Department of Mathematical Sciences Colloquium

ALEXANDER J. ROPELEWSKI

Pittsburgh Supercomputing Center

Adapting Dynamic Programming for Biological Problems on Diverse High Performing Computer Architectures

Dynamic programming is a rigorous mathematical technique that works by breaking a problem into a table of partial solutions that are combined to give the optimal solution to the problem. It has found use for many biological sequence analysis problems including sequence database searching, RNA folding and Multiple Sequence Alignment. This talk will discuss some of the common ways in which dynamic programming can be implemented in parallel on a variety of high performance computing architectures as well as the advantages and limitations of those parallel approaches in solving real biological problems.

Friday, October 28, 2005 at 4 pm. in Bell Hall 143 The University of Texas at El Paso

Please note the unusual time for the Colloquium.

Refreshments will be served in front of the colloquium room, 15 minutes before the start of the colloquium.

For further information, please contact Dr. Pavel Šolín, Bell Hall 220. Phone: (915) 747-6770, email: solin@utep.edu.