

## MULTIGENIC DISSECTION AND PROGNOSTIC MODELING OF COMPLEX TRAITS

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Empowered by the new tools emerged from the Human Genome Project and by its genome-wide perspective, today genetic research is shifting its focus from the traditional high-penetrance/low-incidence diseases to the far-more challenging low-penetrance/high incidence ones. This shift holds the promise to uncover the genetic bases of traits shared by large portions of the population and to change the way in which medical practice is able forecast, prevent and manage chronic and late-onset diseases. This new perspective, however, challenges traditional genetic methods and require the development of novel design and analysis techniques, able to tackle complex phenotypes, epistatic interactions, and multigenic traits. This poster will describe these emerging methods to design genomic studies and analyze their results using two examples: a late-onset disease – stroke – and a chronic disease – asthma. In particular, it will describe the novel biomedical informatics methods required for the design and analysis of a study to identify the complex genomic profile underpinning the risk of stroke in sickle cell anemia patients and the integration of multiple genes to track down the genomic profile of adult-onset asthma. It will also describe the novel mechanism for sharing and distributing genomic data using as an example the Human Variation Omnibus, a comprehensive genome/phenome database under development at Harvard Medical School.

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