# **Simulating Beta-coalescents**

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#### **Abstract**

We describe C++ code for simulating a particular class of  $\Lambda$ -coalescents referred to as Beta-coalescents, adapting the algorithm in<sup>(2)</sup>. The incomplete Beta-coalescent is derived in<sup>(1)</sup>, and is a variant of the complete Beta-coalescent<sup>(3)</sup>.

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incbeta: simulate (incomplete) Beta-coalescents

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#### 2 Background

A  $\Lambda$ -coalescent is a continuous-time Markov chain on the partitions of  $\mathbb{N} := \{1, 2, ...\}$ ; restricted to  $\{1, ..., n\}$  for some  $n \in \mathbb{N}$  it has rates, for  $2 \le k \le n$ ,

$$\lambda_{n,k} = \int_0^1 t^{k-2} (1-t)^{n-k} \Lambda(dt) + a \mathbb{1}_{\{k=2\}}$$
 (1)

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where  $\Lambda$  is a finite measure on (0,1], i.e. without an atom at zero. A Beta-coalescent is a  $\Lambda$ -coalescent with rate, for  $1 \le \alpha < 2$ ,

$$\lambda_{n,k}^{\text{Beta}} = \frac{1}{B(M; 2 - \alpha, \alpha)} \int_{0}^{M} t^{k - \alpha - 1} (1 - t)^{n + \alpha - k - 1} dt$$
 (2)

where B(M; a, b) is the (incomplete) beta-function  $B(M; a, b) := \int_0^M t^{a-1} (1-t)^{b-1} dt$  for a given constant  $M \in (0, 1]$ .

An obvious approach to sample the process would be to compute the total rate of merging k blocks,

$$\mu_{n,k}^{\text{Beta}} := \binom{n}{k} \lambda_{n,k}^{\text{Beta}} \tag{3}$$

for all  $k \in \{2, ..., m\}$  and for all  $2 \le m \le n$ , with n the given sample size, and use the resulting probability distribution, sampling a merger size as

$$\max \left\{ i \in \{2, \dots, m\} : u < \frac{\mu_{m,i}^{\text{Beta}}}{\sum_{i=2}^{m} \mu_{m,i}^{\text{Beta}}} \right\}$$
 (4)

where u is a random uniform on the unit interval. However, for large n it may not be feasible to numerically evaluate  $\mu_{n,k}^{\text{Beta}}$ .

The code returns estimates of  $\mathbb{E}[B_i(n)/B(n)]$  where  $B_i(n)$  is the random length of branches supporting  $i \in \{1, ..., n-1\}$  leaves, and  $B(n) := B_1(n) + \cdots + B_{n-1}(n)$  is the total tree length. The ratio  $B_i(n)/B(n)$  is well defined since B(n) > 0 almost surely, and  $0 \le B_i(n)/B(n) \le 1$  almost surely.

### 3 Compilation and call

Compile the document with

latex -shell-escape clambdabetalargen.tex

Compile the code with

c++ -Wall -Wextra -Wshadow -Wnon-virtual-dtor -m64 -std=c++20
-march=native -pedantic -DNDEBUG clambdabetalargen\_minimal.cpp
-lm -lgsl -lgslcblas

The call is (see § 12 and § 13), given the executable is a.out:

./a.out <sample size> <alpha parameter> <K parameter>
\$(shuf -i 1000-100000 -n1)

#### 4 Includes

The included libraries.

```
#include <iostream>
#include <vector>
#include <random>
#include <functional>
#include <memory>
#include <utility>
#include <algorithm>
#include <ctime>
#include <cstdlib>
#include <assert.h>
#include <math.h>
#include <unistd.h>
#include <omp.h>
```

### 5 Random number generators

```
// obtain a seed out of thin air for the random number engine
std::random_device randomseed;
// Standard mersenne twister random number engine
// seeded with randomseed()
std::mt19937_64 rng(randomseed());
// the GSL random number generator
gsl_rng * rngtype;
// initialising rngtype
static void setup_rng(unsigned long int s)
{
const gsl_rng_type *T;
gsl_rng_env_setup();
T= gsl_rng_default;
rngtype= gsl_rng_alloc(T);
gsl_rng_set(rngtype,s);
}
```

#### 6 Sample from a beta-distribution

Use rejection sampling to sample from a beta-distribution Beta(M;  $2 - \alpha$ ,  $\alpha$ ) in case of incomplete Beta-coalescent Eq (2).

```
static double xreject( const double a, const double M)
{
  double x = gsl_ran_beta(rngtype, 2.0 - a, a);
  while( (x > M) || ( x <= 0.) ){
    x = gsl_ran_beta(rngtype, 2.0 - a, a); }
  assert( x > 0. );
  assert( x <= M);
  return( x);
}</pre>
```

### 7 Sample sojourn time

Sample time during which we see a given number of blocks, and a variate from a betadistribution. Note the total rate of mergers in a  $\Lambda$ -coalescent without an atom at zero can be written

$$\lambda_n = \int_0^1 \mathbb{1}_{\{0 < t \le M\}} \Big( 1 - (1 - t)^n - nt(1 - t)^{n-1} \Big) t^{-2} \Lambda(dt). \tag{5}$$

```
while ( gsl_rng_uniform(rngtype) >
   (((1. - pow(1.-x[0], n) - (n*x[0]*pow(1.-x[0], n-1.)))/(x[0]*x[0]))/R));
}
else{
   timi = ( -log(1. - gsl_rng_uniform(rngtype) )/R);}

return ( timi );
}
```

#### 8 Sample merger size

Sample a merger size given a probability of participating in a merger computed in § 7.

```
static size_t samplek( const size_t n, const double x )
{
    size_t k = 2 + (x > 0.0 ? gsl_ran_binomial(rngtype, x, n - 2) : 0);
    while(gsl_rng_uniform(rngtype) > 2./static_cast<double>(k*(k - 1))){
        k = 2 + (x > 0.0 ? gsl_ran_binomial(rngtype, x, n - 2) : 0);}
    return(k);
}
```

### 9 Update branch lengths

Update branch lengths of the branch length spectrum  $(B_1(n), ..., B_{n-1}(n))$  given a realised sojourn time from § 7.

### 10 Sum merging blocks

Sum the blocks sampled to merge given merger size sampled in  $\S$  8; returns the size of the new block. Given merger size k, the last k blocks of the shuffled tree (vector of block sizes) are merged.

### 11 Update estimate of $\mathbb{E}[B_i(n)/B(n)]$

Update estimate of  $\mathbb{E}[B_i(n)/B(n)]$  given a realisation of branch lengths.

#### 12 Estimate $\mathbb{E}[B_i(n)/B(n)]$

Estimate  $\mathbb{E}[B_i(n)/B(n)]$  by sampling trees and realisations of branch lengths.

```
// param_K is the cutoff parameter on the number of
// juveniles
  const int number_experiments = 100 ;
  int trials = number_experiments + 1;
  double timeTk {} ;
  size_t merger_size {};
  // compute the upper bound on the beta integral
  const double integral_upper_bound_M =
  (param_K > 0.0 ?
  param_K/(param_K + 1 + pow(2.0, 1.0 - param_alpha)/(param_alpha - 1.0))
                                                                   : 1.0);
  size_t new_block {} ;
  std::vector<double> v_branch_lengths (n + 1, 0.0);
  std::vector<double> v_ebib(n, 0.0);
  std::vector< size_t> tree__array__ (n, 1);
  double * prob_heads = (double *)malloc( sizeof(double));
  while( --trials > 0){
    /* run lots of experiments */
    tree__array__.clear();
    tree__array__.assign( n, 1);
   // initialise branch lengths vector
    std::fill( std::begin( v_branch_lengths),
           std::end( v_branch_lengths), 0.0);
   // generate a tree
    while( tree__array__.size() > 1 ){
      // sample time Tk
      timeTk = sample_interval_time(
                static_cast<double>( tree__array__.size() ),
                param_alpha, integral_upper_bound_M, prob_heads );
      // update branch lengths
      updateBranchLengths(v_branch_lengths,
                    tree__array__, timeTk);
      // sample merger size
     merger_size = samplek( tree__array__.size(),
                                  prob_heads[0] );
      // merge blocks and update tree
      std::shuffle( std::begin( tree__array__),
```

```
std::end(tree__array__), rng) ;
     new_block = sum_merging_blocks( tree__array__,
                                       merger_size);
      // remove the merged blocks from the tree
      tree__array__.erase( std::begin(tree__array__)
             + tree__array__.size() - merger_size,
                         std::end( tree__array__) );
      tree__array__.push_back( new_block);
    }
    // generated one tree
    assert( tree__array__.size() == 1);
    // add to estimate of E[B_i(n)/B(n)]
    update_estimate_ebib(v_ebib, v_branch_lengths, n);
  }
  // write out estimate of E[B_i(n)/B(n)]
  for( const auto &y: v_ebib){
    std::cout << y/static_cast<double>(number_experiments)
                                                 << '\n'; }
  // free memory
 free( prob_heads) ;
}
```

#### 13 The main function

## References

- [1] JA Chetwyn-Diggle, Bjarki Eldon, and Alison M. Etheridge. Beta-coalescents when sample size is large. in preparation.
- [2] Jere Koskela. Multi-locus data distinguishes between population growth and multiple merger coalescents. *Stat. Appl. Genet. Mol. Biol.*, 17(3):20170011, 21, 2018.
- [3] J Schweinsberg. Coalescent processes obtained from supercritical Galton-Watson processes. *Stoch Proc Appl*, 106:107–139, 2003.