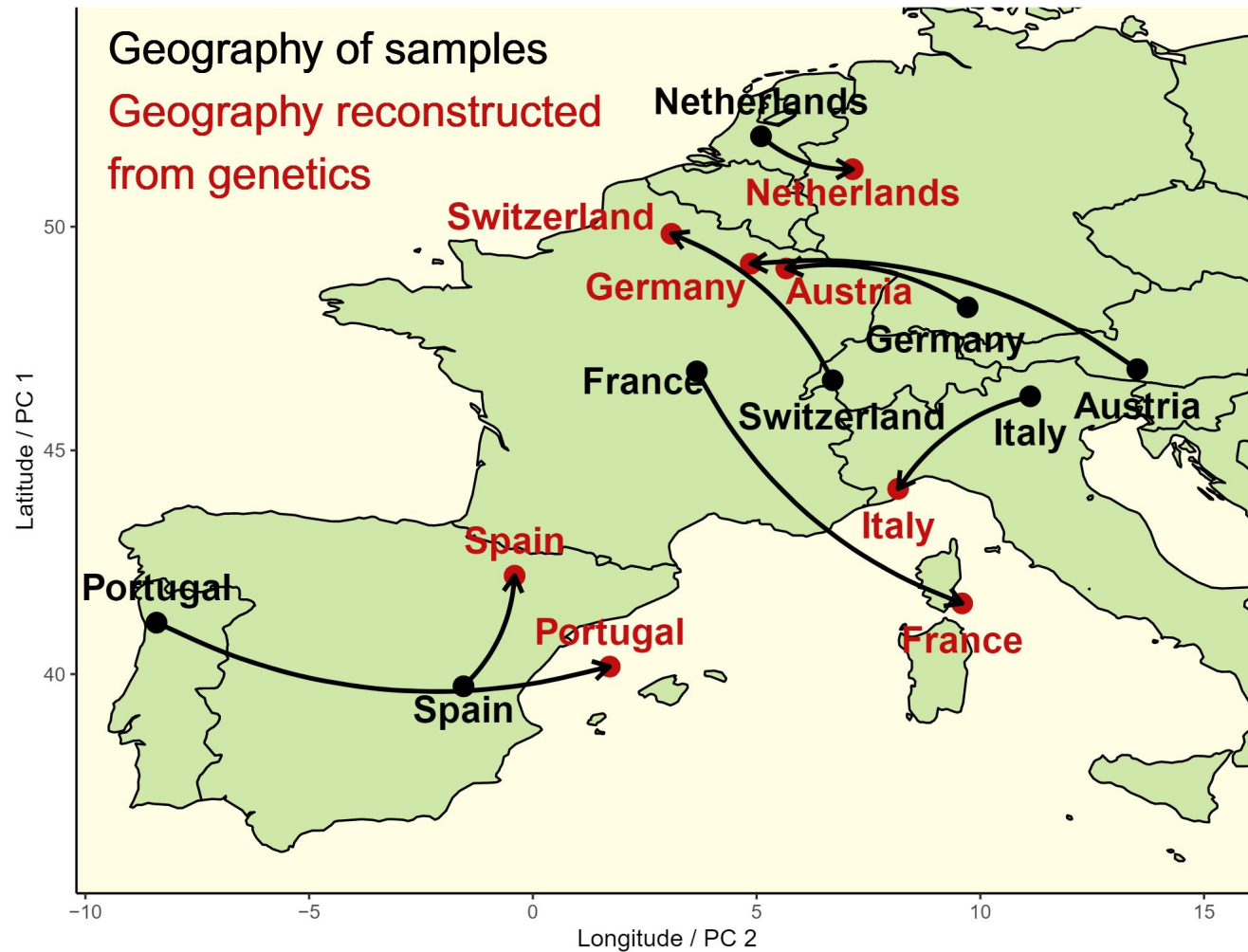




Reconstructing fruit fly geography from genetics

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Project Objective

Develop a method for visualizing a type of geospatial data common in population genetics

Reconstruct the geography of biological samples of *D. melanogaster* fruit flies solely from genetic variation information

Visualize the transformation from geographic space to PC-space

Dataset used

Drosophila Evolution over Space and Time (DEST)

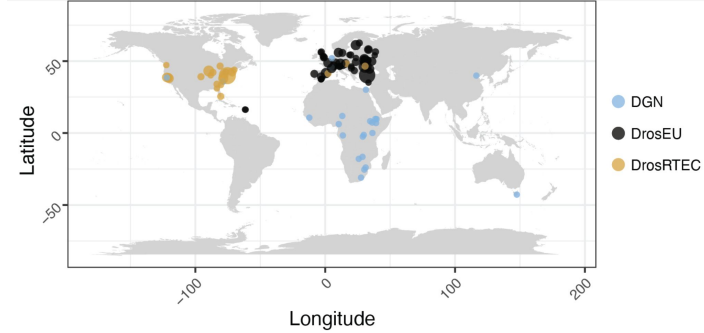
Genetic variation of more than 13,000 *D. melanogaster* fruit flies

272 samples across four continents over several years

We use, latitude, longitude, country of origin, and genetic variation of samples

Unused variables include environmental information, genome sequencing technique, locality, and date

We focus on Western Europe



Kapun et al. (2021), Fig. 1a

Our method

Apply principal component analysis (PCA) to genetic variation information of fruit fly samples

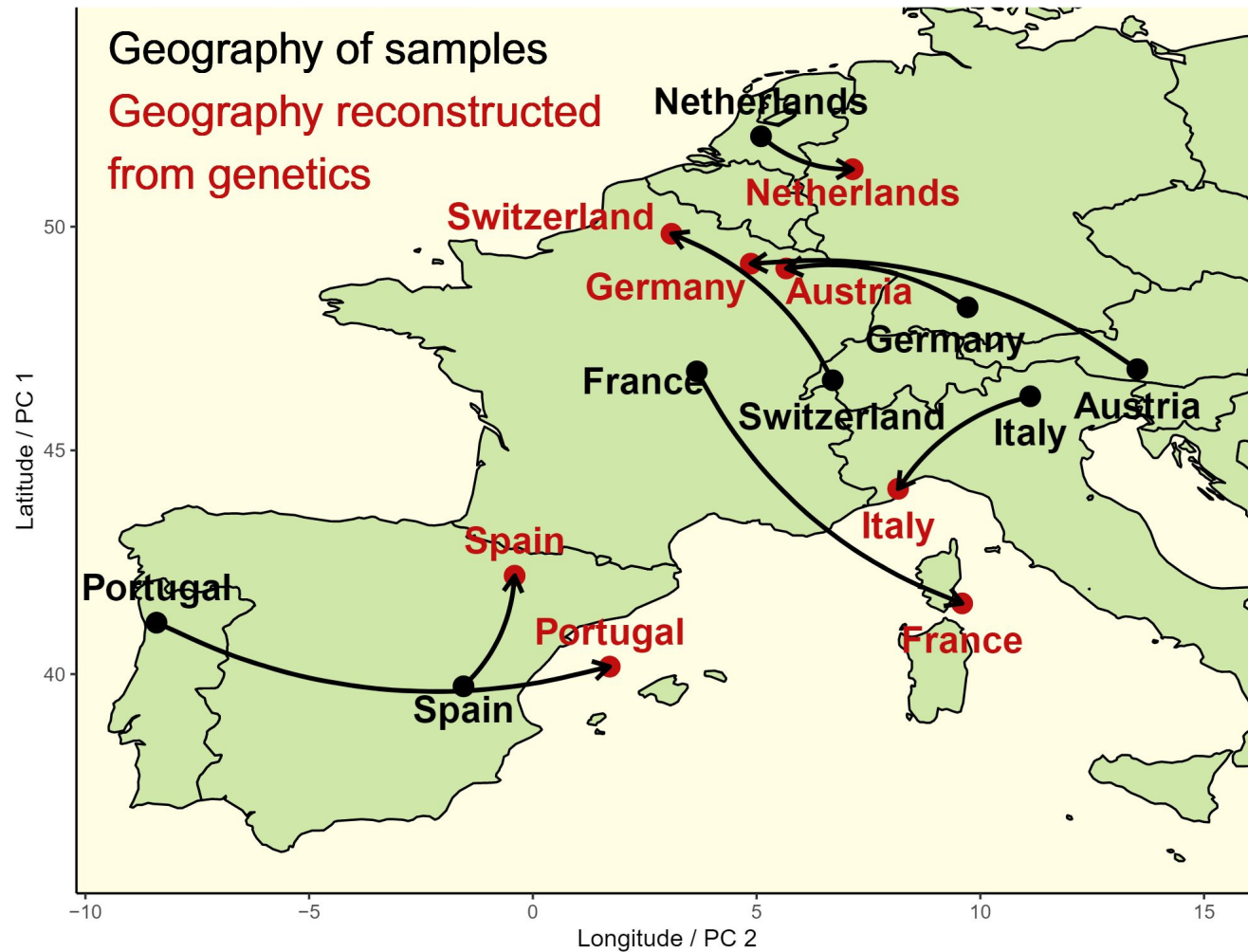
Find that PC1 and PC2 strongly correlated with latitude and longitude

Average latitude and longitude of each country to display geographic information in one point per country (**black**)

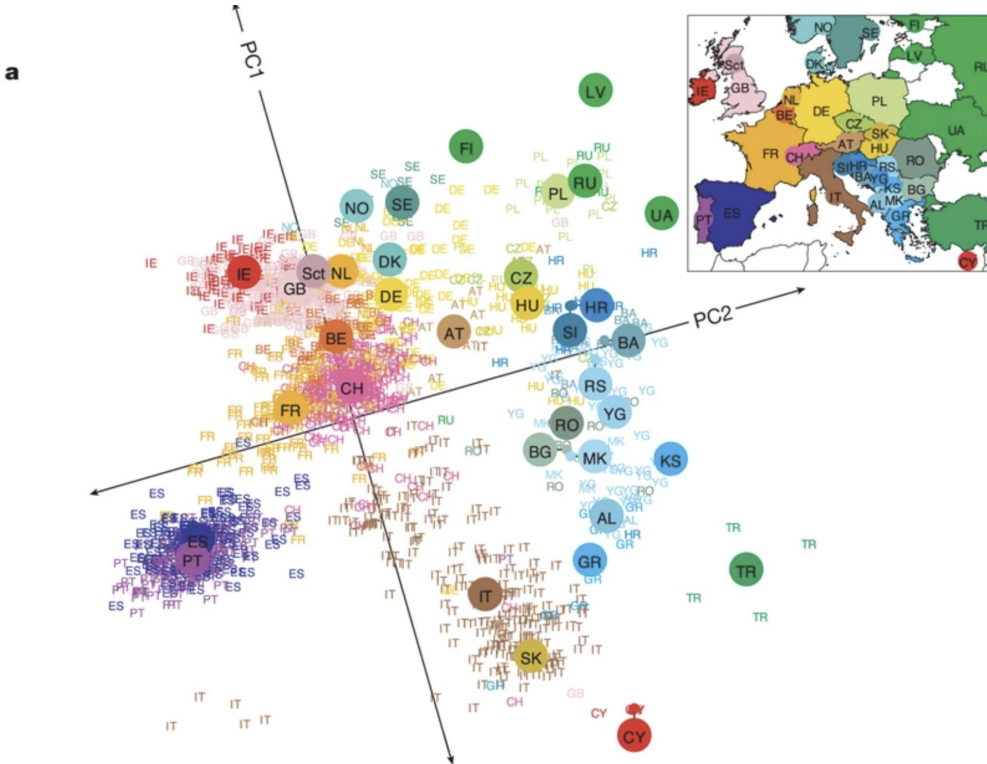
Apply Procrustes analysis to PC-space to align it with geographic space

Display PC-space in single points divided by country of relevance (**red**)

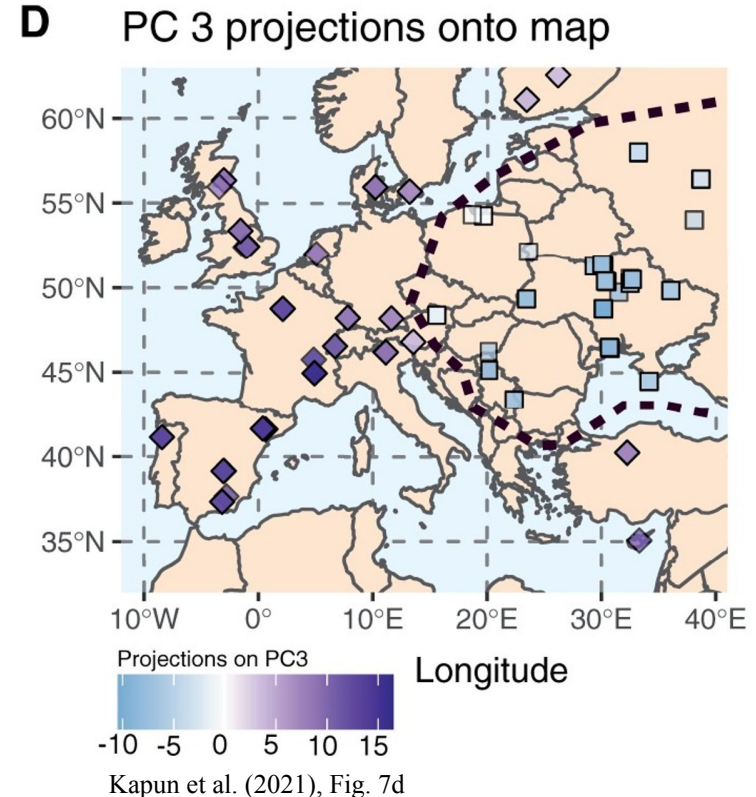
Connect the geographic information and PC information with arrows



Limitations of current methods previous figures



Novembre et al. (2009), Fig. 1a



Resolving limitations

We apply Procrustes analysis to align PC-space to geographic space

We plot points for both geographic space and PC-space

We emphasize the transformation from geographic space to PC-space with arrows connecting pairs of corresponding points

We group the data so as to only display one point per country in either space

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Questions?

