Body Size Data Processing

NEON collects macroinvertebrate data via fixed-area samplers (e.g., Surber samples) and measures insect body sizes using XXXXX. In contrast, fish are collected using 3-pass removal electrofishing within stream reaches that vary in area across study sites. For each collection, the first 50 fish per taxon are measured for total length in mm (Monahan et al. 2020). Thus, the fish data consist of two subsets of data, one for counts of the total number of fish per pass per reach, and another with the length of the first 50 fish caught per taxon per reach (but not per pass). To convert both types of samples into a single format containing abundance (per square meter) of each dry mass, whether macroinvertebrate or fish, multiple data steps were required as described below.

*Macroinvertebrates*

*Fish*

We obtained measurements of individual fish total lengths (mm) from the *fsh\_perFish* table in data product DP1.20107.001 (NEON 2022). For each collection event (i.e., collection date, reach, and site), *fsh\_perFish* contains up to 50 individual measurements per species. Most species have fewer than 50 measurements, though in some cases there are more than 50. Length measurements were converted to dry mass estimates (mg) using published length-weight equations specific to the fish species or family (FISHBASE).

After measuring the first 50 or so fish, NEON then bulk counts the rest and reports those counts per pass in the table *fsh\_bulkCount*. For example, if 100 Rainbow Trout were collected on the first pass, then *fsh\_bulkCount* would indicate 50 fish with the other 50 indicated by the total count in *fsh\_perFish*. Adding these totals gives the total number of fish per reach per pass per taxon. We used these data to estimate the total population size of each species using the CarleStrub formula in the *removal()* function of the FSA package (CITE). This resulted in estimates of fish abundance per m2. We converted these estimates to fish *size* per m2 by sampling sizes from the fish size measures. To do this, we first converted measures from per\_m2 to 1000\*per\_m2 so that abundance estimates were in integers. We then sampled individual body sizes (mg dry mass) with replacement from the *fsh\_perFish* table relative to the number of individuals estimated from the 3-pass removal. For example, if the *removal()* function estimated 296 individuals of Speckled Dace in a reach, then we sampled 296 body sizes from the Speckled dace body size measurements (at that site/date/reach combination). Since only 50 individuals were measured, that meant that some body sizes are repeated. From this list of body sizes, we obtained a list of counts per body size, which we then converted to body size per m2. These estimates were then combined with macroinvertebrate estimates to generate a list of body sizes (mg dry mass) and their abundance (no/m2) for both fish and macroinvertebrates.