Screw: tools for building reproducible single-cell epigenomics workflows

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Background: Single-cell DNA Methylation Sequencing

DNA methylation is a heritable epigenetic mark that shows a strong correlation with transcriptional activity. The gold standard for detecting DNA methylation is whole genome bisulfite sequencing (WGBS). Recently, WGBS has been performed successfully on single cells (SC-WGBS) [@Schwartzman2015]. The resulting data represents a fundamental shift in the capacity to measure and interpret DNA methylation, especially in rare cell types and contexts where subtle cell-to-cell heterogeneity is crucial, such as in stem cells or cancer.

The mechanism of 5-Aza resistance, and indeed the details of its action in patient bone marrow, has not been clearly determined. We have embarked on a study of purified CD34+CD38-Lin- progenitor cells from paired bone marrow aspirates drawn from patients with myeloid malignancies before and after 5-Aza treatment. We will be investigating both patients who developed resistance, and those for whom therapy was still effective. In this poster, we discuss results from the first patient in this series.

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