

New algorithm for single-cell RNA-seq analysis

March 22, 2018 – The sequencing of RNA from individual cells is an increasingly used, powerful method for studying cellular heterogeneity. However, the analysis of single-cell RNA-seq is limited due to the high technical variability between experiments and the inability to perform true technical replicates on the same cell. David Severson and colleagues from the labs of Benjamin Schuster-Böckler and Xin Lu have developed a new algorithm, BEARsc, published in *Nature Communications*, which uses simulation to improve the biological interpretation of single-cell RNA-seq experiments.