**Time Complexity of Iterative-Deepening A*: The Informativeness Pathology (Abstract)**

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**Introduction**

Korf et al. (2001) developed a formula, KRE, to predict the number of nodes expanded by IDA* for consistent heuristics. They proved that the predictions were exact asymptotically (in the limit of large $d$), and experimentally showed that they were extremely accurate even at depths of practical interest. Zahavi et al. (2010) generalized KRE to work with inconsistent heuristics and to account for the heuristic values of the start states. Their formula, CDP, is intuitively described in the next section. For a full description of CDP the reader is referred to Zahavi et al. (2010).

Our research advances this line of research in three ways. First, we identify a source of prediction error that has hitherto been overlooked. We call it the “discretization effect”. Second, we reverse the intuitively appealing idea that a “more informed” prediction system cannot make worse predictions than a “less informed” one. More informed systems are more susceptible to the discretization effect, and in our experiments the more informed system makes poorer predictions. Our third contribution is a method, called “$\epsilon$-truncation”, which makes a prediction system less informed, in a carefully chosen way, so as to improve its predictions by reducing the discretization effect. In our experiments $\epsilon$-truncation improved predictions substantially.

**The CDP Prediction Framework**

Let $S$ be the set of states, $E \subseteq S \times S$ the set of (directed) edges over $S$ representing the parent-child relation in the underlying state space.

**Definition 1** $T = \{t_1, \ldots, t_n\}$ is a type system for $(S,E)$ if it is a disjoint partitioning of $E$. For every $(\hat{s}, s) \in E$, $T(\hat{s}, s)$ denotes the unique $t \in T$ with $(\hat{s}, s) \in t$. For all $t, t' \in T$, $p(t'|t)$ denotes the probability that a node $s$ with parent $\hat{s}$ such that $T(\hat{s}, s) = t$ generates a node $c$ such that $T(s,c) = t'$. Finally, $b_t$ denotes the average number of nodes $c$ generated from a parent $\hat{s}$ and grandparent $s$ with $T(\hat{s}, s) = t$.

CDP samples the state space in order to estimate $p(t'|t)$ and $b_t$ for all $t, t' \in T$. We denote by $\pi(t'|t)$ and $\beta(t)$ the respective estimates thus obtained. Intuitively, CDP predicts the number of nodes expanded by emulating IDA*’s iteration using $\pi(t'|t)$ and $\beta(t)$ to estimate the number of states of a type at a level of search. Let $N(i, t, s^*, d)$ be the number of pair of states $(\hat{s}, s) \in E$ with $T(\hat{s}, s) = t$, at a level $i$, rooted at the start state $s^*$ and with a depth bound $d$. CDP calculates $N(i, t, s^*, d)$ recursively by multiplying $N(i-1, u, s^*, d)$, $\pi(t(u))$ and $\beta(u)$ for all $u \in T$.

As our basic type system, $T_h$, we use Zahavi et al.’s basic “two-step” model, defined (in our notation) as $T_h(\hat{s}, s) = (h(\hat{s}), h(s))$, with $(\hat{s}, s) \in E$. Another “more informed” type system is $T_{gc}(\hat{s}, s) = c(s, 0), \ldots, c(s, H), \text{gc}(s, 0), \ldots, \text{gc}(s, H))$. Where $c(s,k)$ is the number of children of $s$ whose $h$-value is $k$, and $H$ is the maximum $h$-value observed in the sampling process and $\text{gc}(s,k)$ is the number of grandchildren of $s$ whose $h$-value is $k$.

Intuitively, if $T_1$ is more informed than $T_2$ one would expect predictions using $T_1$ to be at least as accurate as the predictions using $T_2$, since all the information that is being used by $T_2$ to condition its predictions is also being used by $T_1$ (Zahavi et al. 2010), p. 59). However, our experiments show that this is not always true. The underlying cause of poorer predictions by $T_1$ when $T_1$ is more informed than $T_2$ is the discretization effect.

**The $\epsilon$-Truncation Prediction Method**

Consider the problem of predicting the outcome of flipping a biased coin that yields tails in 90% of all trials, modeled in the CDP framework. An initial type $\text{init}$ generates either type $\text{tails}$ or type $\text{heads}$, where $p(\text{tails}|\text{init}) = 0.9, p(\text{heads}|\text{init}) = 0.1$ and $b_{\text{init}} = 1$. Suppose $\pi$ and $\beta(\text{init})$ approximates respectively $p$ and $b_{\text{init}}$ exactly and $N(i, \text{init}, s^*, d) = 1$. Then CDP would predict that 0.9 tails and 0.1 heads will occur at level $i + 1$. However, a prediction of 1.0 tails and 0.0 heads occurring at level $i + 1$ has a smaller expected absolute error when compared to CDP’s prediction. We call this phenomenon (better predictions arising when less accurate probability estimates are used) the discretization effect.

If a type $t'$ is generated with low probability from a type $t$ and if $N(i, t, s^*, d)$ is small, it may be possible to reduce expected absolute error by disregarding $t'$, i.e., by artificially setting $\pi(t'|t)$ to zero at level $i$ of the prediction calculation.

Our approach, which we call $\epsilon$-truncation, avoids the discretization effect and can be summarized as follows.
1. As before, sample the state space to obtain \( \pi(t|u) \).

2. Compute a cutoff value \( \epsilon_i \) for each \( i \) between 1 and \( d \). 

3. Use \( \epsilon_i \) to define \( \pi^i(t|u) \), a version of \( \pi(t|u) \) that is specific to level \( i \). In particular, if \( \pi(t|u) < \epsilon_i \) then \( \pi^i(t|u) = 0 \); the other \( \pi^i(t|u) \) are set by scaling up the corresponding \( \pi(t|u) \) values so that they sum to 1.

4. In computing \( \text{CDP} \) use \( \pi^i(t|u) \) at level \( i \) instead of \( \pi(t|u) \).

The calculation of the \( \epsilon_i \) values requires computing \( \text{CDP} \) predictions for a set of start states and, for each level \( i \) in each of these prediction calculations, solving a set of small linear programs that minimizes the expected error. The solutions of the linear programs suggest an \( \epsilon_i \) (details are omitted due to lack of space).

**Experiments and Conclusion**

Our experiments shows that, 1) more informed type systems can produce poorer predictions and, 2) the \( \epsilon \)-truncation method improves the predictions of a more informed type system and prevents the pathology from occurring.

The choice of the set of start states is the same used by Zahavi et al. (2010): start state \( s \) is included in the experiment with depth bound \( d \) only if \( \text{IDA}^* \) would actually have used \( d \) as a depth bound in its search with \( s \) as the start state. Unlike an actual \( \text{IDA}^* \) run, we count the number of nodes expanded in the entire iteration for a start state even if the goal is encountered during the iteration.

For each prediction system we will report the ratio of the predicted number of nodes expanded, averaged over all the start states, to the actual number of nodes expanded, on average, by \( \text{IDA}^* \). This ratio will be rounded to two decimal places and it is called the (average) signed error. The signed error is the same as the “Ratio” reported by Zahavi et al. (2010) and is appropriate when one is interested in predicting the total number of nodes that will be expanded in solving a set of start states. It is not appropriate for measuring the accuracy of the predictions on individual start states because errors with a positive sign cancel errors with a negative sign. To evaluate the accuracy of individual predictions, the appropriate measure is absolute error. For each instance one computes the absolute value of the difference between the predicted and the actual number of nodes expanded, divide this difference by the actual number of nodes expanded, add these up over all start states, and divides by the total number of start states. A perfect score according to this measure is 0.0.

Zahavi et al. (2010) introduced a method for improving predictions for single start states. Instead of directly predicting how many nodes will be expanded for depth bound \( d \) and start state \( s \), all states, \( S_r \), at depth \( r < d \) are enumerated and one then predicts how many nodes will be expanded for depth bound \( d - r \) when \( S_r \) is the set of start states. We applied this technique in our experiments. The value of \( r \) for each experiment is specified below.

We ran experiments on the 8 and 15 sliding tile puzzles and used the same type system as Zahavi et al. (2010), which is a refinement of \( T_h \) we call \( T_{h,b} \). \( T_{h,b} \) is defined by

\[
T_{h,b}(s, s') = (T_h, \text{blank}(s), \text{blank}(s'))
\]

where \( \text{blank}(s) \) returns the kind of location (corner, edge, or middle) the blank occupies in state \( s \). \( T_{g,c,b} \) is defined analogously. For square versions of the puzzle \( T_{gc} \) is exactly the same as \( T_{gc,b} \) and therefore \( T_{gc} \) is more informed than \( T_{h,b} \).

The inconsistent heuristic we used for the 8-puzzle is the one defined by Zahavi et al. (2010). Two PDBs were built, one based on tiles 1-4, and one based on tiles 5-8. The first PDB is consulted for states having the blank in an even location and the second PDB is consulted otherwise. The results, with \( r=1 \), are shown at the top of Table 1. Here we see the informativeness pathology: \( T_{gc} \)’s predictions are worse than \( T_{h,b} \’s \), despite its being a refinement of \( T_{h,b} \). Applying \( \epsilon \)-truncation substantially reduces \( T_{gc} \’s \) prediction error.

For the 15-puzzle, we used 1,000 random start states to measure prediction accuracy. To define \( \pi(t|u) \) and \( \beta_i \), one billion random states were sampled and, in addition, we used the process described by Zahavi et al. (2010): we sampled the child of a sampled state if the type of that child had not yet been sampled. The bottom of Table 1 gives the results when Manhattan Distance is the heuristic, \( T_{h,b} \) and \( T_{gc} \) are the type systems and \( r=25 \). Here again we see the pathology: \( T_{h,b} \’s \) predictions are better than \( T_{gc} \’s \) which is eliminated by \( \epsilon \)-truncation. Our method also improved considerably the prediction accuracy for the 10 and 15 pancake puzzles (results omitted due to lack of space).

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**References**


Table 1: Informativeness Pathology

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