Limacina workflow- April 2019…or…how to get really frustrated and reanalyze all your data in R….

1. Pull out pteropod and aragonite saturation values from SQL backend
   1. Create a qry that puts the data with the basin scale indices so that data are equally spaced and all there. Plus, you’ll want the basin scale indicators later
   2. Create qry of env parameters that you think will also be useful- chl, temperature at different depths (?? Do you pull in the raw data and average in R or do I qry the data out for the depths I want??), salinity, and all of those parameters on the 26.5 isopycnal
2. Sparse out the data by env and boil vars? Include aragonite or keep all in one large flat file??
   1. Just learned best to keep in large flat file to begin with and then
   2. Save this large flat file- RAW data to be used for later anz
3. Generate a time series variable for each bio and env dataset
   1. Loop over each station
   2. Summary stats for each env var by station
4. Interpolate over Nans
5. Plot
6. Run cross corr with pteropods and env var
7. Check for ACF and PACF
8. What AR process do we have?
9. Decompose
10. Plot
11. Extract the decomposed trends- long term and seasonal and run cross corr with those and env vars
12. Dplyr and tidyverse
13. Generate the time series model- see Will’s class