Interactive Tool Guidance

Managed Access

* Data
  + moz\_ma has 6 features
  + 10 other data from the CRCC
* Process
  + Load data
  + Check field names
    - Rename and reorder if needed
  + Calculate area to check if the area fields are correct
    - st\_area() calculates things in m2 so to get area in ha (1 ha = 10000 m2)
    - Would need to create a new field (can delete later)
  + moz\_ma has multiple features for one managed access area
    - Probably use group\_by() to get 6 unique managed access areas and still use summarise() to get total area afterwards [there are codes for group\_by() and summarise() in the clean and export scripts
      * What could be done is create area field, then group\_by(maa\_name) then summarise(area\_ha = sum(area)) or something like that
  + Bind data
    - May need to change coordinate systems

Reserves

Larval migration

* Can reference the larval connectivity code to see how it has previously been updated
* But data file names (in Explorer / Finder / Q / R / ArcGIS) and codes need to be updated to reflect
* Species codes 🡪 basically first letter of genus and first four of species (all lowercase) for data names
  + Crab (crb) = *Scylla serrata* (ssera)
  + Emperor (emp) = *Lethrunus lentjan*
  + Fusilier (fus) = *Caesio teres* (ctere)
  + Grouper (grp) = *Epinephelus malabaricus* (emala)
  + Parrotfish (pfs) = *Scarus ghobban* (sghob)
* Can very likely search and replace (find “crb” and replace with “ssera”)
  + Maybe start doing it one at a time or can do all together and see if the same numbers match (e.g., each find and replace says it has found 20 instances or something like that; there should always be an even amount being replaced)