E1-57: Low cost, high performance computing for biomedical applications

G I D B S Dharmaratne, D N Ranasinghe
(*Dept of Statistics and Computer Science, University of Colombo, Colombo 3*)

Biochemistry research combined with the tools provided by modern biotechnology have generated massive volumes of genetic and protein sequence data. Biomedical researchers are therefore in need of computational tools to retrieve biological information from these massive databases. Since these are computationally intensive tasks they can benefit from parallel computing techniques.

Here, a parallel computing tool for DNA sequence pattern analysis is developed which runs on a cluster of Pentium PCs. The tool was written in message passing style, using a public domain library known as WPMI v 0.9b which is a Message Passing Interface standard for Microsoft Win32 platforms.

The work demonstrates how most of the commonly available networked hardware resources can be used for cost effective parallel computing.