

optima: an open-source R package for the Tapestri platform for integrative single cell multiomics data analysis

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Abstract

The Tapestri platform offers DNA and protein analysis at the single cell level. Integrating both types of data is beneficial for studying multiple cell populations in heterogeneous microenvironments, such as tumor tissues. Here, we present *optima*, an R package for the processing and analysis of data generated from the Tapestri platform. This package provides streamlined functionality for raw data filtering, integration, normalization, transformation, and visualization. Insights gained from the *optima* package help users to identify unique cell populations and uncover surface protein expression patterns. The results generated by *optima* help researchers elucidate dynamic changes at the single cell level in heterogeneous microenvironments. This package is available in Github: <https://github.com/rachelgriffard/optima>