Bio+MedVis Challenge 2022 @ IEEE VIS

Mouse-Human Hybrids

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We propose a data exploration application that allows for a quick inspection of spatial pattern as well as contrasts between mouse and human version of proteins. Our interface integrates a larger number of data driven pattern detectors by automatically computing candidate pattern that are displayed in a consistent manner using animations. Our solution minimizes visual search strategies to quickly explore the structure of protein modifications.

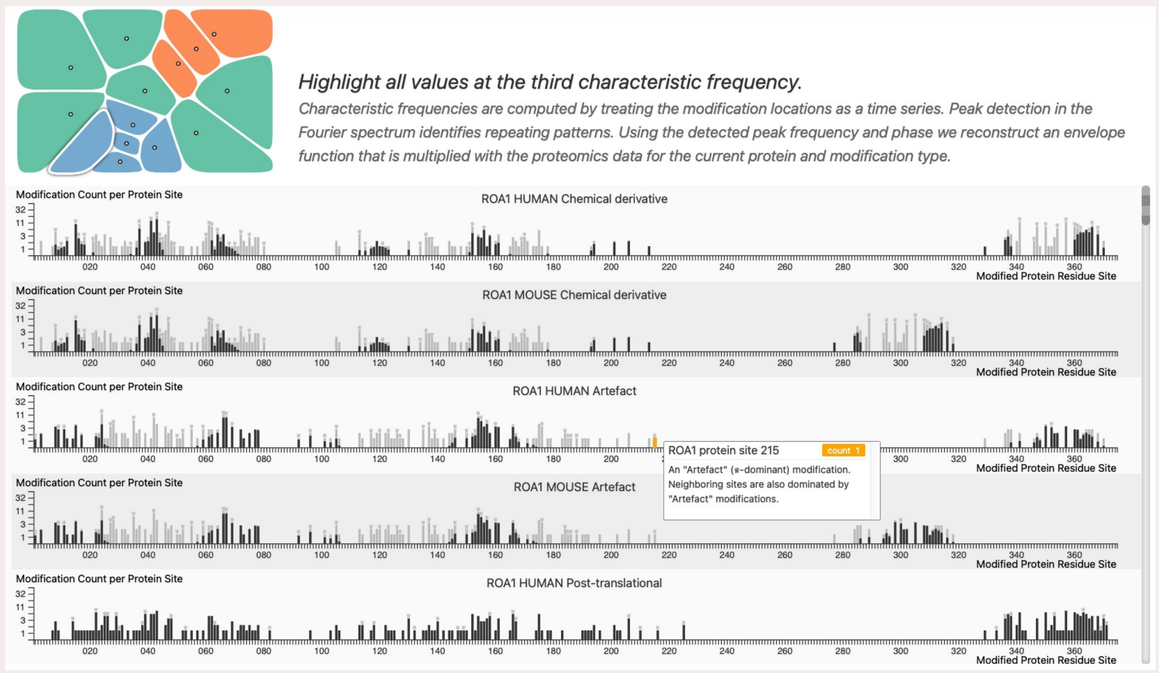


Fig. 1. Control surface and bar-plot animation facilitate identification and comparison of residues with high occurrences of chemical modifications for human and mouse models.

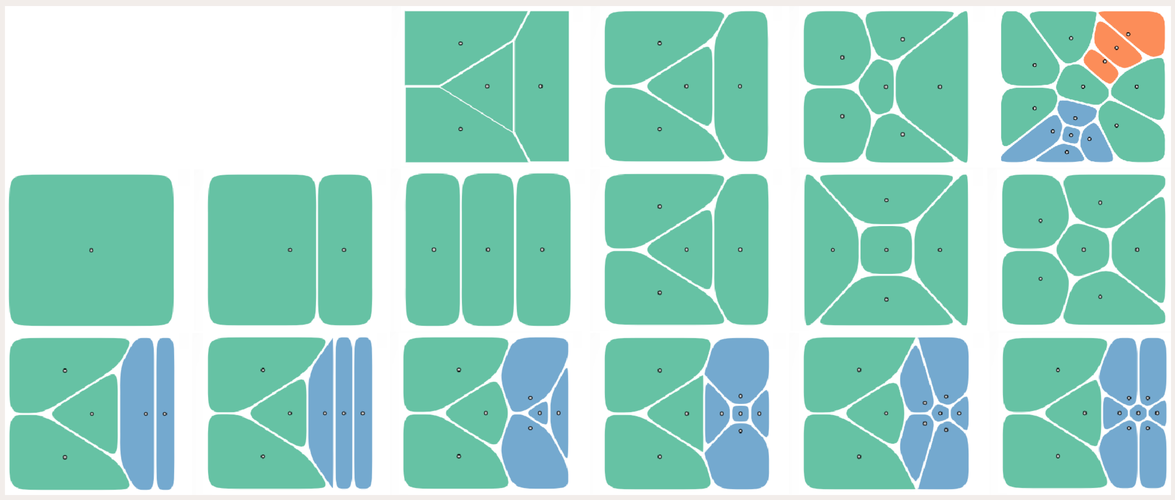
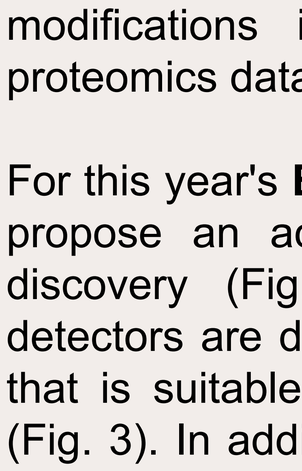


Fig. 2. Control interface examples. The top row shows on the left a Voronoi tessellation (blue zones) of a square space with three control points placed around a central point (black circles). Following images show a smoothed tessellation, a smoothed tessellation with a larger weight of the right-most control point and, on the far right, the more complex arrangement of 14 control zones used in figure 1. The middle row shows six level-0 tessellations (zone numbers one to six). In the bottom row one level-0 zone is sub-divided further into two to seven zones (orange zones).

ABSTRACT

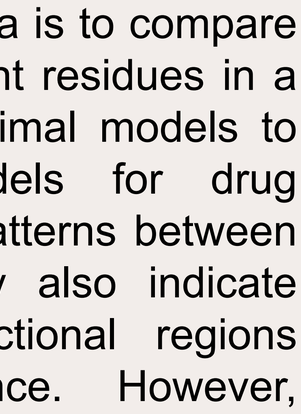
A key goal in the analysis of proteomics data is to compare chemical modifications occurring on different residues in a protein sequence between human and animal models to assess the suitability of animal models for drug development. Differences in modification patterns between mouse and human protein 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 accessible exploratory interface for pattern discovery (Fig. 1). Results from data driven pattern detectors are displayed using a single animation metaphor that is suitable for both comparing and contrasting tasks (Fig. 3). In addition, we propose a compact steel-drum like pattern selector component (Fig. 2) 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.



Sequence of animations (top to bottom) used to highlight a repeated pattern (bottom).

Easing generates intermediate frames for a cyclic animation at 0.5Hz.



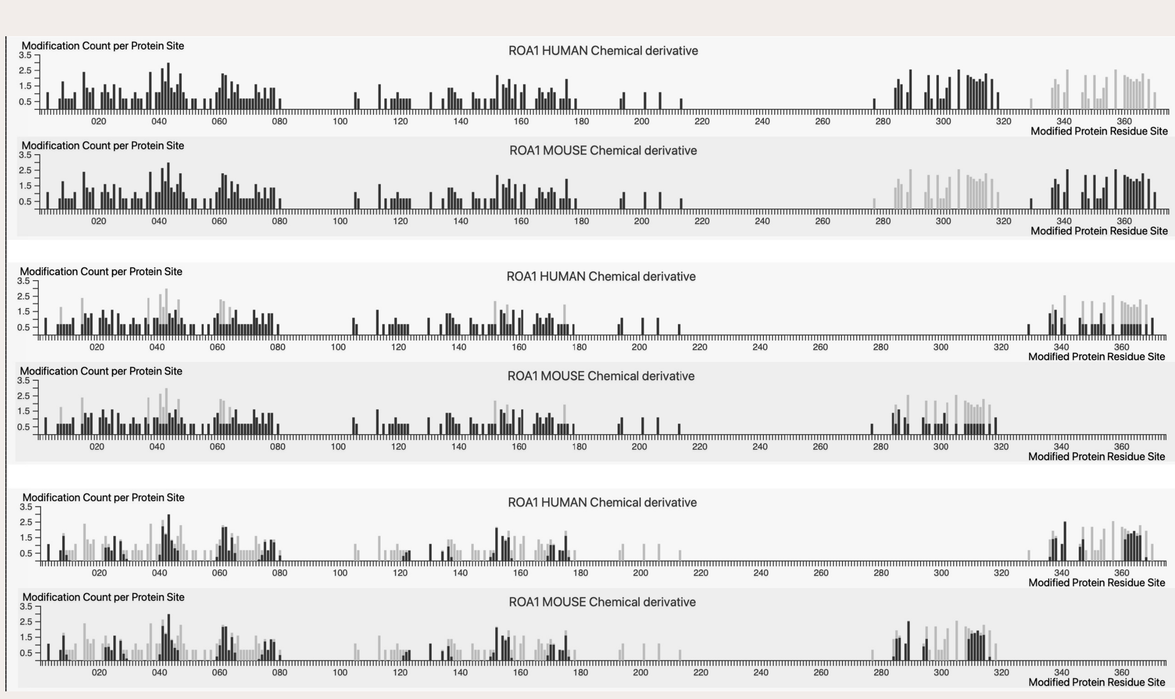


Fig. 3: Example (static) pattern visualized with our application for pairs of mouse/human chemical derivative modifications in the ROA1 protein sequence. The top pair of plots show in lighter gray the baseline human (top) and respectively mouse (bottom) modification data in a mouse-human hybrid visualization. In darker gray the paired mouse / human data are displayed. Note, that in the application the darker bars are animated highlighting the additional contribution of the other species in the hybrid display. The middle pair of bar plots show the extreme value quantile pattern. The bottom row highlights a one of the frequency analysis pattern.

Try exploring our interface yourself!

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