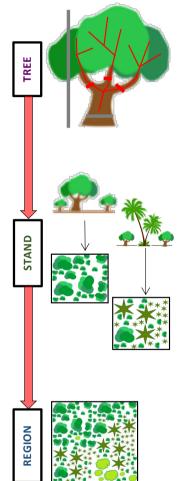


Project main objectives



Non-destructive approaches for tree-level biomass estimation (TLS, QSM, etc.) :

$$AGB_{Tree} = f$$
 (Volume, Density)

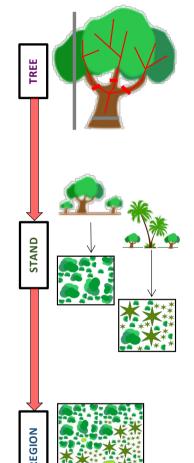
Allometric and RS models to link sensor and field data (plot-level):

$$\Sigma AGB_{Tree} = f (RS signal)$$

Model inversion for large-scale biomass mapping:

$$f^{-1}(RS signal) = AGB$$

Project main objectives



Non destructive approaches for tree-level biomass estimation (TLS, QSM, etc.):

$$AGB_{Tree} = f$$
 (Volume, Density)

Allometric and RS models to link sensor and field data (plot-level):

$$\Sigma AGB_{Tree} = f (RS signal)$$

What is the actual performance of large-scale forest biomass mapping models?

Model inversion for large-scale biomass mapping:

$$f^{-1}(RS signal) = AGB$$



ARTICLE



https://doi.org/10.1038/s41467-020-18321-y

OPEN

Spatial validation reveals poor predictive performance of large-scale ecological mapping models

Pierre Ploton ^{1⊠}, Frédéric Mortier ^{2,3}, Maxime Réjou-Méchain¹, Nicolas Barbier ¹, Nicolas Picard⁴, Vivien Rossi ⁵, Carsten Dormann ⁶, Guillaume Cornu ^{2,3}, Gaëlle Viennois Nicolas Bayol⁷, Alexei Lyapustin⁸, Sylvie Gourlet-Fleury ^{2,3} & Raphaël Pélissier ¹

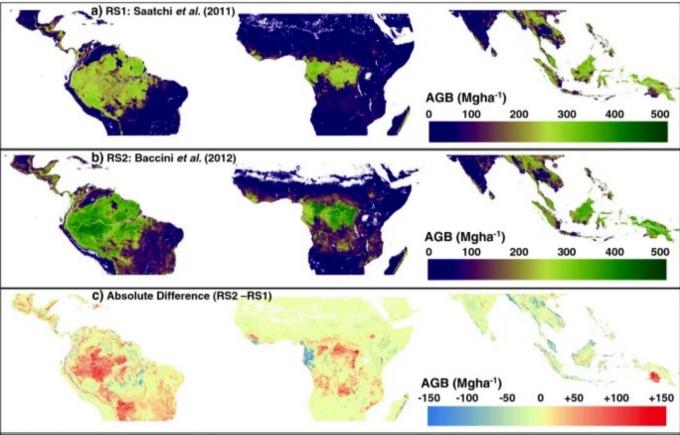


RESEARCH Open Access

Uncertainty in the spatial distribution of tropical forest biomass: a comparison of pan-tropical

maps

Edward TA Mitchard^{1*}, Sassan S Saatchi², Alessandro Baccini³, Gregory P Asner⁴, Scott J Goetz³, Nancy L Harris⁵ and Sandra Brown⁵



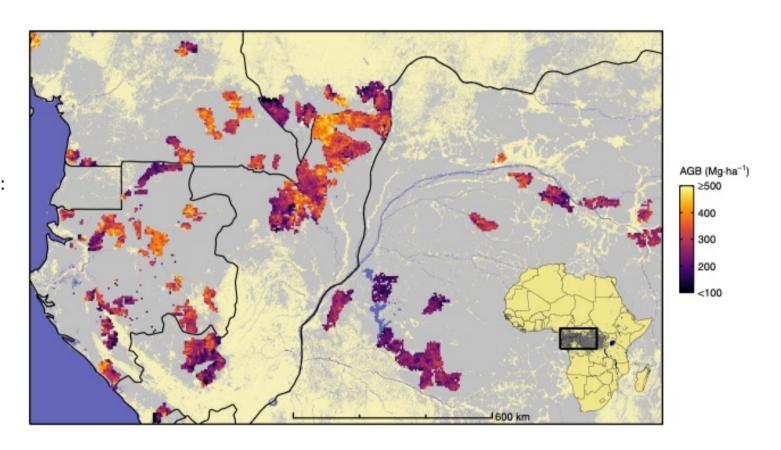
Commercial forest inventories from Central Africa (2000-2010): c. 100 000 ha; 1.8 Million trees

Above-Ground Biomass (AGB) in 60 000 1-km² pixels

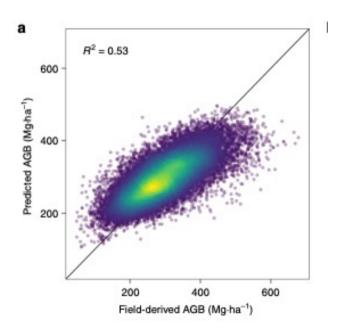
RF model with 22 predictors variables:

- Environmental layers (climate, topography, etc.)
- RS-derived vegetation indices (MODIS)

Wall-to-wall AGB map at 1-km resolution

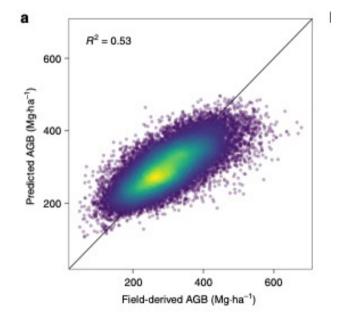


Random K-fold cross-validation with 10% randomly selected test pixels

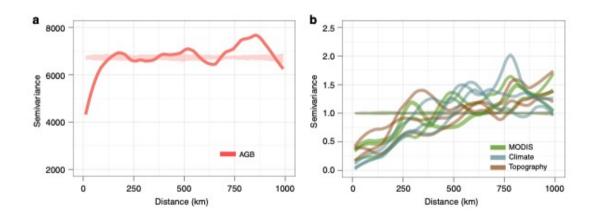


Random K-fold cross-validation

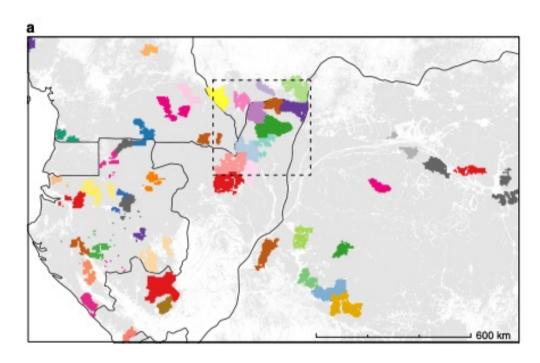
with 10% randomly selected test pixels

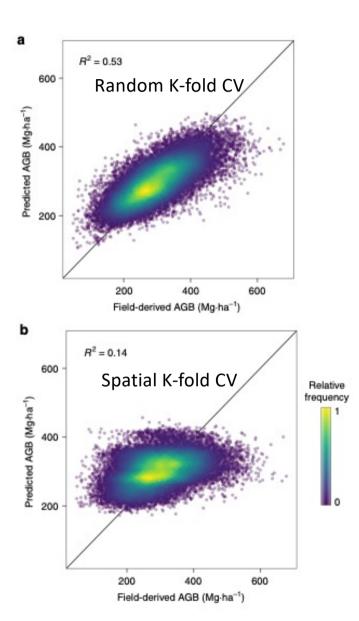


Spatial autocorrelation violate independence between observations



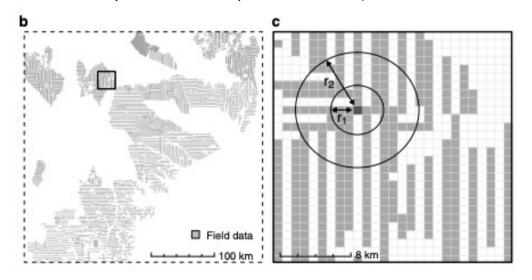
Spatial K-fold cross-validation (blocking)

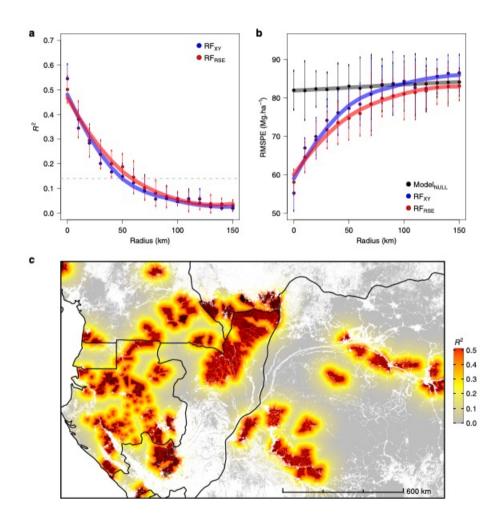




Buffer-Leave-One-Out cross-validation (B-LOO)

100 randomly selected test pixels + buffer (radius 10 to 150 kms)

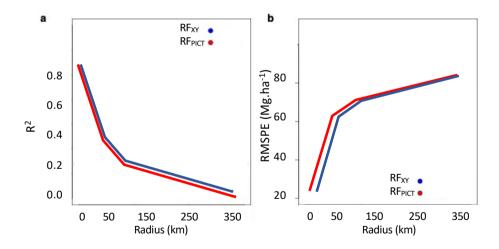












Conclusion

- Biological processes are spatially autocorrelated for reasons independent from the environment (biotic interactions, dispersal, etc.)
- By multiplying spatial combinations of predictors, RF (ML?) creates local overfitting, i.e. predict well local spatial configurations not determined by the environmental predictors
- Spatial cross-validation is mandatory to asses the <u>predictive</u> performance of spatial models
- We still miss the main drivers of tropical forest above-ground biomass

