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High-performance Diagnostics and Biomarker Discovery in Translational Bioinformatics  

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Abstract  
Although serum proteomics demonstrates and exciting promise in the diagnosis of complex diseases, it is still far from being routinely used in clinical practice because of its relatively low diagnostic accuracy and poor data reproducibility. In this study, we present a novel profile-biomarker diagnosis technology to accelerate it into being routinely used in clinical practice while studies on data reproducibility are underway by inventing a novel biomarker discovery technique: Multi-ResoluTion-test (MRT-test) by extending our method. The MRT-test can separate different phenotypes spatially for proteomics and microarray data with few biomarkers. Finally, we develop a novel bottom-up subnetwork marker identification algorithm: network marker synthesis (NMS) by walking from gene markers to network markers to overcome the weakness of the existing subnetwork identification methods. Our work suggests a profile biomarker alternative to accelerate proteomics and microarray technologies into a clinical routine, demonstrates the linear separability of microarray and proteomics data, and has positive impacts on ‘omics’ data analysis in translational bioinformatics.