Early detection is critical in disease control and prevention. Biomarkers provide valuable information about the status of a cell at any given time point. Biomarker research has benefited from recent advances in technologies such as gene expression microarrays, and more recently, proteomics. The long-term translational research goal is that if drugs can be targeted to specific tissues in the body, then dosage can be altered to achieve the desired effect while minimizing side effects such as toxicity. Motivated by specific problems involving such high throughput data, I have developed computer-intensive statistical methods based on nonparametric and semiparametric mixture model assumptions for real-time analysis in the context of biomarker discovery. Most biomarker-discovery projects aim at identifying features in the biomarker profiles (gene expression, phage, SAGE, mass spectrometry proteins) that distinguish cancers from normals, between different stages of disease development, or between experimental conditions (such as different treatment arms or different tissue types). Novel statistical methodology development will be highlighted with direct applications to cancer research challenges that address our long term translational goal.