Grooming-Enhanced Multicast in Multilayer Networks with Bacterial Evolutionary Algorithm

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Abstract: In this paper we introduce new, bacterial evolutionary algorithm (BEA) based methods for routing unicast and multicast demands in grooming capable multi-layer optical wavelength division multiplexing (WDM) networks. The methods introduced are compared with both well known heuristic methods, accumulative shortest path heuristic (ASP) and minimum path heuristic (MPH), and as well as with ILP. We prove the strength of our approach by comprehensive simulations in our versatile simulator.

Keywords: WDM, bacterial evolutionary algorithm, ILP, MPH, multicast, unicast

1 Introduction

In recent years the traffic load of transport networks has increased significantly due to the rapid growth of Internet and network based applications. A time will come when the network providers cannot satisfy the traffic demands by merely enlarging network capacities. An effective routing method is needed to solve the problem.

At the present time network traffic can be divided into two solidly different classes: unicast and multicast demand. While the unicast demand can be

characterized by its source, its only one destination and the required bandwidth, the multicast demand has more than one destination sharing the same bandwidth.

Some of the well known unicast applications are file transport, voice over IP (VoIP), net banking, etc. Multipoint applications include very important broadband services such as digital media broadcasting (e.g. IP-TV, IP-Radio, etc.), VoD streaming, distance learning, virtual private LAN services, etc [1].

The problem of optical routing of unicast demands was mentioned in various cases and places, a detailed classification can be read in [8]. Here we only review those few most closely related. In [6] the problem was solved by genetic programming. In this approach each gene represents the routing of a demand chosen from a previously calculated set. The authors of [7] solved the same problem by a similar approach but the full path stored in the DNA.

Just like the unicast one, multicast routing is also a key issue in network management. In [2] a heuristic method for the problem of multicast routing and wavelength assignment in WDM ring networks was proposed. Several heuristic tree formation algorithms were proposed in [3]. The aim of [4] is to demonstrate the advantage of multicast demands. In this paper an ILP formalism was also given. In [9] a solution for the Steiner-tree problem is given with the use of genetic programming.

2 Problem Formulation

A two-layer network is assumed, where the upper, electronic layer is time switching capable, while the lower, optical layer is a wavelength (space) switching capable one. The electronic layer can perform traffic grooming, i.e. multiplexing low bandwidth demands into a single WL channel. The two layers are assumed to be interconnected, while routing, the control plane has information on both layers and both layers take part in accommodating a demand.

Network topology and the number of fibers are assumed given as well as the description of traffic demands. The capacity of WL channels and the cost of routing, (e.g. space switching, optical to electronic conversion, WL branching, etc.) can also be given. We assume static traffic consisting of unicast and multicast demands. The objective is to reach all destination node(s) from the source while observing all routing and technical constraints (for example: bandwidth limit of the links) and minimizing the cost.

3   Network Model

We use a wavelength graph model for routing in two layer networks with grooming and with different types of nodes and arbitrary topologies. The WL graph corresponding to the logical network is derived from the physical network considering the topology and capabilities of physical devices. A simpler version of the model has been first proposed in [5].

The types of nodes can also be quite different: Optical Add-and-Drop Multiplexers (OADM), Optical Cross-Connects (OXC: optical core) with full or limited, optical or opto-electrical WL conversion or even an Opto-Electrical Cross-Connect (OEXC: electrical core) [17]. Furthermore, some of these nodes support grooming, typically with a limited number of optical ports. All these properties can be considered in the WL graph model, together with different protection techniques of traffic demands.

The network consists of nodes and links connecting the nodes. Both ends of an optical link (fiber) are attached to an interface (IF) of a physical device, which determines the number of supported WLs in the fiber. Every physical device contains an internal switching fabric and some IFs. Each link and every physical device has a specific logical representation in the WL graph.

A physical link is derived to as many logical edges as the number of available WLs in the link. The logical sub-graph of a physical device depends on the capabilities of the device. Every edge in the graph has a capacity and a cost of usage. The capacity of the edge usually equals to the WL capacity, which depends on the used carrier. The cost of the edge is determined by its functionality (WL edge, O/E conversion, etc.).

A physical device is modeled by a sub-graph. It represents all IFs of the device, and the capabilities of its internal switching fabric. The WL graph model (together with our ILP framework) can support devices with different capabilities appearing in the network at the same time. The model is easily extendable; the type of devices can be changed later, if new internal models are introduced.
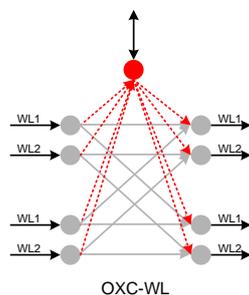

Figure 1

Sub-graph of an OXC-WL device in the wavelength graph

A sub-graph of a versatile physical device is depicted in Figure 1. The equipment is a combination of an OXC with WL-conversion and an OADM: it can originate and terminate traffic demands, as well as perform space-switching. WL-conversion and splitting (branching) of light-trees can only be performed in the electronic layer. This is illustrated by an electronic node in the sub-graph, while other (pairs of) logical nodes correspond to interfaces. Figure 1 assumes two fibers being connected to the device, and two WLs per fiber, which results in two input and two output interfaces – because all edges are directed. We will use this complex node in the simulations.

4 Previous Routing Algorithms

Several algorithms can be applied to route the demands in the network. A simple example illustrating the different outcome of the algorithms is shown in Figure 2.

4.1 ILP Routing and FormulationEquation Section 4

ILP always provides the optimal cost of routing the current demands in the system, thus it serves as a baseline for comparison. On the other hand ILP routing usually consumes much time since the current problem is NP-hard [17]. The ILP formalism that was used can be read in [4].

4.2 Accumulative Shortest Path Heuristic

Accumulative shortest path algorithm (ASP), also known as Dijkstra's algorithm, is fast, simple and easy to use but in the other hand it is rather costly. It can be applied to route demands one-by-one.

The ASP algorithm in case of multicast demands works as follows: routes are calculated between the source and the destination nodes one after the other. The algorithm operates directly on the logical network (wavelength graph). The source and the destination nodes of a sub-demand are the electronic nodes of the corresponding physical device. The cost of already reserved edges of the graph is set to zero, which means it can be used for free. The bandwidth usage is non-additive in case of multicast demands, i.e. if two or more sub-demands of the same demand share the same wavelength the needed bandwidth is the same as one's.

4.3 Minimal Path Heuristic (MPH)

This heuristic is used in case of multicast, since for unicast demands its result is the same as ASP. This heuristic usually gives better results than ASP but it is slightly slower.

The MPH algorithm transforms the original wavelength graph into a virtual graph and applies Prim's algorithm [10] to form a minimum cost spanning tree. A virtual graph is a full mesh, in which only the source and all the destination nodes are presented. The weight of an edge in the virtual graph expresses the cost of the shortest path in the original wavelength graph (which implies that the shortest path has to be calculated for every node pair in both directions). Prim's algorithm is applied in this virtual graph. After the minimal cost spanning tree is found the paths are traced back into the original wavelength graph. A last phase may be needed to meet some physical constraints. Details of the MPH algorithm can be read in [11].
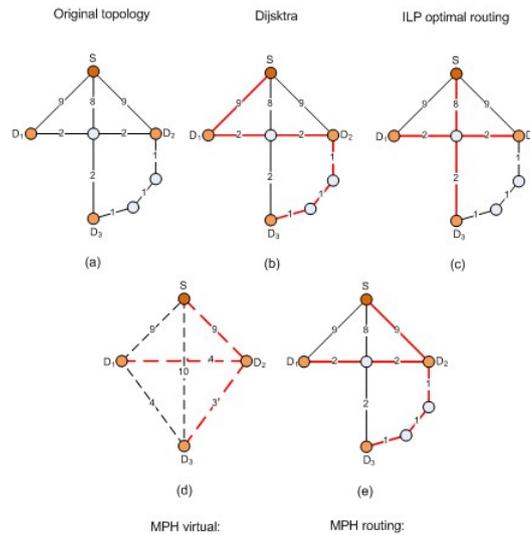

Figure 2

Original topology with the source node and three leave nodes (a), ASP routing (b) , ILP optimal routing (c), MPH virtual topology and routing (d), MPH routing (e)

5 Bacterial Evolutionary Algorithm

There exist various optimization algorithms, which have been inspired by natural selection processes. The advantage of these algorithms is their ability to solve and quasi-optimize problems with non-linear, high-dimensional, multimodal, and discontinuous character. These processes can easily be applied in optimization problems where one individual corresponds to one possible solution of the problem. The original Genetic Algorithm (GA) was developed by Holland [15] and was based on the process of evolution of biological organisms. Recognized as a powerful global search technique, genetic algorithms have been applied to a wide variety of problems.

A slightly different evolutionary technique is called bacterial evolutionary algorithm (BEA) which was inspired by the microbial evolution phenomenon [16]. BEA has already been successfully applied to rule learning [14] and feature selection [13].

The BEA works on a given population of bacteria. Every bacterium represents a solution for the problem. The size of the population, i.e. the number of bacteria, is predefined. A bacterium has a genotype and a phenotype. The genotype is the knowledge of the bacterium, while the phenotype is the concrete solution calculated from the previous one. A function, called fitness function, is given to measure the quality of the solution.

There are two operators in the BEA: the bacterial mutation and the gene transfer. These operators are applied as it can be seen in .
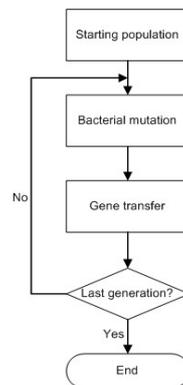

Figure 3
Flowchart of Bacterial Evolutionary Algorithm

During the bacterial mutation at once one part of the gene sequence is selected, and a previously given number of clones are generated. A clone only differs from the original bacterium in the currently examined part of the gene sequence. If a

clone is better, i.e. its fitness is bigger then the original bacterium is replaced. The length of the examined part is specified with its ratio to the full length. Mutation step is finished only when all the bacteria have been examined in full length.

The goal of the gene transfer is to distribute knowledge among bacteria. Bacteria are ordered according to their fitness value. One bacterium is randomly chosen from the better half, one from the worse half population. If their fitness values are not equal, than the better one gives a part of its gene sequence to the worse one. The length of the transfer is an input parameter for the algorithm as well the number of gene transfers during a bacterial cycle.

6   The Proposed Encoding

6.1   Fitness Function

The goal is to minimize the cost of the routing. Hence the fitness should be the routing cost multiplied by minus one. However, usually a cheaper solution can be obtained by not routing one or more demands. For this reason a penalty cost is added to the base fitness for every unrouted demand. Therefore in case of inadequate bandwidth, i.e. it is not possible to route all the demands, the algorithm tries to find a solution with maximal number of routed demands and with the cheapest cost.

6.2   Genotypes and Phenotypes

In our approach the goal is to avoid the well known faults of the heuristic algorithms. Thus heuristic algorithms (see Session 0 and 0) are applied to calculate the phenotype and the fitness, but the routing order and cost conditions are encoded in the genotype. Thus genotype of a bacterium is divided into two different parts: the first one is the set of virtual costs; the second one is the order of routing.

For every edge in the net there is a corresponding virtual cost in every bacterium. The heuristic routing algorithm, that currently takes place during BEA to evaluate the phenotype from the genotype, uses these values as the costs of the edges, meanwhile the fitness is still calculated with the original costs. An example is given in Figure 4.
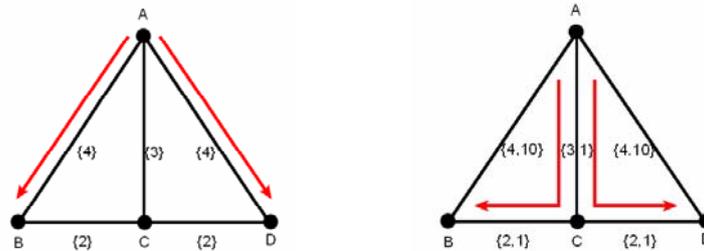
Figure 4

Faults of routing algorithms, two demands AB and AD, original ASP routing (left) with cost 8, routing on virtual costs (right), with cost 7

The genotype contains the routing order, too. An example is given in Figure 5 to show the advantage of this idea.
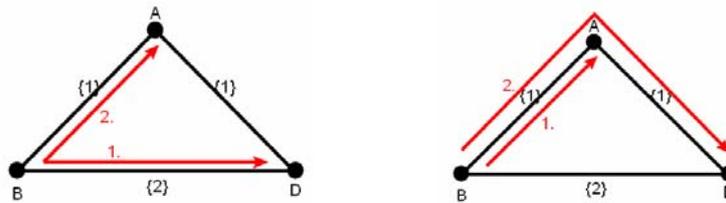

Figure 5

Faults of routing algorithms, two demands BA and BD, original routing order (left), better routing order (right)

7 Results

To optimize the application of our approach the first goal is to find a suitable setting for the further usage. A suitable setting means that the likelihood of finding a good solution is as great as possible whilst time is not wasted. During the search for it at each simulation sequence only one parameter is modified meanwhile the others are fixed. For simulation the COST266 reference network was used [12], with tree wavelength in every link, 2500 GB capacity pro link. Every demand has bandwidth of 500 GB and its source and destination(s) are chosen randomly.

7.1 Unicast

During the search for the best settings 15 unicast demands were inserted into the network.

7.1.1 Number of Bacteria

Figure 6 shows the changing of the fitness and time with different numbers of bacteria. The time dependence is linear. The optimal number of bacteria is about 6.
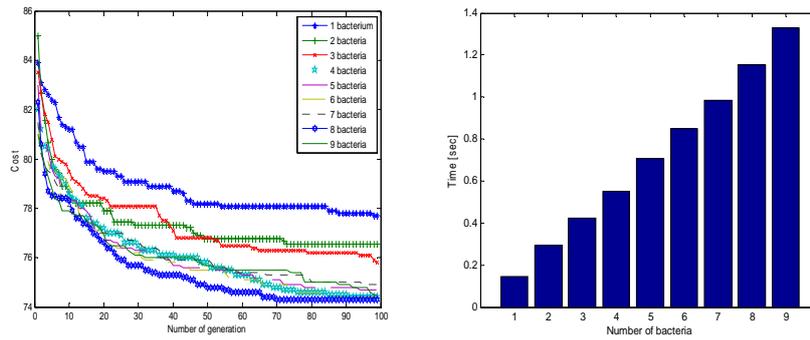

Figure 6

Change in cost (left) and time (right) according to the generation and the number of bacteria

7.1.2 Number of Clones

Figure 7 shows the change of the cost with different number of clones. Applying more clones means faster convergence in the first few generations. But the gain with an additional clone is less and less significant as the number of generations increases.
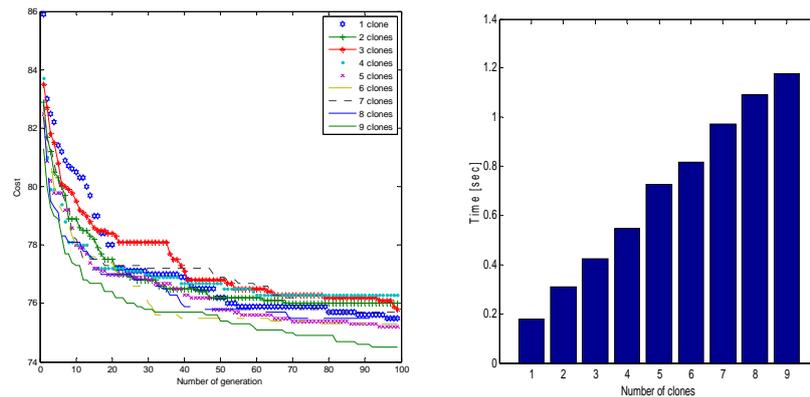
Figure 7

Change in cost (left) and time (right) according to the generation and the number of clones

7.1.3 Mutation Ratio

Mutation ratio tells the length of the examined part during a bacterial mutation for a bacterium. Larger value means smaller part. As Figure 8 illustrates, its best value is about 5, too. There is quite small number of demands in the net to saturating thus there are big unused parts in the genome that can be freely manipulated. However, during BEA improvements are searched locally, thus a large mutation length may be the wrong choice.
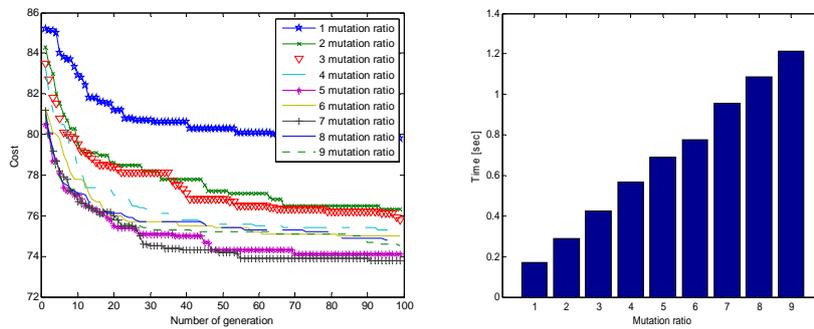

Figure 8

Change in cost (left) and time (right) according to the generation and the mutation ratio

7.1.4 Gene Transfer Length and Number of Gene Transfers

As Figure 9 illustrates, these two parameters are not as important as the ones before. However they can not be omitted to maintain knowledge distribution. The run time of the algorithm is nearly independent from their values.
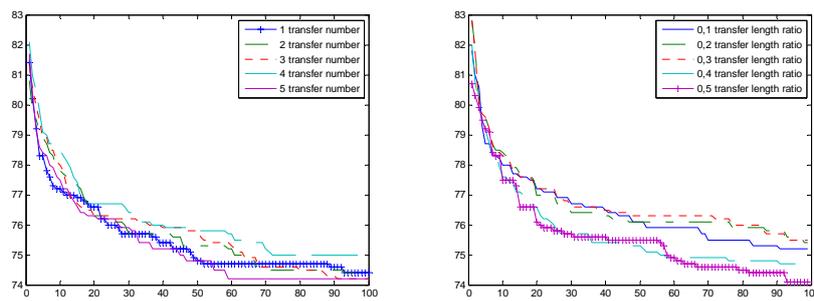

Figure 9

Change in cost according to the generation with the transfer number (left) and transfer length ratio

(right)

7.1.5 Generation Number

All the simulations showed that in the first 10-20 generation the improvement of every generation is usually good. After this period the gain of another generation falls radically. Thus in most cases 30 generation is enough to find an adequate solution and after the 100th generation the improvement is not considerable.

7.1.6 Suggested Settings

According to the previous studies the good setting is something like as follows: 30-100 generations, 5-6 bacteria, 4-5 clones, mutation ratio is 4-5, 3 gene transfers in a cycle and 0.3 part of gene sequence is transported in every gene transfer.

7.1.7 Performance

The performances of the algorithms are displayed in Figure 10. ILP is always the cheapest, as expected, but also the slowest. Heuristic method (ASP) is the fastest but also the worst. Meanwhile the BEA offers something between these two. During 30-100 generations the results of the ILP method can be achieved in notably less time. Even there is only time for the first generation the result is still better than the heuristic one whereas time is affordable.
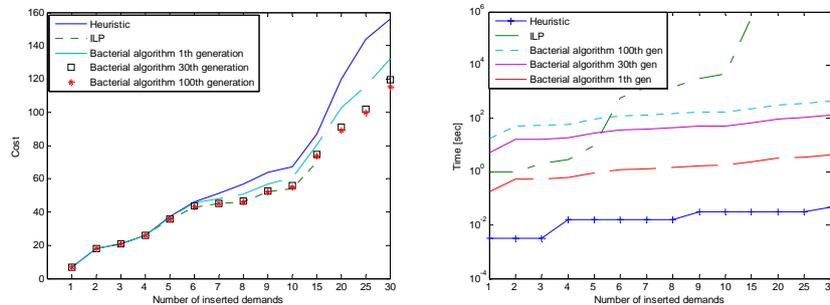

Figure 10
Performance of the methods in cost (left) and time (right)

7.2 Multicast

For multicast demands two well known heuristics were implemented to evaluate the genotype (see Section 0). The same search for affordable settings was done for these two as in the unicast case. In this case four multicast demands with eight destinations for each were inserted. The results were almost the same as before. The suitable setting is as follows: 30-100 generations, 5-6 bacteria, 4-5 clones, mutation ratio is 4-5, gene transfer is 3 and 0.3 part of gene sequence is

transported in every gene transfer for both type. The solution is linear with the number of bacteria, number of clones and mutation rate and nearly independent from the other parameters.

7.2.1   Comparison of the Evaluation Methods for BEA

As Figure 11 illustrates, at the same generation the MPH evaluation almost always gives better results than ASP evaluation. With the growth of the complexity the gain is increasing.

However, if the solution time is also measured the picture is changing a bit. The MPH evaluation in average is twice slower than the ASP evaluation and this ratio is increasing with the complexity although not significantly. Consequently if the speed is important then the ASP evaluation is suggested, if the quality of the solution is relevant then the MPH evaluation is proposed.
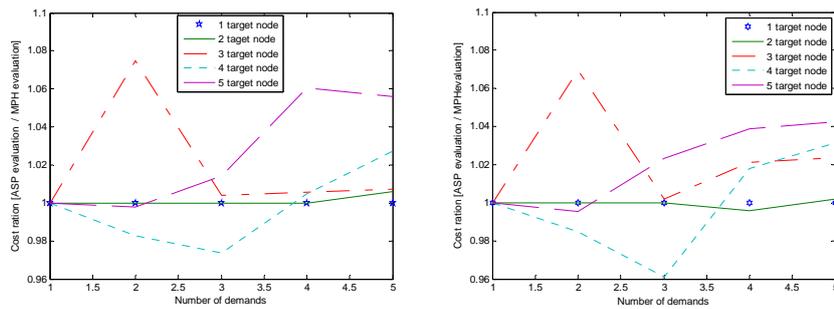

Figure 11

ASP evaluation pro MPH evaluation in cost, 1st generation (left), 30th generation (right)

7.2.2   BEA and the Heuristic Algorithms

In Figure 12 the solution cost of the heuristic algorithms is compared to the first generation result of ASP evaluation BEA. In Figure 13 the same is displayed but in term of the elapsed time. The first generation of BEA is almost always better than the classical heuristics, especially in complex cases with affordable time.

If a later generation is mentioned then the gain of the BEA is increasing, but the time difference is growing, too as shown in Figure 14.
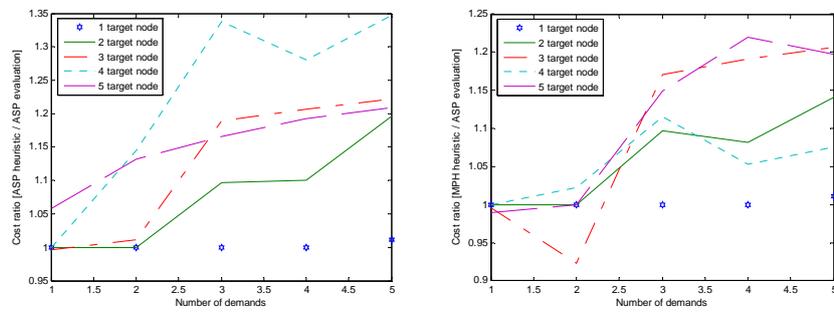
Figure 12

Heuristics pro ASP evaluation 1st generation in cost, ASP heuristic (left), MPH heuristic (right)
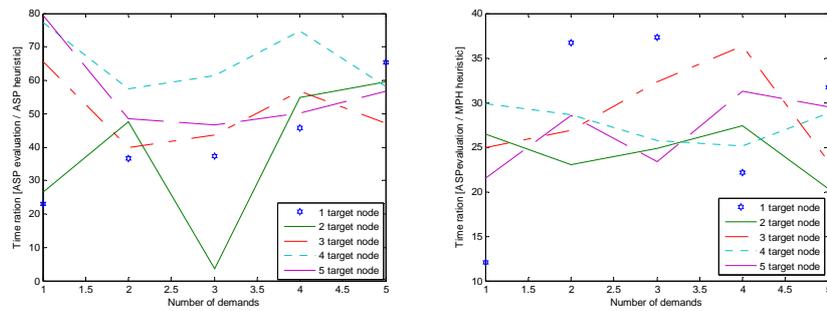

Figure 13

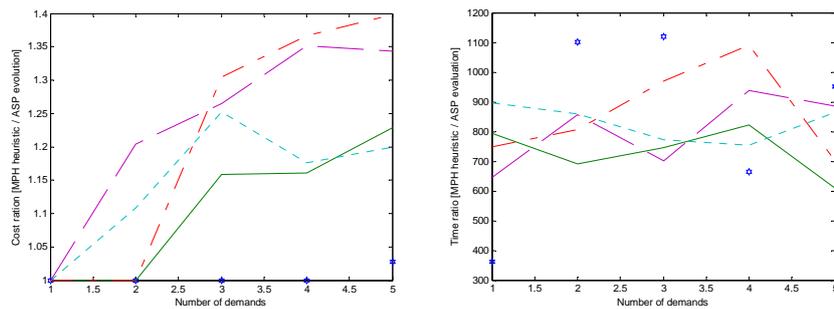Heuristics pro ASP evaluation 1st generation in time, ASP heuristic (left), MPH heuristic (right)

Figure 14

MPH heuristic pro ASP evaluation 30th generation in cost (left) and time (right)

7.2.3 Bacterial Evaluation and ILP

In this case the goal was to find as good results as possible. Hence MPH evaluation with 100 generation is used. The result is shown in Figure 15. The MPH evaluation is always near to the ILP result but its speed is up to 200 times faster.
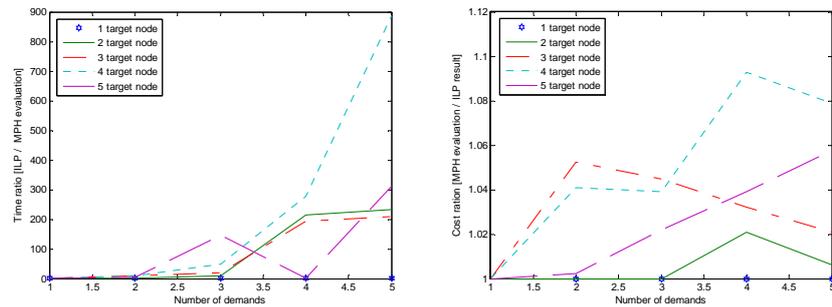

Figure 15

ILP pro MPH evaluation 100th generation in time (left), MPH evaluation pro ILP in cost (right)

Conclusions

We have presented a new and powerful way to find optimal routing in WDM networks. This method can be applied for unicast and multicast demand as well. Usually it finds nearly as good solution as the ILP but its time dependence is polynomial.

The proposed encoding can be easily extended for nearly all routing and other selected problems in connection with network.

Acknowledgements

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