mvMapper: interactive spatial mapping of genetic structures

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ABSTRACT

Characterizing genetic structure across geographic space is a fundamental challenge in population genetics. Multivariate statistical analyses are powerful tools for summarizing genetic variability, but geographic information and accompanying metadata is not always easily integrated into these methods in a user-friendly fashion. Here, we present a deployable Python-based web-tool, mvMapper, for visualizing and exploring results of multivariate analyses in geographic space. This tool can be used to map results of virtually any multivariate analysis of georeferenced data and routines for exporting results from a number of standard methods have been integrated in the R package adegenet, including principal components analysis (PCA), spatial PCA (sPCA), discriminant analysis of principal components (DAPC), principal coordinates analysis (PCoA), non-metric dimensional scaling (NMDS), and correspondence analysis (CA). mvMapper’s greatest strength is facilitating dynamic and interactive exploration of the statistical and geographic frameworks side-by-side, a task that is difficult and time-consuming with currently available tools. Source code and deployment instructions, as well as a link to a hosted instance of mvMapper, can be found at https://popphylotools.github.io/mvMapper/.
Assessing patterns of genetic structure is one of the foundational challenges of population genetics (Pritchard et al. 2000; Slatkin 1987; Verity & Nichols 2016; Wright 1949), and characterizing this structure across geographic space is one of the first steps in most population genetic studies. Such contextualization of genetic structure allows in-depth evolutionary investigations, such as characterizing dispersal and invasion pathways (Genton et al. 2005; Janes et al. 2014; Mori et al. 2016), assessing and prioritizing conservation efforts (Austin et al. 2011; Proshek et al. 2015; Zenboudji et al. 2016), quantifying hybridization (Chatfield et al. 2010; Dupuis & Sperling 2016), and even utilizing genomic information to predict human origins (Das et al. 2016; Elhaik et al. 2014; Flegontov et al. 2016). Some analyses explicitly incorporate spatial information in the assessment of population structure (e.g. TESS: Caye et al. (2016), BAPS: Cheng et al. (2013), GENELAND: Guillot et al. (2005), EEMS: Petkova et al. (2016), SCAT: Wasser et al. (2004), sPCA: Jombart et al. (2008)), and landscape genetics is a fast growing field of statistics combining population genetics and landscape ecology (Manel & Holderegger 2013; Manel et al. 2003; Storfer et al. 2007).

Multivariate analyses stand out as powerful tools for summarizing genetic variability (Jombart et al. 2009). A wide diversity of such methods exist, each with their own particular applications (reviewed in Jombart et al. 2009). As a whole, these statistics provide many analytical advantages for population genetics, including, but not limited to: few overarching assumptions regarding the data (e.g. Hardy-Weinberg expectations and linkage equilibria, which can mask subtle clinal population structure (Jombart et al. 2008)), low computational requirements for the analysis of large datasets (e.g. thousands of markers and individuals.
(Jombart & Ahmed 2011; Patterson et al. 2006)), and the statistical flexibility to address complex population genetic questions (Jombart et al. 2009 and references therein). While some methods explicitly incorporate geographic information (e.g. spatial principal components analysis (sPCA) (Jombart et al. 2008) and spatial correspondence analysis (Dray et al. 2008)) and provide valuable geographic context to population genetic data, non-spatial analyses also benefit from visualization in geographic space (Cavalli-Sforza et al. 1994; Wang et al. 2012). However, incorporating geographic context into multivariate analyses often requires the laborious comparison of ordination plots to maps of sampling localities, or technical expertise in map-making or geographic information systems (GIS) that may be beyond the comfort zone of the average researcher. While some streamlined tools exist for specific geographic visualizations (e.g. the Geography of Genetic Variants browser (Marcus & Novembre 2017)), generalized tools for straightforward visualization are lacking.

Here, we present a tool for the visualization and exploration of multivariate analyses in geographic space. mvMapper is a Python-based, deployable web-based tool that can process outputs of virtually any multivariate analysis as well as sample locality information and allows users to interactively explore the statistical framework of the multivariate analysis in both ordination and geographical space (Figure 1). The input format is a simple comma-delimited tabular file that can either be assembled manually, or generated using mvMapper’s input generation function in the adegenet library (Jombart 2008) in R (R Core Team 2016), giving access to a wide range of commonly used methods.

METHODS
Implementation

mvMapper is implemented in Python v3.6 (Python Software Foundation 2017), and makes extensive use of the following libraries: Bokeh v0.12.4 for data visualization (Bokeh Development Team 2014), Pandas v0.19.2 for data structure and analysis (McKinney 2010), colorcet v0.9.1 for color utilities (Kovesi 2015), and pyproj v1.9.5.1 (Whitaker 2016), a python interface for cartographic transformations using PROJ.4 (Warmerdam 2001). Map tiles and map data are by Stamen Design under CC BY 3.0 (Stamen Design 2017) and OpenStreetMap under CC BY SA (OpenStreetMap contributors 2017), respectively, and use the WGS84 (ESPG 4326) spatial reference system. The automated data preparation script is implemented in the adegenet library (Jombart 2008) in R (R Core Team 2016). Links to mvMapper’s source code, documentation, a ready to deploy Docker container (Merkel 2014, see https://www.docker.com/), and a hosted instance of the web application can be found on our project page at https://popphylotools.github.io/mvMapper/. Although deploying a stand-alone instance of mvMapper provides a great deal of flexibility through the customization of the configuration file (default displayed statistical parameters, dataset, etc.), here, we generally refer to the default configuration available on our hosted instance. All modern desktop web browsers support mvMapper.

Data input

The primary input for mvMapper is a comma-delimited tabular file that contains individuals in rows and information about those individuals in columns. A typical file contains columns such as: specimen identification code (we refer to this unique identifier as key),
collection locality information (latitude and longitude, or \texttt{lat} and \texttt{lon}), a population identifier, results of the multivariate analysis (specimen coordinates across multiple dimensions of an analysis, e.g. principal components), and any other metadata related to the specimens (sex, host, morphological characteristics, etc.). Given that many of these analyses are conducted in R (R Core Team 2016), we have incorporated a data preparation function to the widely used R library \texttt{adegenet} (Jombart 2008). This function, \texttt{export_to_mvmapper}, combines an active R object from a multivariate analysis with locality information for each specimen. Currently, multivariate analyses conducted in \texttt{adegenet} and those based on the duality diagram (\texttt{dudi}.* functions) in \texttt{ade4} (Dray & Dufour 2007) are supported, including: sPCA and discriminant analysis of principal components (DAPC: Jombart \textit{et al.} (2010)) in \texttt{adegenet}, and principal components analysis (PCA), principal coordinates analysis (PCoA), non-metric dimensional scaling (NMDS), correspondence analysis (CA), and others in \texttt{ade4}. Locality information is then incorporated into the multivariate analysis through another R object. This is most easily done by preparing an additional file with at least three columns, \texttt{key}, \texttt{lat}, and \texttt{lon}, where \texttt{key} matches the unique individual identifiers used in the multivariate analysis. After reading this locality file into R, \texttt{export_to_mvmapper} will combine the two R objects (the multivariate analysis and the locality information) into \texttt{mvMapper} input format, which can be manually written to a comma-delimited file (e.g. using R’s \texttt{write.csv} function). Locality information can be incorporated via other means (e.g. when latitude and longitude are already part of a \texttt{genind} object), however the advantage of creating an additional file, as described here, is that any additional specimen-based information can be included in that file (named \texttt{localities.csv} in the following example), such as: specimen sex, host information, and
morphological or ecological characters. Alternatively, rather than using

\texttt{export_to_mvmapper}, the input data file can be generated manually from results of

multivariate analyses in different programs or R libraries, as the tabular format is general and

user-friendly.

Below we provide an example of data preparation from a DAPC, which in addition to

standard multivariate analyses results (distribution of individuals along principal components)

provides additional components recognized by \texttt{mvMapper}, such as membership to \textit{a priori-}

assigned and DAPC-assigned groups, and the posterior probabilities of the DAPC-assigned

groups. See \url{https://github.com/popphylo tools/mvMapper/tree/master/dataPrepExampleFiles} for

an example of this file generated from a dataset of 783 autosomal microsatellite loci genotyped

for 1,048 human individuals from 53 populations (Rosenberg \textit{et al.} 2005).

```r
> # An example using the microsatellite dataset of Rosenberg \textit{et al.} 2005
> # Using adegenet devel version
> Rosenberg <- read.structure("Rosenberg_783msats.str", n.ind=1048,
> n.loc=783, onerowperind=F, col.lab=1, col.pop=2, row.marknames=NULL,
> NA.char="-9", ask=F, quiet=F)
> # DAPC (n.pca determined using xvalDapc, see ??xvalDapc)
> dapc1 <- dapc(Rosenberg, n.pca=20, n.da=200)
> # read in localities.csv, which contains "key", "lat", and "lon" columns
> # with column headers (this example contains a fourth column "population" which
> # is a text-based population name based on geography)
> localities <- read.csv(file="localities.csv", header=T)
> # generate mvmapper input file and write to "rosenbergData.csv"
> out <- export_to_webapp(dapc1,localities)
> write.csv(out, "RosenbergData.csv", row.names=F)
```

By default, \texttt{mvMapper} is configured to display the microsatellite dataset of Rosenberg \textit{et

al.} (2005) from the example above. Users can upload their own datasets through the upload tab

linked in the navigation bar at the top of the page (Figure 1, top). Files uploaded in this manner
are named using an alphanumeric random string that is integrated into the web address used to select that dataset; users can return to a previously uploaded dataset using its unique web address until it expires after 14 days.

Interface and functionality

The main interface of mvMapper consists of three components: a statistical panel, a mapping panel, and a metadata panel (Figure 1). Aspects of these panels are linked, so that, for example, selecting individuals in the ordination of the statistical panel will highlight those individuals on the map and their metadata will appear in the metadata panel. Pull-down menus to the left of the statistical panel allows users to select which data is displayed in the ordination plot. In a general multivariate analysis, the most informative principal axes (or principal components) would be plotted against each other (e.g. PC1 vs. PC2) (Figure 1); in mvMapper, any of the multivariate analysis results (all principal axes) or specimen-based metadata can be plotted in the statistical panel. For example, the distribution of individuals along a particular principal component can be plotted against populations of origin (Figure 2A), assigned group membership from DAPC, or latitude or longitude (Figure 2B). Individual specimen points in both the statistical and mapping panels can be colored (with several palette choices) or sized according to any column in the input data file, except when discrete data values outnumber available colors/sizes, in which case those attributes are excluded from the dropdowns.

Automatic binning supports coloring and sizing of numeric attributes. Specific attributes can be configured to be treated as discrete values, even if numeric, and by default these include key, grp, and assigned_grp. These coloring and sizing abilities facilitate rapid exploration of
metadata with regard to population structure; for example, individuals can be colored by
collection locality, group membership, host, sex, or other genetic attribute (Figure 2C), or be
sized by the posterior probability of group membership in a DAPC, all with a few mouse clicks.

Both the statistical and mapping panels are interactive with tools for panning, zooming in
and out, and saving the image. Individuals can be selected singly with a mouse click, or multiply
by shift clicking or using the dragged box tool. In the mapping panel, overlapping points can be
separated with a jitter function, and the zoom tool is dynamic: zooming in or out will access
finer-scale or coarser-scale map tiles with more or less detail, respectively (e.g. labeling
countries, cities, roads, or other scale-appropriate geographical features). This allows
mvMapper to function at both global and local geographic scales (Figure 2C). Selecting
individuals in either the statistical or mapping panel displays their metadata in the lower panel,
which can be sorted by clicking on column headers. Selected data can also be downloaded (as a
comma-delimited file) to facilitate downstream analysis, for example re-analysis of individual
population groups or hierarchical analysis (Vähä et al. 2007).

DISCUSSION

Visualizing population structure across geographic space is fundamental to most
population genetic studies. However, combining multiple “data wrangling” tools (Kandel et al.
2011), including population genetic data processing, multivariate analysis, and particularly map-
making or GIS, is a time-consuming, error-prone, and generally daunting task (e.g. Fletcher-
Lartey & Caprarelli 2016; Rickles & Ellul 2014; Sipe & Dale 2003). mvMapper greatly
facilitates this process by providing an accessible, open access, user-friendly interface for
exploring and visualizing results of multivariate analysis in geographic space, and perhaps most importantly facilitates dynamic and interactive exploration of these spaces. Interactivity, in particular, is key to enable users to quickly assess the geographic patterns of any combinations of principal components, population groupings, additional statistical parameters (assignments to groups based on discriminant functions in DAPC or lag-vectors of principal components in sPCA), and any other specimen-based metadata with a few mouse clicks in the drop-down menus to the left of the statistical panel. Given these characteristics, we envision mvMapper to be of wide interest to a broad range of researchers as well as for teaching and training purposes. Additionally, mvMapper’s highly generalized and modular approach allows it to be modified for more specific uses; for example, including metadata corresponding to whether specimens of an invasive species were collected in its native versus introduced range allows mvMapper to become a tool for source determination of intercepted material (Roderick 2004).

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Research Unit for Modelling Methodology. Mention of trade names or commercial products in this publication is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the USDA. USDA is an equal opportunity employer.

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**DATA ACCESSIBILITY**

Software, documentation, and example data are available at https://popphylotools.github.io/mvMapper/, and a stable release at the time of publishing is available at http://zenodo.org DOI: XXXXXXX.
AUTHOR CONTRIBUTIONS

JRD, FTB, SSB, and SMG conceptualized software; JRD, FTB, and TJ implemented software. JRD wrote the manuscript with input from all authors.

FIGURE LEGENDS

Figure 1. The user interface of mvMapper in a web browser, displaying the human microsatellite dataset of Rosenberg et al. (2005). Features include the statistical panel (left), mapping panel (right), metadata panel (lower), and navigation bar (top).

Figure 2. Various visualization options for the human and swallowtail butterfly microsatellite datasets of Rosenberg et al. (2005) (A and B) and Dupuis and Sperling (2016) (C), respectively. A) population grouping vs. principal component 3, B) latitude vs. principal component 3, and C) principal component 2 vs. 1, colored by COI clade and zoomed in to the Red Deer River valley in southeast Alberta, Canada.