

High Performance Computing: Harnessing Computational Power for Scientific Research

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Abstract:

With the advent of the genome project and techniques such as micro array or sequence alignment, the complexity and volume of data collected by biological scientists have increased exponentially in recent years. At the same time there have been great advances in computational power, and with the rise of multiple core processors we can expect this trend to continue. However, this computational power has not been made fully accessible to scientists due to learning curve imposed by the inherent complexity of the computing infrastructure. Grid computing and parallel computers are two areas of High Performance Computing that promise to provide technologically and economically feasible solutions to more efficiently manage and analyze the large quantities of data produced in biological research.

My research has focused on facilitating and automating the interaction with High Performance computers by end-users, being scientists or programmers. In this talk I will present my work in simplifying the development of Grid and parallel applications. In particular I will present GAUGE, a workflow-based Grid Computing Environment that permits the rapid creation of Grid applications, and a generative programming approach aimed at increasing the productivity of programmers working with master/worker parallel applications.