STATS 700-002 Class 7. Complex Population Dynamics and the Coalescent Under Neutrality

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Outline

Volz, E. M. (2012) Complex population dynamics and the coalescent under neutrality. Genetics **190**: 187–201. doi:10.1534/genetics.111.134627

- The first approach to phylodynamic likelihood for a compartment model with a structured population
- Supposes that the model dynamics are determined by a system of differential equations

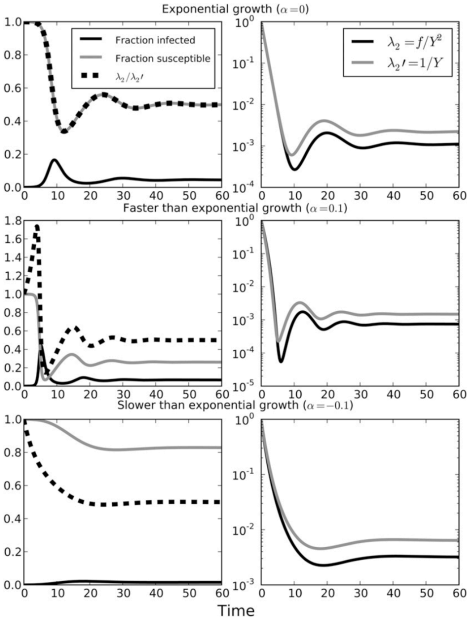


Figure 1 (Left) The fraction of the population susceptible and infected is shown over time for model (16). (Right) The rates of coalescence $\lambda_2 = f/Y^2$ and $\lambda_2' = 1/Y$. In all solutions to Equation 16, $N = 10^4$, $\beta = 2$, $\gamma = 1$, $\eta = \frac{1}{10}$. The incidence scaling factor α is varied for each row: $\alpha = 0$ (top), $\alpha = \frac{1}{10}$ (middle), and $\alpha = -\frac{1}{10}$ (bottom).

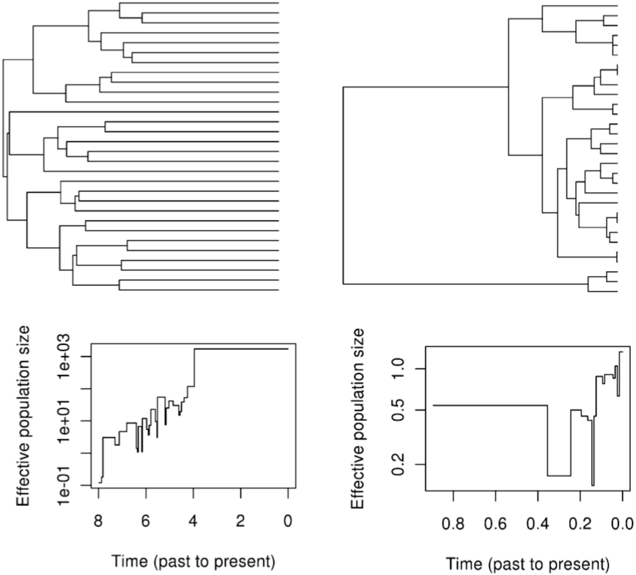


Figure 2 Simulated genealogies (top) and corresponding skyline estimates of N_e (bottom) for exponential growth (left) and FTE growth (right). Simulations were of a pure-birth process with monotonically increasing population sizes. Samples of 30 taxa were taken during a period of growth (either exponential or FTE) at the point when a population size of $Y = 2 \times 10^4$ was reached. In the exponential case, the skyline is unbiased for the harmonic mean of $Y/2\beta$ within each interval. In the FTE case, the skyline underestimates population size.

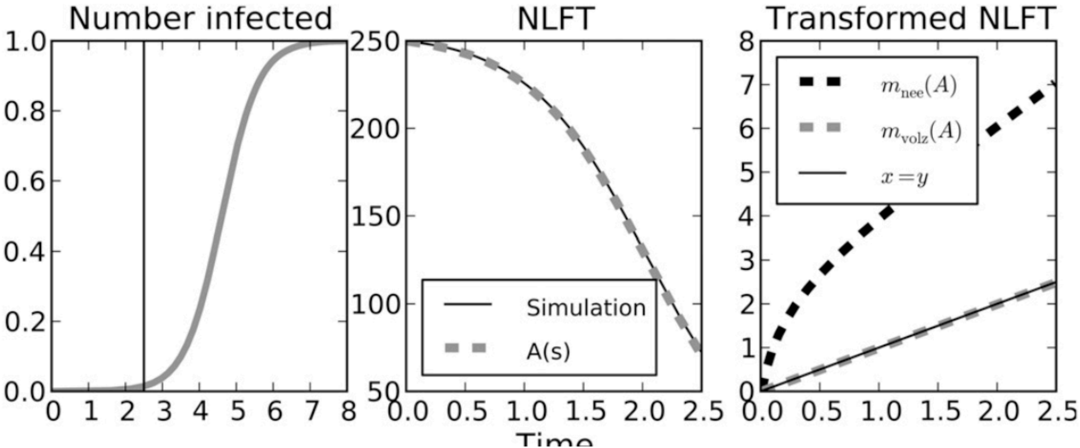


Fig 3. $n = 250$ samples at $t = 2.5$.

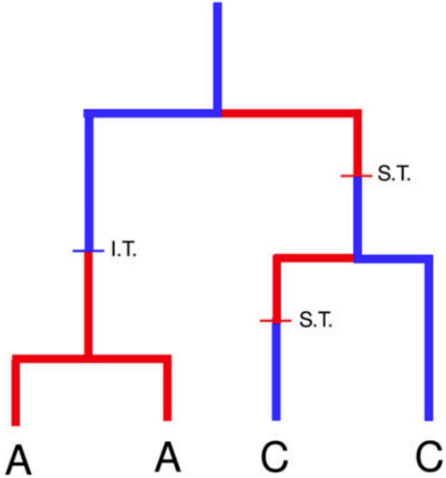
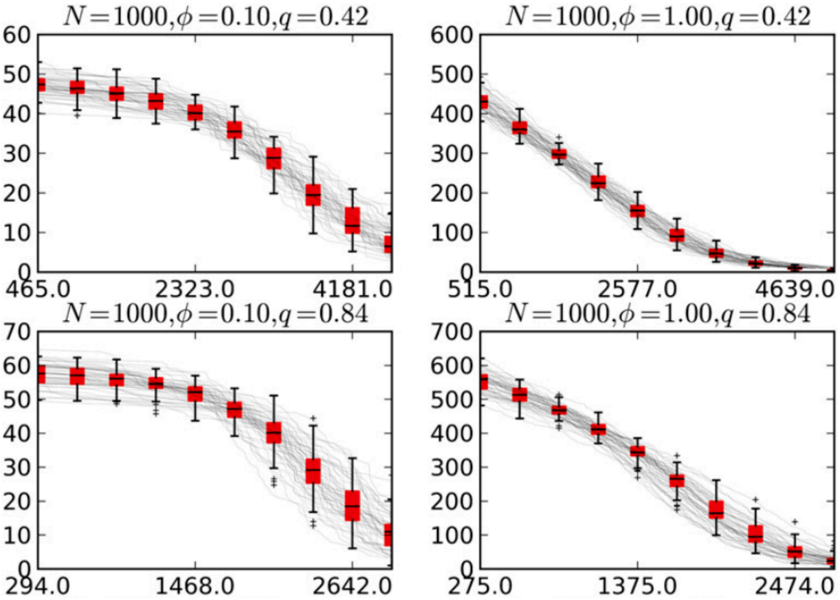
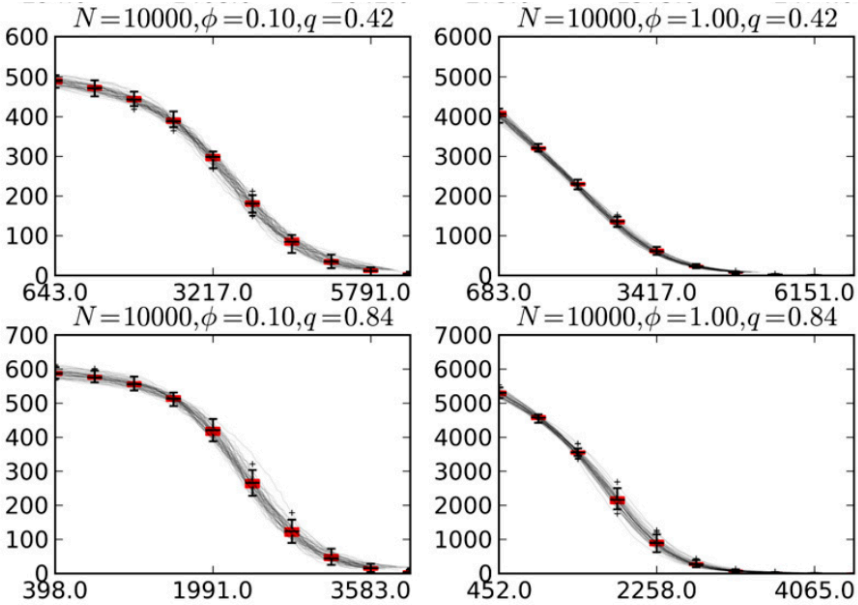


Figure 4 An example gene genealogy that could be generated by the HIV model (Equation 29). Red branches correspond to stage-1 infected hosts. Blue branches correspond to stage 2.



N=1000,ϕ=0.10,q=0.42
N=1000,ϕ=1.00,q=0.42
N=1000,ϕ=0.10,q=0.84
N=1000,ϕ=1.00,q=0.84

NLFT (Fig 5)



$N=10000, \phi=0.10, q=0.42$
600
500
400
300
200
100
0
643.0
3217.0
5791.0
$N=10000, \phi=1.00, q=0.42$
6000
5000
4000
3000
2000
1000
0
683.0
3417.0
6151.0
$N=10000, \phi=0.10, q=0.84$
700
600
500
400
300
200
100
0
398.0
1991.0
3583.0
$N=10000, \phi=1.00, q=0.84$
7000
6000
5000
4000
3000
2000
1000
0
452.0
2258.0
4065.0

NLFT (Fig 5)

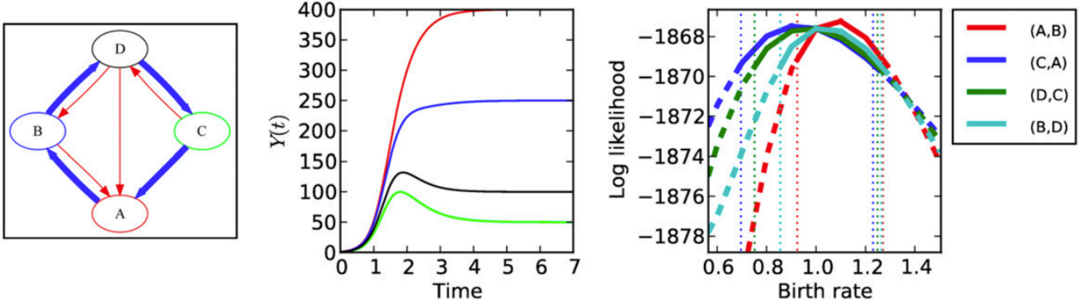


Fig 6. (Left) Model with m = 5 states, four birth terms, and seven migration terms. Blue arrows are logistic birth terms. Red arrows are migration. (Center) The population size Y_k over time for each of 5 states. (Right) Likelihood profile of four (relative) birth rates and 95% CIs.

Branching process approximations

- Why does Volz describe his method as a branching process approximation?
- How is the branching process approximation related to the assumption of a large population with a low sampling fraction?
- How would you assess the inaccuracy incurred by the branching process approximation in a particular application?

Deterministic population dynamics

- What are the benefits and weaknesses for data analysis of making an assumption of deterministic population dynamics?
  - This is a question about the population model, not its relationship to phylodynamic data.
- Is a branching process approximation to the phylodynamic model more suitable in a deterministic or stochastic population model, or are those decisions separate?

The Riccati equation

- How do you solve Eq. (20)?
- Is the proposed solution in Eq. (22) correct?