



Automated Inference Optimizations in the Probabilistic Programming Language Miking CorePPL

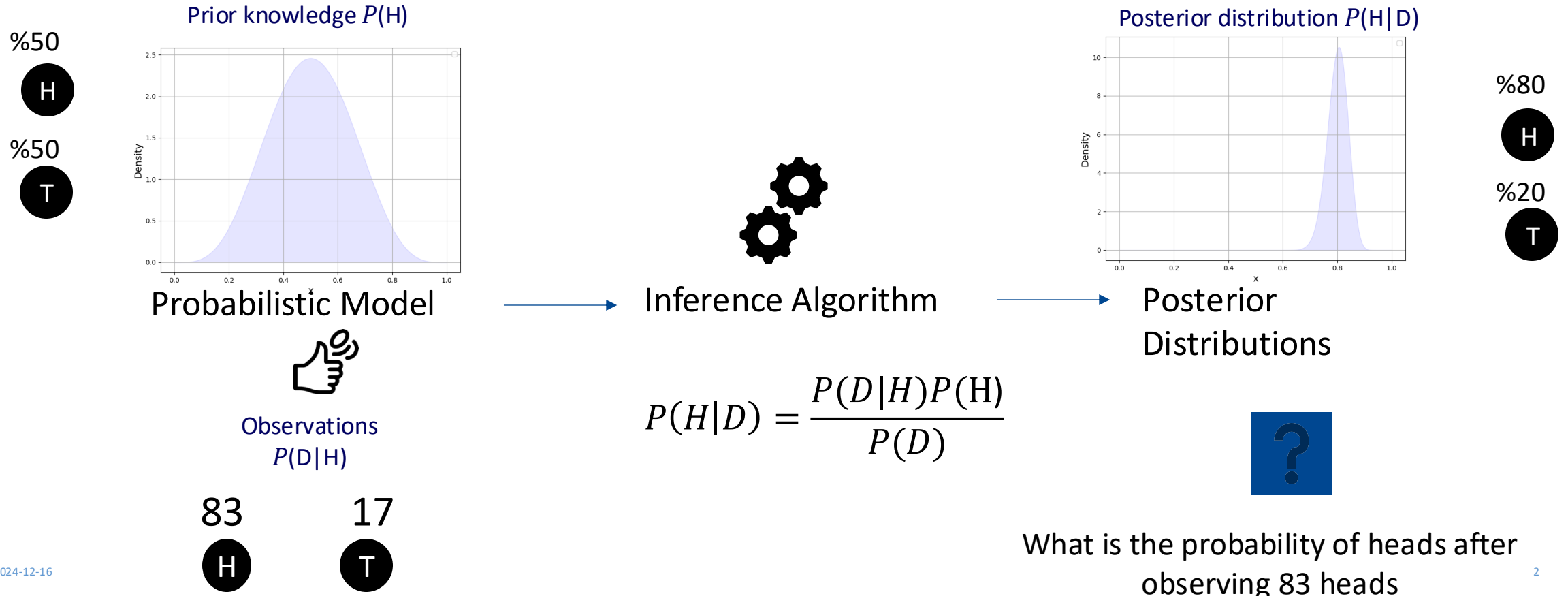
Gizem Caylak

Collaborators: David Broman, Daniel Lundén, Emma Granqvist, Fredrik Ronquist, Viktor Senderov

2024-12-16

Introduction: Probabilistic Programming Languages

- Probabilistic programming languages (PPLs) provide tools to write probabilistic models and run statistical inference over these models.



Introduction: Probabilistic Programming Languages

Monte Carlo Methods



Stan



Anglican



Birch



WebPPL



Miking CorePPL

Variational Inference



Edward



Pyro

Exact Inference

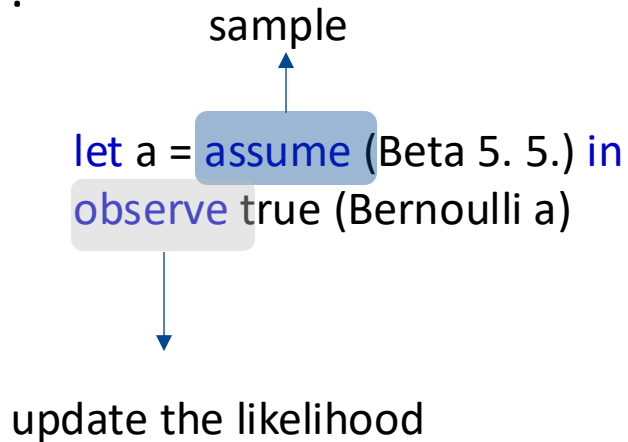
IBAL

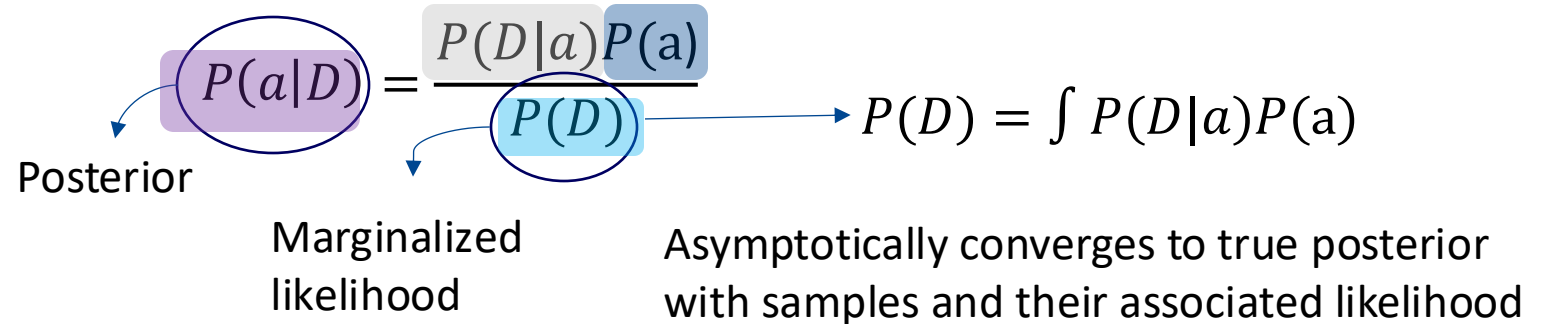
ProbZelus

PERPL

Introduction: Miking CorePPL

- Statically typed **universal** probabilistic programming language
- Calculate posterior distributions through **compiled** probabilistic code!



$$\begin{array}{c}
 \text{Posterior } P(a|D) = \frac{P(D|a)P(a)}{P(D)} \\
 \text{Marginalized likelihood } P(D) \rightarrow P(D) = \int P(D|a)P(a) \\
 \text{Asymptotically converges to true posterior with samples and their associated likelihood}
 \end{array}$$


Introduction: Problem definition

- Trade-off between approximate vs exact methods



$$P(D) = \int P(D|\theta)P(\theta)$$

$$P(\theta|D) = \frac{P(D|\theta)P(\theta)}{P(D)}$$

Approximate Inference



Exact Inference

Expressiveness

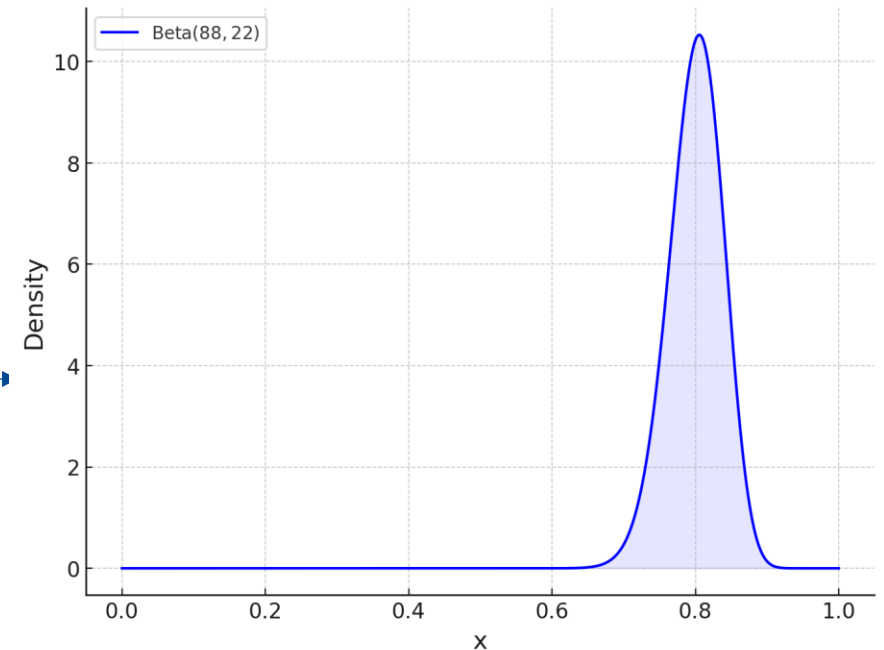
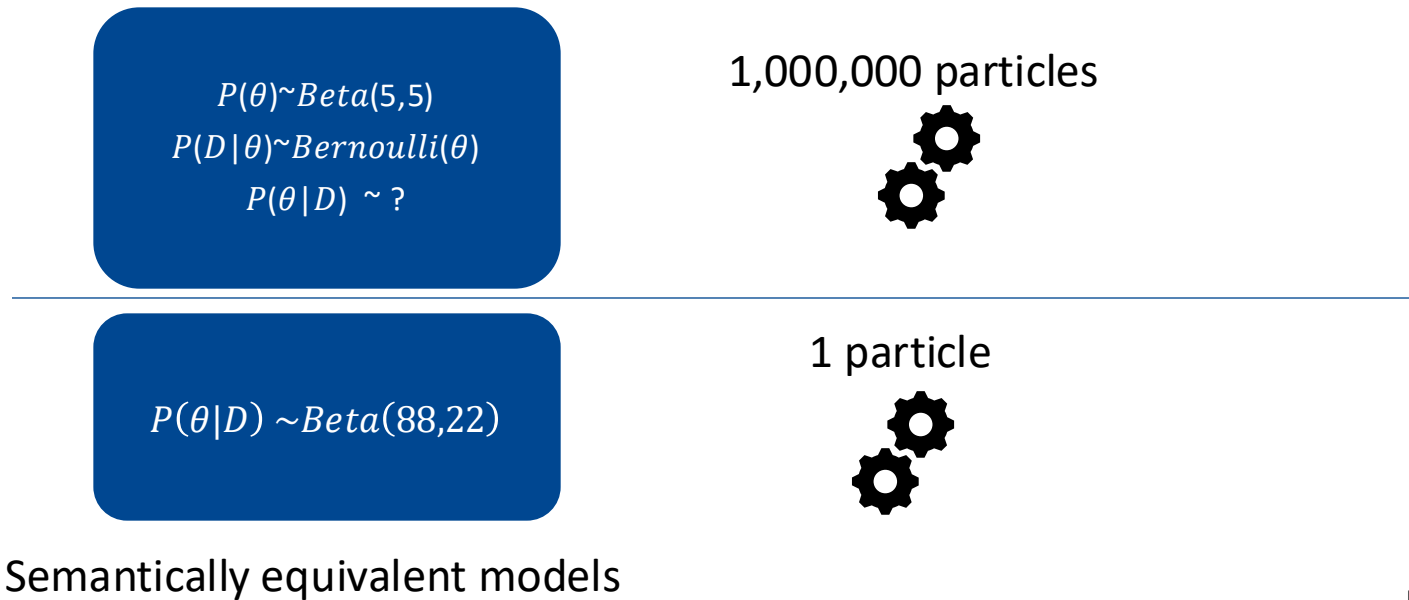
Accuracy

Dynamic Adaptation

Computational Efficiency

Introduction: Problem definition

- By utilizing exact inference techniques, we can improve the efficiency of approximate methods.



Both models converge to the same posterior with different execution times

Approaches

When

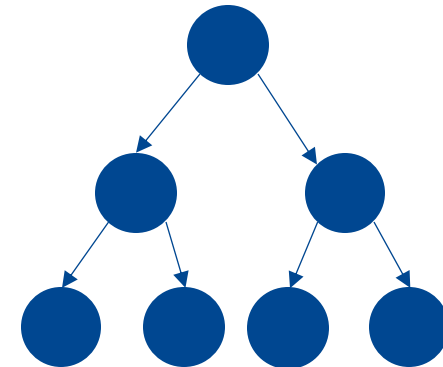
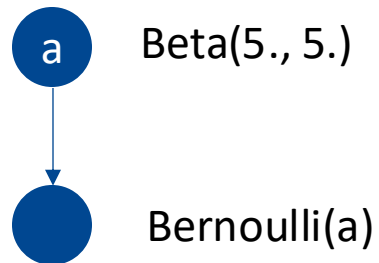
Compile-time approaches

Runtime approaches

What

- Topology of the model
- Conjugate prior relations between random variables

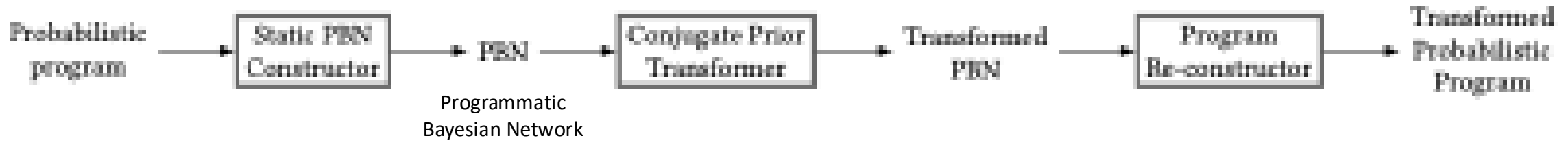
How



Delayed sampling by Murray et al. (2018): An approach utilizing conjugate prior relations at runtime

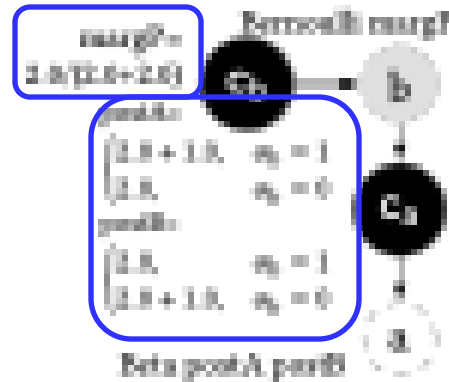
Belief propagation by Pearl (1986) gives exact solution for models forming tree structures.

Statically Delayed Sampling Algorithm



```

1 let a = assume
2 (Beta 2.0 2.0) in
3 observe b (Bernoulli a)
  
```



```

1 let margP = divf 2. (addf 2. 2.) in
2 observe b (Bernoulli margP);
3 let postA = if b then addf 2. 1.
4   else 2. in
5 let postB = if b then 2.
6   else addf 2. 1. in
7 let a = assume (Beta postA postB) in ()
  
```

Marginalize

$$P(b) = \int_a P(b|a)P(a) da$$

$$p(\tilde{x} = 1) = \frac{\alpha'}{\alpha' + \beta'}$$

Condition

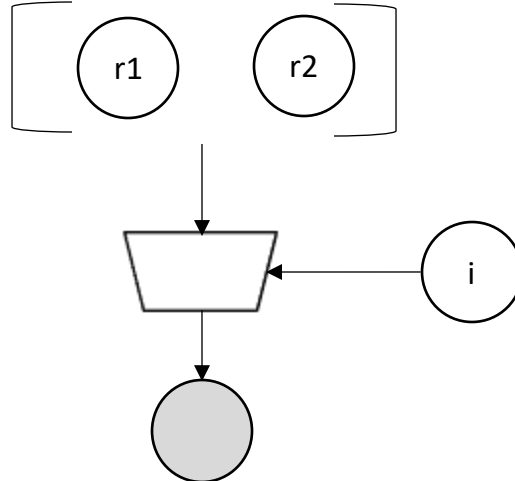
$$P(a|b) = \frac{P(b|a)P(a)}{P(b)}$$

$$\alpha + \sum_{i=1}^n x_i, \beta + n - \sum_{i=1}^n x_i$$

Programmatic Bayesian Network

```
1 let r1 = assume (Gaussian 0. 1.) in
2 let r2 = assume (Gaussian 1. 2.) in
3 let lst = [r1, r2] in
4 let i = assume (Categorical [0.6, 0.4]) in
5 let mu = get lst i in
6 observe 0.9 (Gaussian mu 1.)
```

Programmatic Bayesian Network



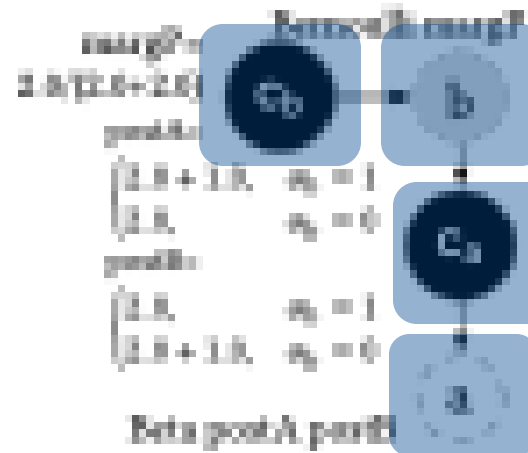
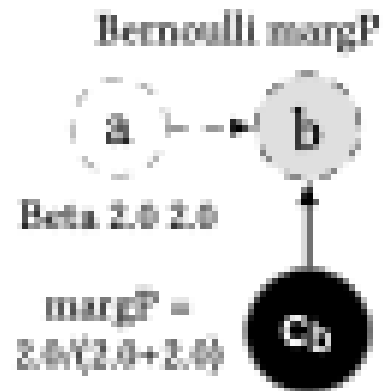
Reconstruct

- Topologically sort the graph and then reconstruct each node

```

1 let a = assume
2 (Beta 2.0 2.0) in
3 observe b (Bernoulli a)

```



```

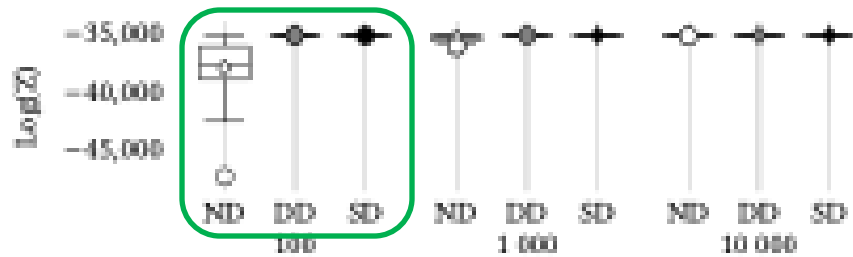
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2 observe b (Bernoulli margP);
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4   else 2. in
5 let postB = if b then 2.
6   else addf 2. 1. in
7 let a = assume (Beta postA postB) in ()

```

Results

No delayed (ND)
 Dynamically delayed (DD)
 Statically delayed (SD)

Bayesian linear regression

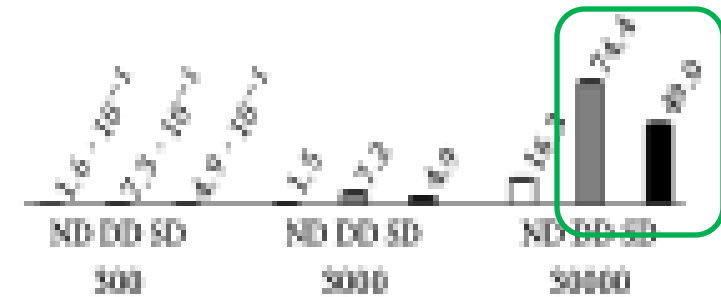
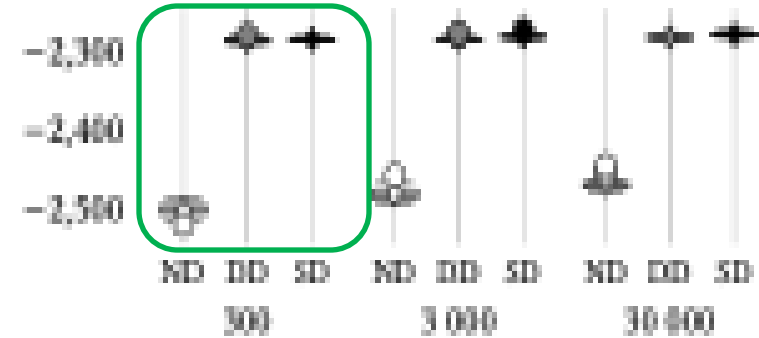


(a) Log normalizing constants.



(b) Execution times

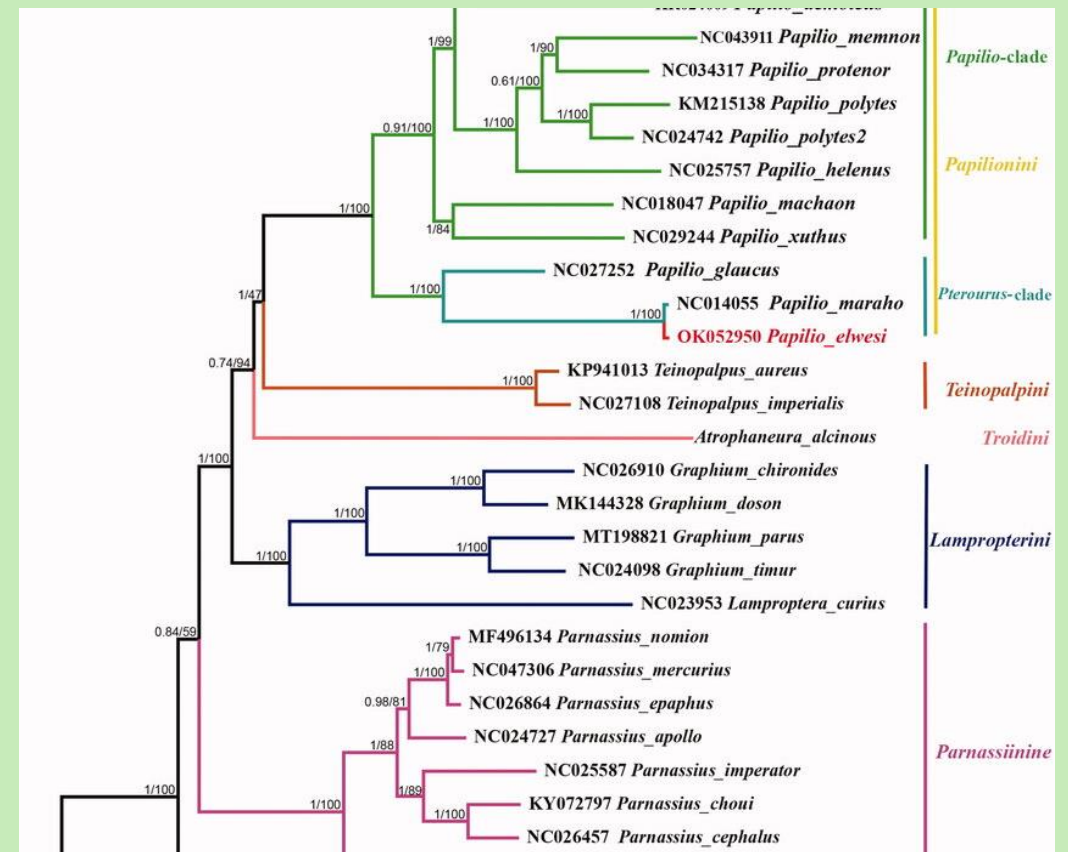
Latent Dirichlet allocation



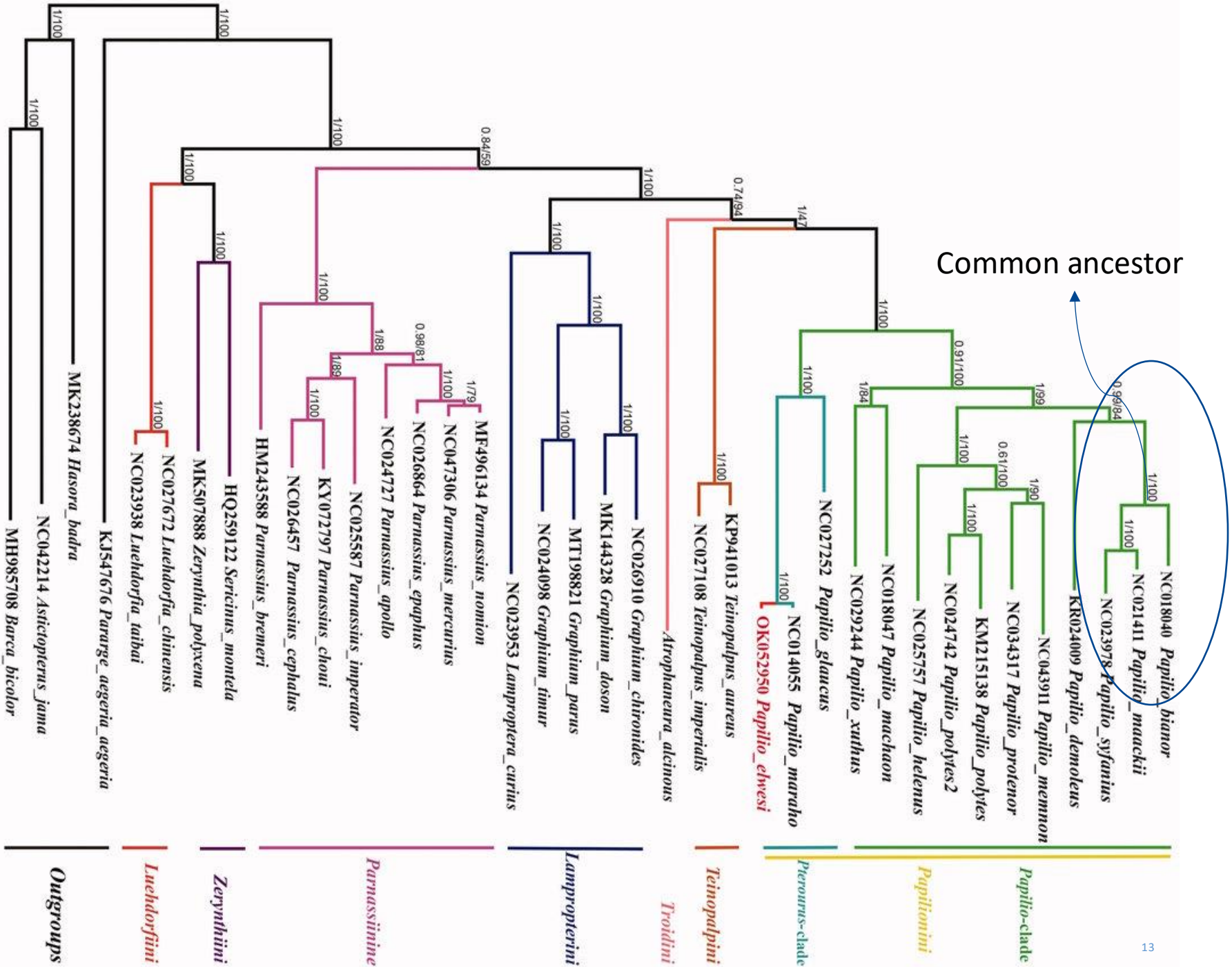
Automating the Forward Pass of Belief Propagation

- Tree inference is a fundamental problem in evolutionary biology
- Given the current species, what is the most likelihood evolutionary tree or distribution of trees?
- Can we answer this question efficiently?

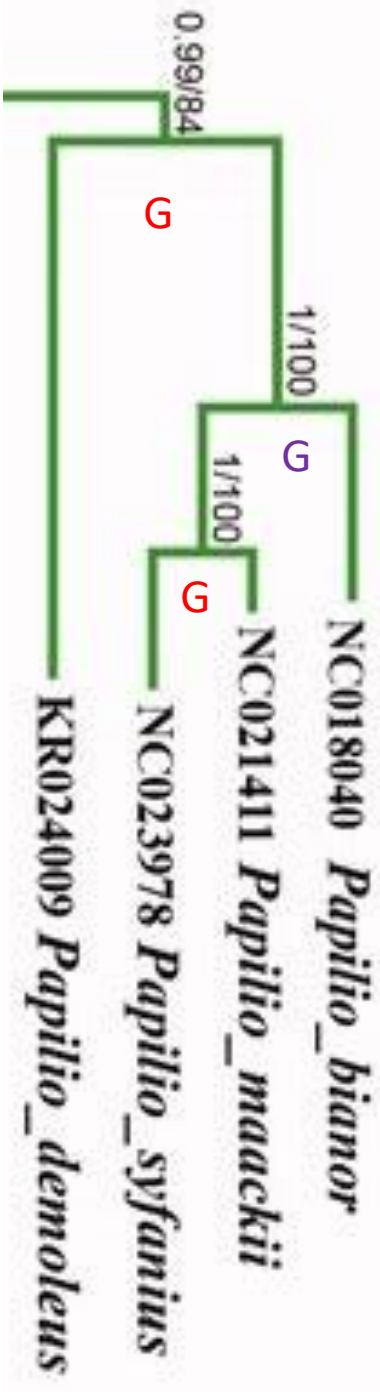
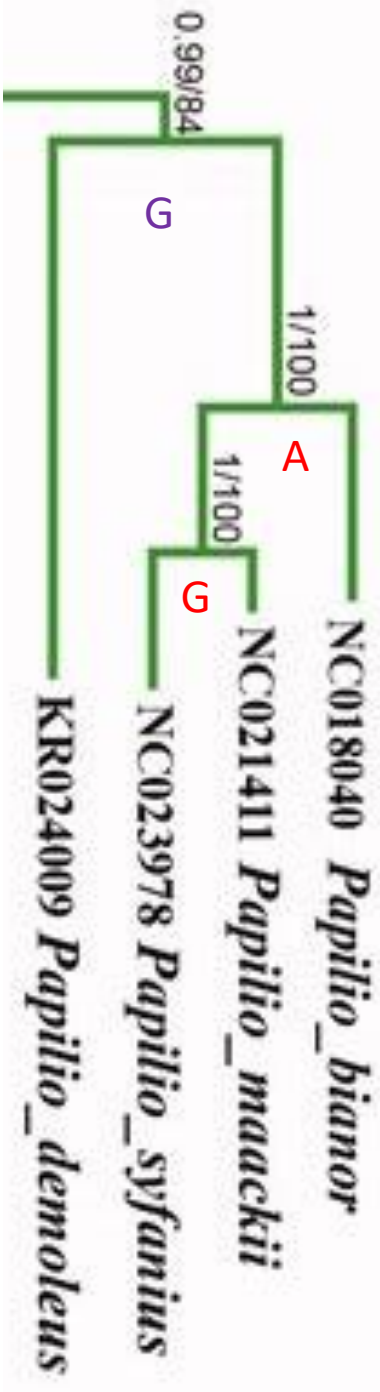
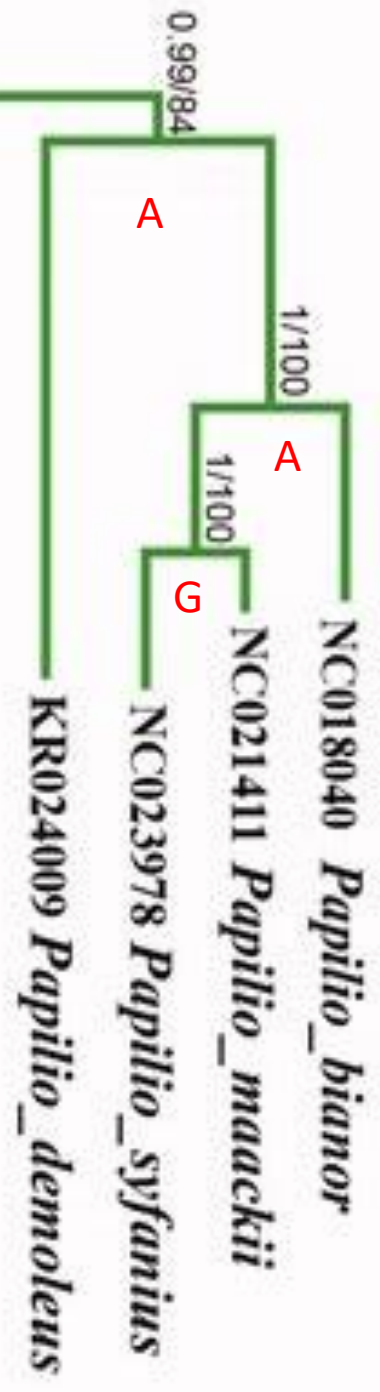
Complete mitochondrial genome of *Papilio elwesi* and its phylogenetic analyses with other swallowtail butterflies (Lepidoptera, Papilionidae) - Scientific Figure on ResearchGate. Available from: https://www.researchgate.net/figure/Phylogenetic-tree-using-Bayesian-inference-BI-and-maximum-likelihood-ML-analysis_fig1_359347159 [accessed 2 Dec 2024]



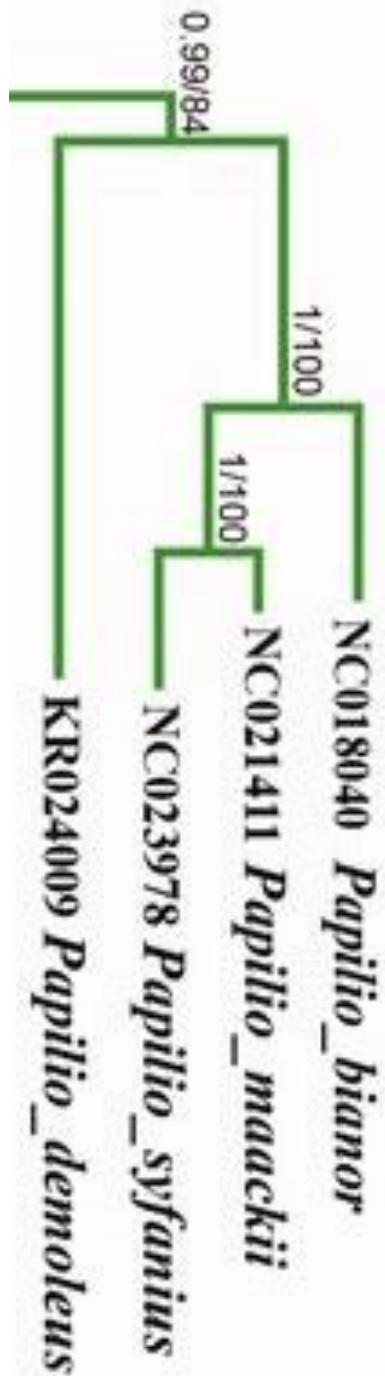
The purpose is to calculate the likelihood of this tree



Common ancestor

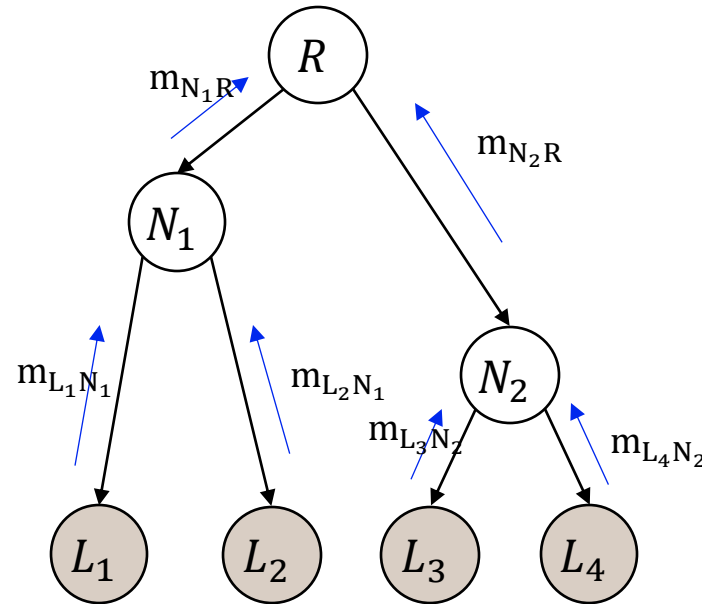


...



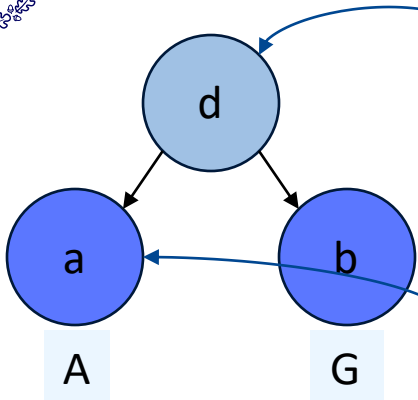
- The important information is the topology of the tree not specific information about internal nodes such as their genetic code
- Can we summarize this information:
For all the possible values internal nodes can take, what is the likelihood of this tree?

Belief Propagation on Tree Inference Problem



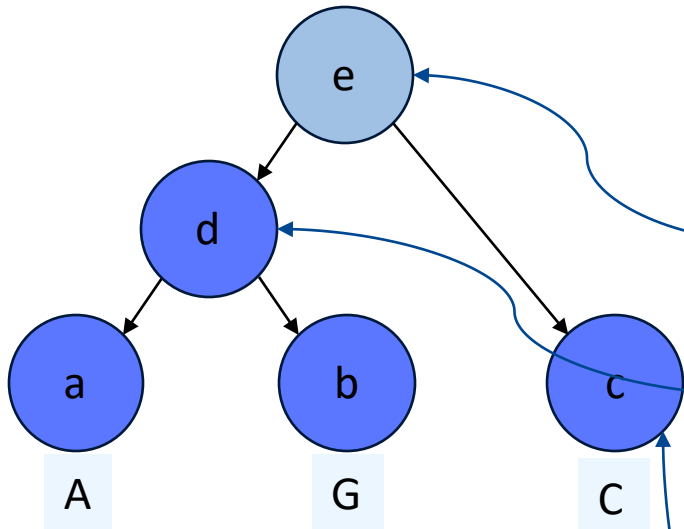
Marginalize out the internal nodes

Propagate the messages to the root to calculate the likelihood of observations given the tree topology



```
let d_seq = prune (Categorical [0.25,0.25,0.25,0.25]) in
```

```
let p1 = ctmc (pruned d_seq) q (subf age (getAge a)) in
observe (getSeq a) (Categorical p1);
```

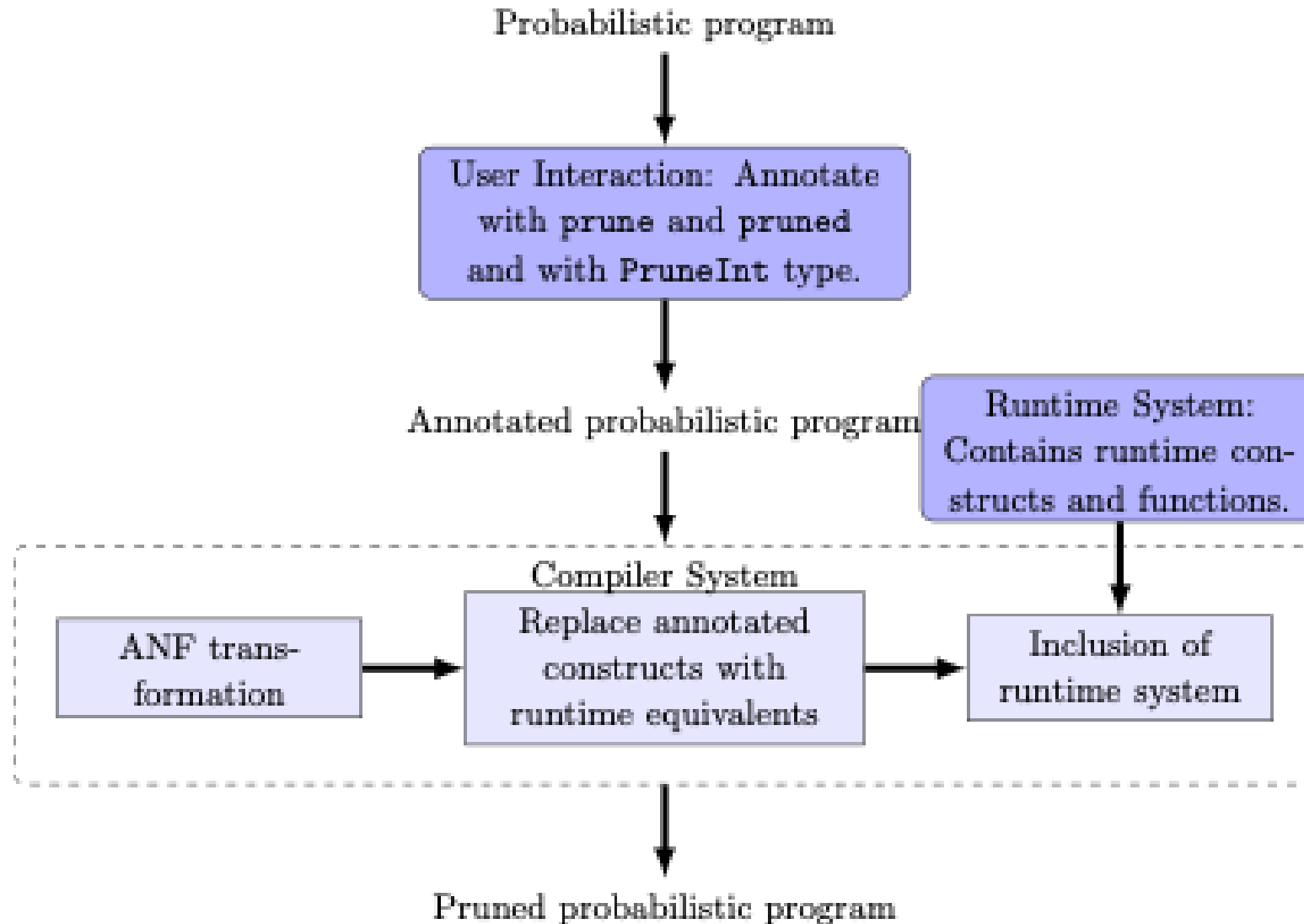


```
let p2 = ctmc (pruned d_seq) q (subf age (getAge b)) in
observe (getSeq b) (Categorical p2);
```

```
let e_seq = prune (Categorical [0.25,0.25,0.25,0.25]) in
let p3 = ctmc (pruned e_seq) q (subf age (getAge d)) in
observe (pruned (getNodeSeq d)) (Categorical p3);
```

```
cancel (observe (pruned (getNodeSeq d))
(Categorical [0.25,0.25,0.25,0.25]));
```

```
let p4 = ctmc (pruned e_seq) q (subf age (getAge c)) in
observe (getSeq c) (Categorical p4)
```



Results

Generalized time reversible model– Primates data

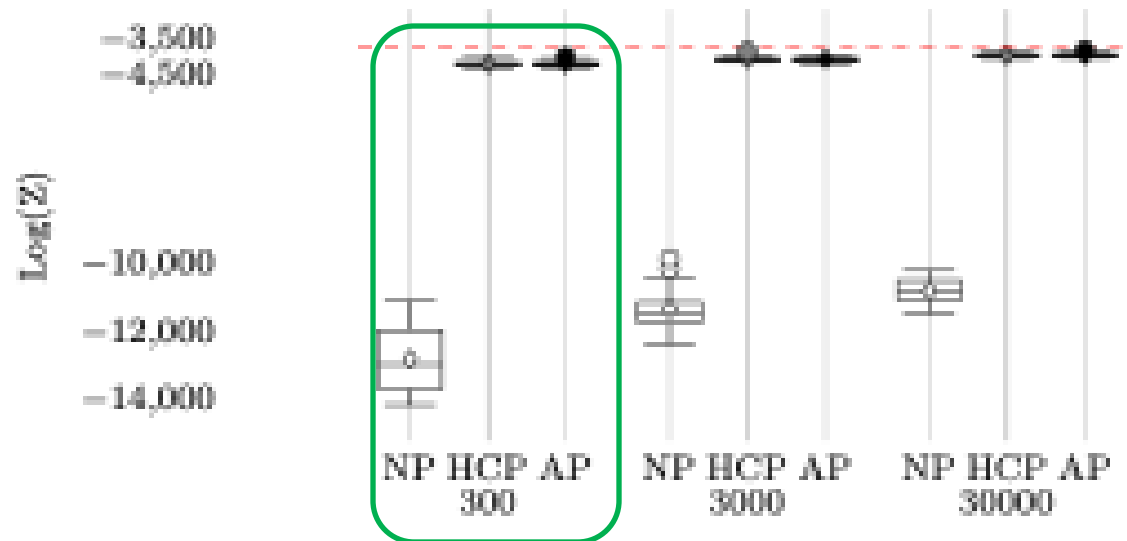
Without pruning, GTR model is encoded in 110 lines

The number of lines that need to be changed for

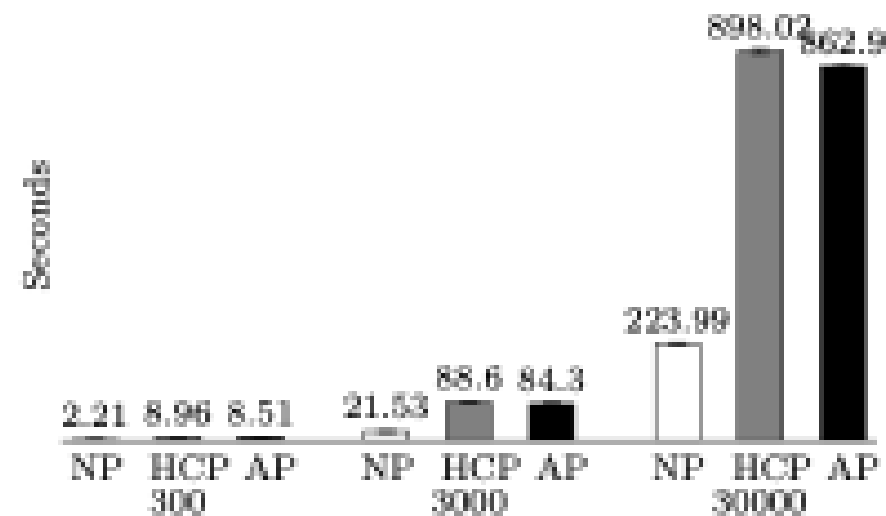
Automated pruning: 18

Hard-coded pruning: 107

No pruning (NP)
 Hard-coded pruning (HCP)
 Automated pruning (AP)



(a) Log normalizing constants.



(b) Execution times



Conclusion