I have developed a pipeline to create plots for my third PhD paper. This pipeline allows for the efficient generation of plots from several data files, requiring only minor changes to the path and limits, so that the plots are quickly ready for inclusion in a manuscript.

To clarify, I used this pipeline for **Figure 8** in my manuscript, which is structured to show several variations. **Figure 8** depicts the **catch share rate** and **retention probability** for **Krill** species using mesh sizes of **14, 20, and 30 mm** in the **belly section** of the trawl net. This method allows us to examine the catch share between test nets and a control net (10 mm) and to predict the catch pattern in the tested nets.

As detailed in the manuscript, the figure is titled: "Size selectivity in belly section for krill (trials in 2022). Left column: experimental catch share points (circles) with the modelled catch sharing rate (black curve) for the belly sections for krill. The size distribution of krill captured in the test and control compartment are represented by the black and grey lines, respectively. Right column: Size selection curve (black curve) with corresponding 95% confidence bands (dashed lines)."

The excel data files used in these plots are generated by a statistical software called SELNET. This pipeline can be utilized for analysis immediately after retrieving data from this software, with each column in the plot representing a specific part of the analysis.

I tried to minimize the manual manipulation of the code after changing path names. It can be developed further; it still needs some work. For now, this is enough for one species, but for different data ranges, it can be edited to adjust according to the data type or range. My plan is to develop the code so people using this specific statistical software tool can plot more easily.

For the script and data paths please see:

https://github.com/eniskostak/enk/tree/5430375cd7d59082ef7955eb9ce14132a9334312/final_assignment