

Invited Speakers

Modeling, Global Constraints, and Decomposition

J. Christopher Beck

Unlike mathematical programming and SAT solving, constraint programming (CP) is based on the idea that both modeling and solving of combinatorial optimization problems can be based on conjunctions of loosely coupled, recurring, combinatorial subproblems (also known as "global constraints"). This rich representational approach means that, for better or for worse, pretty much anything can be expressed as a global constraint. Much of CP's success, however, has come from exploiting only one aspect of the rich constraint definition: global constraint propagation. In this talk, I will investigate how work in CP, SAT, AI planning, and mathematical programming can be understood as more seriously pursuing the implications of a rich constraint definition and how the interplay between local and global information can lead to dynamic problem reformulations and a flexible hybrid solver architecture.

J. Christopher Beck is an associate professor and associate chair, research in the Department of Mechanical and Industrial Engineering, University of Toronto. Beck's MSc and PhD degrees both come from the Department of Computer Science, University of Toronto, in the area of artificial intelligence. Beck spent three years at ILOG as a senior scientist and software engineer on the ILOG Scheduler team before spending two years as a staff scientist at the Cork Constraint Computation Centre. He returned to Toronto in 2004 to join the Department of Mechanical and Industrial Engineering. Beck's research interests include scheduling, constraint programming, AI planning, reasoning under uncertainty, queueing theory, mixed integer programming, and hybrid optimization techniques. Beck currently serves in an editorial capacity for four journals and one website in AI and OR. He is the president-elect of the Executive Council for the International Conference on Automated Planning and Scheduling.

Applications of Graph Search in Group Theory and Proteomics

Gene Cooperman

Two domains of graph search are described that lie at two different extremes. The first domain is computational group theory. In this domain, there is a natural series of ever larger graphs whose vertices must be enumerated, along with certain other properties. This work led to a permutation representation acting on 13,571,955,000 points for the Baby Monster group; an early upper bound on the number of moves to solve Rubik's Cube; and the Roomy software package, providing a minimally invasive method to extend RAM-based space-limited algorithms to data-parallel implementations over parallel disks or other secondary storage. The second domain is structural alignment of proteins, a part of bioinformatics. A Delaunay triangulation approach to protein matching is described. Matching all pairs in the PDB protein database then leads to a billion small graph search problems.

Gene Cooperman received his Ph.D. from Brown University in 1978. He spent two years as a post-doc, followed by six years in a basic research group at GTE Laboratories. He has been a professor at Northeastern University since 1986, and a full professor since 1992. He is the head of the High Performance Computing Laboratory at Northeastern University, where he has graduated nine Ph.D. students. He has over 90 refereed publications. His interests lie in high performance computation and symbolic algebra. His group currently supports such packages for parallel computing as: TOP-C (task oriented parallel C/C++); ParGAP (a parallel version of the GAP language for computational group theory); and Geant4-MT (a multithreaded version of the Geant4 software package for high energy physics). His group also supports DMTCP (distributed multithreaded checkpointing), the most widely used package for transparent user-space checkpointing.