This manuscript is very welcome for at least two reasons, a general and a specific one.

Far too often, data matrices for phylogenetic analyses are taken as observed facts by reviewers, editors and readers, or, conversely, as matters of taste that are likewise beyond discussion. Consequently, in successive publications (by the same authors or altogether different ones), matrices are usually little modified beyond the addition of taxa and sometimes characters; this is indeed documented here in appendix 8. In reality, errors abound, ranging – as the manuscript shows – from genuine typographic errors over correct scores placed in the wrong line or column to artificially missing data (features that are known and could have been scored but somehow weren't), scores based on reconstructions that are themselves based on misinterpretations of other reconstructions (rather than directly on specimens or even on specimen drawings) and even intellectually dishonest scores where body parts that are unknown were scored after presumed relatives of the taxa in question, a practice that is logically circular if a matrix is to be used for phylogenetic analysis. I have published on this before (Marjanović & Laurin, 2008, 2009, 2019; Marjanović & Witzmann, 2015), and so has the author (Gee, 2020b); it is good to see an investigation of another matrix, indeed a set of matrices derived from each other. Consequently, I applaud the use of such words as "correction" and "error".

The specific reason is that the phylogeny, and to a lesser extent the phylogenetic position, of Dissorophidae has been unclear. The present manuscript is by far the most thorough investigation of that problem yet undertaken, and its largely negative result (Dissorophidae is phylogenetic grass) will be very productive in the longer run because it will prevent the field from taking any of the existing phylogenetic hypotheses for granted (and basing far-reaching hypotheses in evolutionary biology on them).

Arguably as a prerequisite for the latter, the manuscript also presents for the first time the problem of identifying the holotype of *Platyhystrix rugosus* – a species that has made it into a lot of children's books.

I recommend publication in PeerJ after revision of the text and the figures; it would also be good to repeat the analyses after the changes to the matrix suggested below.

Comments on science

Scores and codings

Characters 10 and 21/22 in appendix 1 seem at least partially redundant with each other. If the state of one of these is predictable from the state of another, it should be scored as inapplicable or the characters should be merged. I haven't had time to look into this, so please check if they're redundant and either explain in the note to ch. 21/22 why they're not, or describe what you did to avoid redundancy. This is important to allow other people to reproduce and extend your matrix.

Character 22 should be ordered because it is clearly continuous, and because state 1 of ch. 21 is the same as the entire range of ch. 22, state 0 of ch. 21 should be added to ch. 22 on the "0" end. The fact that this state 0 may not occur in some restricted taxon samples does not pose any problem for the analyses. It cannot distort the trees or the Bremer values, and I don't think it would distort the bootstrap values either; it would only (slightly) increase the consistency index, but PAUP*, at least, calculates the CI both with and without the parsimony-informative characters.

Ch. 23 and 32 depend on each other, too: when the prefrontal contacts the jugal (32:0), that means the lacrimal is excluded from the orbit margin (23:1). Did you score that twice, or did you score ch. 23 as inapplicable for all taxa with 32:1?

Is ch. 29 redundant with 10 or 21/22, too?

Ch. 30 definitely is: without the elongation of the naris (state 10:1), only state 30:0 is possible.

Does state 42:1 necessitate state 20:2?

The note to ch. 46 makes it sound like the character is parsimony-uninformative. If so, you can of course delete it.

Ch. 84 claims: "In *Doleserpeton*, it [the ectopterygoid] is reduced to a thin edentulous strut". Unless you have studied unpublished material (which I know is possible), it is not known whether *Doleserpeton* had that bone, and if it did, what shape the bone had (Sigurdsen & Bolt, 2010). It could easily have been like in *Gerobatrachus*: small and toothless, but too short and wide to be called a strut. If indeed you have studied unpublished material that shows the condition you mention, say so. – But whether or not *Doleserpeton* has state 1, if state 1 doesn't occur anywhere else in your taxon samples, the character is parsimony-uninformative and can safely be deleted.

"Carapace" makes me think of a turtle shell; is state 91:2 the complete osteoderm cover of *Ecolsonia*? If so, does it occur anywhere else in your taxon samples? If it doesn't, this state is parsimony-uninformative, and you could replace it by a question mark. In any case, please spell out what you did.

Note to ch. 92: Then what is the difference between the two states? The length/width ratio of the osteoderms? Please find out how you scored this character and spell it out to make it reproducible.

I'm not sure why ch. 102 is ordered in this order and not in 1-0-2. If both are equally likely, the character should be unordered.

Does state 112:1 occur in non-dissorophids you sampled?

Tables S1 and S2 are a good idea!

In appendix 2 you state you've changed the score of *Mordex* for ch. 19 from state 0 to unknown because "while the maxilla terminates posterior to the orbit, the termination of the tooth row cannot be confidently determined." But the character has three states, and the described condition makes state 2 (where the maxilla does not terminate posterior to the orbit) impossible. The correct score is therefore partial uncertainty between states 0 and 1, not total uncertainty.

Wildcards, and deleting them

I question the value of "permutations" 1B and 2, if the intent is to elucidate olsoniform phylogeny rather than to evaluate the performance of historical approaches for comparison. (If the latter is the intent, that should be spelled out – as it is in lines 280–281, but explicitly contradicted in lines 259–260 for the first four "permutations".) Rather contrary to lines 1583–1584 in the Conclusions, every OTU in a matrix has an effect on the position(s) of every other OTU in the same matrix, let alone on the support values. (Three references are cited in Marjanović & Laurin [2019:91], and the analyses with added taxa in that paper illustrate the phenomenon further – some of the added taxa are very fragmentary indeed.)

If wildcards turn the strict consensus into phylogenetic grass, one option is to prune them from the MPTs and recalculate the strict consensus; that way, the trees are not distorted by an artificial lack of data. The disadvantage is that this way you don't get to see if the

wildcards are really all over the place or perhaps just have two widely separated positions each. In Marjanović & Laurin (2019), where most strict consensus trees (not shown there) were very grassy, I used another method: as described below, I looked at a sample of MPTs and represented the equally most parsimonious positions of all wildcards graphically. The disadvantage is that it's more time-consuming.

PAUP vs. TNT*

Although PAUP* and TNT differ in the default settings for some things like the collapsing rules for zero-length branches, each can be set to imitate the other's default settings. I agree with lines 30–31 and 1081–1085 that the settings are a matter of personal preference. However, perhaps contrary to lines 1071–1080, another source for divergent results are simple user errors: both programs can be set so that they don't necessarily find all MPTs, or even any MPTs at all – most easily by just not running enough addition-sequence replicates in a heuristic search or not running any of them for long enough. Likewise, they can be set to perform too few bootstrap replicates, and I think they often are. (In my experience, really a lot of replicates are necessary to make replication of a bootstrap analysis possible – even with the same program.) All this actually occurs in the literature, because many people who use these programs don't quite understand how they work, or even how parsimony analysis works in general. (On top of that, TNT is so poorly documented that I don't think anybody without good contacts to Argentina has ever learned to use it well. I certainly haven't.) I listed a number of clearly spurious discrepancies between PAUP* and TNT results on p. 4 of Marjanović & Laurin (2019); in addition, Maddin et al. (2012) did not find any of the MPTs for their matrix, and only found 34 of the > 150,000 trees that are one step longer, because – I'm told – they didn't know what addition-sequence replicates are good for and only performed a single one. Given the size of their matrix, they should have done a thousand.

Line 1086: Schoch (2013) claimed to have recovered less resolution using TNT, but this is one of the examples I (& Laurin, 2019:4) cited: his PAUP 3.1 analysis **failed to find any MPTs at all.** We know this because he reported (p. 682) that his TNT trees is had 633 steps but his PAUP trees had 638 steps (and worse CI and RI, too). Given that there aren't any polymorphisms in that matrix, it is impossible that differences in collapsing rules or whatever could have such an effect. The only possible way to explain this result is that Rainer made some kind of mistake in his PAUP analysis. (Without repeating the analysis I can only speculate what exactly; perhaps he set too few addition-sequence replicates, perhaps he accidentally used an older version of his matrix…) There is no point in comparing the resolution of the consensus of (I hope) optimal with that of suboptimal trees. To state that "Schoch, 2013, recovered less resolution using TNT" (line 1086) is misleading, and the statement that "[t]hese specific programs have recovered different topologies for the same matrix" (1085) will require a valid example. The same holds for the conclusion of that section (1087–1090).

However, setting too few replicates is only possible for heuristic searches. It cannot explain the differences between your runs of "Permutations" 8 and 9A, where you used branch-and-bound searches. Supposedly, branch-and-bound is mathematically guaranteed to find all MPTs, and no errors in its implementation in PAUP* have yet been reported. Perhaps branch-and-bound and implicit enumeration aren't exactly the same thing after all?

Polymorphism

Line 1009: You can't cite a 22-year-old paper for the observation that the treatment of polymorphisms "remains", present tense, "a contentious topic". I suggest "has been a contentious topic for a long time (e.g. Wiens, 1999; Watanabe, 2015)." – Note that what you cite as Watanabe (2016) was published on 15 July 2015 and should consequently be cited as "2015" in the text and "2015 (for 2016)" in line 1994 if PeerJ lets you.

Line 1033–1036: The interpretation of polymorphism as a state of its own would require some discussion before it could be used, let alone recommended. I don't have time to check if there is such a discussion in Wiens (2000), but I've never seen any anywhere. Off the top of my head, I suppose it could work in unordered characters, but I can't see how it would work in ordered ones…

By the way, is there any partial uncertainty in the matrix? Above I mention a case where you corrected a score and described the situation as partial uncertainty, but claimed to have scored complete uncertainty…

Other

Line 62: But that is only possible if the character sampling of the novel matrix overlaps little enough with the previous matrix. Depending on how large the latter is, that may not be possible. In this case, however, where e.g. the postcranium is heavily underrepresented in the traditional matrix, that may not be an issue…

Lines 347–351: "I did factor in the datedness of literature sources as well. Therefore, some of the revised scores will differ from the equivalent score in my own matrix. These approaches minimize personal scoring philosophy and should provide an acceptable derivation of this matrix should other workers continue to use it." – The last sentence contradicts the other two. If the matrix is to be used, it will need those updates that you have withheld in, it appears, the interest of an experiment that belongs not so much to science as to the history of science. Is the question of what Dilkes would have found last year if he had corrected Schoch's untenable scores really interesting enough to hamper the goal of providing "an acceptable derivation"? (Or indeed "derivate"?) I decided otherwise in 2008 when I began to correct and update the matrix of Ruta & Coates (2007) for what became Marjanović & Laurin (2019).

Line 1426: Eurasia? What Eurasia? There was no Eurasia. Laurussia had recently collided with Kazakhstania instead, as one of the last steps in the formation of Pangea. While I have no opinion on *Nooxobeia*, chroniosuchians should have been present in inland North America at least from the Capitanian onward, because there was nothing to stop them from just walking there.

Lines 1490–1491: Quite the opposite – intraspecific niche partitioning prevents interspecific partitioning of the same niches and therefore (if all else is equal) leads to lower biodiversity.

Maybe mention somewhere that skulls without visible sutures might reveal sutures in a synchrotron. Of course that won't help with lost specimens like *Zygosaurus*.

Comments on the presentation of the results

Majority-rule consensus trees of parsimony analyses should **never** be used. I have not been able to find any situation where the majority-rule consensus of a parsimony analysis would contain any useful information. Bootstrap and Bayesian analyses are designed so that their majority-rule consensus is a support measure; that is not the case with plain non-bootstrap parsimony. All most parsimonious trees from the same analysis are **exactly** equal. If you get 1180 MPTs, and one node appears in one MPT while an alternative node appears in all 1179 other MPTs, those two nodes are **exactly** equally likely to be correct given the dataset – parsimony cannot discriminate between them. Worse yet, as first pointed out to me by none less than Joe Felsenstein, it is not uncommon that a majority-rule consensus tree is not even identical to any single MPT: the most common resolutions of different parts of the tree need not be able to coexist. And finally, at least PAUP* rounds the percentages: a node marked "100" in a majority-rule consensus tree may only occur in 99.5% of the MPTs and can therefore be absent from the strict consensus (pers. obs.).

Therefore, I must insist that all mentions that a node appears in some percentage of the MPTs, throughout the text, appendices and figures, must be removed, or replaced by completely non-committal wording such as "this node occurs in some trees" or "this clade is sometimes found in that clade" (not "most", "many", "few" or anything else quantitative). I did this in Marjanović & Laurin (2019), mentioning percentages only for the bootstrap and Bayesian analyses.

This will have the advantage of shortening the most descriptive and therefore necessarily most boring section of the text.

When the strict consensus is too poorly resolved, there are other methods than the majority-rule consensus to extract information from the result of an analysis. One is to take a look at a sample of the MPTs; in my experience (Marjanović & Laurin, 2019), about 20 are enough if they're evenly spaced (e.g., if there are 103 MPTs, take the first, the last, and every fifth for a total of 22). Admittedly, that gets time-consuming if the trees are large and numerous, especially when the results are to be represented as figures (as I did in Marjanović & Laurin, 2019: fig. 10–17). Another method is to prune suspected wildcard taxa from the MPTs (not from the matrix!) and recalculate the strict consensus; one issue here is to identify the wildcards, which is sometimes very easy (it is what the Adams consensus is meant to do) but can sometimes only be done by comparing individual trees, i.e. by using the other method, and another issue is that wildcards can be larger clades and need not be single terminal taxa. In short, I recommend using either method depending on how time-consuming it is to compare MPTs and draw figures to represent them, and how easy wildcards are to identify.

Incidentally, the claim that "majority-rule consensus trees are used only to identify nodes that occur in an overwhelming majority of most parsimonious trees" (lines 416–418) contradicts the very first percentage mentioned (line 443), which is only 59%, and many others later…

Lines 580–583: The Adams consensus is not intended, and is not, a good representation of the results of a phylogenetic analysis. No MPT needs to be congruent with all its resolved nodes. It is meant to identify wildcard taxa by placing them as close to the root as possible, but sometimes fails at that.

Appendix 2: In the revised scoring of *Acheloma*, do the brackets mean polymorphism (parentheses in NEXUS format, "&" in Mesquite) or partial uncertainty (curly braces in NEXUS format, "/" in Mesquite)? Or is TNT unable to distinguish between the two? (The difference doesn't have an impact on the topologies, because ancestors cannot be reconstructed as polymorphic; compared to partial uncertainty, each count of polymorphism just adds one step to every tree. As a drastic example, the MPTs of Ruta & Coates [2007] are 1584 steps long when polymorphism is treated as partial uncertainty, but 1621 steps long if they're distinguished [Marjanović & Laurin, 2019:60]. It is also possible in PAUP* to treat both as polymorphism. Mesquite cannot even treat them the same.)

Comments on nomenclature and terminology

Throughout the text, the figures, the tables and the appendices, replace "***locklardi***" by "***lockardi***". Daly (1994) consistently used the latter spelling and explained she was naming the species after a Mr. Lockard.

Throughout the figures, replace "*angustus*" by "*angusta*".

Throughout the text, the figures, the tables and the appendices, replace "*neglecta*" by "*neglectus*". As Schoch & Milner (2014:78) acknowledged, although ops is feminine in the original Greek, the ICZN (1999) has an article (30.1.4.3) that declares it masculine: "A compound genus-group name ending in -ops is to be treated as masculine, regardless of its derivation or of its treatment by its author." (I don't know why; maybe it was introduced in order to preserve e.g. *Eryops megacephal**us*** and *Triceratops horrid**us***.)

Epoch names like "Late Carboniferous", "Early Permian" and "Middle Triassic" are official names defined by the International Commission on Stratigraphy and therefore begin with an uppercase letter. The same holds for the corresponding series names ("Upper Carboniferous", "Lower Permian"). Please fix this throughout the manuscript.

The "permutations" aren't really permutations; they don't differ in the reshuffling of data. I would just call them "analyses", as I did in Marjanović & Laurin (2019).

Line 23: "temnospondyl amphibians", and line 68: "Temnospondyli, often referred to as 'amphibians' in a broad sense" – in the last 20 years or so, whenever temnospondyls have been called amphibians, that has instead been meant to imply the definition of Amphibia now formalized by Laurin et al. (2020): the total group of the extant amphibians, assuming those form a clade exclusive of Amniota. Whether the temnospondyls are amphibians is an unresolved question (Danto et al., 2019; Daza et al., 2020 – please add at least the latter to line 74), so for line 23 I recommend "temnospondyls" or "temnospondyl anamniotes", and for line 68 I recommend "Temnospondyli, often considered the amphibian stem-group".

The nomenclatural note (383–402) is presented in a somewhat confusing manner and omits a crucial fact, namely that "Eucacopinae" is impossible because there is no "Eucacops". I would present everything in chronological order, perhaps like this:

"The name Cacopinae, used here for the clade of all taxa more closely related to *Cacops aspidephorus* than to *Dissorophus multicinctus*, has a complex history. For a long

time, *Cacops* was referred to Aspidosaurinae (e.g. Williston, 1914; De Mar, 1966b; Milner, 2003; Witzmann & Soler-Gijón, 2010). Daly (1994:52) considered the poorly known *Aspidosaurus* to be a dissorophine, making Aspidosaurinae a junior synonym of Dissorophinae and necessitating a new name for the remainder of the taxa referred up to then to Aspidosaurinae; she coined Cacopinae for that purpose. Because Daly (1994) did not substantiate her classification, the name Cacopinae went unused until Schoch & Rubidge (2005), who used it for an OTU composed of *Cacops aspidephorus* and *Kamacops acervalis*; they did not sample the poorly known *Aspidosaurus*. All following works on dissorophids (except Witzmann & Soler-Gijón, 2010) used the name in its modern meaning (although, curiously, only Berman et al. [2010] cited its source) until Schoch & Sues (2013) pointed out that Cacopinae Daly, 1994, was preoccupied by Cacopinae Noble, 1931, which is named for the microhylid frog genus *Cacopus* (long since sunk into *Uperodon*, and 'Cacopinae' into Microhylinae). To remedy the situation, they claimed to change the name of the dissorophid subfamily to Eucacopinae. This change was widely adopted. However, as David Marjanović has brought to my attention, there are two grave problems with this. First, the name 'Eucacopinae' cannot exist: Article 11.7.1.1 of the International Code of Zoological Nomenclature (ICZN, 1999) states that the names of taxa at the family group of ranks 'must be […] formed from the stem of an available generic name', and there is no such genus name ('Eucacops' or similar). Second, according to the same article, 'Cacopinae' Noble, 1931, is likewise unavailable because it is formed from only part of the stem of an available generic name, the stem of *Cacopus* being Cacopod- rather than Cacop- (which is the stem of *Cacops*). (Günther [1864: 415–416 – https://books.google.com/books?id=SRxAAQAAMAAJ&pg=PA415] did not explain the etymology of *Cacopus*, which looks like a Greek compound for 'bad foot', but he pointed out several times how short the limbs of this frog are, the hindlimbs and the toes in particular. The stem of the 'foot' word is pod-.) Thus, Cacopinae Daly, 1994, is not preoccupied, so there is no need to replace it. This fact may be the unstated reason why Schoch (2018a), Atkins, Reisz & Maddin (2019), Anderson, Scott & Reisz (2020) and Schoch & Milner (2021) used this name again. I follow this usage. Cacopinae may still eventually turn out to be a junior synonym of Aspidosaurinae, but this does not seem likely from my results discussed below."

Line 431: "post-micromelerpetid dissorophoids" is an example of a misguided and occasionally misleading terminology used exclusively by Rainer Schoch so far. I recommend "non-micromelerpetid dissorophoids" or, better yet, "the sister group of Micromelerpetidae".

573: "Dissorophinae is not recovered. Cacopinae is recovered" – In any results of any analysis that contains *Dissorophus multicinctus* and *Cacops aspidephorus*, Dissorophinae and Cacopinae are automatically, inevitably and trivially present by definition; the interesting question is whether Dissorophinae contains anything other than *Dissorophus multicinctus* and whether Cacopinae contains anything other than *Cacops aspidephorus*. Please reword this passage.

575: "Kamacopini is not recovered" – that name has not been mentioned in the manuscript before. If it is defined as everything closer to *Kamacops* than to *Cacops*, then see above – I would recommend "*Anakamacops* and *Zygosaurus* are not recovered as kamacopines". It appears later in the text, but likewise without explanation.

582–583: Rather, "and *Broiliellus* and *Diploseira* are recovered as dissorophines."

Similar wordings occur throughout the Results section.

1220–1221: These aren't scenarios, and there is no "truly", because genera aren't real. They're personal, unscientific preferences about classifications, and classifications are conventions at best. I would write the sentence as follows: "If genera are to be monophyletic, this topology is equally compatible with *C. woehri* remaining in *Cacops* or receiving its own genus that is closely related to *Cacops*."

Comments on style

The style is sometimes overwrought. The text is a bit difficult to read in places; it requires that the readers will have a large vocabulary and will readily consider interpreting various words as having meanings similar but not identical to their usual ones. There are even sentences that I don't understand. In the interest of time, I will limit myself to just a few concrete examples in the "details" list below, but the entire text including the figure & table legends could and should be made simpler and easier to understand. Most likely, it would become shorter as a consequence. Even though the manuscript is rather long – the PDF of the main manuscript has 100 pages, and that of the appendices another 42 – I do not advocate cutting anything of substance (except maybe "permutations" 1B and 2, see above); the various analyses and discussions form a coherent whole, it is good to have them all in one place. Still, it seems to me that many of the stylistic infelicities make the text longer than it needs to be.

I will dissect one example, the very beginning of the abstract (lines 16–22): "Phylogenetic relationships of most extinct tetrapod clades remain poorly resolved, which may be variably attributed to a lack of study, the limitations of inference from phenotypic data, and constant revision of best practices. While methodological refinement continues to be essential, any phylogenetic analysis is inherently constrained by the underlying dataset that it analyzes. Therefore, it becomes equally important to assess the integrity of these datasets, especially when certain ones are repeatedly propagated, thus appearing to constitute a working consensus of sorts, in order to assess whether such a consensus is robust."

First, why "Phylogenetic relationships", implying "some"/"any", and not "The phylogenetic relationships"? The fact that not all are meant is already made explicit two words later by "most".

Next, "most extinct tetrapod clades" is still far too wide; you are probably thinking of Paleozoic or non-amniote tetrapods, and should say so.

At the same time, "tetrapod" is too narrow now that Tetrapoda has been defined as the crown group of limbed vertebrates (Laurin, 2020a). The alternatives I can come up with are Tetrapodomorpha, which is a less widely known name and refers to a much larger clade (though it is accurate that the phylogeny of Paleozoic tetrapodomorphs is poorly understood), Stegocephali or Labyrinthodontia (two names that used to be obsolete and used to refer to grades, but were repurposed as clade names by Laurin [2020b, c]; this is rather too little known to be assumed in an abstract), or simply "clades of early limbed vertebrates". (Stegocephali is everything closer to Tetrapoda than *Tiktaalik* is; Labyrinthodontia begins at the *Acanthostega*/*Ichthyostega* node.)

"may be variably attributed to […] and" is also odd. I would try to decide between "may be attributed to […] or", "is variably attributed to […] and" and "has been variably attributed to […] and".

I am not completely sure what "methodological refinement continues to be essential" means exactly. If it means "it continues to be important that the methods be refined", just write that. Or does it mean "refinement of the methods continues to have a large impact"?

What is “underlying” about the dataset? I think this word can just be omitted.

Why “becomes” and not “is”?

Why “integrity”, a rather vague term, and not “accuracy”, which is what you have in fact assessed?

I find that “certain ones” sounds a bit awkward and would use “the same few ones”.

The last sentence consists of two intertwined sentences; at the end of the sentence, I had to go back and read the beginning again to see that one sentence is placed in the middle of the other. They should be unraveled.

In short, here is one suggestion for improving this passage: “The phylogenetic relationships of most clades of Paleozoic limbed vertebrates remain poorly resolved, which may be attributed to a lack of study, the limitations of inference from phenotypic data, and constant revision of best practices. While it continues to be important that the methods be refined, any phylogenetic analysis is inherently constrained by the dataset it uses. Therefore, it is equally important to assess the accuracy of these datasets. There are fields where the same few datasets are repeatedly propagated with minimal changes, so that the analyses of these datasets appear to constitute a working consensus of sorts but are not in fact independent; in such cases it is especially important to evaluate the accuracy of these datasets in order to assess whether such a seeming consensus is robust.”

I definitely don’t want to impose my own style! I only mean to provide a starting point for improvements and to show that improvements are necessary.

Details

The character #, occasionally used in the main file and the appendices as the American number symbol, can be deleted throughout the manuscript because it is always obvious from context that whatever follows is a number that belongs to an ordered list. Outside the US, “number” is indicated by different means (e.g. “no.” in the UK), and # may not be readily understood everywhere.

46: Replace “labiality” by “lability”.
89: Since you’re already using “nominal”, replace “taxa” by “species”.
92: Replace “eryopoids” by “eryopids” because Eryopoidea, on the rare occasions that that term is used, is much larger than Eryopidae. Replace “zatracheidids” by “zatracheids” because I’ve figured out just enough Greek grammar to tell that the latter is the correct form. http://www.perseus.tufts.edu/hopper/text?doc=Perseus%3Atext%3A1999.04.0057%3Aentry%3Dtraxu%2Fs
113: Remove the comma.
116: Replace “2020” by “2019”. (You got it right in the references list.)
123: Add a comma after the parenthesis.
142–143: If the lissamphibians are dissorophoids, all non-lissamphibian dissorophoids are stem-dissorophoids. If the lissamphibians are not dissorophoids, there aren’t any stem-dissorophoids because there aren’t any crown-dissorophoids; instead, all dissorophoids are stem-tetrapodomorphs. I suggest “and *Perryella olsoni*, variously thought to be a ‘basal’ dissorophoid or a ‘basal’ dvinosaur (see below)”.
168: Replace “*Perreylla*” by “*Perryella*”.
173–174: Replace “a ‘stem dissorophoid,’ diverging before *P. olsoni*, so the former” by “the sister-group of all other dissorophoids, so it”. By the way, there may be another reason not to

include it in a dissorophoid analysis: I don't trust the redescription. *Macrerpeton* comes across as a pretty unremarkable cochleosaurid, except for a handful of unambiguous dissorophoid features that are duly emphasized in the text and the reconstruction drawings but not discernible in the very coarse-grained, practically useless grayscale photos.
182–183: Good, because *C.* "*lewisi*" is just a baby *C. milleri* anyway (Reisz et al., 2005; not contradicted by pers. obs.).
192: Replace "LEP" by "the lateral exposure of the palatine" just to be sure.
197, 264, 1018: No need for a hyphen in the free-standing noun "species level".
245: Replace "index" by "indices".
270: Replace "is" by "are".
286: Replace "assessi" by "assess".
319: Replace "2020" by "2020b".
333: Replace "cannot be scored are" by "were spuriously scored were", and "other members of a relatively exclusive in-group" by "presumed close relatives".
412: Replace "MH" by "MI".
433–434: Replace "employed in color swatches" by "color-coded in the figures".
440, 530, 589, 625, 696, 787, 1458, 1461: "earliest-diverging taxon" needs a hyphen to avoid the meaning 'the earliest one of the diverging taxa'.
461, 1531: "early-diverging" for the same reason.
462: "higher-nested" or "more highly nested" for the same reason.
486–487: By "the cacopine and trematopid", do you mean "Cacopinae and Trematopidae"?
581: Remove the comma, and replace "to" by "than".
659: Remove "for", and insert "branch-and-bound" after "PAUP*".
694: Replace "kamacopinines" by "kamacopins" (like 'hominins' from Hominini).
829: Either "the" or the apostrophe. I would write "the derivate by Dilkes (2020)".
850: "integrity" sounds like you're concerned about the matrix literally falling apart. Why not just "accuracy"?
859: No, the corrections are precisely not errors. How about "the corrections I made concern unequivocal errors" or even "correct unequivocal errors"?
867–868: By "propagated score [sic!] created by Holmes, Berman & Anderson", do you mean "first added to the matrix by Holmes, Berman & Anderson, 2013"?
875: Replace "scored" by "a score".
917: Replace "the data" by "data".
921: Replace "their" by "its".
927: Replace the hyphen by an n-dash.
931: "therein" – wherein? In the occiput? If so, I recommend replacing "therein" by "thus".
934: Replace "asymmetric" by "inconsistent".
938: In the appendices you say you've replaced "otic notch" by "squamosal embayment"…
949–950: "earliest-appearing" needs a hyphen.
956: Oh yes, they are unjustified. They may not be wrong, but they're unjustified – if they're correct, they just happen to be correct by lucky guessing: they're right for the wrong reasons. Replace "unjustified" by "wrong", "incorrect" or "inaccurate".
977: Replace "therein," by "thereby" (without a comma).
988: The same matrix except for added taxa, as you say in appendix 8.
1003: Replace "work" by "worker" or a synonym of "worker".
1024: Replace the hyphen by a dash.
1032: Either drop "most", or replace "rarely" by "not".
1047: Replace "ontogenetically related" by "ontogeny-related".

1048: Remove “explicitly”, or replace “is explicitly known” by “has been explicitly stated” and cite a source.
1063: Replace “Eucacopinae” by “Cacopinae” or by “Cacopinae (‘Eucacopinae’)”.
In line 1063, you use “who” to refer to the authors of a paper, but in line 1064, you use “which” to refer to the paper itself. Both choices are fine with me, but to see them both in the same sentence is rather confusing.
1097, 1313, 1536: By “asymmetrical”, do you mean “uneven”?
1111: Replace “taxa…but” by “taxa […] but” to make clear that “taxa…but” does not occur in the original.
1112: You should replace “…"” by “”.”, i.e. a formatted closing quotation mark and then a period. I hope PeerJ’s secret house style has improved since late 2018, and they let you do that. If not, use “ […].”, i.e. put the three dots in brackets and put a space in front of that.
1112–1116: Have you actually seen a Bayesian analysis presented without support metrics? I can’t think of any off the top of my head.
1117–1118: I misread this at first, taking “regardless of support or interpreting topologies” as a unit before I read on and found that’s not intended. Therefore, please put commas around “or interpreting topologies without consideration of support”.
1133 (twice), 1136: Insert a space at least after “<”.
1134–1135: Well, I have (& Laurin, 2019), but that was with a larger and messier matrix.
1162–1164: In the analyses with added taxa, we also sampled a composite of *Mordex* and *Mattauschia*. But the result was the same. In addition to the limited taxon sample, I also blame the limited character sample.
1178: Replace “post-” by “non-”.
1189: Replace “newly” by “recently” to avoid the interpretation that you’re naming it in this manuscript.
1201: Remove the first comma.
1202: Replace “subclades” by “subfamilies” – Dissorophidae has more subclades, they’re just not all mutually exclusive (e.g., the smallest clade that contains Cacopinae and Dissorophinae is not Dissorophidae).
1213: Insert a space at least after “>”.
1230: Insert “genus” after “dissorophid”.
1241: Insert “the” at the end of the line.
1261: I don’t understand what you mean by material being valid. Do you mean the species?
1262: Mention that *A. chiton* is the type species!
1337: Rather than coining the wholly new term “taxonomic brevity”, replace it by “short-lived species” or even “short-lived genera”, or by “rapid taxonomic turnover”.
1350: Add a comma at the end of the line.
1351: As written, this means that the holotype of *P. rugosus* still represents two taxa. therefore, insert “that number” after “despite”.
1373–1374: “this specimen” refers to two different specimens in the same sentence; I would replace the second “this” by “that”.
1266–1267: To make clear that all these pieces form the holotype (…they do, don’t they?…), insert “consisting of” after the comma.
1272: Replace “define” by “diagnose”. Taxon names do have definitions under the rank-based codes, but they’re more boring: the definition of *Platyhystrix* is “the genus that contains *P. rugosus*”.
1284: Replace “augmented” (which means ‘added something to it’) by “strengthened”.
1302: “2003” is an insertion into the sentence and needs to be followed by another comma.

1453: Replace the hyphen by a dash.
1456: What “other large-bodied terrestrial temnospondyls” do you have in mind? *Eryops*, which was certainly capable of walking on land, but apparently unable to eat on land? Or have I underestimated the size of *Zatrachys*?
1473–1474: By “which size class diverges first (*Ca. morrisi*)”, do you mean “the smallest specimen diverges first (*Ca. morrisi*)”?
1487: Insert a space at least after “=”.
1500: Replace “untenable” (‘cannot be [up]held’, said e.g. of a conclusion) by “unfeasible”, “infeasible” or “not feasible” (‘cannot be done’).
1550: Replace “taxonomic experts” by “experts on phylogeny”.
1562: Do you mean “exhaustive”, “exhausting”, or both?
1570: Remove “explicitly”, or replace it by “unequivocally” or “unambiguously”.
1643: Replace “PLoS one” by “PLOS ONE”. “ONE” has (for, presumably, some reason) always been in all-caps; in 2012, the PLOS journals switched from “PLoS” to “PLOS”, announced the change on their blog, changed their logos and everything except the suggested citation in each paper. I even wrote to them about this evident oversight (having published in PLOS ONE myself) and never got a reply. Absent that, I recomment citing PLOS papers from 2012 or later as all-uppercase “PLOS”.
1680, 1705, 2026: No italics in the originals?
1730–1734: These two references are in the wrong order.
1734: Replace “Akademiya” by “Akademii” or “Akademiyi” (the genitive, variously transcribed).
1785: Spell out “Paläontologische Zeitschrift”.
1814: Replace both hyphens by dashes.
1852, 1855, 1933, 1948, 1952, 2032, and the appendix-references to Milner (1985) and Schoch (1999): Abhandlungen (“treatises”) and Monatshefte (“monthly notebooks”) are the two journals titled N. Jb. Geol. Paläont.; replace the hyphen by a space and whatever you find appropriate (a comma, colon, dash…).
1881, 1944: If PeerJ doesn’t let you write “PNAS”, I’m afraid you’ll have to add the rest of its name, “of the United States of America”.
1951: A hyphen is definitely wrong here. I’d replace it by a dash, preferably surrounded by spaces.
1981–1982: That’s version a166, which has expired; in line 251, you claim to have used the current version, a169. Also, mention that a169 is available at http://phylosolutionscom/paup-test/ – not at Sinauer, which has nothing to do with it!
1985: Uppercase for “Morphology”.
2017: Replace “Marcello R” by “Ruta M”.
2029: That might be “eye- and jaw musculature”, carried over from German where “eye musculature” and “jaw musculature” would be written without spaces; but it’s definitely not “eye-and”. Please check.
Fig. 2: It would be useful to add your present matrices.
Legend to fig. 3: Everything except the first sentence is copied from the legend to fig. 2 and doesn’t refer to anything in fig. 3.
Fig. 3, 5: Replace “Nominal” by “Traditional”.
Fig. 4A: Spell out “Holmes, Berman & Anderson”.
Fig. 4C: Copy the green circle to the other side.
Fig. 7B: Replace “*Dissorphus*” by “*Dissorophus*”.
Legend to fig. 10: Remove “1.”.

Fig. 11: It would be useful to mark the type specimens, e.g. with an asterisk after the number.
Fig. 12 and its legend don't match: the legend says there's a part C which isn't there in the figure.
Legends to fig. 13–17: Replace all occurrences of "resultant tree" by "tree resulting".
Legends to fig. 18, 19: Replace the first two hyphens, and the last, by dashes.
Fig. 18: As the species differ in the exposure of bones, it would be good to mention what the red and the yellow ones are (ectopterygoid and quadrate, I suppose).
Legend to fig. 20: What does "Identifiers are not named for any specimen" mean?
Legend to table 1: I'm sure all programs treat - as ? by default; the only alternative is to treat it as a 5^{th} base/21^{st} amino acid.
Table 1: Since you break down the US by state, can't you break down China and Russia by province?
Table 2: It would be very useful to add here which matrix was used in each analysis.
Legends to tables 3, 4: Make explicit that these are the Bremer and bootstrap values.
Appendices, second line: Remove "online" – the entire journal is purely online.
Appendix 1, note to character 8: Which one is the derived state? I've seen papers whose authors – I think Rainer Schoch is one – seem to believe there's some kind of requirement that all plesiomorphies be called 0, but there isn't. The software doesn't care. If you mean state 1, just say so. I would also reword the whole sentence to "Note that, in *Cacops woehri*, state 1 only occurs in small individuals" to make clear that the state also occurs outside of *C. woehri* – this is clear from the preceding sentence, but nonetheless confused me at first.
Character 17: Explain what sort of zone.
Note to ch. 18: Replace "eucacopines" by "cacopines".
Note to ch. 20: Replace "second derived" by "third" or "additional".
Note to ch. 22: Replace "plesiomorphic state's language" by "wording of state 0".
Notes to ch. 25, 47: Replace "derived condition"/"derived state" by whichever state it is.
Note to ch. 40: Put "ventrolateral expansion of the nasal" in quotation marks; the nasal is expanded, not the character… I stumbled over that while reading.
Characters 48–51, 54, and their notes: Here you use "otic notch" throughout, after you just abandoned that in favor of "squamosal embayment" in ch. 46. Is that deliberate? (…Personally, I think dissorophids had a fully functional tympanic ear, but trematopids and amphibamids did not… but all this needs more research…)
Ch. 52: By "size", do you mean width or area?
Ch. 53: By no means. If a character has three or more states, and one of them is limited to a single OTU, then the distinction between the other two or more remains parsimony-informative. Just that one state would be useless.
Note to ch. 59: Replace "extoses" by "exostoses". (ex-ost- = out-bone-[growths])
Note to ch. 60: There's a word missing after "distinctly".
Ch. 64: "*Broiliellus*" *reiszi* has straight horizontal stapedes, but they're long, not "abbreviated". How did you score it, and why?
Ch. 70: Insert "length" before "reaching", or replace the description of state 2 altogether, e.g. by "basal plate about twice as wide as long or more". In the note, replace "second derived state" by "state 2".
Ch. 76: Don't the transverse ridge and the fossa often occur together, with the ridge forming the caudal margin of the fossa?
Ch. 90: "90." should be in blue.
Note b to ch. 94: Replace "plesiomorphic state" by "state 0".

Ch. 101: All states redundantly mention “slender”; this can be dropped. More importantly, replace “The first derived state” and the second derived state” by “state 1” and “state 2” if those are what you mean. I also wonder how many of the “terrestrial” amphibamiforms were amphibious.
Note to ch. 107: Remove “trunk”.
Note b to ch. 110: This clearly belongs to another character; which one? Also, remove “derived”.
Note to ch. 112: Replace “the derived condition” by “state 1”.
Title of table S2: Replace “dissorophid” by “trematopid”!
Appendix 2: Replace “Corrections are assumed to have been typographic” by “Corrected scores are assumed to have been typographic errors”; at least I think that’s what you mean.
Phonerpeton, ch. 68: Add an apostrophe to “Dilkes”.
Anconastes, ch. 87, and *Dissorophus*, ch. 83: Why “typographic”?
Appendix 3, ch. 26: I would replace “the recency in which” by “how recently”.
Later in app. 3, and in app. 5: I’m not aware of any programs that are able to treat unknown and inapplicable states differently, or of any method to do so. PAUP* at least is able to treat the symbols - and ? differently, because - is defined as a gap in a molecular sequence, which can be treated as unknown (fortunately that’s the default setting) or as a 5th base/21st amino acid (which would seriously distort the results of an analysis of morphological data); so that’s a theoretical danger with using the symbol -.
End of app. 3: I don’t think “specifity” exists, and would replace “specimens of demonstrable conspecifity” by “demonstrably conspecific specimens”.
Appendix 5, *Anconastes*, ch. 18: Replace “the derived state” by “‘1’”.
Tambachia, ch. 30: Replace “are lost” by “is lost”.
Cacops morrisi, ch. 38: Replace “eucacopine” by “cacopine”.
Reiszerpeton, ch. 3: What do you mean by “confluent”? Generally it means that two things flow together, but here is only one, the orbital margin of the maxilla, as far as I understand. Do you mean the margin is not clearly smooth and therefore not clearly completely enough preserved? – Move the comma in the citation to the other side of the space.
Ch. 63: Replace “eucacopine” by “cacopine”.
Appendix 8: Mention that Schoch & Sues (2013:443, but not 444 or fig. 4) erroneously claimed to have excluded *Broiliellus texensis* instead of *B. olsoni*. In the description of Liu (2018), replace the two occurrences of “the second derived state” by “state 2”. Under Dilkes (2020), replace “extoses” by “exostoses”.
Appendix 9, end of 2nd paragraph: Replace “when the taxon was monospecific” by “when *Cacops* was thought to be monospecific”.
Table S3: Given that you refer *Acheloma dunni* to *A. cumminsi*, can the “*Acheloma* sp.” specimen (OMNH 79318) be referred to *A. cumminsi*, too? “sp.” should in any case not be in italics because it is not the abbreviation of an actual species name.
Reference to Efremov (1937): Replace “Akademiya” by “Akademii” or “Akademiyi” (the genitive, variously transcribed).
Reference to Eichwald (1848): Société Impériale des naturalistes. (You got it right in the main text, line 1731.)

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