkv_order markovian order on the markovian matrices used in the MTD

nbseed number of seeds for the EM algorithm

nbiter_max maximum iterations number of the EM algorithm

eps value of the epsilon of the EM algorithm

log true to log the successive likelihood values

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

- **MTDMarkov.h**

6.4 Partition Class Reference

Dealer of alphabet partitions.

`#include <seqpp/Partition.h>`

Public Member Functions

- **Partition** (short alphabet_size)

  constructor with integrated creation of the set of partitions
- **Partition** (const **Translator** &alphabet, const string &pfile)

  Constructor from a file containing the partitions or the list of synonymous tokens.
- virtual ~**Partition** ()

  destructor
- const vector< vector< short > > & **list_possible_elements** ()

  initialize the list_possible_ elements of possible tokens'subset in a partition and return it
- long **tell_nbposs** () const

  returns the number of possible tokens'subset in a partition
- const vector< vector< short > > & **get_synonymous** () const

  returns the synonymous list
- short **tell_size** () const

  returns the size of the space to partition

6.4.1 Detailed Description

Dealer of alphabet partitions.

Let a partition of an alphabet be a set of tokens'subset, i.e. a division of the alphabet into subset. The Partition object gives 2 possibilities:

- to compute the overall set of possible partitions (automatically generated) given the alphabet
- to compute the overall set of possible partitions (automatically generated) given a synonymous pseud-alphabet: by declaring synonymous tokens, it is possible to group tokens as a single predictor so that the number of partitions is lower.

  In this case, a configuration file with the top key word "#Synonymous", containing the lists of synonymous tokens, is required.

  Exple:

  ```
  #Synonymous
  a t
  g c
  ```

- to input a selected set of partitions. In this case, in a configuration file after a "#Partition" on the first line, each partition is represented as a list of tokens'subset delimited by a "|", each subset being composed with tokens of the alphabet separed by space

  Exple:

  ```
  #Partition
  a | g | c | t
  a g | c | t
  a c t | g
  ```

6.4.2 Constructor & Destructor Documentation

6.4.2.1 Partition::Partition (short *alphabet_size*)

constructor with integrated creation of the set of partitions

Parameters:

alphabet_size size of the alphabet

6.4.2.2 Partition::Partition (const Translator & *alphabet*, const string & *pfile*)

Constructor from a file containing the partitions or the list of synonymous tokens.

Parameters:

alphabet a link to a **Translator**(p. 64) object required for the file reading

pfile partitions file

-> 1st possibility: after a "#Partition" on the first line, each partition is represented as a list of tokens'subset delimited by a "|", each subset being composed with tokens of the alphabet separed by space

Example:

```
#Partition
a g | c t
```

-> 2nd possibility: after a "#Synonymous" on the first line, tokens are grouped (separed by spaces) into synonymous classes on each line

Example:

```
#Synonymous
a t
g c
```

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

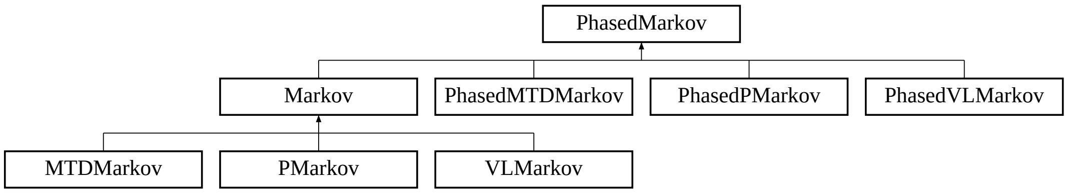
- **Partition.h**
- Partition.cc

6.5 PhasedMarkov Class Reference

Phased **Markov**(p. 14) modelling, estimation and simulation.

`#include <seqpp/PhasedMarkov.h>`

Inheritance diagram for PhasedMarkov::



Public Member Functions

- **PhasedMarkov** (const string &markov_file, bool calc_rank=false)

  Constructor 1 : read a configuration file.

- **PhasedMarkov** (const **SequenceSet** &seqset, short phase, short initial_phase=0, bool calc_rank=false)

  Constructor 2 : Estimate the transition matrices on the sequences of seqset.

- **PhasedMarkov** (const **Sequence** &seq, short phase, short initial_phase=0, bool calc_-rank=false)

  Constructor 3 : Estimate the transition matrices on the sequence seq.

- **PhasedMarkov** (const **PhasedMarkov** &phm)

  Constructor 4 : Copy constructor.

- **PhasedMarkov** ()

  Constructor 5 : Default constructor.

- **PhasedMarkov** (short size, short order, short phase)

  Constructor 6 : Minimal Constructor.

- **PhasedMarkov** (const **PhasedMarkov** &M1, const **PhasedMarkov** &M2, const float p)

  Constructor 7 : Creation of a "mixed" **Markov**(p. 14) *chain M = p*M1 + (1-p)*M2 */.*

- **PhasedMarkov** (const **SequenceSet** &seqset, const vector< int > &Indseq, short phase, short initial_phase=0, bool calc_rank=false)

  Constructor 8 : Estimation of the transition matrix based on the sequences of seqset given in Indseq.

- **PhasedMarkov** (const gsl_rng *r, short size, short order, short phase, bool calc_-rank=false)

  Constructor 9 : random markov matrices.

- **PhasedMarkov** (unsigned long ∗∗count, short size, short order, short phase, short initial_-phase=0, bool calc_rank=false)

  Constructor 10 Estimate the transition matrices on a word-count.

- virtual ∼**PhasedMarkov** ()

  Destructor.

- template<class TSeq> void **estimate** (const TSeq &tseq, short phase, short initial_phase, unsigned long beg, unsigned long end, bool calc_rank=false, bool count_again=true)

  Estimate the transition matrices on the sequence/sequenceset tseq.

- const double ∗∗ **markov_matrices** () const

  access to the markov matrix(ces)

- const double ∗ **markov_matrix** (short numphase) const

  access to the numphase-th markov matrix

- void **draw_markov_matrices** (const gsl_rng ∗r)

  draw at random the markov matrices

- void **free_markov_matrices** ()

  free the memory allocated for markov matrices

- double **total_variation** (const **PhasedMarkov** &M)

  Total variation distance between ∗this and M.

- void **compute_stat_laws** (bool force=false)

  Compute the stationnary laws.

- const double ∗ **stat_law** (short numphase=0) const

  access to the stationnary distrib in phase numphase

- void **free_stat_laws** ()

  free the memory allocated for stationnary laws

- void **compute_init_law** (double ∗MuInit, const **SequenceSet** &seqset) const

  Get the empirical relative frequency of the first order+1 letters on the set of sequences "seqset".

- virtual int **compute_rank** ()

  Computes the rank of convergence of the **Markov**(p. 14) *Chain.*

- virtual long **nb_parameters** () const

  return the number of effective parameters

- void **link_to_translator** (const **Translator** &trans)

  link to a **Translator**(p. 64) *object to use proba methods with strings*

- double **proba_c** (const string &word, **Coder** &coder, short numphase=0) const

  Stationnary proba of a word(size greater than _order) conditionnaly of its first letters (!use link_to_translator before!).

- double **proba** (const string &word, **Coder** &coder, short numphase=0) const

  Stationnary proba of a word.

- double **proba_c** (const vector< short > &word, **Coder** &coder, short numphase=0) const

  Stationnary proba of a word(size greater than _order) conditionnaly of its first letters.

- double **proba** (const vector< short > &word, **Coder** &coder, short numphase=0) const

  Stationnary proba of a word.

- double **proba_c** (long word, int lw=-1, long jump=-1, short numphase=0) const

  Stationnary proba of a word(size greater than _order) conditionnaly of its first letters.

- double **proba** (long word, int lw=-1, long jump=-1, short numphase=0) const

  Stationnary proba of a word.

- double **proba_c** (const long ∗seq, long tbeg, long tend, short numphase=0) const

  Stationnary proba of the word seq[tbeg...tend](size greater than _order) conditionnaly of its first letters.

- double **proba** (const long ∗seq, long tbeg, long tend, short numphase=0) const

  Stationnary proba of the word seq[tbeg...tend].

- double **log_likelihood** (const **SequenceSet** &seqset, short initial_phase=0, short numphase=-1) const

  loglikelihood of a set of sequence

- double **log_ratio_likelihood** (const **SequenceSet** &seqset, const **PhasedMarkov** &M, short initial_phase1=0, short initial_phase2=0) const

  Calculation of the logarithm of the ratio of the probability of observing "seq" under "this" distribution and "M".

- double **log_likelihood** (const **Sequence** &seq, short initial_phase=0, short numphase=-1) const

  loglikelihood of a sequence

- double **log_ratio_likelihood** (const **Sequence** &seq, const **PhasedMarkov** &M, short initial_phase1=0, short initial_phase2=0) const

  Calculation of the logarithm of the ratio of the probability of observing "seq" under "this" distribution and "M".

- template<class TSeq> double **BIC** (const TSeq &tseq, short initial_phase=0) const

  BIC of sequences (BIC = -2∗loglikelihood + nbparam∗log(length)).

- template<class TSeq> double **AIC** (const TSeq &tseq, short initial_phase=0) const

  AIC of a set of sequences (AIC = -2∗loglikelihood + 2∗nbparam).

- void **print** (const string &FileOut)

  Print a summary of the object.

- void **print** (ofstream &Out) const

Print a summary of the object.

- int **tell_size** () const

  Returns the alphabet size.

- int **tell_rank** () const

  Returns the convergence rank.

- int **tell_order** () const

  Returns the order.

- int **tell_phase** () const

  Returns the phase.

- int **nMu** () const

  size of the stat law vector

- int **nPi** () const

  size of the matrix

- double **Pi** (int i, int p=0) const

  Access to **Markov**(p. 14) *matrix Pi.*

- double & **operator()** (int i, int p=0)

  () operator for **Markov**(p. 14) *matrix Pi elements*

- double **Mu** (int i, int p=0) const

  Access to stationnary vector Mu elements.

- bool **isPis** () const

  _Pis != NULL ?

- bool **isMus** () const

  _Mus != NULL ?

- short **nextPhase** (short p) const

  Give the phase following p.

- short **prevPhase** (short p) const

  Give the phase preceding p.

- bool **Stochasticity** ()

  Verify stochasticity of the _Pis[] and eventually rescale it.

Protected Member Functions

- bool **isNextPhase** () const

  _nextPhase != NULL ?

- bool **isPrevPhase** () const

  _prevPhase != NULL ?

Protected Attributes

- short **_phase**

  Phase of the model.

- double ** **_Pis**

  "Matrices" (in vector format) of transition probabilities for each phase

- double ** **_Mus**

  Vector of stationnary probabilities for each phase.

- short **_size**

  Size of the alphabet.

- short **_order**

  Order of the model (the same at each phase).

- long **_nPi**

  Dim of Pi :_size^(_order+1).

- long **_nMu**

  Dim of Mu :_size^_order.

- long **_nb_param**

  number of effective parameters

- int **_rank**

  How many steps to converge to Mu ?

- long **_jump**

  jump to the codes of _order+1 letters when Sequence-like code

- short * **_nextPhase**

  (Optimization) For each phase, give the next phase

- short * **_prevPhase**

  (Optimization) For each phase, give the previous phase

- const **Translator** * **_trans**

  link to a translator object for the use of proba methods

6.5.1 Detailed Description

Phased **Markov**(p. 14) modelling, estimation and simulation.

This is generalization of a **Markov**(p. 14) chain, using different matrices in function of the considered position in the sequence. The phase is variable.

For example, if we consider 3 phases, and we note respectively Pi1, Pi2 and Pi3, the three transition matrices, the **Markov**(p. 14) sequences will be generated by the indices 123123123123... In a DNA modelisation (genomic field), this is useful to take into account the fact that a coding region is read by 3 bases-blocks. The order of the **Markov**(p. 14) Model, i.e. the number of previous states necessary to determine the distribution of the current state, is variable. It is assume here that this order is the same in all the phases.

Methods are implemented for Markovian transition matrix estimation, stationary distribution calculus, word probabilities, total variation distance between two Markovian matrices, and further. The efficiency of eigenproblems computation is ensured by the use of the implicitly restarted Arnoldi algorithm.

Simulations are also possible.

6.5.2 Constructor & Destructor Documentation

6.5.2.1 PhasedMarkov::PhasedMarkov (const SequenceSet & *seqset*, short *phase*, short *initial_phase* = `0`, bool *calc_rank* = `false`)

Constructor 2 : Estimate the transition matrices on the sequences of seqset.

Parameters:

seqset set of sequences for estimation

phase selected phase

initial_phase phase of the first element of each sequence

calc_rank calculus of the convergence rank if true

6.5.2.2 PhasedMarkov::PhasedMarkov (const Sequence & *seq*, short *phase*, short *initial_phase* = `0`, bool *calc_rank* = `false`)

Constructor 3 : Estimate the transition matrices on the sequence seq.

Parameters:

seq sequence for estimation

phase selected phase

initial_phase phase of the first element of each sequence

calc_rank calculus of the convergence rank if true

6.5.2.3 PhasedMarkov::PhasedMarkov (short *size*, short *order*, short *phase*)

Constructor 6 : Minimal Constructor.

Initialises the constants of the model but not the matrices nor the stat laws

Parameters:

size alphabet size

order markovian order

phase selected phase

6.5.2.4 PhasedMarkov::PhasedMarkov (const PhasedMarkov & *M1*, const PhasedMarkov & *M2*, const float *p*)

Constructor 7 : Creation of a "mixed" **Markov**(p. 14) chain M = p∗M1 + (1-p)∗M2 ∗/.

Parameters:

M1 first **Markov**(p. 14) chain object

M2 second **Markov**(p. 14) chain object

p weight of M1 in the resulting M(with 0<=p<=1)

6.5.2.5 PhasedMarkov::PhasedMarkov (const SequenceSet & *seqset*, const vector< int > & *Indseq*, short *phase*, short *initial_phase* = `0`, bool *calc_rank* = `false`)

Constructor 8 : Estimation of the transition matrix based on the sequences of seqset given in Indseq.

Parameters:

seqset set of sequences for estimation

Indseq index of selected sequences

phase selected phase

initial_phase phase of the first element of each sequence

calc_rank calculus of the convergence rank if true

6.5.2.6 PhasedMarkov::PhasedMarkov (const gsl_rng ∗ *r*, short *size*, short *order*, short *phase*, bool *calc_rank* = `false`)

Constructor 9 : random markov matrices.

Parameters:

r gsl random generator

size alphabet size

order markovian order

phase selected phase

calc_rank calculus of the convergence rank if true

GSL use exple:

```
const gsl_rng_type * T;
// Choice a default generator and seed
// from environment variables
gsl_rng_env_setup();
// New created instance of the generator
T = gsl_rng_default;
gsl_rng * r = gsl_rng_alloc (T);
// Initialize/Seeds the random number generator
gsl_rng_set( r, (long)(time( NULL )) );
...
...
gsl_rng_free( r );
```

6.5.2.7 PhasedMarkov::PhasedMarkov (unsigned long ** *count*, short *size*, short *order*, short *phase*, short *initial_phase* = `0`, bool *calc_rank* = `false`)

Constructor 10 Estimate the transition matrices on a word-count.

Parameters:

count count of all the coded word(base size) of size order+1 for each phase,for estimation

size alphabet size

order markovian order

phase selected phase

initial_phase phase of the first element of each sequence

calc_rank calculus of the convergence rank if true

6.5.3 Member Function Documentation

6.5.3.1 template<class TSeq> double PhasedMarkov::AIC (const TSeq & *tseq*, short *initial_phase* = `0`) const `[inline]`

AIC of a set of sequences (AIC = -2*loglikelihood + 2*nbparam).

Parameters:

tseq a sequence or a set of sequences

initial_phase phase of the first element of each sequence

6.5.3.2 template<class TSeq> double PhasedMarkov::BIC (const TSeq & *tseq*, short *initial_phase* = `0`) const `[inline]`

BIC of sequences (BIC = -2*loglikelihood + nbparam*log(length)).

Parameters:

tseq a sequence or a set of sequences

initial_phase phase of the first element of each sequence

6.5.3.3 void PhasedMarkov::draw_markov_matrices (const gsl_rng * *r*)

draw at random the markov matrices

Parameters:

r gsl random generator

GSL use exple:

```
const gsl_rng_type * T;
// Choice a default generator and seed
// from environment variables
gsl_rng_env_setup();
// New created instance of the generator
T = gsl_rng_default;
gsl_rng * r = gsl_rng_alloc (T);
// Initialize/Seeds the random number generator
gsl_rng_set( r, (long)(time( NULL )) );
...
...
gsl_rng_free( r );
```

6.5.3.4 template<class TSeq> void PhasedMarkov::estimate (const TSeq & *tseq*, short *phase*, short *initial_phase*, unsigned long *beg*, unsigned long *end*, bool *calc_rank* = `false`, bool *count_again* = `true`) `[inline]`

Estimate the transition matrices on the sequence/sequenceset tseq.

Parameters:

tseq sequence/sequenceset for estimation

phase selected phase

initial_phase phase of the first element of each sequence

beg begin position in sequence(s) if subsequences

end end position in sequence(s) if subsequences

calc_rank calculus of the convergence rank if true

count_again false if the word-count already performed before the use of this method

6.5.3.5 double PhasedMarkov::log_likelihood (const Sequence & *seq*, short *initial_phase* = `0`, short *numphase* = `-1`) const

loglikelihood of a sequence

Parameters:

seq sequence

initial_phase phase of the first element of each sequence

numphase likelihood in only the numphase phase, -1 if sum of the phases

6.5.3.6 double PhasedMarkov::log_likelihood (const SequenceSet & *seqset*, short *initial_phase* = 0, short *numphase* = -1) const

loglikelihood of a set of sequence

Parameters:

seqset set of sequence

initial_phase phase of the first element of each sequence

numphase likelihood in only the numphase phase, -1 if sum of the phases

6.5.3.7 double PhasedMarkov::log_ratio_likelihood (const Sequence & *seq*, const PhasedMarkov & *M*, short *initial_phase1* = 0, short *initial_phase2* = 0) const

Calculation of the logarithm of the ratio of the probability of observing "seq" under "this" distribution and "M".

Parameters:

seq sequence

M alternative **Markov**(p. 14) chain

initial_phase1 phase of the first element of each sequence considered in model *this

initial_phase2 phase of the first element of each sequence considered in model M

REMARKS : NO verification is done on the compatibility of the **Markov**(p. 14) chains

CAREFUL: this calculus is performed by scanning the sequence to avoid pbm of too low likelihood

6.5.3.8 double PhasedMarkov::log_ratio_likelihood (const SequenceSet & *seqset*, const PhasedMarkov & *M*, short *initial_phase1* = 0, short *initial_phase2* = 0) const

Calculation of the logarithm of the ratio of the probability of observing "seq" under "this" distribution and "M".

Parameters:

seqset set of sequences

M alternative **Markov**(p. 14) chain

initial_phase1 phase of the first element of each sequence considered in model *this

initial_phase2 phase of the first element of each sequence considered in model M

REMARKS : NO verification is done on the compatibility of the **Markov**(p. 14) chains

CAREFUL: this calculus is performed by scanning the sequence to avoid pbm of too low likelihood

6.5.3.9 double PhasedMarkov::Mu (int *i*, int *p* = 0) const `[inline]`

Access to stationnary vector Mu elements.

Parameters:

i index of the word

p selected phase

6.5.3.10 double& PhasedMarkov::operator() (int *i*, int *p* = 0) [inline]

() operator for **Markov**(p. 14) matrix Pi elements

Parameters:

i index of the word

p selected phase

6.5.3.11 double PhasedMarkov::Pi (int *i*, int *p* = 0) const [inline]

Access to **Markov**(p. 14) matrix Pi.

Parameters:

i index of the word

p selected phase

6.5.3.12 void PhasedMarkov::print (const string & *FileOut*) [inline]

Print a summary of the object.

The estimation results can be saved in such a representation:

```
# 1 <- Order of the phased Markov chain
# 2 <- Phase
# 4 <- Alphabet size
# 19 steps <- Convergence to the stationnary distribution
# Phase nř0
# Transition matrix:
0.3945322543    0.1652811616    0.1535033485    0.2866832356
etc..........
# Stationnary Probability:
0.3127105148    0.2114684268    0.1783495332    0.2974715251
# Phase nř1
# Transition matrix:
0.3923961961    0.163516403     0.1521005152    0.2919868858
etc...............
# Stationnary Probability:
0.3135417652    0.2089660861    0.1771006767    0.300391472
```

6.5.3.13 double PhasedMarkov::proba (const long ∗ *seq*, long *tbeg*, long *tend*, short *numphase* = 0) const

Stationnary proba of the word seq[tbeg...tend].

Parameters:

seq Sequence-like coded sequence(see Sequence). The Markov-order for the code must be the same than _order

tbeg begin position of the word

tend end position of the word

numphase phase of the last letter of word

6.5.3.14 double PhasedMarkov::proba (long *word*, int *lw* = `-1`, long *jump* = `-1`, short *numphase* = `0`) const

Stationnary proba of a word.

Parameters:

word word as a Sequence-coded-like integer (see **Sequence**(p. 59))

lw length of the word. Default => order+1

jump Sequence-coded-like jump (see **Sequence**(p. 59)). Default => jump[order]

numphase phase of the last letter of word

6.5.3.15 double PhasedMarkov::proba (const vector< short > & *word*, Coder & *coder*, short *numphase* = `0`) const

Stationnary proba of a word.

Parameters:

word word as a vector of short

coder required **Coder**(p. 11) object, from a **PrimaryCount**(p. 49) object for exple

numphase phase of the last letter of word

6.5.3.16 double PhasedMarkov::proba (const string & *word*, Coder & *coder*, short *numphase* = `0`) const

Stationnary proba of a word.

Parameters:

word word as a string -a **Translator**(p. 64) object is required to process string to int-

coder required **Coder**(p. 11) object, from a **PrimaryCount**(p. 49) object for exple

numphase phase of the last letter of word

6.5.3.17 double PhasedMarkov::proba_c (const long ∗ *seq*, long *tbeg*, long *tend*, short *numphase* = `0`) const

Stationnary proba of the word seq[tbeg...tend](size greater than _order) conditionnaly of its first letters.

Parameters:

seq Sequence-like coded sequence(see Sequence). The Markov-order for the code must be the same than _order

tbeg begin position of the word

tend end position of the word

numphase phase of the last letter of word

6.5.3.18 double PhasedMarkov::proba_c (long *word*, int *lw* = -1, long *jump* = -1, short *numphase* = 0) const

Stationnary proba of a word(size greater than _order) conditionnaly of its first letters.

Parameters:

word word as a Sequence-coded-like integer (see **Sequence**(p. 59))

lw length of the word. Default => order+1

jump Sequence-coded-like jump (see **Sequence**(p. 59)). Default => jump[order]

numphase phase of the last letter of word

6.5.3.19 double PhasedMarkov::proba_c (const vector< short > & *word*, Coder & *coder*, short *numphase* = 0) const

Stationnary proba of a word(size greater than _order) conditionnaly of its first letters.

Parameters:

word word as a vector of short

coder required **Coder**(p. 11) object, from a **PrimaryCount**(p. 49) object for exple

numphase phase of the last letter of word

6.5.3.20 double PhasedMarkov::proba_c (const string & *word*, Coder & *coder*, short *numphase* = 0) const

Stationnary proba of a word(size greater than _order) conditionnaly of its first letters (!use link_-to_translator before!).

Parameters:

word word as a string -a **Translator**(p. 64) object is required to process string to int-

coder required **Coder**(p. 11) object, from a **PrimaryCount**(p. 49) object for exple

numphase phase of the last letter of word

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

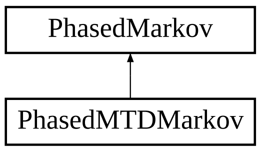
- **PhasedMarkov.h**
- PhasedMarkov.cc

6.6 PhasedMTDMarkov Class Reference

Phased Mixture Transition Distribution **Markov**(p. 14) modelling, estimation and simulation.

`#include <seqpp/PhasedMTDMarkov.h>`

Inheritance diagram for PhasedMTDMarkov::



Public Member Functions

- template<class TSeq> **PhasedMTDMarkov** (const TSeq &tseq, short mkv_order, short phase, short initial_phase=0, short nbseed=NBSEED, int nbiter_max=NBITERMAX, double eps=EPS, bool log=false)

  Constructor 1 from a **SequenceSet**(p. 62) *or a* **Sequence**(p. 59).

- **PhasedMTDMarkov** (unsigned long **count, short size, short mtd_order, short mkv_order, short phase, short initial_phase=0, short nbseed=NBSEED, int nbiter_-max=NBITERMAX, double eps=EPS, bool log=false)

  Constructor 2 from a coded-word count.

- void **estimate** (unsigned long **count, bool decal_required, short mkv_order, short phase, short initial_phase, short nbseed, int nbiter_max, double eps, bool log)

  performs the estimation [used by each constructor]

- ~**PhasedMTDMarkov** ()

  Destructor.

Protected Attributes

- mtd_core * **_mtdcore**

  Parcimonious Context Trees.

6.6.1 Detailed Description

Phased Mixture Transition Distribution **Markov**(p. 14) modelling, estimation and simulation.

PhasedMTDMarkov is a **PhasedMarkov**(p. 24) object with a different estimation step. This object performs the estimation with the Mixture Transition Distribution algorithm and then transfoms, once per phase, the MTD model in a markovian matrix.

6.6.2 Constructor & Destructor Documentation

6.6.2.1 template<class TSeq> PhasedMTDMarkov::PhasedMTDMarkov (const TSeq & *tseq*, short *mkv_order*, short *phase*, short *initial_phase* = `0`, short *nbseed* = `NBSEED`, int *nbiter_max* = `NBITERMAX`, double *eps* = `EPS`, bool *log* = `false`) `[inline]`

Constructor 1 from a **SequenceSet**(p. 62) or a **Sequence**(p. 59).

Parameters:

tseq a set of sequences or a sequence for estimation

mkv_order markovian order on the markovian matrix of the MTD

phase phase short

initial_phase phase of the first element of each sequence

nbseed number of seeds for the EM algorithm

nbiter_max maximum iterations number of the EM algorithm

eps value of the epsilon of the EM algorithm

log true to log the successive likelihood values

6.6.2.2 PhasedMTDMarkov::PhasedMTDMarkov (unsigned long ** *count*, short *size*, short *mtd_order*, short *mkv_order*, short *phase*, short *initial_phase* = `0`, short *nbseed* = `NBSEED`, int *nbiter_max* = `NBITERMAX`, double *eps* = `EPS`, bool *log* = `false`) `[inline]`

Constructor 2 from a coded-word count.

Parameters:

count count of all the coded word(base size) of size order+1 for each phase, for estimation

size alphabet size

mtd_order markovian order for the resulting model

mkv_order markovian order on the markovian matrices used in the MTD

phase phase

initial_phase phase of the first element of each sequence

nbseed number of seeds for the EM algorithm

nbiter_max maximum iterations number of the EM algorithm

eps value of the epsilon of the EM algorithm

log true to log the successive likelihood values

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

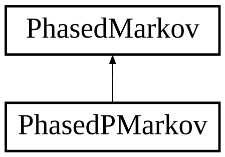
- **PhasedMTDMarkov.h**

6.7 PhasedPMarkov Class Reference

Phased Parcimonious **Markov**(p. 14) modelling, estimation and simulation.

`#include <seqpp/PhasedPMarkov.h>`

Inheritance diagram for PhasedPMarkov::



Public Member Functions

- **PhasedPMarkov** (const **SequenceSet** &seqset, short phase, short initial_phase=0, double prior_alpha=-1., double penalty=0., const string &xmlfile=string())

  Constructor 1 from a **SequenceSet**(p. 62).

- **PhasedPMarkov** (const **Sequence** &seq, short phase, short initial_phase=0, double prior_alpha=-1., double penalty=0., const **Translator** &trans=**Translator**(), const string &xmlfile=string())

  Constructor 2 from a **Sequence**(p. 59).

- **PhasedPMarkov** (const string &partitionfile, const **SequenceSet** &seqset, short phase, short initial_phase=0, double prior_alpha=-1., double penalty=0., const string &xmlfile=string())

  Constructor 3 from a **SequenceSet**(p. 62) *and a* **Partition**(p. 22) *-file.*

- **PhasedPMarkov** (const string &partitionfile, const **Translator** &trans, const **Sequence** &seq, short phase, short initial_phase=0, double prior_alpha=-1., double penalty=0., const string &xmlfile=string())

  Constructor 4 from a **Sequence**(p. 59) *and a* **Partition**(p. 22) *-file.*

- **PhasedPMarkov** (unsigned long **count, short size, short order, short phase, short initial_phase=0, double prior_alpha=-1., double penalty=0., const **Translator** &trans=**Translator**(), const string &xmlfile=string())

  Constructor 5 from a coded-word count.

- **PhasedPMarkov** (const string &partitionfile, const **Translator** &trans, unsigned long **count, short order, short phase, short initial_phase=0, double prior_alpha=-1., double penalty=0., const string &xmlfile=string())

  Constructor 6 from a coded-word count and a **Partition**(p. 22) *-file.*

- void **estimate** (unsigned long **count, bool decal_required, const **Translator** &trans, **Partition** &p, short phase, short initial_phase, double prior_alpha, double penalty, const string &xmlfile)

  performs the estimation [used by each constructor]

- ~**PhasedPMarkov** ()

Destructor.

Protected Attributes

- pmm_tree * **_pmmtree**
  Parcimonious Context Trees.

6.7.1 Detailed Description

Phased Parcimonious **Markov**(p. 14) modelling, estimation and simulation.

PhasedPMarkov is a **PhasedMarkov**(p. 24) object with a different estimation step. This object performs the estimation with the Parcimonious **Markov**(p. 14) algorithm and then transfoms, once per phase, the parcimonious context tree in a markovian matrix. xml outputs can be activated to save the associated trees.

6.7.2 Constructor & Destructor Documentation

6.7.2.1 PhasedPMarkov::PhasedPMarkov (const SequenceSet & *seqset*, short *phase*, short *initial_phase* = `0`, double *prior_alpha* = `-1.`, double *penalty* = `0.`, const string & *xmlfile* = `string()`) `[inline]`

Constructor 1 from a **SequenceSet**(p. 62).

Parameters:

seqset a set of sequences for estimation

phase phase

initial_phase phase of the first element of each sequence

prior_alpha alpha for the a priori law, by default -1. means 1./alphabet_size

penalty penalty on the leaves number, by default 0

xmlfile xmlfile for tree saving (if xml2 activated)

6.7.2.2 PhasedPMarkov::PhasedPMarkov (const Sequence & *seq*, short *phase*, short *initial_phase* = `0`, double *prior_alpha* = `-1.`, double *penalty* = `0.`, const Translator & *trans* = Translator(), const string & *xmlfile* = `string()`) `[inline]`

Constructor 2 from a **Sequence**(p. 59).

Parameters:

seq sequence for estimation

phase phase

initial_phase phase of the first element of each sequence

prior_alpha alpha for the a priori law, by default -1. means 1./alphabet_size

penalty penalty on the leaves number, by default 0

trans a **Translator**(p. 64) is required only for the xml saving

xmlfile xmlfile for tree saving (if xml2 activated)

6.7.2.3 PhasedPMarkov::PhasedPMarkov (const string & *partitionfile*, const SequenceSet & *seqset*, short *phase*, short *initial_phase* = `0`, double *prior_alpha* = `-1.`, double *penalty* = `0.`, const string & *xmlfile* = `string()`) `[inline]`

Constructor 3 from a **SequenceSet**(p. 62) and a **Partition**(p. 22) -file.

Parameters:

partitionfile file containing a selected partition, when default overall partition is too heavy

seqset a set of sequences for estimation

phase phase

initial_phase phase of the first element of each sequence

prior_alpha alpha for the a priori law, by default -1. means 1./alphabet_size

penalty penalty on the leaves number, by default 0

xmlfile xmlfile for tree saving (if xml2 activated)

Exple of partitionfile (grouped tokens, separed with a "|", beware the spaces) with 4 partitions

```
a c | g t
a c | g | t
a | c | g | t
c g t | a
```

6.7.2.4 PhasedPMarkov::PhasedPMarkov (const string & *partitionfile*, const Translator & *trans*, const Sequence & *seq*, short *phase*, short *initial_phase* = `0`, double *prior_alpha* = `-1.`, double *penalty* = `0.`, const string & *xmlfile* = `string()`) `[inline]`

Constructor 4 from a **Sequence**(p. 59) and a **Partition**(p. 22) -file.

Parameters:

partitionfile file containing a selected partition, when default overall partition is too heavy

trans a **Translator**(p. 64) is required for the partition reading

seq sequence for estimation

phase phase

initial_phase phase of the first element of each sequence

prior_alpha alpha for the a priori law, by default -1. means 1./alphabet_size

penalty penalty on the leaves number, by default 0

xmlfile xmlfile for tree saving (if xml2 activated)

Exple of partitionfile (grouped tokens, separed with a "|", beware the spaces) with 4 partitions

```
a c | g t
a c | g | t
a | c | g | t
c g t | a
```

6.7.2.5 PhasedPMarkov::PhasedPMarkov (unsigned long ** *count*, short *size*, short *order*, short *phase*, short *initial_phase* = `0`, double *prior_alpha* = `-1.`, double *penalty* = `0.`, const Translator & *trans* = `Translator()`, const string & *xmlfile* = `string()`) `[inline]`

Constructor 5 from a coded-word count.

Parameters:

count count of all the coded word(base size) of size order+1 for each phase, for estimation

size alphabet size

order markovian order associated to the word count

phase phase

initial_phase phase of the first element of each sequence

prior_alpha alpha for the a priori law, by default -1. means 1./alphabet_size

penalty penalty on the leaves number, by default 0

trans a **Translator**(p. 64) is required only for the xml saving

xmlfile xmlfile for tree saving (if xml2 activated)

6.7.2.6 PhasedPMarkov::PhasedPMarkov (const string & *partitionfile*, const Translator & *trans*, unsigned long ** *count*, short *order*, short *phase*, short *initial_phase* = `0`, double *prior_alpha* = `-1.`, double *penalty* = `0.`, const string & *xmlfile* = `string()`) `[inline]`

Constructor 6 from a coded-word count and a **Partition**(p. 22) -file.

Parameters:

partitionfile file containing a selected partition, when default overall partition is too heavy

trans a **Translator**(p. 64) is required for the partition reading

count count of all the coded word(base size) of size order+1 for each phase, for estimation

order markovian order associated to the word count

phase phase

initial_phase phase of the first element of each sequence

prior_alpha alpha for the a priori law, by default -1. means 1./alphabet_size

penalty penalty on the leaves number, by default 0

xmlfile xmlfile for tree saving (if xml2 activated)

Exple of partitionfile (grouped tokens, separed with a "|", beware the spaces) with 4 partitions

```
a c | g t
a c | g | t
a | c | g | t
c g t | a
```

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

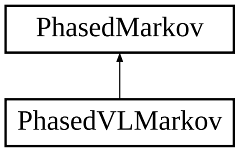
- **PhasedPMarkov.h**

6.8 PhasedVLMarkov Class Reference

Phased Variable Length **Markov**(p. 14) modelling, estimation and simulation.

`#include <seqpp/PhasedVLMarkov.h>`

Inheritance diagram for PhasedVLMarkov::



Public Member Functions

- template<class TSeq> **PhasedVLMarkov** (const TSeq &tseq, vector< double > &init, double cutoff, short phase, short initial_phase=0)

  Constructor 1 from a **SequenceSet**(p. 62) *or a* **Sequence**(p. 59).

- template<class TSeq> **PhasedVLMarkov** (const TSeq &tseq, double cutoff, short phase, short initial_phase=0)

  Constructor 2 from a **SequenceSet**(p. 62) *or a* **Sequence**(p. 59) *with random init.*

- ∼**PhasedVLMarkov** ()

  destructor

Protected Attributes

- vlm_tree ∗ **_vlmtree**

  Variable Length Context Trees.

6.8.1 Detailed Description

Phased Variable Length **Markov**(p. 14) modelling, estimation and simulation.

PhasedVLMarkov is a **PhasedMarkov**(p. 24) object with a different estimation step. This object performs the estimation with the Variable Length **Markov**(p. 14) algorithm and then transfoms, once per phase, the variable length context tree in a markovian matrix. One difference is that a cutoff is required for the selection of the tree.

6.8.2 Constructor & Destructor Documentation

6.8.2.1 template<class TSeq> PhasedVLMarkov::PhasedVLMarkov (const TSeq & *tseq*, vector< double > & *init*, double *cutoff*, short *phase*, short *initial_phase* = 0) `[inline]`

Constructor 1 from a **SequenceSet**(p. 62) or a **Sequence**(p. 59).

Parameters:

tseq a (set of) sequence(s) for estimation

init initial law in the leaves

cutoff tree selection cutoff

phase phase

initial_phase phase of the first element of each sequence

6.8.2.2 template<class TSeq> PhasedVLMarkov::PhasedVLMarkov (const TSeq & *tseq*, double *cutoff*, short *phase*, short *initial_phase* = 0) `[inline]`

Constructor 2 from a **SequenceSet**(p. 62) or a **Sequence**(p. 59) with random init.

Parameters:

tseq a (set of) sequence(s) for estimation

cutoff tree selection cutoff

phase phase

initial_phase phase of the first element of each sequence

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

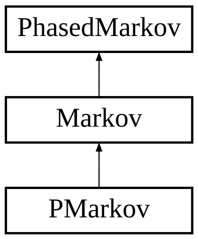
- **PhasedVLMarkov.h**

6.9 PMarkov Class Reference

Parcimonious **Markov**(p. 14) modelling, estimation and simulation.

`#include <seqpp/PMarkov.h>`

Inheritance diagram for PMarkov::



Public Member Functions

- **PMarkov** (const **SequenceSet** &seqset, double prior_alpha=-1, double penalty=0., const string &xmlfile=string())
  Constructor 1 from a **SequenceSet**(p. 62).
- **PMarkov** (const **Sequence** &seq, double prior_alpha=-1, double penalty=0., const **Translator** &trans=**Translator**(), const string &xmlfile=string())
  Constructor 2 from a **Sequence**(p. 59).
- **PMarkov** (const string &partitionfile, const **SequenceSet** &seqset, double prior_alpha=-1, double penalty=0., const string &xmlfile=string())
  Constructor 3 from a **SequenceSet**(p. 62) *and a* **Partition**(p. 22) *-file.*
- **PMarkov** (const string &partitionfile, const **Translator** &trans, const **Sequence** &seq, double prior_alpha=-1, double penalty=0., const string &xmlfile=string())
  Constructor 4 from a **Sequence**(p. 59) *and a* **Partition**(p. 22) *-file.*
- **PMarkov** (unsigned long ∗count, short size, short order, double prior_alpha=-1, double penalty=0., const **Translator** &trans=**Translator**(), const string &xmlfile=string())
  Constructor 5 from a coded-word count.
- **PMarkov** (const string &partitionfile, const **Translator** &trans, unsigned long ∗count, short order, double prior_alpha=-1, double penalty=0., const string &xmlfile=string())
  Constructor 6 from a coded-word count.
- void **estimate** (unsigned long ∗count, bool decal_required, const **Translator** &trans, **Partition** &p, double prior_alpha, double penalty=0., const string &xmlfile=string())
  performs the estimation [used in each constructor]

Protected Attributes

- pmm_tree ∗ **_pmmtree**
  Parcimonious Context Tree.

6.9.1 Detailed Description

Parcimonious **Markov**(p. 14) modelling, estimation and simulation.

This is a special case of a phased Parcimonious **Markov**(p. 14) [**PhasedPMarkov**(p. 39)] model when only one phase is considered, and also a **Markov**(p. 14) object.

6.9.2 Constructor & Destructor Documentation

6.9.2.1 PMarkov::PMarkov (const SequenceSet & *seqset*, double *prior_alpha* = `-1`, double *penalty* = `0.`, const string & *xmlfile* = `string()`) `[inline]`

Constructor 1 from a **SequenceSet**(p. 62).

Parameters:

seqset a set of sequences for estimation

prior_alpha alpha for the a priori law, by default -1 means 1./alphabet_size

penalty penalty on the leaves number, by default 0

xmlfile xmlfile for tree saving (if xml2 activated)

6.9.2.2 PMarkov::PMarkov (const Sequence & *seq*, double *prior_alpha* = `-1`, double *penalty* = `0.`, const Translator & *trans* = Translator`()`, const string & *xmlfile* = `string()`) `[inline]`

Constructor 2 from a **Sequence**(p. 59).

Parameters:

seq sequence for estimation

prior_alpha alpha for the a priori law, by default -1 means 1./alphabet_size

penalty penalty on the leaves number, by default 0

trans a **Translator**(p. 64) is required only for the xml saving

xmlfile xmlfile for tree saving (if xml2 activated)

6.9.2.3 PMarkov::PMarkov (const string & *partitionfile*, const SequenceSet & *seqset*, double *prior_alpha* = `-1`, double *penalty* = `0.`, const string & *xmlfile* = `string()`) `[inline]`

Constructor 3 from a **SequenceSet**(p. 62) and a **Partition**(p. 22) -file.

Parameters:

partitionfile file containing a selected partition, when default overall partition is too heavy

seqset a set of sequences for estimation

prior_alpha alpha for the a priori law, by default -1 means 1./alphabet_size

penalty penalty on the leaves number, by default 0

xmlfile xmlfile for tree saving (if xml2 activated)

Exple of partitionfile (grouped tokens, separed with a "|", beware the spaces) with 4 partitions

```
a c | g t
a c | g | t
a | c | g | t
c g t | a
```

6.9.2.4 PMarkov::PMarkov (const string & *partitionfile*, const Translator & *trans*, const Sequence & *seq*, double *prior_alpha* = `-1`, double *penalty* = `0.`, const string & *xmlfile* = `string()`) `[inline]`

Constructor 4 from a **Sequence**(p. 59) and a **Partition**(p. 22) -file.

Parameters:

partitionfile file containing a selected partition, when default overall partition is too heavy

seq sequence for estimation

trans a **Translator**(p. 64) is required for the partition reading

prior_alpha alpha for the a priori law, by default -1 means 1./alphabet_size

penalty penalty on the leaves number, by default 0

xmlfile xmlfile for tree saving (if xml2 activated)

Exple of partitionfile (grouped tokens, separed with a "|", beware the spaces) with 4 partitions

```
a c | g t
a c | g | t
a | c | g | t
c g t | a
```

6.9.2.5 PMarkov::PMarkov (unsigned long ∗ *count*, short *size*, short *order*, double *prior_alpha* = `-1`, double *penalty* = `0.`, const Translator & *trans* = Translator`()`, const string & *xmlfile* = `string()`) `[inline]`

Constructor 5 from a coded-word count.

Parameters:

count count of all the coded word(base size) of size order+1 for each phase, for estimation

size alphabet size

order markovian order associated to the word count

prior_alpha alpha for the a priori law, by default -1 means 1./alphabet_size

penalty penalty on the leaves number, by default 0

trans a **Translator**(p. 64) is required only for the xml saving

xmlfile xmlfile for tree saving (if xml2 activated)

6.9.2.6 PMarkov::PMarkov (const string & *partitionfile*, const Translator & *trans*, unsigned long ∗ *count*, short *order*, double *prior_alpha* = `-1`, double *penalty* = `0.`, const string & *xmlfile* = `string()`) `[inline]`

Constructor 6 from a coded-word count.

Parameters:

partitionfile file containing a selected partition, when default overall partition is too heavy

trans a **Translator**(p. 64) is required for the partition reading

count count of all the coded word(base size) of size order+1 for each phase, for estimation

order markovian order associated to the word count

prior_alpha alpha for the a priori law, by default -1 means 1./alphabet_size

penalty penalty on the leaves number, by default 0

xmlfile xmlfile for tree saving (if xml2 activated)

Exple of partitionfile (grouped tokens, separed with a "|", beware the spaces) with 4 partitions

```
a c | g t
a c | g | t
a | c | g | t
c g t | a
```

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

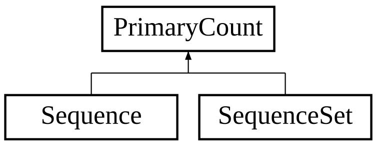
- **PMarkov.h**

6.10 PrimaryCount Class Reference

Abstract class designed for the (coded)word count.

`#include <seqpp/PrimaryCount.h>`

Inheritance diagram for PrimaryCount::



Public Member Functions

- virtual ~**PrimaryCount** ()

  destructor

- void **clear_count** () const

  clear the count

- void **null_count** () const

  put all counts down to 0

- short **tell_order** () const

  returns the markovian order

- int **tell_nb_value** () const

  returns the nber of codes/words taking into interest

- long **tell_jump** () const

  returns the jump to the codes of _order+1 letters

- long * **get_jump** () const

  returns the vector of the jumps to the codes of i letters, 0<i<=order+2

- **Coder** & **get_coder** () const

  allows a const access to the coder

- bool **is_count_ok** () const

  checks if the count is available

- unsigned long ** **get_p_count** () const

  get the total count, in the phased case

- unsigned long * **get_count** (short p=0) const

  get the total count in a phase p, or in the unphased case

- short **tell_phase** () const

returns nb of phase

- void **count_p_occurencies** (short phase, short initial_phase, unsigned long beg, unsigned long end) const

  Phased count the number of occurencies of all the nbvalue codes (in the sub-sequence [beg...end])... beware: beg>=0 but not >0.

- void **count_p_occurencies** (unsigned long **extern_count, short phase, short initial_-phase, unsigned long beg, unsigned long end) const

  Phased extern count the number of occurencies of all the nbvalue codes (in the sub-sequence [beg...end])... beware: beg>=0 but not >0.

- void **count_p_occurencies** (unsigned long **extern_count, short phase, short initial_-phase=0) const

  Phased extern count the number of occurencies of all the nbvalue codes in the whole sequence.

- void **count_p_occurencies** (short phase, short initial_phase=0) const

  Phased count the number of occurencies of all the nbvalue codes in the whole sequence.

- void **count_occurencies** (unsigned long beg, unsigned long end) const

  Extern count the number of occurencies of all the nbvalue codes (in the sub-sequence [beg...end])... beware: beg>=0 but not >0.

- void **count_occurencies** () const

  Count the number of occurencies of all the nbvalue codes in the whole sequence.

- unsigned long **tell_p_occurencies** (long code, short numphase) const

  extract the number of occurencies of code in phase

- unsigned long **tell_occurencies** (long code) const

  extract the number of occurencies of obs

Protected Member Functions

- void **init_count** () const

  initialize the count

- virtual unsigned long **tell_max_count** () const =0

  return the max length for the count

- virtual void **compute_count** (unsigned long **extern_count, short phase, short initial_-phase, unsigned long beg, unsigned long end) const =0

  compute the count

Protected Attributes

- short **_order**

  Order of the model.

- long **_nbvalue**

  nber of codes/words taking into interest

- short **_nbinv**

  number of invalid negative code

- **Coder** ∗ **_coder**

  markovian coder associated to the order of the sequence

- bool **_coder_in**

  true if _coder is build in the class

- unsigned long ∗∗ **_count**

  count of each code/word, even invalid (-1)

- bool **_count_ok**

  if the count is available

- short **_phase**

  phase for the count

6.10.1 Detailed Description

Abstract class designed for the (coded)word count.

This object is based on integer codes to store words as required for a markov modelling (see **Sequence**(p. 59)). The words are coded in alphabet_size base, coding the 1-token words, then the 2-tokens words, the 3-tokens words... Let call jump(i) the first code of a i-tokens words, a PrimaryCount object is designed to count all words:

```
(example with alphabet AGCT and order=2)
0              first word ( 0 -> A)
..
..             1-token words (from A to T)
..
jump(1)        (4 -> AA)
..
..             2-tokens words (from AA to TT)
..
jump(2)        (20 -> AAA)
..
..             3-tokens words (from AAA to TTT)
..
..
..             last word (TTT)
jump(order+1)  (64 -> /end)
```

The count can also be phased.

6.10.2 Member Function Documentation

6.10.2.1 void PrimaryCount::count_occurencies (unsigned long *beg*, unsigned long *end*) const `[inline]`

Extern count the number of occurencies of all the nbvalue codes (in the sub-sequence [beg...end])... beware: beg>=0 but not >0.

Parameters:

beg the sub-sequence [beg...

end the sub-sequence ...end]

6.10.2.2 void PrimaryCount::count_p_occurencies (short *phase*, short *initial_phase* = `0`) const `[inline]`

Phased count the number of occurencies of all the nbvalue codes in the whole sequence.

Parameters:

phase phase

initial_phase phase of the first element of associated sequence

6.10.2.3 void PrimaryCount::count_p_occurencies (unsigned long ** *extern_count*, short *phase*, short *initial_phase* = `0`) const `[inline]`

Phased extern count the number of occurencies of all the nbvalue codes in the whole sequence.

Parameters:

extern_count extern count storage

phase phase

initial_phase phase of the first element of associated sequence

6.10.2.4 void PrimaryCount::count_p_occurencies (unsigned long ** *extern_count*, short *phase*, short *initial_phase*, unsigned long *beg*, unsigned long *end*) const `[inline]`

Phased extern count the number of occurencies of all the nbvalue codes (in the sub-sequence [beg...end])... beware: beg>=0 but not >0.

Parameters:

extern_count extern count storage

phase phase

initial_phase phase of the first element of associated sequence

beg the sub-sequence [beg...

end the sub-sequence ...end]

6.10.2.5 void PrimaryCount::count_p_occurencies (short *phase*, short *initial_phase*, unsigned long *beg*, unsigned long *end*) const `[inline]`

Phased count the number of occurencies of all the nbvalue codes (in the sub-sequence [beg...end])... beware: beg>=0 but not >0.

Parameters:

phase phase

initial_phase phase of the first element of associated sequence

beg the sub-sequence [beg...

end the sub-sequence ...end]

6.10.2.6 unsigned long* PrimaryCount::get_count (short *p* = 0) const `[inline]`

get the total count in a phase p, or in the unphased case

Parameters:

p selected phase, default 0 if unphased case.

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

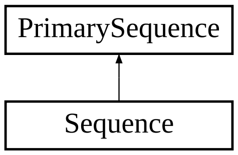
- **PrimaryCount.h**
- PrimaryCount.cc

6.11 PrimarySequence Class Reference

Virtual class corresponding to a generic sequence.

`#include <seqpp/PrimarySequence.h>`

Inheritance diagram for PrimarySequence::



Public Member Functions

- virtual ~**PrimarySequence** ()=0

  Destructor.

- const **Translator** & **ref_translator** () const

  allows a const access to the alphabet

- short **tell_alphabet_size** () const

  returns the alphabet size

- short **tell_nb_inv** () const

  returns the nber of invalid codes in alphabet

- virtual unsigned long **tell_length** () const

  returns the length

- string **tell_seq_name** () const

  return the sequence name

- string **tell_file_name** () const

  return the file name

- void **set_pos** (unsigned long t)

  sets the current position

- unsigned long **tell_pos** ()

  returns the current position

- virtual short **tell_int** (unsigned long pos) const =0

  returns the int value of the single letter on position pos

- short **tell_int** ()

  Return the code on current position.

- short **tell_int_compl** (unsigned long pos) const

Returns the complementary code on position i.

- short **tell_int_compl** () const

  Returns the complementary code on position i.

- string **tell_pattern** (unsigned long pos) const

  returns the pattern for a position

- string **tell_pattern_compl** (unsigned long pos)

  returns complementary pattern on position pos

- string **tell_patterns** (unsigned long beg, unsigned long stop) const

  returns the patterns between position beg and stop

- string **tell_label** (unsigned long pos) const

  return the label(if defined in the alphabet) for a position

- string **tell_labels** (unsigned long beg, unsigned long stop) const

  returns the label(if defined in the alphabet)-sequence between position beg and stop

- void **print** (const string &file) const

  print the sequence in fasta format

Protected Attributes

- const **Translator** ∗ **_transl**

  a **Translator**(p. 64) *alphabet pointer*

- short **_sizecode**

  the number of char for a letter of the alphabet (alphabet mode)

- short **_nmodal**

  number of possible observable value

- long ∗ **_obs**

  Vector of the observed datas.

- unsigned long **_length**

  length of the sequence

- unsigned long **_ipos**

  current position

- string **_name**

  name of the sequence

- string **_name_file**

  name of the file

6.11.1 Detailed Description

Virtual class corresponding to a generic sequence.

Note that a Primarysequence is associated with a **Translator**(p. 64) object.

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

- **PrimarySequence.h**
- PrimarySequence.cc

6.12 PrimarySequenceSet< TSequence > Class Template Reference

Class corresponding to a generic sequence set.

`#include <seqpp/PrimarySequenceSet.h>`

Public Member Functions

- **PrimarySequenceSet** ()
  default constructor
- virtual ~**PrimarySequenceSet** ()
  destructor
- const **Translator** & **get_translator** () const
  allows a const access to the alphabet via a reference
- short **tell_alphabet_size** () const
  returns the alphabet size
- short **tell_nb_inv** () const
  returns the nber of invalid codes
- TSequence & **get_sequence** (int i) const
  allows a const access to ith sequence via a reference
- TSequence & **operator()** (int i) const
  allows a const access to ith sequence via a reference
- int **tell_nb_sequence** () const
  returns the number of sequences
- virtual unsigned long **tell_length** () const
  returns the total length
- unsigned long **tell_length_max** () const
  returns the length max
- unsigned long **tell_length_seq** (int i) const
  returns the length of sequence i
- string **tell_seq_name** (int i) const
  gives the name oh the ith file
- string **tell_file_name** (int i) const
  gives the name oh the ith file
- void **weight_matrix** (double **wmat) const
  compute the weight matrix associated to the sequences wmat[token][position in the sequence]

Protected Attributes

- const **Translator** ∗ **_transl**

  Associated alphabet.
- short **_nmodal**

  number of possible observable value
- int **_nb_seq**

  Number of sequences in the array.
- unsigned long **_total_length**

  Total length.
- unsigned long **_length_max**

  Maximum length of a sequence.
- TSequence ∗∗ **_array_seq**

  Array of sequences.

6.12.1 Detailed Description

template<class TSequence> class PrimarySequenceSet< TSequence >

Class corresponding to a generic sequence set.

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

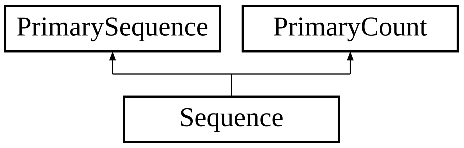
- **PrimarySequenceSet.h**

6.13 Sequence Class Reference

The Sequence class has been designed for Markovian analysis of a single sequence.

`#include <seqpp/Sequence.h>`

Inheritance diagram for Sequence::



Public Member Functions

- **Sequence** (ifstream &ifile, short order, const **Translator** &transl, **Coder** &coder, const string &name_file="noname")

  Constructor from a flow ifile from a fasta file.

- **Sequence** (short order, unsigned long length, const **Translator** &transl)

  minimal constructor

- **Sequence** (const string &name_file, short order, const **Translator** &transl)

  Constructor from a Fasta or Genbank file containing a single sequence.

- **Sequence** (const **Sequence** &seq)

  Copy constructor.

- **Sequence** (const **Sequence** &seq, short order)

  Deduction constructor from an order 0-sequence.

- virtual ∼**Sequence** ()

  destructor

- short **tell_int** (unsigned long pos) const

  Returns the int value of the token on position pos.

- long **tell_code** (unsigned long pos) const

  Returns the code on position pos.

- long **tell_code** () const

  Returns the code on current position.

- const long ∗ **seq** () const

  Returns the coded sequence as a vector.

- const long ∗ **get_code** () const

  Returns the coded sequence as a vector.

- void **simule** (const double ∗m_trans, const double ∗v_init, const gsl_rng ∗r)

    simulate the observations from a transition matrix and a vector for initial _order-word proba

- void **simule** (const double ∗m_trans, const gsl_rng ∗r)

    simulate the observations from a transition matrix, random initial law

- void **simule_phased** (short phase, const double ∗∗m_trans, const double ∗v_init, const gsl_rng ∗r)

    simulate the observations from a vector of transition matrices and a vector for initial _order word proba

- void **simule** (unsigned long position, double ∗proba, const gsl_rng ∗r)

    simulate the observation on position from a alphabet size vector

Protected Member Functions

- virtual unsigned long **tell_max_count** () const

    return the max length for the count

- virtual void **compute_count** (unsigned long ∗∗extern_count, short phase, short initial_-phase, unsigned long beg, unsigned long end) const

6.13.1 Detailed Description

The Sequence class has been designed for Markovian analysis of a single sequence.

On each position, the markovian predictor is coded and store (see **PrimaryCount**(p. 49)):

```
Exple with the alphabet AGCT:
sequence position  .... 7  8  9 ...
token              .... A  G  A ...
code stored        .........24
```

Sequence object of integer values corresponding to the code of the word considered on a position t for a **Markov**(p. 14) model of order _order... this code corresponds to the number of smaller words and the calculus in base |A| of this word, with A the alphabet.

ex : from A to GGG for order 2 with dna alphabet

6.13.2 Constructor & Destructor Documentation

6.13.2.1 Sequence::Sequence (ifstream & *ifile*, short *order*, const Translator & *transl*, Coder & *coder*, const string & *name_file* = "noname")

Constructor from a flow ifile from a fasta file.

on the position of the char '>', create an object until the next '>' generating his name by the concatenation of the sentence after the char '>'. The flow is or eof or on a '>' at the end.

Parameters:

ifile iftream flow

order markovian order

transsl reference to a **Translator**(p. 64)

coder reference to a **Coder**(p. 11)

name_file file name corresponding to ifile

6.13.2.2 Sequence::Sequence (short *order*, unsigned long *length*, const Translator & *transl*)

minimal constructor

Parameters:

order markovian order

length default length

transl reference to a **Translator**(p. 64)

6.13.2.3 Sequence::Sequence (const string & *name_file*, short *order*, const Translator & *transl*)

Constructor from a Fasta or Genbank file containing a single sequence.

Parameters:

name_file file name to open

order markovian order

transl reference to a **Translator**(p. 64)

6.13.3 Member Function Documentation

6.13.3.1 void Sequence::compute_count (unsigned long ** *extern_count*, short *phase*, short *initial_phase*, unsigned long *beg*, unsigned long *end*) const `[protected, virtual]`

total length case

Implements **PrimaryCount** (p. 50).

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

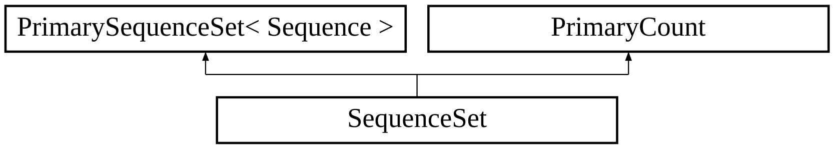
- **Sequence.h**
- Sequence.cc

6.14 SequenceSet Class Reference

Set of **Sequence**(p. 59) objects.

`#include <seqpp/SequenceSet.h>`

Inheritance diagram for SequenceSet::



Public Member Functions

- **SequenceSet** (const string &seq_list_file, const string &alpha_file, short order, int nbseq=BUFFERSEQ)

  constructor with a alphabet-needed file

- **SequenceSet** (const string &seq_list_file, short mode, const string &line2parse, bool case_sensitivity, short order, int nbseq=BUFFERSEQ)

  constructor with a alphabet-needed line2parse

6.14.1 Detailed Description

Set of **Sequence**(p. 59) objects.

from :

- a Fasta file (with 1 or more sequences inside separated by a line beginning with a SKIPCHAR) or a Genbank file
- or a file containing the name of many Fasta (or a Genbank) sequence files

6.14.2 Constructor & Destructor Documentation

6.14.2.1 SequenceSet::SequenceSet (const string & *seq_list_file*, const string & *alpha_file*, short *order*, int *nbseq* = `BUFFERSEQ`)

constructor with a alphabet-needed file

Parameters:

seq_list_file file, among the 3 possibilities of files.

alpha_file file for initializing the alphabet (see **Translator**(p. 64) doc)

order Markovian order,

nbseq number of sequences

6.14.2.2 SequenceSet::SequenceSet (const string & *seq_list_file*, short *mode*, const string & *line2parse*, bool *case_sensitivity*, short *order*, int *nbseq* = `BUFFERSEQ`)

constructor with a alphabet-needed line2parse

Parameters:

seq_list_file file, among the 3 possibilities of files.

mode number of char for a token in the alphabet

line2parse string for initializing the alphabet (see **Translator**(p. 64) doc)

case_sensitivity true for being case sensitive

order Markovian order,

nbseq number of sequences

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

- **SequenceSet.h**
- SequenceSet.cc

6.15 Translator Class Reference

Alphabet designer tool.

`#include <seqpp/Translator.h>`

Public Member Functions

- **Translator** (const string &alpha_file)

  Constructor from a configuration file.

- **Translator** (const string &line2parse, short mode, bool case_sensivity=true)

  Constructor from an expression.

- **Translator** (const **Translator** &t)

  Copy constructor.

- **Translator** ()

  Default constructor.

- ∼**Translator** ()

  Destructor.

- short **tell_alphabet_size** () const

  Returns alphabet size.

- short **tell_nb_inv** () const

  Return the number of invalid code.

- short **tell_alphabet_mode** () const

  Return alphabet mode, the number of characters of a token.

- bool **is_complementary_ok** () const

  Checks if complementary codes are defined.

- bool **is_label_ok** () const

  Checks if labels are defined.

- short int **char_to_int** (const char ∗source) const

  Returns the int code for a given char ∗.

- short int **str_to_int** (const string &source) const

  Returns the int code for a given string.

- short **complementary_char_to_int** (const char ∗source) const

  Returns the complementary int code for a given char ∗.

- short int **complementary_str_to_int** (const string &source) const

  Returns the complementary int code for a given string.

- short **complementary_int** (short source) const
  Returns the complementary int code for a given code.
- void **int_to_char** (char ∗dest, short source) const
  Initialize dest to the word corresponding to the int source.
- string **int_to_str** (short source) const
  returns the word corresponding to the int source
- void **complementary_char** (char ∗dest, const char ∗source) const
  Initialize dest to the word corresponding to the complementary of word source.
- string **complementary_str** (const string &source) const
  returns the token corresponding to the inverse complementary of a token source
- string **complementary_int_to_str** (short source) const
  returns the string corresponding to the complementary of int source
- string **complementary_strw** (const string &wordsource) const
  returns the inverse complementary string-word of source
- void **vect_to_word** (char ∗worddest, const short ∗vectsource, short sizeword) const
  a char-word <- an int-vect
- void **vect_to_word** (char ∗worddest, const vector< short > &vectsource) const
  a char-word <- an int-vect
- string **vect_to_strw** (const short ∗vectsource, short sizeword) const
  a string-word <- an int-vect
- string **vect_to_strw** (const vector< short > &vectsource) const
  a string-word <- an int-vect
- void **word_to_vect** (short ∗vectdest, const char ∗wordsource, short sizeword) const
  a char-word -> an int-vect
- void **word_to_vect** (vector< short > &vectdest, const char ∗wordsource) const
  a char-word -> an int-vect
- void **strw_to_vect** (vector< short > &vectdest, const string &wordsource) const
  a char-word -> an int-vect
- long **word_to_coded_int** (const char ∗wordsource, int &l) const
  a char-word -> an int code (base alphabet_size)
- long **strw_to_coded_int** (const string &wordsource) const
  a string-word -> an int code (base alphabet_size)
- long **complementary_coded_int** (long codesource, short sizeword) const
  Returns the complementary int code for a given coded int.

- short **isInvalid** (const char ∗source) const
  checks if source is invalid
- short **isInvalid** (const string &source) const
  checks if source is invalid
- string **int_to_label** (short source) const
  returns the label corresponding to the source
- string **vect_to_labelstrw** (const vector< short > &vectsource) const
  a string-word of label <- an int-vect

Protected Attributes

- short **_alphabet_size**
  number of tokens describing the alphabet
- short **_alphabet_mode**
  number of characters of each token
- short **_nb_inv**
  number of invalid tokens
- bool **_complementary_ok**
  checks if complementary is defined
- bool **_label_ok**
  checks if labels are defined

6.15.1 Detailed Description

Alphabet designer tool.

The key of the seq++ flexibility is the translator object. It defines a mapping between the alphabet and integer values. In seq++, a letter of an alphabet, called a token, can be made of one or more characters, for instance to manage n-uplets like codons. It is associated to its rank integer position in the alphabet.

A simple configuration file is required, containing synonymous tokens, complementary tokens (if exist) and labels. A label aims to be the explicit name of a token. Moreover, invalid tokens can be declared and associated to negative values.

Use a initial file containing same size(alphabet_mode characters) tokens (the letters of the alphabet)

- on a same line, all the synonymous tokens (beware lower and upper case)
- (if necessary) on a line beginning with a "?", single characters or tokens (same size than others) to declare a class of invalid tokens. NB: a default class contains all the tokens not declared (neither belonging to alphabet nor to known invalids)

- (if necessary) their associated label (formally the common name) after a " $\rightarrow$ "
- (if necessary) their complementary after a ":"
  Beware the spaces between each tokens !

exple :

```
  #codons
  ttt TTT -> F1
  ttc TTC -> F2
  tta TTA -> L1
  ...
  ggg GGG -> G4
  ? taa TAA tag TAG tga TGA


  #dna
  a A : t T
  g G : c C
  c C : g G
  t T : a A
  ? n N


#secondary structures
  H -> HELIX
  B -> BETA
  C -> COIL
```

OR

Use an expression to parse ("line2parse") where all the same size ("mode") tokens are concatened, with a ":" to define the inverse complementary with same size tokens. No synonyms supported. exple :

```
  acgt:tgca         # dna alphabet, mode = 1
  R1R2T1T2T3X1Y1Y2  # other alphabet, with mode = 2 (R1 is the first token...)
```

6.15.2 Constructor & Destructor Documentation

6.15.2.1 Translator::Translator (const string & *alpha_file*)

Constructor from a configuration file.

Parameters:
alpha_file configuration file

6.15.2.2 Translator::Translator (const string & *line2parse*, short *mode*, bool *case_sensivity* = `true`)

Constructor from an expression.

Parameters:
line2parse alphabet expression
mode number of characters of a token
case_sensivity false if no case sensitivity required

6.15.3 Member Function Documentation

6.15.3.1 short int Translator::char_to_int (const char * *source*) const

Returns the int code for a given char *.

Parameters:

source pointer to the first character of a token to translate in int Beware that source must be the beginning of a word of size _alphabet_mode, or -1 is returned

6.15.3.2 void Translator::complementary_char (char * *dest*, const char * *source*) const `[inline]`

Initialize dest to the word corresponding to the complementary of word source.

Parameters:

dest must be allocated with _alphabet_mode+1 space, empty word if bad query.

source pointer to the first position of the source token

6.15.3.3 short int Translator::complementary_char_to_int (const char * *source*) const

Returns the complementary int code for a given char *.

Parameters:

source pointer to the first character of a token to complementary translate in int Beware that source must be the beginning of a word of size _alphabet_mode, or -1 is returned

6.15.3.4 short Translator::complementary_int (short *source*) const `[inline]`

Returns the complementary int code for a given code.

Parameters:

source integer code

6.15.3.5 short int Translator::complementary_str_to_int (const string & *source*) const

Returns the complementary int code for a given string.

Parameters:

source string-token to complementary translate in int

6.15.3.6 void Translator::int_to_char (char ∗ *dest*, short *source*) const

Initialize dest to the word corresponding to the int source.

Parameters:

dest must be allocated with _alphabet_mode+1 space, empty word if bad query.

source integer to translate

6.15.3.7 short int Translator::str_to_int (const string & *source*) const

Returns the int code for a given string.

Parameters:

source string-token to translate in int

6.15.3.8 long Translator::strw_to_coded_int (const string & *wordsource*) const

a string-word -> an int code (base alphabet_size)

Parameters:

wordsource word to code

6.15.3.9 void Translator::strw_to_vect (vector< short > & *vectdest*, const string & *wordsource*) const

a char-word -> an int-vect

a string-word -> an int-vect

6.15.3.10 void Translator::vect_to_word (char ∗ *worddest*, const short ∗ *vectsource*, short *sizeword*) const

a char-word <- an int-vect

Parameters:

worddest word (must be allocated sizeword∗_alphabet_mode + 1 space) corresponding to the sequential translation of source

vectsource vector of integer to translate

sizeword size of the vectsource to translate

6.15.3.11 long Translator::word_to_coded_int (const char ∗ *wordsource*, int & *l*) const

a char-word -> an int code (base alphabet_size)

Parameters:

wordsource pointer to the character word to code

l its length

6.15.3.12 void Translator::word_to_vect (short ∗ *vectdest*, const char ∗ *wordsource*, short *sizeword*) const

a char-word -> an int-vect

Parameters:

vectdest integer vector (must be sizeword-allocated)

wordsource character word to sequentially translate

sizeword size of the word

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

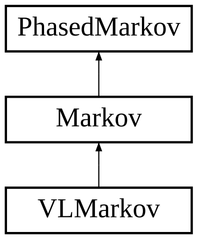
- **Translator.h**
- Translator.cc

6.16 VLMarkov Class Reference

Variable **Markov**(p. 14) modelling, estimation and simulation.

`#include <seqpp/VLMarkov.h>`

Inheritance diagram for VLMarkov::



Public Member Functions

- template<class TSeq> **VLMarkov** (const TSeq &tseq, vector< double > &init, double cutoff)

  Constructor 1 from a **SequenceSet**(p. 62) *or a* **Sequence**(p. 59)*.*

- template<class TSeq> **VLMarkov** (const TSeq &tseq, double cutoff)

  Constructor 2 from a **SequenceSet**(p. 62) *or a* **Sequence**(p. 59) *with random init.*

Protected Attributes

- vlm_tree * **_vlmtree**

  Variable Length Context Tree.

6.16.1 Detailed Description

Variable **Markov**(p. 14) modelling, estimation and simulation.

This is a special case of a phased Variable LengthMarkov [**PhasedVLMarkov**(p. 43)] model when only one phase is considered, and also a **Markov**(p. 14) object.

6.16.2 Constructor & Destructor Documentation

6.16.2.1 template<class TSeq> VLMarkov::VLMarkov (const TSeq & *tseq*, vector< double > & *init*, double *cutoff*) `[inline]`

Constructor 1 from a **SequenceSet**(p. 62) or a **Sequence**(p. 59).

Parameters:

tseq a (set of) sequence(s) for estimation

init initial law in the leaves

cutoff tree selection cutoff

6.16.2.2 template<class TSeq> VLMarkov::VLMarkov (const TSeq & *tseq*, double *cutoff*) `[inline]`

Constructor 2 from a **SequenceSet**(p. 62) or a **Sequence**(p. 59) with random init.

Parameters:

tseq a (set of) sequence(s) for estimation

cutoff tree selection cutoff

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

- **VLMarkov.h**

Chapter 7

seqpp File Documentation

7.1 Coder.h File Reference

Coder(p. 11).

`#include <vector>`

`#include <iostream>`

Classes

- class **Coder**

  Coded abstract representation of a word.

7.1.1 Detailed Description

Coder(p. 11).

Author:
Vincent Miele

07/2004

Coded abstract representation of a word

7.2 const.h File Reference

Configuration file.

Namespaces

- namespace **seqplusplus_space**

Variables

- const int **BUFFERSEQ** = 100

  for **SequenceSet**(p. 62)*, number of sequence per buffer*

- const int **LGBLOC** = 1000

  for **Sequence**(p. 59)*,length of a bloc used to memory the sequence*

- const char **SKIPCHAR** = '>'

  for **Sequence**(p. 59)*, character definig the line to skip on top of a sequence (cf. fasta file)*

- const char **INVCHAR** = '?'

  for **Translator**(p. 64)*, for invalid declaration file*

- const char **COMCHAR** = '#'

  comments characters

- const char **LABPATT** [3] = " → "

  label prefix before a declaration

- const char **LABINV** [4] = "INV"

  invalid label

- const int **LGSTRING** = 256

  string name max length

- const int **LG_FILENAME** = 200

  file name max length

- const int **STREAM_PRECISION** = 8

  precision for the o/ofstream

- const double **PRECISION** = 1e-7

  precision for comparing a double to 0, must be = 1e-(STREAM_PRECISION-1)

- const double **EPS** = 1e-5

  for MTD E.M. Algorithm

- const short **DEBUG** = 0

  debug level, for the compilation

7.2.1 Detailed Description

Configuration file.

Author:
Vincent Miele

12/2003

7.3 DOXYMAINPAGE.h File Reference

7.3.1 Detailed Description

Main page

7.4 Markov.h File Reference

Markov(p. 14) model.

`#include <seqpp/PhasedMarkov.h>`

`#include <seqpp/arnoldi.h>`

Classes

- class **Markov**

  Markov modelling, estimation and simulation.

7.4.1 Detailed Description

Markov(p. 14) model.

Author:

David Robelin - Vincent Miele

01/2004

7.5 MTDMarkov.h File Reference

Mixture Transition Distribution **Markov**(p. 14) model.

`#include <seqpp/Markov.h>`

`#include <seqpp/mtd_core.h>`

Classes

- class **MTDMarkov**

  Mixture Transition Distribution **Markov**(p. 14) *modelling, estimation and simulation.*

7.5.1 Detailed Description

Mixture Transition Distribution **Markov**(p. 14) model.

Author:
Vincent Miele

01/2004

7.6 Partition.h File Reference

Partition(p. 22).

`#include <seqpp/Partition_box.h>`

`#include <seqpp/Translator.h>`

`#include <list>`

`#include <set>`

`#include <map>`

Classes

- class **Partition**

  Dealer of alphabet partitions.

7.6.1 Detailed Description

Partition(p. 22).

Author:
Vincent Miele

23/02/2004

7.7 Partition_box.h File Reference

Partition_box.

`#include <iostream>`

`#include <fstream>`

`#include <vector>`

`#include <cmath>`

7.7.1 Detailed Description

Partition_box.

Author:

Vincent Miele

23/02/2004

display the set of |A|-vectors containing the num of group for each letter. exple: a c g t 1 1 1 1 1 2 1 1 1 2 2 1 etc... 1 2 3 4 and those vector must be processed and stored in a Tpart

7.8 PhasedMarkov.h File Reference

Phased **Markov**(p. 14) model.

`#include <seqpp/SequenceSet.h>`

`#include <seqpp/arnoldi.h>`

`#include <vector>`

`#include <string>`

Classes

- class **PhasedMarkov**

  Phased **Markov**(p. 14) *modelling, estimation and simulation.*

7.8.1 Detailed Description

Phased **Markov**(p. 14) model.

Author:

David Robelin - Vincent Miele

01/2004

7.9 PhasedMTDMarkov.h File Reference

Phased Mixture Transition Distribution **Markov**(p. 14) model.

```
#include <seqpp/PhasedMarkov.h>
#include <seqpp/mtd_core.h>
```

Classes

- class **PhasedMTDMarkov**

  Phased Mixture Transition Distribution **Markov**(p. 14) *modelling, estimation and simulation.*

7.9.1 Detailed Description

Phased Mixture Transition Distribution **Markov**(p. 14) model.

Author:
Vincent Miele

01/2004

7.10 PhasedPMarkov.h File Reference

Phased Parcimonious **Markov**(p. 14) model.

`#include <seqpp/PhasedMarkov.h>`

`#include <seqpp/pmm_tree.h>`

Classes

- class **PhasedPMarkov**

  Phased Parcimonious **Markov**(p. 14) *modelling, estimation and simulation.*

7.10.1 Detailed Description

Phased Parcimonious **Markov**(p. 14) model.

Author:

Vincent Miele

01/2004

7.11 PhasedVLMarkov.h File Reference

Phased Variable Length **Markov**(p. 14) model.

```
#include <seqpp/PhasedMarkov.h>
#include <seqpp/vlm_tree.h>
```

Classes

- class **PhasedVLMarkov**

  Phased Variable Length **Markov**(p. 14) *modelling, estimation and simulation.*

7.11.1 Detailed Description

Phased Variable Length **Markov**(p. 14) model.

Author:

Vincent Miele

01/2004

7.12 PMarkov.h File Reference

Parcimonious **Markov**(p. 14) model.

```
#include <seqpp/Markov.h>
```

```
#include <seqpp/PhasedPMarkov.h>
```

```
#include <seqpp/pmm_tree.h>
```

Classes

- class **PMarkov**

  Parcimonious **Markov**(p. 14) *modelling, estimation and simulation.*

7.12.1 Detailed Description

Parcimonious **Markov**(p. 14) model.

Author:
Vincent Miele

01/2004

7.13 PrimaryCount.h File Reference

Abstract class designed for the (coded)word count.

`#include <seqpp/Coder.h>`

Classes

- class **PrimaryCount**

  Abstract class designed for the (coded)word count.

7.13.1 Detailed Description

Abstract class designed for the (coded)word count.

Author:

Vincent Miele

23/04/2003

7.14 PrimarySequence.h File Reference

Abstract generic sequence.

```
#include <seqpp/Translator.h>
```

```
#include <fstream>
```

```
#include <iostream>
```

```
#include <string>
```

Classes

- class **PrimarySequence**

  Virtual class corresponding to a generic sequence.

7.14.1 Detailed Description

Abstract generic sequence.

Author:

Vincent Miele - Florence Muri - Pierre Nicolas

23/04/2003

7.15 PrimarySequenceSet.h File Reference

Generic set of sequence objects.

`#include <seqpp/Sequence.h>`

`#include <seqpp/Translator.h>`

`#include <iomanip>`

Classes

- class **PrimarySequenceSet< TSequence >**

  Class corresponding to a generic sequence set.

7.15.1 Detailed Description

Generic set of sequence objects.

Author:
Vincent Miele

23/04/2003

7.16 Sequence.h File Reference

Sequence(p. 59) class has been designed for Markovian analysis.

```
#include <seqpp/PrimarySequence.h>
#include <seqpp/PrimaryCount.h>
#include <seqpp/Coder.h>
#include <set>
#include <gsl/gsl_rng.h>
#include <gsl/gsl_randist.h>
```

Classes

- class **Sequence**

  The Sequence class has been designed for Markovian analysis of a single sequence.

7.16.1 Detailed Description

Sequence(p. 59) class has been designed for Markovian analysis.

Author:

Vincent Miele - Florence Muri - Pierre Nicolas

23/04/2003

7.17 SequenceSet.h File Reference

Set of **Sequence**(p. 59) objects.

`#include <seqpp/PrimarySequenceSet.h>`

`#include <iomanip>`

Classes

- class **SequenceSet**

  Set of **Sequence**(p. 59) *objects.*

7.17.1 Detailed Description

Set of **Sequence**(p. 59) objects.

Author:

Vincent Miele

23/04/2003

7.18 Translator.h File Reference

General Alphabet class.

`#include <seqpp/const.h>`

`#include <iostream>`

`#include <fstream>`

`#include <string>`

`#include <map>`

`#include <vector>`

Classes

- class **Translator**

  Alphabet designer tool.

7.18.1 Detailed Description

General Alphabet class.

Author:

Vincent Miele - Pierre Yves Bourguignon

23/04/2003

7.19 VLMarkov.h File Reference

Variable Length **Markov**(p. 14) model 01/2004.

`#include <seqpp/Markov.h>`

`#include <seqpp/PhasedVLMarkov.h>`

`#include <seqpp/vlm_tree.h>`

Classes

- class **VLMarkov**

  Variable **Markov**(p. 14) *modelling, estimation and simulation.*

7.19.1 Detailed Description

Variable Length **Markov**(p. 14) model 01/2004.

Author:
Vincent Miele

Chapter 8

seqpp Page Documentation

8.1 Library

The inheritance links between classes are essential to understand the design of seq++ and the behaviour of each object. Please browse the top task bar to discover the `Class Hierarchy`.

Basicaly seq++ focuses on both aspects:

- Sequence manipulation:

1. the key of the seq++ flexibility is the possibility to customize any alphabet thanks to the **Translator**(p. 64) class. Therefore a seq++-based software can support alphabets of DNA, codons, proteins, secondary structure, hydrophobicity class and so on.
2. the **SequenceSet**(p. 62) and **Sequence**(p. 59) classes are dedicated to the storage and the manipulation of external sequences provided by the user. This is done keeping in mind the purpose of modeling sequences with Markov models: at each position of the sequences the associated markovian-predictor (word, see **PrimaryCount**(p. 49)) is coded and stored.

- Markovian modelling (estimation, simulation...)

1. the **PhasedMarkov**(p. 24) object represents the general Markov model: the order and the number of phases have to be selected. **Markov**(p. 14) focuses on non-phased models.
2. **PhasedPMarkov**(p. 39) and **PMarkov**(p. 45) are dedicated to Parcimonious Markov models. Note that the definition of a set of partitions of the alphabet (see **Partition**(p. 22)) can be required.
3. **PhasedMTDMarkov**(p. 37) and **MTDMarkov**(p. 20) are dedicated to Mixture Transition Distribution Markov models. Note that the estimation is performed by a E.M. algorithm so that E.M. parameters have to be set up.
4. **PhasedVLMarkov**(p. 43) and **VLMarkov**(p. 71) are dedicated to Variable Length Markov models. Beware that these models require a cutoff value which can be estimated by optimizing the BIC criteria.

Please watch the **References**(p. 101) page for more details on the models.

8.2 Programs

When installing the package seq++, both the libary and a set of binary programs are available on your system:

1. **estim_m** is dedicated to Phased Markov model estimation (based on the **PhasedMarkov**(p. 24) object).
2. **estim_vlm** is dedicated to Variable Length Markov model estimation (based on the **PhasedVLMarkov**(p. 43) object).
3. **estim_pm** is dedicated to Parcimonious Markov model estimation (based on the **PhasedPMarkov**(p. 39) object).
4. **estim_mtd** is dedicated to Mixture Transition Distribution Markov model estimation (based on the **PhasedMTDMarkov**(p. 37) object).
5. **simul_m** is dedicated to sequence simulation from a markovian matrix (previously estimated) or a base sequence (based on the **PhasedMarkov**(p. 24) object).
6. **dist_m** computes the Total Variation Distance between two Markov models previously estimated with estim_∗.

Nota bene: the `estim_*` programs differs only on the way the estimation of the markovian matrix is performed.

Basicaly the best way to discover the possibilities of these programs is the Unix way:

```
program_name --help  OR man program_name
```

The estimation results can be saved in such a representation:

```
# 1 <- Order of the phased Markov chain
# 2 <- Phase
# 4 <- Alphabet size
# Phase nř0
# Transition matrix:
0.3945322543    0.1652811616    0.1535033485    0.2866832356
0.2758032675    0.208204727     0.2605722039    0.2554198016
0.3496152294    0.2310568942    0.1708121974    0.248515679
0.2312234494    0.2503993203    0.1515293118    0.3668479184
# Stationnary Probability:
0.3127105148    0.2114684268    0.1783495332    0.2974715251
# Phase nř1
# Transition matrix:
0.3923961961    0.163516403     0.1521005152    0.2919868858
0.2789719005    0.2082462898    0.2570550517    0.2557267579
0.352109549     0.2297549901    0.1679259742    0.2502094867
0.2320996136    0.2447917561    0.1520437956    0.3710648347
# Stationnary Probability:
0.3135417652    0.2089660861    0.1771006767    0.300391472
```

8.3 What's new

	[02/17/05]		Version 4.0.0: Mixture Transition Distribution models are available in the library, as the program estim_mtd and the **Phased-MTDMarkov**(p. 37) and **MTD-Markov**(p. 20) objects.
	[02/02/05]		New version 3.1.3, with man pages. No more limitations for **SequenceSet**(p. 62) in terms of sequences number.
	[01/24/05]		MTD model development starts with 1.75 (1 +1/2+1/4...) developers.
	[01/24/05]		Happy new year with version 3.1.2 available. estim_pm: time performance increases up to 40% (nice!) with an increase of 0.5% memory. Be careful: some programs options have slightly been modified.
	[12/14/04]		Stable version 3.1 available. Parcimonious **Markov**(p. 14): note a new **Partition**(p. 22) possibility where you can define a restricted alphabet of synonymous tokens for the markovian predictor -> usefull for proteins.
	[11/29/04]		Stable version 3.1 is currently tested by 5 beta testers, fixing a few bugs appearing in versions 3.0.x. Updated version 3.0.4 is also available. Improvments: libxml2

8.4 Bug and Feedback

- Bug report:

  If you experiment any bug with seq++, please send a mail to Vincent Miele `name@genopole.cnrs.fr` with the following subject "bug report". At last, feel free to add any relevant comments to that bug report. We will try to answer to most of those reports.

- Other feedback:

  seq++ is an emerging project which is still in evolution. Thus, your feedback is more than welcome to help us to get seq++ better than it is. For any suggestion or comment, please send a mail to Vincent Miele `name@genopole.cnrs.fr` with the following subject "feedback".

8.5 ToDo

Forthcoming developments:

- implementation of Mixture Transition Model (MTD) in release seq++-4.0 [in progress, released in February].

  Please send a mail to Sophie Lebre `name@genopole.cnrs.fr` for information on the topic.

- algorithm for Transcription factor binding site detection using seq++ modules [in test, released in February 2005].

8.6 Download and Installation

The package is written in ANSI C++ and developed on x86 GNU/Linux systems with GCC 3.3. It has been successfully tested with Intel ICC 8.0, on Sun systems using GCC 3.3 and Apple Mac OSX systems with GCC 3.1. Compilation and installation are compliant with the GNU standard procedure. seq++ is licensed under the GNU General Public License (**Licence**(p. 100)). Please visit the bottom links to download seq++.

NOTICE: The following procedure installs on your system both the library as a shared library and associated include files and the binaries such as estimation and simulation programs.

0/ Requirements : compilators C++ and F77, library GSL and XML2(optionnal).

1/ The installation procedure is explained in ./INSTALL. The classical way, compliant with the GNU standard procedure:

- ./configure (add "–enable-xml" to activate xml options, libxml2 required)
- make
- make install
- make docs (if you want to generate the html doc)

NB: for a debug compilation, add "–enable-debug and then le library name becomes "seqpp_g"

2/ You can then include files from seqpp by such an include

- exple: #include <seqpp/.....>

2'/ You can then use the binary programs.

- exple: estim_m –help

3/ You now must compile with the -lseqpp or use in your configure.in the set of instructions :

- AC_CHECK_LIB(seqpp, main)

4/ Don't forget to fit your $LD_LIBRARY_PATH for the linkage

8.7 Licence

Please visit the `GNU licences` web site.

8.8 References

Please feel to free to contact:

- Pierre-Yves Bourguignon `name@genopole.cnrs.fr` for details on Parcimonious models.
- David Robelin `name@genopole.cnrs.fr` for details on phased models and statistical calculus.
- Gregory Nuel `name@genopole.cnrs.fr` for details on Arnoldi algorithms.
- Sophie Lèbre `name@genopole.cnrs.fr` for details on Mixture Transition Distribution models.

Several references:

- Bourguignon,P.Y., Robelin,D. (2004) `Modeles de Markov parcimonieux` , Actes de JOBIM.
- Bourguignon,P.Y. (2005)`Parcimonious Markov Models`, submitted.
- Bühlmann,P., Wyner,A.J. (1999) Variable length Markov chains. Annals of Statistics, 27, 480-513.
- Bulyk M.L., (2003) Computational prediction of transcription-factor binding site locations, Genome Biology, 5:201.
- Borodovsky,M., McIninch,J.D., Koonin,E.V., Rudd,K.E., Medigue,C., Danchin,A., (1995) Detection of new genes in a bacterial genome using Markov models for three gene classes, Nucleic Acids Res., 25, 3554-62.
- Lebre,S. (2004) Estimation de modèle MTD, Evry Univ. Internal Report.
- Lehoucq R.B., Sorensen B., Yang C. (1996) ARPACK user's guide: solution of large-scale eigenvalue problems by implicitly restarted Arnoldi methods. Technical report, Rice University.
- Richard H., Nuel G., (2003) SPA: simple web tool to assess statistical significance of DNA patterns. Nucl. Acids. Res., 31(13):3679-81.
- Robelin D., Richard H., Prum B., (2003) `SIC: a tool to detect short inverted segments in a biological sequence.` Nucl. Acids. Res., 31(13):3669-71.
- Ron D., Singer Y., Tishby N., (1996) The power of amnesia: learning probabilistic automata with Variable Memory Length, Machine Learning, 25.
- Schbath S., Prum B., Turckheim E. d. (1995) Exceptional motifs in different Markov chain models for a statistical analysis of DNA sequences. J. Comp. Biol., 2:417-437.
- Stormo G.D. (1990) Consensus patterns in DNA. Methods Enzymol., 183:211-221.

Index