



An Application of a Multivariate Estimation of Distribution Algorithm to Cancer Chemotherapy

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Abstract

Chemotherapy treatment for cancer is a complex optimisation problem with a large number of interacting variables and constraints. A number of different probabilistic algorithms have been applied to it with varying success. Here we apply two further estimation of distribution algorithms to the problem; UMDA and hBOA. The latter is the first EDA using a multivariate probabilistic model to be applied to the chemotherapy problem. While instinct would lead us to predict that the more sophisticated algorithm would yield better performance on a complex problem like this, we show that it is outperformed by the algorithms using the simpler univariate model.

Chemotherapy and EAs

- Highly complex method of treatment
- Requires balancing the tumour reducing effect of several drugs against their toxic side effects.
- In this instance: 10 drugs, 16 dose levels, 10 treatment intervals
- With binary representation chromosomes are 400 bits



We have previously described [1] the application of numerous evolutionary algorithms to the chemotherapy problem using a mathematical model of tumour response to drug treatment.

Problem Complexity

Like many other real-world problems, the chemotherapy problem has a large number of interactions between variables.

- 400 variables
- 79800 possible bivariate interactions
- We ran the Linkage Detection Algorithm [2] to find interactions (linkage) present between variables
- 50491 interactions found (mean over 30 runs, SD 109.5)
- Does not necessarily mean that a multivariate model is needed for optimisation of this problem, but provides motivation to consider applying a multivariate EDA

