Responses to editor’s and reviewers’ comments

Please make sure that you adhere to our data and code policy: refer to our website for author instructions.

# Editor’s comments

The Reviewers have provided helpful suggestions below to improve the manuscript.

Both reviewers identified areas for improvement, but they state, and I agree, that these are minor changes overall. Most of the changes focus on clarifications and additional information to provide context and increase reproducibility. Reviewer 1’s suggestion to evaluate whether non-native species tend to be disproportionately sampled is a good one. I think this would be very helpful and suggest that you implement this change and report the results, and incorporate it briefly into your discussion. If you do find disproportionate sampling, I think it is sufficient to state that, and not necessary to adjust the analysis by, for example, down-weighting non-native results in any way. It just needs to be discussed in terms of potential caveats. Similarly, I think that addressing “on average across each non-native species x region combination, what fraction of traits were measured within that region?” would provide very useful context for average trait completeness in the invaded range. Addressing phylogentic correction would also strengthen the analysis.

Answer: We thank the editor and the reviewers for their comments. Addressing them really strengthened the manuscript. We provide detailed point-by-point replies to the comments of the reviewers below.

As suggested by Reviewer 1, we have added a comparison with native species globally, showing that there is a disproportionately high sampling of non-native ones, with a greater than expected number of traits measured for non-native species than for natives.

Regarding the suggestion of location of the trait measurement in specific regions, although we think this would give us further insights into our trait knowledge of non-native species, for the sake of simplicity and data completeness, we have not considered any location data for the trait measurements. This is a non-trivial task to perform and would heavily reduce our dataset, because the locality where traits were measured is only available for 42% of all trait data. We think this would be a quite different set of analyses to be performed in a different manuscript and therefore opted not to address this point.

We also added a phylogenetic model, showing that all coefficients had a consistent effect with the non-phylogenetic model.

Please provide a more comprehensive (and reproducible) workflow so that someone can more easily reproduce your results, including for the sections noted by Reviewer 2 (taxonomic harmonization, trait imputation). Include a workflow in the repository (this can be a detailed outline of steps and specific code filenames to run and/or a diagram listing these specifics with the order of code clearly shown). You use the term “workflow” in \_targets.R but it is not commented enough. This workflow diagram or outline can exist in the README. In this workflow, please include specific reference to the input and output data (including their sources) so that someone can read it and understand how you go from input data to results. You state that you will host the data and code via Zenodo but I only see the code in the link you provided and then found cleaned data (but not metadata I could find). Page 52 of the Supplement begins a long data table which lacks metadata. I will need to review the data and its metadata before making the next decision on your manuscript, so please include that in the repository (or if it is too large, host it elsewhere, for example Environmental Data Initiative). Please omit data from the supplement and include it only with your online repository, adding complete metadata. This repository should contain the code and any relevant information on the workflow such that someone can reproduce your results (e.g., relative filepaths, specific naming of each figure in the manuscript, etc.). Currently it has a lot of useful information but needs a little more to make it more reproducible and accessible.

I may have missed this, but because you’ve run this analysis on a certain date you have worked with a specific version of the trait data. But these databases change all the time in terms of edits and in terms of amount of data. It would be best if you could include any unedited input data (raw data) in the data repository as the exact version you use in the manuscript, otherwise it is not reproducible (also note the date / version of each data source in the data repository).

Answer: We would like to thank the editor for such a detailed comment. We agree that it is important to adhere fully to the principles of FAIR and open science. Making a study truly accessible and well-documented for someone else to use, especially in our case, where we merged so many different heterogeneous datasets, is a challenge in itself. We have now detailed our workflow by a general scheme (available both on the GitHub version of the code and data, as well as the permanently archived Zenodo version). We explain step by step what the code is doing.

Regarding the raw data, we do understand the problem of the availability of metadata. Given our extensive workflow, we cannot provide detailed metadata for all intermediate datasets. We, however, now have fully documented the table that was initially shared as a supplement. It also is now available as an online supplement that is searchable in itself at <https://rekyt.github.io/alientraitgaps/> (which is also archived permanently on Zenodo).

We are aware of the brittleness of the online service that we have used in our work. That is why we provide a computationally tractable environment through the renv package, which tracks the version of all the R packages we used. Furthermore, on the Zenodo version of our code (not on GitHub due to size constraints), we now share the entirety of our raw and processed data from our workflow (generated by the targets package). People can thus load any object of the workflow by copying that folder to a local repository and leveraging the targets R package. Regarding the version of the trait and taxonomy databases we are using, they are now properly specified in the README file at the root of the repository, as well as in the Material and Methods section of the manuscript.

# Reviewers’ comments

## Referee: 1

In this work, the authors synthesize four major plant trait databases (a major work in itself) and provide information on the current state of knowledge (and some potential drivers) of trait data for plant species that have been introduced globally. The manuscript highlights the major gaps in our knowledge, building on previous work on both database integration and data availability. The methods are reasonable (although I provide a few suggestions below about potential things the authors might also consider), and the results mostly make sense (aside from the direction of some of the predictor variables), and the methods are clearly presented (plus the code is provided and is clear, with well-named and intuitive functions). Further, the authors not only highlight the problem, but provide reasonable methods forward (which I would love to see implemented). I think the manuscript is in good shape and will be well-cited. I have only a few minor comments and suggestions which should be relatively easy to implement in most cases.

Answer: We thank the reviewer for these thoughtful comments. We think their many detailed comments have greatly improved the reach and the reproducibility of the manuscript.

Line 41: I’d argue that the evidence supporting invasions as major drivers of extinction is relatively weak (particularly with plants). At the very least, this is a contentious claim in the literature. Thus, I would either provide some strong citations to back this up (and possibly include some “but see ….” citations), or else modify this to something like “Biological invasions are an important component of global change”. Or you could highlight that some plant invasions have major economic or environmental impacts, which is certainly true (and part of why having trait data to try to understand which species will have the bigger impacts is so important).

Answer: There is clear evidence that biological invasions in general are a major driver of extinctions. As shown by the recent IPBES report on invasive and alien species, which we now cite to support our statement, invasions contribute to 60% of all observed extinctions (Key Message A2 in the Summary for Policymakers, see also chapter 4.3.1). It is certainly more nuanced for plants, but invasions as a whole strongly impact biodiversity directly, notably through local extinctions. We, however, agree with the reviewer that the picture is more nuanced; so, we changed our wording to reflect this nuance:

L42-L44: “Biological invasions are an important component of global changes (Roy et al., 2024); we need a better understanding of their underlying ecological processes for effective management (Díaz et al., 2019; Roy et al., 2023).”

We also added a sentence detailing the ecosystem consequences of invasive plants:

L45-L54: “Plant invasions are known to cause many long lasting impacts on terrestrial and aquatic ecosystems, above- and belowground. Consequences include, e.g., severely changing ecosystem processes, leading to biotic homogenization of formerly distinct biotas, changing local abundance and species richness of outcompeted native biota (Pyšek et al., 2012; D’Antonio & Flory, 2017; Kumar Rai & Singh, 2020; Lázaro-Lobo et al., 2023; Dostál, 2024). Global invasion of plants led to approximately four percent of the global flora being established outside of its native range (van Kleunen et al., 2015), becoming alien (i.e. non-native, exotic) somewhere on this planet. Identifying plant traits promoting successful species introductions, establishment and dispersal is one of the major aims of plant invasion ecology (e.g., Pyšek et al., 2008; Drenovsky et al., 2012; Knapp & Kühn, 2012; van Kleunen et al., 2015; Gallien & Carboni, 2017).”

Line 186: since the model is at the species-level, it would be good to check whether phylogenetic correction is needed. I don’t expect it will be, or will change the overall conclusions, but worth doing a quick check anyway, especially since you found taxonomic biases in trait availability. (Li’s rtree package would be an easy source of phylogenies).

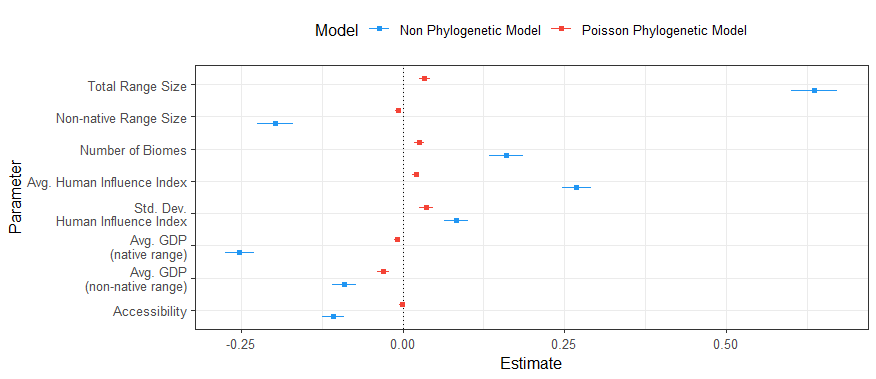
Answer:

On the one hand, we don’t think we need to provide a phylogenetic correction for the model, as we’re interested in knowing the determinants of the number of available traits for all species, whatever its identity. With this model, whether there is a phylogenetic effect or not doesn’t matter for the user of trait data.

On the other hand, testing the phylogenetic correction effect would help showing if there is an effect of closely-related species having a close number of measured traits. So we did fit a phylogenetic model. We first generated a phylogenetic tree of species using Li’s rtree package, we managed to position our 14,529 species. Using the generated tree, we identified a phylogenetic signal in the residuals of our trait measure model, so clearly a phylogenetic correction was needed.

We couldn’t identify an easy method to perform negative binomial phylogenetic models, so we decided to fit a Poisson model with a phylogenetic structure through the phylolm package with the phyloglm() function. The Poisson model assumes a mean-variance relationship which is relaxed under the negative binomial model, but given we were using the phylolm package, none of the classical diagnostics plots and tools were available, so we couldn’t make sure that assumption was actually met. If the reviewer has any strong suggestion regarding this point, we would be very open to implement it.

Under the phylogenetic model, the same variables affected the number of measured traits in a similar fashion (those increasing the number of measured traits were still increasing, respectively decreasing). The relative importance of the factors were slightly changed, but didn’t change our overall conclusions as shown in the figure below



We now mention the phylogenetic model briefly in the methods section, as well as the results section and provide the above figure as a supplementary figure for reference.

L222-L227: “*Phylogenetic model*. Because our trait knowledge model was species based we wanted to test the effect of adding phylogenetic correction to the model. We fitted a Poisson phylogenetic regression model, based on the same predictors as our non-phylogenetic model, using the phyloglm() function in the phylolm package (Ho & Ane, 2014). We provided a phylogenetic tree of all of our non-native species, assembled through the rtrees package (Li, 2023) using a reference global plant phylogeny (Smith & Brown, 2018).”

L378-L379: “Considering the phylogeny in the model didn’t affect the direction of the effect of all of the variables, which all remained with p-values < 0.001 (Figure S4).”

This is just a suggestion, please ignore it if it seems like too much work (e.g, more than say 10 lines of code): It would be interesting to compare the coverage of traits for introduced species with the overall coverage (or coverage for a comparably sized random sample of species). Then we’d know whether non-native species tend to be disproportionately sampled. I know you do the invasive vs non-invasive, but native vs non-native is also interesting (if it isn’t a hassle).

Answer: We have now added a section that compares the coverage between naturalized species and random subsamples of the same size of native species. We see that native species show much lower proportions of measured traits combinations then naturalized species. More generally, we found that naturalized plants have many more trait measures in our dataset than native plants. These results are now part of the Results section.

L330-L333: “Non-native species referred to as invasive in at least one region in GloNAF (“invasive” in this section) had a greater coverage in all trait combinations than non-native species never reported as invasive (“non-invasive” in this section), **which themselves showed higher coverage than species never referenced as non-natives (“natives” in this section).**”

L339-L341: “**The number of traits available per species followed the same pattern, invasive species had 74.8 traits available on average, while non-invasives had 34.7 and native ones 7.44 (All pairwise t-tests showed p-values < 0.001).**”

Given potential phenotypic differences between native and non-native regions, it would be interesting to know how complete the trait matrices tend to be when we only consider traits known to be measured within a given region. In other words, on average across each non-native species x region combination, what fraction of traits were measured within that region? I expect this is a very small fraction (as you mention), but if this could be assessed quickly it would be a useful addition. I wouldn’t think the full set of analyses (e.g., different trait spectra or family-level completeness) would be needed, but if a quick measure of the average trait completeness in the invaded range was available, I think that could be a nice addition and would fit in very nicely with the paragraph on lines 392 - 402.

Answer: We understand the reviewer’s idea on comparing trait availability within or outside the native region of each species. However, given that location is not available for a substantial number of trait data, we made the simplifying assumption not to consider the location of the trait measurement when estimating the amount of available data. This location information is available for all AusTraits and BIEN trait records, but only for about 40% of the trait records in TRY (see Kattge et al. 2020). The GIFT database that leverages floras to extract trait information and, as such, each trait record could be reported as the geographical span of the flora from which it was extracted. We now explicitly mention in the Methods section that we do not consider the location information as it’s available for only 42% of the trait records of TRY:

L134-L137: “We didn’t consider the geographical provenance of our data, though available for all of AusTraits and BIEN data, because it is only available for 42% of TRY data [(Kattge *et al.*, 2020)](https://www.zotero.org/google-docs/?eKFvqr), and isn’t easily tractable in GIFT as the trait measurements are coming from floras.”

L 437-L440! “Although we know that the provenance of the traits, i.e. where the measurements come from (e.g. native or non-native range), is relevant in invasion ecology [(e.g. Parker *et al.*, 2013)](https://www.zotero.org/google-docs/?Tczrot), we could not consider this factor. The main reason is the lack of georeferenced measures [(e.g., only 42% of trait observations are georeferenced in TRY v.5.0; Kattge *et al.*, 2020)](https://www.zotero.org/google-docs/?i5Yeot).”

Furthermore, identifying which part of the range of the species was the trait reported from requires knowing the exact delineation of native vs. naturalized range of species, which is a research question in itself. As such, this great suggestion is not achievable in this manuscript the main focus of which is to identify trait gaps.

Line 302: If I understand correctly, the comparison here is between non-native, non-invasive and non-native, invasive? Perhaps explicitly specify this as to clarify you’re not comparing native vs invasive.

Answer: This is correct. The sentence before tries to specify our definition of invasives and non-invasives in this section:

L330-L333: “Non-native species referred to as invasive in at least one region in GloNAF (“invasive” in this section) had a greater coverage in all trait combinations than non-native species never reported as invasive (“non-invasive” in this section), which themselves showed higher coverage than species never referenced as non-natives (“natives” in this section).”

We updated the next sentence to be clearer:

L333-L335: “We found strong evidence that LHS traits are more frequently measured for invasive species (48.2% of species) than for non-invasive species (24.8%; χ2 = 325, df = 1, p-value < 0.001).”

The negative effects of some of the predictors on trait completeness seem counterintuitive in some cases. It would be a nice inclusion if you revisited these relationships in the discussion and speculated a bit on what might be going on.

Answer: We have now added a full paragraph in the discussion detailing these negative effects

L413-L422: “As we expected, we found that non-native plants with larger ranges and occurring in more biomes had more traits measured across the databases. Opposite to our expectations, we found negative relationships between the number of traits measured and the average GDP in countries in both their native and non-native ranges. While average GDP should correlate with research effort, and as such collection effort, this negative relationship could be due to the relationships between average GDP over species ranges and the area of their ranges. Large-range species, which tend to have more traits measured, will show lower average GDP over their ranges. Small-range species may occur over higher GDP areas, but show a lower number of traits measured because of their overall smaller range. These findings call for additional studies on the determinants of trait knowledge for both native and non-natives plants.”

Line 342: Remind readers what this threshold refers to here (predictor completeness), and that the analyses you just told us about was based on an 80% threshold.

Answer: The sentence was indeed unclear. It now reads:

L375-L378: “The analyses were performed considering species for which the predictors were available for at least 80% of their total range, we obtained similar results when performing the same analyses with a threshold of 70% and 90% (Figure S4)”

I appreciate that you included the figures in the text, I hate having to scroll down to the bottom of a manuscript 🙂

Love the Open Code.

Answer: We’d like to reiterate our thanks to the reviewer for such nice comments.

## Referee: 2

I very much enjoyed reading this manuscript. It presents a comprehensive treatment of an important issue: the (lack of) availability of data on biological traits for a large subset of a group of interesting species - in this case, non-native plants. The compiled dataset is impressive, the analyses and visualisations are really impactful, and overall this is a valuable contribution to the ‘biodiversity data gaps and biases’ literature. There are a few places where a little more explanation or discussion could improve the work, but I have no major concerns. I’ll outline a couple of more general points and then some minor suggestions to consider, referencing relevant line numbers within the submitted manuscript.

Answer: We’d like to thank the reviewer for their nice comments that helped make our manuscript stronger and clearer.

Taxonomic harmonisation

I fully appreciate (from bitter experience!) that this is a significant endeavour, and a major consideration for this kind of synthetic work. As such, I would appreciate a little more detail in the main ms text about how exactly you performed this harmonisation. You state (in the section from L100) that you “merg[ed] the accepted binomial species names between GloNAF and each trait database” - what does that mean in practice? You point to Supplementary Information 1 but this does not appear to include any further information on the taxonomic harmonisation process.

Answer: That is correct, the manuscript actually didn’t contain the supplementary information; it should have contained a description of taxonomic harmonization. We now explain briefly our taxonomic harmonization procedure in the main text as well as a fully detailed explanation in Supplementary Information 1. The main text reads as follows:

L119-L128: “As the different databases used different taxonomic backbones to standardize species names, we performed a full taxonomic harmonization workflow (Grenié et al., 2022). For the four trait databases as well as GloNAF, we referred to the raw available names with authors and subspecific epithets if available (i.e., the name from the original source). We leveraged the speed and reliability of the Taxonomic Name Resolution Service (TNRS, v. 5.1 Boyle et al., 2021, 2013) with its R package TNRS v.0.3.6 (Maitner, 2024) to match all of these names against the World Checklist of Vascular Plants (Govaerts R (ed.), 2023). We set TNRS to only return the best match. To merge all datasets, we only retained the accepted binomial names for all species. In the end, we had 14,073 matched species names between GloNAF and all trait databases (see Supplementary Information 1 and Figure S1).”

Trait definitions

The section on aligning trait definitions (from L128) and associated detail in Supplementary Information is clear and well described - this was clearly a significant amount of work. I applaud the fact you make your cross-database table available to make it useful to others (L423), however as the saying goes, “Supplementary Material is where data go to die”. Do you have plans to serve this somewhere more obviously visible to the community? For instance, you go on to mention Open Trait Networks - is there infrastructure there that could host your cross-database matrix? That could of course be in addition to the Supp Mat version.

Answer: First of all, we thank the reviewer for this very relevant point. We agree that this represents a great amount of work that we wouldn’t like to see lost. Also, we know that Supplementary Materials are less read and more difficult to cite and reuse than actual papers. We’re in the process of writing a specific data manuscript solely on the trait network, and insights we can gain from this trait network, which are beyond the scope of this manuscript. This manuscript will be accompanied by a fully functional website and an R package to explore the network. To avoid having it hidden in this manuscript, we added an online supplementary material (<https://rekyt.github.io/alientraitgaps/>) that would be more accessible and specifically citable through the Zenodo archive (<https://doi.org/10.5281/zenodo.13940200>). We tend to think that OpenTraits is not exactly the best venue for this data, but we will discuss with the people behind the architecture to see how we could host it there or at least make it visible.

On the same topic of trait definitions, I come from a background of trait-based ecology in animal systems, where we might typically consider 10 or so traits, and so I am always amazed by the sheer number of traits considered in plant studies - here, well over 2000. You present some discussion of ‘key’ traits in different contexts - for instance, the groupings used in fig 2 - but I did wonder if there is any mileage in setting out some minimum set of broad traits that would be especially useful for the study of plant invasions. In a plant ecology context, I’m thinking of the work of e.g. Salguero-Gómez and colleagues attempting to identify key traits to define simple axes of plant life history (for example https://doi.org/10.1073/pnas.1315179111) - is there any potential to pare down the 2000+ traits to a much smaller number? You do this to some extent, although that’s largely based on data availability. Perhaps some consideration of key sets of traits could feed into your discussion (from L431) of prioritising future efforts.

Answer: We agree that this number of distinct traits seems well over a reasonable amount, especially compared to animal traits. As stated above, we aim to publish a full manuscript studying this trait network, detailing the classification of traits by type or organs. One of the issues with plant traits, which could be mentioned here, is the immense context-dependency of some traits, which inflate the total number of traits. For example, flammability traits can be quite diverse: post-fire resprouting ability, resistance against actual fire, propagule possibilities after a fire, etc., but they are only relevant and measured in fire-prone ecosystems. As such, they contribute traits that are very rarely measured. Also, most unique traits are brought by the TRY database, and looking at the actual traits can explain this trait inflation: element concentrations in leaves or barks can be explained through many traits. For example, thanks to mass spectrometry, it’s possible to report concentrations in more than 20 different elements across plant organs, even if their ecological meaning isn’t clear (for example, there are four traits in TRY for concentration of antimony, in leaves, stems, roots, and coarse root, but we lack an ecological interpretation of antimony concentration apart from it’s ecotoxicity). Similarly, TRY reports hundreds of litter decomposition rates, which are not considered traits by many, that differ based on what has been considered in the actual litter (only leaves, only wood, etc.). We think a collective reflection should be done to point out and solve this problem of trait inflation.

With focus on something like trait syndromes for plant invasions it is also obviously very context- specific. However, there are some trait, or trait combinations, which are more often analysed and associated with invasion success than others. But be aware that those analyzed traits are per se biased based on the data availability (you can’t analyze what you don’t have).

We now mention it explicitly in the manuscript:

L490-L491: “It seems unrealistic to expect all trait gaps to be filled with in-situ measurements in the near future. **Given the immense diversity of the plant traits reported here (more than 2,764 different traits), prioritizing the most commonly studied traits would seem more tractable.**”

Trait accuracy

In the section from L392 in the discussion you touch on the fact that a single measure of a trait per species does not capture the full range of variation present, using the example of different trait expression by the same species in native and non-native ranges. But I think there is a broader point to be made here about how much we trust these large data compilations - incredible resources though they surely are. In your ms, you are quantifying the completeness of the species x trait matrix, with the implicit assumption that all trait measurements are accurate. This is almost certainly not the case. For instance, across marine metazoa, documented estimates of maximum size can vary by 2-3 orders of magnitude within species (see https://doi.org/10.1002/ece3.11506) - whilst some of this variation is ecologically interesting, there are clear instances of mistakes in databases too (and these often propagate from primary sources into various secondary compilations). Perhaps more directly relevant to your study is this recent critique of data quality in TRY: https://doi.org/10.1111/gcb.17116. None of this is to denigrate the data sources, or your analyses of them. But I think it would be good to acknowledge somewhere that \*even if\* the full species x trait matrix were somehow to be completed, there would likely still be considerable uncertainty remaining, owing to mistakes / measurement error, as well as the fact that individual species vary.

Answer: This is a great point! We agree that not all trait measurements are precise and well reported. We, ourselves, have identified several errors in trait measurements due to unit inversion or implausible trait values. We decided not to consider it explicitly as a factor to take the least conservative possible estimates (exactly like we didn’t consider the estimation of intraspecific variation in our completeness assessments). This way, if our estimates, taken the least conservative approach, are concerning, they should be even more concerning considering ITV and measurement errors.

We now acknowledge measurement errors and intraspecific variation explicitly in the discussion by adding a full paragraph about it:

L448-L457: “We here made the simplifying assumption that all trait measurements have been perfectly recorded, with neither measurement nor reporting errors. Considering these errors would certainly reduce even further our trait knowledge. It was recently shown for the TRY database that only 23% of the original SLA measurements from TRY were actually original, representative, logical, comparable, and traceable (Augustine et al., 2024). While we know the ecological importance of intraspecific trait variation for plants (Westerband et al., 2021), we also simplified our trait matrix by considering any single trait measurement for a single species enough to know the trait value for the species. Our study could be further extended by studying the number of trait measurements known for each trait and each species to estimate how well we know the intraspecific variation for each species.”

Trait imputation

As part of your useful overview of strategies to increase trait knowledge, Fig 6 includes trait imputation. Clearly this is potentially a very effective and extremely cost effective way of filling some gaps, and there’s now a fairly well developed literature which includes details on various methods, such as those including phylogenetic structure (e.g. (r)phylopars) and more general methods (e.g. missForest). However, you do not go into this in the text, which feels like an omission. I don’t think you need to add much, but 2-3 sentences to give a quick overview and a few references (for instance https://doi.org/10.1111/2041-210X.14339, https://doi.org/10.1111/geb.13185) would be a useful addition to show you have considered this issue.

Answer: That’s correct. We thank the reviewer for this great remark. We now add some details about trait imputation in the discussion of the paper:

L576-L583: “The above-mentioned strategies help fill the trait gaps by acquiring new data. Trait imputation (also known as trait gap filling) is a complementary strategy that leverages trait correlations as well as additional data (whether spatial and/or phylogenetic depends on the exact method) to infer the trait values for species with missing values (Joswig et al., 2023). Trait imputation should be performed carefully, considering the strengths and weaknesses of the different imputation methods as well as the ecological context of the original trait measurements used to fit the imputation models (Penone et al., 2014; Johnson et al., 2021; Blomberg & Todorov; Gorné et al.).”

### Minor points

L122, 407 spelling - this should be ‘complementary’ (which means combining together to provide a more complete picture) not complimentary (free).

Answer: Fixed!

L153 - you note that ‘521 traits were never observed across our set of target species’ - to what extent are these important traits? Does this further impact your conclusions around trait data availability or completeness - i.e. your percentages are in reality even lower? Are any of these fully missing traits important in an invasion context?

Answer: Given the context dependency of traits, and the fact that TRY basically accepts any trait submission, which leads to trait inflation (= increasing by a large fraction the number of traits measured), we can say confidently that these traits mustn’t be important for an invasion context, or at least not for a global comparison.

L222 - sentence incomplete

Answer: Fixed!

Fig2A is great. Fig2B expands this and is a really nice idea but not sure it’s successful, as it quickly becomes hard to make out detail in any but the biggest few families. You could maybe show some exemplar families (big / small, well known / poorly known) at the same size, and then include the existing figure as a supplementary figure. Or could it be presented online in a zoomable format? I think it is OK as it is, and would not insist on any changes, so these are just suggestions.

Answer: We now have a fully zoomable version through our online supplement (<https://rekyt.github.io/alientraitgaps>), which is archived long-term on Zenodo (<https://doi.org/10.5281/zenodo.13940200>).

Fig3A - To what extent is alien species richness a function of study effort? In other words, are there likely to be more undetected alien species in some parts of the world, perhaps with similar covariates as those you identify as being important for trait data availability. I appreciate you can only speculate on this, but it seems like a relevant point which would make your assessments of data availability generous, if anything.

Answer: Study effort is for sure a strong determinant of the known alien species richness. GloNAF is the most complete global compilation of regional alien plants. GloNAF offers a completeness score that judges to what extent the original species lists are completeness based on expert opinion. It shows that completeness is highest for North America, many European regions, China, Southern Africa and Australia and New Zealand. As we wanted to get the most complete global picture, we decided not to leverage these scores to limit ourselves, but we do understand the concern of the data completeness.

L299 ‘More measured’ does not read quite right. ‘…measured more often’ perhaps? Or ‘Trait data is more often available for widespread and invasive species’?

Answer: We opted for “Traits of widespread invasives are measured more often”

Fig 5 - can you put SE values around these coefficients? Also would it be worth noting that units on the x axis are standard deviations of the relevant predictors (I think)?

Answer: The confidence intervals were on the figure, but they were too small to be seen. This was because the figure displayed Incidence Rate Ratios on a log scale, because we are using a negative-binomial regression. We changed the figure to display exponentiated coefficients, which are easier to interpret, and added confidence interval values to the label of the average estimate to know exactly how well they are estimated.

L364 - I think you have this point well covered but a couple of other relevant papers are https://doi.org/10.1098/rstb.2019.0445 (various dimensions of marine animal diversity) and https://doi.org/10.1111/j.1466-8238.2011.00726.x (specifically on correlates of trait data availability)

Answer: Thank you for suggesting these papers that broaden the perspective. We now cite them both in this paragraph.

L405 ‘interoperable’ is a good choice of word here - you could maybe make the more general point about FAIRness of data here (in my experience, the I in FAIR is often the hardest one to achieve!) - I appreciate you do raise this in your conclusion but it could be good to mention it here too.

Answer: Great suggestion! We now mention FAIR principles explicitly:

L459-L462: “Even though there are efforts in unifying the format of plant trait databases, they are far from being interoperable or even automatically integrable, both of which are criteria to follow FAIR principles (i.e. Findability, Accessibility, Interoperability, and Reusability) in data stewardship (Wilkinson et al., 2016; Keller et al., 2023).”

With the following references:  
Wilkinson, M.D., Dumontier, M., Aalbersberg, Ij.J., Appleton, G., Axton, M., Baak, A., Blomberg, N., Boiten, J.-W., da Silva Santos, L.B., Bourne, P.E., 2016. The FAIR Guiding Principles for scientific data management and stewardship. Scientific data 3, 1–9.

Keller, A., Ankenbrand, M.J., Bruelheide, H., Dekeyzer, S., Enquist, B.J., Erfanian, M.B., Falster, D.S., Gallagher, R.V., Hammock, J., Kattge, J., Leonhardt, S.D., Madin, J.S., Maitner, B., Neyret, M., Onstein, R.E., Pearse, W.D., Poelen, J.H., Salguero-Gomez, R., Schneider, F.D., Tóth, A.B., Penone, C., 2023. Ten (mostly) simple rules to future-proof trait data in ecological and evolutionary sciences. Methods in Ecology and Evolution 14, 444–458. https://doi.org/10.1111/2041-210X.14033