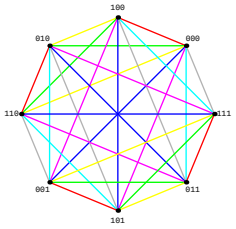
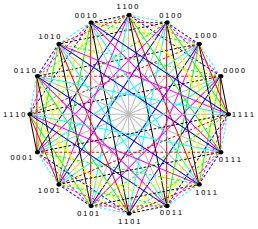
Discrete Mathematics and Optimization Seminar

F2002



Jointly Organized by
School of Computer Science and
Department of Mathematics and Statistics



October 21 (Monday), 17:15 – 18:30, Macdonald Harrington G-10

Proteins, Petaflops and Algorithms

by

Dr. W.R. Pulleyblank
Director, Deep Computing Institute
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Abstract. Computational biology is an important, rapidly growing area of deep computing. The protein folding problem is one of the most intriguing problems - how does a protein form a three dimensional structure when it is placed in water? Modeling this process goes far beyond the capabilities of current supercomputers. I will discuss the problem as well as different solution approaches currently being tried. I will also discuss a project called Blue Gene which will build a petaflop scale supercomputer suitable for one approach to this problem within the next three years.

Organizers: D. Avis(CS), W. Brown(Math), D. Bryant(CS/Math), L. Devroye(CS), K. Fukuda(CS), B. Reed(CS), V. Rosta(Math), G. Toussaint(CS) and S. Whitesides(CS).
Information: http://www.cs.mcgill.ca/~fukuda/semi/discmath.html