

Biomarkers in the age of integromics

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Despite the rapid technological advances in the omics high throughput data generation, mining the data biomarkers or biological significance remain challenging. This is attributed to the lack of adequate analytical tools that take into consideration the biological heterogeneity, and to the confusion stemming from the imposition of a pathology-type immunohistochemical (IHC) biomarker concept on omics data. In most cases, the characteristics of the IHC biomarkers are not compatible with and cannot be compared to those from omics datasets. An omics biomarker cannot be assigned and validated without prior modeling and subtyping of the disease to reveal the extent of its heterogeneity, ontogenic classes, and omics' clonal aberrations (driver changes) underlying its subtypes and pathways' complexity.

In the age of integromics, a systems biology method such as parsimony phylogenetic analysis is better suited for data analysis, where disease modeling and the unraveling of clonal from non-expanded mutations should precede biomarker delineation. The analytical paradigm is based on phylogenetic principles, which aim to identify groups of patients (clades) that share clonal aberrations, and models these clades into a tree-like diagram termed cladogram. The cladogram is our dynamic tool of disease modeling; it spans a hierarchical arrangement of the normal, the transitional (at risk), and the diseased phenotypes. It offers a multidimensional systematic approach that is dynamic and highly predictive, and permits the recognition of biomarkers at various levels of the hierarchical classification--within and between clades. The universality of the data parsing approach offers a suitable platform for omics data integration and biomarkers discovery.

Biography

Hakima Amri holds a Ph.D. in Biochemistry and MS in Reproductive Biology from Pierre and Marie Curie University, Paris, France. After completing her post-doctoral training in Molecular Endocrinology, she joined the department of Biochemistry and Cellular and Molecular Biology at Georgetown University to research natural therapeutics for cancer. Dr. Amri's background in developmental biology and her interest and work in cancer research led to the creative application of phylogenetics to mutation-based diseases, such as cancer. This multi-disciplinary background provides Dr. Amri with a profound understanding of the disease biochemical pathways and the limitations facing biomedical research. Most recently, she has been advocating the application of phylogenetics analysis to high-throughput omics data. Dr. Amri shows that parsimony phylogenetics is a multidimensional dynamic analytical tool that is useful for disease modeling, profiling, and subtyping as well as biomarker discovery.