

Interactive exploration of single-cell trajectories with Cell Journey

Damian Panas^{*a,b}, Marcin Tabaka^{#a,b}

^aInternational Centre for Translational Eye Research, Skierniewicka 10A, Warsaw, 01-230, Poland

^bInstitute of Physical Chemistry, Polish Academy of Sciences, Kasprzaka 44/52, Warsaw, 01-224, Poland

^{*}corresponding author email: mtabaka@ichf.edu.pl

[#]Presenting author

1. Main Text

High-throughput single-cell sequencing enables precise reconstruction of cell state differentiation pathways. Existing visualization approaches are constrained mainly to two-dimensional embeddings, which fail to capture the complexity of branched or multipartite transition topologies. Cell Journey is an open-source tool that overcomes this limitation. The software allows for interactive exploration and analysis of single-cell trajectories.

2. Methods and results

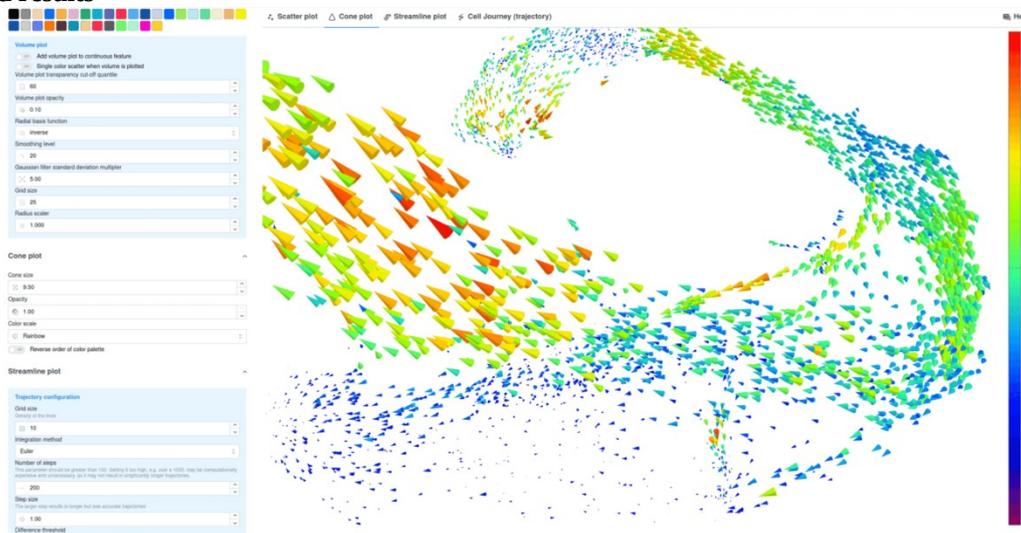


Fig. 1. A part of the interface of the Cell Journey. The software has a main window on the right and a drop-down panel on the left.

3. Acknowledgement

D.P. and M.T. are supported by the International Centre for Translational Eye Research (FENG.02.01-IP.05-T005/23) project, which is carried out within the International Research Agendas Program of the Foundation for Polish Science, co-financed by the European Union under the European Regional Development Fund; and grant funded by National Science Center, Poland: the Sonata Bis 12 grant 2022/46/E/NZ2/0037 (M.T.).

4. References

- [1] Rutkowski P, Tabaka M. Ocelli: an open-source tool for the analysis and visualization of developmental multimodal single-cell data, *NAR Genomics and Bioinformatics* 7(2), 2025.
- [2] La Manno G, Soldatov R, Zeisel A *et al.* RNA velocity of single cells, *Nature* 560, 2018.