05-Apr-2025  
  
Dear Dr Boyko:  
  
Decision on USYB-2024-270, Automatic Discovery of Optimal Discrete Character Models:  
  
Major revisions.  
  
Thank you for your Systematic Biology submission. It has been reviewed by Associate Editor Professor Josef Uyeda and two expert reviewers. Their comments are listed at the end of this letter. The reviewers and the AE provide some excellent constructive suggestions that I am sure you will appreciate. I really want to emphasize that I found the suggestions from both reviewers and the AE extremely constructive.  
**Thank you for..**

E.1. The main concerns are (1) the lack of discussion to the RJ-MCMC approach of Pagel, and (2) a better description of the models and algorithms that were newly developed. I absolutely agree with this assessment.

**A: I have taken steps to correct both problems. In the introduction I have added a description of the RJ-MCMC approach and how it compares to what is being proposed here (Reviewer 1 was kind enough to point out several key differences). I have also added a more detailed description and figure for the main dredging algorithm. This algorithms for searching model structures have changed significantly from the original version in order to provide theoretical grantees of a global optimum.**

E.2. I also struggled a bit to fully understand each specific step in the dredge procedure. Maybe some more visual examples, also including the hidden states, could help.

**A: Agreed, I have added a figure to visualize the dredging process.**   
  
Some minor comments from my own reading:  
E.4: Please check in the entire manuscript that in-line equations and math symbols have spaces around them.  
**A: Apologies, I had originally used an open text document format, and during conversion to docx, some of the formatting was changed. This should be corrected now.**

E.5: line 33-39: This could have more broader background and citations. Also, please define what you mean by complex characters.

**A: I meant multistate, rather than complex. I have chanted to wording.**

E.6: line 73: Could you please consider adding the equation k=(2^s)\*(2^s-1), where s is the number of binary characters.

**A: Done.**

E.7: line 77: I would not say "likelihood-based" but instead Maximum Likelihood, as Bayesian inference is also likelihood-based and might show different behaviour.

**A: Corrected.**

E.8: line 111: Please cite the original pruning algorithm by Felsenstein

**A: Corrected.**

E.9: line 117-119: Please add citations.

**A: Corrected.**

E.10: line 166: Could you explain your approach to ensure the identifiability better? More specifics would help.

**A: Apologies, I have added some additional description and the relevant citation which describes the issue in detail.**

E.11: line 190-209: Perhaps you could briefly emphasize how your cross-validation approach connects and is different from this one <https://doi.org/10.1093/sysbio/syad004>

**A: A fascinating paper, I had not seen it! In this paper, the sampling is based on.. Whereas my implementation is a basic type of k-fold cross-validation differing only in the sampling being weighted by phylogenetic distance.**

E.12: Results: The Mk model represents the unconstrained model, i.e., the ARD model? Why not call it ARD? Also, in my understanding the Mk is the same as the ER model.

**A: You are correct, this error has been corrected.**

E.13: Results: Since for rates the fold changes is more important than the actual change, please consider re-evaluating the simulations by computing the bias and variance on the the log-rates.

**A: True. The choice was made for empirical settings, but I’ve done both. Log rates make more sense in terms of bias versus variance.**

E.14: Simulations: Would it be possible to plot, e.g., a histogram, the number of transition across the phylogeny? I'm curios if the shown power has to do with the number of transitions.

**A:**

E.15: Empirical Example: Could you provide confidence intervals for the parameter estimates?

**A: Added.**

Associate Editor Recommendation: Recommendation #1: Major Revision  
  
Associate Editor's comments to author (if any):  
Associate Editor: Uyeda, Josef  
Comments to the Author:  
Dear Dr. Boyko,  
Thank you for your submission "Automatic Discovery of Optimal Discrete Character Models". Your manuscript has been reviewed by two expert reviewers, and both find that the manuscript is very timely and likely of substantial interest to the readers of Systematic Biology. I concur with these assessments. Both reviewers also have provided extensive comments to improve the manuscript.

**A: Thanks**

AE.1: Reviewer 1 points out the similarity of the approach to the Reversible-Jump approach developed by Pagel and Meade. No discussion is made of this approach or a Bayesian framework, despite the similarity in objectives.

**A: Will do**

AE.2: Furthermore, both reviewers ask for how the dredge approach works for a "negative control" of two independently evolving characters.

**A: I have added a negative control. In fact, the original simulation did include a negative control in the form of independent relationships (only half of the states had dependent relationships). However, for the original submission, it had not occurred to me to report the success of finding true independent relationships. Thus, there is no additional simulation, but I now report the success rates for both dependent and independent relationships.**    
  
AE.3: Line 156 - should be "within the regularized model are"

**A: Corrected.**  
  
AE.4: Line 265, 419, 422 - The order here for condition 3 doesn't make sense, and is in conflict with line 282. Should be q34 (=10) > q21 (=5) > qij (=1?); although it's not clear what qij refers to.

**A: The final test (q34 (=10) > q21 (=5) > qij (=1?)) was meant to determine if the model correctly inferred the relative rates with qij being all other rates not q34 or q21. This test has been removed in favor of focusing on the correlated trait dynamics (finding dependent and independent relationships).**

AE.5: Line 467 - "better behaved" and "clean likelihood peaks and reasonable confidence intervals". I see what is meant regarding information but it gives the impression we can evaluate models by the cleanliness of their peaks and the reasonableness of their CI's, but it's unclear to me exactly what model selection philosophy supports that, or how those can be quantitatively evaluated. I'm not sure that's the implication that's intended, but it's possibly what could be received by the reader. True models can presumably sometimes have wide confidence intervals and poorly behaved likelihood peaks. The answer is provided later in Line 484, but again no citations to indicate that this necessarily "demonstrates the value" of the approach. *How is this different from, for example, choosing the model in statistical phylogenetics that maximizes your bootstrap scores or posterior probabilities in your topology ?* This would be a very poor way of evaluating models, as we want our models to reflect our true uncertainty on our target of inference, not arbitrarily choose models that necessarily give us "cleaner" results.

**A: This is a great point. I did not intend to imply that model selection should be based on the width of a model’s CI, but I can see how the text would lead a reader to that conclusion. I have changed the text to be clear that we should not compare models based on the behavior of their profile likelihoods. I do believe there is legitimate value in both examining the likelihood surface (more common in Bayesian settings to be sure) and having a model where the dataset is informative of the parameters (sensu Fisher information). But I would not want to suggest forgoing classic model selection techniques in favor of using a model with the lowest possible CI (or maximizing bootstrap scores from your example). I think what interested me about these dredge results was the fact that I did not forgo classic model selection, but by expanding the set of models being examined the optimal model was one which had parameters which are well informed by the data. I think I’m suffering from the same problem pointed out in AE.11 where I am overgeneralizing a single empirical result, and I have been more careful with discussing the implications of this result. Also note that a large part of this section was changed because of new empirical results (adding hidden states to the dredge).**   
  
AE.6: The use of "standard corHMM model" throughout is a bit confusing/misleading. The model used is a standard Pagel model for correlated traits implemented in corHMM, and does not contain hidden states. Nothing about a Pagel model is the standard approach for how corHMM models discrete traits is it? It's one of many models that can be implemented in the package.

**A: True, when I say standard corHMM model I mean default settings. Poor wording on my part and this has been corrected throughout the text.**   
  
AE.7: Figure 5 - It's kind of ambiguous if the lower right panel of profile likelihoods falls under the b) or d). I'd also say that it's somewhat hard to compare them because the x-axes are in strange and not common units. e.g. it takes a fair amount of work to compare Theta\_1 in a) and b) and Theta\_2 to Theta\_3 in a) and b).

**A: Good point. I have made new figures based on these comments.**

AE.8: Line 479 - Adding to Reviewer 1's flagging of this issue, this is an additional location in the text where an apparent conflict between what is stated and what is in Figure 4. It says there is a slight preference for multimale mating, but in the figure it says it's monogamy that is slightly preferred. Figure 4 shows monogamy being preferred.

**A: Yes, this should be… I have corrected it.**   
  
AE.9: Line 497 - In light of the simulation study, the great uncertainty among models, and the very variable outcomes to ancestral state estimation, I think this discussion overinterprets the results. It is striking to say on the one hand that the dredged model changes the ancestral state reconstructions to a previously undescribed one but that is supporting a previous hypothesis, discuss its implications at length, and then in the next section, point out that regularization doesn't improve ancestral state estimation. Are readers to cite this study as providing evidence for one hypothesis of primate evolution over another, or should we simply view any ancestral state reconstruction with this dataset with great skepticism?

**A: Yes, ASR is overinterpreted. Model selection matters though. Honestly, who knows? This is even more relevant with the new results because in adding a hidden state I found a different strongly supported model….**  
  
AE.10: Line 525 - "state reconstructions" not "state reconstructs"

**A: Corrected.**  
  
AE.11: Line 524-530 - This discussion is not clear to me. That the marginal reconstructions can change across slight differences in models is one thing, but it does not speak to accuracy like your simulation results do, because we don't know the truth there. However, you're not comparing the same thing in this discussion. On the one hand you're talking about the consistency of the reconstructions across alternative models in the empirical study, while in the other you're discussing accuracy of reconstructions in the simulations. It's not clear to me what you're saying in Line 527. For example, suppose that in your simulation study your Mk model compared to your L2 model both recover ancestral states at the same rate under a particular set of conditions. It's unclear to me what this number would mean for how often they differed in their reconstructions at a set of key nodes that change biological interpretations. It could easily be quite common, I would think. The fact is the empirical study is one realization. Overall, I'm just confused on the relationship between accuracy and "robustness" of ancestral estimations that is being implied. I may be being dense here.

**A: Good point. You’re right to point out that I have overinterpreted a single empirical result. I suppose I was just struck by how minor differences in model structure would lead to very different ancestral reconstructions, but “walking along” the likelihood ridge and examining the same model structure with parameter estimates orders of magnitude apart led to very similar ancestral reconstructions. But it’s true this was not something I set out to test and thus my simulations don’t speak to this. So as not to overstate the generality of this point, I have removed this as its own section and included a more modest version at the end of the first discussion section. It’s stated more as an area of future research rather than as a concrete finding.**

AE.12: Line 556 - Shouldn't this be "homology over homoplasy"?

**A: Yes, thank you for pointing that out.**   
  
AE.13: Line 584-586 - Is this referring just to hidden state models? Otherwise I don't know what rate classes mean in this context.

A:  
  
AE.14: Figure S2 - Related to the discussion above about lines 524-530, I don't think I understand the procedure for Figure S2. From which models 95% CI are these high rates sampled? Jointly or independently for each transition rate? Or is it for the corHMMDredge model? I think the discussion of increasing rates is worth discussing within the context of phylogenetic signal. If all transition rates are arbitrarily large, the assumption is that the process has no phylogenetic signal and all nodes should be a their stationary distribution. This is usually what I assume leads to likelihood ridges (or as stated, low frequency states). However, that's clearly not the case for Figure S2, or the empirical example generally. Is it the case for the simulation results? Should this be factored in to how they are summarized? Presumably, across complicated model structures, many equivalent stationary distributions could be obtained with a variety of high transition rates configurations.

**A: Apologies for the lack of clarity. The 95% CI are generated via profile likelihood, so they are generated independently. I then take a value that is 1000x the MLE for only one of the rates. This 1000xMLE is still within the 95% CI. I then do a marginal reconstruction replacing one of the MLEs with the 1000xMLE – the expectation being such a biologically meaningful difference in rates would lead to a different ASR. But that is not what I find. The ASR estimates are essentially the same. Nonetheless, as you point out in AE.11, I have overinterpreted this result. I would need to know the true reconstructions and test this type of problem (influence of sampling CI vs alternative model structures) in a more systematic way across many simulation scenarios to have confidence in this pattern. As such I have removed this point from the paper. This is in-line with the changes made based on AE.11.**

Reviewer(s)' comments to author (if any):  
Reviewer: 1  
  
Comments to the Author  
Automatic discovery of optimal discrete character models  
Systematic Biology  
Review, January 2025  
  
Reviewer expertise: phylogenetic comparative methods, discrete character models, vertebrate evolution  
  
Evolutionary models for discrete (or categorical) characters are ubiquitous in evolutionary biology, anthropology, linguistics, and beyond; however, as these models increase in complexity, so do the number of potential models to explain a given dataset. The author presents a dredge framework for automatically detecting the optimal model structure that balances model fit (likelihood) and complexity (number of parameters). The framework uses a regularization scheme to penalize more complex models and a parameter sharing method for equating and reducing the number of rate parameters. The study conducts simulations to compare the performance of the regularized models over traditional ones, and how often the automatic model selection recovers the models used to simulate the data. Then, the author applies this framework to the study of primate mating systems and compares their results with those of previous studies.  
  
R1.1: Overall, the dredge framework is a welcome and complementary contribution to modeling the evolution of discrete characters. I particularly appreciate the integration of this framework into the corHMM R package to include hidden Markov models and >2 binary characters. I agree with the author's goal of automating the search for a wider set of potential models while balancing model fit and complexity. I think this is a promising approach. However, I'm concerned about the dredge procedure's ability to explore a wide enough set of potential models. The current manuscript also lacks comparisons with the reversible-jump Markov chain Monte Carlo procedure described by Pagel and Meade (2006), which attempts to accomplish the same goal. And, in some ways, I would argue the RJMCMC procedure is better equipped to do this than the current implementation of the dredge procedure.

**A: Absolutely agree. RJMCMC is the gold standard with theoretical garuntees I simply can’t provide. As you point out, the main advantage is computation.**   
  
**Major concerns**  
R1.2 One of my main concerns is that, while referencing Pagel and Meade (2006) many times in the manuscript, and even using its data, the author refrains from mentioning that Pagel and Meade (2006) already devised an approach for automatically exploring different model structures while accounting for model complexity. There are a few details that distinguish Pagel and Meade’s model from the proposed dredge framework: 1) it is implemented in a Bayesian framework using reversible-jump Markov chain Monte Carlo (RJMCMC); 2) it doesn’t settle on one optimal model but quantifies the frequency of accepted models proposed throughout the MCMC; and 3) that model currently doesn’t allow for >2 binary characters or HMM. Despite these key differences, I found the lack of comparisons or discussion of the RJMCMC procedure surprising given that it seems to accomplish what the author has set out to do. This manuscript would be much improved by adding that context and some comparisons with Pagel and Meade’s RJMCMC procedure. For example, how does the author's parameter sharing procedure compare with the merging/splitting and augmenting/reducing operations of Pagel and Meade’s RJMCMC model?

**A: It is an oversight, no doubt about it. I was mainly concerned with outlining what I see as the problem of standard model sets only being applied. I should have written more extensively about the methodological similarities.**   
  
R1.3 The two approaches (the author’s dredge framework, and Pagel and Meade’s RJMCMC) also seem to differ in modeling philosophy. The author states the dredge approach is more parsimonious (lines 554-556 of PDF document), whereas Pagel and Meade’s RJMCMC uses a Bayesian framework to assess the frequency and probability of competing models. In my opinion, a parsimony-inspired framework seems antithetical to a model-based approach to study evolution. However, regardless of opinion on which framework is best to use, I think it would make this manuscript more holistic if the author discussed and compared these two approaches and philosophies.

**A: Interesting. What do I think about the differences in philosophy? I’m not sure.**   
  
R1.4: I’m also concerned that the author’s parameter sharing procedure doesn’t adequately explore the suite of potential models. Namely, the procedure only moves in one direction toward reducing the model and, therefore, does not evaluate other combinations of rate parameters that do not directly reduce from the initial model. For example, other simple models may fit the Old World primate data just as well as the one chosen through the dredge procedure (Figure 5c), but the rate parameters of those models were removed from consideration because they were estimated as close to 0 in the initial model. In contrast, Pagel and Meade’s RJMCMC allows rate parameters to either split after previously being equated or to be allowed back into the model (augment) after being reduced or removed from the model (i.e., set to 0). Indeed, Pagel and Meade (2006) find that there are many simple models with two or fewer non-zero rate classes that equally explain the primate data. Many of these models overlap with the model chosen by the author’s dredge procedure (if you compare Figure 5c with Table 2 in Pagel and Meade 2006). Of course, Bayesian RJMCMC is more computationally intensive than the author’s dredge framework; however, if the author’s intended goal is to explore a larger model space while overcoming problems of over-parameterization, I’m afraid the dredge framework in its current implementation may not accomplish this as thoroughly as RJMCMC.

**A: Yes, I agree. RJMCMC is the gold standard and comes with theoretical guarantees on top of that. I make this abundantly clear. Ultimately, this is meant to be a first step. This is not on the level of RJMCMC, for many reasons you have pointed out. But I think it is an improvement over how things are commonly done (as I often see them). My perspective could be biased, but I believe that individuals already emailing methods developers represent a biased sample of folks who are already going above and beyond. Of those who contact me, many are running default sets of models. Additionally, in papers I see model selection often a nuisance on route to ASR. So, in a sense, the goal is not so much to explore model space thoroughly, this would be a solved problem of RJMCMC. The goal is to provide a simple, better than current practices, while highlighting some of the issues that I hope empiricists will care about.**

**I have also put a warning at the start of the dredge function and, although this was not suggested by any specific review, I think it would be prudent to change the title of this paper, the original of which was inaccurate.**

R1.5: Lastly, I appreciate the author’s use of simulations to demonstrate the effectiveness of the dredge framework. However, for the second simulation study, I recommend the author include a negative control group, where the author simulates two randomly evolving characters independently and tests how often the automatic model selection procedure selects an independent model.

**A: A negative control was included actually as part of the original correlated test. Not all of it is correlated and so we can check to see if the dependent relationships are there. I have been more clear about this in the text. However, if the reviewer is still concerned I have added a blah in the supplemental and maybe did the tests anyways. I am hesistant to include a pure negative control as we shouldn’t be thinking in the absolute of correlatd vs not, as with this my hope is we will examine parametesr to look for negative controls vs not.**

R1.6: I found the change in the use of the mapping matrix and Q matrix to be a bit confusing. For example, when the author described the correlated model (lines 258-283), they predominately used the notation for the rate’s location in the Q matrix (e.g., q1,2) without providing the same notation in the matrix on line 284. It might help the reader to give the location notation in the same matrix or state very clearly that q1,2 is on the first row and second column. Ideally, they could have both notations or matrices side-by-side so the reader doesn’t have to count or remember where the rates are located.

**A: I will improve this.**

R1.7: Figure 4: The standard model in the figure does not seem to match the standard model described in the text (lines 455-458). In the figure, the standard corHMM slightly prefers a root state with monogamy and estrus display (dark blue). However, the results describe a model with a 61% marginal probability of the root state having multimale mating and estrus display (lines 455-458). Is this the wrong figure?

**A: Oops.**  
  
R1.8: Lines 27, 341, 351, 355, 475, 488, and 524: Inconsistent hyphenation of Old World monkeys (or primates) throughout the text. I don’t think it needs to be hyphenated.

**A: Thank you, corrected.**   
  
R1.9: Line 50: Please remove the apostrophe after ‘models’

**A: Corrected.**  
  
R1.10: Line 63: Replace ‘by’ with ‘as’

**A: Corrected.**  
  
R1.11: Line 94: Add a space between ‘model’ and before the start of the parentheses

**A: Corrected.**  
  
R1.12: Line 154: Spaces are needed around ‘C’ and ‘S’

**A: Corrected.**  
  
R1.13: Line 155: Please define Lreg. Is this the likelihood for any of the regularized models?

A: **A definition has been added. I also point the readers to the equations where Lreg is actually different for the different regularization schemes.**  
  
R1.14: Line 169: Space is needed after ‘AIC’

**A: Corrected.**  
R1.15: Figure 2: Please define the shorthand ‘lnLik’ and ‘dAIC’ in the figure caption.  
**A: This figure has been replaced in response to other comments which desired a clearer description of the dredge algorithm. I have kept this comment in mind for all abbreviations in figure captions.**

R1.16: Figure 2: “(c) Based on model (c)" -- I think the first ‘(c)’ should be ‘(d)’.

**A: See response to R1.15**  
  
R1.17: Line 203: Add ‘is’ after “because it”

**A: Corrected.**  
R1.18: Line 260: Add a period and space after 1  
**A: Corrected.**

R1.19: Line 260: Add a comma and space after ‘e.g.’

**A: Corrected.**  
  
R1.20: Line 262: Add an ‘=’ sign after ‘birth rate’

**A: Corrected.**  
  
R1.21: Line 267: Remove the comma after ‘character’

**A: Corrected.**  
  
R1.22: Lines 269-270: Spaces may be needed before or after each of the Xs and Ys. There may be some formatting issues with the equations in Word.

**A: Yes, there were. I have corrected all the formatting errors.**   
  
R1.23: Line 289: Remove the comma after ‘(1)’

**A: Corrected.**  
  
R1.24: Line 290: Add a comma and space before ‘(2)’

**A: Corrected.**  
  
R1.25: Lines 317-318: Test #4 is misplaced in the next sentence on line 318.

**A: Corrected.**  
  
R1.26: Line 324: Make ‘transition’ plural

**A: Corrected.**  
  
R1.27: Line 332: Is JS Divergence a function in corHMM?

**A: Yes, I have added it for this manuscript. However, it is currently not exported. It can be accessed through corHMM:::** **js\_divergence and it uses corHMM:::kl\_divergence to calculate the divergence. If the reviewer believes it would be of general interest, I’d be happy to export the function and add documentation.**   
  
R1.28: Line 451: Are these the “default settings” in corHMM? Please remind the reader that this is an all rates different model. I recommend that the author continues referring to this as the 'all rates different model' because other programs or packages may have different default settings.

**A: Yes, this was pointed out in other comments as well. I have removed all mentions of “default corHMM settings” or “corHMM models” and have replaced them with the common model names (all rates different, equal rates, etc.)**  
  
R1.29: Lines 451-452: I’m confused by the AIC comparison here. Why is this AIC used to support regularization if the AIC score was from a comparison between two unregularized models?

**A: Good point, I have removed the statement. I had wanted to demonstrate that there are “better” models beyond the typical set tested (ER, SYM, ARD) and hence running dredge without regularization (for valid AIC comparisons). But you are right to point out that this is confusing, and I don’t believe it is necessary. This section as has also changed substantially with new empirical results where I tested an additional rate class.**   
  
R1.30: Line 453: Remove ‘the’ after ‘estimated’

**A: Corrected.**   
  
R1.31: Line 477: Again, I recommend that the author refers to this model as the 'all rates different model' even though it is the default setting for this particular R package.

**A: Agreed, corrected throughout the manuscript.**   
  
R1.32: Figure S1: I agree that there are issues of non-independence here, and I’m glad the author acknowledges this. I also recognize that the author is trying not to make a big deal out of these results (because of the non-independence issue). However, it is very difficult to see the points in this plot, and the author doesn’t provide any slopes, p-values, or R2 values, which makes it difficult to believe even their qualitative claims of an increase in predictive performance toward the root.

**A: Yes, I do wonder if it is worth including at all. The non-independence issues make any conclusions from an already messy pattern even more dubious. However, I think it is natural for a reader to wonder what effect regularization would have on ASR so I will keep this section. I have added a supplementary table with the requested values. I don’t think this changes the qualitative interpretations as I think the overwhelming pattern is that there are very minor differences in the ASR performance.**   
  
R1.33: Figure S2: I assume the left is the upper 95% CI, but is this for the standard all rates different model or from a regularized model?

**A: This is from the standard all rates different model. The AE pointed out the lack of clarity in this figure and it has been changed to improve the clarity.**

Reviewer: 2  
  
Comments to the Author  
This manuscript is an interesting and timely contribution. When analyzing discrete traits, the number of potential evolutionary models (Q matrices) is vast, which makes navigating the model space challenging. Comparative phylogenetics has largely lacked robust methods for selecting the optimal model from this pool. To my knowledge, this is the first study that attempts to address this problem using maximum likelihood framework.  
  
The author  proposes using regularization techniques (lasso and ridge), which have been widely employed in other statistical fields, to penalize parameters in the Q matrices in order to identify the optimal model. Additionally, this appears to be the first application of these techniques to Q matrices and CTMCs. Similar approaches exist in Bayesian frameworks using a horseshoe prior, which shares similarities with the lasso method. Consequently, the study is novel and will be of high interest to the readership of Systematic Biology, particularly those working with discrete traits.  
  
Overall, the manuscript is well written; however, I believe it would benefit from additional details and discussion in some areas. I recommend its publication in Systematic Biology once these points are addressed, placing my recommendation between minor and major revision.  
**A: Thanks**  
  
R2.1: Clarification on the Dredge Algorithm (L152). I am a bit lost of how the dredge algorithm functions, particularly how the regularization component is linked to model exploration. From my understanding, the algorithm calculates the penalized likelihood for a broader model, then merges parameters and estimates the merged model. Could the authors clarify whether the algorithm compares the wider model with the merged model using AIC or only the penalized log-likelihood? Additionally, how is AIC calculated for a penalized model—does it include the lambda parameter? It would be helpful to know the criteria for merging and dropping parameters; and an estimate of how many models the dredge algorithm explores on average for a single dataset.

**A: I have provided a more detailed conceptual figure which addresses these points (now Figure 2). However, note that I have changed how the model structure search is conducted (see also responses to: ), so some of**   
     
R2.2: I would appreciate more practical tips for using cross-validation. For example, does the user need to repeat the entire dredge algorithm with varying values of the lambda parameter and then select the set that minimizes the chosen statistic (e.g., JS)? A separate section briefly describing the best practices for the dredge algorithm  would be very useful.

**A: Can do.**  
     
R3.3: Dredge and Hypothesis Testing. Correct me if I am mistaken, but it appears that dredge explores the model space by sequentially penalizing models and eventually selects the one with the best AIC. While this approach is reasonable, there is no guarantee—either theoretically or practically—that the dredge algorithm will converge on the true model, as there are no simulations presented to show the convergence rate. It seems that the decision is made based on parameter estimates that reduce variance, essentially dredge is a mix of approaches: AIC + parameter estimations. I would welcome a more detailed discussion of these issues. For instance, if dredge selects model M1 as the best model, but a user identifies an alternative model M2 (which was not explored by dredge) that has a better AIC, which model should be chosen? What practical considerations should guide this decision? Can dredge mislead hypothesis testing?

**A: So true! And interesting. I should have been more clear about this. Hence the warning I added to dredge now. It’s meant as a compliment. I don’t have theoretical garuntees (this is now discussed in more depth following R1 comments).**   
  
R2.4: Furthermore, in L. 605, the author states "In a dredge run, one is not testing specific hypotheses but rather comparing parameter estimates across" . Does it mean that the main values of dredge is parameter estimation rather than hypothesis testing? To me, it seems like it is more for parameter estimation. I think it is important for users to know it before hand. Consider adding an explanation to Introduction that clarifies the usage of dredge.

**A: Ya I should clarify this.**   
     
R2.5:  It would be helpful to include a comparison of AIC scores between dredge-selected models and non-dredge models in Tables 1–2.

**A: Can do!**  
     
R2.6: In the simulations, the author demonstrated the performance of dredge for correlated models. It would be interesting to see how the dredge algorithm performs when the generative model is independent but contains several  parameters. Will dredge converge in identifying the independent model?

**A: Good point. Can do.**   
     
R2.7: In Figures 4 and 5, dredge selects a model where the state X1Y0 is inaccessible (resulting essentially in a three-state model as shown in Fig. 5c), which is logical because this state is absent among the tips of the tree in Fig. 4. Generally, as a rule of thumb, in CTMCs, a model with an unobserved state always has a worse  likelihood than a model where that state is removed. Thus, to a certain extent, the performance of the models in Figs. 5c and 5d is deterministic. While it is encouraging that dredge can identify such cases—given that many users may not be familiar with this property—it would be interesting to see a discussion on this topic. How should such "deterministic" correlations, indicated by zero transitions, be treated in practice as such cases might be common?

**A: God what a question… there has been some discussion of this topic elsewhere. For the moment I have nothing new to add to it. I don’t think dredge has any specific insights into what a zero means here.**   
     
R2.8. Unfortunately, I was unable to locate any code associated with the analyses presented in the paper despite following the links provided. I encourage the author to publish an R tutorial that explains how to implement the dredge algorithm.

**A: I have one! I polished it more though.**   
  
R2.9: (L127–128, L145) It would be helpful for readers to have more details about the mechanism of the regularization technique. In particular, please explain how the method penalizes models and provide an intuitive interpretation of the lambda parameter.

A:

R.10: (L89)  Should this be “corHMMDredge function”?

**A: Yes, thank you. Corrected.**

R.11: (L134)  What does “k” represent in the formula? Please clarify the notation.

**A: The number of freely estimated parameters. Added to main text.**

R.12: (L155) Please explain what is meant by Lreg​.

**A: Corrected.**

R.13: (L200) Does the term “observed likelihood” refer to the character states at the tips (e.g., vectors such as (1,0) or (0,1) for a binary character? Clarification here would be appreciated.

**A: Yes, that’s correct. Though for an HMM the vector could be (0.5,0,0.5,0)/(0,0.5,0,0.5) and for unknown states it would be (0.5,0.5). I have clarified this in the main text.**

R.14: (L203)   it a symmetric” should be  “it is a symmetric.”

**A: Corrected.**

R.15: (L209)  Please explain the terms in the equation for "w=…"

**A: It is inversely proportional to the amount of phylogenetic similarity, so for the text I have described it as “phylogenetic uniqueness”.**

R.16: (L276)  Consider providing a Q matrix that defines terms such as q34​, as these terms are not introduced  elsewhere.

**A: Reviewer 1 made a similar point, so I have provided a point of comparison as suggested in R1.6.**

R.17: (L282)   “whether the the” remove “the.”

**A: Corrected.**

R.18. (L62)  The Mk model is typically understood to refer to a morphological model with a single rate parameter (similar to the Jukes-Cantor model) used for tree inference. Using “Mk” in this context may be confusing. I recommend renaming  to e.g.,  Pagel’s model or a correlated model.

**A: Yes, thanks for point this out. Corrected.**

R.19: (L378)  When referring to a “reduction in variance,”  clarify which variance is being discussed (e.g., total variance or another specific type).

**A: Excellent point, corrected.**

R.20: (L395)  Define the “absolute average bias.”

**A: Corrected.**

R.21: (L428)  Explain what the values in the right-hand columns of Table 2 represent.

**A: Thanks for pointing this out! Corrected.**