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Mathematical Optimization Society Newsletter

Note from the Editors

This issue of Optima is a special one – it is due to come out around the one-year anniversary of the tragic accidental death of Alberto Caprara. Alberto had served as an Optima editor for many years and the current editorial board and Alberto's friends felt it would be fitting to dedicate this issue to the overview of his work and some of the fond memories shared by Alberto's colleagues. We are very grateful to Andrea Lodi who compiled multiple contributions of many of Alberto's colleagues into a comprehensive overview. He also collected personal memories from Alberto's friends, which help present Alberto's personality for those, who may not have had a chance to know him so closely. Thank you, Andrea and all the contributors.

Due to the special nature of this issue, and also due to his 60th birthday, we allowed Philippe Toint to take a break from his usual chair's column. The next issue will contain his farewell column as the MOS chair before he hands over to Bill Cook.

Sam Burer,
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Optima editors

Nikhil Bansal, Matteo Fischetti, Giuseppe Lancia, Adam N. Letchford, Andrea Lodi, Michele Monaci, Ulrich Pferschy, David Pisinger, Juan-José Salazar-González, Maxim Sviridenko, and Paolo Toth

Alberto Caprara (1968–2012): Scientific Contributions

Alberto Caprara died unexpectedly and tragically in a mountaineering accident on April 21, 2012. This tragedy has left his friends and colleagues with a terrible grief and the feeling of how much our personal and professional lives will be emptier without him. This feeling has been shared by many people all over the world that suggested multiple ways to remember Alberto. The invitation by the *Optima* editors to devote the current issue to Alberto has been especially welcome not only because Alberto has been an editor and a supporter of *Optima* for a long time but also because it gave his friends and co-authors the chance of getting together and writing a paper outlining the important, often fundamental, scientific contributions Alberto gave in the five areas of

1. Integer Programming,
2. Knapsack and related problems,
3. (Multi-dimensional) Bin Packing problems,
4. Computational Biology,
5. Railway applications.

The article is organized precisely to follow these five topics in the next five sections, and ends with a farewell section.

1 Integer Programming

Alberto Caprara made an important and sustained contribution to the field of *Integer Programming* during his career. He was notable for having used a wide variety of modeling frameworks and solution techniques. We cover some of these in the following subsections.

1.1 General-purpose cutting planes

Many algorithms for solving Integer Programs to proven optimality use *cutting planes*, which are linear inequalities that are known to be satisfied by all feasible integer solutions. Over the years, researchers have discovered several families of cutting planes that are 'general purpose', in the sense of being applicable to a wide range of problems. Among these are the so-called *Chvátal-Gomory* (CG) cuts, applicable to any Integer Linear Program (ILP), and the *split* cuts, applicable to any Mixed-Integer Linear Program (MILP).

Caprara and Fischetti (25) considered a special case of the CG cuts, which they called $\{0, \frac{1}{2}\}$-cuts. They showed that the associated separation problem (i.e., the problem of detecting whether or not a given fractional point violates one of the cuts) is strongly $\mathcal{NP}$-hard. On the other hand, they showed that it is polynomially-solvable in some important special cases. These results have been used by many authors since. See also the follow-up article (3), by Caprara and co-authors, where several effective separation heuristics for $\{0, \frac{1}{2}\}$-cuts were described and tested.

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Caprara et al. (26) described the so-called mod-k cuts, which, for any integer $k \geq 2$, form a subclass of the CG cuts. They gave an efficient algorithm for testing whether there exists a mod-k cut that is violated by the maximum possible amount. By applying these results to the traveling salesman problem, they were able to unify and generalize several previously-known results for that problem.

As for the split cuts, the complexity of separation for them was a long-standing open problem. It was finally settled in Caprara and Letchford (48), where it was shown that the problem is strongly $\mathcal{NP}$-hard, even under certain special conditions. Along the way, hardness was shown for several other classes of inequalities.

1.2 Special-purpose cutting planes

In parallel with the work on general-purpose cutting planes, a huge effort has been devoted in the literature to the development of *special-purpose* ones, by which we mean those that are tailored to specific combinatorial optimization problems. Alberto made several nice contributions here, too.

Caprara and Salazar (59; 60) described branch-and-cut algorithms for the *Index Selection Problem* (ISP), which is a fundamental problem arising in the physical design of databases. In (59), the cutting planes were traditional *odd-hole* inequalities, which have been used for several other problems in the past. Nevertheless, the separation algorithm given in (59) exploits the special structure of the ISP in an elegant manner to obtain a significant speed up. The follow-up article (60) presented a stronger class of *lifted* odd-hole inequalities, and showed that they too could be separated efficiently.

Caprara et al. (50) presented various families of cutting planes for a very challenging graph layout problem known as the *Minimum Linear Arrangement problem*. A cutting-plane algorithm based on these inequalities provided lower bounds that were typically far stronger than any of the previously-known lower bounds. In many cases, the bounds were an order of magnitude larger.

In Caprara and Letchford (49), it was shown that cutting planes could be applied not only to various combinatorial optimization problems, but also to certain cooperative games associated with those problems. Specifically, it was shown that, if a class of cutting planes for a specific problem satisfies a certain condition, then it can be used to compute good 'cost shares' for the corresponding games. By applying this idea to various games (e.g., the assignment, 2-matching, facility location, traveling salesman and vehicle routing games), they were able to unify and generalize several results in the literature.

Alberto also developed cutting-plane algorithms for certain problems arising in computational biology and railway applications, which are discussed in later sections.

On the negative side, Caprara (15) showed that a natural way of formulating certain 'partitioning' problems as ILPs is guaranteed to perform badly. In particular, he showed that the lower bound from the LP relaxation of such models will always be both weak and trivial, even if all cutting planes of a particular kind are added. He argued that such problems would be better solved via either Dantzig-Wolfe decomposition or Lagrangian relaxation, discussed next.

1.3 Lagrangian relaxation

Lagrangian relaxation is a standard Integer Programming tool in which certain 'complicating' constraints are moved to the objective function, leaving a relaxed problem that is typically much easier to solve. Alberto used this technique to very good effect in several articles.

Caprara et al. (28) considered a family of very large-scale *Set Covering Problems* (SCPs) that arise in railway and mass-transit applications. A Lagrangian-based heuristic approach was devised, which includes several innovative features, such as (i) a dynamic variable pricing scheme using 'Lagrangian reduced costs', (ii) a greedy heuristic that gives priority to variables with low Lagrangian reduced cost, (iii) the systematic use of variable fixing to reduce the problem dimension and (iv) new ways of controlling the step-size and ascent direction within the subgradient optimization procedure. This algorithm gave the best known solution value for all instances considered, and won the 'FASTER' prize (see Section 5).

In Caprara et al. (29), it was shown that Lagrangian relaxation can be useful even in the context of an exact algorithm for the SCP, by providing a way to eliminate (fix at zero) a significant proportion of the variables before entering the branch-and-bound procedure.

Another paper putting Lagrangian relaxation to good effect is Caprara et al. (58), concerned with the *Quadratic Knapsack Problem* (QKP). An exact algorithm was presented, which embeds a Lagrangian relaxation within a branch-and-bound scheme (see Section 2). The innovative feature was a new way of relaxing the QKP, which results in a small number of independent continuous knapsack problems. Although these subproblems can be solved quickly, the resulting upper bounds were surprisingly good. As a result, the algorithm was able to solve instances with up to 400 binary variables, which was a real breakthrough.

The method for the QKP described in (58) was extended to general *0-1 Quadratic Programs* (0-1 QPs) in Caprara (22). As he explained in that article, a similar approach had in fact been used in the past by researchers working on the Quadratic Assignment Problem. Nevertheless, it was Alberto who was the first to realize that the same framework could be used for general 0-1 QPs.

Alberto also applied Lagrangian relaxation to problems in computational biology and railway applications; see the later sections.

1.4 Some other methods

Although Alberto had a strong interest in cutting planes and Lagrangian relaxation, his work was by no means restricted to those tools. For the sake of brevity, we mention just three articles of his that presented completely different approaches to certain specific problems in Integer Programming:

- Caprara and Salazar (61) describes an exact algorithm for the *bandwidth* problem, a hard combinatorial optimization problem that has been studied since the 1960s. Rather than using linear programming relaxations, they used an elegant and non-trivial ILP relaxation that, despite being a discrete problem, can be solved efficiently. The resulting strong lower bounds were the key to computing optimal or near-optimal solutions for instances with up to 1,000 nodes, which represented a real breakthrough.
- The paper (8) (see also Section 2) presents an algorithm that takes an ILP or MILP, and automatically identifies substructures that are likely to be amenable to Dantzig-Wolfe decomposition. Interestingly, the algorithm gives rather good results even when applied to ILPs and MILPs that do not at first sight look like promising candidates for decomposition.
- The article (9) describes a branch-and-bound algorithm for minimizing a convex quadratic objective function over integer variables, subject to convex constraints. The innovative feature here is that, rather than using the original objective function to compute lower bounds, a simpler objective function, that can be minimized much more quickly, is used whenever possible. The resulting algorithm is very fast, because all expensive calculations are done in a pre-processing phase, whereas each node in the enumeration tree is processed in linear time.

2 Knapsack and related problems

Receiving his scientific education in Bologna, the origin of the classical textbook on knapsack problems (78), it should come as no surprise that Alberto Caprara also contributed to problems of the knapsack family. As an avid mountaineer the practical side of packing a knapsack in an optimal way was also clearly well known to him.

It is more astonishing that his first paper in this direction (39) appeared only in 1999, preceded by various earlier papers on other topics. It considers the quadratic knapsack problem (QKP), an extension of the standard 0-1 knapsack problem where any pair of packed items yields an additional profit value. The paper (58) by Caprara and co-authors still forms the basis in development of exact algorithms for QKP. By use of Lagrangian relaxation, the problem is split into a number of ordinary knapsack problems that can be solved either to optimality or further LP-relaxed. The resulting bounds are quite tight, and can be used to reduce the problem by variable fixing, such that the remaining problem can be solved through branch-and-bound. Instances with up to 400 variables were reported to be solved to optimality.

Staying more closely to the standard 0-1 knapsack problem, Alberto made significant contributions to the cardinality constrained variants of the knapsack and subset sum problem (39). In these problems there is an additional constraint on the number of packed items. Due to the practical relevance of this problem, it belongs to the most frequently cited papers of Alberto.

In (39) dynamic programming algorithms are developed both for the knapsack version (rather straightforward) and for the subset sum version (more involved) of the problem. Both allow scaling of the profit space to reach a fully polynomial time approximation scheme (FPTAS).

Further collaboration of the authors of that work resulted in a series of three papers on approximation of the multiple subset sum problem. This consists of a setting with a fixed number of knapsacks (=subsets), where each item can be packed into one of them or not at all. Since no FPTAS can exist for this problem even for the case of only two knapsacks with equal capacity, Caprara and co-authors proceeded to develop polynomial time approximation schemes (PTAS). The first paper (35) presents a PTAS for the case of knapsacks of equal capacity. This is a fairly complicated construction building on the classical asymptotic PTAS for the bin packing problem by Fernandez de la Vega and Lueker (66) but requiring a much more involved approach. Also the bottleneck variant which maximizes the lowest load over all knapsacks was considered. As a by-product a linear time 3/4-approximation algorithm was given in (37). In the subsequent paper (36) a PTAS was developed also for the case of different knapsack capacities. Strangely enough, it requires to leave some knapsacks empty in order to partition the knapsacks into subsets with capacities that differ only by a certain factor. This chapter was finally closed by Chekuri and Khanna (63) who gave a PTAS for the multiple knapsack problem, where profits and weights of items differ.

Moving from packing one-dimensional items to higher dimensions, we encounter on the one hand two-dimensional geometric packing problems which are discussed in Section 3. On the other, we can also consider vectors representing d-dimensional data and ask for a packing of items into bins such that for each bin the capacity constraint is fulfilled in all d dimensions. In (38) Caprara and co-authors considered the special case where vectors are correlated such that there exists a strict ordering on the set of items, i.e., vectors. Note that this case contains also the cardinality constrained bin packing problem. The main result of this paper is an asymptotic PTAS for the strictly ordered d-dimensional bin packing problem which can also be extended to sets of vectors with constant Dilworth number. Papers such as (38), but also (35) and (36), showed that Alberto not only contributed significantly to theory and application of integer programming but also mastered the art of building approximation schemes based on ILP structures.

The special case of a vector packing problem with $d = 2$ was considered in (62). Even this special case does not allow an asymptotic PTAS. However, Alberto developed heuristic algorithms and an exact branch and bound scheme with highly competitive practical performance. The introduced lower bounds are analyzed also from a worst-case point of view and a dominance relation is shown by graph theoretical arguments. Recalling that the implementational details also involve red-black trees, (62) shows the comprehensive approach Alberto was able to undertake.

Combining knapsack and bin packing problems, Alberto investigated the interesting question of the behavior of the following heuristic for the bin packing problem: Pack the first bin as full as possible, i.e., solve the corresponding subset sum problem. Then close the bin and continue with the remaining items and the second bin, etc. While it is easy to see that this very natural, greedy-type (although not polynomial) approach will not yield an optimal solution in general, its worst-case performance was mostly settled by Caprara and Pferschy in 2004 (56). They showed that the ratio is in [1.6067, 1.6210] for general item weights, which is – somewhat surprisingly – only slightly better than the 1.7 given by the elementary first-fit heuristic. The analysis is extended to depend parametrically on the largest item weight. Note that the upper bound uses a mathematical programming formulation which is solved analytically by exploiting LP-duality and applying classical calculus.

Since worst-case scenarios of packing problems often depend on the "wrong" treatment of large items, a follow-up paper (57) considered two variants of the natural subset sum heuristic which perform a special treatment for "large" items. Capara and Pferschy (57) could show that this simple modification yields a significant improvement of the worst-case performance ratio.

Alberto's most recent contribution to the area of knapsack type problems considered a knapsack problem with a time-dependent resource consumption (33) motivated by a railway application problem. In this so-called temporal knapsack problem, or unsplittable flow on a line problem, a number of items is given, each item j being active for a time interval $[s_j, f_j]$. The task is to select a subset of items to pack in the knapsack of capacity c such that at any time the set of active items do not exceed the capacity constraint. In (33), Caprara and co-authors describe a Dantzig-Wolfe decompostion of the problem and show that decomposed problem is significantly easier to solve. The paper is interesting since Dantzig-Wolfe decomposition normally is used when the problem at hand admits a natural decomposition, but this is not the case for the temporal knapsack problem. The results contribute to a general framework for Dantzig-Wolfe decomposition of MIPs presented in (8). In this paper the temporal knapsack problem is used as an example for automated Dantzig-Wolfe decomposition.

The knapsack problem also frequently appeared as a subproblem in Alberto's application oriented papers, where sometimes his roots in electronic engineering came through. In (27) a knapsack problem is solved as part of a heuristic for the index selection problem in physical database design. Similarly, a knapsack-type problem is solved in (4) when designing a partitioning algorithm for on-chip scratchpad memory partitioning.

When the authors of the knapsack monograph (71) asked Alberto to join their effort he politely refused, stating that in his opinion one should write monographs towards the end of a career when one is looking back with more insight and a broad understanding. Unfortu-

nately, Alberto never reached this stage but stayed at the top of his scientific productivity throughout his much too short life.

3 (Multi-dimensional) Bin Packing problems

In this section we review some of the fundamental contributions of Alberto for multi-dimensional packing problems.

We restrict our discussion to results around the *two-dimensional bin packing problem* (2BP), in which one is required to pack a given set of n rectangular items, the j-th item having width w_j and height h_j, into a minimum number of identical bins of size $W \times H$. In the most basic variant of the problem, the items can be packed arbitrarily in a bin, as long as they are not rotated and their sides are parallel to the edges of the bin. By scaling, it can be assumed without loss of generality that all bins are unit squares.

Two-dimensional packing problems have received considerable attention in the literature since the sixties. As with most packing problems, a right measure here is the asymptotic approximation ratio, where an algorithm A has asymptotic approximation ratio ρ if $A(I) \leq \rho \cdot \mathrm{OPT}(I) + c$ for every instance I and some fixed constant c independent of I. While the classic one dimensional bin packing (1BP) admits an asymptotic polynomial time approximation scheme (APTAS), i.e., $\rho = 1 + \epsilon$ for any fixed $\epsilon > 0$, such a possibility is ruled out for 2BP (though the known lower bounds are quite weak, roughly like $\rho \geq 1 + 1/3000$ (64)). For a long time, the best known result for 2BP was a $\frac{17}{8}$ asymptotic approximation achieved by the *Hybrid First-Fit* algorithm due to Chung et al. (65). Later, an improved $(2 + \epsilon)$ asymptotic approximation was given by Kenyon and Rémila (72) as a byproduct of a $1 + \epsilon$ approximation for the *two-dimensional strip packing* (2SP), i.e., the problem of minimizing the height used to pack a given set of rectangular items into a unique strip of fixed width and infinite height.

The first contribution of Alberto for such problems was an APTAS for a variant of 2BP, known as *shelf bin packing* (2SBP) (52). This variant is motivated by viewing bin-packing as a cutting stock problem, where the items are rectangular patterns that need to be cut out from the minimum number of square sheets. For mechanical reasons of the cutting tool, it is desirable that the packing of items in the bin should not be too complicated. In particular, in the 2SBP variant, the items must be packed such that each item can be recovered by recursively applying at most two side to side cuts to the bin (such cuts are known as guillotine cuts). Figure 1 shows such a packing (technically, one also needs an additional cut for separating the item from the wasted area).

It is not hard to see that such packing is composed of *shelves*, where each shelf includes a subset of items placed with their bottom edge at the same level. The APTAS in (52), the first result of this type for a multi-bin variant of 2BP, was based on an elegant combination of various techniques such as rounding, linear grouping, geometric grouping, and enumeration of a constant number of feasible patterns

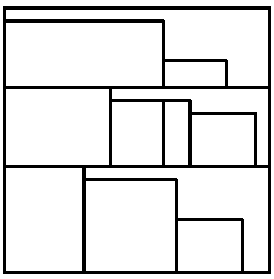

Figure 1. *An example of a feasible pattern for shelf bin packing*

(i.e., shelves in this context). For each configuration of shelves, the algorithm required solving an Integer Linear Program with a constant number of variables and constraints, which can be done in polynomial time (76). Later in (53), it was observed that the step of optimally solving the ILP can be replaced by rounding an optimum solution of a certain natural Linear Programming relaxation. This lead to an asymptotic fully PTAS (AFPTAS).

The next major contribution (20) of Alberto was to break the barrier for $2 + \epsilon$ for 2BP and give an asymptotic approximation of $T_\infty + \epsilon$, where $T_\infty = 1.691\ldots$ is the well-known guarantee of the harmonic algorithm for the *one-dimensional bin packing* (1BP) (74). Consider the sequence defined by $t_1 = 1$ and $t_{i+1} = t_i(t_i + 1)$ for $i \geq 2$, then T_∞ is given by

$$T_\infty = \sum_{i \geq 1} \frac{1}{t_i} = 1 + \frac{1}{1 \cdot 2} + \frac{1}{2 \cdot 3} + \frac{1}{6 \cdot 7} + \frac{1}{42 \cdot 43} + \ldots$$

Interestingly, Alberto's algorithm for 2BP was inspired by his investigations into 2SBP. In particular a corollary of his result is that even though shelf packing may appear quite restrictive, for any instance the ratio between the optimal 2SBP solution and the optimal 2BP solution is bounded above by $T_\infty = 1.691\ldots$

His beautiful algorithm for 2BP is the following. Fix some large constant number k that depends on the precision parameter $\varepsilon > 0$ and classify all items into k classes $C_1, \ldots, C_k$ according to the width. Formally, $C_r = \left\{ j : w_j \in (\frac{1}{r+1}, \frac{1}{r}] \right\}$ for $r = 1, \ldots, k-1$ and $C_k = \left\{ j : w_j \leq \frac{1}{k} \right\}$. The widths of items from class C_r are rounded up to $1/r$. Order all the items within each class according to their height and form shelves in a greedy way, each shelf except the last one gets r items for each class C_r, $r = 1, \ldots, k-1$. The class C_k is treated separately but in a similar way.

After assigning the items to shelves, the algorithm defines the height of a shelf to be the largest height out of all items assigned there. The problem of packing the shelves in the best way possible now reduces to a 1BP instance that can be solved almost optimally. Despite the simplicity of the algorithm, proving that it has an asymptotic approximation ratio of $T_\infty + \varepsilon$ required brilliant new insights. In his journal paper (23), Alberto showed how to generalize this idea to the d-dimensional bin packing problem to obtain an algorithm with asymptotic approximation ratio of $T_\infty^{d-1} + \varepsilon$.

In subsequent work (6; 7), Alberto and co-authors improved the approximation ratio for 2BP even further to $1 + \ln T_\infty = 1.525\ldots$. But more importantly, a general framework to obtain improved approximations for various other packing problems was developed. The idea is the following. Suppose there is a ρ-approximation algorithm for some packing problem (e.g., 2BP) with the property that it is "subset oblivious". Roughly, this means that if we pick a random subset I' of items from the given instance I, by picking each item with probability p, then the value of algorithm on I' is about p times the value on the instance I. It turns out that many known algorithms, such as Alberto's algorithm for 2BP from (20), satisfy this subset obliviousness property. Alberto and co-authors showed a general result that if there exists a ρ subset-oblivious algorithm for a problem, then a $1 + \ln \rho$ approximation can be obtained using a combination of linear programming and randomized rounding like techniques. In addition to the $1.525 + \epsilon$ approximation for 2BP, this also gives other results like $1.525 + \epsilon$ approximation for 2BP with rotations, and a $(1 + \ln d + \varepsilon)-$approximation for the vector d-dimensional packing problem.

The following beautiful open problem is due to Alberto. Let OPT_{2BP} be the optimal value of the $2BP$ and let OPT_{G2BP} be the optimal value of the so-called Guillotine 2BP, i.e., the problem where we are allowed to pack each item only in an area that can be obtained by a sequence of edge to edge cuts. Clearly,

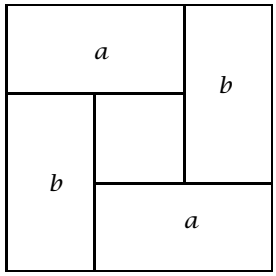

Figure 2. *A non-guillotine packing of one bin for the ratio* OPT_{G2BP}/OPT_{2BP}

$OPT_{2BP} \leq OPT_{G2BP}$. Since any shelf packing is a feasible guillotine packing, the algorithms from (20; 23) imply that $OPT_{G2BP} \leq T_\infty \cdot OPT_{2BP}$. On the other side, the following instance, due to Alberto, shows that OPT_{G2BP}/OPT_{2BP} could be as large as $4/3$. We are given 12 items, 6 of size $(\frac{2}{3}-\epsilon, \frac{1}{3}+\epsilon)$ (type a) and 6 of size $(\frac{1}{3}+\epsilon, \frac{2}{3}-\epsilon)$ (type b). Figure 2 shows a non-guillotine packing of one bin packing 2 items of type a and 2 of type b, yielding $OPT_{2BP} = 3$. It is easy to check that any guillotine solution can pack at most 3 items per bin (either 2 of type a and 1 of type b, or vice versa), thus $OPT_{G2BP} \geq 4$.

Finding the precise value of the worst case ratio OPT_{G2BP}/OPT_{2BP} is a major open problem in the area.

Alberto's contributions on two-dimensional packing also had impacts on bilinear programming. In particular, the problem of defining the pair of dual feasible functions (see, Lueker (77)) producing the best lower bound for 2BP was formulated as a bilinear program in (51). Further attempts to the problem of checking whether a given set of rectangles fit into a bin have been conducted in (54), where it is proved that the asymptotic worst-case performance ratio between the optimal 2BP solution and the best bound provided by dual feasible functions belongs to the range $[\frac{9}{8}, T_\infty]$, and that similar results hold for the two-dimensional version of the knapsack problem.

4 Computational Biology

In the mid nineties, while visiting Carnegie Mellon University as a PhD student, Alberto became involved in the emerging field of Computational Biology. Even in this field he was soon able to contribute with some major results. His contributions can be roughly divided into three application areas, i.e., *genome rearrangements*, *protein structure alignment* and *sequence alignment*. We will now elaborate on each of these topics.

Genome rearrangements and Sorting By Reversals. One of the evolutionary events that, by altering the genome of the living organisms, eventually lead to the birth of new species, is the inversion of a large DNA region. In million of years of evolution and after many such events, the genomes of two different species may carry the same genes but in a different order, and we may be interested in determining how many inversions have happened in the evolutionary process from their closest common ancestor.

In order to give a precise mathematical formulation of the problem, denote the set of common genes between two species by $[n] := \{1, \ldots, n\}$ and let S_n denote the set of the $n!$ permutations of $[n]$. Without loss of generality, we may assume that the order of the genes in the first species is $\iota = (1, \ldots, n)$, while in the second species it is represented by a permutation $\pi = (\pi_1, \ldots, \pi_n)$.

For each pair of indices i and j, with $1 \leq i < j \leq n$, we denote by ρ_{ij} the *reversal* operator $\rho_{ij} : S_n \mapsto S_n$ such that

$$\rho_{ij}(\pi) = (\pi_1, \ldots, \pi_{i-1}, \pi_j, \pi_{j-1}, \ldots, \pi_{i+1}, \pi_i, \pi_{j+1}, \ldots, \pi_n)$$

i.e., the application of ρ_{ij} to π reverses the order of the elements between π_i and π_j (included). A sequence of reversals $\rho^1, \ldots, \rho^D$ is called a *sorting sequence* for π if $\rho^1(\cdots(\rho^D(\pi))\cdots) = \iota$. The minimum value D for which $\rho^1(\cdots(\rho^D(\pi))\cdots) = \iota$ is called the *reversal distance* of π, and is denoted by $d(\pi)$. The problem of finding $d(\pi)$ and a sorting sequence $\rho^1, \rho^2, \ldots, \rho^{d(\pi)}$ is called *Sorting by Reversals* (SBR).

The idea of comparing genomes by looking at which inversions make them identical was introduced by Watterson et al. in 1982 (83). In that paper the authors formalized the problem of SBR, discussed some lower and upper bounds and proposed a simple (but rather ineffective) greedy heuristic for its solution. A thorough computational study of SBR did not start before 1993, when Kececioglu and Sankoff (69; 70) conjectured the problem to be NP-hard and provided the first branch-and-bound method, a combinatorial approach suitable only for small instances ($n \leq 30$). In 1997 Alberto was eventually able to show that SBR is NP-hard (14), thus settling a longstanding open question. For this result, he received the "Best Paper by a Young Scientist" prize, awarded by the 1st International Conference on Computational Molecular Biology (RECOMB) committee.

While the complexity status of SBR was still unknown, Caprara, Lancia and Ng (45) proposed a branch-and-price approach based on a nice graph representation of the problem, namely, the *breakpoint graph* introduced by Bafna and Pevzner (5). In order to describe the breakpoint graph, we have to introduce the concept of a breakpoint. For technical reasons, extend π so that it starts with $\pi_0 := 0$ and it ends with $\pi_{n+1} := n + 1$. Then, for $i = 0, \ldots, n$, there is a breakpoint at position i, if $|\pi_i - \pi_{i+1}| > 1$, i.e., if two elements of π are consecutive while they should not be in the target permutation ι. Let us denote the number of breakpoints in π by $b(\pi)$. The breakpoint graph $G(\pi)$ has a node for each element of π and edges of two colors, say, red and blue. For each position $i \in \{0, \ldots, n\}$ such that there is a breakpoint at i in π there is a red edge between π_i and π_{i+1} in $G(\pi)$. Similarly, for each value $v \in \{0, \ldots, n\}$ such that v and $v + 1$ are not adjacent in π there is a blue edge between v and $v + 1$ in $G(\pi)$. $G(\pi)$ is Eulerian and its edges can always be partitioned into edge-disjoint color-alternating cycles. Let $c(\pi)$ be the maximum number of edge-disjoint alternating cycles in $G(\pi)$. Since a reversal can remove at most two breakpoints, and ι has no breakpoints, a valid lower bound for SBR is $d(\pi) \geq \lfloor b(\pi)/2 \rfloor$, but this bound is usually quite weak. Bafna and Pevzner (5) proved that a better valid lower bound is $b(\pi) - c(\pi)$. This bound turns out to be very tight, as observed first experimentally by various authors and then proved to be almost always the case by Alberto (16; 17), who showed that determining $c(\pi)$ is essentially the same problem as determining $d(\pi)$.

In (16) Alberto proved that for a random permutation π of n elements, the probability that the bound $b(\pi) - c(\pi)$ is not tight is asymptotically $\Theta(1/n^5)$. This work received the "Best Paper Award" by the editors of the Journal of Combinatorial Optimization, as the best paper published by the journal in the year 1999.

In (17) Alberto proved that decomposing a bicolored Eulerian graph into a maximum set of alternating cycles is NP-hard, and in particular, that it is NP-hard to compute $c(\pi)$. Although this may look as a major drawback in the use of $c(\pi)$ for a practical solution of SBR, this is not the case. Indeed, for any upper bound $c'(\pi)$ to $c(\pi)$, the value $b(\pi) - c'(\pi)$ is a lower bound to $d(\pi)$ which can be used in a branch-and-bound algorithm for SBR. The bound is tight

as long as $c'(\pi)$ is a tight bound to $c(\pi)$. Such a tight bound can be provided by the LP-relaxation of the following, exponential-size, ILP model for the maximum cycle decomposition problem.

Let $\mathcal{C}$ denote the set of all the alternating cycles of $G(\pi) = (V, E)$, and for each $C \in \mathcal{C}$ introduce a binary variable x_C. The maximum cycle decomposition problem is:

$$c(\pi) := \max \left\{ \sum_{C \in \mathcal{C}} x_C \mid \sum_{C \ni e} x_C \leq 1, \ \forall e \in E, \quad x \in \{0,1\}^{\mathcal{C}} \right\}. \quad (1)$$

The LP relaxation of (1) has an exponential number of variables, but in (45) it is shown that it can be solved in polynomial time by column-generation techniques, where the pricing requires the solution of non-bipartite min-cost perfect matching problems. By using this approach, Alberto and co-authors were able to solve SBR instances with n up to one hundred, including a famous "man vs mouse" instance whose optimal solution was found for the first time.

In (46; 47) Caprara et al. experimented with a different (weaker) bound obtained by enlarging the set $\mathcal{C}$ in (1) to include also the *pseudo-alternating* cycles, i.e., alternating cycles that may possibly use a same edge twice. With this new set of variables, the pricing becomes much faster, since only bipartite matching problems must be solved. Extensive computational experiments showed that the resulting algorithm for SBR can consistently solve to optimality within seconds random permutations of up to 200 elements. Moreover, a diving heuristic based on greedily fixing some variables to one, depending on the current LP solution, performs remarkably well for permutations with n up to 1000, yielding feasible solutions within 2 % of the optimum.

While SBR can be employed to estimate a lower bound to the evolutionary distance between two genomes, other models that pursue a different objective may produce a closer estimate to the actual distance value. In (42), Caprara and Lancia introduced the idea of using a probabilistic approach for computing the length of a most likely sequence of reveresals between two genomes. The problem can be illustrated by the following experiment. Consider the graph $\hat{G} = (S_n, \hat{E})$ in which every permutation is a node, and there is an edge between two permutations π and σ if there exist a reversal ρ such that $\pi = \rho(\sigma)$. Starting from ι, perform a random walk in $\hat{G}$ and stop at a random permutation π. Let K be the length of this random walk. The problem is then: *given π obtained by the above process, return an estimate $\tilde{K}$ as close as possible to K.*

Let X_k denote the number of breakpoints in a permutation obtained after a random walk of length k. Caprara and Lancia proved that $E[X_k] = (n-1) - (n-3)^k/(n-1)^{k-1}$. Given a permutation π, and under the assumption that Nature applied its reversals following a random walk, the method of maximum likelihood suggests that $b(\pi)$ should be the average value. Hence, the most likely value is $\tilde{K} = \text{argmin}_K |E[X_K] - b(\pi)|$. In a further model analyzed in (42), it is assumed that the reversals were applied according to a Bernoullian process with a given probability p, and then by using conditional probabilities, it is shown how to estimate the odds that a certain number of reversals were applied, given that we observe $b(\pi)$ breakpoints. The computational results showed that the the probabilistic approach provides a much better estimate of K than the reversal distance, except for the cases in which K is rather small.

After working on the reversal distance between two genomes, Alberto turned his attention to the case of multiple genomes. In (18) he introduced the problem of finding a signed permutation which minimizes the total reversal distance from a set of given signed permutations $\pi^1, \ldots, \pi^q$. This problem is called *Reversal Median Problem* (RMP). A signed permutation is a permutation in which each element is signed either "+" or "-". For a signed permutation, a reversal not only flips a block of consecutive elements, but it also swaps the sign of the elements within the block. Hannenhalli and Pevzner had shown that computing the reversal distance between two signed permutations is polynomial (68). In (18), Alberto showed that RMP is NP-hard, and that the same complexity holds for the Steiner Tree problem (called *Tree SBR*, or TSBR) with centers in the given set of signed permutations. For both RMP and TSBR he described a $(2 - 2/q)$-approximation algorithm. Median problems are generally aimed at the reconstruction of evolutionary trees. In particular, the *Breakpoint Median Problem (BMP)*, introduced by Sankoff and Blanchette in (81) calls for determining a permutation which minimizes the total breakpoint distance from a set of given permutations, and was widely used as a subroutine by algorithms reconstructing evolutionary trees. While it was recognized that RMP would be a more realistic model than BMP, it was a common belief that RMP would not be practically solvable by an exact algorithm, and even heursitics would run in trouble on all but small instances. In (19; 21) Alberto showed that this is not the case and proposed effective algorithms (both exact and heuristic) capable of solving instances whose size was quite beyond the current limits. Now Alberto's approach is implemented and used within many state-of-the art software packages for evolutionary trees (such as the program GRAPPA by Moret et al. (79)).

Protein structures and Contact Map Overlap. A protein is a complex molecule for which a simple linear structure, given by the sequence of its aminoacids (also called *residues*), determines a unique three-dimensional structure. When left in its natural environment, driven by the forces between its residues, the protein folds into the structure minimizing the total free energy, called its *native fold*. The fold fully defines how the protein functions and interacts with other molecules, and in the past few years many tools have emerged which allow the comparison of 3D protein structures. While the problem of computing a similarity measure between folds has become extremely important in structural biology, many models for structure comparison turn out to be NP-hard.

The main features of a fold are conveniently represented by a graph, called the protein's *contact map* (CM). This is a graph $G = (V, E)$ in which the vertices are the protein residues and the edges represent the *contacts*, i.e., the pairs of residues that lie in close proximity (e.g., within 5Å) when the protein is in its native fold.

The problem of computing the similarity of two contact maps is called the *Contact Map Overlap* (CMO) problem and was originated in the the mid nineties. Formally, the problem can be phrased in graph–theoretic language as follows: We are given two undirected graphs $G_1 = (V_1, E_1)$ and $G_2 = (V_2, E_2)$, with $V_i = \{1, \ldots, n_i\}$ for $i = 1, 2$. To avoid confusion with the *edges* in G_1 and G_2, we hereafter call a pair (i, j) with $i \in V_1$ and $j \in V_2$ a *line* (since it *aligns* i with j), and we denote it by $[i, j]$. An *alignment* of V_1 in V_2 is defined by a subset of lines $\{[i_1, j_1], \ldots, [i_p, j_p]\} \subset V_1 \times V_2$ such that, for $1 \leq h < k \leq p$, it is $i_h < i_k$ and $j_h < j_k$ (i.e., an alignment corresponds to a *noncrossing matching* in the complete bipartite graph $B = (V_1 \cup V_2, V_1 \times V_2)$). Two contacts $\{l_1, r_1\} \in E_1$ and $\{l_2, r_2\} \in E_2$ are *shared* by the alignment if there are $h, k \leq p$ s.t. $l_1 = i_h$, $r_1 = i_k$, $l_2 = j_h$ and $r_2 = j_k$. Each pair of shared edges contributes a *sharing* to the objective function. The problem consists in finding the alignment which maximizes the number of sharings. In the context of protein structure comparison, this objective scores how many pairs of residues are in contact in the first protein and are aligned to residues which are also in contact in the second protein. This value is called the *overlap* of the alignment, and the problem requires to

find an alignment of maximum overlap. It is not difficult to see that CMO is NP-hard.

In 2000 a group at Sandia National Laboratories formulated the CMO problem as an ILP and solved it by Branch–and–Cut (73). The model employs binary variables x_{iu} for $i \in V_1$ and $u \in V_2$, to select the lines of a noncrossing matching, and binary variables y_{ef} for $e \in E_1$ and $f \in E_2$ to select which pairs of contacts are sharings in the solution. The objective of CMO is the maximization of $\sum y_{ef}$ over all $(e, f) \in E_1 \times E_2$. Among the constraints, particularly important are those enforcing the lines of the solution to be noncrossing. Let $L = V_1 \times V_2$ be the set of all lines. We say that two lines $l = [i_1, j_1]$ and $m = [i_2, j_2]$ in L are *incompatible* if no feasible alignment can contain both lines. Let $\mathcal{I}$ denote the collection of all maximal sets of pairwise incompatible lines $I \subset L$. Then, we have the following constraints:

$$\sum_{l \in I} x_l \leq 1, \ \forall I \in \mathcal{I}. \tag{2}$$

In (73) it is shown that $\mathcal{I}$ is exponentially large, but there is an effective polynomial-time separation algorithm for inequalities (2). The resulting branch-and-cut algorithm made possible, for the first time, to find the optimal alignment for a set of about 300 pairs of proteins from the Protein Data Bank, with up to 80 amino acids and about 150 contacts each. The CMO was also validated by a clustering experiment involving 33 proteins classified into four families. The running time of the branch-and-cut was, on average, in the order of minutes up to an hour.

Shortly after the publication of (73), Alberto became interested in the CMO problem, and suggested the use of a Quadratic Programming approach for its solution. Binary Quadratic Programming problems require the selection of a set of variables under a quadratic objective function, in which some profits p_{ij} are attained when two binary variables x_i and x_j are *both* set to 1 in a solution. Analogously, in the CMO problem, there can be a profit for aligning two specific residues provided some other two are *also* aligned.

The quadratic model is still based on binary variables x_l for each line $l \in L$. For $l = [i_1, j_1]$, $m = [i_2, j_2] \in L$, define $a_{lm} = 1$ if $\{i_1, i_2\} \in E_1$ and $\{j_1, j_2\} \in E_2$, $a_{lm} = 0$ otherwise. The objective function contains terms of the form $a_{lm} x_l x_m$, indicating that a contribution of a sharing is achieved if the three terms in the product take the value 1, i.e., a profit of 1 is attained if both x_l and x_m are equal to 1. In fact, in order to illustrate the method, it is necessary to introduce separately products $x_l x_m$ and $x_m x_l$ in the objective function. To this end, define separate profits b_{lm} for $x_l x_m$ and b_{ml} for $x_m x_l$ such that $b_{lm} + b_{ml} = a_{lm} (= a_{ml})$ for all $l, m \in L$. For instance, a valid choice is $b_{lm} = b_{ml} = a_{lm}/2$.

The problem can now be stated as the following *Binary Quadratic Program*:

$$\max \sum_{l \in L} \sum_{m \in L} b_{lm} x_l x_m \tag{3}$$

subject to constraints (2) and binary variables x. The main difference between this problem and a standard quadratic assignment is that CMO is in maximization form and the matching to be found does not have to be perfect and must be noncrossing. The model can then be linearized by using a standard technique that is described by Caprara and Lancia in (43) together with a Lagrangian approach for its solution. In particular, Caprara and Lancia showed how the Lagrangian relaxation can be solved in quadratic time with respect to the number of contacts and proposed both a branch-and-bound and a heuristic based on the Lagrangian relaxation, which they further developed in (44). The approach considerably improved over the results in (73), obtaining a speed-up of at least one order of magnitude. For the first time, it was possible to optimally align some proteins with up to 1000 residues and 2000 contacts each. Furthermore, 10,000 pairs of proteins from a test set of 269 proteins in the literature, were aligned to optimality or near-optimality within a few hours. Eventually, Alberto and the group from Sandia Labs merged their results and published a joint journal paper (see Caprara et al. (24)). In the paper, an extensive set of computational experiments showed how the CMO score can be practically employed for assessing protein fold similarity.

Multiple sequence alignment. While the CMO problem focuses on the alignment of two protein *structures*, there is another type of alignment of paramount importance in computational biology, i.e., the *sequence* alignment. Genomic sequences are strings over either the 4-letter nucleotide alphabet {A, C, G, T} or the 20-letter aminoacid alphabet. The alignment of two sequences s^1 and s^2 aims at determining their degree of similarity, usually expressed in the form of an edit distance, i.e., the number of edit operations (such as insertion, deletion or overwriting) necessary to turn s^1 into s^2. The edit distance between two strings of length n can be computed effectively in time $O(n^2)$ via Dynamic Programming.

When the comparison has to be made between more than two sequences at once, we talk of a *multiple sequence alignment* (MSA) problem. MSA is one of the fundamental problems in computational molecular biology. By aligning a set of sequences it is possible to identify highly conserved, functionally relevant, genomic regions, spot fatal mutations, and suggest evolutionary relationships. The alignment of a set of sequences is a matrix with each row containing one of the sequences. The alignment may possibly insert some symbols "-" in each sequence to make them become all of the same length. The following is a simple example of an alignment of the sequences ACCGGAC, ATTCCGGTG, ACCGGTC and CCGGATG:

```
A-CCGGA-C
ATTCCGG-TG
A-CCGG-TC
--CCGGATG
```

The alignment shows how the subsequence CCGG is highly conserved within this family, and how the last nucletotide has mutated from C to G in some of the sequences.

A popular objective function for the MSA problem is the *Sum-of-pairs (SP)* objective, which attempts to minimize the average edit distance between each pair of rows in the multiple alignment. The generalization of the Dynamic Programming approach to the case of multiple sequences leads to an exponential algorithm, and, in fact, MSA is NP-hard for the SP objective as well as many other biologically relevant objective functions (82).

One of the difficult issues in the computation of "biologically good" multiple alignments is the scoring of the gaps. A *gap* is a run of consecutive "-" within a row of the alignment. For instance, the above alignment contains altogether six gaps, two of which are in the first row. The length of the longest gap is 3, while the shortest gap has length 1.

One way to score a gap (called the *linear gap* model) is that of considering a gap of length k to be identical to k gaps of length one each. In particular, for a given cost δ (called *indel* cost), the cost of a gap of length k is equal to $k\delta$. This is the simplest possible way of scoring gaps, and therefore it was the first to be considered when the first MSA algorithms were proposed. The fact that it is already NP-hard to minimize the SP objective under the linear gap model prevented many researchers from trying to consider more complex gap cost functions. However, from a biological point of view, the linear model is unsatisfactory: In the linear model, a gap of length k can be seen as k events of deletion of one nucleotide each, while

it should more likely correspond to a unique event deleting k nucleotides at once. A more "biologically-sound" way of scoring the gaps is the *affine* gap cost model, in which there are two costs, α (a *gap-opening* cost) and β (a *gap-extension* cost, usually much smaller than α), and a gap of length k has cost $\alpha + (k-1)\beta$.

By the year 2000, the MSA problem provided two big challenges for computer scientists interested in its solution. First, because of its computational complexity, the vast majority of MSA programs were of heuristic nature, and it was believed that no exact algorithm would be effective on instances of practical interest. Secondly, the affine gap cost model was too complex to be optimized and henceforth no method in the literature dealt with truly affine gap costs (although a "quasi"-affine model had been considered in (80)). Around that time, Alberto came in contact with a group of German researchers who had already successfully applied combinatorial optimization techniques in the solution of several computational biology problems, such as RNA secondary structure alignment (Lenhof et al. (75)) and protein-protein docking (Althaus et al. (80)).

Alberto joined the group with the objective of applying mathematical programming techniques to obtain an effective exact method for the solution of MSA under the affine gap cost model. Their effort resulted in two papers (1; 2) in which they proposed a branch-and-cut approach which not only could be applied to the affine model, but to any gap cost function including convex and position-dependent gap costs. The algorithm was evaluated using BAliBase, a benchmark library of sequence alignments. The results showed that their method ranks among the best algorithms for MSA, and for small- to moderately-sized instances it outperforms most methods in the literature.

5 Railway applications

Alberto was deeply involved in the definition of mathematical models and in the design of effective exact and heuristic algorithms for the solution of important real-world *Railway Optimization Problems*: *Crew Planning*, *Train Timetabling*, *Train Platforming*, *Train Unit Assignment*. His contributions to the railway optimization field have been highly appreciated by the international research community, and he has been invited as plenary speaker at several international conferences and schools, and as co-author of two recent reviews on the considered topics (see (41) and (40)). Alberto was also involved in several research contracts with *Ferrovie dello Stato* (*FS*, the main Italian railway company), and in the European Union Projects: *TRIO*, *TRIS*, *PARTNER* (Path Allocation Reengineering of Timetable Networks for European Railways), *REORIENT* (Implementing Change in the European Railway System), *ARRIVAL* (Algorithms for Robust and online Railway optimization: Improving the Validity and reliAbility of Large scale systems), *ON TIME* (Optimal Networks for Train Integration Management across Europe).

The *Crew Planning Problem* (CPP) is concerned with covering each trip of a given timetable with the required numbers of *crews* (drivers and conductors). CPP represents a very complex and challenging problem, due to both the size of the instances to be solved and the type and number of operational constraints. It is usually decomposed into the following two phases. In the *crew scheduling* phase, the short-term schedule of the crews is considered, and a convenient set of *duties* covering all the trips is constructed. Each duty represents a sequence of trips to be covered by a single crew member within a short time period overlapping at most one or two consecutive days. In the *crew rostering* phase, the duties selected in the crew scheduling phase are sequenced to obtain the final *rosters*, which describe for each crew member the sequence of duties to be carried out on consecutive days.

In 1994, *FS* promoted the development of new techniques for the effective solution of the very large *Set Covering Problem* (SCP) instances that arise in their crew scheduling applications, involving up to 5,000 rows (trips) and 1,000,000 columns (duties). To this end, *FS* and *AIRO* (the Italian Operations Research Society) set up a competition among universities, named *FASTER*, calling for the best heuristic code for very large set covering problems. The heuristic proposed by Caprara, Fischetti and Toth (28) outperformed the previously available methods, and was awarded the first prize in the *FASTER* competition. The method, called CFT, was based on dual information associated with the Lagrangian relaxation of the set covering model, and was organized in three main phases. The first one (subgradient phase) was aimed at quickly finding a near-optimal Lagrangian multiplier vector. In the second one (heuristic phase), a sequence of near-optimal Lagrangian vectors was given as input to a greedy heuristic procedure to possibly update the incumbent solution. In the third phase (refining and fixing phase), a refining procedure was applied and a subset of "good" columns (duties) of the incumbent solution were fixed. The three-phase procedure was iterated until certain termination conditions were met. When very large instances were tackled, the computing time spent on the first two phases became excessively large. To overcome this difficulty, a *core problem* containing a suitable subset of columns (duties) was defined. The definition of the core problem turned out to be very critical, so CFT used a variable pricing scheme to update the core problem iteratively, in a vein similar to that used for solving large scale linear programs. The use of pricing within Lagrangian optimization drastically reduced the computing time, and was one of the main ingredients for the success of the overall CFT scheme.

Alberto was also involved in a follow-up competition setup in 1995 by *FS* and *AIRO*, named *FARO*, that was aimed at developing effective heuristics for the crew rostering problem. In Caprara et al. (31), a new relaxed model was introduced that took explicitly into account all the rules for sequencing two consecutive duties within a roster, along with some main constraints on the total number of weekly rests. Based on that model, a constructive heuristic was proposed to build feasible rosters, one at a time, by sequencing duties in the roster according to dual information taken from the relaxed model. Once a roster was completed, all its duties were removed from the problem, and the process was iterated on the remaining duties. The resulting heuristic proved very effective, and ranked first in the FARO competition.

A global approach for the effective solution of the *Crew Planning Problem* is presented in Caprara et al. (32).

The general aim of the *Train Timetabling Problem* (TTP) is to provide a timetable for the trains required to be run by several *Train Operators* (TOs) on a certain part of the railway network. Each TO generates its own *ideal timetable* and submits this to the *Infrastructure Manager* (IM). Then the IM, in cooperation with the TOs, integrates the ideal timetables of the TOs into one single feasible timetable by minimizing the changes with respect to the ideal timetables.

Caprara, Fischetti and Toth (30) considered a TTP defined on a main single line (*corridor*), and proposed an ILP model based on the discretization of the time horizon. The problem is represented in a directed space-time graph whose nodes represent departures or arrivals of trains at stations along specific tracks. The arcs of this graph represent either a train traveling between two adjacent stations (in case they join a departure node to an arrival node), or a train stopping at a station (in case they join an arrival node to a departure node). The timetable for a single train corresponds to a path in this graph. The authors also proposed an effective heuristic algorithm based on the Lagrangian relaxation of the ILP model, where, for each train, the resulting Lagrangian problem calls for a

path having maximum Lagrangian profit. In Caprara et al. (55) and in Cacchiani, Caprara and Toth (11) the ILP model and the heuristic algorithm are extended for dealing with additional real-world constraints and with a railway network, respectively. Cacchiani, Caprara and Toth (10) proposed an alternative ILP model, in which each variable corresponds to a full timetable for a train, and heuristic and exact algorithms based on the solution of the LP relaxation of the ILP model.

The definition of the actual timetables within TTP generally does not take into account the actual routing of the trains within the stations. This is the purpose of the *Train Platforming Problem* (TPP), that must be solved separately for each station, in which one has to find for each train a so-called *route* from the point where it enters the station to the point where it leaves the station. Assuming that each train has to stop at a platform, a route is specified by the platform itself plus arrival/departure *paths* joining the entry/exit points of the train to the platform. Several objectives are generally taken into account, such as the minimization of the number of platforms used and the penalties incurred if a train is not assigned to a platform within a given preference list or possible conflicts on the arrival/departure paths arise.

Caprara, Galli and Toth (34) presented a general formulation of the problem, along with a MIP model which considers explicitly the full list of routes for each train (which is generally acceptably long) and has a quadratic objective function. The authors propose an efficient way to linearize the objective function by using a small number of additional variables along with a set of constraints that can be separated efficiently by solving an appropriate linear program.The LP relaxation of the corresponding MILP, solved through separation and pricing procedures, is used to drive a heuristic algorithm.

The rolling stock to be assigned to the trains whose timetable has been found by TTP can either be locomotives and train carriages, or aggregated modules, called *train units*. The latter are composed of a number of carriages in a fixed composition, and can move in both directions without the need of an extra locomotive. A train can then be composed of several coupled train units. Train units may exist in different types, representing technical characteristics and capacity. In order to obtain a better match between the available train units and the passengers' seat demand, the compositions of the trains usually can be changed at several stations by adding or removing train units from the trains. Let a *trip* be a part of a train timetable that must be performed by the same train unit without changes. The *Train Unit Assignment Problem* (TUAP) calls for the minimum cost assignment of the train units to the trips, possibly combining more than one train unit for a given trip, so as to fulfill the seat requests.

Cacchiani, Caprara and Toth (12) represented TUAP as a directed multigraph $G = (V, A)$ with a node in V for each trip. The arc set A is partitioned into different sets A^t, one for each train unit type t. An arc $(i, j) \in A^t$ represents the fact that trip j can appear right after trip i in a feasible sequence for train unit type t. With this representation, TUAP can be modeled as a multi-commodity flow problem. Namely, it calls for a min-cost collection of *paths* of G, each associated with arcs of the same type, such that each node is visited by a sufficient number of paths, with several constraints on the path feasibility. The authors proposed an ILP model having one variable for each possible path of each train unit type. A diving heuristic algorithm based on the LP relaxation of this model is developed, combined with a local search procedure. In Cacchiani, Caprara and Toth (13) a slightly different graph representation of the problem is presented, an alternative ILP model is proposed and a fast heuristic algorithm, based on the Lagrangian relaxation of the ILP model, is developed. The solution of the relaxed problem is computed by solving a sequence of assignment problems.

6 Farewell

Surveying Alberto's results has been a great opportunity for us to realize once again how lucky we have been in knowing him so closely, working with him and enjoying his creativity and his humor. But it confirms sadly how much we have lost. We believe Alberto's work will continue to be an inspiration for us, for the community at large and especially for the young generations of which Alberto was caring so much.

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Alberto Caprara (Foto: Juan-José Salazar González)

Alberto Caprara (1968–2012): Memories

by Valentina Cacchiani (U Bologna), Andrea Lodi (U Bologna), Enrico Malaguti (U Bologna), Ulrich Pferschy (U Graz), Juan-José Salazar-González (U La Laguna), Emiliano Traversi (TU Dortmund), and Gerhard Woeginger (TU Eindhoven)

Alberto and Aussois*

Alberto was used to celebrating his birthday here, he would have turned 45 tomorrow (January 9th). It is hard to explain why celebrating Alberto in Aussois is so special for us and how grateful we are to Mike, Gerd and Giovanni for this opportunity. It is certainly because of the picture you have just seen [printed on the right], the passion of Alberto for the mountains, passion for which Aussois might be responsible. But there is more to Albertos' connection with Aussois. Right after Alberto's death, Denis Naddef, Aussois inventor back in 1996, wrote in the webpage we dedicated to Alberto (http://albertocaprara.people.ing.unibo.it/gbook.php?page=1):

> *This is a very sad news. Alberto attended all Aussois meetings, except this very last one. He gave a talk in every one and we all enjoyed the scientific content but also the jokes at the end towards the politics of Italy. We will miss you.*

Many other memories and messages left by friends and colleagues on the webpage mentioned Aussois.

Mike in his welcome speech and introduction to the workshop yesterday reminded us that the goal of the Aussois organizers is not only to offer a fantastic scientific program but also to take care of creating a nice, warm and fun atmosphere. I think Alberto over the first 15 years of the workshop series has been instrumental to both goals. *Andrea*

*From the introductory speech to the two sessions dedicated to Alberto in the Aussois Combinatorial Optimization Workshop 2013. Five scientific talks by Alberto's more recent and former students, Michele Monaci, Valentina Cacchiani, Margarida Carvalho, Tiziano Parriani and Laura Galli, were presented.

Visits to Alberto

Growing up in the stimulating scientific environment of DEIS in Bologna, with mentors Paolo Toth and Silvano Martello and colleagues Daniele Vigo and Andrea Lodi, Alberto quickly became much sought by visitors. From a fairly young age he attracted colleagues from many countries who wished to spend some time with him and pursue joint research topics.

These visits did not require formal project proposals, but topics of common interest were quickly identified and work began. Thus, no time was wasted with writing proposals, accounts and reports; one could focus quickly on discussing problems. The cordial hospitality offered by Alberto and his wife Cristina helped to keep the costs low and the spirits high.

It should be pointed out that the working conditions of a researcher with a permanent position in the world-famous group of Bologna were quite modest. Alberto started with a desk in the corridor shielded by only two cubicle walls. This had the advantage that his visitors were immediately spotted by everyone else in the group and lively discussions frequently arose during the day. It seems that only when he became an associate professor, could Alberto move into a real office, of course sharing with three or four people. This did not change when he became a full professor. It would have been totally against his personality (and probably useless) to fight for vane status symbols such as door plates and a higher number of square meters.

Alberto's special talent for finding tucked away places in the country side serving delicious food of Emilia Romagna at a reasonable price but in large quantities ("items of high efficiency" in the knapsack terminology), was well-known at the department and to all his visitors. Many pleasant evenings were spent driving to places on tracks which seemed to lead absolutely nowhere, but ended up in some converted "castello" or extended farm house where the "padrone" himself served a seemingly infinite number of different authentic Italian dishes. Complicated bills were unknown, but rather very reasonable fixed amounts were charged in these places.

Alberto's thorough knowledge of railway systems was particularly helpful once when a visitor was dropped off at the Bologna railway station some Friday evening to catch the night train back home. Alberto noticed that Bologna Centrale was unusually quiet. Accompanying his guest to the platform of a completely deserted station, he realized that one of the traditional railway strikes was taking place. This was no problem for Alberto, who happily kept his guest for the weekend. After paying back this prolonged hospitality by mowing the lawn, the visitor shared some more time with Smokey, the beloved family dog. Being the reason for long walks, accompanied by stimulating discussions while wandering through the shrubs around Bologna, Smokey made it on the list of co-authors of a conference talk, but (according to SCOPUS) not on a real journal paper. He passed away shortly after his master. *Ulrich*

Studying with Alberto

Since the beginning Alberto was a brilliant student, a bit shy, with lots of scientific curiosity and creativity. He had the best qualities, studying deeply all the theoretical details in articles and books, and also with the best skill of a computer programmer in Fortran. Like other PhD students, he had his desk in the corridor of the department, implementing on a Digital DECstation 5000/240 (Boder1), by the time of Cplex 1. He was always kind and fully available to others in the department. Immediately it was easy for other PhD students to work with him, Alberto being the leader of the research and at the same time ready to prove and disprove conjectures or debug computer codes. Since very early in his scientific carrier he was the ideal co-author. But more than a PhD student, he was a friend, bringing others even to the house of his Grandmother for lunch (by the way, a wonderful cook that probably was the responsible for enlarging Alberto's remarkable stomach). As an example of the excellent integration of Alberto, he attended for example the "EURO Summer Institute X", on Combinatorial Optimization (Paris, July 2–15, 1994), where he met several colleagues that after became his co-authors of many good articles. *Juan José*

Studying under Alberto's supervision

A late-winter day Alberto took four of his current at the time and former students to a mountain trip on the snow. Emiliano was about to leave Italy for a post-doc in Germany, André was going back to his University in Brasil after a long period in Bologna, Paolo was starting his PhD in Bologna and I had just got an assistant professor position in Bologna. It was a changing time for everyone and an occasion to say goodbye to those that were leaving.

We started walking on the snow at sunrise, Alberto led the group with his relaxed rate, which was almost running for those not used to it. He showed us his woods, the creek, the lost trails that he discovered on the mountain, and of which he was the only hiker. This was his secret playground, he shared it with us on that very special day [see the picture taken by Alberto printed on the right], and it was a privilege to be there.

Picture taken by Alberto of his students during a mountain trip on the snow (Corno alle Scale, April 3, 2011): Alberto's comment on the webpage http://www.on-ice.it/onice/onice_view_report.php?type=4&id=2198 roughly said "How can people say that the PhD in Italy is not tough?"

Alberto was a bright researcher and strong alpinist. But where he was really extreme was eating. You could not leave a table where he was sitting before all the food was eaten, no matter how much, and all the wine was drunk. An Aussois fondue night at his table meant al least two bowls of fondue, many ile-flottante and an uncountable number of wine bottles. And later at night, as he used to say, you could even "see the dragons".

"Hey, is everything OK?" he appeared every day at the door of our office, always smiling, to hear the news about our work, or just to say hello, and to tell us of his beloved dog that he had to take for a walk at 3 in the morning, or about the next incredible mountain trip he had in mind to do. It was great to hear his stories, always ironic and never trivial, his jokes said under his breath and his valuable advice. Alberto was without compromise, he was one who did not spare himself, but brought on his ideas and passions without limits.

Humbleness and brightness, these are two aspects of Alberto I enjoyed a lot while talking to him. I think he was not fully aware of his positive impact on the people around him. For example, one of the many things Alberto left to me is one sentence during his speech as head of the committee for my master thesis: "In life there are no choices that are right or wrong *a priori*. What makes a choice right or wrong is the commitment that day by day we show in order to pursue it." At that time, my PhD with him was not started yet, but he already started teaching me important lessons …

Enrico, Valentina, Emiliano

Alberto's Talks

I do not remember precisely when I attended the first talk by Alberto. Perhaps it was at IPCO'1996 in Vancouver, when he presented his heuristic (with Matteo Fischetti and Paolo Toth) for the set covering problem, but more likely it was at some smaller European meeting around the same time.

Alberto liked to build up tension and then break it. He would say something like: *"The most fascinating question in this area concerns […]. This is important since […], and one needs deep insight and fundamentally new ideas for making progress on it. Hence, I will not talk about this, but about something completely different."* Anyway, his talks were never aseptic or overly polished. His overhead slides were of-

ten monochrome, written in black (until the black pen ran out of ink) and then blue (until the blue pen ran out of ink). The slides did not matter at all, since he was so enthusiastic and electrifying in presenting his results.

Whenever Alberto gave a talk at the Aussois meeting on combinatorial optimization, his last slide would contain a report on the latest wrongdoings of Silvio Berlusconi. I remember a slide on a mausoleum, for which Berlusconi had to bend and rewrite the local water protection laws. I remember a slide on the past life of one of Berlusconi's incompetent ministers, and I remember that after that talk Matteo got worried and told Alberto to be more cautious and diplomatic in his public statements. *Gerhard*

Announcements

Workshop: Nonlinear Optimization – A Bridge from Theory to Applications

Erice, Italy June 10–17, 2013. This is the 59th Workshop of the International School of Mathematics "G. Stampacchia" at the Ettore Majorana Centre and Fondation for Scientific Culture (EMCFSC). It is the seventh Workshop on Nonlinear Optimization and related topics. The preceding ones have been held every three years starting from 1995.

The Workshop aims to review and discuss recent advances and promising research trends in Nonlinear Optimization and to provide a forum for fruitful interactions in strictly related fields of research, with a particular focus on applications. Topics include

- constrained and unconstrained nonlinear optimization
- global optimization
- mixed integer nonlinear programming
- derivative-free methods
- nonsmooth optimization
- nonlinear complementarity problems
- variational inequalities
- equilibrium problems
- game theory
- bilevel optimization
- optimization and machine learning
- applications of nonlinear optimization

The Workshop will include invited lectures (1 hour) and contributed lectures (30 minutes). Members of the international scientific community are invited to contribute a lecture describing their current research and applications.

Invited lecturers who have confirmed the participation are:

- Alfio Borzi', University of Wurzburg, Germany
- Vladimir Demyanov, University of St. Petersburg, Russia
- Daniela Di Serafino, II Università di Napoli, Italy
- Francisco Facchinei, Sapienza Università di Roma, Italy
- David Y. Gao, University of Ballarat, Australia
- Manlio Gaudioso, Università della Calabria, Italy
- Tom Luo, University of Minnesota, USA
- Kaisa Miettinen , University of Jyväskylä, Finland
- Laura Palagi, Sapienza Università di Roma, Italy
- Jong-Shi Pang, University of Illinois, USA
- Stephen Robinson, University of Wisconsin, USA
- Gesualdo Scutari, State University of New York at Buffalo, USA
- Gerhard W. Weber, Middle East Technical University, Ankara, Turkey
- Ya-Xian Yuan, Chinese Academy of Science, China

The Scientific and Organizing Committe:

- Gianni Di Pillo, Sapienza, University of Rome, Italy
- Franco Giannessi, International School of Mathematics, EMCFSC, Erice, Italy
- Massimo Roma, Sapienza, University of Rome, Italy

Further information: www.dis.uniroma1.it/~erice2013
Email: erice2013@dis.uniroma1.it.

11th EUROPT Workshop on Advances in Continuous Optimization

June 26–28, 2013, Florence, Italy. We announce the 11th EUROPT Workshop which will be held in Florence on June 26–28, 2013. The Organizing Committee is chaired by Laura Palagi (Sapienza, Università di Roma) and Fabio Schoen (Università degli Studi di Firenze). EUROPT 2013 will be a satellite meeting of the XXVI EURO/INFORMS joint meeting held in Rome July 1–4, 2013.

The primary objectives of EUROPT are to disseminate state-of-the-art knowledge and to support research in the broad area of continuous optimization. The Workshop will feature a series of invited lectures, together with invited and contributed sessions. Each session will consist of three or four talks.

Topics include – but are not limited to – the following areas:

- Linear and nonlinear local optimization
- Large-scale optimization
- Mixed integer nonlinear optimization
- Derivative-free optimization
- Global optimization
- Complementarity and variational problems
- Conic optimization and semi-definite programming
- Complexity and efficiency of optimization algorithms
- Convex and non-smooth optimization
- Optimal control
- Multi-objective optimization
- Robust optimization
- Semi-infinite programming
- Stochastic optimization
- Optimization in data mining
- Optimization in industry, business and finance
- Analysis and engineering of optimization algorithms
- Optimization software development

Invited speakers

- Jacek Gondzio (School of Mathematics, University of Edinburgh, Scotland, U.K.)
- Chih-Jen Lin (Department of Computer Science, National Taiwan University, Taiwan)
- Marco Locatelli (Dipartimento Ingegneria Informatica, Università di Parma, Italy)

Registration fees: Regular: 200 EUR (early) / 300 EUR (late)
Student: 140 EUR (early) / 160 EUR (late)
Accompanying person: 120 EUR
Extra ticket for the conference dinner: 60 EUR
Early registration deadline: May 10th, 2013

Please visit www.europt2013.org for more information or contact europt2013@gmail.com.

Florence is one of the top destinations for culture, art and tourism, and it is widely recognized as one of the most beautiful cities of the world. Since the end of June is high tourist season, we strongly recommend to book as early as possible accommodation and flight.

MIP 2013

July 22–25, 2013, University of Wisconsin-Madison, Madison, WI, USA. You are cordially invited to participate in the upcoming workshop in Mixed Integer Programming (MIP 2013). The 2013 Mixed Integer Programming workshop will be the tenth in a series of annual workshops held in North America designed to bring the integer programming community together to discuss very recent developments in the field. The workshop series consists of a single track of invited talks and a poster session.

This year's confirmed speakers are:

- Tobias Achterberg, IBM CPLEX Optimization
- Pietro Belotti, Clemson University
- Greg Blekherman, Georgia Institute of Technology
- Sergei Chubanov, University of Siegen
- Daniel Dadush, New York University
- Marco Di Summa, University of Padova
- Yuri Faenza, EPFL Lausanne
- Oktay Gunluk, IBM T.J. Watson Research
- John Hooker, Carnegie Mellon University
- Matthias Koeppe, University of California, Davis
- Quentin Louveaux, University of Liege
- Carla Michini, ETH Zurich
- Marco Molinaro, Carnegie Mellon University
- Eduardo Moreno, Universidad Adolfo Ibanez
- George Nemhauser, Georgia Institute of Technology
- Thomas Rothvoss, MIT
- Mohit Singh, McGill University
- Gautier Stauffer, Grenoble Institute of Technology
- Mathieu Van Vyve, Catholic University of Louvain
- Juan Pablo Vielma, MIT
- Laurence Wolsey, Catholic University of Louvain
- Bo Zeng, University of South Florida
- Muhong Zhang, Arizona State University

The workshop is designed to provide ample time for discussion and interaction between the participants, as one of its aims is to facilitate research collaboration. A poster session will be held on the first evening of the workshop (July 22). Thanks to the generous support by our sponsors, registration is free.

MIP 2013 Organizing Committee: Amitabh Basu, University of California, Davis; Daniel Bienstock, Columbia University; Alberto Del Pia, ETH Zurich; Santanu Dey, Georgia Tech; Jim Luedtke, University of Wisconsin-Madison.

Information and registration:
https://events.discovery.wisc.edu/mip2013/ or
mip2013@discovery.wisc.edu

Recent Advances on Optimization

July 24–26, 2013, Toulouse, France. An international conference on optimization will be organized under the umbrella of a research programme supported by the RTRA STAE foundation in Toulouse.

The conference will address topics in unconstrained and constrained optimization, with and without derivatives. It will be also the occasion to celebrate the many contributions made by Philippe L. Toint to the field. A half-day session related to the RTRA data assimilation project "ADTAO" will be part of this conference.

Contributed talks and posters related to the topics of the conference are welcome, and will be added to the programme as far as schedule constraints permit.

Confirmed invited speakers:

- Stefania Bellavia – University of Florence (Italy)
- Andrew Conn – IBM T. J. Watson Research Center (USA)
- John Dennis – Rice University (USA)
- Andreas Griewank – Humboldt University of Berlin (Germany)
- Michael Kocvara – The University of Birmingham (UK)
- Jorge More – Argonne National Laboratory (USA)
- Benedetta Morini – University of Florence (Italy)
- Jorge Nocedal – Northwestern University (USA)
- Michael Powell – Cambridge University (UK)
- Annick Sartenaer - University of Namur (Belgium)
- Mike Saunders – Stanford University (USA)
- Katya Scheinberg – Lehigh University (USA)
- Luis Nunes Vicente – University of Coimbra (Portugal)
- Ya-xiang Yuan – Chinese Academy of Sciences (China)
- Stephen Wright – University of Wisconsin (USA)

Registration: Thanks to our sponsors, no registration fees are required. However registration is mandatory. Registration information (name, firstname, affiliation) should be sent directly to Brigitte Yzel (yzel@cerfacs.fr). Registration deadline: May 15, 2013.

Information on how to submit your contribution can be found on the webpage of the conference: www.fondation-stae.net/fr/optimization-july2013.html

Looking forward to welcoming you in Toulouse! On behalf of the scientific and local organization committees: Coralia Cartis, Nick Gould, Serge Gratton and Xavier Vasseur

MOPTA 2013

August 14–16, 2013, Lehigh University, Rauch Business Center, Bethlehem, PA, USA. MOPTA aims at bringing together a diverse group of people from both discrete and continuous optimization, working on both theoretical and applied aspects. There will be a small number of invited talks from distinguished speakers and contributed talks, spread over three days. Our target is to present a diverse set of exciting new developments from different optimization areas while at the same time providing a setting which will allow increased interaction among the participants. We aim to bring together researchers from both the theoretical and applied communities who do not usually have the chance to interact in the framework of a medium-scale event.

Confirmed plenary speakers:

- Brian Denton (U. of Michigan)
- Abhijit Deshmukh (Purdue U.)
- Omar Ghattas (U. of Texas at Austin)
- Ignacio Grossmann (Carnegie Mellon U.)
- Zhi-Quan (Tom) Luo (U. of Minnesota)
- Jorge Nocedal (Northwestern U.)
- Henry Wolkowicz (U. of Waterloo)

Organizing Committee:

- Frank E. Curtis (Chair)
- Tamás Terlaky
- Katya Scheinberg
- Ted K. Ralphs
- Robert H. Storer
- Aurélie C. Thiele
- Larry V. Snyder
- Eugene Perevalov
- Luis F. Zuluaga

Further information: http://coral.ie.lehigh.edu/~mopta/

We look forward to seeing you at MOPTA 2013!

GeoLMI 2013: Conference on Geometry and Algebra of Linear Matrix Inequalities

November 12–16, 2013, Centre International de Rencontres Mathématiques (CIRM), University of Marseille, Luminy, France. This is a conference organized by Didier Henrion and Monique Laurent, jointly with the 3rd official meeting of the GeoLMI project funded by the French National Research Agency.

The conference aims at bringing together various researchers in pure and applied mathematics (real algebraic geometry, commutative algebra, functional analysis, continuous and discrete optimization) interested in linear matrix inequalities and their application areas (operations research, system control, performance analysis of dynamical systems).

For details and how to register please consult the webpage of the conference: http://homepages.laas.fr/henrion/geolmi13

PRELIMINARY ANNOUNCEMENT SIAM Conference on Optimization 2014

May 19–22, 2014, Town and Country Resort & Convention Center, San Diego, California, USA.

Conference themes:

- Applications in health care
- Applications in engineering
- Conic optimization
- Derivative-free optimization
- Mixed integer nonlinear optimization
- Nonlinear optimization
- Polynomial optimization
- Stochastic optimization

Organizing committee:

- Miguel Anjos, Ecole Polytechnique de Montreal, Canada (co-chair)
- Michael Jeremy Todd, Cornell University, USA (co-chair)
- Aharon Ben-Tal, Technion – Israel Institute of Technology, Israel
- Andrew Conn, IBM Research, USA
- Mirjam Dür, University of Trier, Germany
- Michael Hintermüller, Humboldt-Universität zu Berlin, Germany
- Etienne de Klerk, Nanyang University of Technology, Singapore
- Jon Lee, University of Michigan, USA
- Todd Munson, Argonne National Laboratory, USA
- Warren Powell, Princeton University, USA
- Daniel Ralph, University of Cambridge, United Kingdom
- Ariela Sofer, George Mason University, USA
- Akiko Yoshise, University of Tsukuba, Japan

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iccopt 2013

International Conference on Continuous Optimization

Caparica - Lisbon - Portugal
http://eventos.fct.unl.pt/iccopt2013

Department of Mathematics, FCT, Universidade Nova de Lisboa
Mathematical Optimization Society

Conference
July 27 - August 1

Plenary Speakers

Paul I. Barton
Michael C. Ferris
Yurii Nesterov
Yinyu Ye

Semi-Plenary Speakers

Amir Beck
Regina Burachik
Sam Burer
Coralia Cartis
Michel De Lara
Victor DeMiguel
Michael Hintermüller
Ya-xiang Yuan

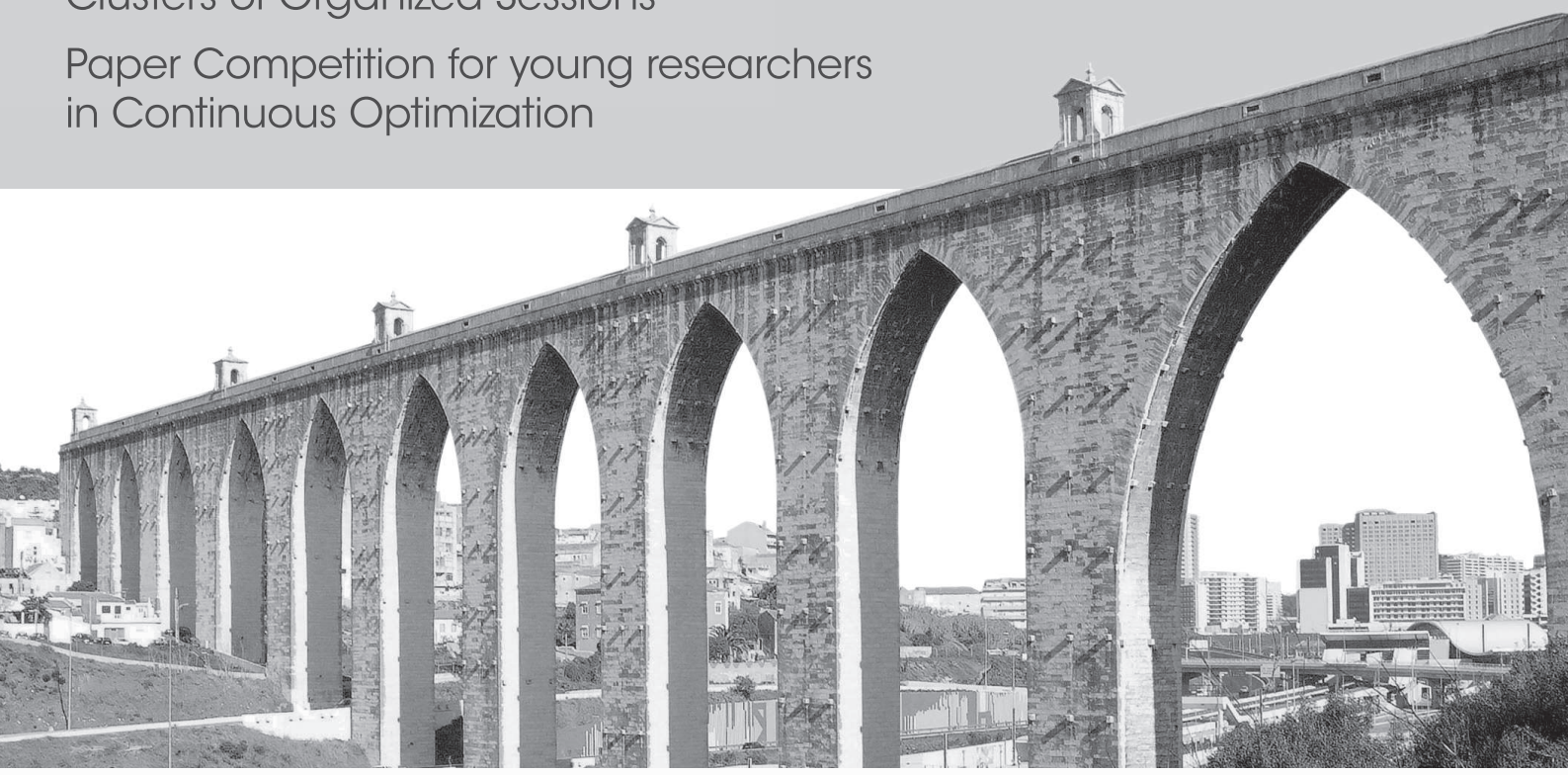
Summer School
July 27 - 28

PDE-Constrained Optimization
by M. Ulbrich, C. Meyer

Sparse Optimization and Applications to Information Processing
by M. A. T. Figueiredo, S. J. Wright

Clusters of Organized Sessions

Paper Competition for young researchers in Continuous Optimization



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