

When studying the behavior and diets of marine predators, there are many limitations to data collection that can make it difficult to generalize results. Systems that allow for direct observation of feeding are typically limited either to a very specific region or by financial factors. Many indirect diet estimation methods, such as stomach content analysis, are lethal and can be biased towards the last meal and the recording of prey with hard parts that take longer to digest. Quantitative Fatty Acid Signature Analysis (or QFASA) is a statistical model that ameliorates these concerns, using proportions of fatty acids stored in the adipose tissue of a marine predator's body to estimate diet over longer periods of time without killing or harming predators during data collection. The QFASA model requires a database of fatty acid signatures for all potential prey in the predator's diet and attempts to match the fatty acid signature of the predator to the prey. Since the QFASA model is used by biologists worldwide and is regularly updated with new functionality for model assessment and inference, a QFASA R package was developed. However, the R package still requires a multi-step process of data formatting and manipulation to function, a process that can be intimidating for users without a background in R. This project aims to create a user-friendly interface through the Shiny package in R that receives a set of simpler inputs and runs the QFASA process in the background, displaying a boxplot of the QFASA output. This would allow users new to R to run QFASA, as well as reducing the tedium of running the process repeatedly for statisticians to observe changes in the data after changing inputs.