

# Mapping functional diversity of canopy physiological traits using UAS imaging spectroscopy

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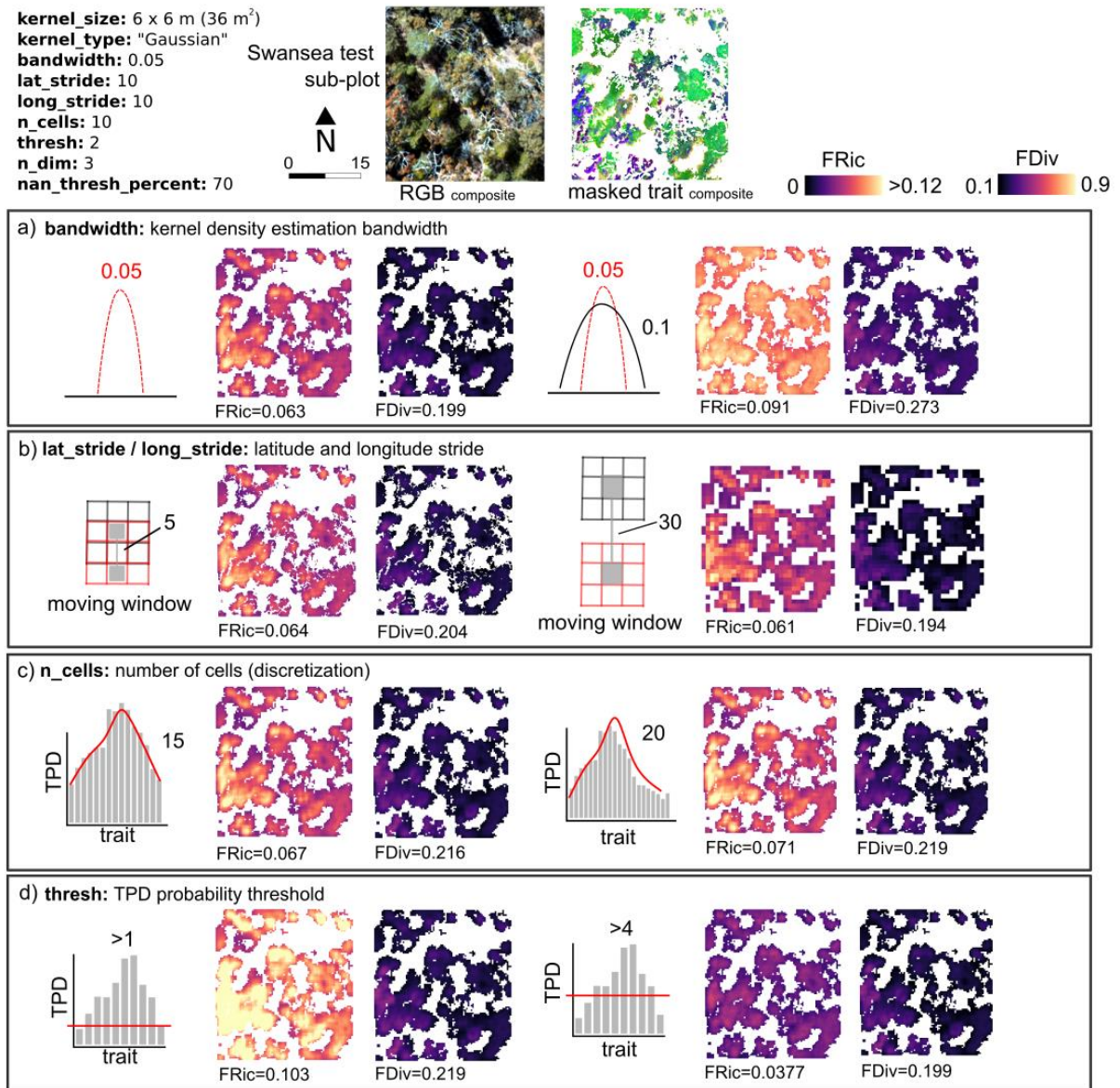
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## APPENDIX D: Functional Trait Diversity (FTD) Python repository.

In support of the crucial demand for research repeatability and systematic open-access biodiversity conservation assessments (Cavender-Bares et al., 2022), we provide here documented algorithms developed through the first iteration of an open-source Python repository named Functional Trait Diversity (FTD) (<https://github.com/ecimoli/Functional-Trait-Diversity-FTD->).

The repository targets specifically TPD computations from stacked physiological (but can be also used for morphological) traits' maps derived from remote sensing observations. To authors' knowledge, this is the first Python programming language approach developed to map pixel-based functional diversity (FD) of stacked image traits with moving window approaches and dealing with the hypervolume problem from an ecological perspective. In previous approaches, a convex hull was used to determine and quantify the hypervolume in traits space as a proxy for functional richness (FRic). The convex hull is defined by the positions of values with the most extreme trait values. On the other hand, TPD functions estimate a probabilistic hypervolume in which the frequencies of different trait values are accounted for. This approach is less sensitive to outliers compared to the convex hull approach thus it truly harnesses the large amount of data provided by high resolution platforms (e.g., UAS). This FTD repository was built on the DASK-empowered *Xarray* data architecture designed for temporal monitoring of large high-resolution datasets (Annala et al., 2018; Hoyer and Hamman, 2017). It is noted that this is just a test release facilitating collaborative improvement and the addition of functionalities. Alternatives in R programming language, that include components of this research, are the hypervolume package (Global Ecology and Biogeography, 23, 2014, 595–609), BAT (Biodiversity Assessment Tools), an

R package for biodiversity assessments, the fundiversity package (Grenié and Gruson, 2022) and the TPD package (<https://CRAN.R-project.org/package=TPD>).



**Figure D1** Effects of different parameters tuneable in the Functional Trait Diversity (FTD) Python repository to compute pixel-based functional diversity (FD) metrics and produce maps of functional richness (FRic) and divergence (FDiv). An exemplar test subplot within the Swansea area was selected to display the effects. The UAS FD maps derived with a 6 x 6 m window size are selected as a reference with the final parameter values selected for this study. **a)** Observed effects for changes in the Kernel Density Estimation (KDE) bandwidth used to produce the TPD. **b)** Observed effects of different window strides lowering final resolution but reducing computation times. **c)** Observed effect of changes in cell size (or the number of cells) used to discretise the continuous TPD. **d)** Observed effects with changes in density threshold for the occupied functional space. Colorbar ranges are maintained constant throughout the figure to allow comparison. Theoretical illustrations on parameter tuning for **c)** and **d)** are based on 1D Trait Probability Density (TPD) for simplicity.

The only input required for the repository is a folder with the selected trait maps in the GeoTIFF format (or similar). The trait maps must be co-registered and of the same resolution and size.

Following the selection of spectral indices as trait proxies or directly the trait maps, FTD allows their normalization between a specific range (e.g., 0 to 1) and the filtering of extreme values via percentiles. FD is always measured within a certain geographical unit defined by the window size (in m<sup>2</sup>) resulting from the multiplication of the number of pixels and the native resolution of the trait map products (see Figure 4a in the main manuscript).

For the KDE, the package allows selecting kernel window size (number of pixels) defining the size of the area accounting for the TPD build (by considering the image resolution), kernel type (e.g., gaussian, exponential, linear etc.) and kernel bandwidth (affecting the “smoothness” of the probability density function or TPD). It also allows to select of the latitudinal and longitudinal stride of the moving window (or the distance the window moves vertically and laterally at each step-in measured in the number pixels), the number of cells for the TPD to be discretised (Figure 4b), and the probability density threshold (selected for making FD metrics less susceptible to outliers). Because different windows will have a varying number of available pixels following mask application, the algorithms also permit to select the threshold percentage of available pixels within each window upon which the entire window is ignored (*nan\_thresh\_percent*). Remaining masked pixels can also be optionally filled any desired value (e.g., zero) or a random value sampled from the same kernel. The filling approach can allow to compute the metrics as a spatial continuum, and to account for canopy gaps as valuable information for biodiversity such as microclimatic, and biological functional gradients relative to the forest interior and crown edges with high biotic heterogeneity. Some examples on how varying TPDs calculation parameters can affect FD metrics can be seen in Figure C1.

The repository allows to make it faster, easier to manipulate and explore parameter space, and more open and accessible such that anyone can run it using their trait-maps data on their own workstation (i.e., without the need for high-performance computing facilities in the case of reasonable size datasets). Our repository is synergetic with a new open-source repository to compute spectral indices associated with a wide range of plant biochemical traits: Spyndex (<https://github.com/awesome-spectral-indices/spyndex>).

## References

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