**Table 4.** Comparison of normalization methods used, including execution time (rounded to nearest five seconds), visualization, and classification rate across all data sets. A ‘\*\*\*’ indicates that the method showed exemplary performance overall, a ‘\*\*’ indicates satisfactory performance overall, and a ‘\*’ indicates some shortcoming in performance compared to other methods. ‘\_’ indicates that the method is not applicable for this type of data. Two variants exist for the Mouse Embryonic Sim Data, but they had negligible differences in execution time.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Category | BASiCS | GRM | Linnorm | SAMstrt | SCnorm | scran | Simple Norm |
| Mouse Embryonic Data (sec) | 230 | 35 | <5 | <5 | 760 | <5 | <5 |
| Mouse Lung Data (sec) | 510 | 60 | <5 | 5 | 1180 | <5 | <5 |
| Mouse Embryonic Sim Data (sec) | 110 | 15 | <5 | <5 | 110 | <5 | <5 |
| Human Embryonic Data (sec) | \_ | \_ | <5 | \_ | 370 | <5 | <5 |
| Classification (Spike-In Genes) | \*\*\* | \* | \*\* | \* | \*\*\* | \*\* | \*\* |
| Visualization (Spike-In Genes) | \*\* | \* | \*\* | \* | \*\* | \*\* | \*\* |
| Classification (Non-Spike-In) | \_ | \_ | \* | \_ | \*\* | \*\* | \*\* |
| Visualization (Non-Spike-In) | \_ | \_ | \* | \_ | \*\* | \* | \*\* |