**S3 Table.** Wilcoxon Signed-Ranked Test for Spring 2017 & 2018 300-level biotechnology course matched Pre and Retrospective Pre-/Post-Student Perceptions Bioinformatics Activity Survey\*

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| --- | --- | --- | --- | --- | --- |
| **Item** | **Survey Item:** Strongly agree (5) to strongly disagree (1) | **Pre** Median | **Retro Pre** Median | **Post** Median | **P-value** |
| Scoring Matrix | I can use a sequence scoring matrix to quantitatively compare sequence similarity between two sequences. | 2 | 1 | 5 | <0.0001 |
| BLAST Algorithm | I can describe how the BLAST algorithm finds partial regions of similarly within two sequence records. | 1 | 1 | 4 | <0.0001 |
| Seq Conservation | I know at which level (nucleotide or protein) coding sequences exhibit the most conservation. | 2 | 1 | 4 | <0.0001 |
| NCBI Database | I am confident in my ability to obtain sequence data housed in databases within NCBI. | 4 | 2 | 5 | <0.0001 |
| FASTA Format | I can describe the FASTA file format. | 1 | 1 | 4 | <0.0001 |
| Distance Matrix | I can describe how a neighbor-joining distance matrix is calculated | 1 | 1 | 4 | <0.0001 |
| MSA Generation | I am confident in my ability to generate a multiple sequence alignment (MSA) using provided sequences and ClustalOmega | 1 | 1 | 4 | <0.0001 |
| Phylogram Analysis | I am confident in my ability to analyze a phylogram constructed with the use of sequence data. | 1 | 1 | 4 | <0.0001 |

\*n=25, non-parametric Wicoxon Signed-Ranks Test (two-tailed) with values represented as a median (typical analysis for ordinal data)

\*\* p-value was independently calculated using the pre and retro pre with the post median and was <0.0001 for all tests with the exceptions being the NCBI database (p=0.0013) and Seq Conservation (p=0.0002) questions with the true pre/post.