**Independent projects – variation partitioning (Wubing)**

**Option 1. Perform variation partitioning on simulated communities**

There are two metacommunities simulated with Thompson metacommunity model (introduced by Shane in Tuesday). In one metacommunity, species have broad niche breadth but have weak dispersal ability. In the second metacommunity, species have narrow niche breadth but have strong dispersal ability. You can find the data in the file “Simulated\_2metacommunities.RDATA”, which were simulated with the R -script “metacommunity\_simulation.R” (You can run the R-script and simulate the metacommunities yourself). In the RDATA, there are 4 files: **meta1\_comp** (community composition data, sites\*species), **meta1\_env\_xy** (environment, column 2, only one variable; and spatial coordinates, column 3 and 4), **meta2\_comp** (community compositions for the second metacommunity), **meta2\_env\_xy** (environment and spatial coordinates for the second metacommunity). You could use these simulated metacommunities to perform variation partitioning to understand whether these methods are useful.

1) The main target:

* Use the multiple/partial regression to partitioning variation in beta-diversity between sites into the fractions due to space and environment;
* Use the RDA/partial RDA to partitioning variation in the community composition data table into fractions due to space and environment

2) Suggestions:

Follow the r-script for variation partitioning step by step:

* explore the metacommunity data, such as spatial patterns of sites, richness and environment, etc.
* calculate the beta-diversity, spatial distance, environmental distance; and perform variation partitioning using multiple/partial regression (function ‘varpart’ in ‘vegan’).
* perform PCNM to generate spatial variable describing spatial structures; and perform variable selection.
* use the RDA/partial RDA to perform variation partitioning.

3) Expectation for presentation:

* Questions, and figures describing the used datasets;
* Compare the results using the two methods of variation partitioning;
* Compare the fractions of variation explained by space and environment between metacommunity 1 and metacommunity 2.
* Some discussion on your results, e.g. why more fraction of variation explained by space in one metacommunity, and more explained by environment in another metacommunity.

4) Optional task:

Simulate some metacommunities using different levels of dispersal possibility and/or niche breadth. And then perform variation partitioning using one or two methods. Compare the relationships between fractions explained by space/environment and the parameters (dispersal and niche) that are used to simulate metacommunities.

**Option 2. Perform variation partitioning on empirical datasets**

Find empirical datasets from the literature or use your study datasets. There is a data paper [(Jeliazkov et al. 2020](https://www.nature.com/articles/s41597-019-0344-7)) that provide 80 datasets (metacommunities) which are open accessible. You can find this database from the figshare: <https://doi.org/10.6084/m9.figshare.c.4459637>. I chose two datasets that were collected from the same region (Arid steppes, Eastern Morocco) and have similar sampling areas. These two datasets are Frenette2012b\_AJ.xlsx (plants)and Frenette2013\_AJ.xlsx (ants). You can choose some datasets that you are interested in and use them to perform variation partitioning. Each of these datasets provide species composition table, environments and spatial coordinates. You could use these empirical metacommunities to perform variation partitioning to address some questions, e.g. difference among taxon groups, the effects of sampling areas on results, comparison between low (tropical) and high (temperate) latitudinal regions.

1) The main target:

* Use the multiple/partial regression to partitioning variation in beta-diversity between sites into the fractions due to space and environment;
* Use the RDA/partial RDA to partitioning variation in the community composition data table into fractions due to space and environment

2) Suggestions:

Follow the r-script for variation partitioning step by step:

* explore the metacommunity data, such as spatial patterns of sites, richness and environment, etc.
* calculate the beta-diversity, spatial distance, environmental distance; and perform variation partitioning using multiple/partial regression (function ‘varpart’ in ‘vegan’).
* perform PCNM to generate spatial variable describing spatial structures; and perform variable selection. If none of PCNM variables are selected, use all variables for next step.
* use the RDA/partial RDA to perform variation partitioning.

3) Expectation for presentation:

* Questions, and figures describing the used datasets;
* Compare the results using the two methods of variation partitioning;
* Compare the fractions of variation explained by space and environment among different metacommunities.
* Some discussion on your results, e.g. the possibilities why more fraction of variation explained by space in some metacommunities, and more explained by environment in other metacommunities.

4) Optional task:

Not just use the two datasets I selected in data analyses. You could perform variation partitioning to all 80 datasets from the data paper (Jeliazkov et al. 2020). You could explore which fractions (pure spatial ) are generally more important. You could also explore the relationships between variation in different fractions explained and some attributes of the datasets (e.g. taxon groups, sampling extent, regions, latitudinal zones etc.)