Editorial

The completion of more than 30 mammalian genome sequences has triggered world-wide efforts to unravel their information content. Many genomics and proteomics projects have been successfully completed in areas such as gene hunting, functional annotation, prediction of post-translational modifications, identification of protein-protein interactions, and so on; others have been stimulated across the fields of transcriptomics and systems biology. These projects have resulted in the design and deployment of large numbers of novel analytic and predictive computer programs throughout the global life science community.

The majority of these developments have necessarily focused on harvesting the fruits of the human genome, transcriptome, proteome, epigenome, etc., given the universal pursuit of pinnacles in human health, wealth and happiness. Today, however, we live in interesting times (as the saying goes), experiencing a revolution in which thousands of other genomes relating to a host of unicellular organisms, plants and non-human animals are being sequenced in diverse research fields across the life sciences. This has been made possible by the advent of Next Generation Sequencing (NGS) (and, more recently, 3Gen) technologies, allowing vast amounts of genomic information to be generated at drastically reduced cost. Analysis of the rapidly accumulating sequence data brings new challenges: above all, it requires integration of bioinformatics and statistical approaches, throwing computational biology, computer science and mathematics into the melting pot in order to extract the wealth of information sequestered in the ever-growing pool of sequenced genomes.

It is in this context that the COST Action "SeqAhead" is working to help address the urgent community need for new and improved approaches to facilitate NGS data management and analysis. EMBnet.journal is honored to publish this Supplement, which has been generated by the SeqAhead consortium following its first combined Management Committee Business Meeting and Scientific Meeting, held in Brussels from November 7th-9th, 2011.

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Ana Conesa explaining their approach using RNA-seq for calculating differential gene expression

Contents

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