

Integrating single-cell multiomics data

Dilyara Grafova, Karina Díaz-Barba, Martijn van der Werff, Roya Charehbeiklou
Supervisors: Dan Kaptijn, Maryna Korshevniuk, Monique van der Wijst, Roy Oelen



Background



- Opportunity to analyse cell-to-cell variability
- Multiomics data can provide a broader understanding of cellular processes

Goal:

To see if there is an effect on gene regulatory network (GRN) reconstruction using multiomics data with/without prior integration

Results

- 4% of cells were filtered out during QC for scRNA-seq
- After performing QC on scATAC-seq data 15% of cells were left out
- Intersection of **scRNA** and **scATAC** resulted in **9,763** barcodes

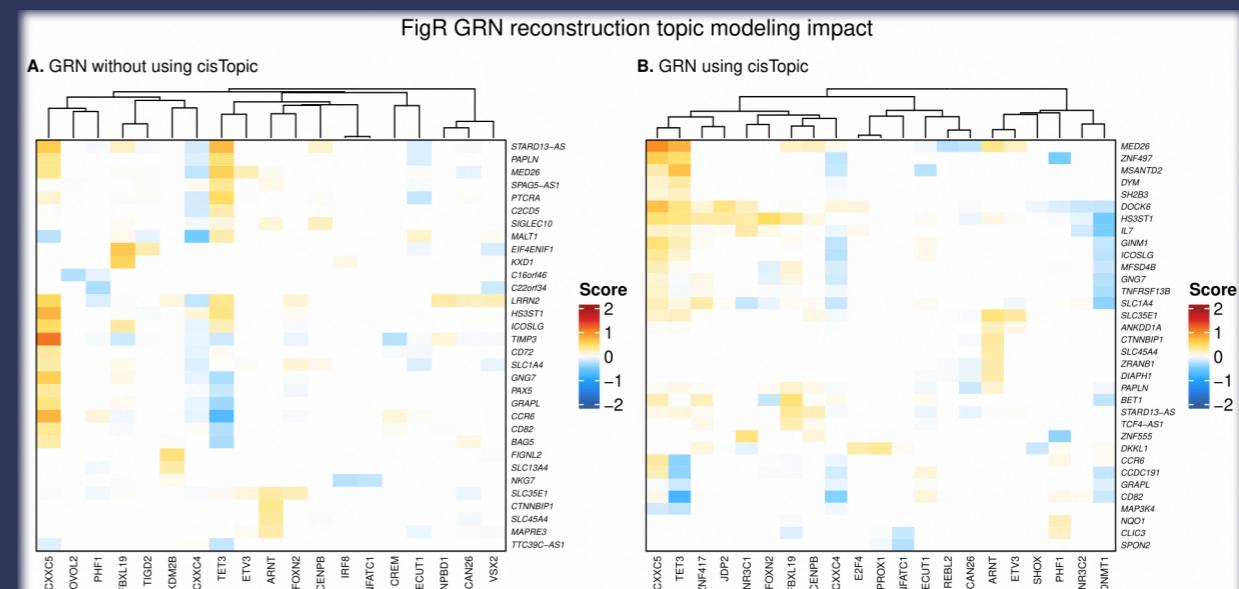


Fig.1 Comparison of running FigR with and without topic modelling
• 32 DORCs and 17 TFs • 34 DORCs and 21 TFs

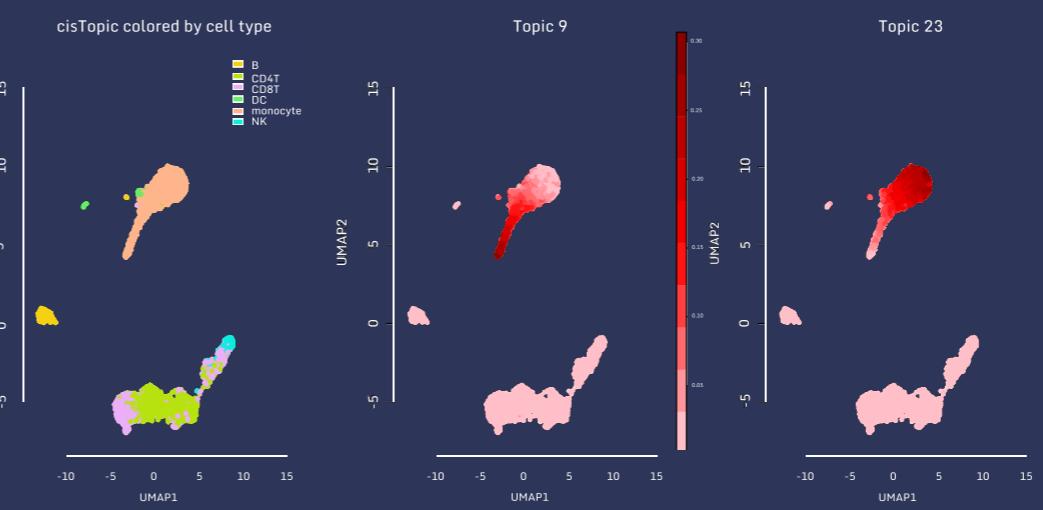


Fig.2 Topic modelling results for FigR

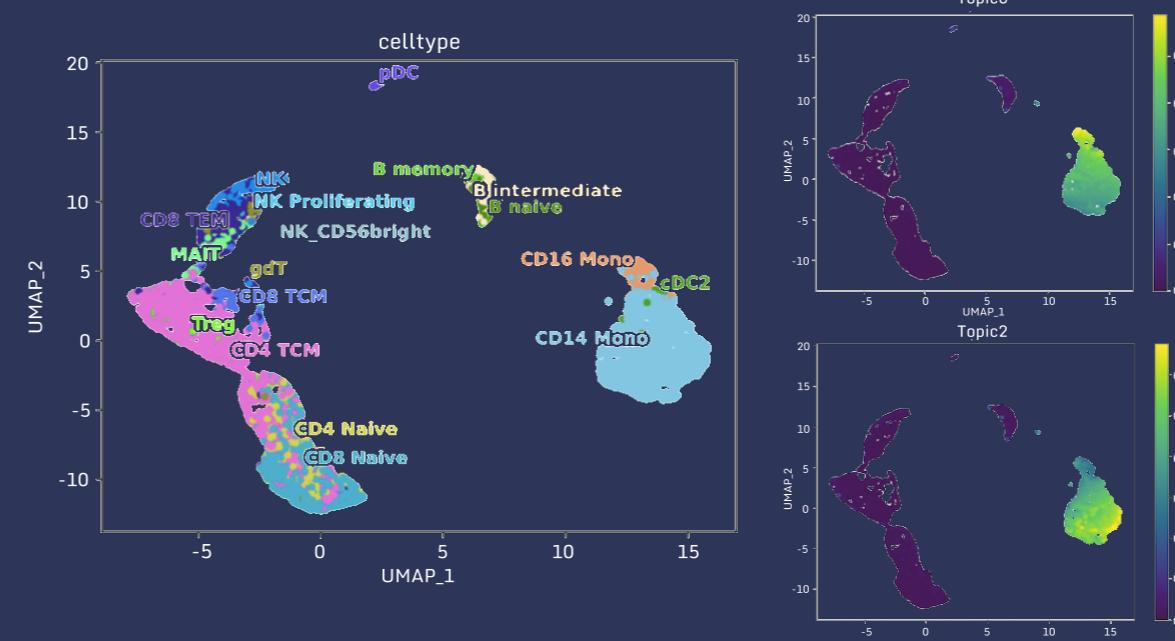


Fig.3 Topic modelling results for SCENIC+

- 9,763 intersections were also used for data integration using Portal, a UMAP similar to SCENIC+ was generated

Research outcome

- Advantageous** effect of creating **cisTopic** object in order to reconstruct GRN in FigR
- Possibility of data integration, but challenges appear in the process of GRN reconstruction

What's next?

- Since we derived top TF-DORC* associations, further research can include **pathway analysis**.
- We may be able to run the analysis for certain topic to see which particular cell type is involved.

* TF - Transcription factor

DORC - Domain of regulatory chromatin

References

- Brombacher, E., Hackenberg, M., Kreutz, C., Binder, H., & Treppner, M. (2022). The performance of deep generative models for learning joint embeddings of single-cell multi-omics data. *Frontiers in Molecular Biosciences*, 9. <https://doi.org/10.3389/fmolb.2022.962644>
- Stuart, T., Butler, A., Hoffman, P., Hafemeister, C., Papalexi, E., Mauck, W. M., Hao, Y., Stoeckius, M., Smibert, P., & Satija, R. (2019). Comprehensive integration of single-cell data. *Cell*, 177(7). <https://doi.org/10.1016/j.cell.2019.05.031>
- González-Blas, C. B., De Winter, S., Hulselmans, G., Hecker, N., Matetovici, I., Christiaens, V., Poovathingal, S., Wouters, J., Albar, S., & Aerts, S. (2022). Scenic+: Single-Cell Multiomic Inference of Enhancers and Gene Regulatory Networks. <https://doi.org/10.1101/2022.08.19.504505>

