

Massively Parallel Programming in the Bioinformatics Domain

Shannon I Steinfadt

Abstract

Parallel programming is highly dependent upon the parallel model of computation being used. Often the style and language used are predetermined. An adaptation and redesign of the Smith-Waterman algorithm for local sequence alignment is being researched and implemented for two different but related models of computation.

The programming languages, style of programming, and programming environments will be explored for the Associative Model of Computation (ASC) as well as the SIMD PCI WorldScape PCX board.

Contact person

Ms Shannon I Steinfadt
4457 Woodglen St.
Apt. F
Kent, OH 44240
Email: ssteinfa@cs.kent.edu
Phone: 330-672-2074