Unchaining the full potential of public single-cell RNA-Seq data for drug discovery

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Abstract
Single-Cell RNA-Seq technologies have transformed our understanding of health and disease. This is reflected in the recent exponential increase of publicly available single-cell RNA-Seq studies. As for other types of public data, studies deposited in public repositories are heterogeneous on many levels, which hinders the simple reuse of this data. To overcome this limitation and allow multi-study and cross-study analyses, we expanded the functionalities of our state-of-the-art GENEVESTIGATOR® knowledge base and analysis tool. Here, we present our single-cell RNA-Seq curation pipeline and demonstrate how to easily analyze high-quality public single-cell RNA-seq data in GENEVESTIGATOR® across different biological contexts such as diseases, drug treatments, tissues, cancers, cell lines, or genotypes. Our tool is helping scientists to unveil exciting new data and speed up drugs discovery processes.

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