ajuanp@gmail.com, Teresa Oliveira, Maria Martinez, Amilcar Oliveira, Javier Faulin, Sven Trenholm

Web-based technologies have driven the growth of new learning opportunities in the Operations Research (OR) arena. We analyze how these technologies facilitate the shifting to an educational paradigm which considers students as active and central actors in their learning process. Use of computer software and collaborative learning as methodological policies to increase students' motivation for OR are also discussed, and some real experiences regarding the design and implementation of OR courses in Web-based environments are described.

4 - Modeling operations research problems with middle school students

Susana Colaco, Departamento de Ciências Matemáticas e Naturais, Escola Suerior de Educação- Instituto politécnico de Santarém, Compexo Andaluz, Apartado 131, 2000, Santarem, Portugal, susana.colaco@ese.ipsantarem.pt, Margarida Pato, Cecilia Rebelo

This talk describes a classroom modeling tasks for middle school students using classical operations research problems, such as linear programming in single and multi-objective versions, set covering, set packing and set partitioning. Some students' productions to model real world problems are presented. The potentialities of using these contexts to develop communication skills, mathematical reasoning and identification of connections among mathematical ideas will be discussed.

■ MA-23

Monday, 9:00-10:20 6.2.49

MOO: Algorithms for Multi-Objective Combinatorial Optimization I

Stream: Multi-Objective Optimization Invited session

Chair: Luis Paquete, Department of Informatics Engineering, University of Coimbra, Polo II, 3030-290, Coimbra, Portugal, paquete@dei.uc.pt

1 - Finite representation of nondominated sets in multiobjective linear programming

Matthias Ehrgott, Engineering Science, University of Auckland, Private Bag 92019, 1001, Auckland, New Zealand, m.ehrgott@auckland.ac.nz

Can a continuous set of nondominated solutions of a multiobjective linear programme be represented by a finite subset? We prove that a related optimisation problem is NP-hard and show that some earlier methods may perform badly. We propose a new combined method which overcomes the limitations of these methods. We show that our method computes a set of evenly distributed nondominated points for which the coverage error and the uniformity level can be measured. Finally, we apply this method to an optimization problem in radiation therapy and present illustrative results for some clinical cases.

2 - Large neighborhood search for solving the multiobjective multidimensional knapsack problem

Thibaut Lust, Laboratory of Mathematics and Operatonial Research, University of Mons, 9, rue de Houdain, 7000, Mons, Belgium, thibaut.lust@umons.ac.be, *Jacques Teghem*

We present a large neighborhood search (LNS) to solve the multiobjective multidimensional knapsack problem. The LNS is integrated into the two-phase Pareto local search method (Lust and Teghem, 2007). Different ratios are used to identify the items that interfere in the generation of the neighbors. The neighborhood is solved with an exact method or with a heuristic method, depending on the size of the neighborhood. We show that we obtain results never reached before (about 90% of the non-dominated points of a 250 items instance can be generated in less than 45 seconds).

3 - A polynomial time algorithm for a cardinality constrained multicriteria knapsack problem

Florian Seipp, Mathematics, University of Kaiserslautern, Paul-Ehrlich-Str. 14 -459, 67663, Kaiserslautern, Germany, seipp@mathematik.uni-kl.de, Luis Paquete, Stefan Ruzika This talk is concerned with the cardinality constrained multicriteria knapsack problem. In this combinatorial optimization problem two binary weight functions and a real valued profit function on the items are given. The task is to choose k out of the n given items with the aim of minimizing the weights and maximizing the profit. Whereas the general multicriteria knapsack problem is known to be NP-hard, we propose an exact algorithm with polynomial running time for our problem. This algorithm computes all nondominated points by efficiently exploring the weight space.

4 - Three Algorithms for Finding Mines in a Line

Luis Paquete, Department of Informatics Engineering, University of Coimbra, Polo II, 3030-290, Coimbra, Portugal, paquete@dei.uc.pt, Jochen Gorski, Mathias Jaschob, Kathrin Klamroth

We introduce three algorithms for the problem of finding mines in a line. In this problem we are given a line partitioned into small segments, the time taken to either search in or travel through each segment, as well as a score value assigned to each segment. The goal is to choose the segments to visit such that the sum of the corresponding scores is maximized and the total travel and search time is minimized. The two algorithms are based on dynamic programming approaches for the multi-criteria knapsack problem. The third algorithm solves a bi-criteria shortest path problem formulation.

■ MA-24

Monday, 9:00-10:20 6.2.50

Bioinformatics I

Stream: Computational Biology, Bioinformatics and Medicine

Invited session

Chair: Jacek Blazewicz, Instytut Informatyki, Politechnika Poznanska, ul.Piotrowo 2, 60-965, Poznan, Poland, jblazewicz@cs.put.poznan.pl

Chair: *Piotr Formanowicz*, Institute of Computing Science, Poznan University of Technology, Piotrowo 2, 60-965, Poznan, Poland, piotr@cs.put.poznan.pl

1 - A new approach for measuring and visualizing quality of 3D protein models

Piotr Lukasiak, Institute of Computing Science, Poznan University of Technology, ul.Piotrowo 2, 60-965, Poznan, Poland, Piotr.Lukasiak@cs.put.poznan.pl, Krzysztof Fidelis, Jacek Blazewicz

Nowadays, there are a lot of computational methods in bioinformatics that can build protein 3D models based on the sequence, however even if real 3D protein structure is known it is hard to clearly evaluate which method is the most efficient. Accurate assessment of quality of protein models can be a crucial point for evaluation of currently available 3D protein prediction methods. In our approach one based on the idea of local descriptors similarity building appropriate measure to distinguish between "good' and "bad' models followed by new ways of visualization of models quality.

2 - Prediction of protein-protein interaction network

Xiang-Sun Zhang, Academy of Mathematics and Systems Science, Zhongguancun East Road 55, 100190, Beijing, China, zxs@amt.ac.cn

Protein-protein interaction network (PPIN) plays an indispensable role in systems biology research. In this research we predict the unknown part of the PPIN by not only collecting all predicted PPIs based on the Domain-Domain Interaction (DDI) information but also satisfying the characteristics of the PPIN as a complex network, such as a small-world network, a network without rich club. Parsimony principle is used to find a spanning DDI structure through solving an integer linear programming.

3 - Minimal Information for Automated Protein Function Prediction

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