A Decision-tree-based Multi-objective Estimation of Distribution Algorithm

Zhong, Xiaoping Li, Weiji

A new decision-tree-based multi-objective estimation of distribution algorithm (DT-MEDA) for optimization problems with continuous variables is developed Decision-tree-based probabilistic models are used to encode conditional dependencies among variables in DT-MEDA. By building and sampling the probabilistic models, the algorithm reproduces the genetic information of the next generation. Incorporating this reproduction mechanism together with the ranking method and the truncated selection, DT-MEDA can approximate the Pareto front. Polynomial mutation operator is used to enhance exploration and maintain diversities in the populations. Furthermore, DT-MEDA adopts a procedure to eliminate a solution with smallest crowding distance at a time in the truncated selection, so that it can obtain a well spread solution set. The performance of the proposed algorithm is evaluated on four biobjective test problems and metrics from literature. Simulation results show that the proposed approach is competitive with NSGA-II and DT-MEDA is a general and effective method for multi-objective optimization.

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Adaptive estimated maximum-entropy distribution model

Tan, Ling Taniar, David

Estimation of Distribution Algorithm (EDA) model is an optimization procedure through learning and sampling a conditional probabilistic function. The use of conditional density function permits multivariate dependency modelling, which is not captured in a population-based representation, like the classical Genetic Algorithms. The Gaussian model is a simple and widely used model for density estimation. However, an assumption of normality is not realistic for many real-life problems. Alternatively, the maximum-entropy model can be used, which makes no assumption of a normal distribution. One disadvantage of the maximum-entropy model is the learning cost of its parameters. This paper proposes an A daptiue Estimated Maximurn-Entropy Distribution (Adaptive MEED) model, which aims to reduce learning complexity of building a model. Adaptive MEED exploits the fact that samples have a low average fitness in the early stage, but they gradually converge to an optima towards the end of the search. Hence, it is not necessary to inference the model with a fall account of observed constraints in the early stage of the search. The proposed model attempts to estimate the density function with a dynamic set of samples and active constraints. In addition, the proposed model includes a global sampling function to address the issue of a missing mutation operator. The ergodic convergence properties ot"the proposed model are discussed with the Markov Chain analysis. The preliminary experimental evaluation shows that the proposed model performs well against genetic algorithms on several clustering problems. (c) 2007 Elsevier Inc. All rights reserved.

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Ambient cardiac expert: A cardiac patient monitoring system using genetic and clinical knowledge fusion

Gondal, Iqbal Sehgal, Shoaib Iqbal, Mudasser Kamruzzaman, Joarder

Cardiac patients can be regularly monitored using low cast sensor networks which can save many lives and valuable time of experts. This monitoring can be more effective if in addition to standard clinical parameters genetic information is used because of its ability to predict hereditary diseases like cardiac problems. Current clinical practices, however, only stress on physiological observation to predict heart failure rate which could miss the important information which could lead to fatal consequences. This paper presents Ambient Cardiac Expert (ACE) which combines physiological parameters observed using sensor networks with gene expression data to predict the heart failure rate. The system uses well established Support Vector Machines (SVM) for class prediction and uses Wrapper Evolutionary Algorithm based on Gaussian Estimation of Distribution Algorithm (EDA) to determine cardiac patient's criticality. Results suggest that ACE can be successfully applied for cardiac patient monitoring and has ability to integrate the information from both clinical and genetic sources.

[Paper](https://www.webofscience.com/wos/alldb/full-record/WOS:000248597700083)

An estimation of distribution algorithm for nurse scheduling

Aickelin, Uwe Li, Jingpeng

Schedules can be built in a similar way to a human scheduler by using a set of rules that involve domain knowledge. This paper presents an Estimation of Distribution Algorithm (EDA) for the nurse scheduling problem, which involves choosing a suitable scheduling rule from a set for the assignment of each nurse. Unlike previous work that used Genetic Algorithms (GAs) to implement implicit learning, the learning in the proposed algorithm is explicit, i.e. we identify and mix building blocks directly. The EDA is applied to implement such explicit learning by building a Bayesian network of the joint distribution of solutions. The conditional probability of each variable in the network is computed according to an initial set of promising solutions. Subsequently, each new instance for each variable is generated by using the corresponding conditional probabilities, until all variables have been generated, i.e. in our case, a new rule string has been obtained. Another set of rule strings will be generated in this way, some of which will replace previous strings based on fitness selection. If stopping conditions are not met, the conditional probabilities for all nodes in the Bayesian network are updated again using the current set of promising rule strings. Computational results from 52 real data instances demonstrate the success of this approach. It is also suggested that the learning mechanism in the proposed approach might be suitable for other scheduling problems.

[Paper](https://www.webofscience.com/wos/alldb/full-record/WOS:000248940200016)

An Incremental Approach for Niching and Building Block Detection via Clustering

Emmendorfer, Leonardo Ramos Ramirez Pozo, Aurora Trinidad

A new decision-tree-based multi-objective estimation of distribution algorithm (DT-MEDA) for optimization problems with continuous variables is developed Decision-tree-based probabilistic models are used to encode conditional dependencies among variables in DT-MEDA. By building and sampling the probabilistic models, the algorithm reproduces the genetic information of the next generation. Incorporating this reproduction mechanism together with the ranking method and the truncated selection, DT-MEDA can approximate the Pareto front. Polynomial mutation operator is used to enhance exploration and maintain diversities in the populations. Furthermore, DT-MEDA adopts a procedure to eliminate a solution with smallest crowding distance at a time in the truncated selection, so that it can obtain a well spread solution set. The performance of the proposed algorithm is evaluated on four biobjective test problems and metrics from literature. Simulation results show that the proposed approach is competitive with NSGA-II and DT-MEDA is a general and effective method for multi-objective optimization.

[Paper](https://www.webofscience.com/wos/alldb/full-record/WOS:000253372500025)

Bayesian inference in estimation of distribution algorithms

Gallagher, Marcus Wood, Ian Keith, Jonathan Sofronov, George

Metaheuristics such as Estimation of Distribution Algorithms and the Cross-Entropy method use probabilistic modelling and inference to generate candidate solutions in optimization problems. The model fitting task in this class of algorithms has largely been carried out to date based on maximum likelihood. An alternative approach that is prevalent in statistics and machine learning is to use Bayesian inference. In this paper, we provide a framework for the application of Bayesian inference techniques in probabilistic model-based optimization. Based on this framework, a simple continuous Bayesian Estimation of Distribution Algorithm is described. We evaluate and compare this algorithm experimentally with its maximum likelihood equivalent, UMDA(c)(G).

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Estimation of distribution algorithm based on probabilistic grammar with latent annotations

Hasegawa, Yoshihiko Iba, Hitoshi

Genetic Programming (GP) which mimics the natural evolution to optimize functions and programs, has been applied to many problems. In recent years, evolutionary algorithms are seen from the viewpoint of the estimation of distribution. Many algorithms called EDAs (Estimation of Distribution Algorithms) based on probabilistic techniques have been proposed. Although probabilistic context free grammar (PCFG) is often used for the function and program evolution, it assumes the independence among the production rules. With this simple PCFG, it is not able to induce the building-blocks from promising solutions. We have proposed a new function evolution algorithm based on PCFG using latent annotations which weaken the independence assumption. Computational experiments on two subjects (the royal tree problem and the DMAX problem) demonstrate that our new approach is highly effective compared to prior approaches.

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