Integrating phylogenetic and hyperspectral information to map forest communities from space

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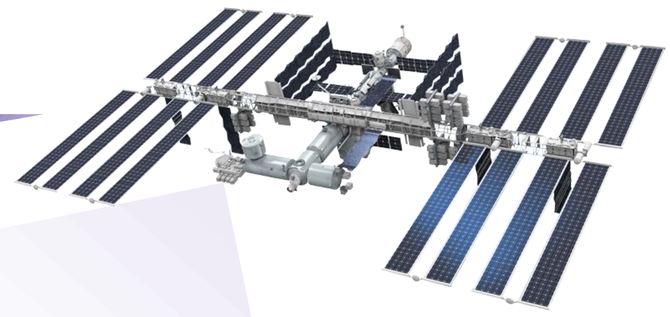

1. Background

- Spaceborne spectroscopy has long been recognized as a key tool for mapping tree species and forest communities and will become increasingly important with forthcoming NASA missions.
- However, the feasibility of mapping forest communities at large spatial extents using space-borne data is not yet clear.
- Unlike species mapping using airborne spectroscopy, space-borne spectroscopy faces ecological and technological challenges:

  ✓Greater numbers of species with greater spatial extents
  ✓Imagery with coarse pixels (e.g., 30m)
  ✓Potential atmospheric effects

2. Goal and hypothesis

Goal

Our goal is to develop an approach that helps to integrate forest inventories, phylogenetic information and space-borne spectroscopy to map forest communities and species at large scales (**Fig. 1**).

Hypothesis

We hypothesize that phylogenetically similar forest communities (low phylogenetic beta diversity) will show greater spectral similarity than phylogenetically dissimilar forest communities (high phylogenetic beta diversity). We are testing the extent to which integrating space-borne spectroscopy with phylogenetic information of trees within forest communities can help remotely sense tree community composition.

3. Materials and Methods

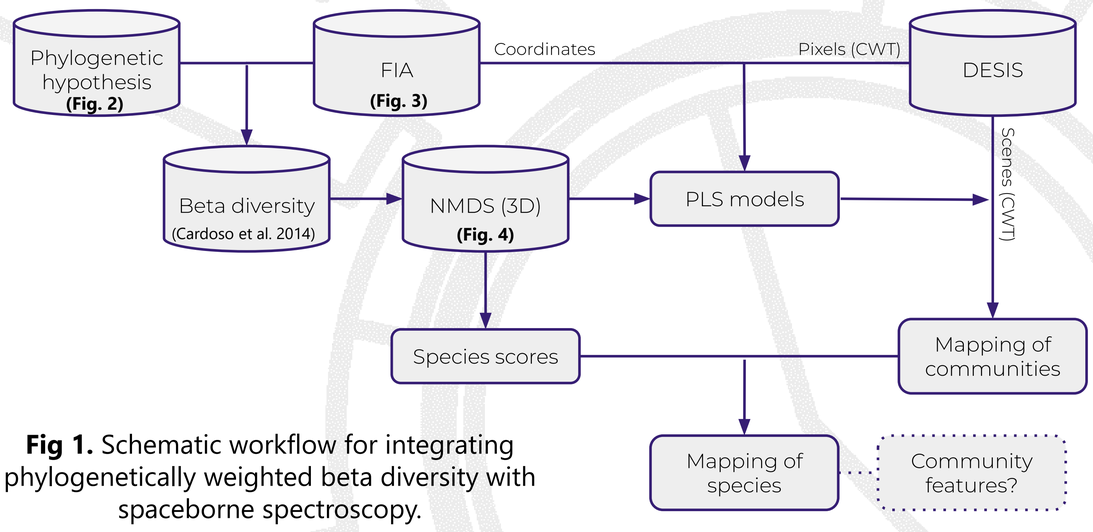

Fig 1. Schematic workflow for integrating phylogenetically weighted beta diversity with spaceborne spectroscopy.

4. Ordination of communities

Fig 2. Phylogeny of forest trees in the Upper Midwest (72 species).

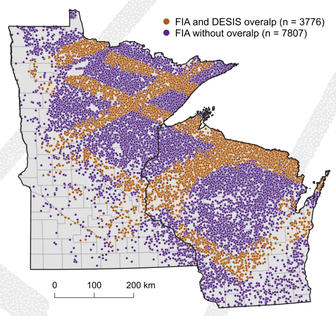

Fig 3. Spatial overlap between FIA and DESIS scenes.

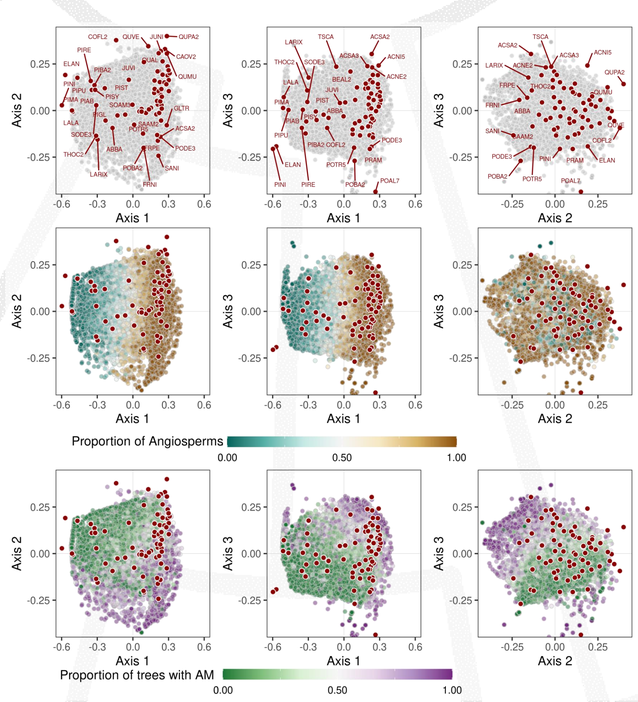

Fig 4. Non-metric Multi-Dimensional Scaling of phylogenetically-weighted total beta diversity. Colors in the middle and bottom panels represent gradients of tree community composition.

5. Predicting models

- We used Partial Least Square Regression models (PLS) to predict each axis of the NMDS ordination.
- These were trained using 60% of the observations in an iterative spatial-cross validation framework.
- We first establish the optimal number of components required to then predict each NMDS axis (**Fig. 5**), to then extract their coefficients (**Fig. 6**) and the variable of importance (**Fig. 7**).
- The model performance was validated using 40% of the remaining dataset (**Fig. 8**).

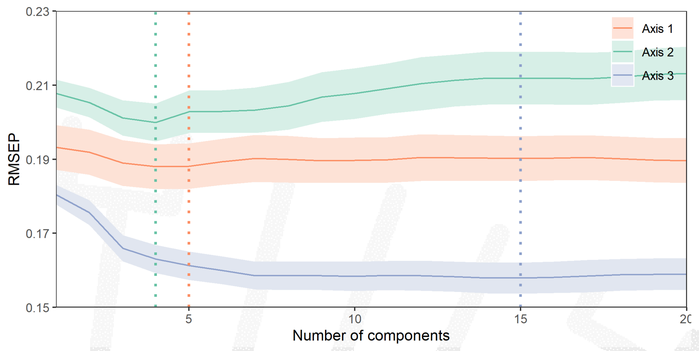

Fig 5. Root Mean Square Error of Prediction (RMSP) associated with the number of components used to predict the NMDS axes.

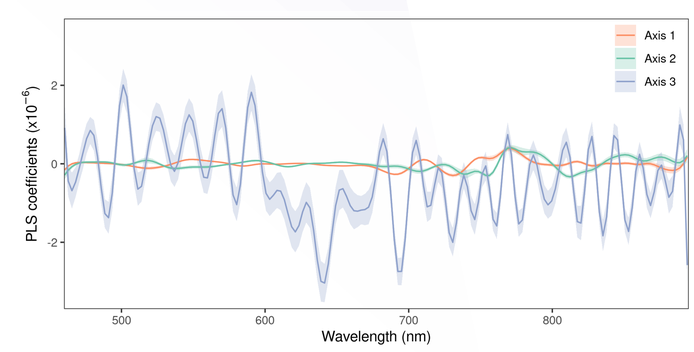

Fig 6. PLS coefficients associated with the spectral bands used to predict the NMDS axes.

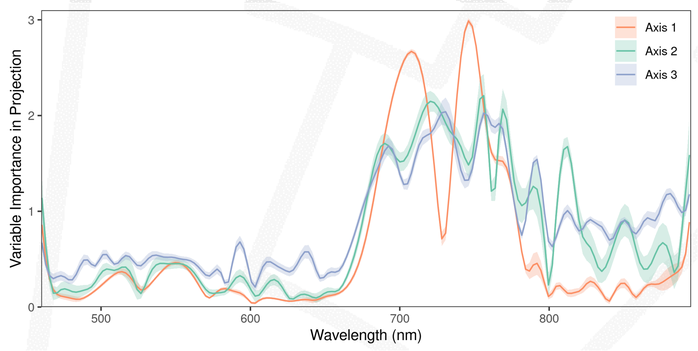

Fig 7. Variable Importance in Projection associated with the spectral bands that predict the NMDS axes.

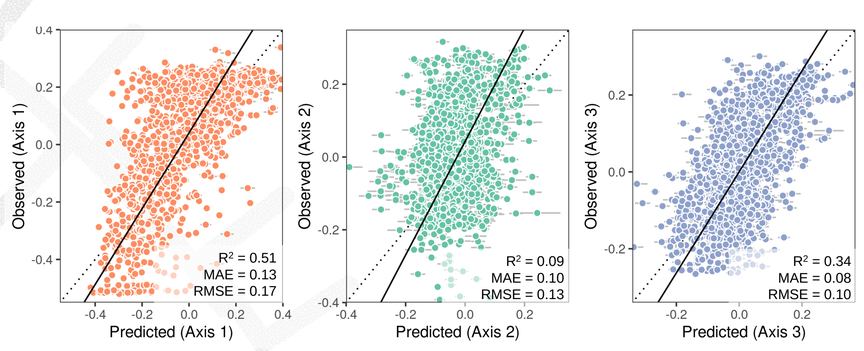

Fig 8. Relationships between observed and predicted NMDS axes.

6. Mapping of communities

- Iterative PLSR models were applied to DESIS scenes, and the probability of species occurrence was approximated using inverse distance weighting (**Fig. 8**).

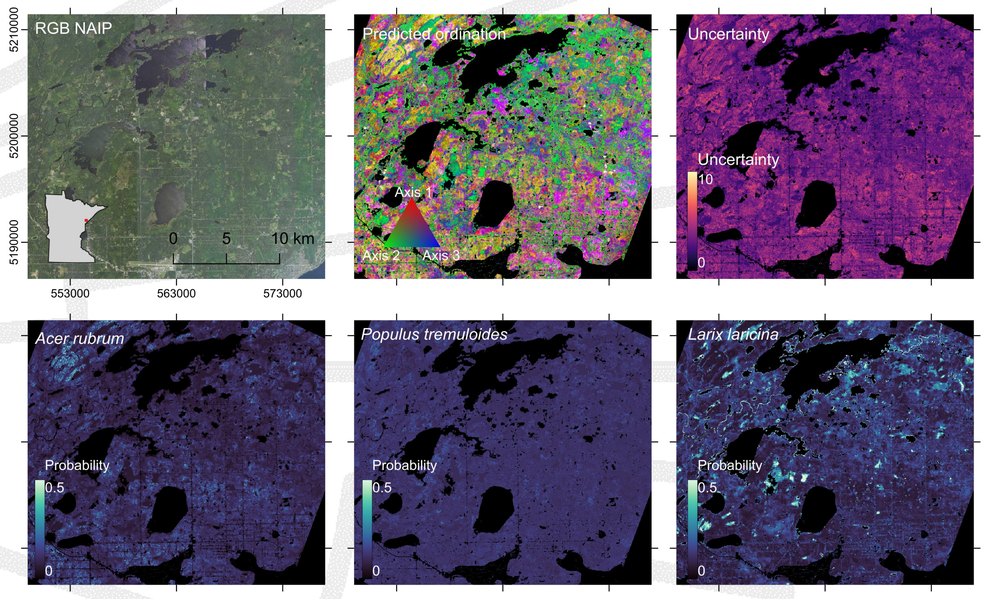

Fig 9. Mapping of the three community ordination axes (phylogenetic beta diversity) and their model uncertainties (top panels) and the approximate species distributions predicted from these models (bottom panels).

7. Conclusions and future directions

- Our results suggest that it is feasible to predict the ordination axes of forest communities using space-borne spectroscopy.
- Mapping of forest community ordinations for the Upper Midwest based on phylogenetic beta diversity can be scaled in space and time, providing a means to detect the distribution of forest communities and their constituent species or any plant hierarchal grouping (e.g., lineages, angiosperms/gymnosperm, AM/EM) of interest.
- Our current work is focused on expanding our approach across Eastern US to include a diverse group of forest communities and exploring potential challenges of these methods applied at even larger scales.

References

Cardoso, P., Rigal, F., Carvalho, J.C., Fortelius, M., Borges, P.A.V., Podani, J. & Schmera, D. (2014) Partitioning taxon, phylogenetic and functional beta diversity into replacement and richness difference components. *Journal of Biogeography*, 41, 749– 761.

Acknowledgments

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