**S1 Table**. Comparison between *BingleSeq*’s Bulk RNA-Seq pipeline and other similar applications.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Functionality** | ***BingleSeq*** | *DEapp* | *DEBrowser* | *Omics Playground* |
| Filter Low Gene Counts | **✓** | **✓** | **✓** | **✓** |
| Batch-effect Correction | **✓** |  | **✓** | **✓** |
| Implements *DESeq2* | **✓** | **✓** | **✓** | **✓** |
| Implements *EdgeR* | **✓** | **✓** | **✓** | **✓** |
| Implements *limma* | **✓** | **✓** | **✓** | **✓** |
| Additional DE methods |  |  |  | **✓** |
| PCA plot | **✓** | **✓** | **✓** | **✓** |
| Summary Barchart | **✓** |  |  | **✓** |
| MA plot | **✓** |  | **✓** | **✓** |
| Volcano plot | **✓** | **✓** | **✓** | **✓** |
| All to all scatter plot |  |  | **✓** | **✓** |
| Heatmap | **✓** |  | **✓** | **✓** |
| Interquartile Range plot |  | **✓** | **✓** | **✓** |