Mapping Phyllopshere and Soil Fungal Function Using AVRIS-NG Hyperspectral Data

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Challenge

Microbial communities play a crucial role in forest ecosystems, where they are fundamental to the health, structure, and sustainability of the forest. Developments in molecular research allow for the evaluation of these understudied communities but are generally too costly and labour intensive for large-scale assessments. In temperate forests, the collection of samples from the top canopy (phyllopshere) especially poses challenges due to the accessibility of the crown of tall (30+ meter) trees, greatly limiting the spatial and temporal density of existing sample points. Advances in hyperspectral sensors offers a solution for bridging these data gaps, enabling the extrapolation of environmental DNA (eDNA)-based microbial profiles across extensive regions.

Methodology

To demonstrate the utilisation of hyperspectral airborne data to predict and map microbial functions of temperate European forests, we modelled the spatial distribution of fungal trophic groups in the soil and top-canopy using AVRIS-NG hyperspectral airborne data collected from the Bavarian Forest National Park in Germany. Putative functional profiles were created from eDNA (genetic material obtained from environmental samples [e.g. canopy, soil] without capturing the organisms themselves) samples from soil and top-canopy leaf material. The public data base "Funguild" was used to concatenate eDNA taxonomic data to functional profiles, allowing linking microbial profiles to ecosystem functions. The fungal functional profiles were used as training and validation data for the models (using PLSR and gaussian processing algorithms), which were consecutive inverted for prediction and mapping.

Results

Our results show for the first time that microbial function in the soil and canopy can accurately predicted for temperate European forests when combining eDNA point profiles with AVRIS-NG hyperspectral airborne data. The findings demonstrate that fungal trophic groups show substantial variation in their spatial distribution across a forest landscape. Furthermore, top canopy functions were predicted with higher reliability than soil microbial functions, presumably due to the stronger link between the phyllosphere and host-tree attributes (chemical, compositional, and functional characteristics) that can be sensed remotely using spectral reflectance.

Outlook for the future (800 - 1000 characters incl. spaces)

This study demonstrates a clear example of how spaceborne next generation hyperspectral data could be used to effectively predict putative microbial functions, providing maps and models with high relevance for forest ecology and management. The findings of this study highlight a significant breakthrough in utilizing airborne or spaceborne next-generation hyperspectral data to effectively predict putative microbial functions, and this research offers valuable insights and tools essential for the sustainable management of forests. Looking ahead, novel next-generation remote sensing platforms, such as the imminent launch of the CHIME satellite, holds the promise of revolutionizing the utilisation and upscaling of environmental DNA (eDNA) point-based information, offering innovative solutions for addressing ecological challenges on a global scale.
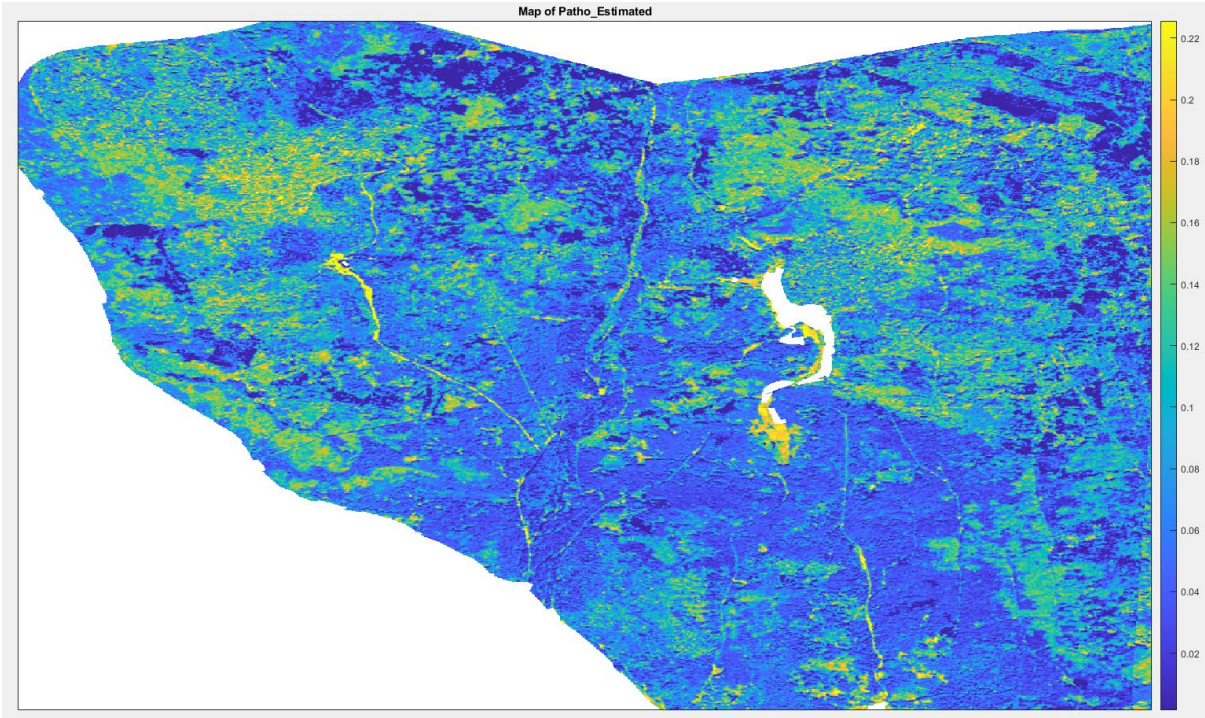
Figure Detail of map showing estimated relative abundance of Pathotrophic fungi in the phyllopshere of Bavaria National Park, Germany. Colour gradient represents the estimated proportion of DNA reads belonging to Pathotrophic fungi in the top-canopy phyllopshere.