

BioE241 labs

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Of all natural systems, living matter preserves inscribed in its organization the largest amount of its own past history no other system is better aufgehoben: constantly abolished and simultaneously preserved. [Pauling and Zuckerkandl, 1963]

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Introduction

This handout describes a series of labs for BioE241, accompanying the theoretical lectures in that class, which describe various statistical models for biological data.

The class has a (non-exclusive) emphasis on models that describe the evolution of DNA, RNA and amino acid sequences on phylogenetic trees.

The BioE241 class page is here: <http://biowiki.org/BioE241>

Most of the labs use the DART software: <http://biowiki.org/DART>

Other software tools are also used. The labs also ask you to develop some pseudocode and actual implementations (generally in a programming language of your choice) and to do a small amount of elementary math.

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[Gillespie, 1977]

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12 Use PRISM to prototype probabilistic models using statistical logic programming

13 Simulate and analyze spatiotemporal models of evolution, epidemiology, ecology, and population dynamics

14 Analyze and fit data to continuous-valued diffusion processes

References

- [Gillespie, 1977] Gillespie, D. T. (1977). Exact stochastic simulation of coupled chemical reactions. *Journal of Physical Chemistry*, 81:2340–2361.
- [Pauling and Zuckerkandl, 1963] Pauling, L. and Zuckerkandl, E. (1963). Chemical paleogenetics, molecular “restoration studies” of extinct forms of life. *Acta Chemica Scandinavica*, 17:S9–S16.