

1 Methods

1.1 Obtaining sequencing data

We obtained single-cell sequencing data. [3] The pre-processed gene counts are accessible through GEO using accession no. GSE147082. To obtain the spliced-unsplliced ratios required for cell velocity calculation, we retrieved the full sequences from SRA using accession no. PRJNA612966.

1.2 RNA velocity calculation

The data was retrieved as FASTA files. We then used `kallisto|bustools` to compute the RNA velocity using the method developed by LaManno et al. [1,2].

References

- [1] Gioele La Manno, Ruslan Soldatov, Amit Zeisel, Emelie Braun, Hannah Hochgerner, Viktor Petukhov, Katja Lidschreiber, Maria E Kastriti, Peter Lönnerberg, Alessandro Furlan, et al. Rna velocity of single cells. *Nature*, 560(7719):494–498, 2018.
- [2] Kyung Hoi (Joseph) Min and A. Sina Boeshaghi. Pre-processing and rna velocity analysis of single-cell rna-seq data with kallisto—bustools, 2021. Accessed Nov. 11, 2023. https://www.kallistobus.tools/tutorials/kb_velocity/python/kb_velocity.
- [3] Susan Olalekan, Bingqing Xie, Rebecca Back, Heather Eckart, and Anindita Basu. Characterizing the tumor microenvironment of metastatic ovarian cancer by single-cell transcriptomics. *Cell reports*, 35(8), 2021.