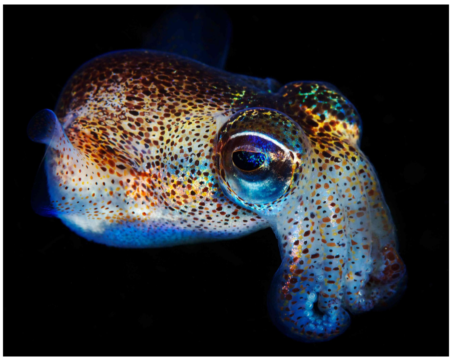
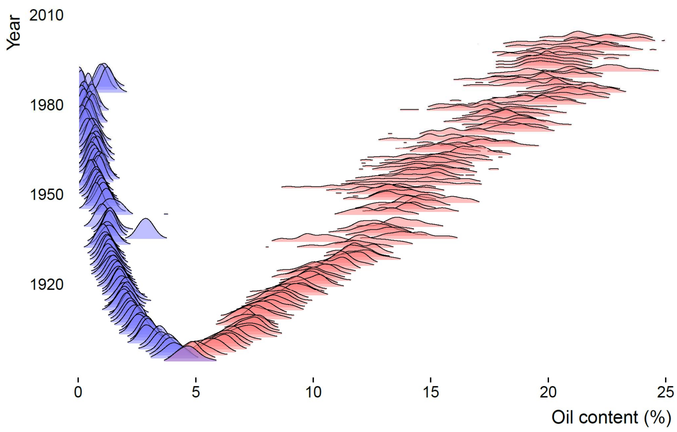
Quantitative principles in biological systems

10. Evolution and evolutionary dynamics

Spring 2025

Surprises again





CGTN
Coop

Some numbers

E. coli genome L ~ 10^6 bp
Mutation rate μ ~ 10^{-9} mutations / bp / gen
→ $L\mu$ ~ 10^{-3} mutations / genome / gen

Population size N ~ 10^9 cells in an overnight culture
→ $N\mu$ ~ 1 mutation produced at each site overnight

… but double mutants are rare $\mathrm{N} \times \mu \times \mu \ll 1$

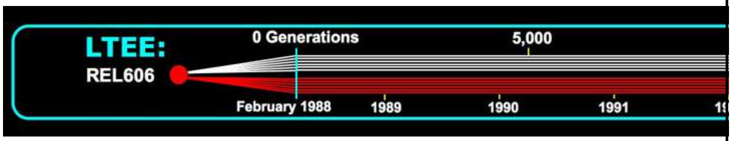
Some numbers

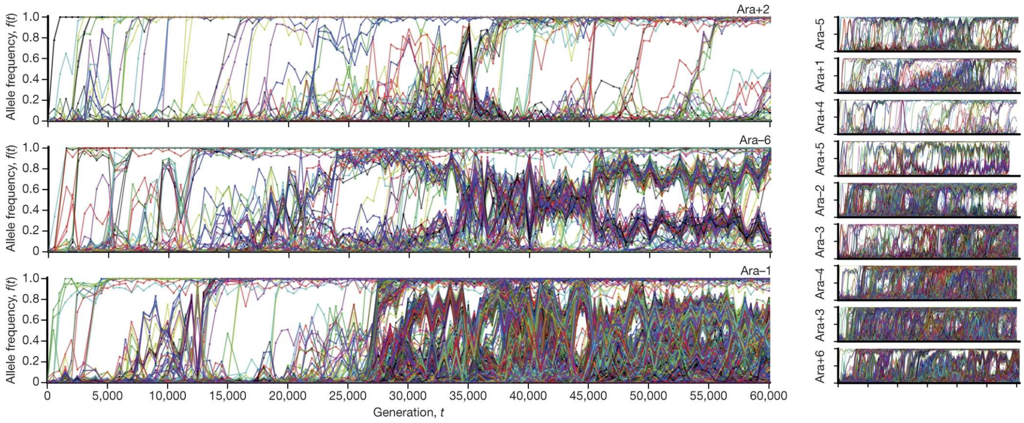
Human genome L ~ 10^9 bp
Mutation rate μ ~ 10^{-8} mutations / bp / gen
→ $L\mu$ ~ 10 mutations / genome / gen

Population size N ~ 10^{10} humans
→ $N\mu$ ~ 100 mutations produced at each site per gen in some individual

… but your genome and my genome only differ at 10^{-3} of the genome

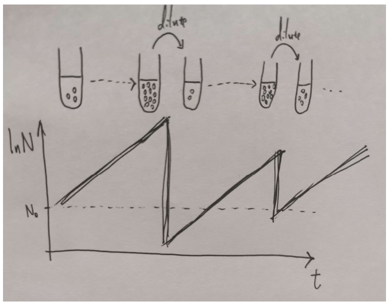
Crash course in evolutionary dynamics

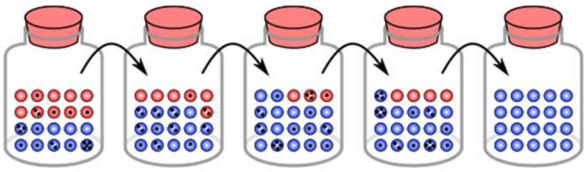


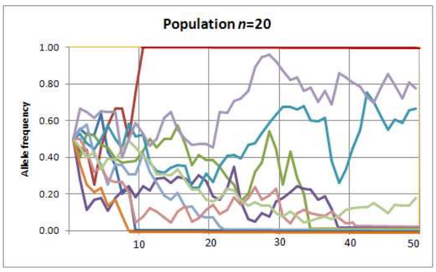


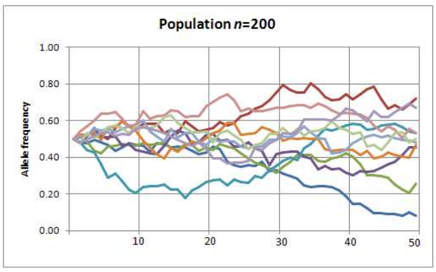
Good et al. *Nature* (2017)

Crash course in evolutionary dynamics – genetic drift



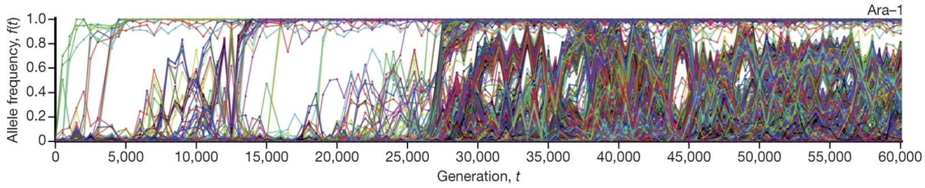


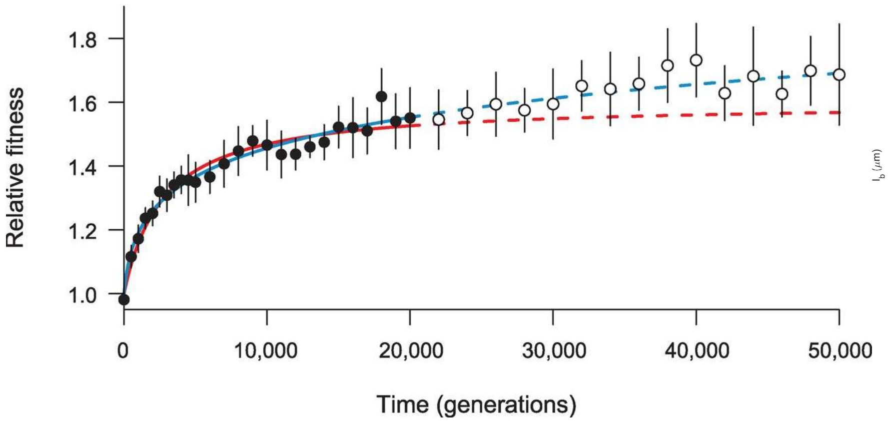


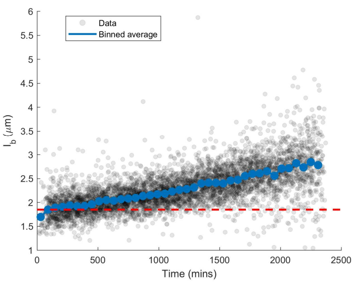


Wikipedia

Crash course in evolutionary dynamics – selection

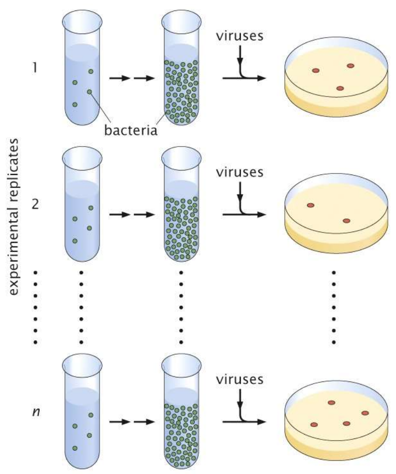


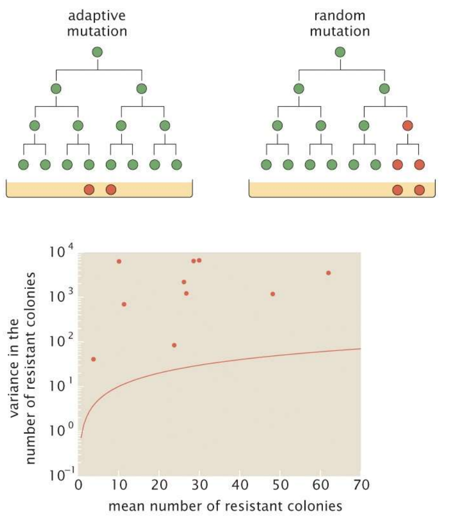




Unpublished data
Wiser et al. *Science* (2013)
Good et al. *Nature* (2017)

Crash course in evolutionary dynamics – mutation

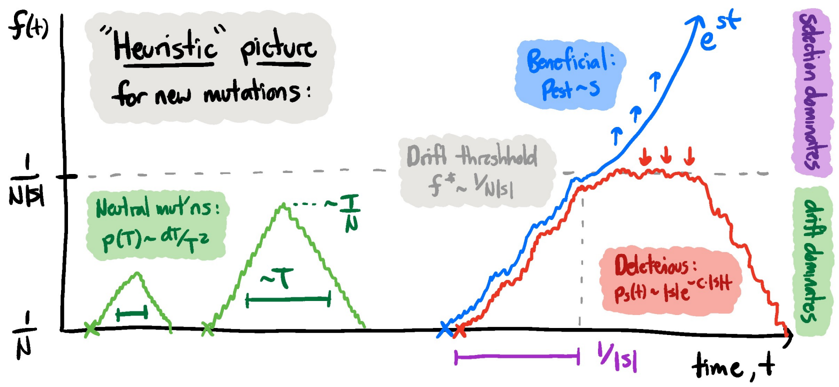




Phillips et al

Crash course in evolutionary dynamics – selection + mutation + drift

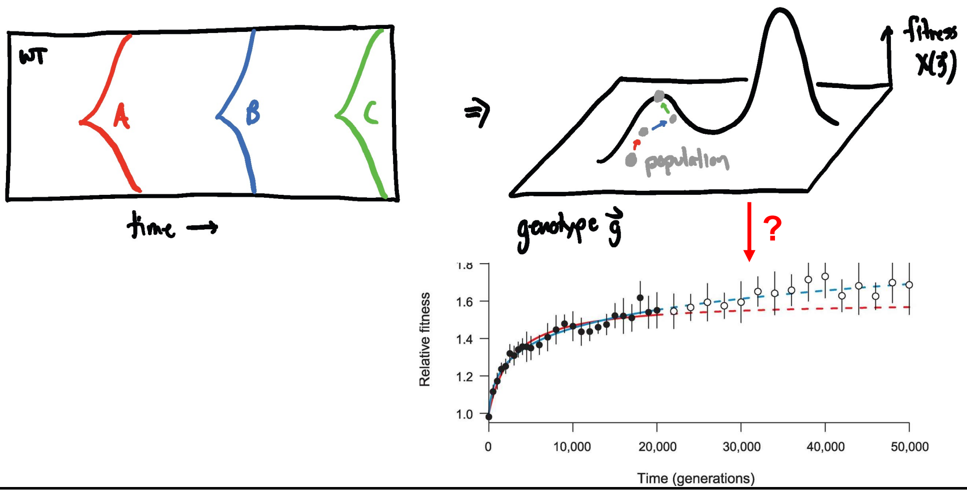
$$\frac{df}{dt} = sf(1-f) + (\mu(1-f) - \nu f) + \sqrt{\frac{f(1-f)}{N}}\xi$$



Good

Crash course in evolutionary dynamics – "strong selection weak mutation"

$$\frac{df}{dt} = sf(1-f) + (\mu(1-f) - \nu f) + \sqrt{\frac{f(1-f)}{N}}\xi$$



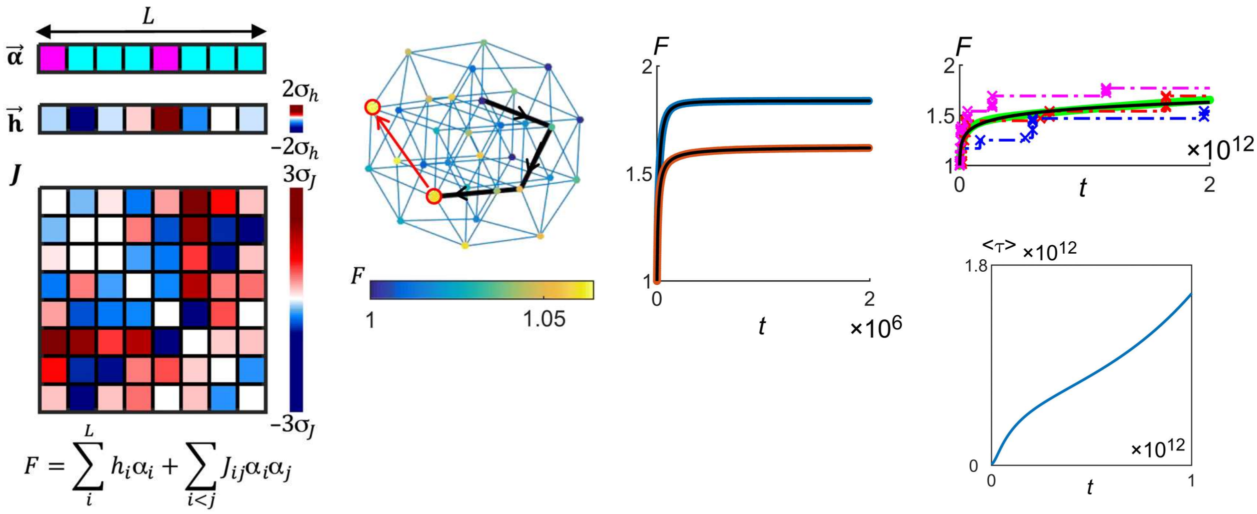
Good

Spin glass for slow fitness trajectories

Genotype-to-Fitness map

No double mutants

Double mutants allowed

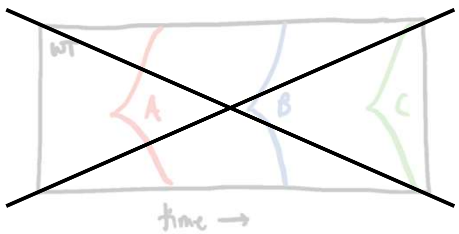


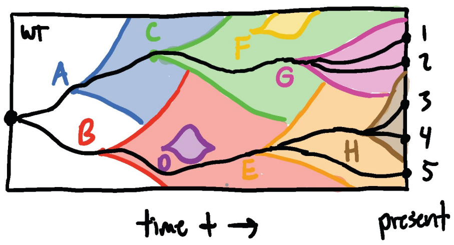
$$F = \sum_{i}^{L} h_i \alpha_i + \sum_{i<j} J_{ij} \alpha_i \alpha_j$$

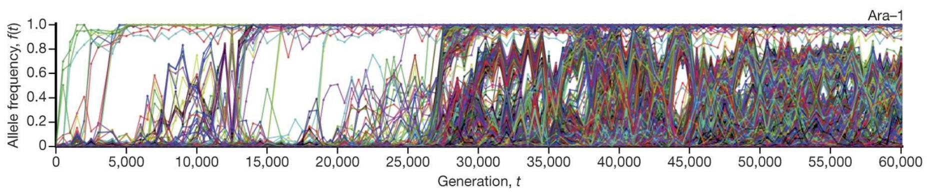
Yipei Guo et al. *Sci Adv* (2019)

Crash course in evolutionary dynamics – “clonal interference”

$$\frac{df}{dt} = sf(1-f) + (\mu(1-f) - \nu f) + \sqrt{\frac{f(1-f)}{N}}\xi$$

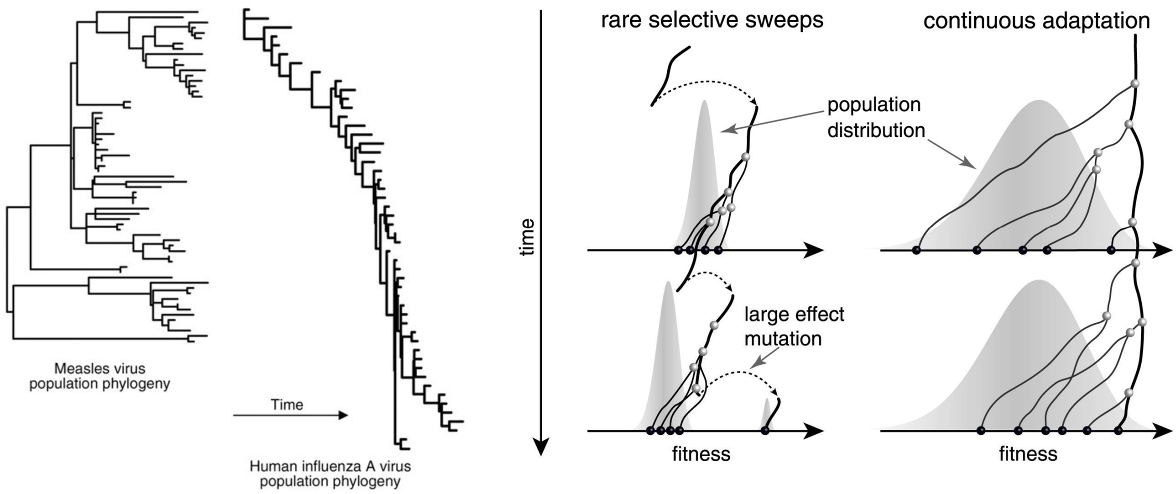






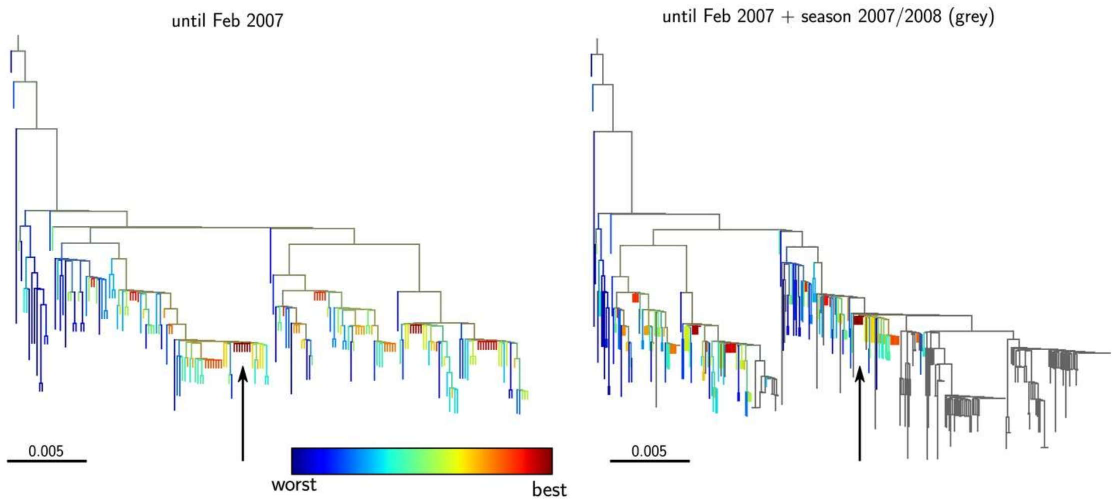
Good

Predicting the next flu strain from the shape of genealogical trees:



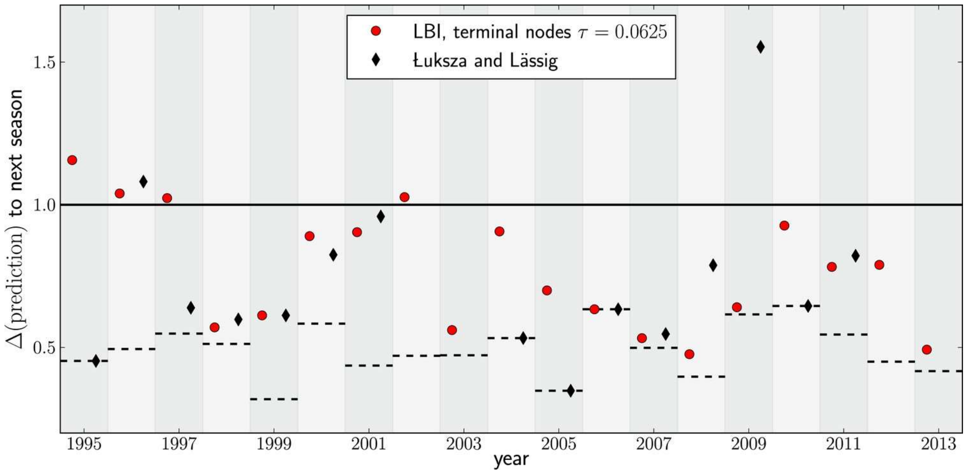
Neher et al. *eLife* (2014)
Grenfell et al. *Science* (2004)

Predicting the next flu strain from the shape of genealogical trees:



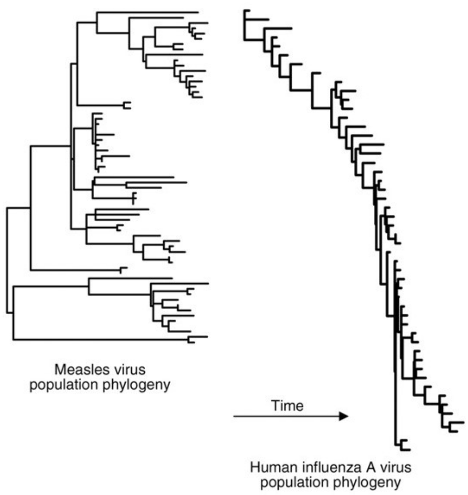
Neher et al. *eLife* (2014)

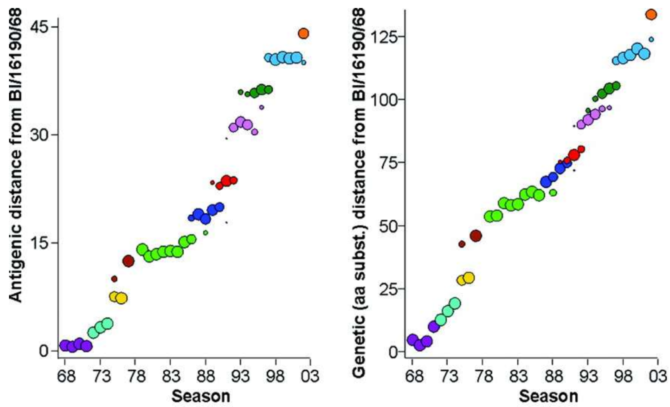
Predicting the next flu strain from the shape of genealogical trees:



Neher et al. *eLife* (2014)

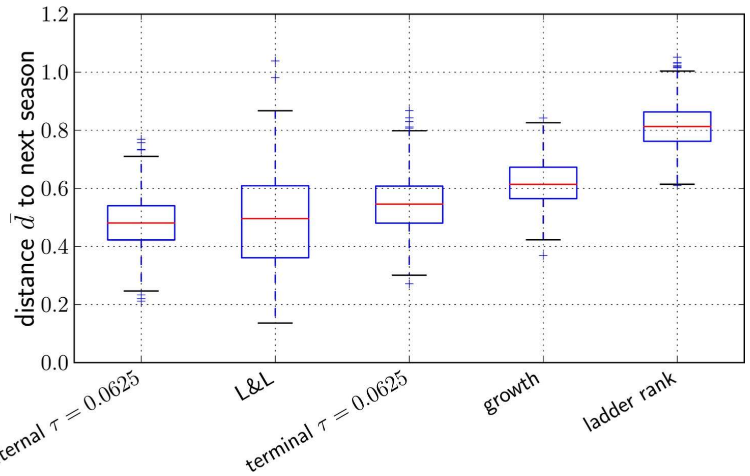
Predicting the next flu strain from the shape of genealogical trees:



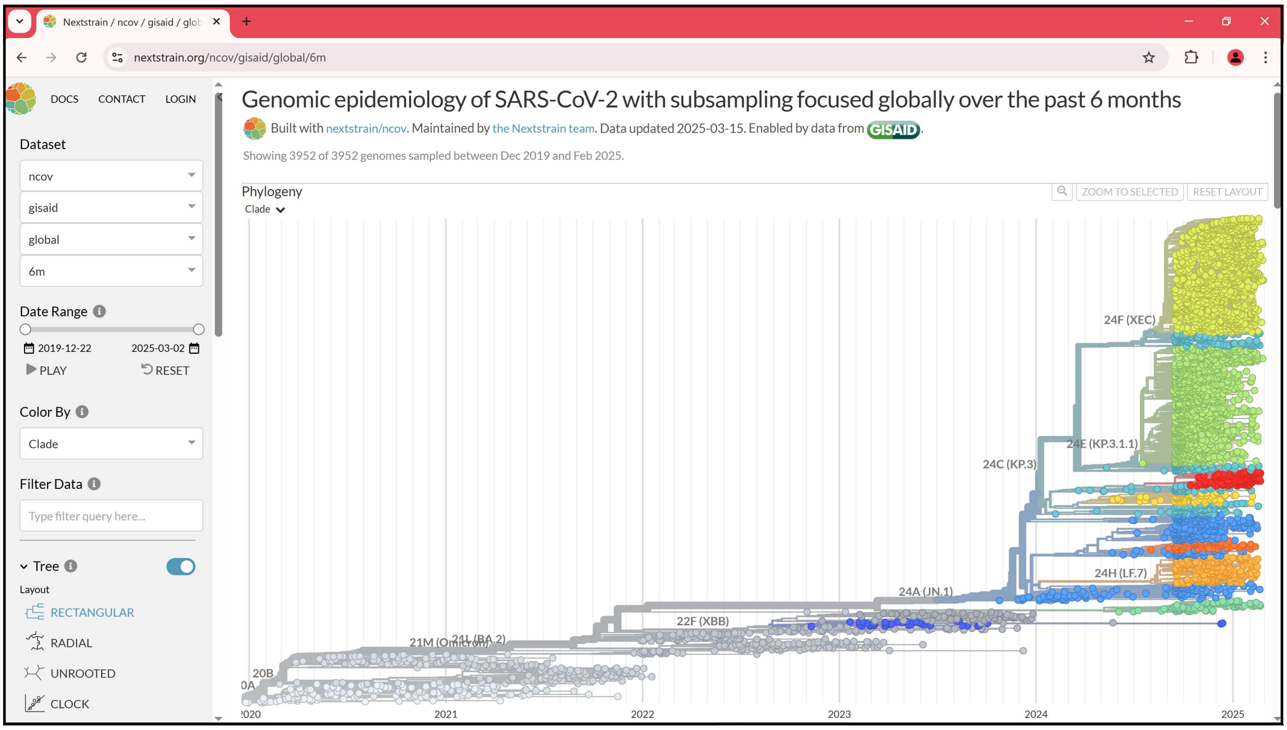


Smith et al. *Science* (2004)
Grenfell et al. *Science* (2004)

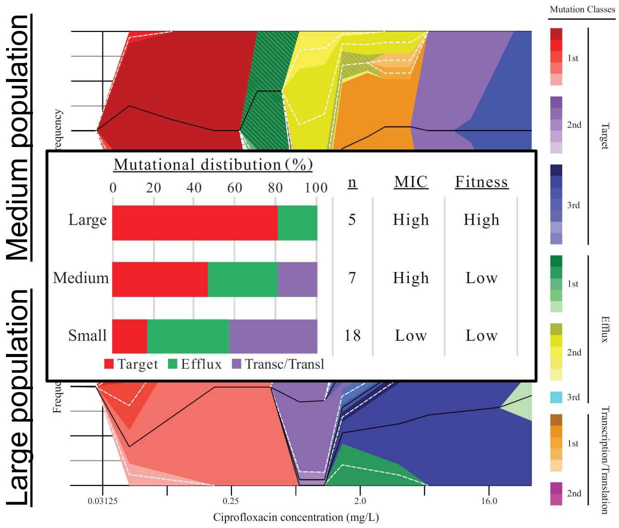
Predicting the next flu strain from the shape of genealogical trees:

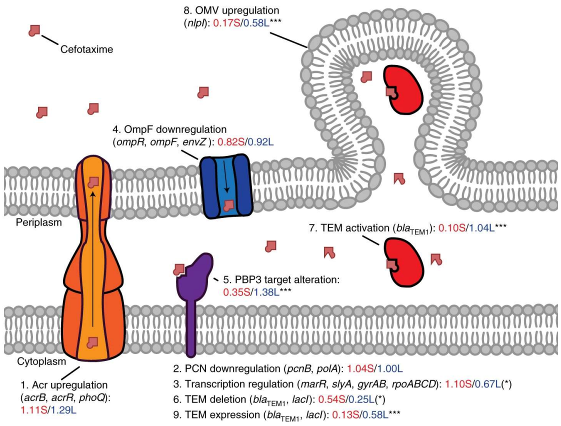


Neher et al. *eLife* (2014)



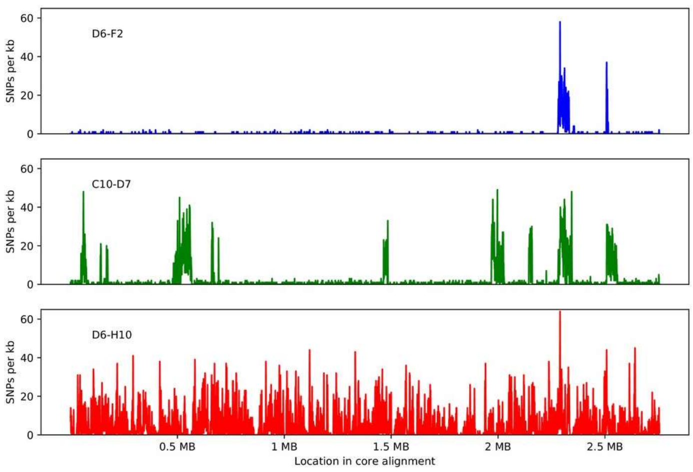
Evolutionary dynamics affects mode of emergence of antibiotic resistance.

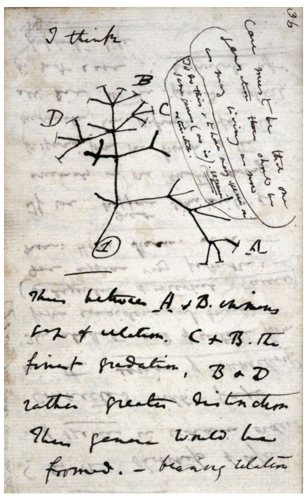




Schenk et al. *Nat Ecol Evol* (2022)
Garoff et al. *Mol Biol Evol* (2020)

Crash course in evolutionary dynamics – recombination





Sakoparnig et al. *eLife* (2021)

Summary

- Evolution can be predictable.