

BCB 503: RevBayes Intro



First session: Setup, Intro, Basics

Orlando Schwery, 24. Aug. 2021, University of Idaho

Quick Intro

Orlando Schwery

- BSc & MSc U of Zürich, Switzerland [[H.P. Linder](#)]
- PhD U of Tennessee [[B. O'Meara](#)]
- Postdoc New Mexico Consortium/U of Idaho [[E. Goldberg](#)]
- Next: Southeastern Louisiana U/LSU [[A. Wright](#) / [J. Brown](#)]
- Next-next: Virginia Tech [[J. Uyeda](#)]

- Phylogenetics, Diversification, Biogeography, Model Adequacy
- Ericaceae, Dung Beetles, ...?



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And who are you?

Disclaimer & the Actual People Behind This

Höhna, Landis, Heath, Boussau, Lartillot, Moore, Huelsenbeck, Ronquist. **2016**. RevBayes: Bayesian phylogenetic inference using graphical models and an interactive model-specification language. *Systematic Biology*, 65:726-736.

Höhna, Heath, Boussau, Landis, Ronquist, Huelsenbeck. **2014**. Probabilistic graphical model representation in phylogenetics. *Systematic Biology* 63:753–771.



Sebastian
Höhna



Fredrik
Ronquist



John P.
Huelsenbeck



Michael J.
Landis



Bastien
Boussau



Tracy A.
Heath



Nicolas
Lartillot



Walker
Pett



William A.
Freyman

Course Plan and Schedule

- 3:30pm Pacific, TLC 139 (or on Zoom)
 - 24. Aug.: Intro
 - **31. Aug.:** Trait Evolution
 - **07. Sep.:** Biogeography
 - **14. Sep.:** Diversification
 - **21. Sep.:** [Model Testing/Adequacy]
 - **28. Sep.:** [Hierarchical Models, FBD, ...?]
- Possible Absences, Recording, Remote, Add-On, ...

Starting RevBayes & Basic Operations

- Use from command-line

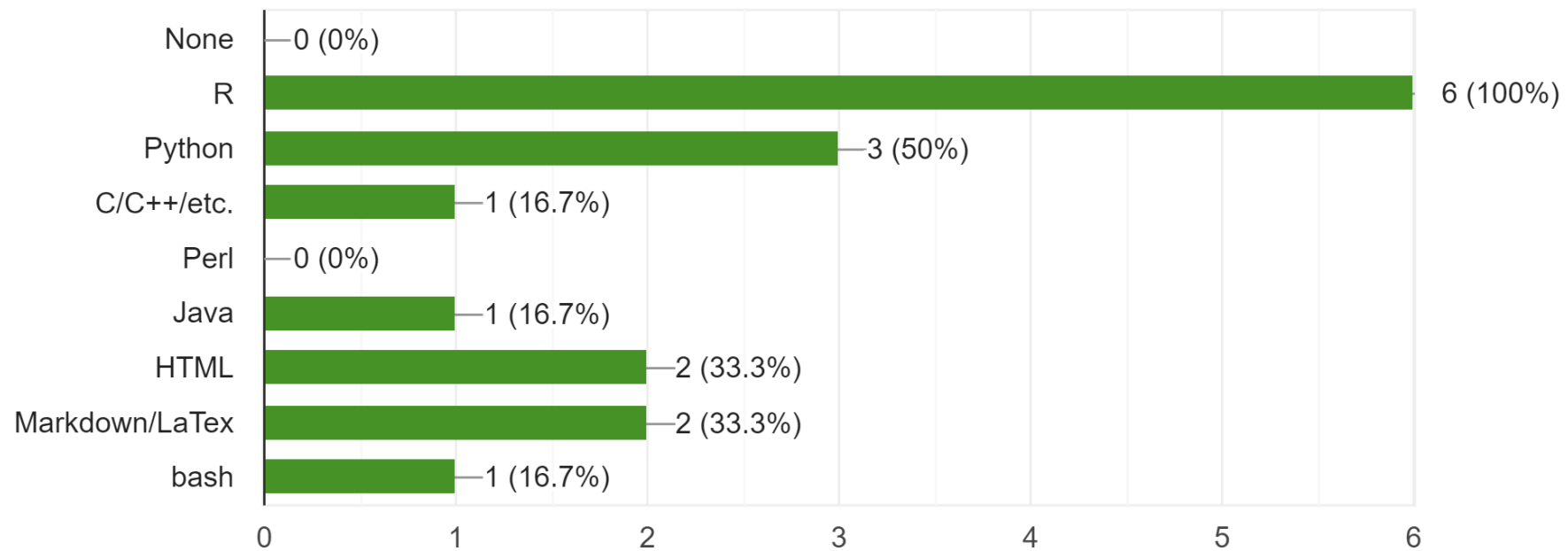
[code-time]

- Possibility to use RStudio or Jupyter as GUI...

Can't we do all that in R...?

Which other languages do you have experience in?

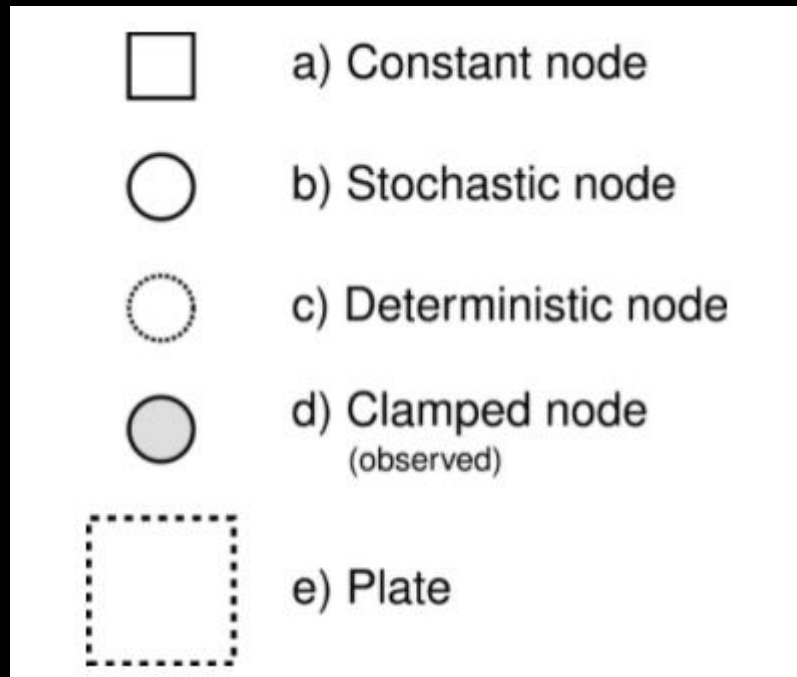
6 responses



Can't we do all that in R...?

- Initial reaction:
“Why not just use the well-established phylo-universe in the R-framework?”
- Probabilistic graphical model framework
 - Modularity, flexibility, customizability (esp. MCMC)
 - Transparency and reproducibility
 - Explicit representation of assumptions and variable dependencies
 - Some advantages for method development
- Speed (*Rev* front-end and *C++* back-end)
- More unified format

Graphical Models

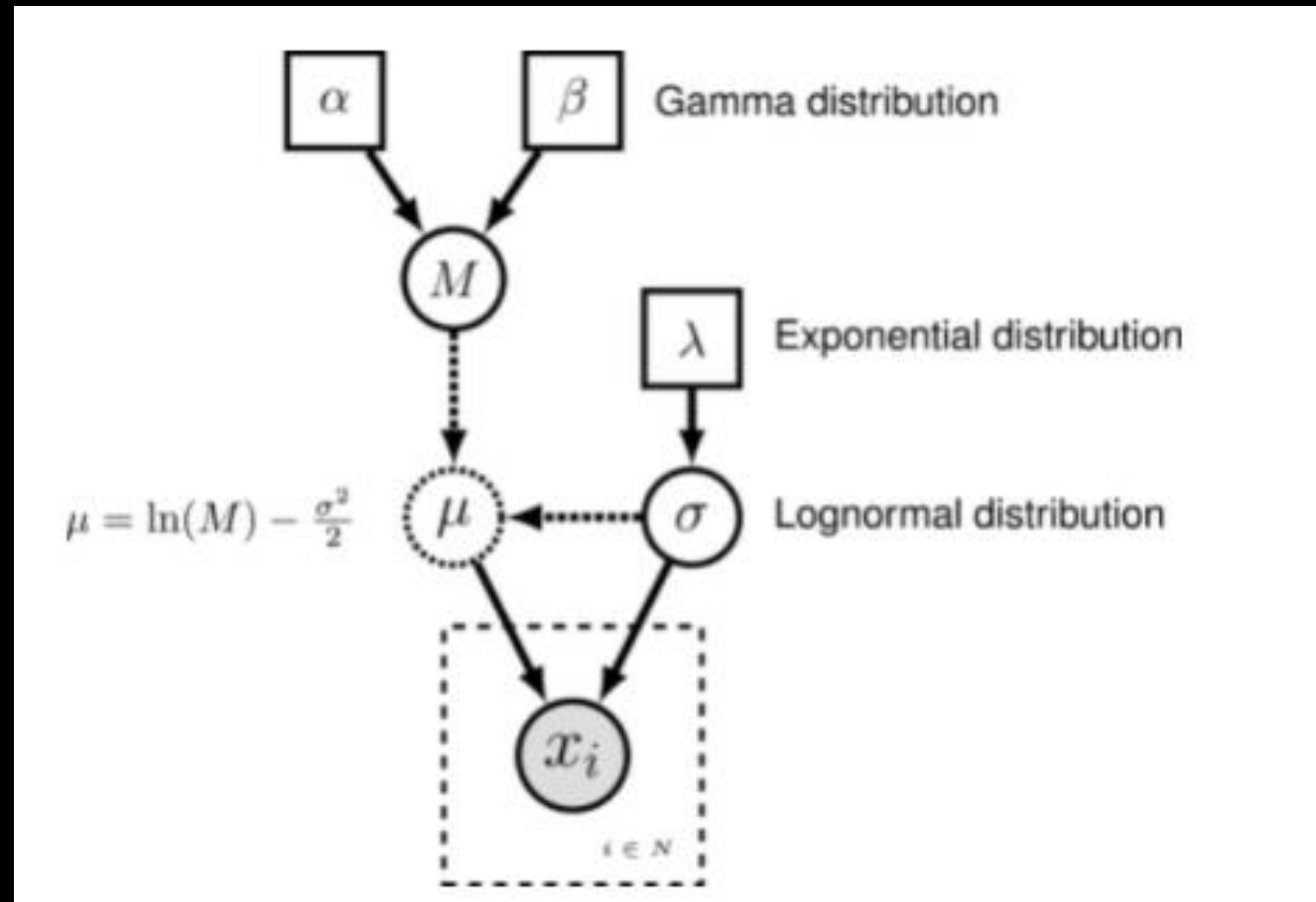
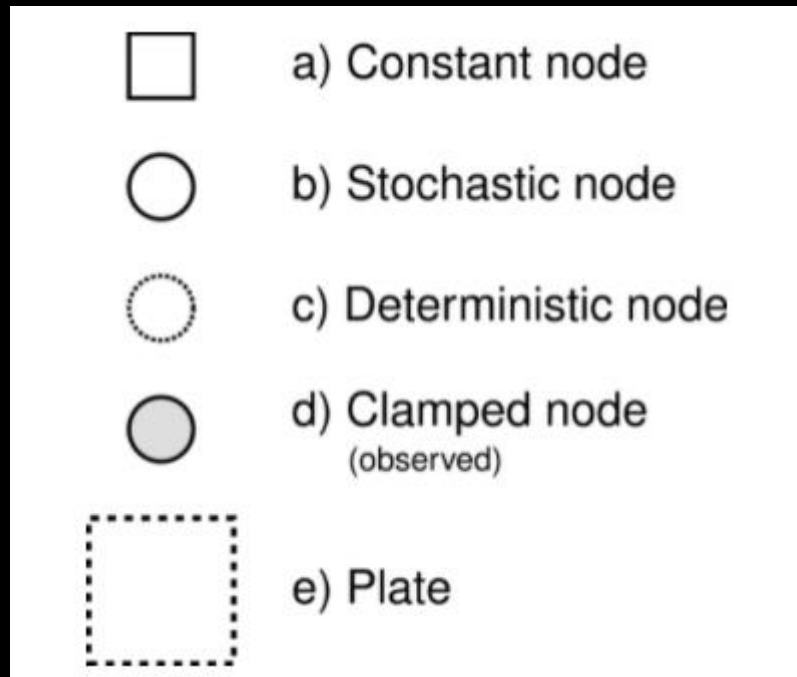


Directed Acyclic Graph (DAG)

→ Nodes (vertices) and Edges (circles/squares and arrows)

a)	<code>p <- 0.5</code>
b)	<code>x ~ dnBernoulli(p)</code>
c)	<code>x := exp(p)</code>
d)	<code>x.clamp(1)</code>
e)	<pre>for (i in 1:N) { x[i] ~ dnBernoulli(p) }</pre>

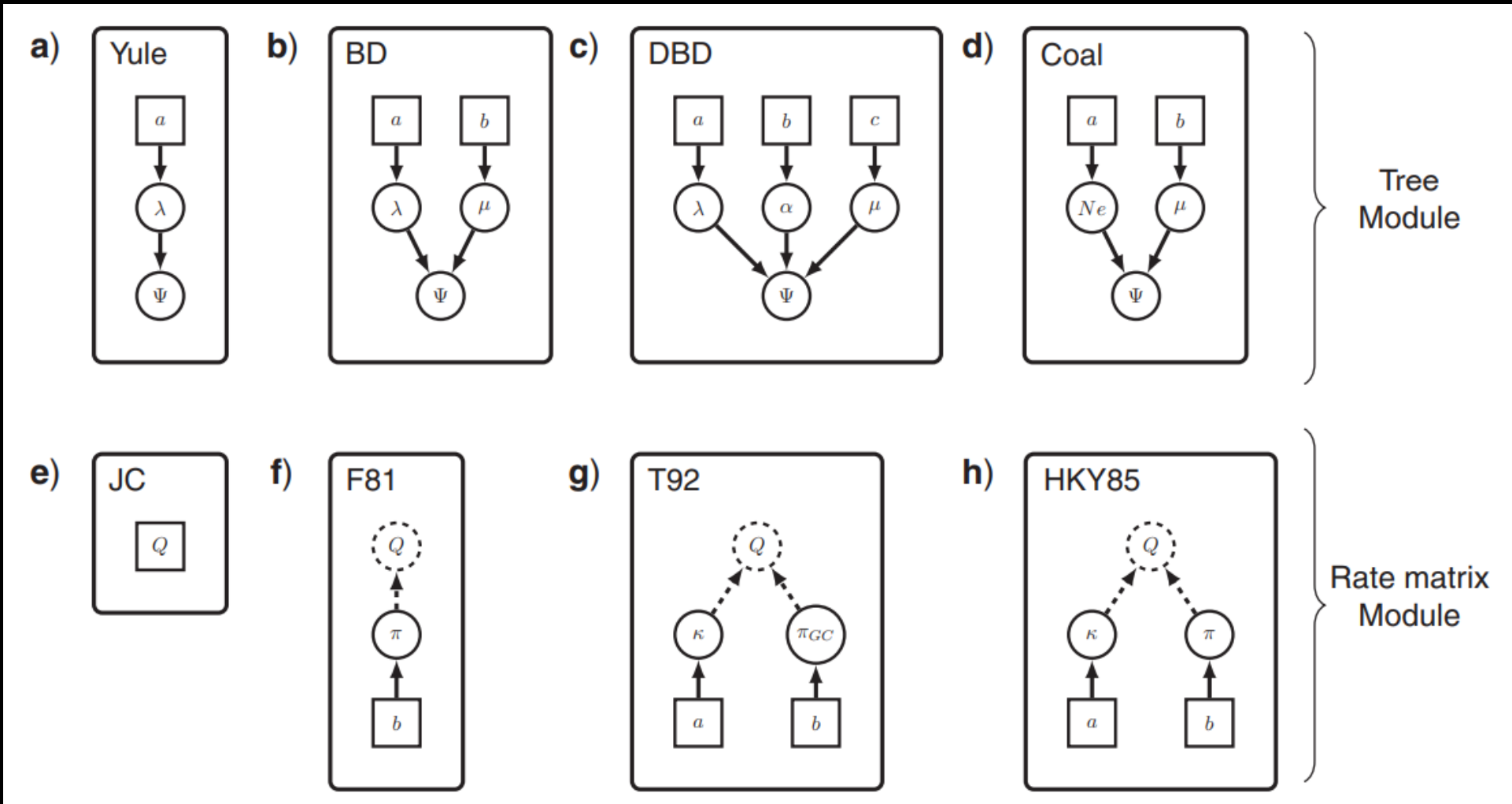
Graphical Models



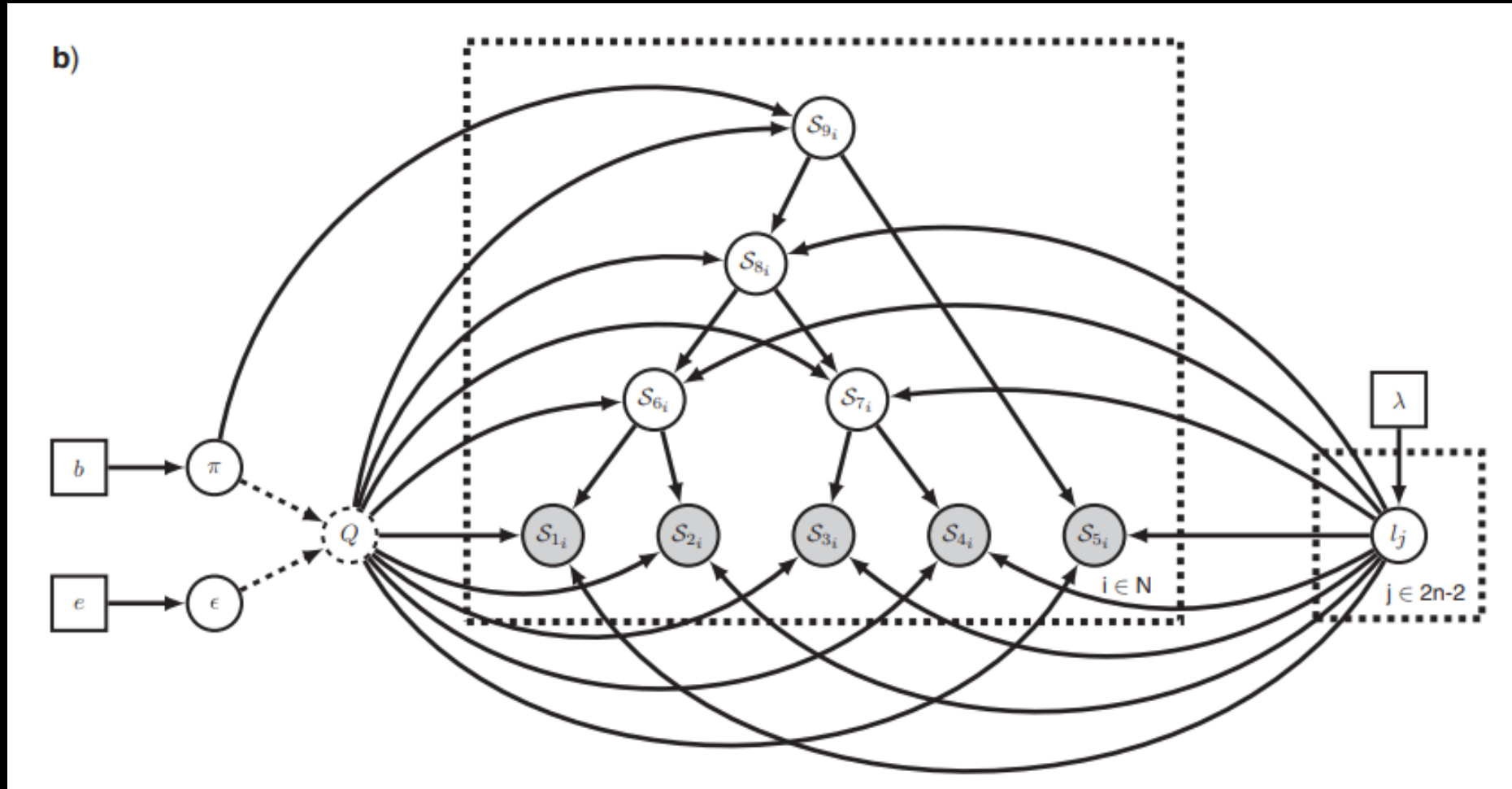
Lognormal Model/Distribution:

$$X = e^{\mu + \sigma z} \quad [\mu: \text{location parameter (log mean)}; \sigma: \text{standard deviation}]$$

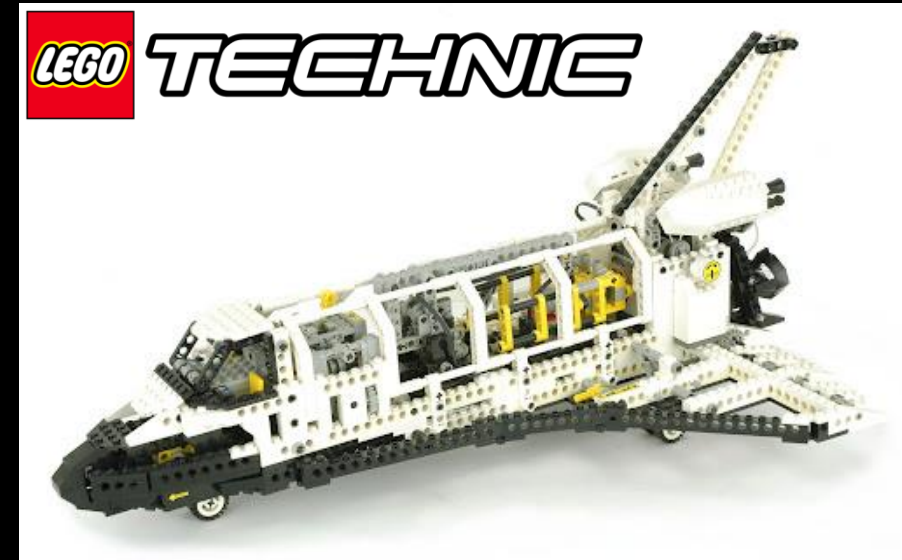
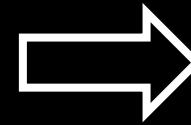
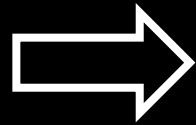
Graphical Models



Graphical Models



Syntax and more...



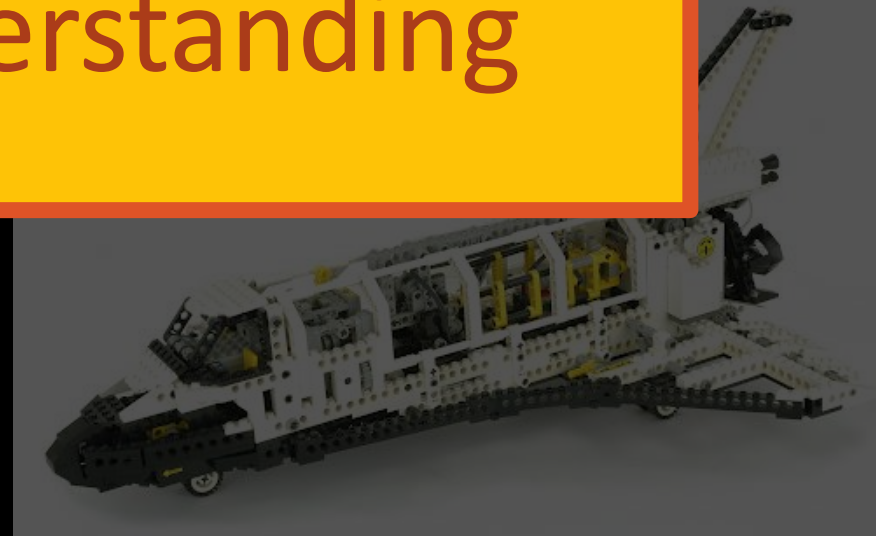
Syntax and more...

Steep learning curve

BUT

increased insight & understanding

duplo



Syntax and more...

[main code-time]