Efficient Inference in Probabilistic Computing

M.Eng Thesis

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Contents

1 Introduction

Probabilistic programming languages are generalizations of programming languages, in which procedures are replaced with random procedures that induce distributions. By allowing for easy description and manipulation of distributions, probabilistic programming languages let one describe classical AI models in compact ways, and provide a language for very richer expression.

A core operation of probabilistic programming languages is inference, which is a difficult computational problem in general[1]. However, Markov chain Monte Carlo (MCMC) methods converge quite quickly to the posterior distribution for a large class of inference problems. Much effort has been devoted to studying in which cases this inference is efficient, and how to make it so.

We explore implementations of a programming language much like Church [2]. A naive implementation of inference uses a database to store all random choices, and re-performs all computations on each transition.

To improve this, we introduce a "traces" data structure, letting us represent the program structure in a way that allows us to do minimal re-computation. During inference, we make one small change and propagate the changes locally.

Unfortunately, the trace structure takes up significantly more space than the random database. Thus we introduce "reduced traces", which takes the same amount of space (asymptotically) as the random database. While it is asymptotically slower than traces for some programs,at we demonstrate thits time complexity is similar in practice.

We also remark on another significant advantage of reduced traces. While writing interpreters in Python is typically considered slow, the PyPy translation toolchain aims to let developers compile their interpreters into lower level languages, such as C. Furthermore, one

can use various hints to generate a tracing JIT. Generating a tracing JIT for inference could potentially improve efficiency greatly, and reduced traces make this far easier to implement.

Thus far, in this project, we hae done the following:

1. Explore the theoretical aspects of the traces and reduced traces inference algorithms.
2. Implement the different inference engines, in RPython, so as to have C versions of the interpreter. All engines conform to a common REST API. [1]
3. Run various benchmarks on the engines to compare the engines' performance on various problems.

There are many research directions to pursue after this, all towards the goal of improving performance of the inference engine:

1. Generate a tracing JIT version of the interpreter.
2. Creating a parallelized version of reduced traces.
3. Potentially exploring some "adaptive" generalizations of Gibbs sampling.

Ultimately like to be able to recover the efficiency of special-cased inference algorithms for topic-modeling, mixture modeling, and Hidden Markov Models, in a much more general setting, and with far fewer lines of code.

2 Language description

2.1 Values and expressions

A **value** is a valid binding for a variable, in our language. For example, integers, floats, and booleans are valid values. We call these primitive values. Another type of value is a **procedure**, a function which gets applied to a tuple of argument values and returns another value. These procedures may, of course, be non-deterministic.

Our language contains some default procedures, from which we can then build up more complicated ones. In fact, as we all see later, the types of procedures we allow will end up being more general than that which is typically thought of as a procedure.

Expressions are syntactic building blocks. Expressions are **evaluated**, so that they take on some value. Their evaluation is relative to an **environment**, in which variable names may be bound to values. All expressions are one of the following:

- A name, e.g. x or y, which refers to a value bound in the current environment.

[1] Server code here: https://github.com/WuTheFWasThat/Church-interpreter

- A constant value, e.g. 3, 3.1415, True, or a default procedure.
- A lambda expression, i.e. $(\lambda\ (x_1 \ldots x_n)$ body_expression), which evaluates to a procedure taking n arguments.
- An application, i.e. $(f\ x_1\ x_2\ \ldots\ x_n)$, where f is a procedure taking n arguments.

2.2 Directives

There are three basic operations, called **directives**, which the language supports. They are:

- `PREDICT [expr]`

  Evaluates with respect to the global environment to sample a value for the expression `expr`.

- `ASSUME [name] [expr]`

  Predicts a value for the expression `expr`, and then binds `name`, a string variable name, to the resulting value in the global environment.

- `OBSERVE [expr] [val]`

  Observes the expression `expr` to have been evaluated to the value `val`. Runs of the program should now be conditioned on the expression evaluating to the value.

There are many other commands. But by far the most interesting and important one is inference.

- `INFER [rerun] [iters]`

  Runs `iters` steps of the Markov Chain, also deciding whether to first rerun the entire program. The result of running sufficiently many iterations from the prior, should be that sampling gives the posterior distribution for expressions, conditioned on all the observed values.

Other commands do various useful things like report various benchmarks (including time, space, and entropy use), help us gather statistics, allow seeding of the underlying PRNG, and deleting parts of the program or clearing it entirely.

3 Inference

Inference is by far the most complicated of the directives, and also the most important. Performing inference is the reason we are interested in probabilistic programming languages in the first place.

3.1 First try

Of course, the most obvious way to implement inference is to use rejection sampling. But this scales poorly with the number of observations. We'd like to instead run Metropolis-Hastings on the space of all possible executions of the program.

Our proposal density, which chooses the new state (program execution history) to potentially transition to, does the following:

1. Pick, at random, one of the random choices made, at any point in the program's execution history. Make a new choice for this randomness.

2. Rerun the entire program, changing only this choice. If this causes us to evaluate new sections of the code (e.g. a different side of an if statement, or a procedure called with different arguments) with new choices of randomness, simply run these new sections freshly.

We then use the update rule of Metropolis-Hastings to decide whether we enter this new state, or whether we keep the old one. However, if the new execution history doesn't agree with our observations, we assign it a probability of 0, so that we never transition to such a state.

3.2 Adding noise to observations

Unfortunately, as it has been described, this random walk doesn't converge to the posterior! Consider the following example, in which I flip two weighted coins and observe that they came up the same:

```
ASSUME a (bernoulli 0.5)
ASSUME b (bernoulli 0.5)
ASSUME c (^ a b)
OBSERVE c True
```

It is easy to verify that the posterior distribution should have the state {`a:True, b:True`} with probability $\frac{1}{2}$ and {`a:True, b:True`} with probability $\frac{1}{2}$. However, we can see that if we start in the state {`a:True, b:True`}, we will never walk to either of the two adjacent states {`a:False, b:True`} and {`a:True, b:False`}. So the random walk stays in the initial state forever! The same argument applies if we start from {`a:False, b:False`}. Thus this Markov chain does not mix properly.

To fix this problem, we should allow some small probability of transitioning to states where observations are false. After all, a Bayesian should never trust their eyes 100%! Suppose instead of

```
OBSERVE [expr] [val]
```

we instead used:

```
OBSERVE (bernoulli (if (= [expr] [val]) 0.999 0.001)) True
```

Now, when we run our walk, if the expression `(= [expr] [val])` evaluates to `False` (so the original observation would've failed), we force the outermost `bernoulli` application to be `True`. If the noise level is small, this should not affect results much, since the execution histories in which the original observation was false are weighted against heavily. However, the space of states is always connected in the random walk and our Markov chain will converge properly.

For convenience, our language uses the function `(noisy [observation] [noise])` as syntactic sugar for `(bernoulli (if [observation] (- 1 [noise]) [noise]))`, where you have observed some expression `[observation]` to be true.

3.3 A short example

Let's start with a simple example, to get familiar with our language. We will see how easy it is to write simple Bayes' nets, in our language (and in fact, it is easy to write much larger ones as well).

```
>>> ASSUME cloudy (bernoulli 0.5)
id: 1
value: True
>>> ASSUME sprinkler (if cloudy (bernoulli 0.1) (bernoulli 0.5))
id: 2
value: False
```

Initially, we have this model, and we know nothing else. So our prior tells us that there's a 30% chance the sprinkler is on.

```
>>> INFER_MANY sprinkler 10000 10
False: 6957
True: 3043
```

We now look outside, and see that the sprinkler is in fact on. We're 99.9% sure that our eyes aren't tricking us.

```
>>> OBSERVE (noisy sprinkler .001) True
id: 3
```

Now, we haven't yet looked at the sky, but we have inferred something about the weather.

```
>>> INFER_MANY cloudy 10000 10
False: 8353
True: 1647
```

This is quite close to the correct value of $\frac{5}{6} = 0.8\overline{333}$ False, which is what we'd get if there was no noise in our observation. However, there is still a number of worlds in which the sprinkler was actually on. In those worlds, the weather was more likely to be cloudy. So we should expect error on the order of 0.001, but more error comes from our small sample size.

4 XRPs and Mem

Up until now, we have neglected to mention a crucial aspect of our language. The procedures allowed in our language are much more general than what we typically think of as procedures. In this section, we introduce the most general type of procedures we can allow inference over.

4.1 Exchangeability

Evaluating and unevaluating sections of code is very easy when all random choices are made independently of one another. But actually, it is easy to evaluate and unevaluate so long as the sequence of random choices is **exchangeable sequence**, meaning, roughly speaking, that the probability of some set of outcomes does not depend on the order of the outcomes. In particular, as long as it is safe to pretend that the section of code we're unevaluating was the last section of code evaluated, we're fine!

Thus instead of merely being able to flip independent coins as a source of randomness for procedures, the most general thing we are able to allow what is called an **exchangeable random procedure (XRP)**. An XRP is a type of random procedure, but different applications of it are not guaranteed to be independent; they are guaranteed merely to be an exchangeable sequence. That is, the sequence of `(arguments, result)` tuples is exchangeable. The probability of a sequence is independent of its order (assuming we got the arguments in that order).

For example, if f is an XRP taking one argument, we may find that $f(1) = 3$, and later that $f(2) = 4$. Unlike a typical procedure, the result $f(2) = 4$ was not necessarily

independent from the earlier result $f(1) = 3$. However, the probability that this execution history happens should be the same as the probability that we first apply $f(2)$ and get 4, and then later apply $f(1)$ and get 3. Of course, $f(2)$ can be replaced with $f(1)$ everywhere in this paragraph, as well — multiple applications to the same arguments can also be different and non-independent, so long as they are exchangeable.

4.1.1 Formally specifying XRPs

XRPs used in our probabilistic programs are specified by the following four functions:

- `initialize()`, which returns an initial state.
- `apply(state, args)`, which returns a value.
- `incorporate(state, value, args)`, which returns a new state.
- `remove(state, value, args)`, which returns a new state.
- `prob(state, value, args)`, which returns the (log) probability of returning the value, if the XRP in its current state is applied to the arguments.

The state of the XRP is a sufficient state, meaning it alone lets you determine the XRP's behavior. Minimally, the state may be a history of all previous applications of the XRP, although in most cases, it is much more succinct. Whenever we apply the XRP, we use `apply` to determine the resulting value, and we may use `prob` to determine the probability that we got that value, conditioning on all previous applications. This value can then incorporated into the XRP using `incorporate`, and the state is updated. Finally, `remove` lets you remove a value, undoing an incorporate.

Notice that if applications are independent, then we do not need a state, and both incorporate and remove can do nothing. Thus this recovers the special case of normal random procedures.

XRPs are quite a general object, and replacing random procedures with them significantly increase the expressive power of our language. They also come in a variety of flavors, and we will see some examples later.

4.1.2 Re-apply or re-score

If our XRP is capable of returning any value in its range, regardless of its arguments, then we will say it is a "rescoring" XRP. That is, if we are dynamically changing the program, and the XRP is passed new arguments but wants to retain its old value, we can do so, but perhaps with a modification to the probability.

If our XRP is not capable of this, we call it a "reapplying" XRP. That is, it should reapply these new arguments to get a new value as well.

Essentially, in inference, when values change, and we are propagating the changes upwards, reapplying XRPs will "pass on" the changes, whereas rescoring XRPs will "absorb"

them.

Now, we can allow for something much more general than the noisy observations above. We now simply require that all observed expressions have an outermost rescoring/absorbing XRP application. When running inference, we always force the XRP to give the observed value by using `inc` (without using `apply`). The probability of getting this observed value should always be non-zero.

The noisy expressions obtained with `noisy` are a special case of this, so long as `noise` was non-zero.

4.2 Mem

A special XRP worth noting is `mem`, which lets us memorize procedures. Applying `mem` to a procedure returns another XRP, which is a memoized form of that procedure. That is, when using a `mem`'d procedure, we never reapply randomness, given old arguments. Thus whenever we apply the memoized procedure once to some particular arguments, applying it again to those arguments will result in the same value.

Implementation of `mem` is extremely tricky, and we will decline to work out its details in this paper. However, it is important to understand its utility. As a simple example, consider a naive implementation of Fibonacci:

```
ASSUME fib (lambda (x) (if (< x 2) 1 (+ (fib (- x 1)) (fib (- x 2)))))
```

Of course, evaluating fibonacci in this manner is an exponential time operation. Evaluating `(fib 20)` took nearly 2 seconds.

Simply wrapping a `mem` around the lambda expression will make it so we don't need to recompute `(fib 20)` the next time we call it. Not only that, but when we recurse, we will only compute `(fib [x])` once, for each $x = 0, \ldots, 20$.

```
ASSUME fib (mem (lambda (x) (if (< x 2) 1 (+ (fib (- x 1)) (fib (- x 2))))))
```

Evaluating `(fib 20)` now takes well less than a millisecond.

5 Traces

The random database implementation of inference is not very interesting. The inference engine simply reruns the program after each iteration, remembering all previous randomness chocies, and having only one choice changed. Let's skip to the "traces" implementation.

5.1 Basic overview

In the traces implementation of inference, we create an **evaluation node** for every expression that is evaluated, which keeps track of the expression, environment, values, and many other things.

The evaluation nodes are connected in a directed graph structure, via dependencies. Thus if the evaluation of one node, x, depends on the evaluation of another (e.g. a subexpression, or a variable lookup), y, we say that y is a **child** of x and that x is a **parent** of y. By interpreting these child-parent relationships as edges (from parent to child), these evaluation nodes form a directed acyclic graph, which we refer to as the **trace**.

Each node caches the relative locations and values of all its children. Furthermore, if it is an application node, we also cache the procedure and arguments. And for every node, we cache its most recent value.

5.2 The proposal

When we re-flip the value of some XRP application, we would like to simply remove the old value, and then incorporate a new value directly, asking for the probabilities as we do so, in order to calculate the MH ratio. This appears to be valid, by the exchangeability property.

We'd then like to propagate the new value throughout the trace, by repeatedly propagating new values to parents. If we reach a "re-scoring" XRP application, we simply reuse its old value, so that we do not need to propagate computation any further (even if its arguments have changed). If new branches need to be evaluated, it is done on demand.

However, how do we consider the probabilities of these other applications? Unfortunately, the singular remove and then apply is only valid once. We can't imagine multiple XRP applications to be the last one. We can at best imagine n applications to be the last n. Thus, conceptually, we must remove all old values before applying and incorporating the new ones (and calculating their probabilities).

Unfortunately, doing this would mean that we can't decide the values while we propagate up, and so we cannot stop propagating, even if the values are the same. To fix this, we will use a different MH proposal.

Let's simply apply and incorporate all new values encountered, but refrain from removing the old values, and querying the probabilities as we go. This way, we can still propagate up dynamically. Then, at the end of our calculation, we can remove all old values, again querying the "unevaluation" probabiltiies. This determines our "forwards" transition probability, or the denominator of the MH ratio (with some cancelling).

Then, we essentially do the process in reverse, to calculate the "backwards" transition probability, the numerator of the MH ratio. We simply re-incorporate all the old values, querying the probabilities as we go, and then remove all the new values, querying the "unevaluation" probabilities.

5.3 Propagation

How does propagation actually work? This question is surprisingly interesting, and we explore two different candidate propagation schemes.

5.3.1 Recursive propagation

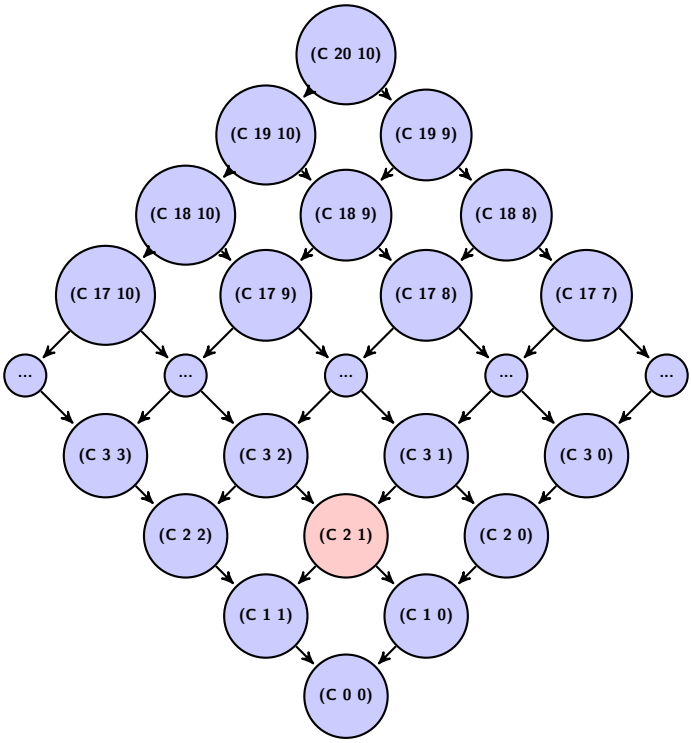
The easiest version of propagation to implement is simply a recursive, "depth-first" implementation. We simply start at the node which we reflipped, and recursively re-evaluate its parents, stopping only when we reach XRP application nodes. However, notice that in a graph where nodes have multiple children and parents, this does not guarantee that we only propagate each node once. In fact, this propagation has exponentially bad worst-case scenarios, and can be poor in some practical settings.

Suppose we have the following program, which computes a familiar multivariate recurrence.

```
ASSUME binom (lambda (n k) (if (or (= k 0) (= k n)) 1
...                            (+ (binom (- n 1) (- k 1)) (binom (- n 1) k))))
```

Let's say we want to randomly replace one of the entry $n = 2, k = 1$ of Pascal's triange with a random real number between 0 and 2. And we are curious in the resulting distribution for the entry $n = 20, k = 10$.

```
ASSUME binom-wrong (lambda (n k c) (if (and (= n 2) (= k 1)) c (binom n k)))
PREDICT (binom-wrong 20 10 (uniform-continuous 0 2))
```



Propagating from the red node upwards. Here the C function is `binom-wrong`.

Now suppose we decided to reflip the `uniform-continuous` application. And suppose we have the policy of always propagating to the right first, if possible. We can then verify that the worst-case number of times we may propagate to the application `(binom-wrong m l)` is essentially `(binom m l)`.

Intuitively, we wanted to propagate to the smaller values first, in this modified Pascal's triangle. Then, we would only have needed to propagate about 100 times; once for each node. Thus we see that the order is extremely important, in general.

However, although the worst case scenario is terrible, this method of propagation is okay in practice for many problems.

5.3.2 Full location

So, we see is that the order of propagation is quite important. How can we know which parents to propagate our values to first? Intuitively, since our trace structure is a DAG, we simply propagate to those "lowest" in the DAG. Essentially, we want to maintain a priority queue, from which we will repeatedly remove the minimum and add his parents to the queue, until the queue is empty. Here, we are simply interpreting the parent-child relationships as comparisons in a partial ordering.

Unfortunately, a heap does not work correctly on a set of elements with only a partial ordering (even with ties arbitrarily broken), and so we must extend to some full ordering.

We cannot simply use timestamps of the initial evaluation, since it is possible for unevaluated branches earlier in the program to be evaluated later.

We could use a full description of the node's location (something like a call stack), but it would be quite expensive, as comparisons would now take $O(h)$, where h is the height of the DAG, defined to be the length of the longest directed path starting from a directive node.

5.3.3 Analysis

As described above, the trace is not static across different runs of the same program. When referring to this dynamic data structure, we will say, the **dynamic trace**. We may think of the dynamic trace as a random variable, where the randomness is over the different runs of the program.

For every node x, we say the **envelope** of x, denoted V_x, is the set of nodes reached by propagating upwards in the dynamic trace until we reach "re-scoring" XRP application nodes (including the application nodes, as well as x), and then propagating down through the bodies of any procedure applications we pass through. We think of V_x a random variable as well, but it is only defined over worlds in which node x is active in the dynamic trace.

Now let p_x be the probability that node x is chosen to be reflipped in the Markov chain. In other words, p_x should represent the distribution where, first, we sample from a run of the program, and then we pick one of the XRP applications uniformly at random. Lastly, we let V be the random variable which first picks some x with probability p_x, and then picks a random V_x, conditioned on x being active.

We then have that the expected propagation time of the "full location" propagation scheme is

$$E_V[|V| \cdot h \log |V|| = h \cdot E_V[|V| \log |V|].$$

This essentially follows directly from our propagation algorithm. We do just as much unevaluating as evaluating, but this introduces just a factor of 2.

6 Reduced Traces

6.1 Motivation

The major downside of the traces implementation is that it is not memory efficient. The number of nodes stored is essentially proportional to the time it takes to compute the original program, since we keep a node for each expression evaluation.

To highlight this, consider the following program, which samples from the categorical distribution, which returns i with probability p_i. The distribution is represented by some procedure `categorical-dist`, which takes an argument i and returns p_i. It is guaranteed that for some finite n, $\sum_{i=0}^{n-1} p_i = 1$

```
ASSUME sample-categorical-loop
        (lambda (v i)
                (if (< v (categorical-dist i))
                    i
                    (sample-categorical-loop
                     (- v (categorical-dist i))
                     (+ i 1))))

ASSUME sample-categorical (lambda ()
                            (sample-categorical-loop (rand) 0)
```

Notice that using traces, we will create a node for each application of the sub-loop. And yet it is clear that this space is un-needed. We feed the function a single choice of randomness, and it creates up to n nodes. But if we were to reflip the application of `rand`, we would need to re-evaluate the entire application again. Thus if n is large, this could be a phenomenal waste of space. Supposing a loop like this were on the critical path of some program, we could be using a multiplicative factor of $O(n)$ more space.

One solution is to "collapse" this sampling into an XRP. That is, we turn `sample-categorical` into an XRP, since applications of it are independent, and thus exchangeable. This is a useful idea which we will turn back to later, but this is clearly not a satisfactory solution in general.

6.2 Reducing the traces graph

The idea of reduced traces is to essentially "contract" all edges of deterministic computation in the traces graph. Whenever we need to perform deterministic computation, we will simply recompute, instead of having nodes all along the way with cached values.

In contracting all these edges, the only nodes which remain will be nodes corresponding to XRP applications, and nodes which correspond to directives [2].

One minor issue which comes up is the locating of child nodes. We need to be able to recover a specific child node, if we perform the computation leading to what should be its evaluation. We also need to be able to figure out the location of children to unevaluate. The relative locations may be long, and we don't want to store them in memory.

In order to do this, we using a rolling hash on the "stack", a list which pins down the relative location of a node within the computation. This technique is also used in the random database implementation of the engine.

[2] There are also nodes corresponding to applications of `mem`.

6.3 Propagation in reduced traces

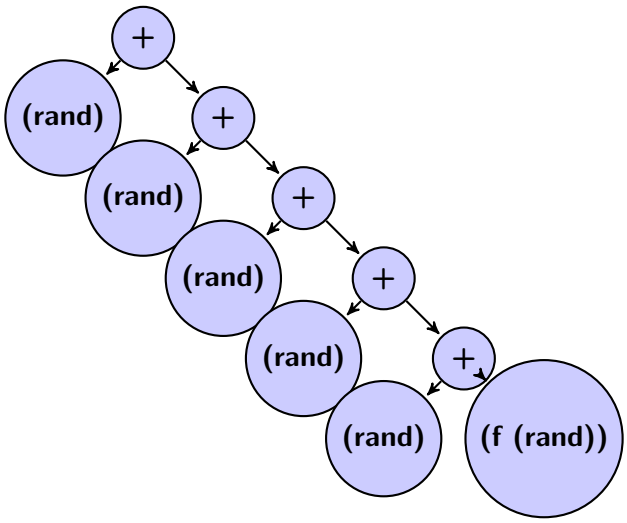
In reduced traces, we essentially have the same options as in regular traces. We won't go into detail explaining again.

However, we will pay a price for our lack of structure. Let's consider the following program, which indexes into an array using the max of two samples from the categorical distribution from the last example:

```
ASSUME categorical-sum (+ (sample-categorical) (sample-categorical))
```

Now, each time we reflip the coin at the bottom of some `sample-categorical`, we must re-evaluate both applications of sample-categorical, in order to propagate up to `x`'s value. Even in the analysis given for the static traces, evaluating this second argument was not necessary.

The structure of a reduced trace is different from that of the traces we saw in the previous section, and this can lead to drastically worse running time. For example, consider the following trace structure:



Now suppose `f` is an extremely expensive deterministic computation, so that the time it takes dominates all other runtime considerations. In regular traces, we only need to recompute `f` with probability 1 in 6, when its argument is reflipped. However, in reduced traces, we must recompute it every time! We no longer have values cached along the edges, and so we have traded in space complexity for some time complexity.

It's clear that we can generalize this example to a class of problems for which reduced traces does drastically worse. However, as we will see, the runtime of reduced traces is empirically comparable to that of traces.

6.4 Analysis

To analyze the propagation, we imagine we were still propagating in the old dynamic trace. Although our notion of nodes is now different, we are really interested in the amount of computation done (essentially, number of expressions evaluated).

Recall that we had defined the envelope to be the set of nodes reached by propagating upwards in a dynamic trace until we reached "re-scoring" XRP application nodes, and then propagating down through the bodies of any procedure applications we passed through. The set of nodes we evaluate is very similar, except that we additionally propagate downward from all other nodes with deterministic computation that we pass through, until we hit another application node (which has its value cached).

Viewing the picture with only reduced traces, the set of nodes we propagate to is extremely analogous to the notion of Markov blankets, and also captures explicitly a notion of conditional independence.

Let us call this set of nodes the **full envelope**, V_x^+. From the reduced trace point of view, we simply propagate to all parents, and then propagate down to their children which needed to be evaluated. However, it is the set of nodes from the traces point of view that we are interested in.

Again, we can consider the reduced trace to be dynamic, in this analysis, using the same sort of amortized analysis we had done earlier. Thus the runtime is

$$E_{V^+}[|V^+| \cdot \log |V^+|],$$

where V^+ is the random variable which first picks some x with probability p_x, and then picks a random full envelope V_x^+, conditioned on x being active.

6.5 Engine Complexity Trade-offs Summary

To summarize, we have the following table of asymptotic complexities:

Table 1: Engine Complexity Trade-offs

	Time / Iteration	**Space**	**Time**
Random DB	T	H + P	T
Traces 1 (recursive)	$E_V[2^V]$	T $(+ H + P)$	T
Traces 2 (full location)	$h \cdot E_V[V \log V]$	T $(+ H + P)$	$h \cdot T$
Reduced Traces (recursive)	$E_{V^+}[2^{V^+}]$	H + P	T
Reduced Traces (full location)	$E_{V^+}[V^+ \log V^+]$	H + P	T

Here, the variables mean the following:

- P = Size of the program description (the directives and their expressions)

- T = Expected runtime of the original program
- H = Expected entropy (number of XRPs)
- V = Envelope size, in dynamic trace
- V^+ = Full envelope size, in dynamic reduced trace
- h = The "height" of the program. That is, the largest number of evaluations any node is away from a directive.

Recall that $T > H$ and $T > P$, and $V < V^+$.

Though none of the traces implementation is strictly dominated by another, we believe the 1st and especially 3rd are more likely to be efficient in practice. And we believe that reduced traces should have much better space usage and only marginally worse run-time. See the appendix for some preliminary empirical results.

7 Extended XRPs

We now discuss some extensions to the XRP interface, to give the user more power over how inference works.

7.1 XRP weights

By default, all XRP applications are equally likely to be reflipped. But what if we would like to reflip some XRP applications more than others? This won't affect the resulting distribution, so long as we correctly calculate transition probabilities, but it could be helpful for making our chain mix much faster.

To achieve this, we will assign each XRP application a weight, which tells us how often we should reflip it relative to other XRP applications. This is extremely useful for certain programs. However, in order to use this, we'd like a data structure supporting the following operations:

- Insert(key, weight) : Insert a key, along with a weight
- Remove(key) : Remove a key
- Sample() : Sample keys, with probability proportional to their weight.

Previously, we needed a data structure to support this in the special case where all weights were 1. In this case, a special augmented hash table can achieve these operations in $O(k)$, where k is the key size. The idea is to keep the keys in an array, as well as a hash table, and to keep a hash table from key to index in that array. When we delete an element, we swap it with the last item of the array and update everything appropriately.

Unfortunately, the weighted case is much more difficult. It is slightly reminiscent of the problem of implementing malloc. A simple solution is to do the following: Maintain the same augmented hash table as before, but also keeping track of weights. Also, keep track of the maximum weight currently held, using a heap. When we sample, use rejection sampling, by dividing by the maximum weight currently held.

Unfortunately, this sampling algorithm has complexity proportional to the ratio of the maximum weight to the average weight, which can get arbitrarily large. However, insertion and removal happen in $O(k \log n)$. Insertion and removal are much more important, as they can happen many times (during propagation), whereas sampling only happens once per round of iteration.

7.2

In addition to sample, incorporate, remove, and apply, we give the user additional optional methods to implement, when implementing their own XRPs.

8 Conclusion and future work

The fact that reduced traces makes it so easy to identify the envelope-like sets is potentially extremely useful.

Firstly, it should be easier to work with for parallelization than other implementations. For parallelization, we'd like to do inference on different parts of the program in parallel. Conditional independence is precisely the property we'd want to be true of the different parts.

Secondly, it should be much easier to generating a tracing JIT for, at the right level of granularity. Essentially, we would like to consider inference loops which have similar structural behavior. Since the randomness choices are sufficient to determine what the computation will be like, all the deterministic structure in-between nodes which is made explicit in the traces data structure is irrelevant. This makes reduced traces much more convenient for implementing a tracing JIT.

These two factors lead us to believe that reduced traces will be crucial in developing even faster versions of this inference engine.

Ultimately we would like to be able to recover the efficiency of special-cased inference algorithms for topic-modeling, mixture modeling, and Hidden Markov Models, in a much more general setting, and with far fewer lines of code.

We're already making large strides towards this goal. In addition to the work mentioned, the Probabilistic Computing group at MIT has developed much shared infrastructure and benchmarking suites, and has made some demos showcasing our engines' ability to perform.

However, with parallelism and JITing still in baby stages, there is undoubtedly much more to be done. Reduced traces were not conceived of or implemented until recently, but will hopefully contribute to the goal of fast, general-purpose inference.

9 Acknowledgements

References

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