

Advances in translational bioinformatics: computational approaches for the hunting of disease genes

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Abstract

Over a 100 years ago, William Bateson provided, through his observations of the transmission of alkaptonuria in first cousin offspring, evidence of the application of Mendelian genetics to certain human traits and diseases. His work was corroborated by Archibald Garrod (Archibald AE. The incidence of alkaptonuria: a study in chemical individuality. *Lancet* 1902;ii:1616–20) and William Farabee (Farabee WC. Inheritance of digital malformations in man. In: *Papers of the Peabody Museum of American Archaeology and Ethnology*. Cambridge, Mass: Harvard University, 1905: 65–78), who recorded the familial tendencies of inheritance of malformations of human hands and feet. These were the pioneers of the hunt for disease genes that would continue through the century and result in the discovery of hundreds of genes that can be associated with different diseases. Despite many ground-breaking discoveries during the last century, we are far from having a complete understanding of the intricate network of molecular processes involved in diseases, and we are still searching for the cures for most complex diseases. In the last few years, new genome sequencing and other high-throughput experimental techniques have generated vast amounts of molecular and clinical data that contain crucial information with the potential of leading to the next major biomedical discoveries. The need to mine, visualize and integrate these data has motivated the development of several informatics approaches that can broadly be grouped in the research area of 'translational bioinformatics'. This review highlights the latest advances in the field of translational bioinformatics, focusing on the advances of computational techniques to search for and classify disease genes.

Keywords: translational bioinformatics; disease genes; computational biology

INTRODUCTION

More than 100 years ago, Archibald Garrod confirmed, with his study of the incidence of alkaptonuria in men, the Mendelian laws of inheritance of this disorder. Dr William Bateson, a keen follower of Mendel, had previously hypothesized that alkaptonuria in offspring resulting from mating of first cousins might be due to the fact that 'first cousins will frequently be the bearer of similar gametes' dispelling the previous notion that mating of first cousins in general might lead to the diseases, and hypothesizing that the disease follows similar

inheritance laws observed by Mendel in plants. Just after the terms genotype and phenotype were coined [1], in 1905, William Farabee [2], a recognized anthropologist, recorded the familial tendencies of inheritance for malformations of human hands and feet and also recognized the Mendelian patterns of inheritance for those anomalies.

It would take over 90 more years of genetic research to identify mutations in the BRCA1 gene with clear relationships to familial breast cancer [3]. This breakthrough knowledge has had important implications for the diagnosis and prognosis of

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Maricel G. Kann is an assistant professor at the University of Maryland, Baltimore County. Her research interests include methods for alignment of protein sequences, prediction of protein–protein interactions and the study of protein domains and their associations with disease. She has co-chaired several sessions at international bioinformatics conferences related to the field of translational bioinformatics.

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