# How does phylodynamics relate to transmission dynamics?

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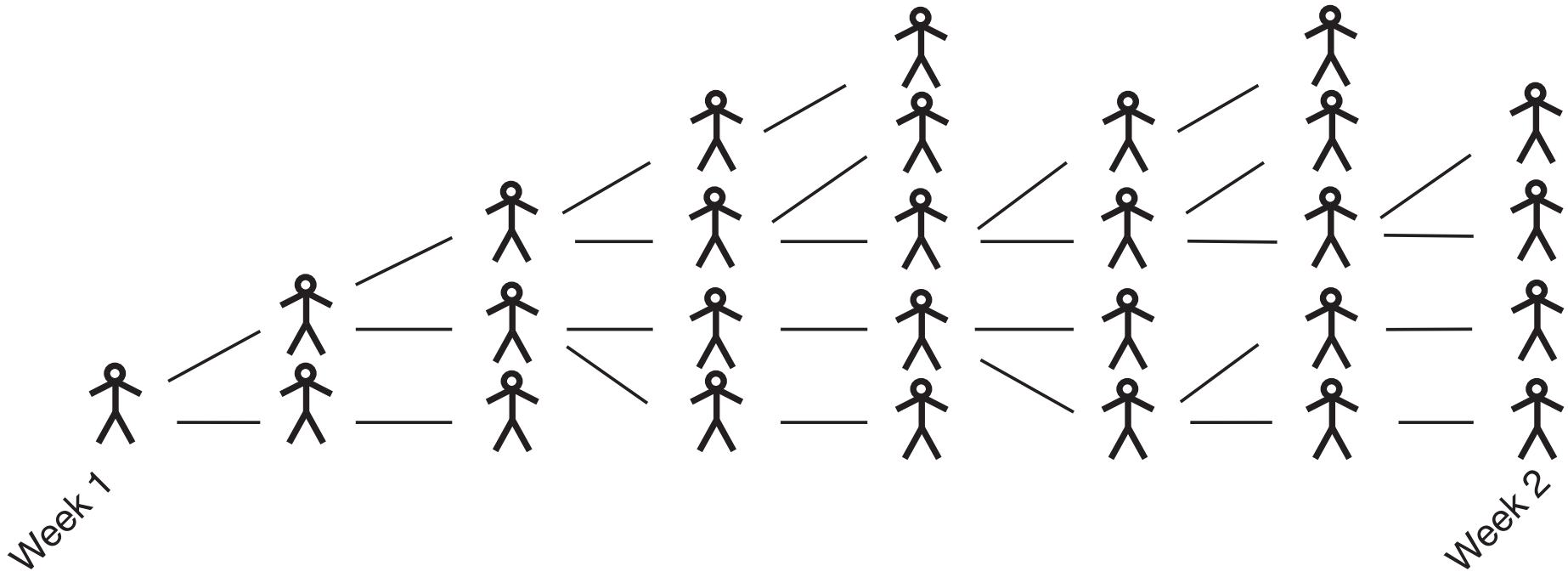
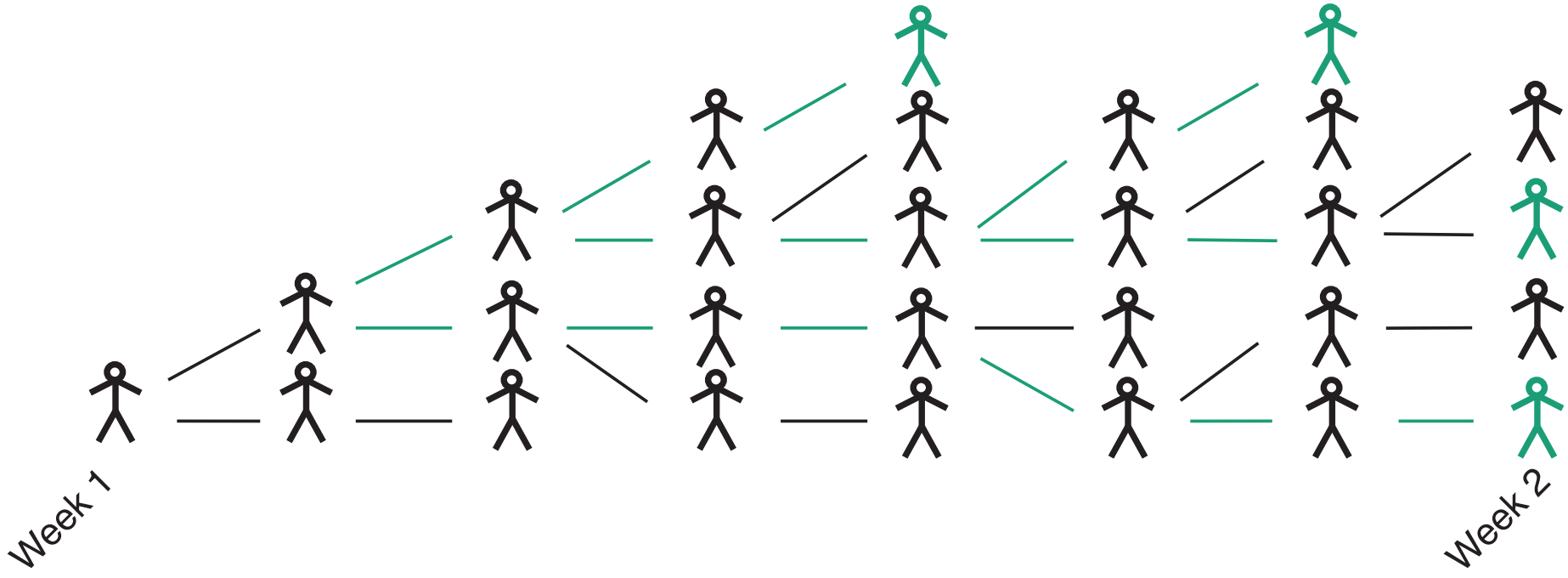
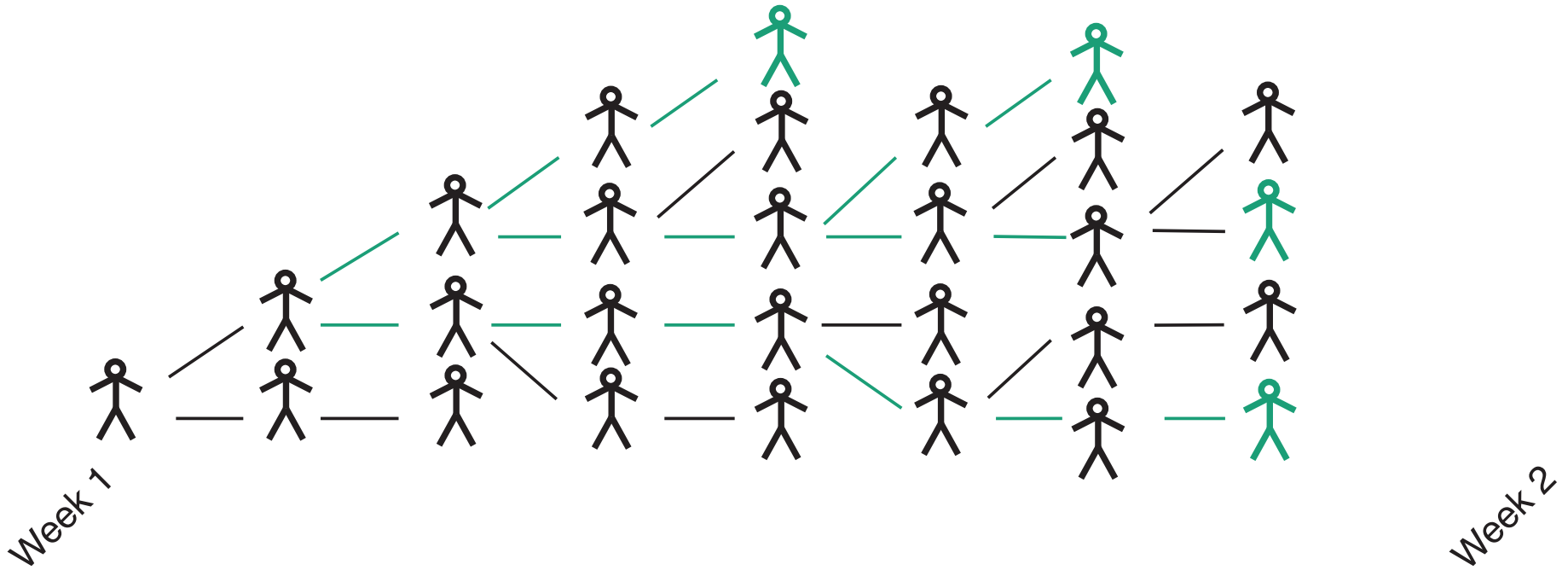
# Genomics allows tracking the shared ancestry.



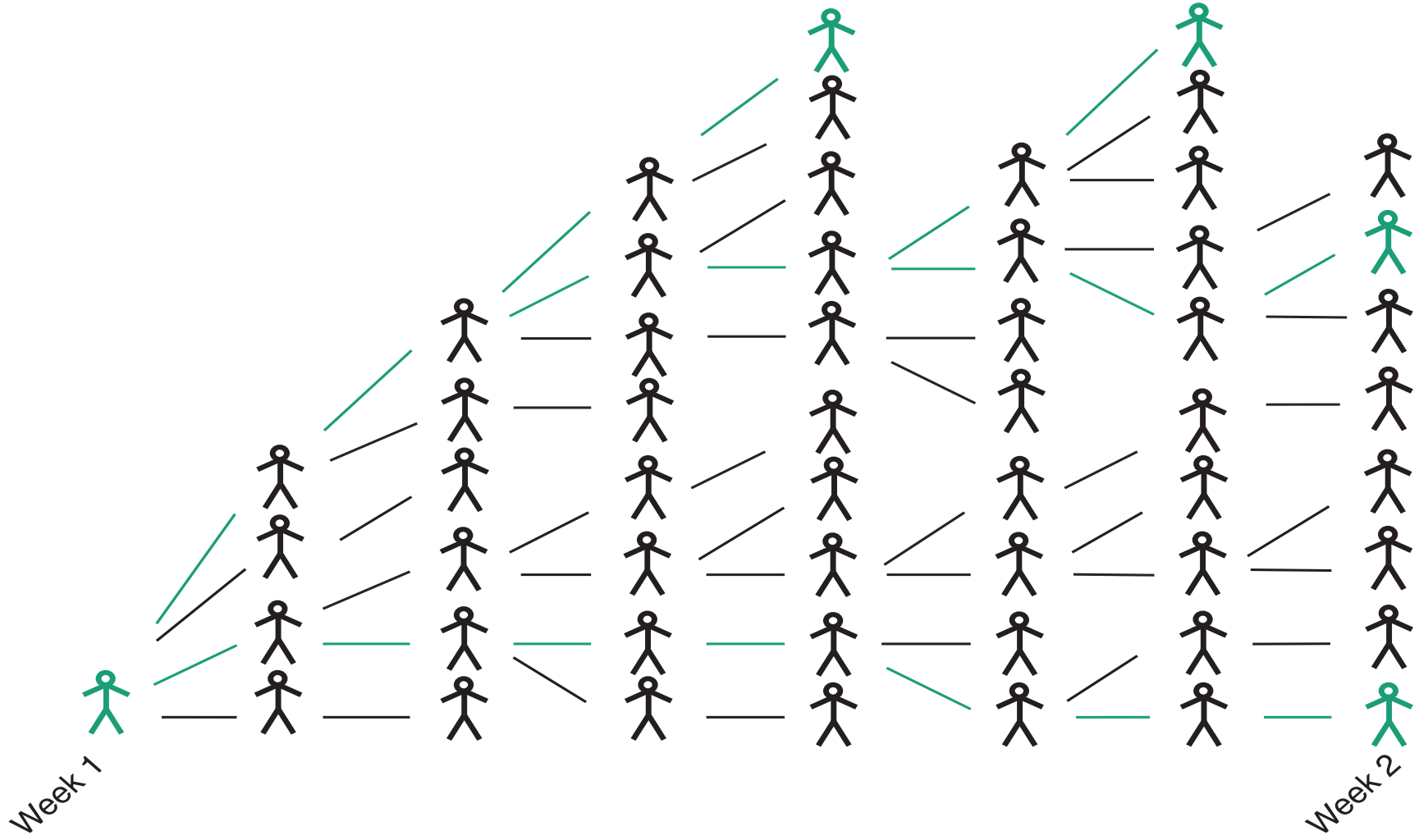
If we track the shared ancestry of the 4 sampled individuals, we will reach a common ancestor more quickly, the smaller the Ne.



# What happens if we have the same number of infected individuals, but higher turnover?



# What happens if we have a higher number of infected individuals and higher turnover?

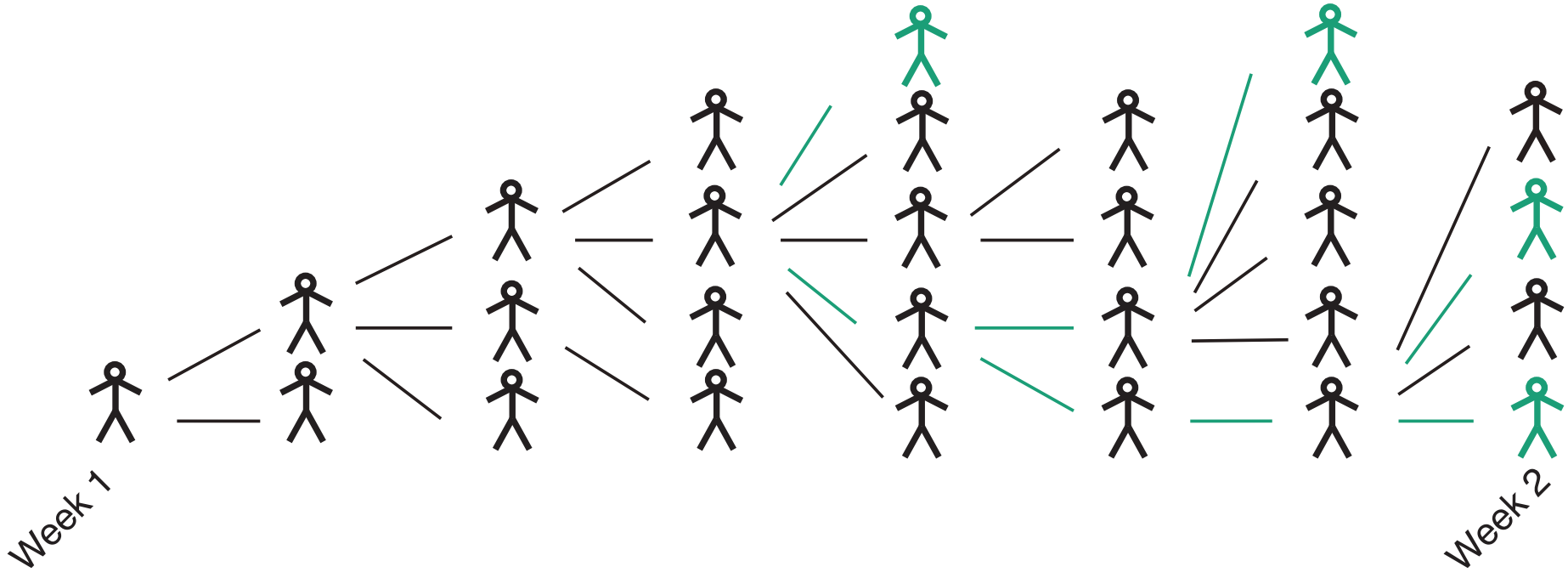


# The effective population size (Ne) can be denoted as a function of epi-parameters for SIR models

$$Ne(t) = \frac{I(t)}{\theta \frac{S(t)}{N}}$$

Volz, E. M. (2012). "*Complex Population Dynamics and the Coalescent Under Neutrality. Genetics*," 190(1), 187-201. https://doi.org/10.1534/genetics.111.134627

# What happens if we have a skewed offspring distribution?

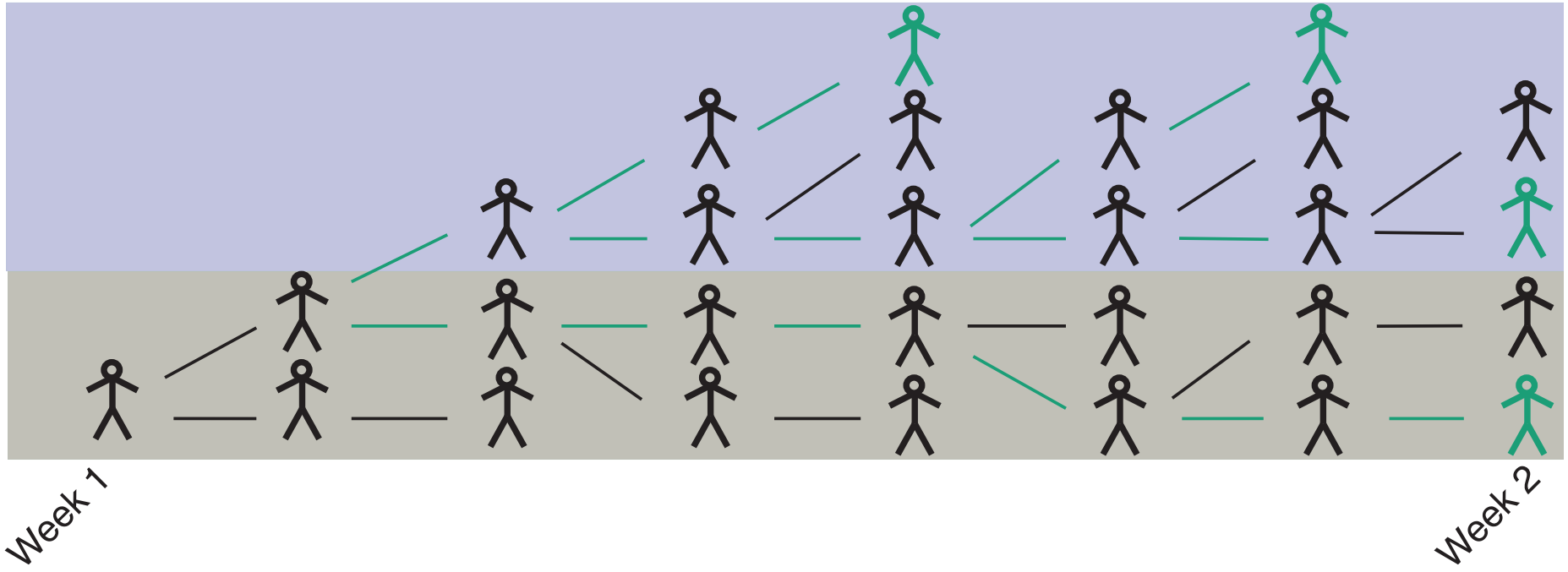


# We can also account for some offspring distributions in the Ne

$$N_e(t) = \frac{I(t)}{\theta\left(1+\frac{1}{k}\right)}$$

Li, L. M., Grassly, N. C., & Fraser, C. (2017). *"Quantifying Transmission Heterogeneity Using Both Pathogen Phylogenies and Incidence Time Series."* Molecular Biology and Evolution, 34(11), 2982-2995. https://doi.org/10.1093/molbev/msx195

# What happens if there is population structure?



Once there is population structure, the meaning of the effective population size is not obvious

$$N_e(t) = ?$$