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To cite this version:

Patrice Calégari, Pierre Kuonen, Frédéric Guidec, Daniel Wagner. A Genetic Approach to Radio Network Optimization for Mobile Systems. VTC'97, May 1997, Phoenix (AZ), United States. pp.755-759. hal-00347016

HAL Id: hal-00347016

https://hal.science/hal-00347016

Submitted on 13 Dec 2008

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A Genetic Approach to Radio Network Optimization for Mobile Systems

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Technical subject area: Mobile communication networks
Key contribution: Automatic optimal BTS placement for mobile communication networks

August 12, 1996

1 Introduction

One of the issues a telecommunication vendor must face when deploying a cellular network is the selection of good locations for base transceiver stations (BTSs). Roughly speaking, the problem comes down to finding out the best possible sites for BTSs, while guaranteeing that all –or at least a given percentage of– the traffic can be served and that the global cost of the radio network is kept at a minimum.

Several approaches are currently investigated to achieve this goal in the STORMS[1] project. This paper describes one of these, which combines computational techniques taken from the graph theory domain together with bio-inspired algorithms.

2 Hypothesis

In the remaining of this paper, we assume that a user-defined set of potential BTS locations is provided as an input to our computation, and that each BTS location is associated a cost.

We also assume that the cell served by a given BTS can be computed and returned by a function ad hoc. The computation that is actually performed by this function may be based on sophisticated wave propagation models, or it may be the result of a draft estimation. Our only requirement is that a cell be discretized, that is, a cell should be described as a finite collection of geographical locations.

3 Model

Our goal is to select a satisfactory subset out of the user-provided set of BTS locations, while ensuring that at least a given percentage of the region considered is served by the selected BTSs.

The approach we consider is based on the notion of dominating set, which originates in the graph theory.

Given a graph $G = (V, E)$ where V is a set of vertices and E is a set of edges, a dominating set[2] of G is a subset $V' \subseteq V$ defined by:

$$\forall u \in V/V', \exists v \in V' \text{ such that } (v, u) \in E$$

A dominating set V' is said to be minimum if no other dominating set has a smaller size (number of vertices).

[1] STORMS (Software Tools for the Optimization of Resources in Mobile Systems) is an ACTS project partly funded by the EC. It aims at the definition, implementation, and validation of a software tool to be used for design and planning of the UMTS network.

[2] Also called a vertex-cover [Cor90]

In the case we consider, V is the union of two sets A and B, where A is the set of all possible BTS locations, and B is the set of all potentially covered locations. There exists an edge (u, v) in E when u is in A (i.e., u is a BTS location), v is in B (i.e., v is a covered location), and the BTS located in u covers the location v.

Finding a set of BTS locations which covers the region considered satisfactorily is equivalent to finding a subset of A which is a minimum dominating set of G. In the case we consider, we know that such a set of G exists because A is itself a dominating set of G (although it is likely not to be the minimum one).

4 The genetic approach

The problem of finding an exact minimum dominating set in a graph requires non-polynomial execution time, because it is a NP-complete problem [Gar79]. Due to the amount of possible BTS locations we must consider (which is typically around 1000 potential BTS locations for a 150 km $\times$x 150 km region), it is not achievable to look for an exact solution. Consequently, we must go round this problem and look for possibly sub-optimal –yet satisfactory– solutions.

To achieve this goal, we are investigating several approaches, which are said to be bio-inspired because they imply the implementation of "heuristics from nature", that is, heuristics that have some analogies with natural or social systems [Col93].

To date, we most especially focus on the so-called genetic approach. A genetic algorithm is a population-based model inspired by evolution that uses selection and recombination operators to generate new sample points in a search space [Hol75]. Each individual in the population is generally encoded as a chromosome-like bit string. The bit strings we consider represent the whole set of possible BTS locations. Whether a location is actually selected in a potential solution depends on the value of the corresponding entry in the bit string.

The first step in the execution of a genetic algorithm consists in the generation of an initial population. In our implementation, the initial population is calculated by constructive methods based on random choices or on greedy algorithms that are capable of computing efficiently satisfactory –yet probably non-minimum– dominating sets.

Each iteration step during the execution of a genetic algorithm can be thought of as a two stage process. Selection is applied to the current population to create an intermediate population. Crossover and mutation are then applied to the intermediate population to create the next population. The execution terminates when a satisfactory individual has been produced or when a predefined number of iteration steps has been run through.

The selection is achieved based on the fitness value associated with each individual, which may be perceived as an allocation of reproductive opportunities: the higher the fitness value of an individual, the likelier it is to "reproduce". In our implementation, the function returning the fitness value may have several implementations depending on which criterion we wish to foster. Typically, though, the evaluation takes into account the number of locations covered by a set of selected BTSs and the cost of this set (remember that each BTS is associated a cost).

Crossover and mutation of individuals which model dominating sets, are likely to generate new individuals that do not model dominating sets anymore. Reconstruction techniques are under investigation in order to "mutate" newly created individuals into individuals that model satisfactory dominating sets.

5 Discussion and future work

The main advantage of the approach that consists in computing a dominating set is that we thus ensure that the set of selected BTSs really permits to cover all (or a given percentage of the surface of) the region considered. One of the drawbacks of this approach is that the graph we have to deal with is large, since each potential BTS location and each covered location is modeled as a vertex in the graph. We are investigating several methods to reduce the size of the graph. One method consists in developing "smart" heuristics to select representative to-be-covered geographical locations. Another most promising approach consists in pre-conditioning input data by computing intersection cells prior to starting the actual search for a dominating set.

Although our algorithm is still under development, preliminary experiments exhibit promising results which confirm the interest of such an approach. Moreover, since genetic algorithms are parallel in essence, we consider implementing a parallel version for MIMD-DM (Multiple Instruction Multiple Data - Distributed Memory) architectures in the near future.

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