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Bioinformatics

Bioinformatics is a new and rapidly evolving research area. Even a consensus on its definition has not been reached yet. For many, myself included, it is the application of mathematical, computational and statistical techniques to data being generated in molecular biology. (Broader definitions would drop 'molecular'.) Whatever definition one chooses, the role of mathematical theory in biology is, without doubt, crucial.

As molecular biology is proceeding towards characterising the genetic basis of biological processes, we find mathematical, computational and statistical sciences playing an increasingly important role. They are forming the basis for the organisation, interpretation and prediction of the burgeoning experimental information. There are many! research avenues that could be explored. Some topical research areas for review could be chosen from, say, the following: Mapping genes and genomes; Measuring the rate of evolution; Alignment of sequences.

An introductory text that includes 'a mathematician's introduction to molecular biology' is

Lander, E.S. and M.S. Waterman, Eds (1995) "Calculating the Secrets of Life", National Academy Press, Washington DC.

Other texts include the following:

Lange, K. (1997) "Mathematical and Statistical Methods for Genetic Analysis", Springer,NY;

Pawlowitzki, I-P, J.H. Edwards, and E.A. Thompson, Eds (1997) "Genetic Mapping of Disease Genes", Academic Press;

Speed, T. and M.S. Waterman, Eds (1996) “Genetic Mapping and DNA Sequencing”, Springer, NY;
Waterman, M.S. (1995) “Introduction to Computational Biology: maps, sequences and genomes”, Chapman & Hall.

Mathematical Genetics: Epistasis

The hunt for genes underlying complex diseases (like heritable cancers, heart disease, autoimmune diseases) is proving elusive. Many reasons have been proposed for this, including the biologically plausible explanation of “epistasis”, namely interaction between the underlying trait loci. Interest in epistasis has re-emerged amongst geneticists, based on recent research that broadly comes under the umbrella of the Human Genome Project; see, for example, ‘Nature Genetics’ 14, 371-3; 465-7; 468-70, and ‘PNAS’ 95, 7502-7.

A review of the background of the mathematical and statistical genetics literature on epistasis would start with:
Hartl, D.L. and T. Maruyama (1968) “Phenogram enumeration: The number of regular genotype-phenotype correspondences in genetic systems” ‘J. Theoret. Biol.’, 20, 129-163;
Strickberger, M.W. (1976) ‘Genetics’, 2nd Edition, MacMillan.

All the above references are in the library, except perhaps the PNAS article which may be too recent, but can be downloaded as a pdf file from http://www.pnas.org/cgi/content/full/95/13/7502.