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MAPPING AVERAGED PAIRWISE INFORMATION (MAPI): A NEW TOOL FOR LANDSCAPE GENETICS ON PLANT VIRUS

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BACKGROUND and OBJECTIVES:

Visualisation of spatial networks based on pairwise metrics such as (dis)similarity coefficients provides direct information on spatial organization of biological systems. However, for large networks, graphical representations are often unreadable as nodes (samples), and edges (links between samples) strongly overlap. We present a new method, MAPI (Mapping Averaged Pairwise Information), allowing translation from spatial networks to variation surfaces.

MATERIALS and METHODS:

MAPI relies on i) a spatial network in which samples are linked by ellipses and, ii) a grid of hexagonal cells encompassing the study area. Pairwise metric values are attributed to ellipses and averaged within the cells they intersect. The resulting surface of variation can be displayed as a colour map in GIS, along with other relevant layers, such as land cover. The method also allows the identification of significant discontinuity in grid cell values through a nonparametric randomisation procedure.

RESULTS.

To illustrate our method we analysed *high- throughput* sequencing data of the Endive Necrotic Mosaic Virus virus obtained from 343 wild salsify collected over ~1500 km2 in South Eastern France. The MAPI analysis revealed a strong spatial genetic structure that could mostly result from host plant population dynamics due to habitat heterogeneity.

CONCLUSIONS:

MAPI is freely provided as a PostgreSQL/PostGIS database extension allowing easy interaction with GIS software and other programming languages. Although developed for spatial and landscape genetics, the method can also be useful to visualise spatial organisation from other kinds of data from which pairwise metrics can be computed.

Building bridges between disciplines for sustainable management of plant virus diseases

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Programme and Abstracts