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 disprove 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 "ϵ-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 ϵ-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 s and grandparent $\hat{s}$ 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 $T_{gc}(\hat{s}, s) = (T_h(\hat{s}, s), c(s, 0), \ldots, c(s, H), gc(s, 0), \ldots, gc(s, H))$. 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 $gc(s, k)$ 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 ϵ-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 *init* generates either type *tails* or type *heads*, where $p(\textit{tails}|\textit{init}) = 0.9$, $p(\textit{heads}|\textit{init}) = 0.1$ and $b_{init} = 1$. Suppose π and $\beta(init)$ approximates respectively p and b_{init} exactly and $N(i, \textit{init}, s^*, d) = 1$. 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 phenonemon (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 ϵ-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 ϵ_i for each i between 1 and d.
3. Use ϵ_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 CDP use $\pi^i(t|u)$ at level i instead of $\pi(t|u)$.

The calculation of the ϵ_i values requires computing 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 ϵ_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 ϵ-trucantion 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 IDA* would actually have used d as a depth bound in its search with s as the start state. Unlike an actual 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 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, adds 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 $T_{h,b}(s, s') = (T_h, blank(s), blank(s'))$ where $blank(s)$ returns the kind of location (corner, edge, or middle) the blank occupies in state s. $T_{gc,b}$ 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 $T_{h,b}$.

		Signed Error			Absolute Error		
d	IDA*	$T_{h,b}$	T_{gc}	ϵ-T_{gc}	$T_{h,b}$	T_{gc}	ϵ-T_{gc}
8-puzzle. Inconsistent Heuristic. r=1							
22	58.5	1.00	1.34	**0.96**	0.47	0.62	**0.41**
23	95.4	1.01	1.39	**0.98**	0.45	0.62	**0.38**
24	135.7	1.03	1.45	**0.93**	0.47	0.66	**0.37**
25	226.7	1.04	1.52	**0.98**	0.42	0.65	**0.34**
15-puzzle. Manhattan Distance. r=25							
52	28,308,808.8	1.25	1.28	**1.14**	0.14	0.17	**0.09**
53	45,086,452.6	1.23	1.29	**1.13**	0.16	0.20	**0.11**
54	85,024,463.5	1.36	1.41	**1.22**	0.21	0.27	**0.15**
55	123,478,361.5	1.36	1.45	**1.24**	0.24	0.31	**0.17**

Table 1: Informativeness Pathology

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 ϵ-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 β_t, 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 ϵ-truncation. Our method also improved considerably the prediction accuracy for the 10 and 15 pancake puzzles (results omitted due to lack of space).

Acknowledgements

This work was supported by the Laboratory for Computational Discovery at the University of Regina. The authors gratefully acknowledge the research support provided by Alberta's Informatics Circle of Research Excellence (iCORE), the Alberta Ingenuity Centre for Machine Learning (AICML), and Canada's Natural Sciences and Engineering Research Council (NSERC).

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