A:\_plot\_data\_sp\_i (trait data taken from species measurements associated with that species and plot)

B:\_study\_data\_sp\_i (trait data taken from that species across all plots)

C:\_plot\_data\_genus\_i (trait data taken from that genus but in the focal plot)

D:\_study\_data\_genus\_i (trait data taken from genus and across all plots)

E:\_plot\_data\_family\_i (trait data taken from the family within the focal plot)

F:\_study\_data\_family\_i (trait data taken from the family across all plots)

G:\_bien\_data\_sp\_i (trait data taken from BIEN measurements for the given species)

H:\_bien\_data\_genus\_ (trait data taken from BIEN measurments for the genus)

I:\_bien\_data\_family\_i (trait data taken from BIEN measurements for the family)