Mouse-Human Hybrids

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Summary:

A key goal in the analysis of proteomics data is to compare chemical modifications occurring on different residues in a protein sequence between human and animal models to assess the suitability of animal models for drug development. Differences in modification patterns between mouse and human protein variants may also indicate evolutionary pressures to preserve functional regions distributed along the protein sequence. However, comparing and contrasting the many possible patterns of modifications is a significant challenge in visualizing proteomics data. For this year's Bio+MedVis Protein Beasts Challenge, we propose an exploratory interface for pattern discovery. Results from data-driven pattern detectors are displayed using an animation metaphor that is suitable for both comparing and contrasting tasks. In addition, we propose a novel, compact steel-drum like pattern selector component that abstracts from the details of the analysis method and focuses instead on the more playful aspects of an exploratory data analysis that favors instant gratification.