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Shifting the paradigm for genetic sample resources

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The current paradigm for biosample collection and genotyping is two-phased: Sample collection and storage, followed by sample retrieval and genotyping. Quite often the second phase is months or years after sample collection, if it occurs at all. This practice is conservative, in that it avoids genotyping expense up front, but at a cost of incurring huge delays in access to data. Furthermore, costs of storing, retrieving and prepping samples prior to genotyping are significant. For these and other technological reasons, we advocate a paradigm in which the genotypic data is generated immediately, upon sample collection, which now places an emphasis on data storage, access, and analysis.

Biography

J Claiborne Stephens has a double major in zoology and mathematics from Duke University preceded by a PhD in Genetics from the University of Georgia, where he specialized in theoretical population genetics. He was fortunate in having postdoctoral training with Bruce Weir at NCSU and subsequently with Masatoshi Nei at UTHSC-H, where his interests began to shift from theory to data analysis, and in particular to the analysis of human molecular genetic data. This pursuit ultimately lead to stints at the Yale-HHMI Human Gene Mapping Library and NCI. As the transformative potential of human genetic research became increasingly more apparent, he made the leap into industry in 1999, first at Genaissance Pharmaceuticals, then Motif BioSciences, and most recently Pfizer. In industry he is continuing his efforts to leverage the application of industrial-scale genomics to human health and drug development.

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