Observing Genomics and Phenotypical Patterns in the Developing Mouse Brain

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Understanding the development of mammalian brains is one of the most intriguing topics in biology. Since the underlying genomics is known to have the most impact on the brain development, it is critical to characterize the gene expression patterns over both space and time. To achieve this goal, in 2013, we created a visual analytic system based on the Allen Developing Mouse Brain Atlas, which included expression data for thousands of genes with spatial structural annotations over multiple developmental stages in the mouse brain. In that prototypical system, we designed the Gene Expression Flow Matrix (GEFM) and the Hierarchical Orientation Structural Tree (HOS-Tree) to visualize temporal patterns in a hierarchy imposed on embedded physical space. However, although the earlier system provided valuable pattern observations, it had two noticeable limitations: the pattern-mining process was not data-driven, and the color encoding of spatial gradients could lead to inaccurate results. To improve the robustness, we applied mutual information corrected K-Means clustering to explore the inherent naturally occurring temporal patterns. Further, to mitigate the inherent uncertainty, we use the union of descendant structures to predict preferred developmental orientations. Additionally, we report preliminary results that pertain to distinct and salient developmental patterns, which were not observable with the previous prototype. In essence, we believe that our new offering could be another step in creating viable and useful visual analytic tools for exploring one of the most enduring and fascinating products of evolution, the mammalian brain.