

1 Coupled MCMC in BEAST 2

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Abstract

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Coupled MCMC has long been used to speed up phylogenetic analyses and to make use of multi-core CPUs. Coupled MCMC uses a number of heated chains with increased acceptance probabilities that are able to traverse unfavourable intermediate states more easily than non heated chains and can be used to propose new states. While more and more complex models are used to study evolution, one of the main software platforms to do so, BEAST 2, was lacking this functionality. Here, we describe an implementation of the coupled MCMC algorithm for the Bayesian phylogenetics platform BEAST 2. This implementation is able to exploit multiple-core CPUs while working with all models and packages in BEAST 2 that affect the likelihood or the priors and not directly the MCMC machinery. We show that the implemented coupled MCMC approach is exploring the same posterior probability space as regular MCMC when MCMC behaves well. We also show our implementation is able to retrieve more consistent estimates of tree distributions on a dataset where convergence with MCMC is problematic.

Introduction

Phylogenetic method are being increasingly used to study complex population dynamics by using ever larger datasets. These analyses however also require an increasingly large amount of computational resources. Tree likelihood calculations (Suchard and Rambaut, 2009) often assume independent evolutionary processes on different branch and nucleotide site and can be easily parallelised (Suchard and Rambaut, 2009). In contrast to that, it can be very complex or even impossible to for example parallelise tree prior calculations to make use of multi-core CPUs. As a results, Markov chain Monte Carlo (MCMC) runs can be very time consuming, which limits the datasets that can be studied and the complexity of models that can be used to do so. Alternatively, coupled Markov Monte Carlo, also called parallel tempering, Metropolis coupled MCMC, or MC3, can be used in Bayesian phylogenetics Altekar *et al.* (2004). This approach is based on running multiple MCMC chains, each at a different “temperature”, which effectively flattens the posterior probability space. This leads to less favourable moves being accepted more often, and in turn increases the chance to travel between local optimas. After some amount of iterations, two chains are randomly exchanged in what is essentially an MCMC move. In such a move, the parameters of the two chains are exchanged, but each chain keeps its temperatures. While the heated chains do not explore the true posterior probabilities, the one cold chain does.

In BEAST 2 (Bouckaert *et al.*, 2014), where a lot of novel Bayesian phylogenetic model development takes place (Bouckaert *et al.*, 2018), this approach is currently missing. Here, we provide such an implementation of the coupled MCMC algorithm of Altekar *et al.* (2004) in BEAST 2. This implementation makes use of multiple CPU cores, allowing virtually any analyses in BEAST 2 to be performed on multi-core machines increasing the size of datasets that can be analysed and the complexity of models that can be used to do so.

We first show the correctness of our implementation of the coupled MCMC by comparing summary statistics of multi type tree distributions sampled under the structured coalescent (Vaughan *et al.*, 2014) to the summary statistics received when using regular MCMC. Additionally, we validate that the inference between regular MCMC and our implementation of coupled MCMC match, when applying both to infer the past population dynamics of Hepatitis C in Egypt (Ray *et al.*, 2000; Pybus *et al.*, 2003). We then compare MCMC with coupled MCMC using different levels of heating on two different datasets. First, we apply it to the Hepatitis C dataset, where we do not expect regular MCMC to be stuck in local optimas. Then, we apply it to a dataset which has been described to be easily stuck in local optimas (Lakner *et al.*, 2008; Höhna and Drummond, 2011).

Methods and Material

Background

Coupled MCMC makes use of running n different chains $i = 1, \dots, n$ at different temperature (Geyer, 1991; Gilks and Roberts, 1996; Altekar *et al.*, 2004). Each of the different chains works similar to a regular MCMC chain. In regular MCMC, a parameter space is explored as follows: Given that the MCMC is currently at state x , we propose a new state x' from a proposal distribution $g(x'|x)$ given the current state. At this new state,

79 we calculate the likelihood $P(D|x')$ of the data D given the state and the
80 prior probability of the new state $P(x')$ and compare it to the old state.
81 The acceptance probability of accepting this new state is then calculated
82 as follows:

$$R = \min \left[1, \frac{P(D|x')P(x')}{P(D|x)P(x)} \frac{g(x|x')}{g(x'|x)} \right] \quad (1)$$

83 If R is greater than a randomly drawn value between $[0, 1]$, the new state
84 x' is accepted as the current state, otherwise it is rejected and we remain
85 in the same state. If we keep proposing new states x' and accept these
86 using (1), we eventually explore parameter space with the frequency at
87 which values of a parameter are visited being its marginal probability
88 (Geyer, 1991).

One of the issues of using this approach is that acceptance probabilities can be quite low, which makes it hard to move between different states in parameter space. Alternatively, an MCMC chain can be heated by using a temperature scaler $\beta_i = \frac{1}{1+(i-1)\Delta\bar{\tau}}$, with i being the number of the chain (Altekar et al., 2004). Heating of an MCMC chain changes its acceptance probability R_{heated} to:

$$R_{heated} = \min \left[1, \left(\frac{P(D|x')P(x')}{P(D|x)P(x)} \right)^{\beta_i} \frac{g(x|x')}{g(x'|x)} \right]$$

For a heated chain however, the frequency at which a value of a parameter is visited does not correspond to its marginal probability any more. However, heated chains can be used as a proposal to update the non heated chain by using what essentially is an MCMC move. This move proposes to swap the current states of two random chains i and j with the temperature β_i and β_j such that $\beta_i < \beta_j$. Exchanging the states of chains i and j is accepted with an acceptance probability R_{ij} of:

$$R_{ij} = \min \left[1, \frac{P(x_i|D)^{\beta_j} P(x_j|D)^{\beta_i}}{P(x_i|D)^{\beta_i} P(x_j|D)^{\beta_j}} \right]$$

89 As for a regular MCMC move, swapping the states of the two chains is
90 accepted when a randomly drawn uniform distribution value in $[0, 1]$ is
91 smaller than R_{ij} .

92 Implementation

93 In our implementation of the coupled MCMC, we run n different MCMC
94 chains, with each chain $i \in [1, \dots, n]$ running at a temperature $\beta_i =$
95 $\frac{1}{1+(i-1)\Delta\bar{\tau}}$. Chain number 1 is therefore the only cold chain and explores
96 the state space like a regular MCMC chain.

97 Upon initialisation, we first sample at random at which iteration the
98 states of two chains with which number are proposed to be exchanged. We
99 then initialise each chain to be run in its own Java thread using multiple
100 CPU cores, if available. Each chain is then run for as many iterations
101 until it reaches the next time an exchange of states with another chain
102 is proposed. This means that every chain runs independently of each
103 other until an iteration at which it actually participates in a proposed
104 exchange, minimising the crosstalk between threads Altekar et al. (2004).
105 If the exchange of states between different chains is accepted, we exchange
106 the temperature of the two chains instead of the states themselves. The
107 states can be quite large and exchanging them across different chains
108 is potentially quite time consuming. Alongside exchanging the states, we

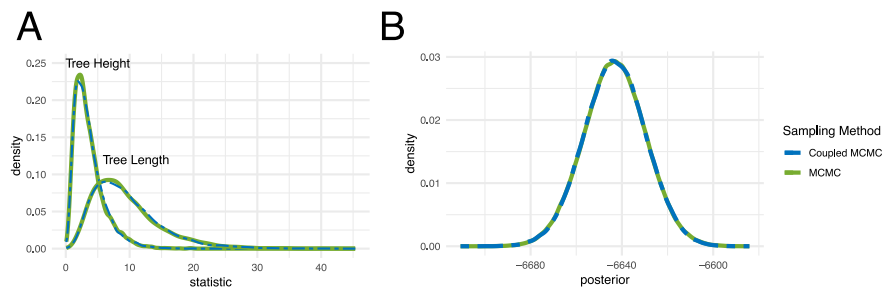


Figure 1: **Comparison of inference between coupled and regular MCMC.** **A** Comparison of the distribution of tree heights and tree lengths sampled under the structured coalescent using MultiTypeTree (Vaughan *et al.*, 2014). The inferred distribution of tree heights and tree lengths match up between MCMC and the cold chains in coupled MCMC. **B** Comparison of the distribution of posterior probability estimates of a Bayesian Coalescent Skyline (Drummond *et al.*, 2005) analysis of Hepatitis C in Egypt (Ray *et al.*, 2000).

109 exchange the operator specifications and logger. We exchange the operator
110 specifications such that the step size of operators can be optimized to run
111 at specific temperatures. The loggers are exchanged such that each heated
112 chain logs its states to the log file that corresponds to its temperature and
113 not the number of the chain.

114 We implemented the coupled MCMC algorithm such that finished runs
115 to be resumed. In case that chains did not fully convergence just yet, it
116 is not necessary to restart the analysis scratch, which is of great practical
117 value.

118 Usually, a graphical user interface called BEAUti is used to set up
119 BEAST 2 analyses. Setting up analyses with coupled MCMC works dif-
120 ferently depending on whether a BEAUti template is needed to set
121 up an analysis as required for some packages. If no such template is
122 needed, an analysis can be set up to run with coupled MCMC directly
123 in BEAUti and we provide a tutorial on how to do this on <https://taming-the-beast.org/tutorials/CoupledMCMC-Tutorial/> (Barido-
124 Sottani *et al.*, 2017).
125

126 Data Availability and Software

127 The BEAST 2 package coupledMCMC can be downloaded by using the
128 package manager in BEAUti. The source code for the software pack-
129 age can be found here: <https://github.com/nicfel/CoupledMCMC>. The
130 XML files used for the analysis performed here can be found in <https://github.com/nicfel/CoupledMCMC-Material>. All plots were done using
131 ggplot2 (Wickham, 2016) in R (Team *et al.*, 2013).
132

133 Validation

134 Similar to the validation of MCMC operators, we can sample under the
135 prior to validate the implementation of the coupled MCMC approach. To
136 do so, we sampled typed trees with 5 taxa and two different states under
137 the structured coalescent using MultiTypeTree (Vaughan *et al.*, 2014).

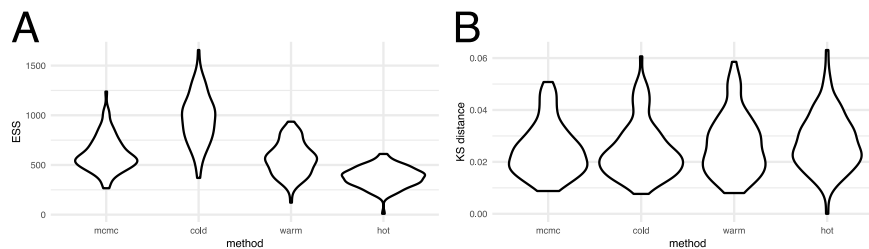


Figure 2: Convergence of coupled MCMC and regular MCMC using posterior ESS values and Kolmogorov Smirnov distances. **A** Here, we show the distribution of posterior ESS values after 4×10^7 for regular MCMC and after 1×10^7 for coupled MCMC with 4 chains. The cold scenario uses coupled MCMC, but does not use any heating. The warm scenario uses slightly heated chains and the hot scenario relatively hotter chains. **B** Here we show the distribution of Kolmogorov Smirnov distances between individual runs and the concatenation of all individual runs. We assume that all 400 runs concatenated describe the true distribution of posterior values and then take the KS distance as a measure of how good an individual run approximates that distribution. The smaller a KS value, the better the true distribution was approximated.

138 We did this sampling once using regular MCMC and once using coupled
139 MCMC. If the implementation of the coupled MCMC algorithm explores
140 the same parameter space as regular MCMC, parameters sampled using
141 both approaches should match. We ran coupled MCMC proposing to
142 exchange states between chains every 1000 iterations. In figure 1A, we
143 compare the distribution of different summary statistics of typed trees
144 between MCMC and coupled MCMC. For all the summary statistics considered
145 here, the distributions are the same.

146 Next, we validate that the coupledMCMC package estimates the same
147 parameters in a Bayesian coalescent skyline (Drummond et al., 2005) analysis
148 of Hepatitis C in Egypt (Ray et al., 2000). To do so, we analysed the
149 Hepatitis C dataset once using coupled MCMC with 4 chains and once using
150 regular MCMC. We find that the inferred posterior probability density
151 is the same between the two approaches(see figure 1B).

152 Results

153 The effect of heating on exploring the posterior

154 In order to explore how heating affects exploring the posterior probability
155 space, we first compare effective sample size (ESS) values between regular
156 and coupled MCMC at different temperatures on a dataset where we do
157 not expect any problems in exploring the posterior space caused by several
158 local optimas. To do so, we ran the Bayesian coalescent skyline (Drummond
159 et al., 2005) analysis of Hepatitis C in Egypt (Ray et al., 2000)
160 for 4×10^7 iterations using regular MCMC in 100 replicates. Additionally,
161 we performed 100 replicates using coupled MCMC on 4 different chains
162 for 1×10^7 iterations using 3 different temperature scalers referred to as
163 cold, warm and hot. The different chains lengths are chosen such that the
164 overall number of iterations over the cold and heated chains is the same
165 for coupled as for regular MCMC. In the cold scenario, we did not use any

166 heating and exchanges between chains were accepted with a probability
167 of about 100%. In the other two scenarios, we used heating such that ex-
168 changes between chains were accepted with around 50% in the warm and
169 with about 25% in the hot scenario. After running all 4 times 100 anal-
170 yses, we computed the ESS values of the posterior probability estimates
171 using loganalyser in BEAST 2 (Bouckaert et al., 2014).

172 As shown in figure 2, the average ESS values are highest for the cold
173 scenario when using coupled MCMC and drop the stronger the temper-
174 ature scaler becomes. Regular MCMC gets in average slightly lower ESS
175 values when using 4 times longer chains. The trends of ESS values are the
176 same when calculating ESS values using coda (Plummer et al., 2006) (see
177 figure S1).

178 In order to assess if coupled MCMC approximates the true distribution
179 of posterior values better than regular MCMC, we compared Kolmogorov-
180 Smirnov (KS) distances between individual runs and the true distribution
181 of posterior values. Since we can not directly calculate the true distribution
182 of posterior values, we concatenated the 400 regular and coupled MCMC
183 runs and used the concatenated distribution of posterior values as the
184 true distribution. Figure 2 shows the distribution of KS distances between
185 individual runs using regular and coupled MCMC to what we assume to
186 be the true distribution. In contrast to the comparison of ESS values,
187 we find that the distribution of KS distances is fairly comparable across
188 all methods. This indicates that in this analysis, coupled MCMC with 4
189 individual chains performs equally well as regular MCMC run for 4 times
190 as long.

191 We next compare the inference of trees on a dataset DS1 that has
192 proved problematic for tree inference using MCMC (Lakner et al., 2008;
193 Höhna and Drummond, 2011; Maturana Russel et al., 2018). This dataset
194 has many different tree island, transitioning between which is highly un-
195 likely due to very unfavourable intermediate states (Höhna and Drum-
196 mond, 2011).

197 We ran the dataset using regular MCMC for $5 * 10^7$ iteration and cou-
198 pled MCMC for $5 * 10^7$ with 4 different chains. We ran coupled MCMC
199 without heating (cold) with a maximum temperature of 0.2 (warm) and
200 the maximum temperature being 1.0 (hot). MCMC converges to different
201 optimas, resulting in differences between inferred clade credibilities across
202 different runs (see figure 3). The clade credibilities are more comparable
203 when using multiple chains but no heating (cold). The increased consis-
204 tency of clade credibilities across runs is in this case due to the main
205 chain essentially being an average over 4 MCMC runs. When using heat-
206 ing (warm and hot), the heated chains are able to more easily cross the
207 unfavourable intermediate states in tree space, resulting in a better con-
208 sistency of clade credibilities across different runs for the warm scenario
209 and essentially the same clade credibilities across different runs in the hot
210 scenario.

211 Conclusion

212 Next generation sequencing has made ever larger datasets of genetic se-
213 quence available to researcher. To study these, more and more complex
214 models are developed, many of which are implemented in the Bayesian
215 phylogenetic software platform BEAST 2 (Bouckaert et al., 2014). Par-
216 allelising these models can often be hard or even impossible and MCMC

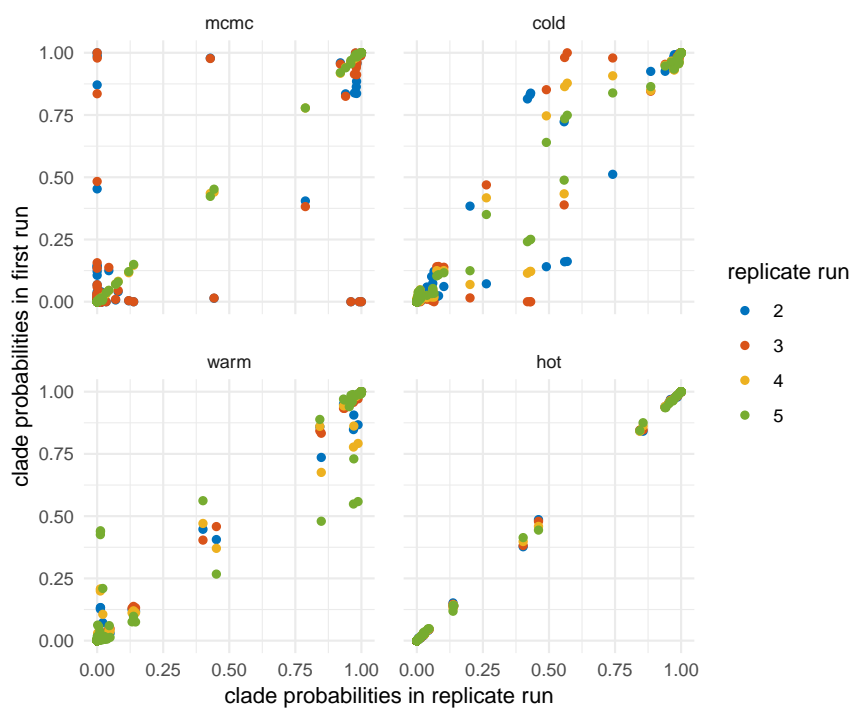


Figure 3: **Inferred clade probabilities between different replicate runs.** Here we compare inferred clade credibilities between one run (y-axis) and four replicates from different starting points (x-axis) using MCMC and coupled MCMC run at different temperature increments.

217 analyses often have to be run on single CPU cores. Alternatively, coupled
218 MCMC can make use of multiple cores, but a full featured version was
219 so far not available in BEAST 2. Here, we provide an implementation of
220 the coupled MCMC algorithm for BEAST 2.5 (Bouckaert *et al.*, 2018).
221 We showed that this implementation explores the same posterior space as
222 regular MCMC and we give an example for when the heating of chains
223 can drastically improve convergence. While ESS values are higher on cou-
224 pled MCMC runs with 4 chains and no heated than on regular MCMC
225 runs that are run for 4 times longer, the distribution of posterior proba-
226 bility values was not better approximated by those runs. This indicates
227 that convergence statistics like the scale reduction factor (Brooks and
228 Gelman, 1998), might be better suited to assess convergence than ESS
229 values. Since the coupled MCMC runs required 4 times less iterations of
230 the cold chain to approximate the distribution of posteriors values as well,
231 coupled MCMC can help speed up analysis by a factor that is approxi-
232 mately proportional to the number of CPU's used. This implementation
233 is compatible with other BEAST 2 packages, so works with any model
234 that works with MCMC.

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238 Authors contribution

239 NFM and RB implemented the code, NFM performed the analyses and
240 NFM and RB wrote the paper.

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