CHEMICAL, PHYSICAL AND MATHEMATICAL SCIENCES

THE STATUS OF PARALLEL COMPUTATION AND HIGH PEFORMANCE COMPUTING IN THE PHILIPPINES

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In technologically advanced countries, solving scientific and technological problems using computer modelling, simulation, and data analysis require supercomputers or high performance computing systems. Conventional supercomputers are very expensive and beyond the budgets of most university research groups especially in developing countries such as the Philippines. However, recent advances in cluster computing technology and parallel computation on Linux-based systems make the cost of supercomputing very low compared with conventional supercomputing platforms.

In the Philippines, a number of science and engineering departments in different universities have begun experimenting with Beowulf clusters or a pile of personal computers connected in parallel through a high-speed network. An example is the High Performance Computing Laboratory of the Ateneo de Manila University which built the AGILA High Performance Computing System intended for computational science and engineering (CSE) applications.

This paper provides an overview of parallel computation on Linux-based high performance clusters. It also discusses recent initiatives by several scientists and engineers engaged in parallel computation and high performance computing in the Philippines.

Keywords: parallel computation, supercomputing, high-performance computing, computational science and engineering, Beowulf cluster, AGILA HPCS.

PERSPECTIVE ON INTERCONNECTION NETWORKS IN THE PHILIPPINES

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Information networks, of which the Internet is the best known and most popular,

are important and very strategic to a country's economy and its people. Competitive advantages are derived by those who have near instantaneous access to relevant information. Thus, a measure of the value of a network to its user is how well that network is interconnected with other networks and thus to the information resources available on them.

In this paper, we discuss the Philippine Internet from the perspective of its interconnectedness. We also offer some recommendations on interconnection of networks run by government, research and education institutions to improve the science and technology capability of the country.

Keywords: internet, information network

BIOINFORMATICS: GENOMIC AND BEYOND

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Bioinformatics tools play key roles in handling biological information at every stage of the research process.

- Scientists analyze existing data to formulate hypothesis, choose experimental targets, map experimental strategies and even design wet lab reagents such as DNA oligonucleotide primers.
- Computation is used in the wet lab as well, from computers that run scientific instruments to tools that gather and digitize data, such as from electrophoresis and microarray images.
- Computational methods are more commonly associated with data analysis. In many cases today, large amounts of experimental data must be stored, organized, and analyzed for patterns in the process of interpretation.
- Access to the databases and exchange of bioinformatics tools have also facilitated the validation of data and results, enhancing the peer review process that is key to the practice of science.

Genomics has received the greatest amount of attention because it has matured to the point of steadily providing genetic information to scientists all over the world. However, the organism is not just the product of genes but rather of the complex interplay between genes and the environment. Genes are turned on, off, and modulated in response to other signals, and mapping this dynamic state of gene function is a major challenge.

Based on the so-called central dogma of molecular biology, scientists have

turned their attention to gene expression through "transcriptomics," or the study of genes that are transcribed into RNA under particular conditions. DNA microarray technology is the major approach used in this area. Other scientists are deep into "proteomics," or studying the protein profile, protein structure and function, as well as predicting gene function through comparison with known those of known proteins. In addition, some researchers are addressing gene function by mapping out interactions between gene products, leading to what some people call the study of the "interactome."

The genome projects, such as that for the human genome, have led the explosion of information on many aspects of the organism. Bioinformatics, together with more efficient wet laboratory tools, have made that explosion possible. Both would be needed to understand more fully the workings of the organism living in its environment.

Keywords: biological information, genomics, human genome, bioinformatics

BIOINFORMATICS FROM THE COMPUTATIONAL POINT OF VIEW

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Bioinformatics is a rapidly developing field that combines computer science and mathematics with the life sciences. The field has emerged from the necessity of acquiring, storing, and analyzing large amounts of biological data from medical, agricultural and scientific applications.

This talk will provide an overview of bioinformatics and review some problems and tools that are important in the sequencing and analysis of genomes. Among the problems discussed are those that deal with sequence alignment, genome comparison, phylogenetic tree reconstruction, and microarray technology. Some compasis will be given on the often contrasting perspectives of the biologist and the computer scientist when it comes to approaching these problems.

Keywords: bioinformatics, genome analysis, microarray, sequence alignment