Contemplating spatial and temporal components of Functional Diversity: Full exploitation of Satellite data for Biodiversity Monitoring

Christian Rossi[1,2,3], Mathias Kneubühler[1], Martin Schütz[2], Rudolf M. Haller[3], Michael E. Schaepman[1], Anita C. Risch[2]

[1]Remote Sensing Laboratories, Dept. of Geography, University of Zurich. [2]Research Unit Community Ecology, Swiss Federal Institute for Forest, Snow and Landscape Research WSL. [3]Department of Research and Geoinformation, Swiss National Park.
E-mail address: christian.rossi@nationalpark.ch

Introduction

In most remote sensing studies temporal effects of biodiversity have been neglected. Single remote sensing dataset offer just a snapshot of a dynamic environment [1]. Here, we present an approach that contemplates both the spatial and temporal dimension of diversity, as well as an interaction term between both dimensions.

Method

- Beta-Functional diversity

$$\beta FD = \beta FD_{RaoQ} = \beta FD_{MI} = \frac{1}{N\,P\,D}\sum_{k=1}^{N}\sum_{t=1}^{D}\sum_{i=1}^{P}(\bar{X}_{itk}-\bar{X}_k)^2$$

- *N* number of traits, *P* is the number of pixels (communities) of an image, *D* is the number of images in time, $\bar{X}_{itk}$ is the value of trait *k* of the *i*th pixel at time *t* and $\bar{X}_k$ is the mean value of trait *k* across all pixels and all datasets.
- FD can be decomposed in time and space components as for the sum of squares (SS_{TOT}) in a two-way ANOVA:

$$SS_{TOT} = SS_W + \overbrace{SS_{FactorT} + SS_{FactorS} + SS_{TxS}}^{SS_B = \boldsymbol{\beta FD} * P * D * N}$$

- SS_W is the sum of square of within-cells, the alpha-functional diversity

$$\beta FD$$

$$= \frac{1}{N\,P\,D}\left\{\overbrace{\sum_{k=1}^{N}\sum_{t=1}^{D}P\left[\left(\frac{1}{P}\sum_{i=1}^{P}\bar{X}_{itk}\right)-\bar{X}_k\right]^2}^{SS_{FactorS} = \boldsymbol{\beta FD_T} * D * N} + \overbrace{\sum_{k=1}^{N}\sum_{i=1}^{P}D\left[\left(\frac{1}{D}\sum_{t=1}^{D}\bar{X}_{itk}\right)-\bar{X}_k\right]^2}^{SS_{FactorT} = \boldsymbol{\beta FD_S} * P * N}\right.$$

$$\left. + \overbrace{\left[\sum_{k=1}^{N}\sum_{t=1}^{D}\sum_{i=1}^{P}(\bar{X}_{itk}-\bar{X}_k)^2 - \sum_{k=1}^{N}\sum_{t=1}^{D}P\left[\left(\frac{1}{P}\sum_{i=1}^{P}\bar{X}_{itk}\right)-\bar{X}_k\right]^2 - \sum_{k=1}^{N}\sum_{i=1}^{P}D\left[\left(\frac{1}{D}\sum_{t=1}^{D}\bar{X}_{itk}\right)-\bar{X}_k\right]^2\right]}^{SS_{FactorSxT} = \boldsymbol{\beta FD_{TS}} * P * D * N}\right\}$$

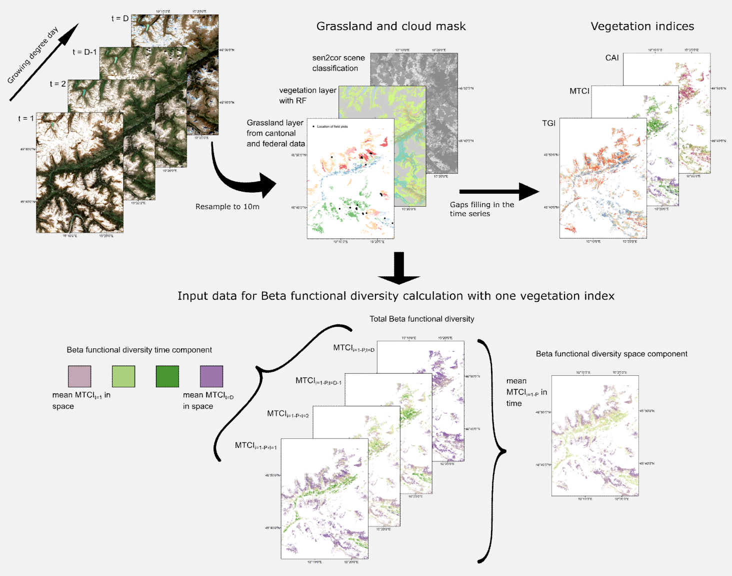
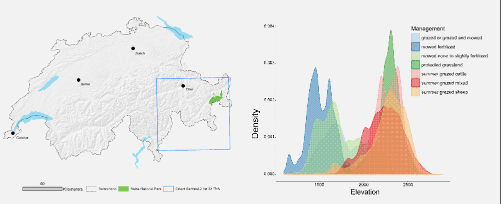


Figure 1: Pre-processing of Sentinel-2 datasets used to calculate the proposed Beta functional diversity (βFD) and its components. Pre-processing included resampling of all bands to 10m spatial resolution and masking out of all cloud and non-grassland pixels. Then, three vegetation indices (TGI, MTCI and CAI) were retrieved for each dataset and gaps in the time series linear interpolated. Each vegetation index was used to calculate βFD and its components.

Study case



- Local contribution of *i*th pixel to βFD

$$LCFD_i = \frac{\sum_{k=1}^{N}\sum_{t=1}^{D}(\bar{X}_{itk}-\bar{X}_k)^2}{N * P * D * \beta FD}$$

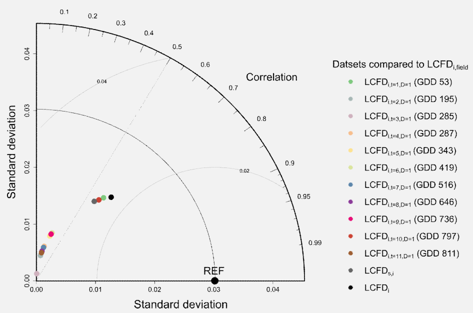


Figure 2: Taylor diagram displaying the statistical comparison between the contribution of each plot to βFD_{field} (REF) and the remotely sensed pixel contribution based on the single datasets (Growing degree day) and the proposed βFD ($LCFD_{S,i}$ and $LCFD_i$).

- Over the whole study area, βFD_S accounted for 49%, βFD_T for 13% and $\beta\text{-}FD_{TS}$ for 38 % of the total βFD.

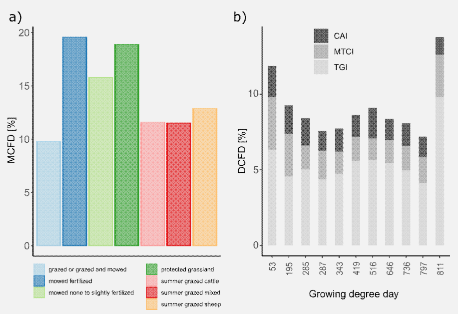


Figure 3: Barplots representing a) the contribution of each management type (MCFD) to the functional beta diversity of the whole study area (βFD) and b) the contribution of each dataset (DCFD) subdivided by vegetation index to βFD.

Conclusions

The partitioning of diversity introduced is an implementation of the analysis of diversity suggested by Rao [2], and the decomposition of the Rao index into within- and among-community diversity [3].

The method allows to partition the spatial and temporal variation in several ways to answer different ecological questions, identify key traits and wavelengths, as well as timing for remote sensing campaigns.

Large scale biodiversity mapping takes advantages of multi-temporal datasets. In particular, areas where a high phenological gradient occurs benefit the most from the proposed approach.

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[2] Rao, C. R. (1982). Diversity and dissimilarity coefficients: a unified approach. Theoretical population biology, 21(1), 24–43.

[3] Pavoine, S., Dufour, A.-B., & Chessel, D. (2004). From dissimilarities among species to dissimilarities among communities: a double principal coordinate analysis. Journal of theoretical biology, 228(4), 523–537.