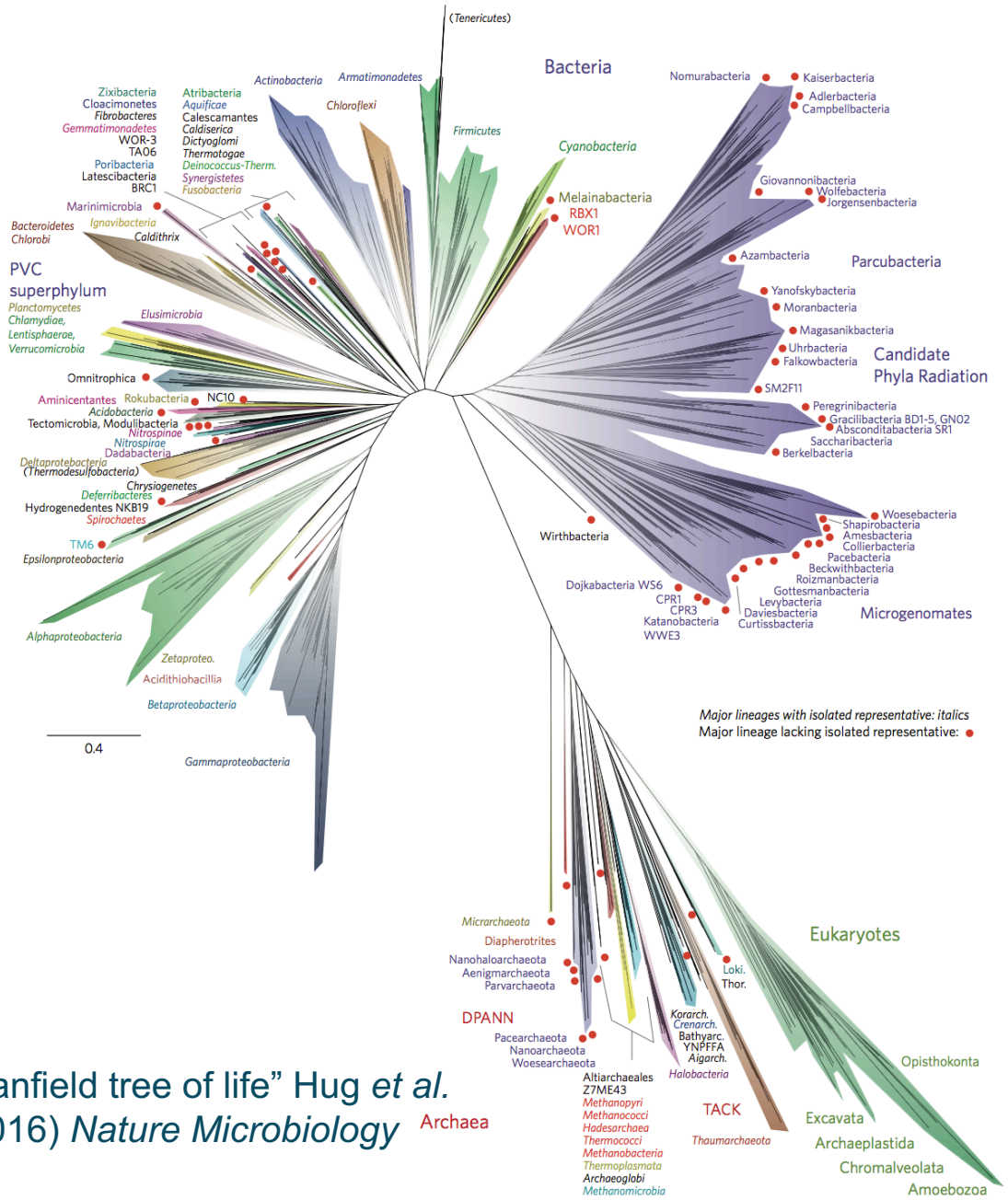
Evolution: Deeper into phylogenetics

Andrew Rominger
Omidyar Postdoctoral Fellow
Santa Fe Institute

- How to infer a phylogeny
- Why the deep past is difficult



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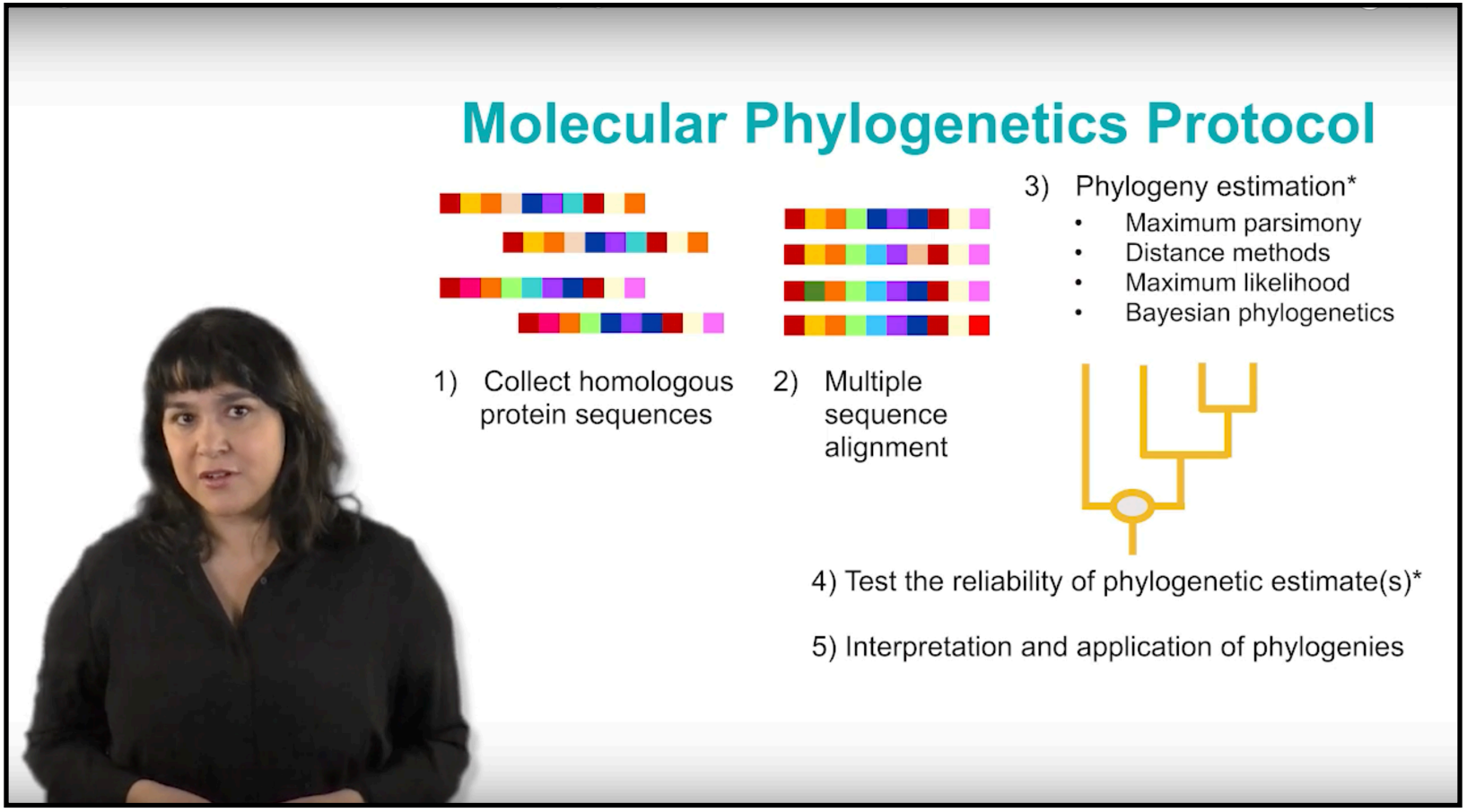
Inferring a phylogeny



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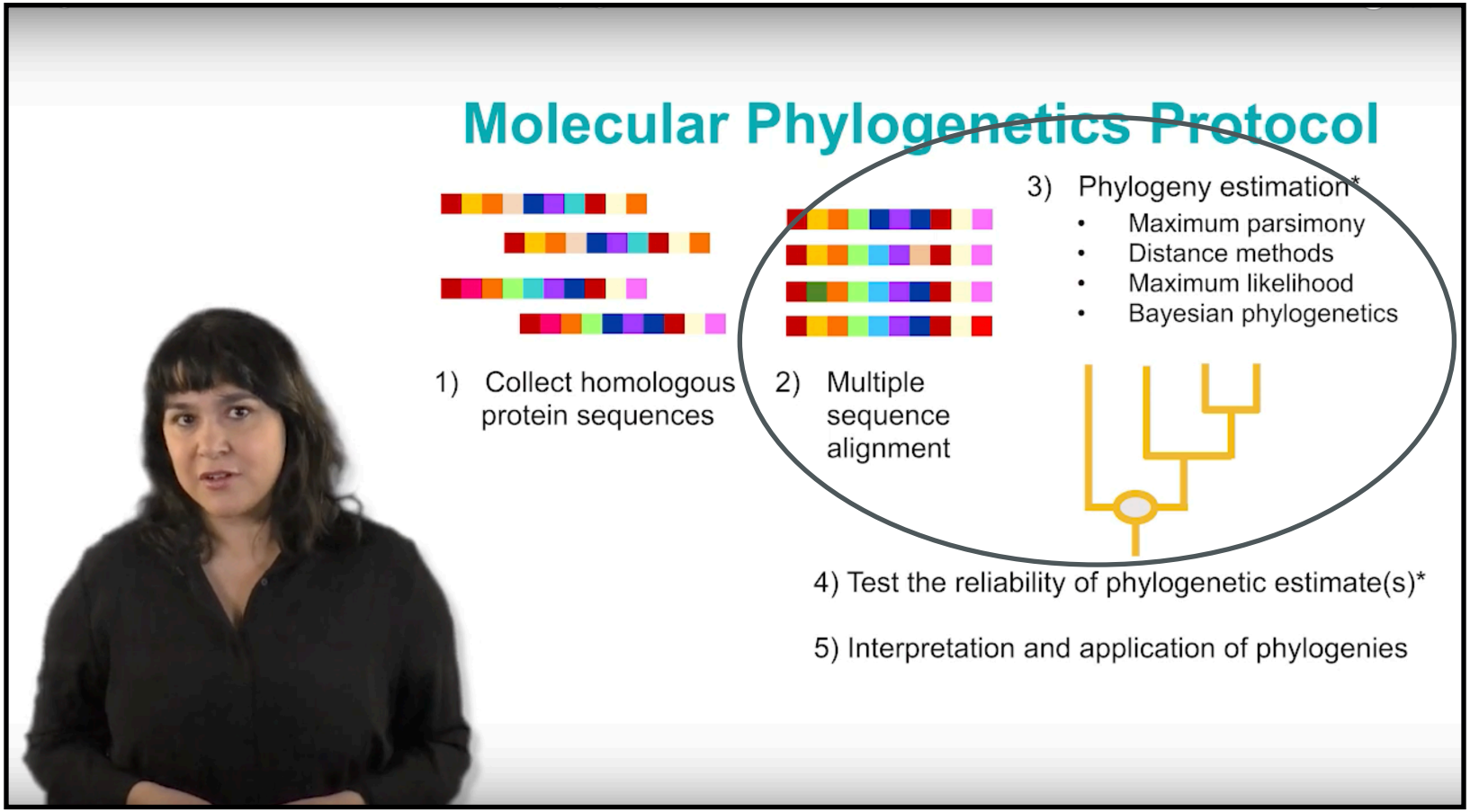
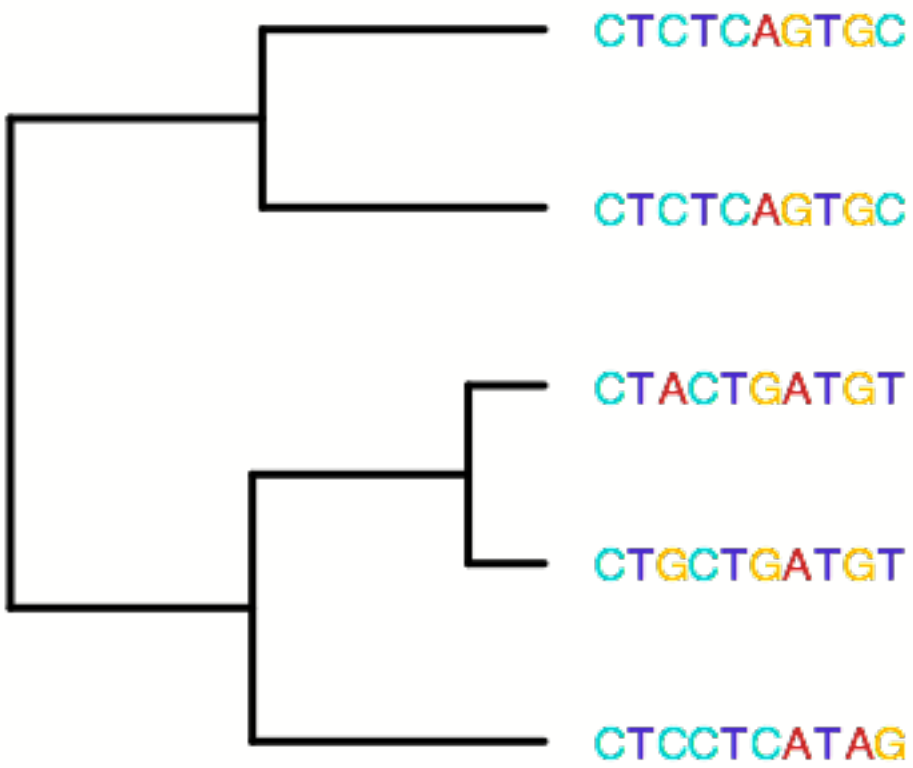


Inferring a phylogeny

Goal: find the process leading to the data



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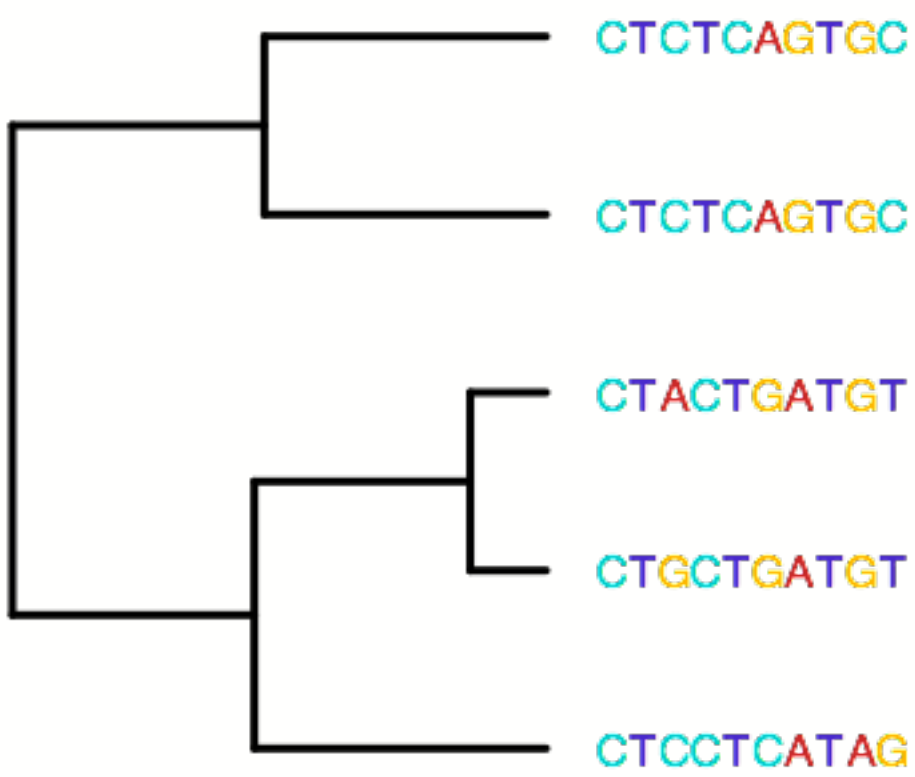

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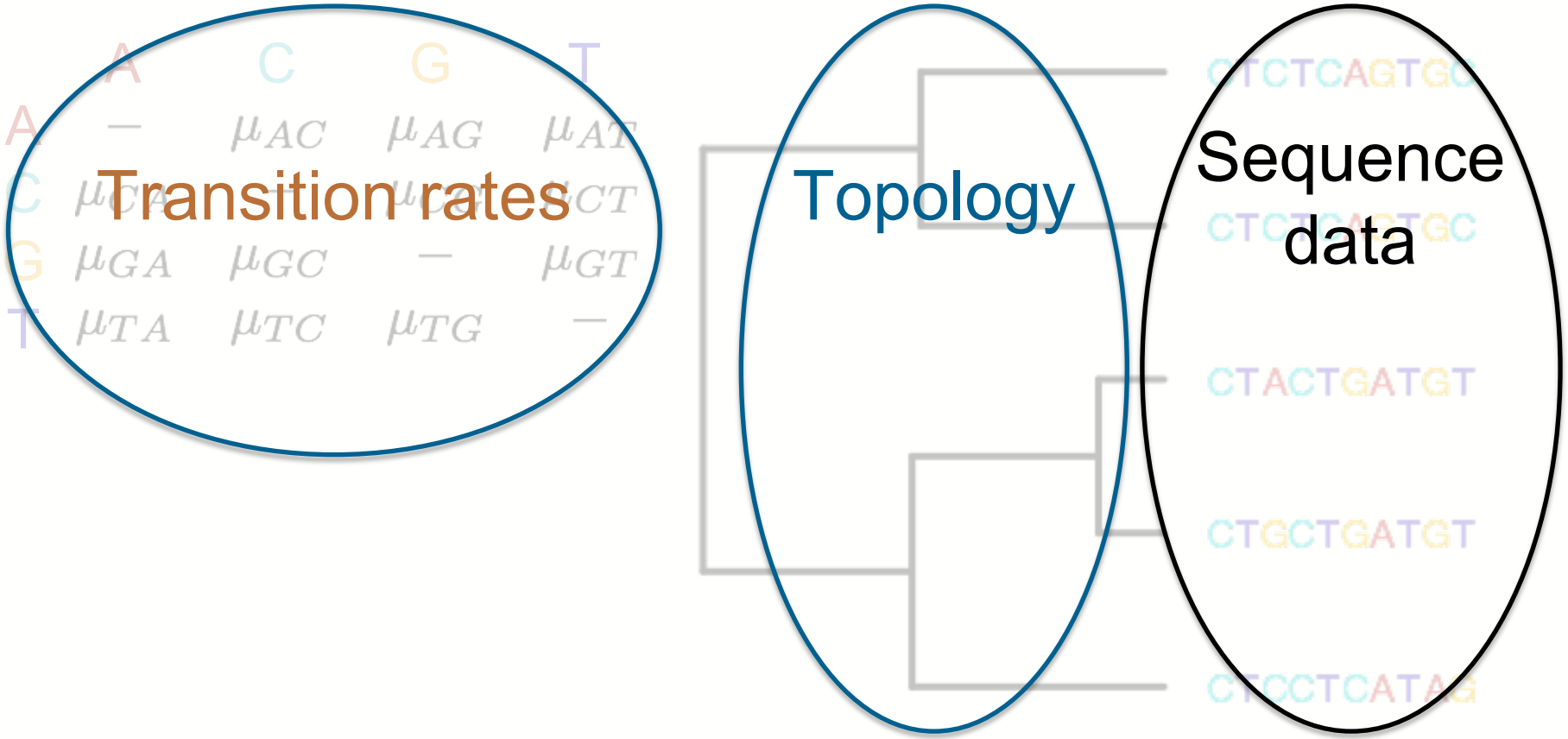

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Goal: find the process leading to the data

Likelihood:

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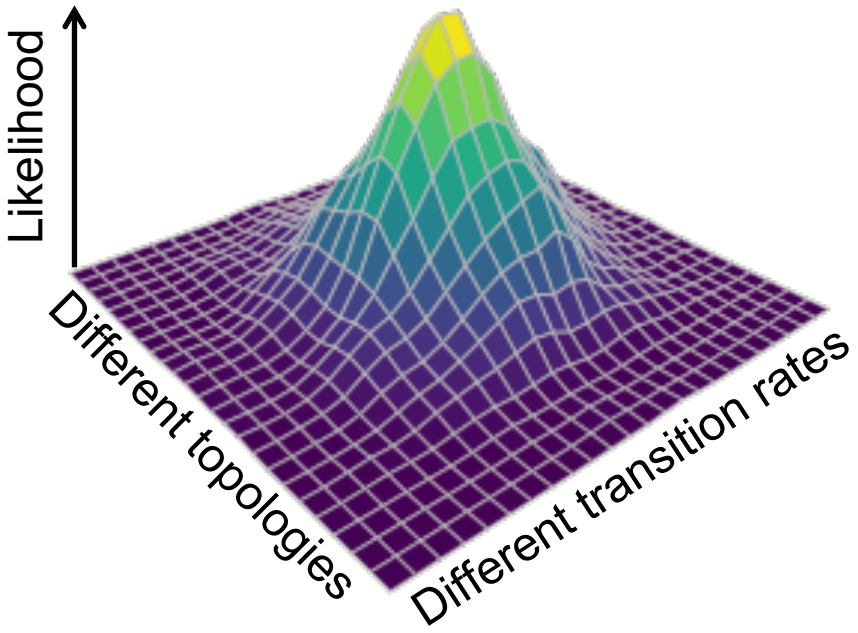

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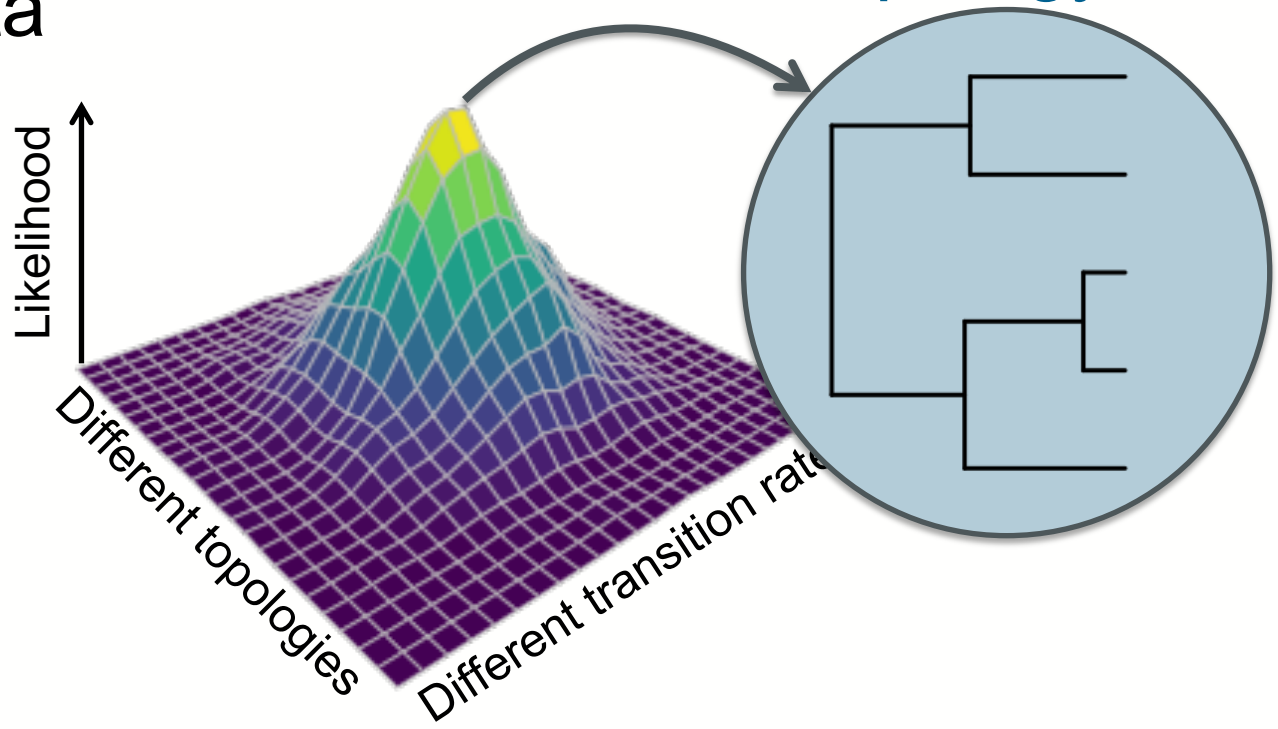
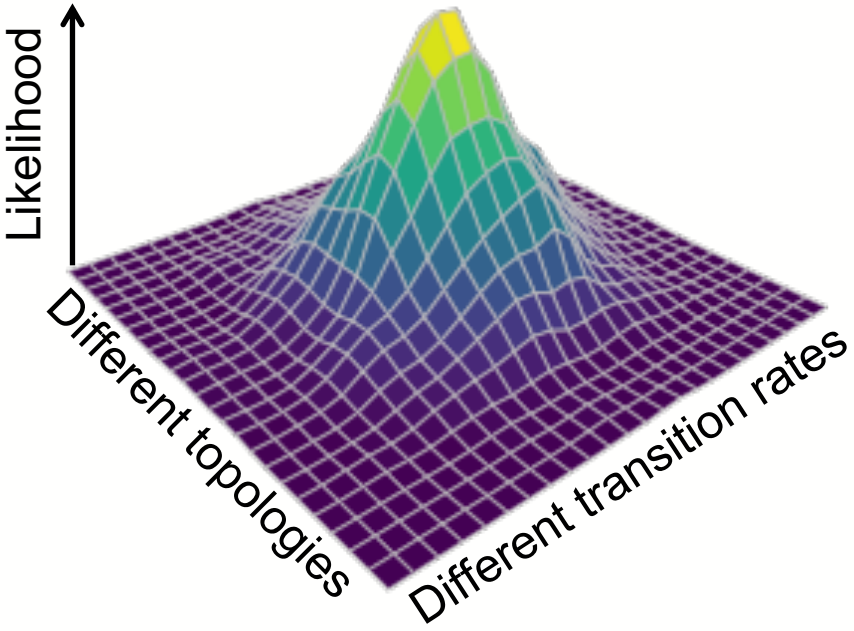


Inferring a phylogeny

Goal: find the process leading to the data

Bayesian inference: traversing the complex topology and rate matrix space lends itself to Bayesian algorithms



Inferring a phylogeny

Goal: find the process leading to the data

Information on parsimony and distance-based methods are left for the Further Reading section

Inferring a phylogeny

Caveats: inferring the past is hard

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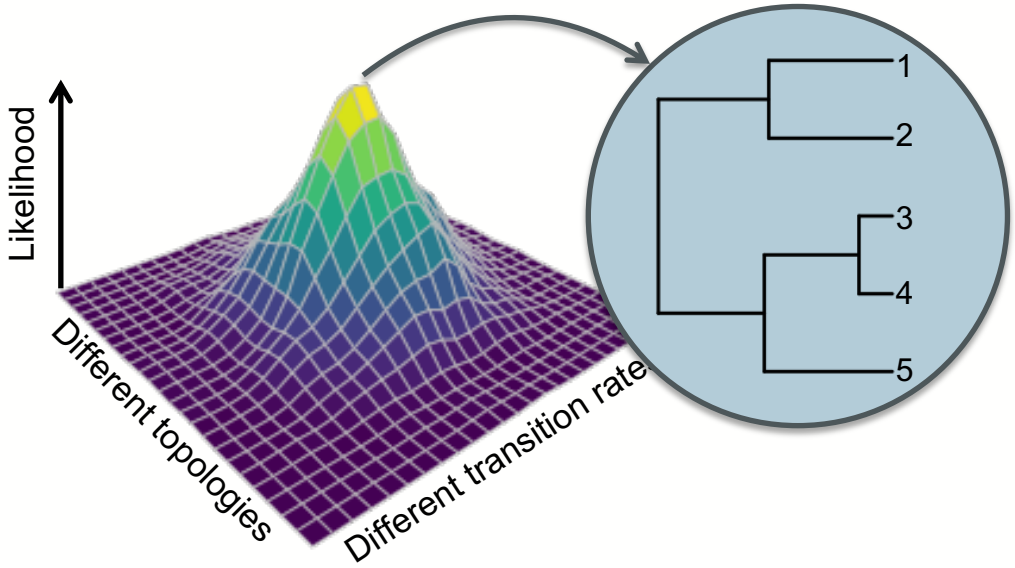

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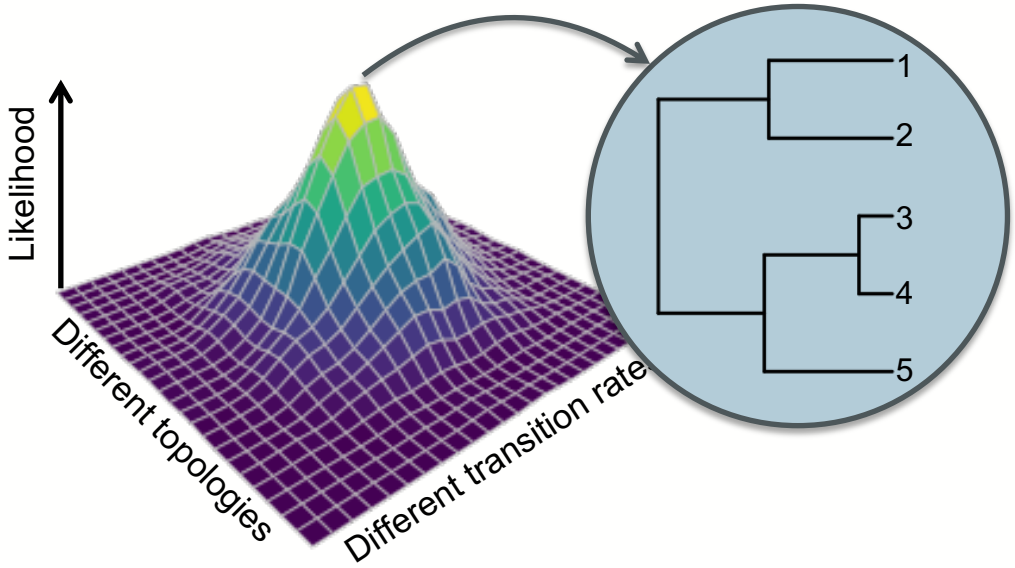
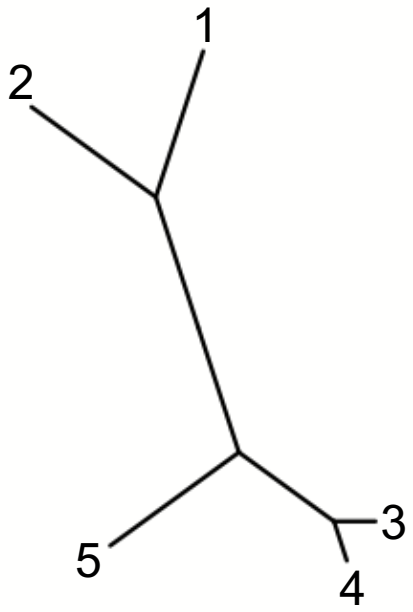


"Unrooted" phylogeny arrises because mutation process is reversible in our models



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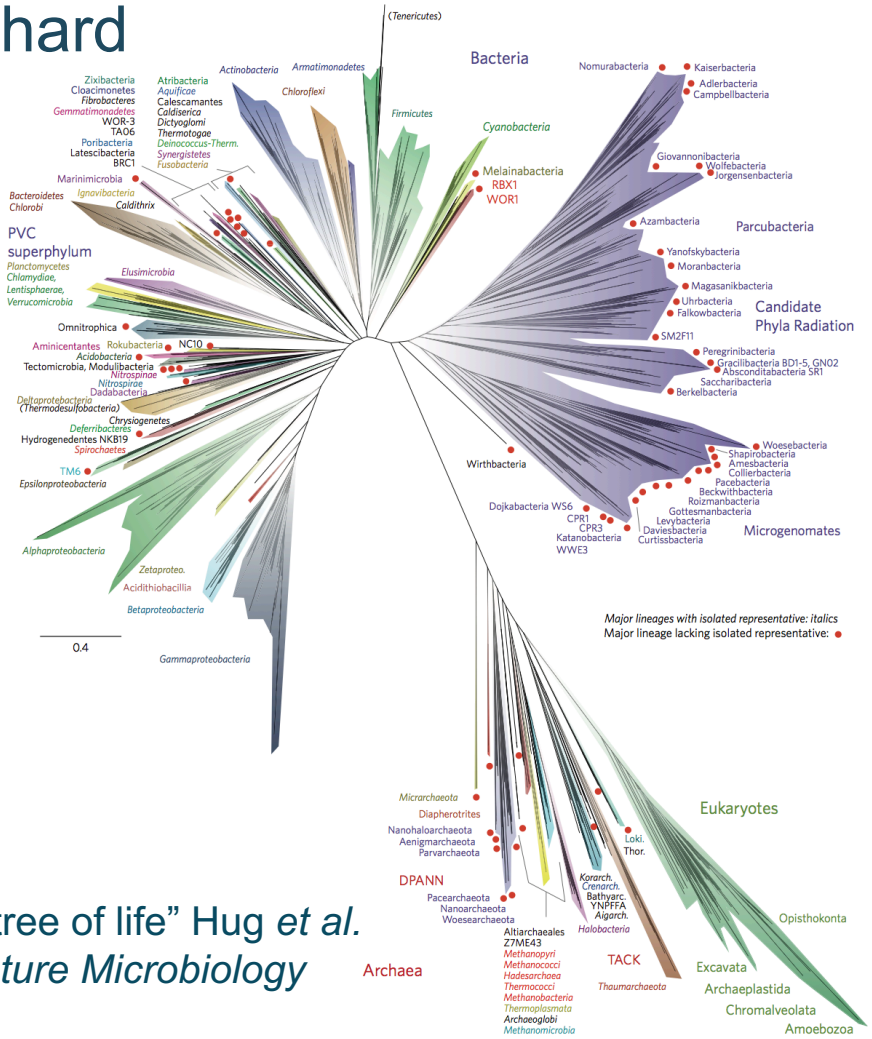

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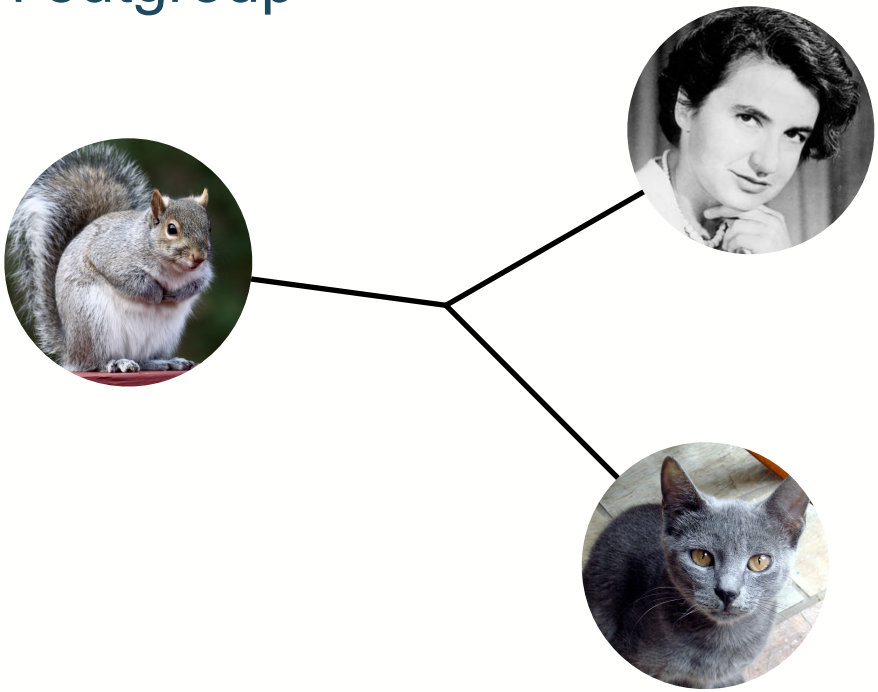

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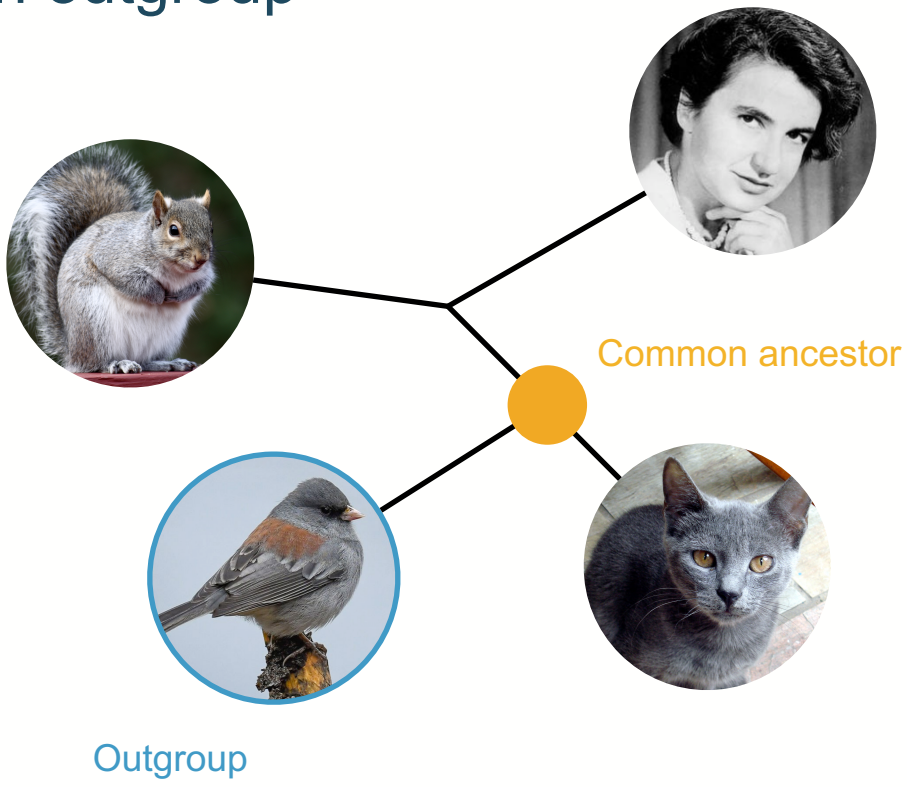

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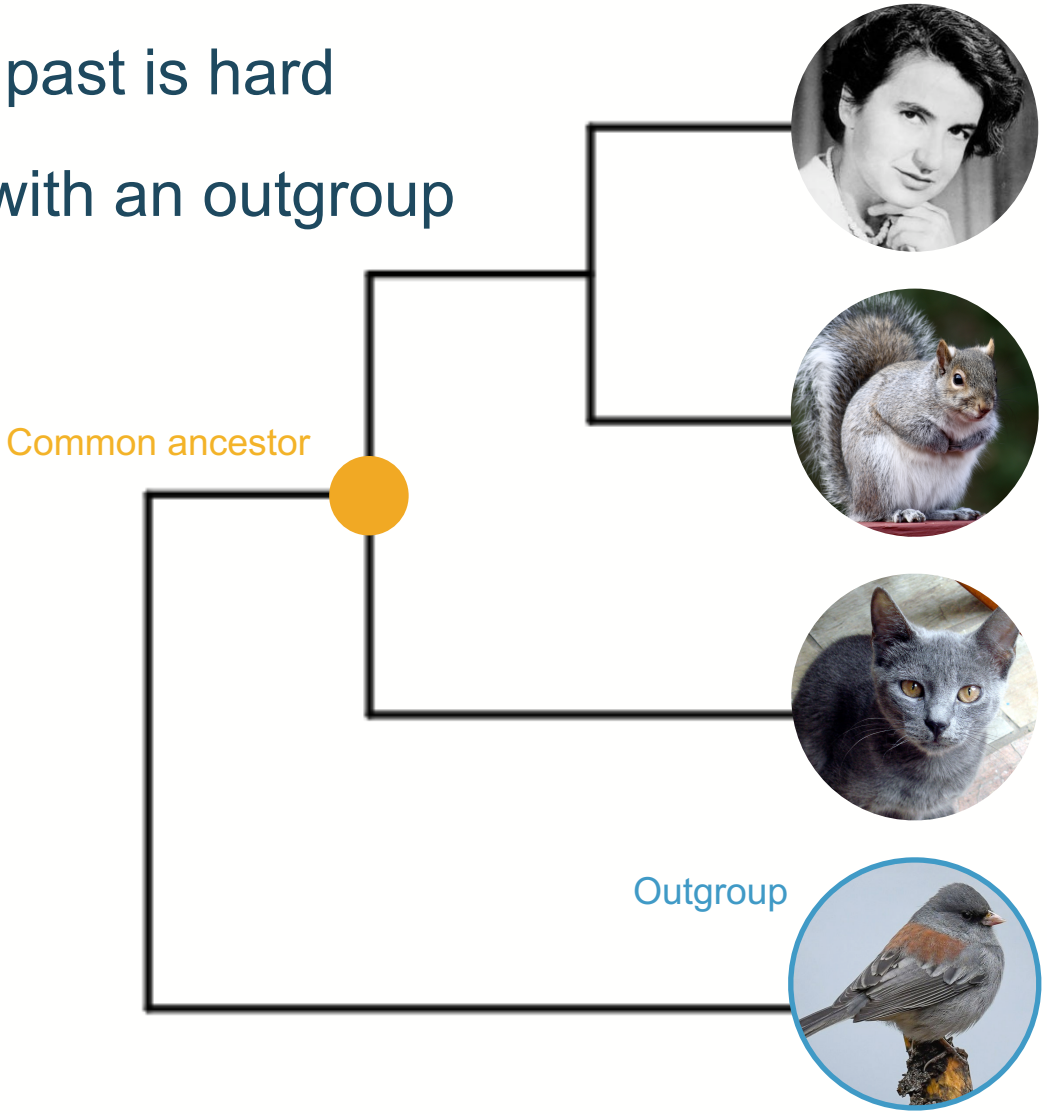

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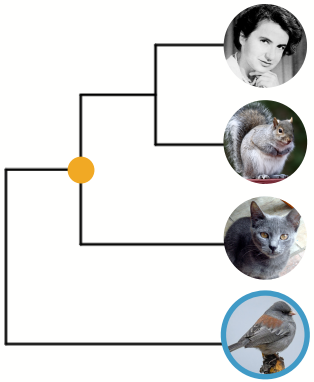
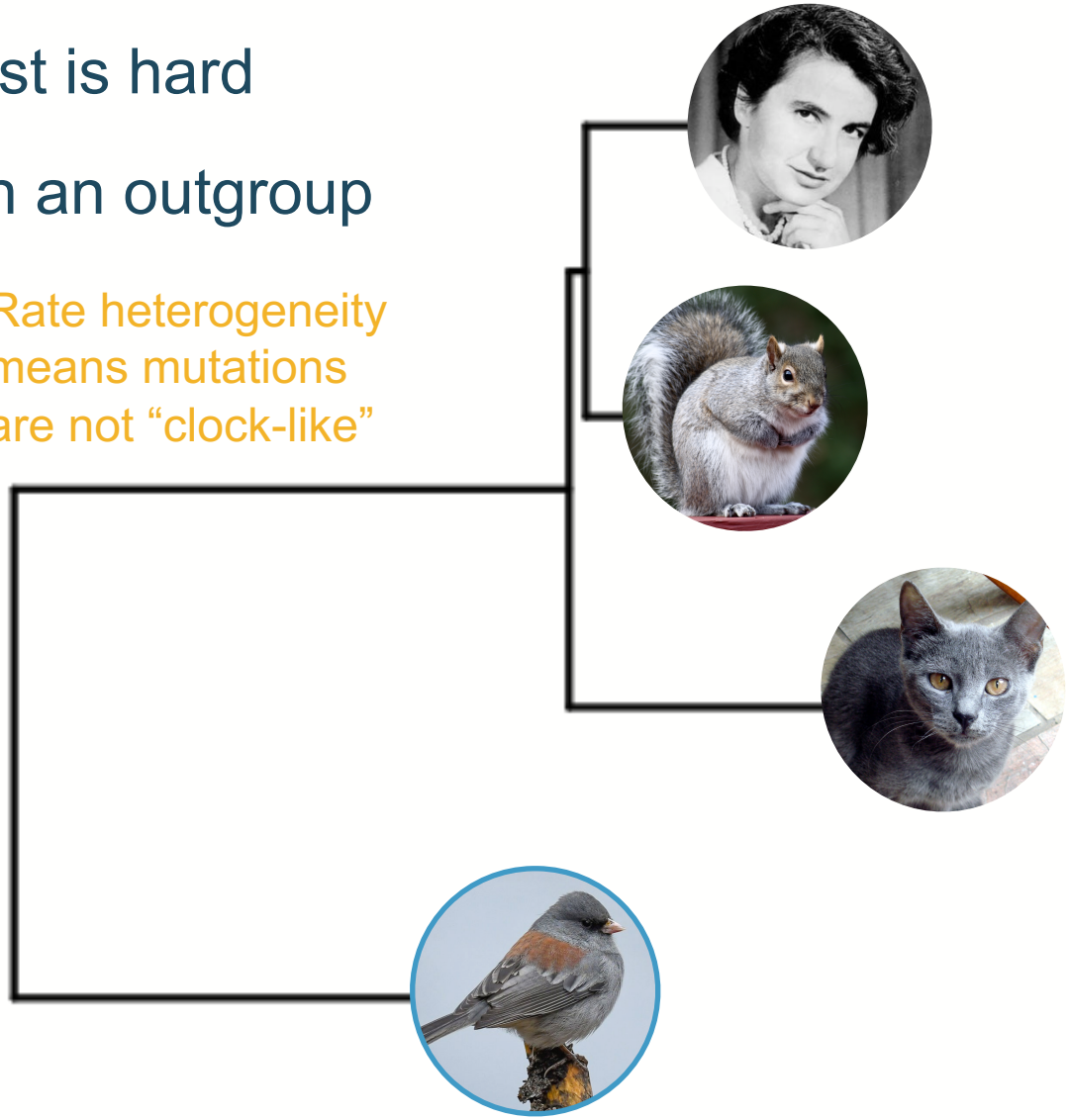


Rate heterogeneity means mutations are not “clock-like”



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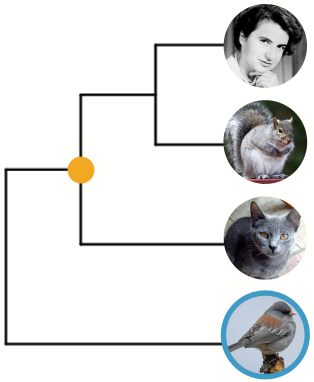

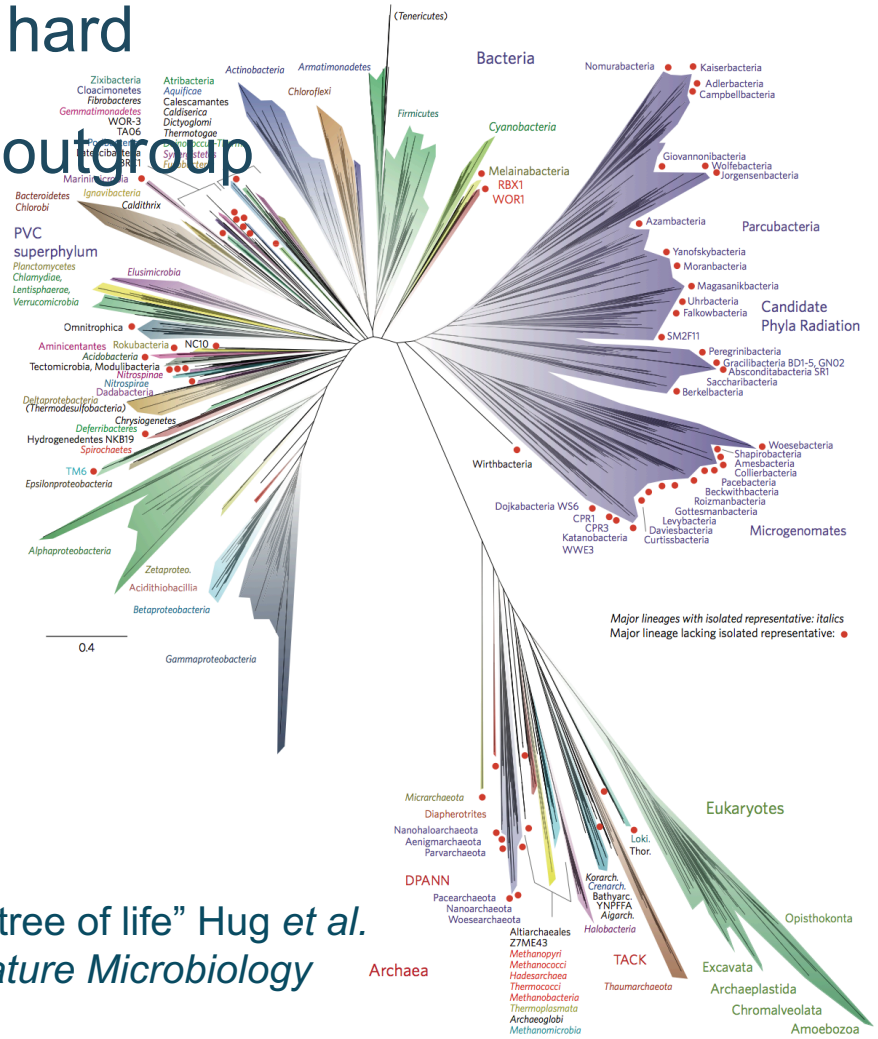

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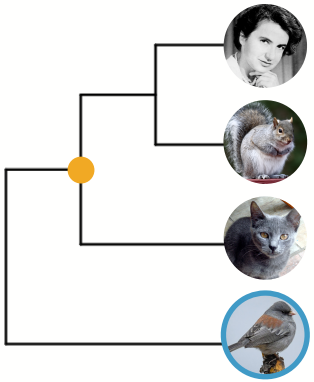

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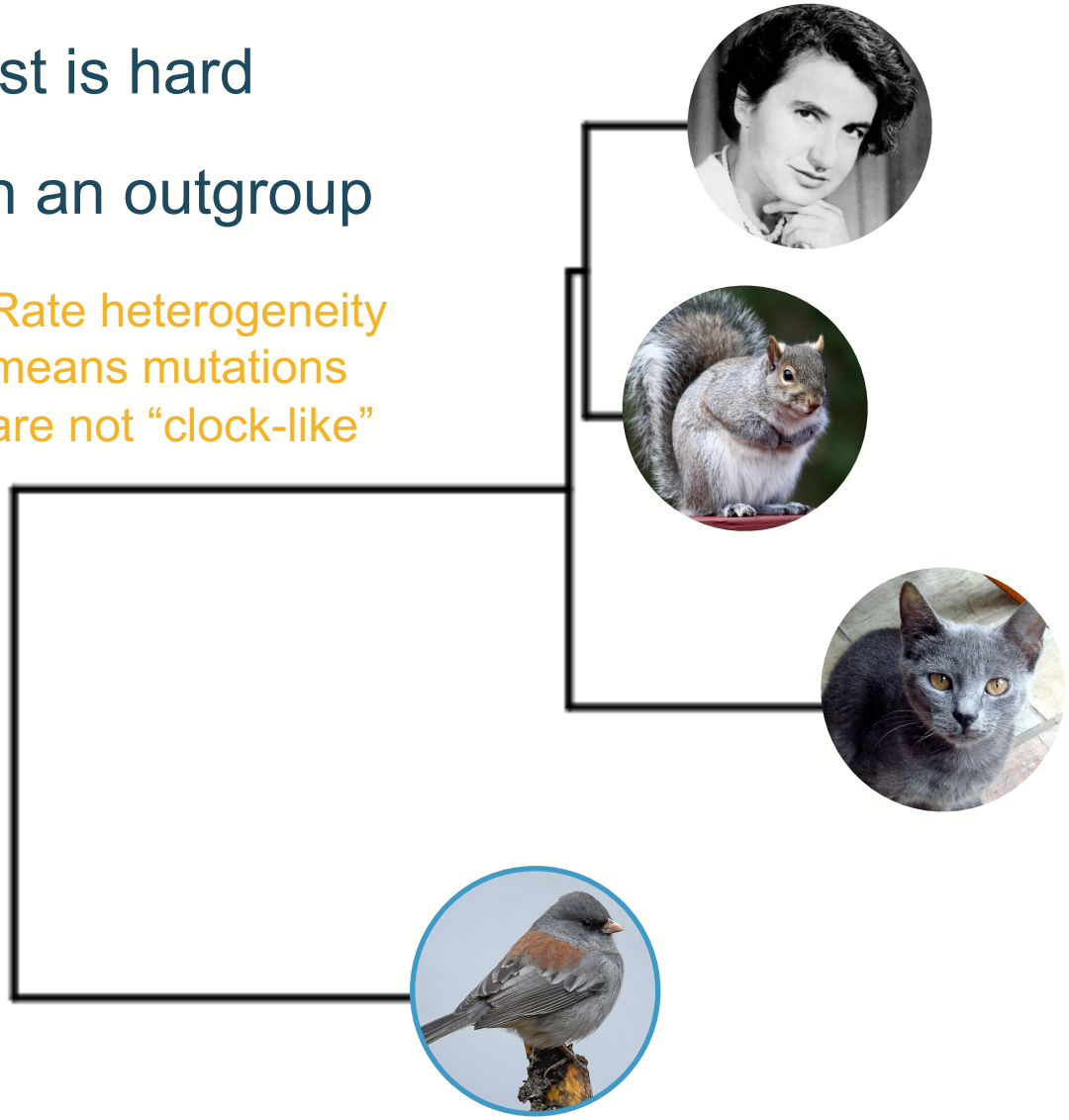

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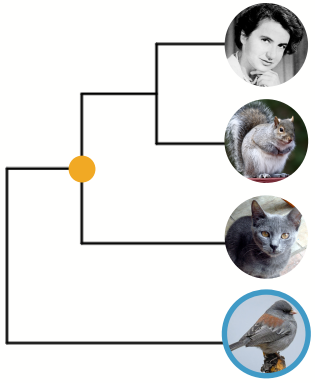

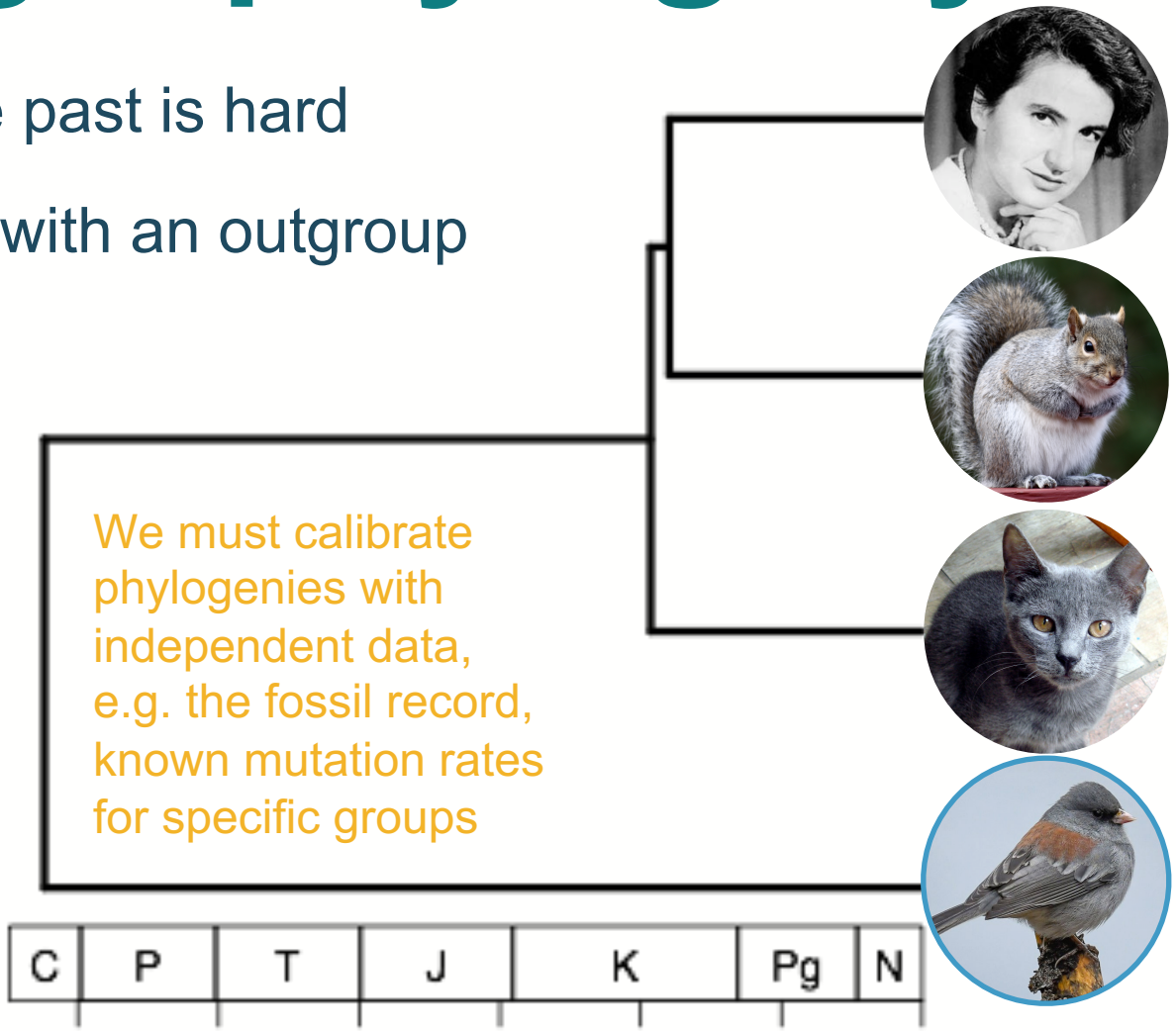

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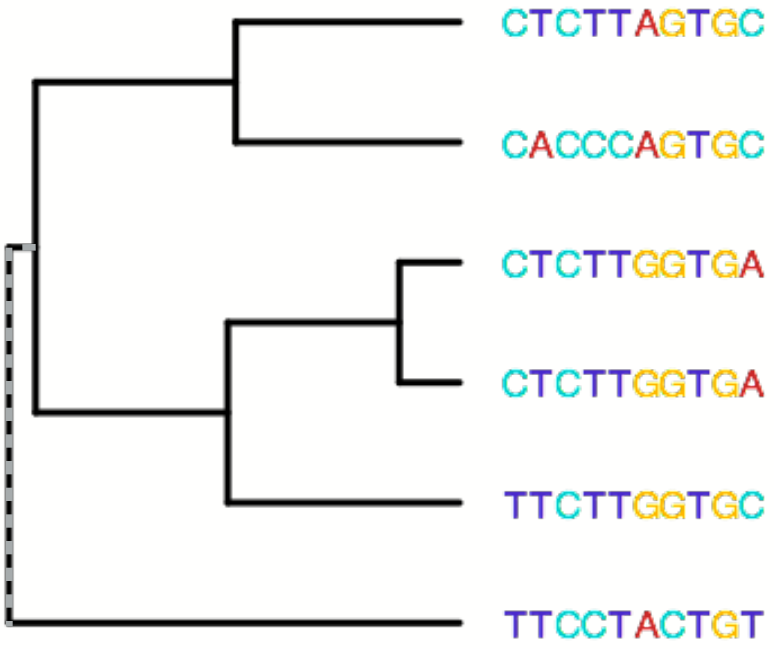
Long branches “attract” each other



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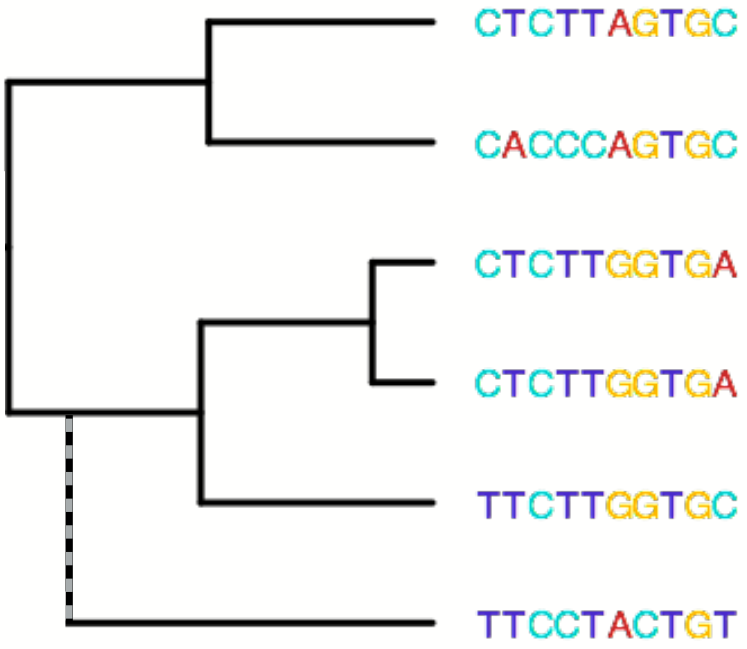

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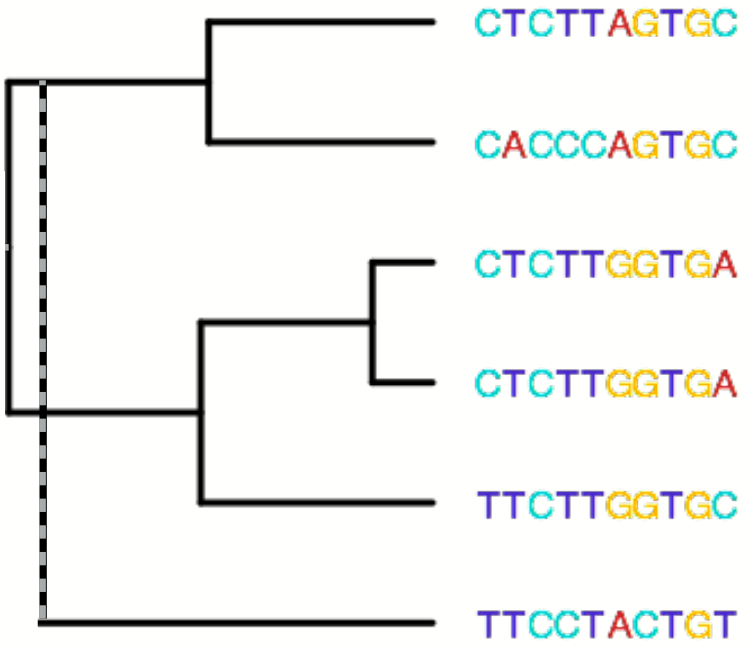

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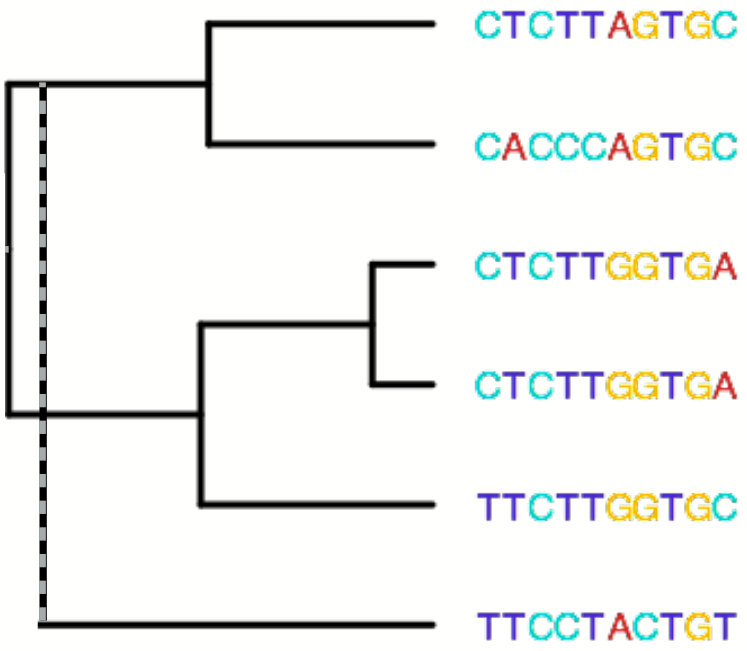

Inferring a phylogeny

Caveats: inferring the past is hard (especially in deep time)

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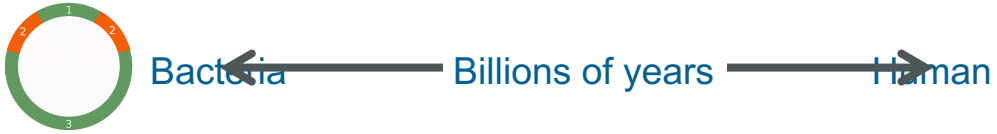
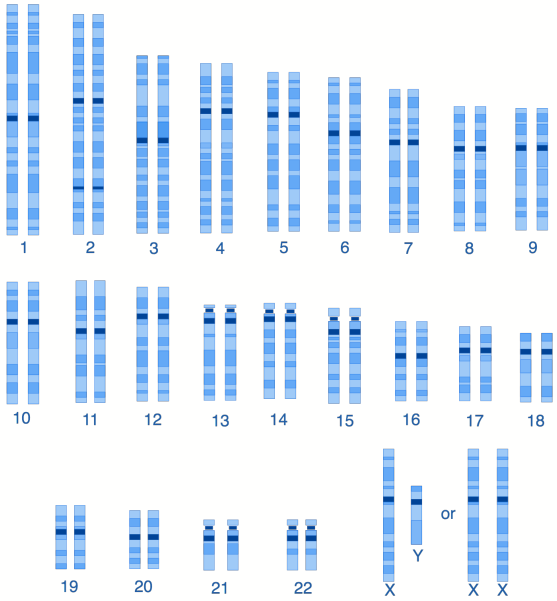
- What genetic information goes back to LUCA?





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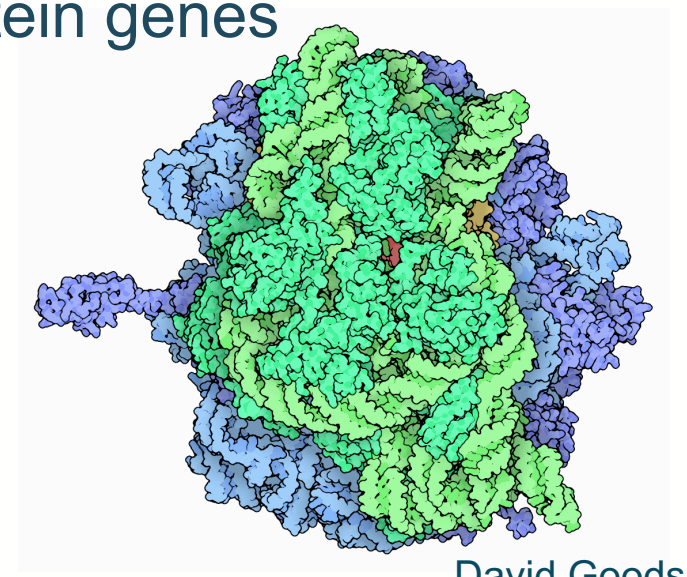
  - Ribosomal RNA and protein genes



David Goodsell

References and Suggested Reading

Huelsenbeck, J. P., & Ronquist, F. (2001). MRBAYES: Bayesian inference of phylogenetic trees. *Bioinformatics*, 17, 754-755.

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