TreePPL—a new DSL in Miking for Phylogenetics

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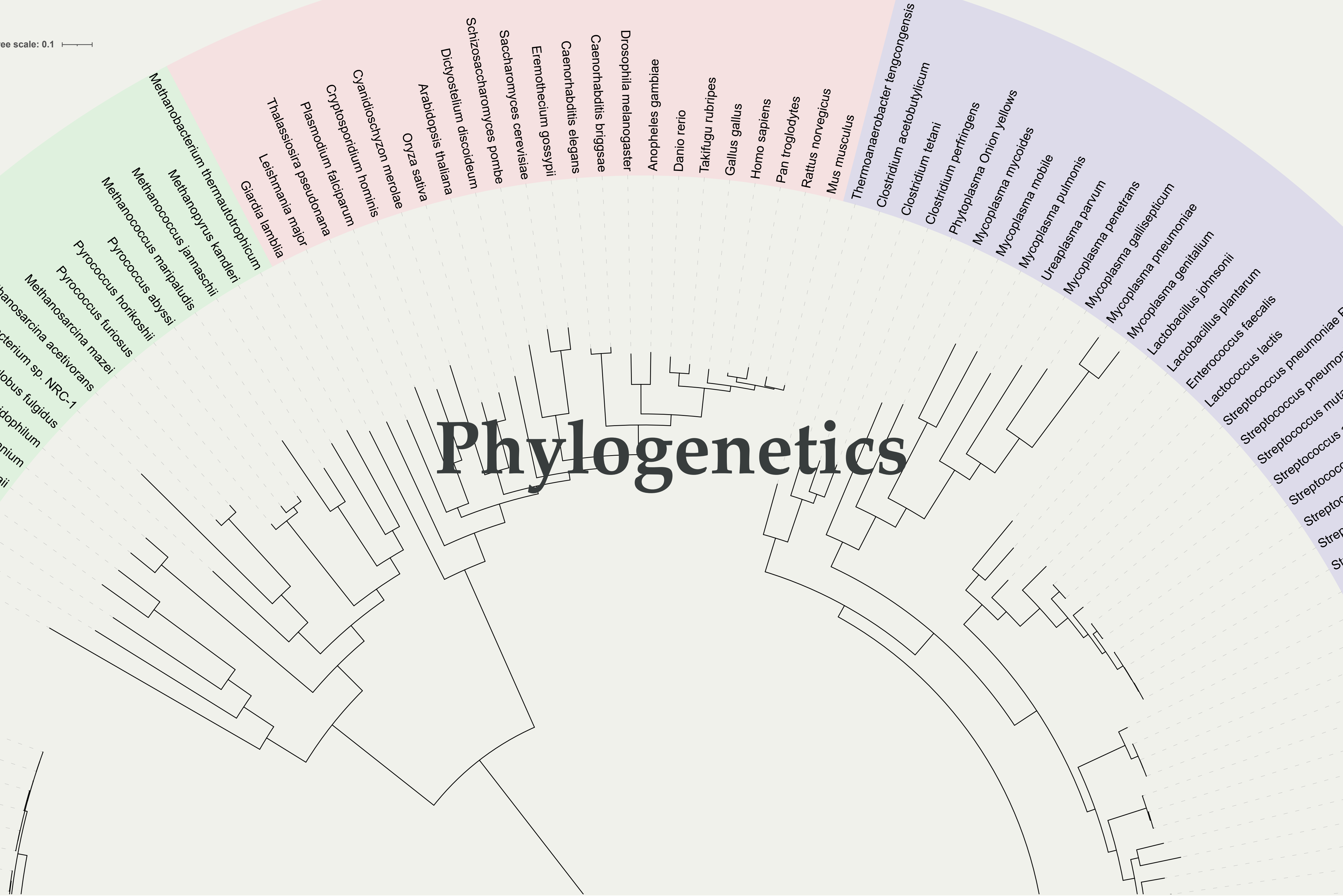
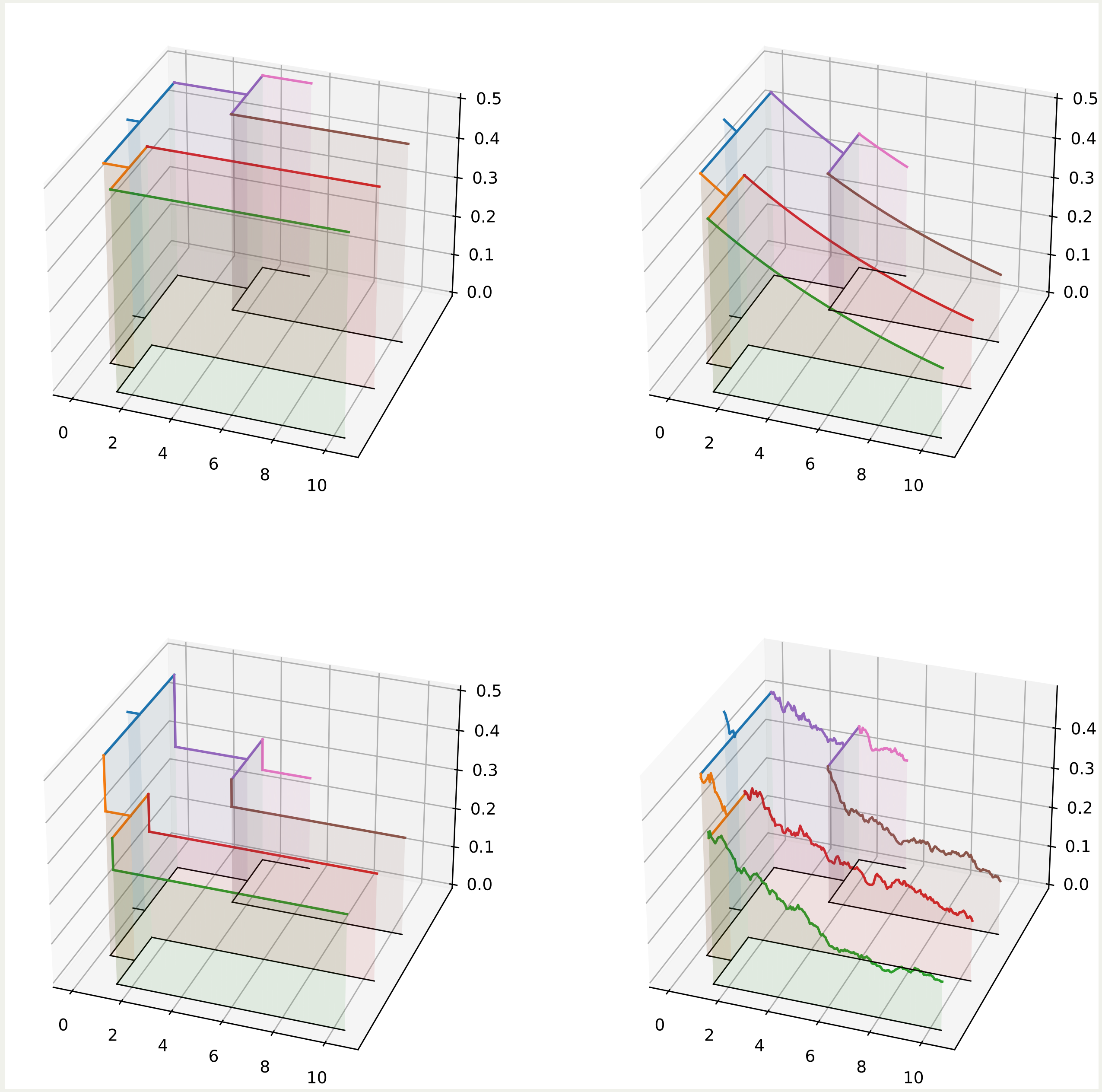
Contents

Phylogenetics



Phylogenetics discussion

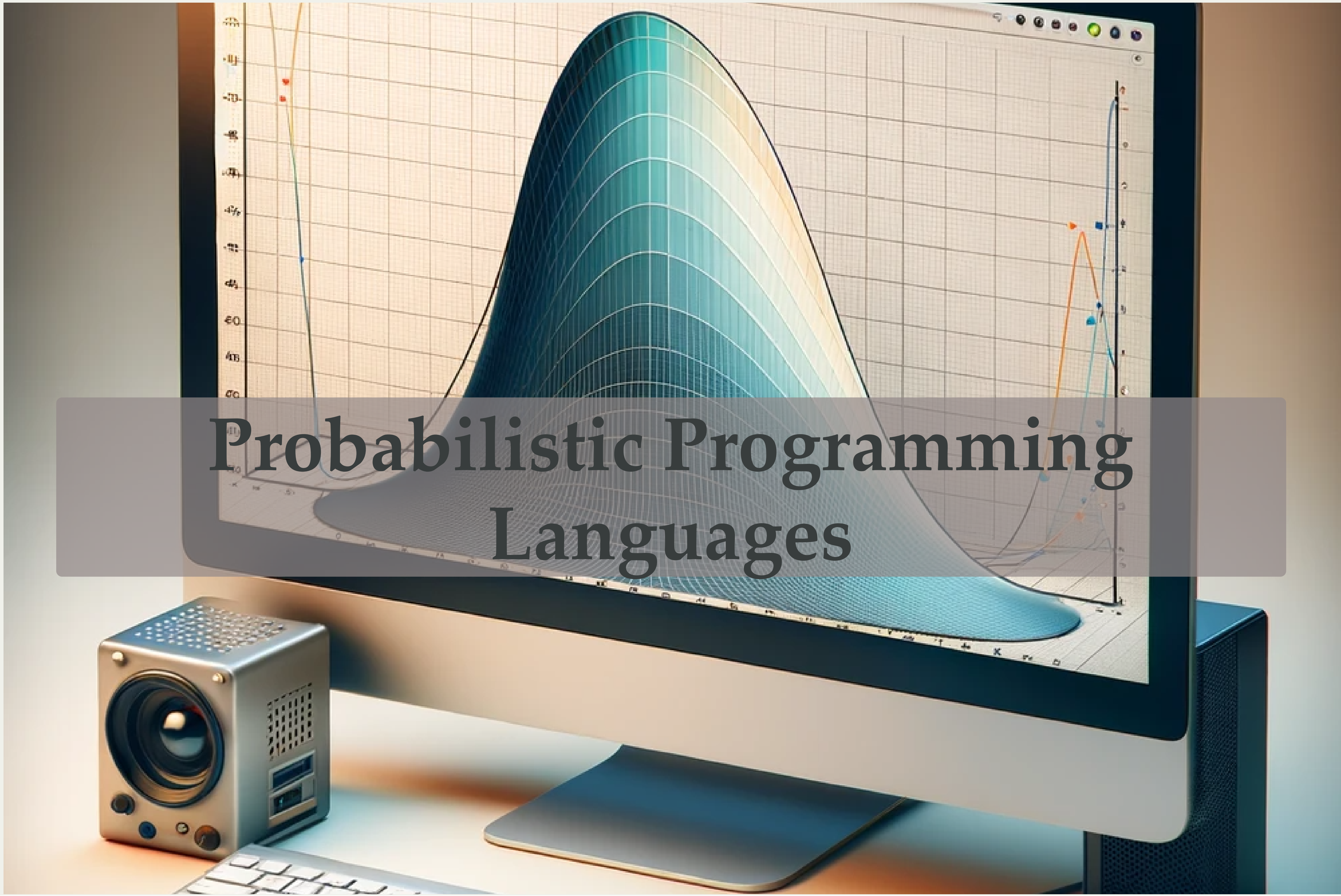
- Problems that phylogenetics deals with
  - Reconstructing phylogenetic trees
  - Using phylogenetic trees to understand evolution and ecology



Diversification models on a phylogenetic tree

What can the users do?

- Methods of phylogenetics
  - Parsimony
  - Statistical methods: ML and Bayesian
- Software for phylogenetics
  - monolithic software: e.g. MrBayes, RAxML
  - extensible software: e.g. BEAST, BEAST2, RevBayes
- Write the model yourself
  - implement in a general-purpose language: e.g. C, Java, Python, or R
  - implement in a probabilistic programming language: e.g. WebPPL, Birch
  - implement in a phylogenic PPL: TreePPL



Probabilistic Programming Languages

Bayes theorem

Let x be some observed data and θ be an unobserved parameter in whose value we are interested in in.

$$\overbrace{p(\theta|x)}^{\text{posterior distribution}} = \frac{\overbrace{p(x|\theta)}^{\substack{\text{data distribution/}\\ \text{likelihood}}} \quad \overbrace{p(\theta)}^{\text{prior distribution}}}{\underbrace{p(x)}_{\text{normalizing constant}}}$$

Bayes theorem

Let x be some observed data and θ be an unobserved parameter in whose value we are interested in in.

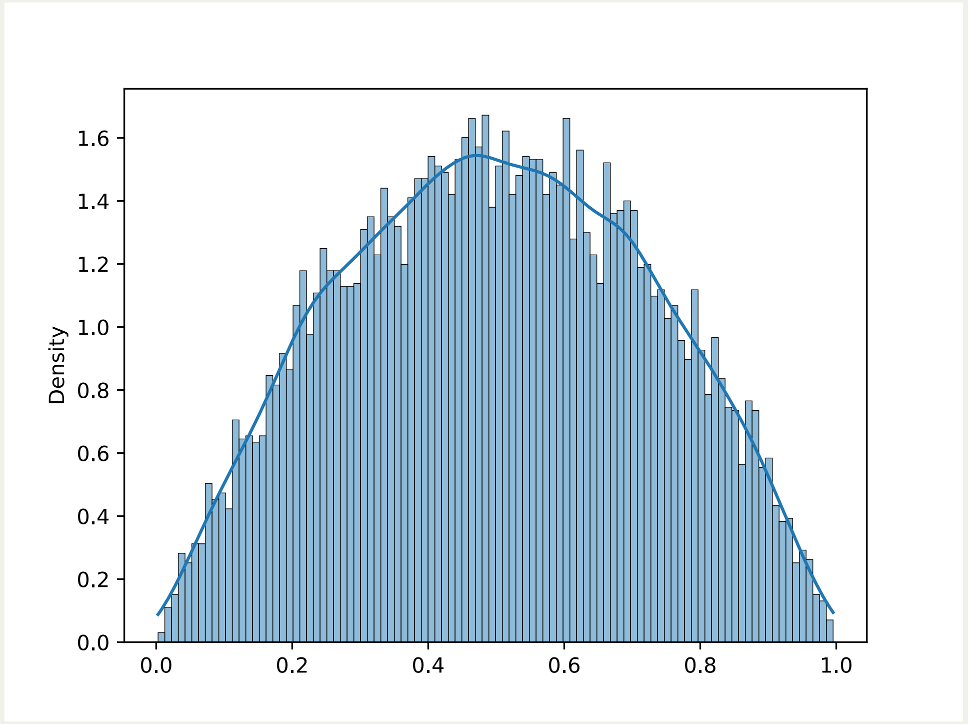
$$\overbrace{p(\theta|x)}^{\text{posterior distribution}} = \frac{\overbrace{p(x|\theta)}^{\substack{\color{red}{\text{observe/factor}} \\ \text{data distribution/} \\ \text{likelihood}}} \quad \overbrace{p(\theta)}^{\substack{\color{red}{\text{assume/sample}} \\ \text{prior distribution}}}}{\underbrace{p(x)}_{\text{normalizing constant}}}$$

Coin example

```python
outcomes=[True, True, True, False, True, False, True, True, True, False,
    False, True, True, False, True, False, False, True, False, False]
```

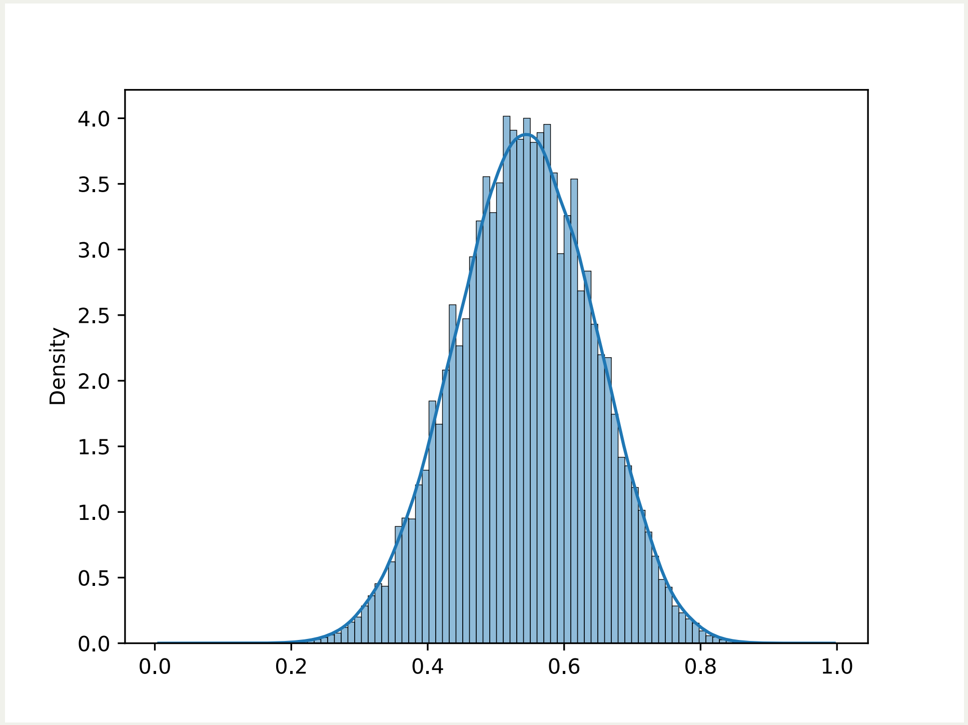
Define prior

```
assume p ~ Beta(2.0, 2.0);
```



Condition on data

```
for i in 1 to (length(outcomes)) {
    observe outcomes[i] ~
Bernoulli(p);
}
```



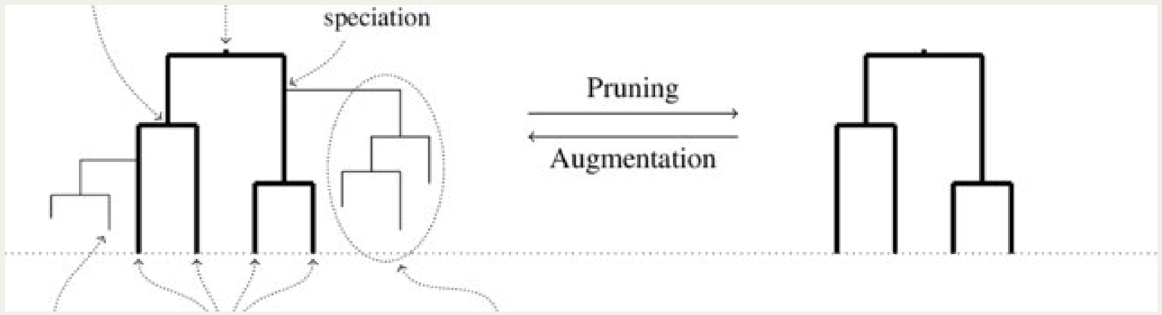
The complete coin example in TreePPL using Python as a wrapper.

```
source = """\
model function coin(outcomes: Bool[]): Real {
  assume p ~ Beta(2.0, 2.0);
  for i in 1 to (length(outcomes)) {
    observe outcomes[i] ~ Bernoulli(p);
  }
  return(p);
}
"""

with treeppl.Model(source=source, samples=10_000, method="is-lw") as coin:
    res = coin(
      outcomes=outcomes
    )
    sns.histplot(
        x=res.samples, weights=res.nweights, bins=100, stat="density", kde=
    )
    plt.show()
```

Universal PPLs

```
function simulateSubtree(time: Real, lambda: Real, mu: Real) {
  assume waitingTime ~ Exponential(lambda + mu);
  if waitingTime > time {
    weight 0.0;
    resample;
  } else {
    assume isSpeciation ~ Bernoulli(lambda / (lambda + mu));
    if isSpeciation {
      simulateSubtree(time - waitingTime, lambda, mu);
      simulateSubtree(time - waitingTime, lambda, mu);
    }
  }
}
```



Simulating unobserved evolutionary lineages

TreePPL

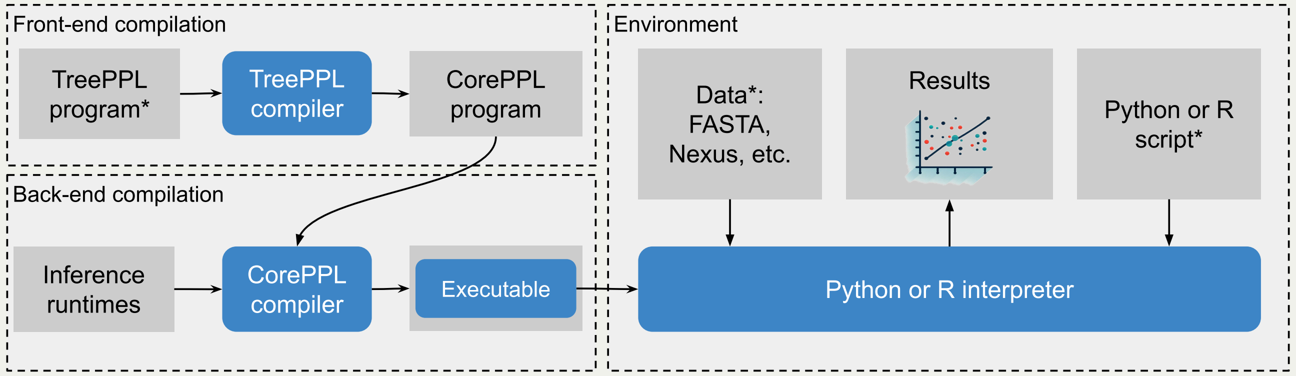
Phylogenetic Data
Supports natively the PhyJSON format for evolutoinary trees

Simplicity
Designed to meet the needs of computational biologists

Rich Model Library
Offers state-of-the art diversificatio
models as templates

Powerful Statistical Inference
Sequential Monte-Carlo (SMC) and Markov-chain Monte-Carlo (MCMC) inference

Architecture



Optimizations

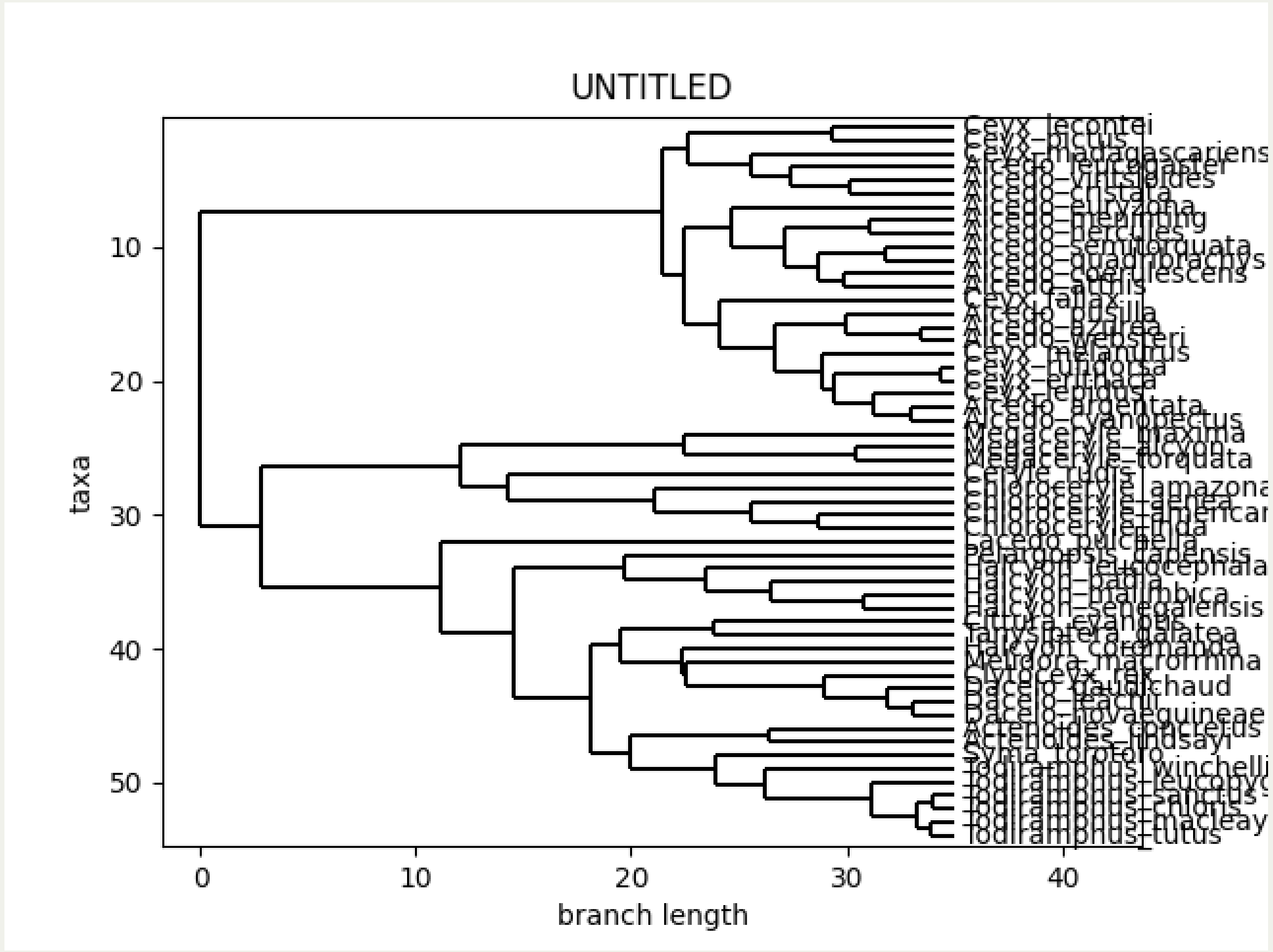
- Partial CPS transformation
- Automatic alignment
- (Delayed sampling/ conjugacy analysis)

Inference strategies

- Lightweight importance sampling
- Sequential Monte Carlo: Bootstrap Particle Filter,
- Sequential Monte Carlo: Alive particle filter
- Lightweight MCMC
- Trace MCMC
- Particle MCMC

Computer demo Challenges

Write a program that infers the bifurcation rate λ and the extinction rate μ under the assumption that they are constant for a given binary evolutionary tree.


UNTITLED
taxa
branch length
0
10
20
30
40
50
Ceyx_lecontei
Ceyx_pictus
Ceyx_madagascariens
Alcedo_leucogaster
Alcedo_vintsioides
Alcedo_cristata
Alcedo_euryzona
Alcedo_meninting
Alcedo_hercules
Alcedo_semitorquata
Alcedo_quadribrachys
Alcedo_coerulescens
Alcedo_atthis
Ceyx_fallax
Alcedo_pusilla
Alcedo_azurea
Alcedo_websteri
Ceyx_melanurus
Ceyx_rufidorsa
Ceyx_erithaca
Ceyx_lepidus
Alcedo_argentata
Alcedo_cyanopectus
Megaceryle_maxima
Megaceryle_alcyon
Megaceryle_torquata
Ceryle_rudis
Chloroceryle_amazona
Chloroceryle_aenea
Chloroceryle_americar
Chloroceryle_inda
Lacedo_pulchella
Pelargopsis_capensis
Halcyon_leucocephala
Halcyon_badia
Halcyon_malimbica
Halcyon_senegalensis
Cittura_cyanotis
Tanysiptera_galatea
Halcyon_coromanda
Melidora_macrorrhina
Clytoceyx_rex
Dacelo_gaudichaud
Dacelo_leachii
Dacelo_novaeguineae
Actenoides_concretus
Actenoides_lindsayi
Syma_torotoro
Todiramphus_winchelli
Todiramphus_leucopyg
Todiramphus_sanctus
Todiramphus_chloris
Todiramphus_macleay
Todiramphus_tutus

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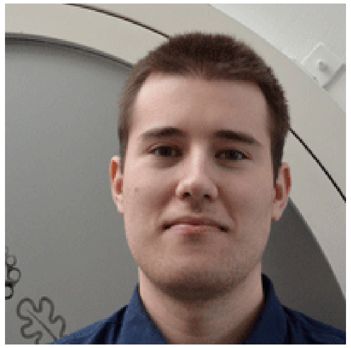

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Thank you

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Downloading

Project homepage: https://treeppl.org

Main repo: https://github.com/treeppl/treeppl

Python library: https://github.com/treeppl/treeppl-python

Paper:
https://www.biorxiv.org/content/10.1101/2023.10.10.561673v1

Citation:

```
TreePPL: A Universal Probabilistic Programming Language for Phylogenetics
Viktor Senderov, Jan Kudlicka, Daniel Lundén, Viktor Palmkvist, Mariana P.
Braga, Emma Granqvist, David Broman, Fredrik Ronquist
bioRxiv 2023.10.10.561673; doi: https://doi.org/10.1101/2023.10.10.561673
```

Bonus material

Discussion of PPLs

- PPL semantics
  - Usual language: *input* $\rightarrow$ *output* + *side effects*
  - PPL: *each program trace describes a sample from a probability distribution*
- Advantages of PPLs
  - natural and generative way of encoding a posterior distribution
  - no need to implement inference
  - enables model comparison as estimation of normalizing constant possible