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Comparative visual analytics for multi-modal single-cell and spatial omics data

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Stellingen behorende bij het proefschrift getiteld

Comparative Visual Analytics for Multi-Modal Single-Cell and Spatial Omics Data

1. Achieving interactive comparative analysis of single-cell transcriptomic data often requires aggregation from cell-level measurements to cluster-level averages (Thesis Chapter 2).

2. Organizing data according to domain-specific conventions (e.g., phylogenetic tree or cell-type colors) can support discovery more effectively than purely algorithmic arrangements, even when the latter are theoretically optimal (Thesis Chapter 3).

3. Interactive spatial gradient exploration enables meaningful cross-dataset comparison despite incomplete gene overlap (Thesis Chapter 4).

4. A modular visual analytics platform suits comparative brain atlas research better than separate single-purpose tools, as new modalities can be integrated without reworking the workflow (Thesis Chapter 5).

5. Linked coordinated views enable pattern discovery in comparative analysis that disconnected single views cannot reveal (Field-specific).

6. Extending multi-species analysis from pairwise to many-species comparisons requires fundamentally different visualization paradigms, not merely scaled versions of pairwise interfaces (Field-specific).

7. On-the-fly computation tightly coupled to visualization supports exploratory analysis better than precomputed outputs inspected afterward (Field-specific).

8. Exploratory visual analysis tools should support the transformation of analytical results into forms suitable for communication (Field-specific).

9. Scientific progress is sustained not by talent alone, but by consistency during periods of uncertainty (General).

10. Well-being is a precondition for creativity, not a reward after productivity (General).