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

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SUMMARY

This thesis develops an interactive visual analytics system for the comparative analysis of multi-species brain atlases. Advances in single-cell and spatial transcriptomics have enabled the systematic study of gene expression and cell-type organization across species, but the resulting datasets are large, heterogeneous, and difficult to interpret using static, batch-oriented workflows. The central objective of this thesis is to design multiple interactive modalities within a unified analytical system that support exploratory, cross-species analysis of transcriptomic and spatial data.

The work is grounded in close collaboration with domain experts and follows a design study methodology. It first characterizes the analytical challenges of comparative brain atlas research, including inconsistent gene coverage, divergent cell-type taxonomies, heterogeneous experimental platforms, and continuous spatial organization that is poorly captured by discrete clustering. These challenges motivate interactive approaches that enable rapid hypothesis generation, iterative refinement, and visual validation of computational results.

[Chapter 2](#) introduces Cytosplore Simian Viewer, a system for pairwise cross-species comparison of single-cell transcriptomic datasets. Through linked views of cell-type hierarchies, gene expression profiles, and species-specific distributions, the system supports interactive identification of conserved and divergent patterns. Validation on primate cortex data demonstrates that interactive analysis can reproduce findings from large comparative studies while enabling additional exploratory insights.

[Chapter 3](#) extends the comparative scope to broader phylogenies with Cytosplore EvoViewer. By integrating evolutionary relationships directly into the visual workflow, the system enables phylogeny-aware exploration of conservation and divergence across multiple species. Interactive branch-based queries support the identification of lineage-specific patterns. Expert evaluation confirms the analytical value of this approach while highlighting scalability limitations related to in-memory data processing.

[Chapter 4](#) presents Cytosplore Gradient Surfer, an interactive method for comparing spatial transcriptomics datasets. Users can probe spatial directions within a reference dataset, identify gradient-associated genes, and project these gradients onto other datasets through a shared feature space. This approach enables cross-dataset comparison even when tissue geometry and gene panels differ. Validation across multiple spatial modalities demonstrates recovery of known biological gradients and robustness to rotation, subsampling, and partial gene overlap.

[Chapter 5](#) introduces Cytosplore Viewer, a modular system that unifies transcriptomic, evolutionary, spatial, and regulatory components within a single interactive environment. By connecting gene expression, phylogenetic context, spatial organization, and chromatin accessibility through consistent interaction principles, the system enables researchers to iteratively refine interpretations while maintaining biological context.

Together, the contributions of this thesis demonstrate that interactive visual analytics can substantially enhance the interpretability, flexibility, and comparative power of large-scale brain atlas research. The work also identifies directions for future development, including scalable out-of-core data management, true multi-species alignment beyond pairwise workflows, automated spatial registration, broader user evaluation, and improved spatial projection and regulatory linking strategies.