Basic Outline of Making Individual Isotope Map for Each Migrant

1. Made a map of hydrogen isotope values in precipitation for N. America in ISOMAP. See ISOMAP Metadata.docx for description of how map was made
2. Brought Isoscape into R and made a raster of the 1) hydrogen isotope precip isoscape and 2) the standard deviation isoscape of the hydrogen isotope precip values
3. To determine the relationship between hydrogen isotopes in precipitation and feathers I used a dataset with hydrogen isotope feather values from breeding WIWA samples captured at known locations. Examination of the relationship between stable hydrogen isotopes in precip and feathers with only AHY birds (i.e., removal of HY birds from the dataset) reduced the R2 value of the regression to 0.64/ slope = 0.8677) compared to R2 = 0.74 / slope = 0.81652 when all birds (AHY and HY) were included. Because the slopes are so similar between the two analyses and R2 improved when you included all birds I used the file with both AHY and HY birds (n=357 – datafile: WIWA\_breeding samples.csv which I assigned the object name of: feather.dat).
4. Extracted hydrogen isotope value of precipitation for each breeding individual from the rasterized isoscape based on the lat/long of the sample location. Also extract the standard deviation of that location from the standard deviation rasterized isoscape.
5. Re-organized the object feather.dat by location of capture and summarized the number of WIWA sampled at that location, the mean and standard deviation of stable hydrogen isotopes of feather samples, and mean and standard deviation of stable hydrogen isotopes of precipitation at the location (values are the same for each indiv).
6. Used rescale function from the vander zanden code to conduct 1000 simulated regressions sampled from normal distributions of data randomly generated from the means and SDs at each site. The output contains the slopes and intercepts of each of the 1000 regression lines, from which a mean intercept and slope can be extracted. The regression equation is: X2H ~ iso with RV = X2H = isotope value from feather, EV = iso = isotope value from precip map. So the equation is predicting the feather isotope value from the precip isotope value.
7. Used the extracted equation of the line for relationship between hydrogen isotopes in precip and feathers calculated in step #6 to rescale the raster map of stable hydrogen isotopes of precipitation from step #2 into a raster map of stable hydrogen isotopes of feathers. Also creates a rescaled raster map of standard deviations associated with the rescaled precip map. This step was done using the raster.conversion function from vander zanden code.
8. Used the assignment function from vander zanden code to create a probability surface of isotope values for migratory WIWAs (datafile: WIWA\_migrants.csv). The probability incorporates the stable hydrogen isotope value of the individual migrant’s feather and associated error. There are three parts to the error: 1) error associated with the original isotope precip map (precip\_SD\_raster), 2) error associated with rescaled precip map (rescaled\_SD\_raster ; parts 1 and 2 vary across the map), 3) error associated with individual calculated from the mean standard deviation of feather isotope values of breeding WIWAs captured at the same location (SD\_indv=mean(fnewcal.dat$sdH); constant value)

I cannot attest to how good the functions from the vander zanden code are constructed. I understand the general idea of what they are doing, but I am new to loop codes and so I have no idea how clunky or poorly written they may be.