scOrange: Single-cell Data Mining for Everyone

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Single-cell RNA sequencing (scRNA-seq) assays pose exciting challenges for computational analysis, visualization and modeling^[1]. We present **scOrange**, enabling data analysis to a broader range of biomedical researchers. It uses visual programming to construct intuitive workflows that deliver fairness, interoperability, accessibility and resuability principles to the single-cell community.



Full interactivity. Users can visually connect hundreds of interoperable **widgets** to construct reusable workflows, designed with emphasis on reproducibility. scOrange assumes no programming knowledge and is accessible to a broader audience than programming language-specific packages^[2].



Built-in templates. scOrange

comes with example datasets and predefined workflows, based on literature-supported methods and parameters.



singlecell.biolab.si



Over 100 widgets. Together with Orange Data Mining^[3], scOrange widgets implement data manipulation, machine learning and visualization tasks.



Projections. Run t-SNE, PCA, MDS to visualize cells in a 2D plane.



Active community. Video tutorials, blogs and docs enable a quick dive straight into action.

Batch effect removal.

Use canonical correlation analysis to remove unwanted, dataset-specific variation^[4].

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Clustering. Identify known cell populations or discover previously un-known subpopulations.

discovery. Validate the clustering with known markers or use statistical tests to find new ones.

Moreover, characterize cell subpopulations through analysis of differentially expressed genes and gene set enrichment, find candidate marker genes, and predict cell types or cell cycle stage^[5].

Support for common data formats (text, 10X, Loom, Excel, ...). Fully-reproducible, standardized analyses without a single line of code. Custom extensions possible through open source.

Visit us for a live demo!

References. [1] DA Jaitin, et al. Massively parallel single-cell RNA-seq for marker-free decomposition of tissues into cell types. Science 343, 6172: 776-779 (2014). [2] Alexander WF, Angerer P, and Theis FJ. SCANPY: large-scale single-cell gene expression data analysis Genome Biology 19.1, 15 (2018). [3] Demšar J, et al. Orange: data mining toolbox in Python. The Journal of Machine Learning Research 14.1, 2349-2353 (2013). [4] Andrew B, et al. Integrating single-cell transcriptomic data across different conditions, technologies, and species. Nature Biotechnology 36.5, 411 (2018). [5] Antonio S, et al. Computational assignment of cell-cycle stage from single-cell transcriptome data. Methods 85, 54-61 (2015).