Responses to #Reviewer 1

This is a well-prepared manuscript. The authors focused on mapping several key plant functional traits in China by integrating three kinds of machine learning algorithms and climate, soil, and vegetation variables. Comprehensive experiments were implemented and all necessary technical details were properly introduced. It could be of great interest to those who are interested in trait ecology, and global vegetation modeling. However, at present, some technical details need to be added and the language of the paper needs to be further improved. In its current form, major revisions are needed before this manuscript could be accepted, thereby further improving the quality and legibility of this manuscript. The main comments are as follows:

[Response]: Thanks for your positive comments and constructive suggestions for our manuscript. We have carefully addressed the comments and suggestions in the revision, and detailed revisions and responses are listed below. In addition, the language of this manuscript has been professionally revised, and we have used tracks to highlight the revisions in the revised manuscript.

1. We are aware that the plant functional traits have strong seasonal variability. However, it seems that the issue of seasonality was not taken into account in the synthesized plant functional traits database by the authors. As a result, I don't know which time period of these estimated plant functional trait maps. Could you please provide some additional explanations regarding the temporal information associated with these plant trait maps?

[Response]: Thanks for your suggestions. In literature and public databases that provided the sampling time used in our study, the sampling time mostly focused on the growing season of a year (i.e., May-October), thus the effect of seasonality is relative minor. In addition, we collected trait data that must meet this criterion: plant trait observations must be made on mature plant individuals, so some specific leaf and plant growth stages (e.g., seedlings, leaf expanding stage or senescent leaves) were excluded to minimize the effect of seasonality. We added the above-mentioned explanation in the section 2.2 in Materials and Methods (see Lines 163–165 in the revised manuscript). And the sampling time of plant functional traits was shown in the dataset used in this study at the figshare link: https://figshare.com/s/c527c12d310cb8156ed2.

2. It is really good you compiled a large plant trait database with more than 50 thousand samples, spanning large geographic regions and species, please present the number of samples for each selected plant functional trait. And how many samples are for model calibration and validation?

[Response]: Thanks for your suggestion. We have added the number of samples for each plant functional trait and the number of samples used for model training and validation in the Table B3 in Appendix B as follows.

Table B3 The number of samples of eight plant functional trait used for model training (80%) and validation (20%).

Traits	No. of samples	No. of samples used for model training	No. of samples used for model validation
SLA	9195	7356	1839
LDMC	3957	3166	791
LNC	7407	5926	1481
LPC	6266	5013	1253
LA	5976	4781	1195
WD	1787	1430	357

3. There are many choices of climate variable products and each product carries varying levels of uncertainty. Why did you choose the WorldClim dataset and did you assess the uncertainties of these datasets?

[Response]: We selected the Worldclim dataset mainly based on two reasons as follows. First, Worldclim version 2.1 dataset includes 19 bioclimatic variables, covering minimum, mean, and maximum temperature, precipitation, solar radiation and total precipitation. When we selected climate datasets in the stage of data processing, we compared Worldclim version 2.1 with some datasets (e.g., CRU v4.0, ERA5-land and China Meteorological Forcing Dataset) from the comprehensiveness of variables, spatial resolution and time period. We used the Worldclim version 2.1 dataset for this study instead of the other three datasets as the latter does not have high resolution and include multiple aspects of climate variables needed in this study. Second, our previous study has proved that climate variability and seasonality variables, in particular, mean temperature of the warmest and coldest seasons of a year and mean precipitation in the wettest and driest seasons of a year, were more important drivers of leaf trait variation than mean annual temperature and mean annual precipitation (An et al., 2021). Therefore, given that Worldclim version 2.1 includes these above-mentioned indicators, we selected it.

Indeed, although WorldClim dataset has been widely applied in different biogeographical applications in the global and regional studies (Loozen et al., 2020; Huang et al., 2021; Liu et al., 2022), and it is classical and recognized by the researchers, we have to admit that climate dataset has certain limitation and uncertainties. We have added the corresponding description about the uncertainties as "*In addition, although Worldclim version 2.1 product has high spatial resolution and includes various aspects of climatic parameters, there exists certain limitation and uncertainty in predicting trait maps. Therefore, integrating satellite remote sensing monitoring methods with in in-situ trait data collection can also provide an effective way to estimate and assess the species diversity at a large scale (Cavender-Bares et al., 2022).*" in the Discussion section (see Lines 625–629 in the revised manuscript).

References

Besnard, S., Koirala, S., Santoro, M., Weber, U., Nelson, J., Gutter, J., Herault, B., Kassi, J., N'Guessan, A., Neigh, C., Poulter, B., Zhang, T., and Carvalhais, N.: Mapping global forest age from forest inventories, biomass and climate data. Earth Syst. Sci. Data, 13, 4881–4896, https://doi.org/10.5194/essd-13-4881-2021, 2021.

Fick, S. E. and Hijmans, R. J.: WorldClim 2: new 1km spatial resolution climate surfaces for global land areas. Int. J. Climatol., 37, 4302–4315, https://doi.org/10.1002/joc.5086, 2017.

Harris, I., Osborn, T. J., Jones P., and Lister D. Version 4 of the CRU TS monthly high-resolution gridded multivariate climate dataset. Sci. Rep., 7, 109, https://doi.org/10.1038/s41597-020-0453-3, 2020.

He, J., Yang, K., Tang, W. Lu, H., Qin, J., Chen, Y. Y., and Li, X.: The first high-resolution meteorological forcing dataset for land process studies over China. Sci. Data, 7, 25, https://doi.org/10.1038/s41597-020-0369-y, 2020.

Huang, Y. Y., Ciais, P., Santoro, M., Makowski, D., Chave, J., Schepaschenko, D., Abramoff, R. Z., Goll, D. S., Yang, H., Chen, Y., Wei, W., and Piao, S. L.: A global map of root biomass across the world's forests. Earth Syst. Sci. Data, 13, 4263–4274, https://doi.org/10.5194/essd-13-4263-2021, 2021.

Liu, X. Q., Su, Y. J., Hu, T. Y., Yang, Q. L., Liu, B. B., Deng, Y. F., Tang, H., Tang, Z. Y., Fang, J. Y., Guo, Q. H.: Neural network guided interpolation for mapping canopy height of China's forests by integrating GEDI and ICESat-2 data. Remote Sens. Environ., 269, 112844, https://doi.org/10.1016/J.RSE.2021.112844, 2022.

Loozen, Y., Rebel, K. T., de Jong, S. M., Lu, M., Ollinger, S. V., Wassen, M. J., and Karssenberg, D.: Mapping canopy nitrogen in European forests using remote sensing and environmental variables with the random forests method. Remote Sens. Environ., 247, 111933, https://doi.org/10.1016/j.rse.2020.111933, 2020.

Munoz-Sabater, J., Dutra, E., Agusti-Panareda, A., Albergel, C., Arduini, G., Balsamo, G., Boussetta, S., Choulga, M., Harrigan, S., Hersbach, H., Martens, B., Miralles, D. G., Piles, M., Rodriguez-Fernandez, N. J., Zsoter, E., Buontempo, C., and Thepaut, J. N.: ERA5-Land: a state-of-the-art global reanalysis dataset for land applications. Earth Syst. Sci. Data, 13, 4349–4383, https://doi.org/10.5194/essd-13-4349-2021, 2021.

4. I found that the time period for bioclimate variables and RAD is from 1970 to 2000, while the AI data is from 1950 to 2000 and the vegetation indices are 2000-2018 & 2002-2011, please explain why the time period of different input variables are not consistent.

[Response]: The bioclimate variables and RAD were extracted from the Worldclim version 2.1 for the period from 1970 to 2000, because this dataset has a high spatial resolution and the comprehensiveness of indicators that are related to plant functional trait variation. There was a mistake in the text, the AI data was from 1970 to 2000 instead of 1950-2000. We have corrected it in the revised manuscript. The AI data was calculated based on WorldClim 2.1 and implementation of a Penman Montieth Reference Evapotranspiration (ET0) equation, and the spatial resolution is 1 km (Trabucco and Zomer, 2018). In addition, vegetation indices included

enhanced vegetation index (EVI) and the MERIS terrestrial chlorophyll index (MTCI) in our study. The EVI data was extracted from the MOD13A3 V006 product, ranging from April 1998 to December 2018 when we began to conduct this study. Due to the incompleteness of January to March in 1998, so we calculated the monthly EVI data from 2000 to 2018. The monthly MTCI data was extracted from MERIS Level 3 MTCI products that only provided the time period for 2002-2011. Given of the data availability and high spatial resolution, the climate and vegetation datasets with different time periods is unavoidable in spatial mapping and biogeographical studies so far (Crowther et al., 2015; Moreno-Martínez et al., 2018; Loozen et al., 2020; Huang et al., 2021; Ma et al., 2021). Indeed, we must admit that the inconsistency in the time period could lead to predictive uncertainty, thus we have added the corresponding content to discuss the possible uncertainties as "*The lack of consistent time period and spatial resolution of predictors due to limitation of data availability is another key challenges in the spatial mapping of plant functional traits.*" in the Discussion section (see Lines 623–625 in the revised manuscript).

References

Crowther, T. W., Glick, H. B., Covey, K. R., Bettigole, C., Maynard, D. S., Thomas, S. M., Smith, J. R., Hintler, G., Duguid, M. C., et al.: Mapping tree density at a global scale, Nature, 532, 268–268, https://doi.org/ 10.1038/nature16178, 2016.

Huang, Y. Y., Ciais, P., Santoro, M., Makowski, D., Chave, J., Schepaschenko, D., Abramoff, R. Z., Goll, D. S., Yang, H., Chen, Y., Wei, W., and Piao, S. L.: A global map of root biomass across the world's forests. Earth Syst. Sci. Data, 13, 4263–4274, https://doi.org/10.5194/essd-13-4263-2021, 2021.

Loozen, Y., Rebel, K. T., de Jong, S. M., Lu, M., Ollinger, S. V., Wassen, M. J., and Karssenberg, D.: Mapping canopy nitrogen in European forests using remote sensing and environmental variables with the random forests method. Remote Sens. Environ., 247, 111933, https://doi.org/10.1016/j.rse.2020.111933, 2020.

Ma, H. Z., Mo, L. D., Crowther, T. W., Maynard, D. S., van den Hoogen, J., Stocker, B. D., Terrer, C., and Zohner, C. M.: The global distribution and environmental drivers of aboveground versus belowground plant biomass. Nat. Ecol. Evol., 5, 1110, https://doi.org/10.1038/s41559-021-01485-1, 2021.

Moreno-Martínez, Á., Camps-Valls, G., Kattge, J., Robinson, N., Reichstein, M., van Bodegom, P., Kramer, K., Cornelissen, J. H. C., Reich, P., Bahn, M., Niinemets, Ü., Peñuelas, J., Craine, J. M., Cerabolini, B. E. L., Minden, V., Laughlin, D. C., Sack, L., Allred, B., Baraloto, C., Byun, C., Soudzilovskaia, N. A., and Running, S. W.: A methodology to derive global maps of leaf traits using remote sensing and climate data. Remote Sens. Environ., 218, 69–88, https://doi.org/10.1016/j.rse.2018.09.006, 2018.

Trabucco, A., and Zomer, R. J.: Global Aridity Index and Potential Evapo-Transpiration (ET0) Climate Database v2. CGIAR Consortium for Spatial Information (CGIAR-CSI), https://cgiarcsi.community, 2018.

5. The authors used the nearest neighborhood method to resample all the input data to a consistent spatial resolution of 1 km. It is fine for the original resolution of the data below 1 km to upscale to 1km. However, Downscaling data to 1km resolution using this method is not meant for datasets with spatial resolutions greater than 1km such as MTCI with 4.63 km spatial resolution.

[Response]: MTCI is an important factor that is closely related to plant functional traits (Loozen et al., 2020). However, MTCI dataset currently available is just 4.63 km in spatial resolution. Although the downscaling data is a common resolution used in spatial mapping studies (Moreno-Martínez et al., 2018; Huang et al., 2021) and a good compromise, we must admit that downscaling data from low spatial resolution may generate the uncertainty. So we have added the relevant contents to discuss this uncertainty as "*The lack of consistent time period and spatial resolution of predictors due to limitation of data availability is another key challenges in the spatial mapping of plant functional traits.*" in the Discussion section (see Lines 623–625 in the revised manuscript).

6. Did you build separate models for each plant trait, or estimated these traits simultaneously? How did you consider the covariance of these traits when you were modeling?

[Response]: We built separate models for each plant trait, so trait covariance need not be considered in the manuscript. To avoid the misleading information in the predictive methods for plant functional traits, we have corrected the relevant content to describe the model predictions more clearly (see Line 286 in the revised manuscript).

7. For the calculations of community-weighted mean values, you first build the relationships between the observed trait values and the input variables with 1km spatial resolution. I think your predicted values of traits present the values of 1km grid cells, so my question is how you applied CWM using the abundance of each PFT in each 1km grid cell.

[Response]: Thanks. We generated the plant functional trait maps in four steps as follows. First, we associated each species with a corresponding PFT based on plant growth form (tree, shrub and grass), leaf type (broadleaf and needleleaf) and leaf phenology (deciduous and evergreen). For example, the information on *Salix matsudana* is: tree, deciduous and broadleaf, thus, we were able to associate the PFT of deciduous broadleaf forest (DBF) to this species (see Lines 177–187). The species that did not correspond to any PFT were discarded. Second, we predicted the trait values for six PFTs separately by building the machine learning models using the field measurement data and predictors at a 1 km spatial resolution. Then, we obtained six prediction layers for each plant functional trait. Third, the classification of natural PFT types includes evergreen needleleaf forest (ENF), evergreen broadleaf forest (EBF), deciduous needleleaf forest (DNF), deciduous broadleaf forest (DBF), shrubland (SHL), grassland (GRL). We

calculated the abundance of individual PFT within 1 km grid cell using a land cover map with a spatial high-resolution of 100 m. Forth, the final community weighted mean trait values were calculated according to the predicted trait values (the second step) and corresponding abundance of each PFT (the third step) refer to the equation of CWM calculation in the community as Eq. (1) (Garnier et al., 2004). As we all know, we cannot obtain the data surrounding species co-occurrence and their relative cover or abundance in ecological communities, which is a key challenges in how scales up from the species to the community levels. The abundance of each PFT can be considered as an alternative way (Moreno-Martínez et al., 2018; Dong et al., 2023) relative to unweighted or equal weight community means methods, in order to scale-up plant trait observations and matching the spatial scales of the local trait observations and environment and vegetation data.

$$\text{CWM} = \sum_{i=1}^{n} W_i X_i \tag{1}$$

where n is the total number of PFT in a given grid, W_i is the relative abundance of the ith PFT, and X_i is the predicted trait value of the ith PFT.

We have revised the relevant content in the sections 2.2 and 2.5 in Materials and Methods (see Lines 177–187, 249–258, 314–322 in the revised manuscript).

Reference

Garnier, E., Cortez, J., Billès, G., Navas, M. L., Roumet, C., Debussche, M., Laurent, G., Blanchard, A., Aubry, D., Bellmann, A., Neill, C., and Toussaint, J. P.: Plant functional markers capture ecosystem properties during secondary succession. Ecology, 85, 2630–2637, https://doi.org/10.1890/03-0799, 2004.

Dong, N., Dechant, B., Wang, H., Wright, I. J., and Prentice, I. C.: Global leaf-trait mapping based on optimality theory. Glob. Ecol. Biogeogr., https://doi.org/10.1111/geb.13680, 2023.

Moreno-Martínez, Á., Camps-Valls, G., Kattge, J., Robinson, N., Reichstein, M., van Bodegom, P., Kramer, K., Cornelissen, J. H. C., Reich, P., Bahn, M., Niinemets, Ü., Peñuelas, J., Craine, J. M., Cerabolini, B. E. L., Minden, V., Laughlin, D. C., Sack, L., Allred, B., Baraloto, C., Byun, C., Soudzilovskaia, N. A., and Running, S. W.: A methodology to derive global maps of leaf traits using remote sensing and climate data. Remote Sens. Environ., 218, 69–88, https://doi.org/10.1016/j.rse.2018.09.006, 2018.

8. What is the ensemble model mean? how to merge the results of RF and boosted regression trees as you presented in line 263. Could you please present more details of the ensemble model?

[Response]: Previous studies have been proved to have differences and uncertainties among different single technique in their modelling performance. Therefore, the ensemble models have the advantages in overcoming the problem of variability in predictions and constructing a more stable and accurate model (Thuiller et al., 2003; 2005). Ensemble models are based on combinative algorithms of the predictions provided by different single-models, and they show

promise for different biogeographical and conservation biological applications (Marmion et al., 2009; Boonman et al., 2020). The most commonly used techniques of ensemble methods include Weighted Average, Mean (All), Median (All), Median (PCA) and Best (Marmion et al., 2009). Previous studies have reported that Weighted Average methods provided significantly more robust predictions than all the single-models and the other consensus methods (Marmion et al., 2009; Bourel et al., 2018).

In this manuscript, we used Weighted Average methods based on the R^2 values of random forest and boosted regression trees to obtain the predictive performance of the ensemble models. First, we calculated the predictive values of ensemble model, in a given grid cell, based on predictive values and the cross-validated R^2 values of random forest and boosted regression trees as described by the following equation (Marmion et al., 2009; Boonman et al., 2020).

$$Pred\_EM_t = \frac{\sum_{m=1}^{2}(pred_{m,t} \times r_{m,t}^2)}{\sum_{m=1}^{2} r_{m,t}^2}$$

where $Pred\_EM_t$ is the predictive values of t trait in ensemble model, $pred_{m,t}$ is the predictive values of t trait in m model, $r_{m,t}^2$ is the cross-validated R^2 of t trait in m model.

Second, the accuracy of the ensemble model was calculated by regressing the predictive values of ensemble model based on the equation above against the observed trait values.

We have added more detailed information of the ensemble model in the section 2.5 in the Materials and Methods (see Lines 326–336 in the revised manuscript).

References

Thuiller, W., Araújo, M. B., and Lavorel, S.: Generalized models vs. classification tree analysis: predicting spatial distributions of plant species at different scales. J. Veg. Sci., 14, 669–680, https://doi.org/10.1658/1100-9233(2003)014[0669:GMVCTA]2.0.CO;2, 2003.

Thuiller, W., Lavorel, S., Araújo, M.B., Sykes, M. T., and Prentice, I. C.: Climate change threats to plant diversity in Europe. P. Nat. Acad. Sci. USA, 102, 8245–8250, https://doi.org/10.1073/pnas.0409902102, 2005.

Marmion, M., Parviainen, M., Luoto, M., Heikkinen, R. K., and Thuiller, W.: Evaluation of consensus methods in predictive species distribution modelling. Divers. Distrib., 15, 59–69, https://doi.org/10.1111/j.1472-4642.2008.00491.x, 2009.

Boonman, C. C. F., Benitez-Lopez, A., Schipper, A. M., Thuiller, W., Anand, M., Cerabolini, B. E. L., Cornelissen, J. H. C., Gonzalez-Melo, A., Hattingh, W. N., Higuchi, P., Laughlin, D. C., Onipchenko, V. G., Penuelas, J., Poorter, L., Soudzilovskaia, N. A., Huijbregts, M. A. J., and Santini, L.: Assessing the reliability of predicted plant trait distributions at the global scale. Glob. Ecol. Biogeogr., 29, 1034–1051, https://doi.org/10.1111/geb.13086, 2020.

Bourel, M., Crisci, C., and Martinez, A.: Consensus methods based on machine learning techniques for marine phytoplankton presence-absence prediction. Ecol. Inform., 42, 46–54, https://doi.org/10.1016/j.ecoinf.2017.09.004, 2017.

9. You just build the models between the 1km spatial resolution data and the filed measurement data. Do you think that is there any spatial mismatch between them?

[Response]: Yes, we have considered this issue when we extracted the predictive variables of sampling sites from the 1 km spatial resolution data. However, it is not avoidable in a meta-analysis at the large scale. It may be mainly attributed into two reasons. First, our study was conducted at a large scale, and was obtained plant functional traits from previous studies on field survey. Given that each study where we collected data focused on different aims and experimental designs, so it is impossible to provide comprehensive auxiliary data such as climate, soil and topography in the original literature and public databases. Indeed, when we extracted the plant functional trait data from literature and public databases, several auxiliary data are always missing. Due to the deficits of original auxiliary data, we have to extract the auxiliary data (i.e., environmental variables and vegetation indices) from public datasets with high spatial resolution to ensure their data match as far as possible. Second, we used environmental variables and vegetation indices with high resolution as much as possible to match field measurement data, in order to minimize the difference between them. In addition, we have found that the MAT and MAP from the original literature agreed well with the values in the dataset (R^2 values were 0.96 and 0.89, $p < 0.05$) in our previous study. Although this method is a most common resolution and accepted practice in similar studies such as large-scale spatial mapping and biogeography based on collected field measurement data (Valverde-Barrantes et al., 2018; Boonman et al., 2020; Ma et al., 2021). We must admit that there exist uncertainties of the spatial mismatch between them, thus we have added the corresponding discussion as "*The environmental information of sampling sites was not always obtained from original literature, thus using the public environmental products is a common resolution used in large-scale plant trait studies (Boonman et al., 2020; Vallicrosa et al., 2022). Such mismatch between in-situ trait measurements and predictors should be resolved in further work.*" in the Discussion section (see Lines 613–616 in the revised manuscript).

References

Boonman, C. C. F., Benitez-Lopez, A., Schipper, A. M., Thuiller, W., Anand, M., Cerabolini, B. E. L., Cornelissen, J. H. C., Gonzalez-Melo, A., Hattingh, W. N., Higuchi, P., Laughlin, D. C., Onipchenko, V. G., Penuelas, J., Poorter, L., Soudzilovskaia, N. A., Huijbregts, M. A. J., and Santini, L.: Assessing the reliability of predicted plant trait distributions at the global scale. Glob. Ecol. Biogeogr., 29, 1034–1051, https://doi.org/10.1111/geb.13086, 2020.

Huang, Y. Y., Ciais, P., Santoro, M., Makowski, D., Chave, J., Schepaschenko, D., Abramoff, R. Z., Goll, D. S., Yang, H., Chen, Y., Wei, W., and Piao, S. L.: A global map of root biomass across the world's forests. Earth Syst. Sci. Data, 13, 4263–4274, https://doi.org/10.5194/essd-13-4263-2021, 2021.

Ma, H. Z., Mo, L. D., Crowther, T. W., Maynard, D. S., van den Hoogen, J., Stocker, B. D., Terrer, C.,

and Zohner, C. M.: The global distribution and environmental drivers of aboveground versus belowground plant biomass. Nat. Ecol. Evol., 5, 1110, https://doi.org/10.1038/s41559-021-01485-1, 2021.

Valverde-Barrantes, O. J., Freschet, G. T., Roumet, C., and Blackwood, C. B.: A worldview of root traits: the influence of ancestry, growth form, climate and mycorrhizal association on the functional trait variation of fine-root tissues in seed plants. New Phytol., 215, https://doi.org/1562–157310.1111/nph.14571, 2017.

Joswig, J. S., Wirth, C., Schuman, M. C., Kattge, J., Reu, B., Wright, I. J., Sippel, S. D., Ruger, N., Richter, R., Schaepman, M. E., et al.: Climatic and soil factors explain the two-dimensional spectrum of global plant trait variation, Nat. Ecol. Evol., 6, 36–48, https://doi.org/10.1038/s41559-021-01616-8, 2022.

10. Please add the units of these traits in Table 2 although you present them in your supplementary table. And I suggest that it is better to use nRMSE in the realm of leaf functional trait estimation (nRMSE = RMSE/range of estimated plant traits).

[Response]: Thanks for your constructive suggestions. We have added the units of these traits in Table 2, and we have also calculated nRMSE to place of RMSE in the revised manuscript (see Line 297, 363–366 and Table 2).

11. When analyzing the spatial patterns of plant functional traits, it is better to have a map to show the readers where the locations you mentioned in the manuscript like Yunnan, Loes Plateau, etc. are.

[Response]: Thanks for your nice suggestion. We have added corresponding locations in the Figs. 3, 4 and 6 according to the result description in the revised manuscript as follows.

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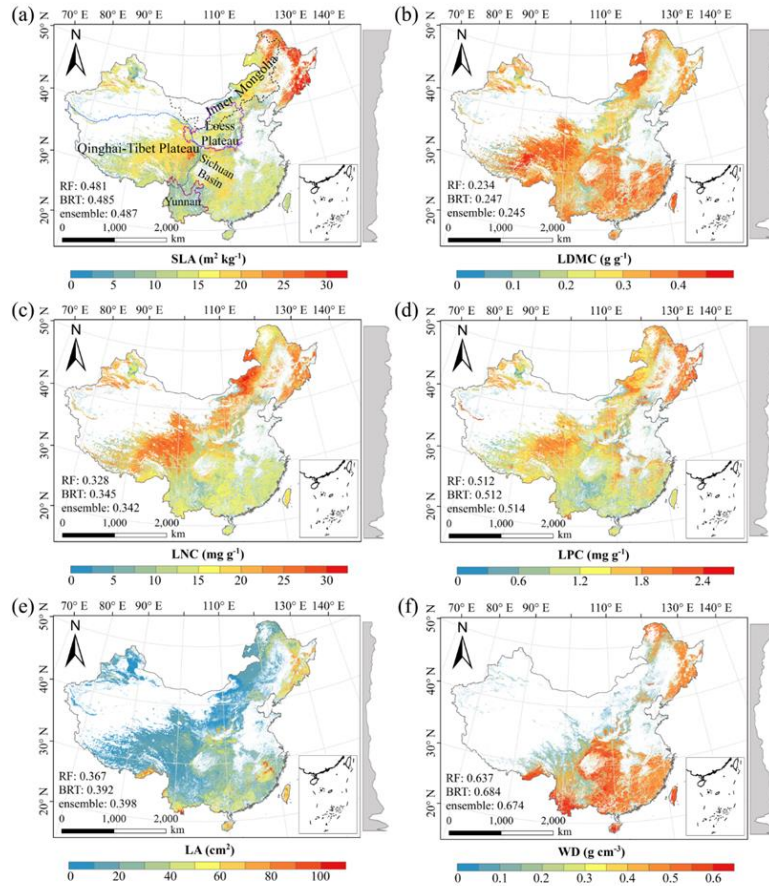
Figure 3. Spatial patterns of predicted plant functional traits in China based on the ensemble model. The grey curves to the right of the maps display trait distribution along with latitude. RF, random forest; BRT, boosted regression trees; ensemble, ensemble model; SLA, specific leaf area; LDMC, leaf dry matter content; LNC, leaf N concentration; LPC, leaf P concentration; LA, leaf area; WD, wood density.
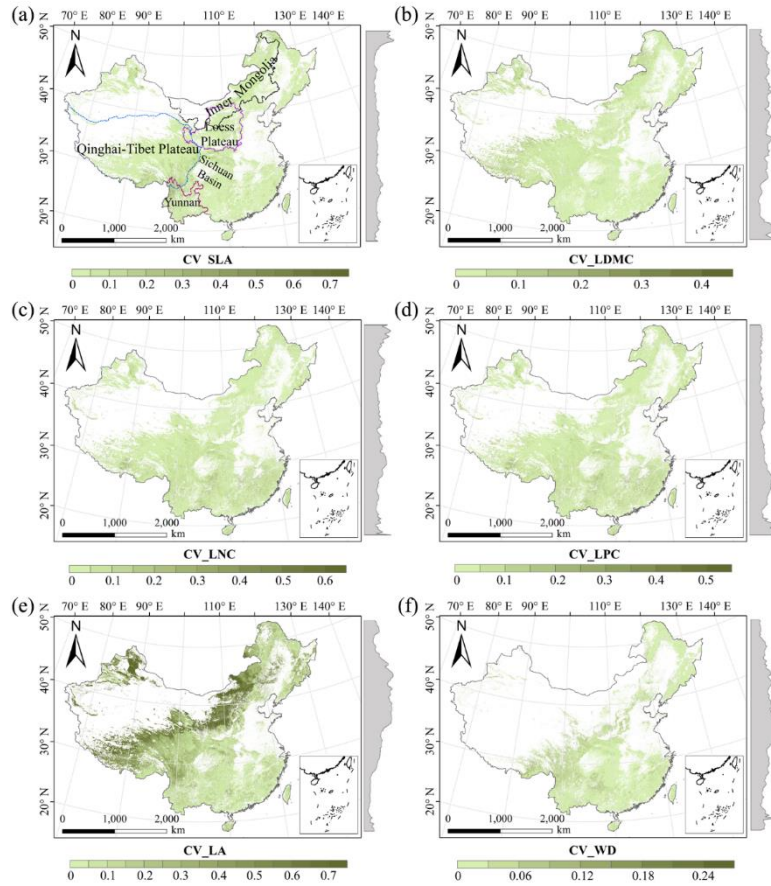
Figure 4. The variability in plant functional trait predictions among random forest, boosted regression trees and ensemble model. The grey curves to the right of the maps display coefficient of variation along with latitude. SLA, specific leaf area; LDMC, leaf dry matter content; LNC, leaf N concentration; LPC, leaf P concentration; LA, leaf area; WD, wood density.
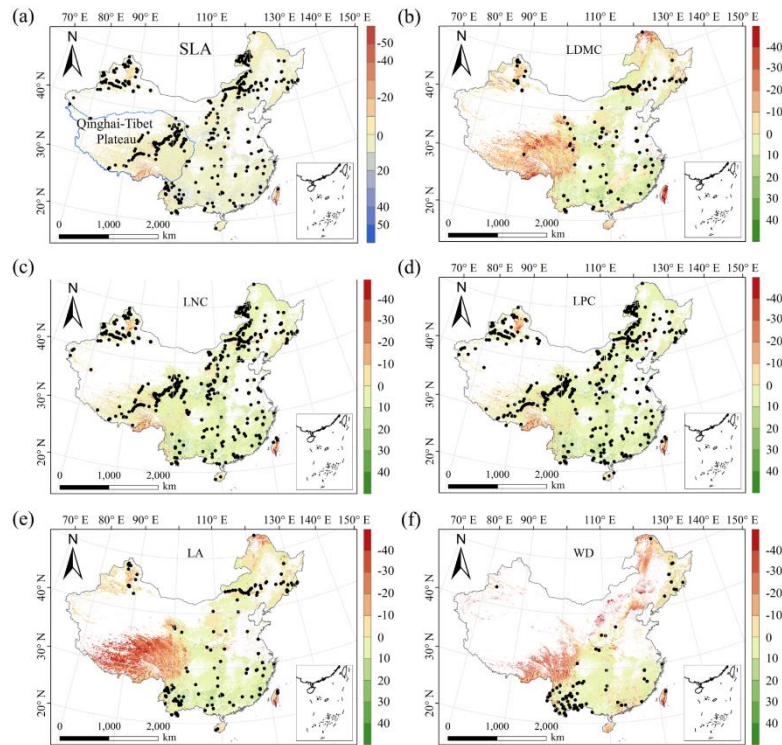
Figure 6. Multivariate environmental similarity surface (MESS) assessments for the six plant functional traits. The black dots represented the locations of trait observations. More intense shades indicate greater similarity (blue) or difference (red) in environmental conditions of the location compared to the predictive factors covered by the training dataset. SLA, specific leaf area; LDMC, leaf dry matter content; LNC, leaf N concentration; LPC, leaf P concentration; LA, leaf area; WD, wood density.

12. For the accuracy of these estimated plant functional traits. The sampling of WD, LPC and SLA is dense, it's reasonable that these three traits have relatively high performance. But LNC and LA also show relatively dense sampling across China as shown in Fig. 5, Could you please tell me why LNC and LA show relatively poor performance?

[Response]: This is a good question. Indeed, LNC and LA had relatively dense sampling across China, whereas they showed relatively poor performance. The main reason is that the environmental variables and vegetation indices were not the primary influencing factors of LNC and LA variations. Our previous study on leaf trait variation has showed that relative to SLA and LPC, LNC and LA were more influenced by phylogeny than environmental variables in China (An et al., 2021). Similar results have been found in other studies. For example, Yang et al. (2016) have reported that LNC and LPC were phylogenetically conserved, but LPC were less conserved than LNC. In addition, Valverde-Barrantes et al. (2017) have suggested that LNC were more influenced by phylogenetic effect rather than climate, while SLA were more controlled by climate. Yang et al. (2017) have also reported that LA and LNC were more

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effected by phylogeny than site or climate in China. Therefore, LNC and LA showed relatively poor performance. We have added the relevant discussion as "*However, LNC and LA showed relatively poor performance, which may be related to the reason that these two traits were more influenced by phylogeny than environmental variables (Yang et al., 2017; An et al., 2021).*" in the Discussion section (see Lines 465–468 in the revised manuscript).

References

An, N. N., Lu, N., Fu, B. J., Wang, M.Y., and He, N.P.: Distinct responses of leaf traits to environment and phylogeny between herbaceous and woody angiosperm species in China. Front. Plant Sci., 12, 799401, https://doi.org/10.3389/fpls.2021.799401, 2021.

Valverde-Barrantes, O. J., Freschet, G. T., Roumet, C., and Blackwood, C. B.: A worldview of root traits: the influence of ancestry, growth form, climate and mycorrhizal association on the functional trait variation of fine-root tissues in seed plants. New Phytol., 215, https://doi.org/1562–157310.1111/nph.14571, 2017.

Yang, X., Chi, X.L., Ji, C.J., Liu, H.Y., Ma, W.H., Mohhammat, A., Shi, Z.Y., Wang, X.P., Yu, S.L., Yue, M., and Tang, Z.Y.: Variations of leaf N and P concentrations in shrubland biomes across northern China: phylogeny, climate, and soil. Biogeosciences, 13, 4429-4438, https://doi.org/10.5194/bg-13-4429-2016, 2016.

Yang, Y. Z., Wang, H., Harrison, S. P., Prentice, I. C., Wright, I. J., Peng, C. H., and Lin, G. H.: Quantifying leaf-trait covariation and its controls across climates and biomes. New Phytol., 221, 155-168, https://doi.org/10.1111/nph.15422, 2018.

13. I suggest that the authors may consider excluding the plant trait of SM and Height, despite their significance in many terrestrial ecosystem processes. The sampling for these traits seems too sparse to accurately represent the trait variability across the entire region of China. As a result, it becomes difficult for me to place trust in the obtained results.

[Response]: Thanks for your suggestion. We have removed the maps of SM and plant height and their relevant content in the revised manuscript.

Responses to #Reviewer 2

This manuscript presented a study on mapping eight key plant traits at 1 km spatial resolution across China using field measurements, environmental variables and vegetation indices. Two machine learning methods were used to develop the trait prediction models. This study is well written and is interesting to the community. The trait dataset of this study has great potential to advance trait-based ecology. However, the methods are not clearly described. Also, it is recommended to perform a quantitative comparison between the trait maps of this study with those from previous studies. I hope that the following comments are helpful to improve the quality of the manuscript.

[Response]: Thanks for your positive comments and constructive suggestions for our manuscript. We have carefully addressed the suggestions and comments on the method description and added a quantitative comparison between the trait maps of this study with those from previous studies. And detailed revisions and responses are listed below. In addition, we have used tracks to highlight the revisions in the revised manuscript.

Specific comments:

1. Line 67: "PROPECT model" should be "PROSPECT model".
[Response]: We have corrected this word in the revised manuscript (see Line 70).

2. Line 125: It is interesting to know the proportion of data excluded by criteria #3. Since the trait values of individual plant were aggregated to community-weighted trait values within 1km, including these data can be helpful to increase the number of measurements.
[Response]: Thanks for your comment. The description was misleading on the criteria #3 in the old version of the manuscript. The aim of criteria #3 was to consider the intraspecific trait variation within the same species. When the same species occurred in the same sampling site from different studies, we included all original observed data from different studies rather than averaging the values at the species level. This criterion can contribute substantially to the trait variation within and between communities, and it also can be helpful to increase the number of trait measurements in subsequent analysis. We have corrected the relevant description about criteria #3 as "*In order to consider the intraspecific trait variation, when the same species occurred in the same sampling site from different studies, we included all original observed data from different studies rather than averaging the values at the species level*" in the section 2.2 in Materials and Methods (see Lines 153–156 in the revised manuscript).

3. Line 135: SLA of sun and shade leaves can be quite different, which may lead to uncertainties

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for later analysis.

[Response]: Thanks. We have checked the literature that these literatures of SLA data that introduced the sampling and measurement methods all sampled the sun leaves according to according to standardized measurement procedures, which require sampling sun leaves during field sampling for trait studies (Perez-Harguindeguy et al., 2013). We have corrected this sentence as "*we included SLA measurements on sun-leaves*" in the section 2.2 in Materials and Methods (see Line 168 in the revised manuscript).

4. Line 159: Specify the full name of AI.

[Response]: We have added the full name of AI (i.e., aridity index) in the section 2.3 in Materials and Methods (see Line 197 in the revised manuscript).

5. Line 167: The soil data was from Shangguan et al., 2013. Please justify that soil properties are time invariant, or their variation across time has little influence on the plant traits.

[Response]: Soil properties are influenced by climate, vegetation, land use and management and human activities over a long period, and to some extent, soil properties may have temporal variability. However, due to the limitation of current technology and the availability of field survey data, a temporal dynamic dataset for multiple soil properties at a large scale is lacking, which is an inadequacy that cannot be resolved in current studies. The soil data that we use is the national-scale dataset that was surveyed based on multiple years during the Second National Soil Survey (1979–1985) and included 2444 counties, 312 national farms, and 44 forest farms in China, which is also a common and widely accepted practice in large-scale spatial mapping and biogeographical studies (Maire et al., 2015; Besnard et al., 2021; Huang et al., 2021; Ma et al., 2021). Soil properties are regarded to be more stable than that of plant traits. A current study has reported that soil organic carbon in most regions in China showed insignificant trend from 1980s to 2010s and slightly inter-decadal declines in North China and Northeast China (Zhang et al., 2023). At the time scale of decades, it is reasonable for being used for large-spatial scale studies.

Reference

Besnard, S., Koirala, S., Santoro, M., Weber, U., Nelson, J., Gutter, J., Herault, B., Kassi, J., N'Guessan, A., Neigh, C., Poulter, B., Zhang, T., and Carvalhais, N.: Mapping global forest age from forest inventories, biomass and climate data. Earth Syst. Sci. Data, 13, 4881–4896, https://doi.org/10.5194/essd-13-4881-2021, 2021.

Huang, Y. Y., Ciais, P., Santoro, M., Makowski, D., Chave, J., Schepaschenko, D., Abramoff, R. Z., Goll, D. S., Yang, H., Chen, Y., Wei, W., and Piao, S. L.: A global map of root biomass across the world's forests. Earth Syst. Sci. Data, 13, 4263–4274, https://doi.org/10.5194/essd-13-4263-2021, 2021.

Ma, H. Z., Mo, L. D., Crowther, T. W., Maynard, D. S., van den Hoogen, J., Stocker, B. D., Terrer, C., and Zohner, C. M.: The global distribution and environmental drivers of aboveground versus belowground plant biomass. Nat. Ecol. Evol., 5, 1110, https://doi.org/10.1038/s41559-021-01485-1, 2021.

Maire, V., Wright, I. J., Prentice, I. C., Batjes, N. H., Bhaskar, R., van Bodegom, P. M., Cornwell, W. K., Ellsworth, D., Niinemets, U., Ordonez, A., Reich, P. B., and Santiago, L. S.: Global effects of soil and climate on leaf photosynthetic traits and rates, Glob. Ecol. Biogeogr., 24, 706–717, https://doi.org/10.1111/geb.12296, 2015.

Zhang, Z. P., Ding, J. L., Zhu, C. M., Wang, J. J., Li, X., Ge, X. Y., Han, L. J., Chen, X. Y., and Wang, J. Z.: Exploring the inter-decadal variability of soil organic carbon in China, Catena, 230, https://doi.org/10.1016/j.catena.2023.107242, 2023.

6. Lines 167-169: Were the soil properties of eight layers averaged? If the topsoil properties are important, it would be good to simply use the soil properties of the first layer (0-45cm).

[Response]: No, we averaged the first four layers. In Shangguan et al. (2013)'s study, the soil characteristics of soil profiles are divided into eight standard layers (i.e., 0–0.045, 0.045–0.091, 0.091–0.166, 0.166–0.289, 0.289–0.493, 0.493–0.829, 0.829–1.383, and 1.383–2.296 m). The first layer is 0-4.5 cm instead of 0-45cm. We averaged the soil data of the first four layers to represent the topsoil. We used the topsoil depth of about 30 cm, because we considered most relevant for community composition via plant establishment and by influencing plants in later life stages, for example, through the potentially high nutrient availability (Vitousek and Sanford, 1986; Boonman et al., 2020).

Reference

Shangguan, W., Dai, Y. J., Liu, B. Y., Zhu, A. X., Duan, Q. Y., Wu, L. Z., Ji, D. Y., Ye, A. Z., Yuan, H., Zhang, Q., Chen, D. D., Chen, M., Chu, J. T., Dou, Y. J., Guo, J. X., Li, H. Q., Li, J. J., Liang, L., Liang, X., Liu, H. P., Liu, S. Y., Miao, C. Y., and Zhang, Y. Z.: A China data set of soil properties for land surface modeling. J. Adv. Model. Earth Syst., 5, 212–224, https://doi.org/10.1002/jame.20026, 2013.

Vitousek, P. M., and Sanford, R. L. Jr. Nutrient cycling in moist tropical forest. Annu. Rev. Ecol. Evol. S., 17, 137–167, https://doi.org/10.1146/annurev.ecolsys.17.1.137, 1986.

Boonman, C. C. F., Benitez-Lopez, A., Schipper, A. M., Thuiller, W., Anand, M., Cerabolini, B. E. L., Cornelissen, J. H. C., Gonzalez-Melo, A., Hattingh, W.N., Higuchi, P., Laughlin, D. C., Onipchenko, V. G., Penuelas, J., Poorter, L., Soudzilovskaia, N. A., Huijbregts, M. A. J., and Santini, L.: Assessing the reliability of predicted plant trait distributions at the global scale. Glob. Ecol. Biogeogr., 29, 1034–1051, https://doi.org/10.1111/geb.13086, 2020.

7. Line 200: Please explain why the MTCT/MIR/etc. of January were used. They are not within the growing season.

[Response]: Thanks. Most selected variables were related to growing seasons because plant functional traits were measured during the growing season. Furthermore, based on the results of collinearity (r values), we found that MTCI, MIR, NIR, red and blue in January showed low correlations with those in other months, thus these variables were included to be used in the machine learning methods (see Lines 239–243 in the revised manuscript).

8. Lines 239-241: What is the difference between the 10-fold cross validation and 80%/20% data split?

[Response]: The description of this section was not clear in the old version. First, we spilt the data into two parts: 80% of the trait data was used to train the models, and the remaining 20% was used to assess model's performance. To obtain a stable and reliable model, this procedure was repeated 10 times, and the model performances (R^2, NRMSE and MAE) were calculated by the average values of these 10 results. We have corrected the description as "*we calibrated the models 10 times using randomly selected 80% of the data for training the models and validating against the remaining 20% based on cross-validation.*" in the section 2.4 in Materials and Methods (See Lines 287–290 in the revised manuscript).

9. Line 252: Please describe the way of obtaining permuted values in more detail.

[Response]: Thanks. The relative importance of each variable is available from model prediction, but it may be model-specific. To overcome this limitation, Thuiller et al. (2009) used a randomisation procedure to estimate the importance of each variable that is independent of the modelling technique, thus enabling direct comparison across models. This method applies correlation between the standard predictions (i.e. fitted values) and predictions where the variable under investigation has been randomly permutated. If the correlation is high, i.e. it is showing little difference between the two predictions, the variable permutated is considered not important for the model. This is repeated multiple times for each variable, and the mean correlation coefficient over runs is recorded. Then the relative importance of each predictor was quantified as one minus the Spearman rank correlation coefficient (see Boonman et al. 2020). We have added more detailed description in the section 2.4 in Materials and Methods (see Lines 302–306 in the revised manuscript).

Reference

Thuiller, W., Lafourcade, B., Engler, R., and Araújo, M. B.: BIOMOD – A platform for ensemble forecasting of species distributions. Ecography, 32, 369–373, https://doi.org/10.1111/j.1600-0587.2008.05742.x, 2009.

Boonman, C. C. F., Benitez-Lopez, A., Schipper, A. M., Thuiller, W., Anand, M., Cerabolini, B. E. L., Cornelissen, J. H. C., Gonzalez-Melo, A., Hattingh, W.N., Higuchi, P., Laughlin, D.C., Onipchenko,

V.G., Penuelas, J., Poorter, L., Soudzilovskaia, N.A., Huijbregts, M.A.J., and Santini, L.: Assessing the reliability of predicted plant trait distributions at the global scale. Glob. Ecol. Biogeogr., 29, 1034–1051, https://doi.org/10.1111/geb.13086, 2020.

10. Line 259: It is not clear how the trait values of individual plant were aggregated with PFT to community-weighted trait values within 1km. Please describe the method in more detail.

[Response]: We generated the plant functional trait maps in four steps as follows. First, we associated each species with a corresponding PFT based on plant growth form (tree, shrub and grass), leaf type (broadleaf and needleleaf) and leaf phenology (deciduous and evergreen). For example, the information on *Salix matsudana* is: tree, deciduous and broadleaf, thus, we were able to associate the PFT of deciduous broadleaf forest (DBF) to this species. The species that did not correspond to any PFT were discarded. Second, we predicted the trait values for six PFTs separately by building the machine learning models using the field measurement data and environmental variables and vegetation indices at a 1 km spatial resolution. Then, we obtained six prediction layers for single plant functional trait. Third, the classification of natural PFT types includes evergreen needleleaf forest (ENF), evergreen broadleaf forest (EBF), deciduous needleleaf forest (DNF), deciduous broadleaf forest (DBF), shrubland (SHL) and grassland (GRL). We calculated the abundance of individual PFT within 1 km grid cell using a land cover map with a spatial high-resolution of 100 m. Forth, the final community weighted mean trait values were calculated according to the predicted trait values (the second step) and corresponding abundance of each PFT (the third step) refer to the equation of CWM calculation in the community as Eq. (1) (Garnier et al., 2004).

$$CWM = \sum_{i=1}^{n} W_i X_i \tag{1}$$

where n is the total number of PFT in a given grid, W_i is the relative abundance of the ith PFT, and X_i is the predicted trait value of the ith PFT.

We have revised the relevant content in the sections 2.2 and 2.5 in Materials and Methods (see Lines 177–187, 249–258, 314–322 in the revised manuscript).

Reference

Garnier, E., Cortez, J., Billès, G., Navas, M.-L., Roumet, C., Debussche, M., Laurent, G., Blanchard, A., Aubry, D., Bellmann, A., Neill, C., and Toussaint, J. P.: Plant functional markers capture ecosystem properties during secondary succession. Ecology, 85, 2630–2637, https://doi.org/10.1890/03-0799, 2004.

11. Lines 263-264: It is not clear how the predictions of the two methods were merged. Did the authors set a threshold for the cross-validated R2? If the accuracies of predictions of one method were too low, it may not be necessary to include them.

[Response]: Thanks for your nice suggestion. In this manuscript, we did not set a threshold for the cross-validated R^2. We used Weighted Average methods based on the R^2 values of single-model to obtain the predictive performance of the ensemble models. Firstly, we calculated the predictive values of ensemble model, in a given grid cell, based on predictive values and the cross-validated R^2 values of random forest and boosted regression trees as described by the following equation (Marmion et al., 2009; Boonman et al., 2020).

$$Pred\_EM_t = \frac{\sum_{m=1}^{2}(pred_{m,t} \times r_{m,t}^2)}{\sum_{m=1}^{2} r_{m,t}^2}$$

where $Pred\_EM_t$ is the predictive values of t trait in ensemble model, $pred_{m,t}$ is the predictive values of t trait in m model, $r_{m,t}^2$ is the cross-validated R^2 of t trait in m model.

Second, the accuracy of the ensemble model was calculated by regressing the predictive values of ensemble model based on the merged predictive values (based on Eq. 5) against the observed trait values. In addition, the accuracies of these two models showed little variability for a given trait.

We have added the relevant description on how the predictions of the two methods were merged in the section 2.5 in Materials and Methods (see Lines 326–336 in the revised manuscript).

12. Lines 403-417: It would be great to perform a quantitative comparison with previous trait maps, for instance, the differences between the trait maps from this study and those of previous studies can be calculated. From such maps, one can easily tell the main differences among the datasets.

[Response]: Thanks for your constructive suggestion. Previous studies mainly focused on the global scale (see Table F1 in Appendix F), we extracted the data of China from the global trait maps. Before the quantitative comparisons with previous studies, we performed two steps to make the products as comparable as possible and improve the consistency between different datasets. First, because the spatial resolution of most global trait maps is 0.5°, we resampled the data products of previous studies and our maps to 0.5° spatial resolution. In addition, Vallicrosa et al. (2022) generated the global maps of LNC and LPC with a 1 km spatial resolution, we also compared the frequency distribution of Vallicrosa et al. (2022) with that of our study at a 1 km spatial resolution. Second, our study focused on natural vegetation, so the global trait maps were used to filter out non-natural vegetation (e.g., croplands). For example, Madani et al. (2018) predicted the spatial distributions of key plant traits for SLA, canopy height and seed mass that include croplands. We quantitatively compared our maps with previous studies from two perspectives. The comparisons among trait maps were made using frequency plots and spatial correlations (Fig. 7 and Table 5, Fig. F1 in Appendix F) in the section 4.1 in

Discussion (see Lines 469–483 in the revised manuscript). And the maps of spatial differences between our study and previous studies were displayed as Figs. F2-F6 in Appendix F in the section 4.2 in Discussion (see Lines 513–542 in the revised manuscript). Please see the Fig. 7 and F1-F6 in the supplement.

Table F1 Summary table of related trait maps used in this study.

References	Related traits	Methods	Predictors	Consideration of PFT	Resolution
Dong et al. (2023)	SLA LNC	Optimality models	Climate	Yes	0.5°
Vallicrosa et al. (2022)	LNC LPC	Neural networks	Climate Soil N and P deposition	Yes	0.0083°
Schiller et al. (2021)	SLA LNC LA WD	Convolutional Neural Networks	Climate In-situ RGB images	No	0.5°
Boonman et al. (2020)	SLA LNC WD	Generalized linear model, Generalized additive model, Random forest, Boosted regression trees, Ensemble model	Climate Soil	No	0.5°
Moreno et al. (2018)	SLA LNC LPC LDMC	Regularized linear regression, Random forest, Neural networks, Kernel networks	Climate Elevation Reflectance	Yes	0.0045°
Madani et al. (2018)	SLA	Generalized additive model	Climate	No	0.5°
Butler et al. (2017)	SLA LNC LPC	Bayesian model	Climate Soil	Yes	0.5°
Bodegom et al. (2014)	SLA WD	Multiple regression analysis	Climate Soil	No	0.5°

The resolutions 0.5°, 0.0083°, and 0.0045° correspond to square grid cell sizes of about 50 km, 1 km and 500 m at the equator. SLA, specific leaf area; LDMC, leaf dry matter content; LNC, leaf N concentration; LPC, leaf P concentration; LA, leaf area; WD, wood density.

Table 5 Spatial correlations for SLA, LNC, LPC, LA and WD between this study and other previous trait maps, labelled by the first author of the corresponding publication (see Table F1 for citations).

Spatial correlation	Dong	Vallicrosa	Schiller	Boonman	Moreno	Madani	Butler	Bodegom
SLA	0.398		-0.082	0.327	0.242	0.136	-0.042	0.319
LNC	0.156	0.359	0.229	0.252			0.394	
LPC		0.136					0.057	
LA			0.514					
WD			0.647	0.107				

SLA, specific leaf area (m^2 kg^{-1}); LNC, leaf N concentration (mg g^{-1}); LPC, leaf P concentration (mg g^{-1}); LA, leaf area (cm^2); WD, wood density (g cm^{-3}).

References

Boonman, C. C. F., Benitez-Lopez, A., Schipper, A. M., Thuiller, W., Anand, M., Cerabolini, B. E. L., Cornelissen, J. H. C., Gonzalez-Melo, A., Hattingh, W. N., Higuchi, P., Laughlin, D. C., Onipchenko, V. G., Penuelas, J., Poorter, L., Soudzilovskaia, N. A., Huijbregts, M. A. J., and Santini, L.: Assessing the reliability of predicted plant trait distributions at the global scale. Glob. Ecol. Biogeogr., 29, 1034–1051, https://doi.org/10.1111/geb.13086, 2020.

Butler, E. E., Datta, A., Flores-Moreno, H., Chen, M., Wythers, K. R., Fazayeli, F., Banerjee, A., Atkin, O. K., Kattge, J., Amiaud, B., Blonder, B., Boenisch, G., Bond-Lamberty, B., Brown, K. A., Byun, C., Campetella, G., Cerabolini, B. E. L., Cornelissen, J. H. C., Craine, J. M., Craven, D., de Vries, F. T., Diaz, S., Domingues, T. F., Forey, E., Gonzalez-Melo, A., Gross, N., Han, W., Hattingh, W. N., Hickler, T., Jansen, S., Kramer, K., Kraft, N. J. B., Kurokawa, H., Laughlin, D. C., Meir, P., Minden, V., Niinemets, U., Onoda, Y., Penuelas, J., Read, Q., Sack, L., Schamp, B., Soudzilovskaia, N. A., Spasojevic, M. J., Sosinski, E., Thornton, P. E., Valladares, F., van Bodegom, P. M., Williams, M., Wirth, C., and Reich, P. B.: Mapping local and global variability in plant trait distributions. P. Nat. Acad. Sci. USA, 114, 10937–10946, https://doi.org/10.1073/pnas.1708984114, 2017.

Dong, N., Dechant, B., Wang, H., Wright, IJ., and Prentice, IC.: Global leaf-trait mapping based on optimality theory. Glob. Ecol. Biogeogr., https://doi.org/10.1111/geb.13680, 2023.

Madani, N., Kimball, J. S., Ballantyne, A. P., Affleck, D. L. R., van Bodegom, P. M., Reich, P. B., Kattge, J., Sala, A., Nazeri, M., Jones, M. O., Zhao, M. S., and Running, S.W.: Future global productivity will be affected by plant trait response to climate. Sci. Rep., 8, 1–10, https://doi.org/10.1038/s41598-018-21172-9, 2018.

Moreno-Martínez, Á., Camps-Valls, G., Kattge, J., Robinson, N., Reichstein, M., van Bodegom, P., Kramer, K., Cornelissen, J. H. C., Reich, P., Bahn, M., Niinemets, Ü., Peñuelas, J., Craine, J. M., Cerabolini, B. E. L., Minden, V., Laughlin, D. C., Sack, L., Allred, B., Baraloto, C., Byun, C., Soudzilovskaia, N. A., and Running, S. W.: A methodology to derive global maps of leaf traits using remote sensing and climate data. Remote Sens. Environ., 218, 69–88, https://doi.org/10.1016/j.rse.2018.09.006, 2018.

Schiller, C., Schmidtlein, S., Boonman, C., Moreno-Martinez, A., and Kattenborn, T.: Deep learning and citizen science enable automated plant trait predictions from photographs. Sci. Rep., 11, https://doi.org/10.1038/s41598-021-95616-0, 2022.

Vallicrosa, H., Sardans, J., Maspons, J., Zuccarini, P., Fernández-Martínez, M., Bauters, M., Goll, D. S., Ciais, P., Obersteiner, M., Janssens, I. A., and Peñuelas, J.: Global maps and factors driving forest foliar elemental composition: the importance of evolutionary history. New Phytol., 233, 169–181, https://doi.org/10.1111/nph.17771, 2022.

van Bodegom, P. M., Douma, J. C., and Verheijen, L. M. A fully traits-based approach to modeling global vegetation distribution. P. Nat. Acad. Sci. USA, 111, 13733–13738, https://doi.org/10.1073/pnas.1304551110, 2014.

Response to #Reviewer 4

The manuscript provides a novel large dataset of 52477 trait measurements on 4291 species for eight relevant traits from 1541 sites across China, compiled from existing datasets and an extensive literature search. Based on these trait data, the authors use environmental drivers, satellite-derived vegetation indices and plant functional type association and abundance to derive high-resolution maps (1km x 1km) across China for these traits. The authors evaluate the maps.

The trait measurements and maps presented fit the scope of the journal.

[Response]: Thanks so much for your encouragement and positive comments on our work. We have carefully addressed the suggestions in the revision, and detailed revisions and responses are listed below. In addition, we have used tracks to highlight the revisions in the revised manuscript.

I have one major and a few minor comments.

1. My major comment: I was not able to completely follow the up-scaling workflow from the leaf-level data to the gridded maps. A figure indicating the different resources and steps might help.

[Response]: Thanks for your constructive suggestion. We have added a methodological workflow for spatial mapping of plant functional traits in China as Figure 1 in the revised manuscript. In addition, we have also added "section 2.1 Overview" to explain the steps of spatial mapping of plant functional traits in the section Methods and Materials (see Lines 119–132 in the revised manuscript).
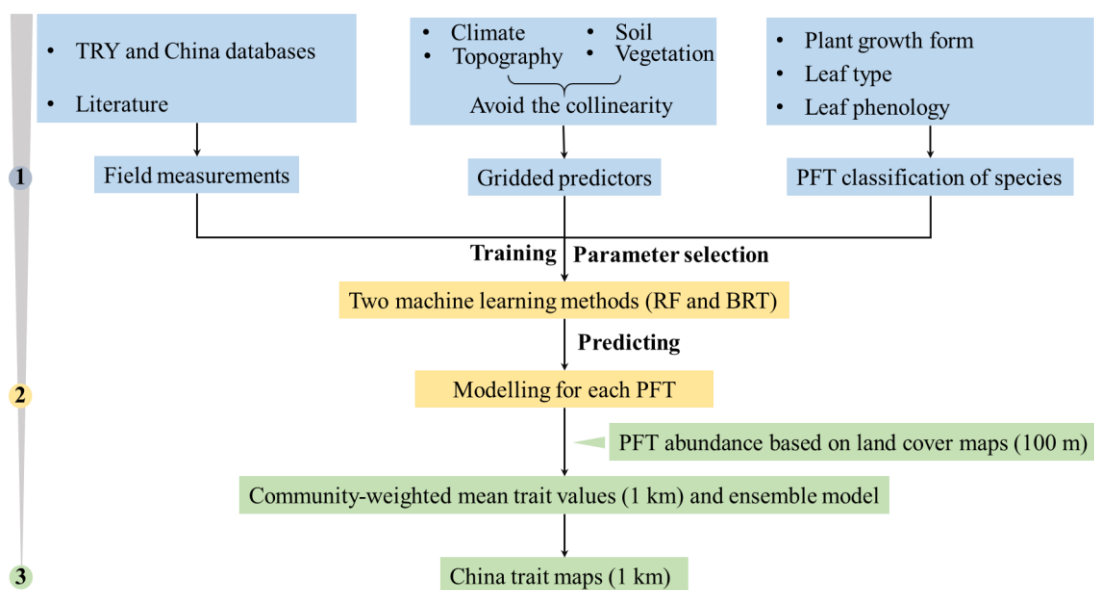
Figure 1. Methodological workflow for spatial mapping of plant functional traits. Trait

mapping is performed in three steps. Step 1: in-situ field measurement of plant functional traits, PFT classification of plant species and gridded predictors were collected. Step 2: two machine learning methods were used to predict trait values by training the field measurements and predictors for each PFT. Step 3: spatialization of trait maps by calculating the abundance of each PFT using 100 m land cover map and predicted trait values within 1 km grid cells. PFT, plant functional type; RF, random forest; BRT, boosted regression trees.

Minor comments:

2. The maps should not be called 'data', as they are rather data products. I would suggest just calling them 'maps'.

[Response]: Thanks for your nice suggestion. We have changed the 'dataset' to 'maps' in the revised manuscript.

3. Line 67: probably the PROSPECT model (not PROPECT).

[Response]: We have corrected PROPECT model to PROSPECT model in the revised manuscript (See Line 70).

4. Line 131: The measurement date or/and time are not provided with the leaf level data.

[Response]: We have added the trait measurement date or/and time into the original dataset when the measurement time has been reported in the literature and public database. However, 45 literatures and three databases from TRY did not provided the measurement time. Please see the updated dataset used in this study at the figshare link: https://figshare.com/s/c527c12d310cb8156ed2.

5. Figure 4: I do not understand the values of the density axes.

[Response]: Density curve is also called as probability density curve, which usually used as a probability density function for continuous variables. The x axis represents of the density curve is the random value of a variable, and the y axis (density axes) is the probability density of this random value.

6. For vegetation modelling it would be excellent to additionally provide a separate map for each PFT per trait.

[Response]: Thanks for your suggestion. We have provided the separate map of each PFT per trait as Figure B1 in Appendix B.
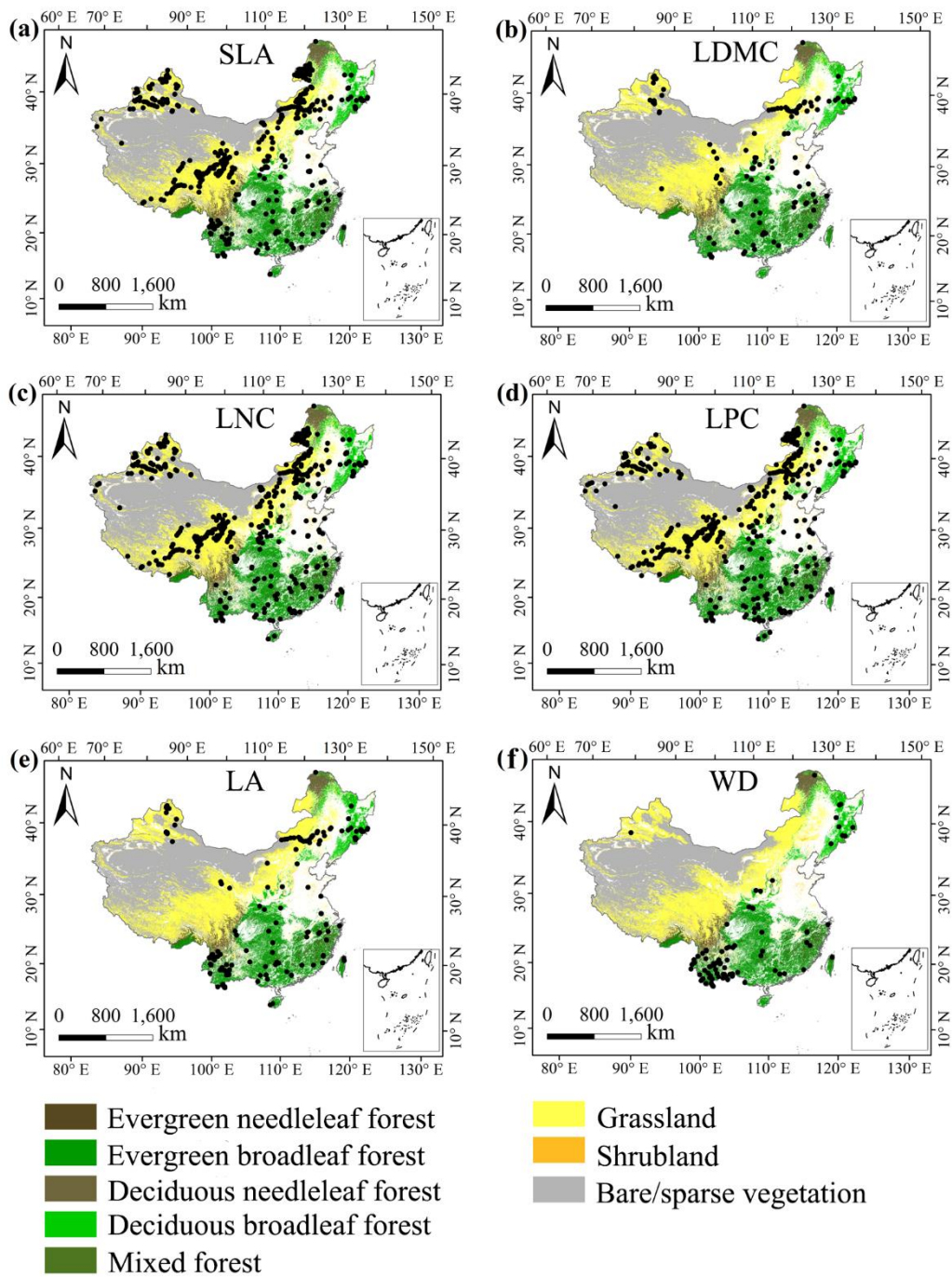
Figure B1. The distribution of sampling site of each plant functional traits across China. The black dots represented the locations of trait observations.