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Omics challenges and unmet translational needs

Clearly, high throughput omics, and related technologies, are advancing quickly. So too are the many challenges to efficient analysis and interpretation of data generated. This issue presents cutting edge research and unmet translational needs related to these challenges. Marcus, et al., address the scarcity of standardized sequencing procedures, data formats and quality management in 'Standardization and quality management in next-generation sequencing. They present current standardization and quality management efforts in documentation and guidelines for validating sequencing workflows as well as the development and implementation of quality metrics for upstream processes and downstream pipeline data management. These standardization issues must be addressed to ensure reliable results and fast processing required for next-generation based clinical diagnostics. Chia, et. al. outline the need for multi-omics data integration and accompanying challenges'. In 'Metabolic modeling with big data and the gut microbiome', they present current limitations to capturing the full potential of omics-based approaches. Calling for a new paradigm for metabolic modeling, Chia et al., offer a framework for characterizing the ecology of the gut microbiome based on a model of metabolic networking. Maher, et al. also address the challenges in understanding complex omics data. They report on the recent Keystone Symposium, 'Human nutrition, environment and health', the first-of-its-kind global meeting on state of the art research in nutritional science, with a focus on personalized nutrition. The main topics were 1) the interaction between human genome, diet and environment; 2) translational models for human nutrition; 3) human nutritional and lifestyle interventions; 4) capturing and monitoring human individuality; 5) nutrigenomics and systems nutrition; 6) Nutrition 2.0 - translational into solution for human health; and 7) global nutrition and sustainability. Finally, Messner et al., present results from the first two rounds of a four round Delphi policy study of 48 multi-stakeholder experts on the importance and tractability of 28 potential barriers to clinical adoption of next-generation sequencing in three major policy domains: 1) intellectual property, coverage and reimbursement and FDA regulation. Not surprisingly overall results indicate a perceived need for policies to promote data-sharing and consistent payer coverage policies. Major findings are that 1) proprietary variant databases represent a formidable challenge to adoption; 2) payer policies are a frequent barrier, in part due to inconsistent coverage policies and; 3) FDA regulation was not perceived as a formidable barrier.

Together these articles propose next stage tasks to harnessing the power of omics technologies.

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