Current Issues in Biomedical Research

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Abstract

The advent of omics techniques, such as microarrays and mass spectrometry of metabolomics and proteomics, and their generated data avalanche has brought in an added level of complexity to biomedical research: mining massively heterogeneous data for biological significance. Two major issues have become the source of "toxic assets" in biomedical research; the first is the researchers' underestimation (or lack of awareness) of populational heterogeneity, and the other is the use of unsuitable analytical bioinformatic paradigms in dealing with heterogeneous data. Consequently, we are still struggling with many standing issues such as disease definition and its molecular boundaries, class discovery (i.e., subtyping of disease), early detection, susceptibility to drug side effects, omics biomarkers discovery, specimen profiling (from genetic, proteomic, metabolomic…etc), sorting out of clonal from non-expanded mutations, genetic versus epigenetic driving events, post-treatment assessment, and figuring out the primary origin of some cancers.

Methods using statistical averaging have their limitations since they are unsuitable for the analysis of heterogeneity; they hide intrapopulational diversity and homogenizes otherwise heterogeneous subpopulations. Many researchers are unaware of alternative methods of analysis that take into account individual variations, and consequently there is a tremendous waste of resources and meaningless interpretation of data. In my presentation, I will outline a systems biology solution through the application of parsimony phylogenetic analysis. Maximum parsimony provides a data-based modeling paradigm that will enable a priori stratification of the study cohort(s) in clinical trials, and permits the assessment of early diagnosis, prognosis, and treatment efficacy within each stratum.