

colleagues refine support vector machine learning of biomarkers by modifying the distance metric comparing expression profiles based on reliable biomarkers reported in the literature. Webb-Robertson and colleagues use a Bayesian framework to integrate proteomic and metabolomic data for improved detection of pathogens. Bush, Dudek, and Ritchie address the combinatoric explosion in GWAS when looking for combinations of SNPs linked to a disease by focusing analysis on SNPs related to pathways or genes linked to the disease under study. Pan and colleagues use local phylogenetic alignments in GWAS to guide the choice of regions under study.

These papers demonstrate all aspects of the focus of this PSB session. While it is very early in the era of knowledge-driven analysis in the biomedical sciences, these papers show that difficult problems are beginning to be solved by new approaches that rely on data integration. These approaches include both tools for linking diverse data across molecular domains and species and methods that leverage prior knowledge to provide new insights into biology. As our data resources continue to grow exponentially, such methods will grow in importance and should provide ever greater insight.

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