2017 Edamame Coding Ability Scale, Chart 1 I can determine the quality of a shotgun metagenome assembly Pre 85% 15% Post 23% 77% I can evaluate the quality of raw sequencing data Pre 54% 46% Post 12% 88% I can find and move files on a computer using terminal 35% Pre 65% Post 4% 96% I can independently execute the steps of microbial AMPLICON metagenomic analysis Pre 81% 19% Post 15% 85% I can make informed choices for analysis parameters for AMPLICON analysis in mothur Pre 96% 4% Post 4% 96% I can move data from at least one other program into R Pre 31% 69% Post 0% 100% I can search for public datasets relevant to my own project 62% 38% Pre Post 15% 85% I can think through the steps of a sequencing analysis from start to finish Pre 65% 35% 92% Post 8% I can use an R package to analyze data Pre 31% 69% Post 0% 100% I CANNOT process and quality control shotgun metagenome unless someone helps Pre 81% 19% Post 69% 31% I know how to map reads in metagenome analysis Pre 77% 23% Post 23% 77% I understand the limitations of unassembled and assembled shotgun metagenomic data Pre 54% 46% Post 12% 88% I understand what a k-mer is Pre 62% 38% 35% Post 65% 100 50 50 100 Percentage

Strongly Disagree

Disagree

Agree

Response

Strongly Agree