Figure 1: Parameter estimation corresponding to λ

1 The algorithm

A reconstruction algorithm to generate complete trees from incomplete trees

begin
    $t = t_0$
  while $t < t_{present}$ do
        Update λ;
        calculate $\sigma = \sum \lambda_j$;
        simulate $\Delta t = rexp(\sigma)$;
        if $t + \Delta t < t_{i+1}$ then
                        $t = t + \Delta t$;
                        simulate extinction $t_{ext} = rexp(\mu_0)$;
                        if $t_{ext} + t < t_{present}$ then
                                update tree with new speciated-extincted specie
                        fi
        fi
        $t =$ next branching time t_i
  od
end

2 Analysis

The plots below shows scaterplots and histograms for each of the three parameter estimator: Each point in the histogram corresponds to one simulated tree; basically we simulate a tree, calculate the MLE of complete tree (x-axis), then drop extinct species, and performs the monte carlo framework using algorithm 1 inside it to get the MLE (y-axes) maximicing the join likelihood described in the apendix
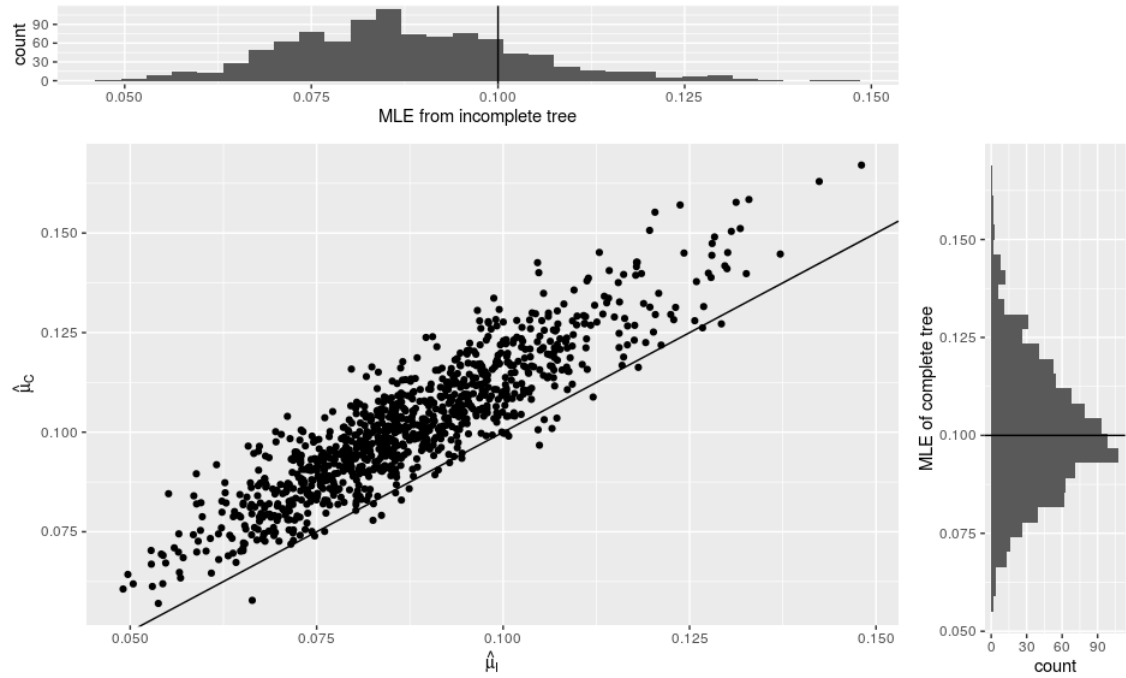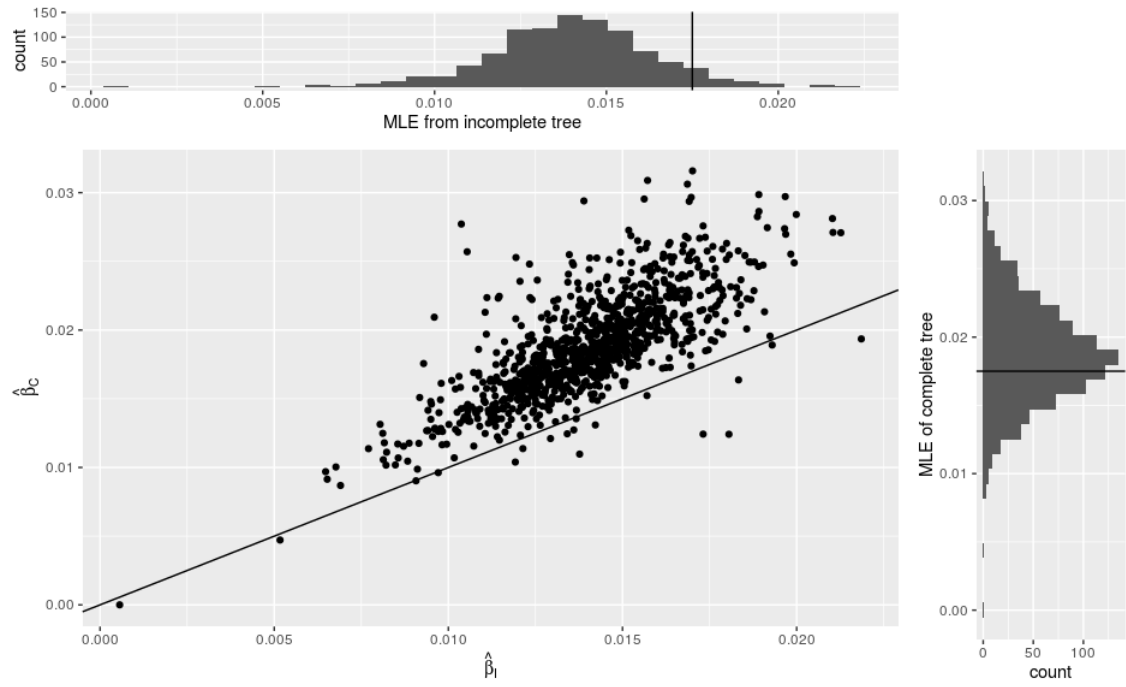
3   Conclusions

The reconstruction of tree using Algorithm 1 and the subsecuence ML estimation gives estimatos precise but not acurate, in other words biased estimators. This is the main potential reason of the non-estability of the EM algorithm (see example in appendix). This is maybe because the algorithm is generating less new species (figuras de los ltt plots y comparacion del numero de nuevas especies), To overcome this issue I see two posible ways:

- Work with algorithm 1 and use statistical tools to overcome the unbiased problem

- Search for an alternative to algorithm 1, it should makes slyghly more species

4   Appendix 1. General way for a multi-trees approach

Let $S = (s_1, ..., s_m)$ be a set of trees and $\mathcal{L} = (l_1(\theta), ..., l_m(\theta))$ the set of log-likelihood functions of S.

Then

$$l_j(\theta) = \sum_{i=1}^{N_j} -\sigma_{i,j} t_{i,j} + log(\rho_{i,j})$$

where N_j is the number of branching times of the $j-$tree, $t_{i,j}$ is the ith branching time of the j-tree and $\sigma_{i,j}$ and $\rho_{i,j}$ are functions of $\lambda_{i,j}(\theta)$ and $\mu_{i,j}(\theta)$, which are the speciation and extinction rates of the species of the tree j at time $t_{i,j}$ as described in previous reports.

In order to solve the E-step on the EM rutine, under the monte-carlo approach, we need to calculate

$$l(\theta) = \sum_{j=1}^{m} l_j(\theta)$$

the M-step corresponds to find $\max_\theta l(\theta)$.

4.1 Diversity dependence model

As described previously, we define

$$l_j(\theta) = log(L(\theta \| s_j))$$

in the case of diversity-dependence, where we have

$\sigma_{i,j} = n_{i,j}\lambda - \beta n_{i,j}^2 + n_{i,j}\mu$
$\rho_{i,j} = E_{i,j}(\lambda - \beta n_{i,j}) + (1 - E_{i,j})\mu$

Thus,

$$l_j((\lambda, \beta, \mu)) = \sum_{i=1}^{N_j} -t_{i,j}[n_{i,j}\lambda - n_{i,j}^2\beta - n_{i,j}\mu] + log(E_{i,j}(\lambda - \beta n_{i,j}) + (1 - E_{i,j})\mu)$$

Moreover,

$$l(\theta) = \sum_{j=1}^{m}\sum_{i=1}^{N_j} -t_{i,j}[n_{i,j}\lambda - n_{i,j}^2\beta + n_{i,j}\mu] + log(E_{i,j}(\lambda - \beta n_{i,j}) + (1 - E_{i,j})\mu)$$

where, as in the case of 1 single tree, we can find an analytical solution for the parameter μ

$$\mu = \frac{\displaystyle\sum_{j=1}^{m}\sum_{i=1}^{N_j}(1 - E_{i,j})}{\displaystyle\sum_{j=1}^{m}\sum_{i=1}^{N_j}t_{i,j}n_{i,j}}$$

and the other two parameters might be calculated under the same framework of the single tree case.

5 EM Example (seed 7)

EM example below.

Table 1: EM iterations

it	λ	β	μ	K
1	1.43	0.015	0.55	58
2	1.09	0.01	0.43	66
3	0.85	0.007	0.36	70
4	0.71	0.0055	0.32	71
5	0.63	0.005	0.28	69
6	0.61	0.0055	0.25	65
7	0.59	0.006	0.23	61
8	0.57	0.0065	0.20	57
9	0.55	0.007	0.18	53
10	0.53	0.0075	0.15	50
11	0.51	0.008	0.13	47
12	0.51	0.009	0.11	44
13	0.51	0.0095	0.10	43
14	0.49	0.0095	0.08	43
15	0.47	0.0095	0.07	42
16	0.45	0.0095	0.06	41
17	0.43	0.0095	0.06	39
18	0.41	0.009	0.05	40
19	0.43	0.01	0.04	39
20	0.39	0.009	0.03	40
21	0.39	0.009	0.03	40
22	0.37	0.0085	0.03	40
23	0.35	0.008	0.02	41
24	0.37	0.009	0.02	39
25	0.37	0.009	0.01	39
26	0.37	0.009	0.01	40
27	0.35	0.0085	0.01	40
28	0.35	0.0085	0.01	40
29	0.35	0.0085	0.01	40
30	0.35	0.0085	0.01	40