**Generating stratified means/swept area biomass estimates** –

There are several steps to generating a stratified mean and then converting it into a swept area biomass estimate. The r scripts necessary to do this are: Poststrat.r (optional), Prestrat.r, Stratmean.r, and Sweptarea.r. The process of each script is outline in the Flow\_diagrams.pptx.

**Step 1** (Optional) – Poststrat.r – changes the stratification scheme of the data using a shapefile. Example – assigning survey catch to EPUs. Make sure to only run this on stations only not survdat data file. (Need to incorporate this into Poststrat)

**Step 2** (Optional) – Segregate by season. Prestrat sums stations by year. If data contains multiple seasons and you want to stratify by season not year, this is when you must segregate. (May consider a toggle to eliminate this step)

**Step 3** – Generate a stratum area table. This can be done by querying the database for survey strata or using the getarea.r script for a shapefile.

**Step 4** – Prestrat.r – this is a preprocessing step. This script sums up the number of stations in each stratum and the weight of each stratum based on area.

**Step 5** (Optional) – Reduce species or combine species. If you are calculating the stratified means on a subset of species or aggregate group of species here is when you would do it. Reducing the number of species before this point may result in stations with zero catch of those species being left out of the calculations.

**Step 6** – Stratmean.r – this calculates the stratified mean biomass and abundance for each group or species. It also calculates the variance and standard error.

**Step 7** – Sweptarea.r – this expands the stratified mean to a total biomass/abundance estimate. The default is to calculate a minimum swept area estimate which assumes a catchability (q) of 1 (i.e. everything in front of the net is caught). Optionally you may supply a data table with q values to increase these estimates.