Greatest Fixed Points of Probabilistic Min/Max Polynomial Equations, and Reachability for Branching Markov Decision Processes

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Abstract. We give polynomial time algorithms for quantitative (and qualitative) reachability analysis for Branching Markov Decision Processes (BMDPs). Specifically, given a BMDP, and given an initial population, where the objective of the controller is to maximize (or minimize) the probability of eventually reaching a population that contains an object of a desired (or undesired) type, we give algorithms for approximating the supremum (infimum) reachability probability, within desired precision \(\epsilon > 0\), in time polynomial in the encoding size of the BMDP and in \(\log(1/\epsilon)\). We furthermore give P-time algorithms for computing \(\epsilon\)-optimal strategies for both maximization and minimization of reachability probabilities. We also give P-time algorithms for all associated qualitative analysis problems, namely: deciding whether the optimal (supremum or infimum) reachability probabilities are 0 or 1. Prior to this paper, approximation of optimal reachability probabilities for BMDPs was not even known to be decidable.

Our algorithms exploit the following basic fact: we show that for any BMDP, its maximum (minimum) non-reachability probabilities are given by the greatest fixed point (GFP) solution \(g^* \in [0,1]^n\) of a corresponding monotone max (min) Probabilistic Polynomial System of equations (max/min-PPS), \(x = P(x)\), which are the Bellman optimality equations for a BMDP with non-reachability objectives. We show how to compute the GFP of max/min PPSs to desired precision in P-time.

1 Introduction

Multi-type branching processes (BPs) are infinite-state purely stochastic processes that model the stochastic evolution of a population of entities of distinct types. The BP specifies for every type a probability distribution for the offspring of entities of this type. Starting from an initial population, the process evolves from each generation to the next according to the probabilistic offspring
rules. Branching processes are a fundamental stochastic model with applications in many areas: physics, biology, population genetics, medicine etc. Branching Markov Decision Processes (BMDPs) provide a natural extension of BPs where the evolution is not purely stochastic but can be partially influenced or controlled: a controller can take actions which affect the probability distribution for the set of offspring of the entities of each type. The goal is to design a policy for choosing the actions in order to optimize a desired objective.

In recent years there has been great progress in resolving algorithmic problems for BMDPs with the objective of maximizing or minimizing the extinction probability, i.e., the probability that the population eventually becomes extinct. Polynomial time algorithms were developed for both maximizing and minimizing BMDPs for qualitative analysis, i.e. to determine whether the optimal extinction probability is 0, 1 or in-between [12], and for quantitative analysis, to compute optimal extinction probabilities to any desired precision [9]. However, key problems for optimizing BMDP reachability probability (probability that the population eventually includes an entity with a target type) have remained open.

Reachability objectives are very natural. Some types may be undesirable, in which case we want to avoid them to the extent possible. Or conversely, we may want to guide the process to reach certain desirable types. For example, branching processes have been used recently to model cancer tumor progression and multiple drug resistance of tumors due to multiple mutations ([1,15]). It could be fruitful to model the introduction of multiple drugs (each of which controls/influences cells with a different type of mutation) via a “controller” that controls the offspring of different types, thus extending the current models (and associated software tools) which are based on BPs only, to controlled models based on BMDPs. A natural question one could ask then is to compute the minimum probability of reaching a bad (malignant) cell type, and compute a drug introduction strategy that achieves (approximately) minimum probability. Doing this efficiently (in P-time) would avoid the combinatorial explosion of trying all possible combinations of drug therapies.

In this paper we provide the first polynomial time algorithms for quantitative (and also qualitative) reachability analysis for BMDPs. Specifically, we provide algorithms for $\epsilon$-approximating the supremum probability, as well as the infimum probability, of reaching a given type (or a set of types) starting from an initial type (or an initial population of types), up to any desired additive error $\epsilon > 0$. We also give algorithms for computing $\epsilon$-optimal strategies which achieve such $\epsilon$-optimal values. The running time of these algorithms (in the standard Turing model of computation) is polynomial in both the encoding size of the BMDP and in $\log(\frac{1}{\epsilon})$. We also give P-time algorithms for the qualitative problems: we determine whether the supremum or infimum probability is 1 (or 0), and if so we actually compute an optimal strategy that achieves 1 (0, respectively).

In prior work [12], we studied optimization of extinction (a.k.a. termination) probabilities for BMDPs, and showed that optimal extinction probabilities are captured by the least fixed point (LFP) solution $q^* \in [0,1]^n$ of a corresponding system of monotone probabilistic max (min) polynomial equations called