Logic in Computational Biology

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Abstract:

There are numerous techniques for dealing with the broad spectrum of bioinformatics problems that have emerged, and more are being proposed every day. In general, papers and talks on bioinformatics tend to focus on the technological and algorithmic aspects of these bioinformatics problems. While these aspects are challenging and exciting, overly focused on them also often masks away essential insight into the bioinformatics problems being solved. In this talk, I want to focus on the *logical* aspect of bioinformatics. In particular, I want to discuss how one starts from some sound biological hypotheses underlining a specific bioinformatics problem, and derive from these hypotheses a logical solution to the problem. The discussion will be illustrated using examples from key mutation site identification, protein interactome analysis, proteomic profile analysis, and gene expression profile analysis.

CV:

Limsoon Wong is a provost's chair professor of computer science and a professor of pathology at the National University of Singapore. He currently works mostly on knowledge discovery technologies and their application to biomedicine. He has/had served on the editorial boards of *Journal of Bioinformatics and Computational Biology*, *Bioinformatics*, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, *Drug Discovery Today*, and *Journal of Biomedical Semantics*. He is a scientific advisor to Semantic Discovery Systems (UK), Molecular Connections (India), and CellSafe International (Malaysia).