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Presentation Title: RIA: a novel Regression-based Imputation Approach for single-cell RNA sequencing
Research focus: single cell, scRNA-seq, imputation, sequencing
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Abstract:

Advances in single-cell technologies have shifted genomics research from the analysis of bulk tissues toward a comprehensive characterization of individual cells. This holds enormous opportunities for both basic biology and clinical research. As such, identification and characterization of shortlived progenitors, stem cells, cancer stem cells, or circulating tumor cells are essential to better understand both normal and diseased tissue biology. However, quantifying gene expression in each cell remains a significant challenge due to the low amount of mRNA available within individual cells. This leads to the excess amount of zero counts caused by dropout events. Here we introduce RIA, a regression-based approach, that is able to reliably recover the missing values in single-cell data and thus can effectively improve the performance of downstream analyses. We compare RIA with state-of-the-art methods using five scRNA-seq datasets with a total of 3,535 cells. In each dataset analyzed, RIA outperforms existing approaches in improving the identification of cell populations while preserving the biological landscape. We also demonstrate that RIA is able to infer temporal trajectories of embryonic development stages.