# 2018 Edamame Coding Ability Scale, Chart 1

### I can determine the quality of a shotgun metagenome assembly

| | | |
|---|---|---|
| Pre | 92% | 8% |
| Post | 8% | 92% |

### I can evaluate the quality of raw sequencing data

| | | |
|---|---|---|
| Pre | 65% | 35% |
| Post | 8% | 92% |

### I can find and move files on a computer using terminal

| | | |
|---|---|---|
| Pre | 35% | 65% |
| Post | 4% | 96% |

### I can independently execute the steps of microbial AMPLICON metagenomic analysis

| | | |
|---|---|---|
| Pre | 73% | 27% |
| Post | 12% | 88% |

### I can make informed choices for analysis parameters for AMPLICON analysis in mothur

| | | |
|---|---|---|
| Pre | 96% | 4% |
| Post | 8% | 92% |

### 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

| | | |
|---|---|---|
| Pre | 50% | 50% |
| Post | 0% | 100% |

### I can think through the steps of a sequencing analysis from start to finish

| | | |
|---|---|---|
| Pre | 73% | 27% |
| Post | 4% | 96% |

### I can use an R package to analyze data

| | | |
|---|---|---|
| Pre | 27% | 73% |
| Post | 8% | 92% |

### I CANNOT process and quality control shotgun metagenome unless someone helps

| | | |
|---|---|---|
| Pre | 8% | 92% |
| Post | 78% | 22% |

### I know how to map reads in metagenome analysis

| | | |
|---|---|---|
| Pre | 92% | 8% |
| Post | 17% | 83% |

### I understand the differences between unassembled and assembled shotgun metagenomic data

| | | |
|---|---|---|
| Pre | 77% | 23% |
| Post | 8% | 92% |

### I understand the limitations of unassembled and assembled shotgun metagenomic data

| | | |
|---|---|---|
| Pre | 92% | 8% |
| Post | 12% | 88% |

### I understand what a k−mer is

| | | |
|---|---|---|
| Pre | 62% | 38% |
| Post | 8% | 92% |

Percentage

Response: Strongly Disagree | Disagree | Agree | Strongly Agree