

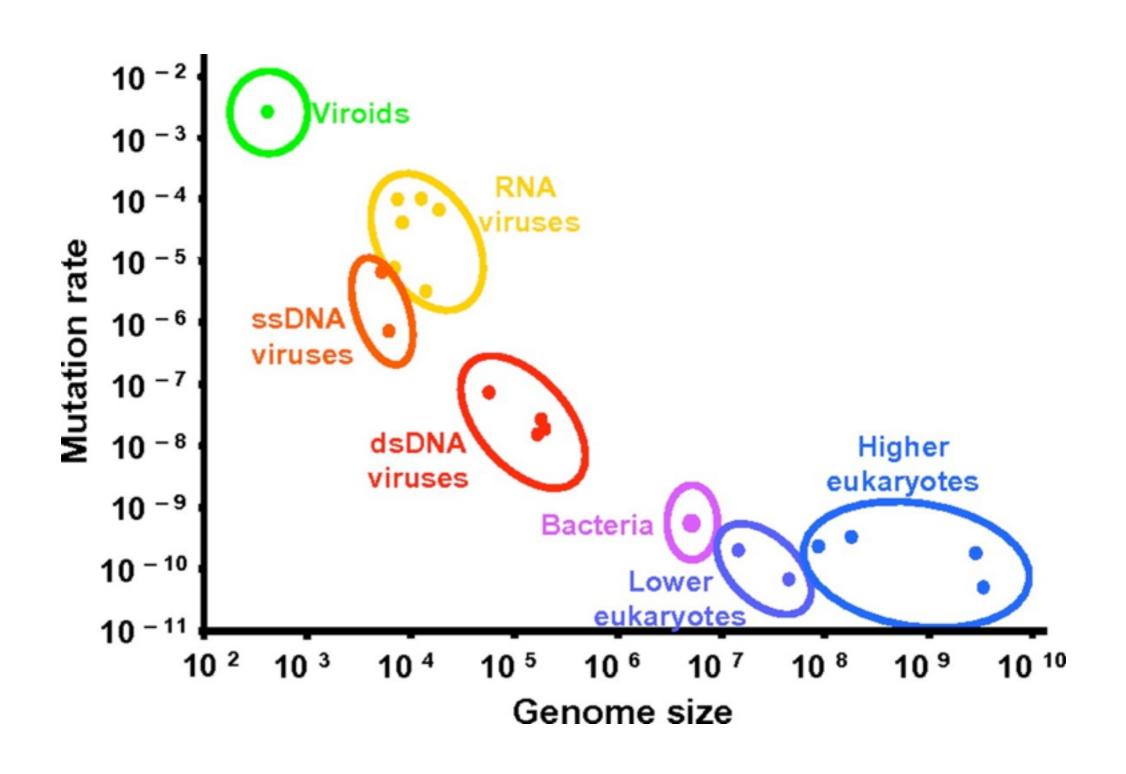
Introduction to infectious disease phylodynamics

Oliver Pybus

What Is Phylodynamics?

Rapidly evolving pathogens are unique in that their ecological and evolutionary dynamics occur on the same timescale and can therefore potentially interact.

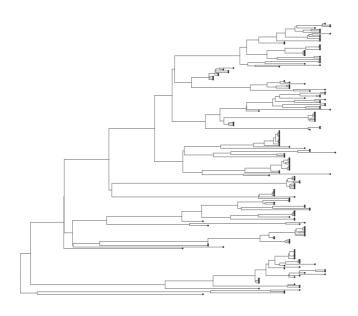
What Is Phylodynamics?

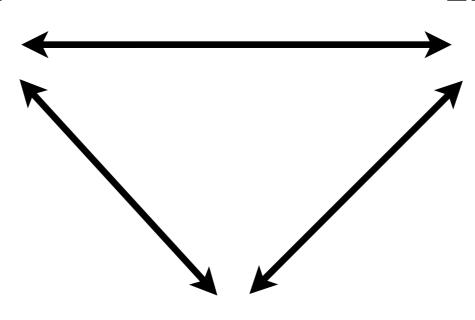


What Is Phylodynamics?

GENETIC DIVERSITY

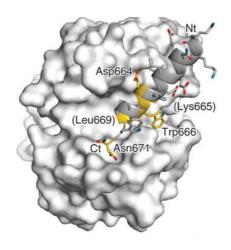
(phylogenetics & population genetics)





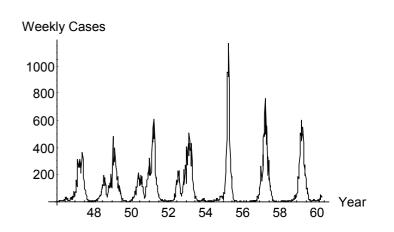
VIRUS PHENOTYPE

(molecular virology & immunology)



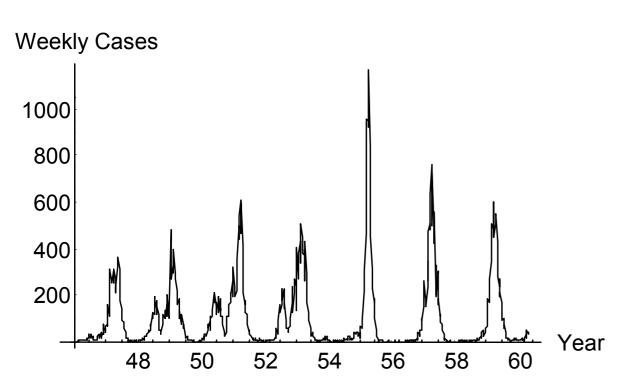
EPIDEMIC DYNAMICS

(mathematical & spatial epidemiology)

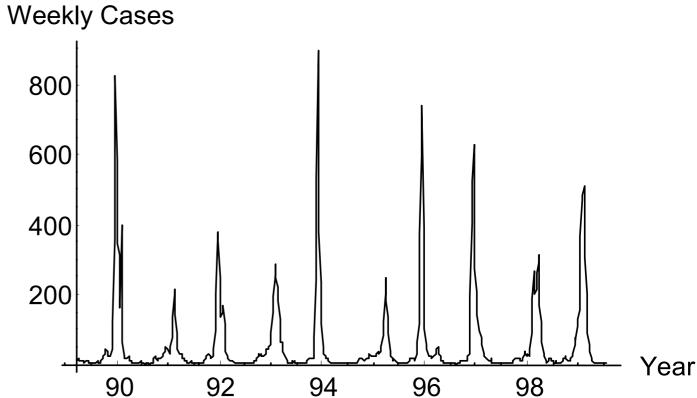




Measles vs Influenza Transmission Dynamics

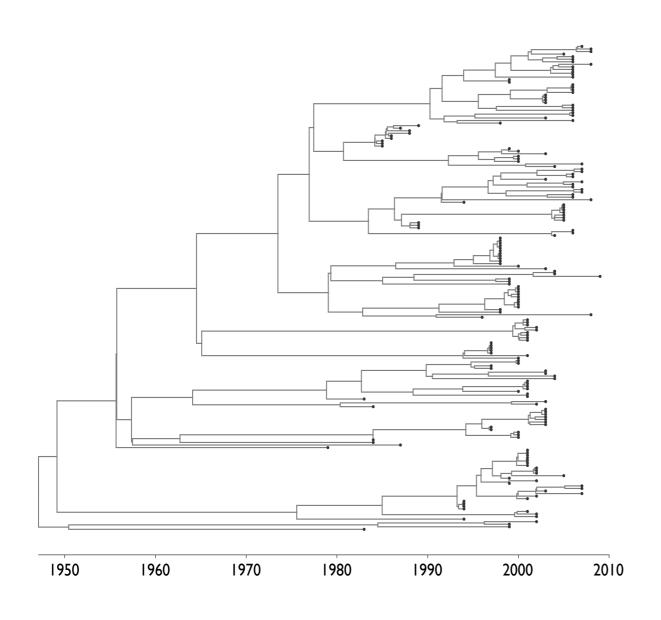


Pre-vaccination dynamics (1940-1960, Leeds UK)

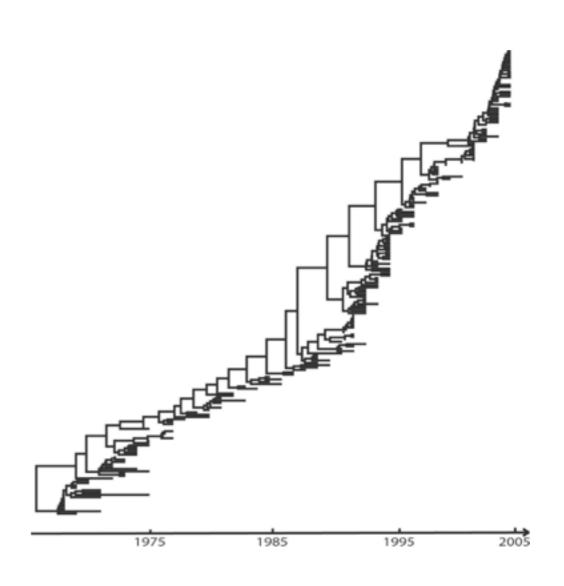


Influenza-like illness (1989-1999, France)

Measles vs Influenza Genetic Dynamics



Global measles virus genetic diversity



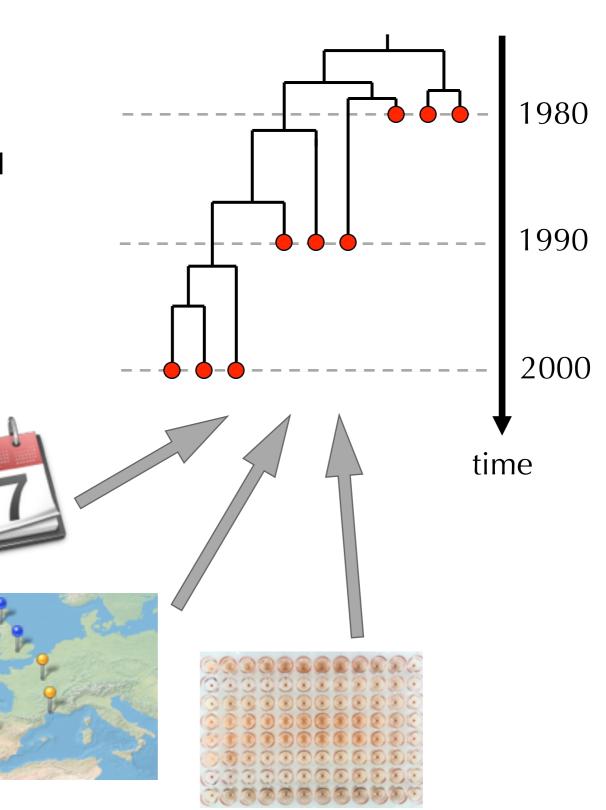
Global human influenza A H3N2 genetic diversity

Phylodynamic Data

• Gene sequences are sampled at different points in time and from different locations.

 Hence transmission history can be estimated on a real time-scale (e.g. years) and in real space (e.g. countries, cities).

• Phenotypic trait data may be available too (e.g. drug resistance, immunological assays).



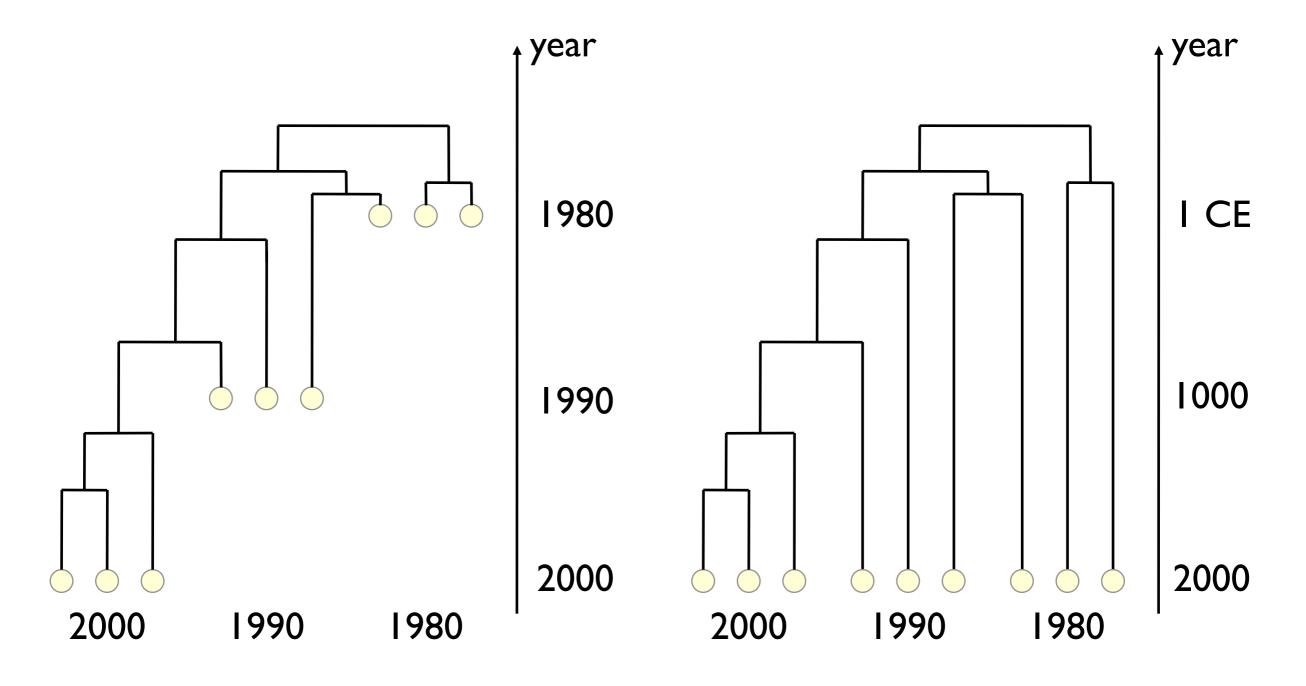
Same sampling times, different rates of evolution

Measurably-evolving population ("heterochronous" or "serially-sampled")

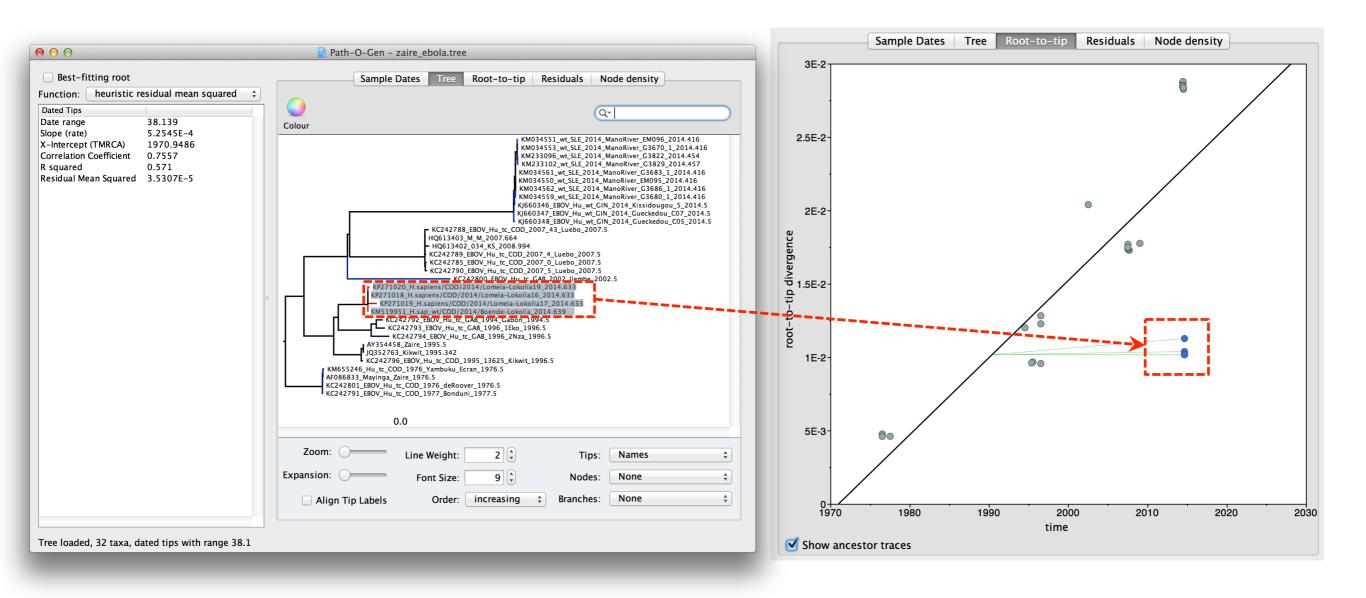
Not measurably-evolving

("isochronous" or

"contemporaneous sampling")



Phylodynamic Data

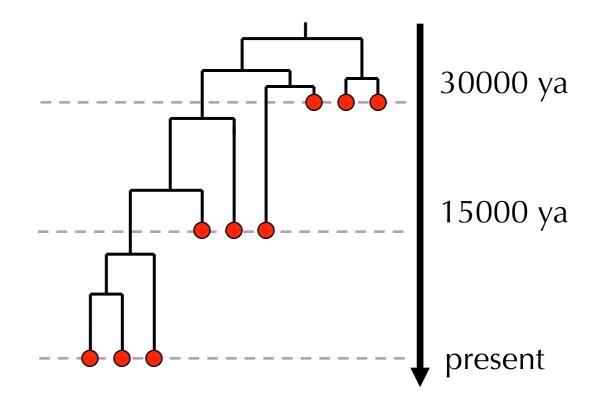


Use TempEst to determine if your sequences are heterochronous. Do they exhibit a correlation between genetic divergence and time?

Phylodynamic Data

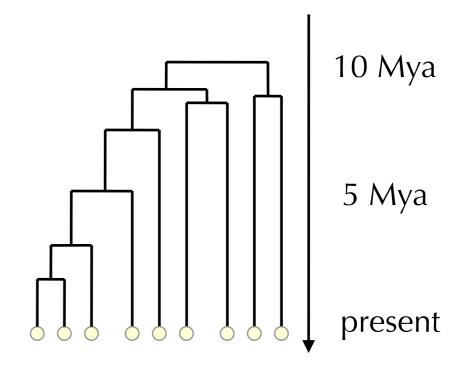
• Are rapidly-evolving pathogens the only source of heterochronous data?

No. Ancient DNA can be recovered from biological material that is > 100,000 years old.



Can phylodynamics be applied to isochronous data?

Yes, although statistical power is weaker. For example, estimating speciation and extinction rates, or investigating the creation and deletion of genes within gene families.



Phylodynamic Questions

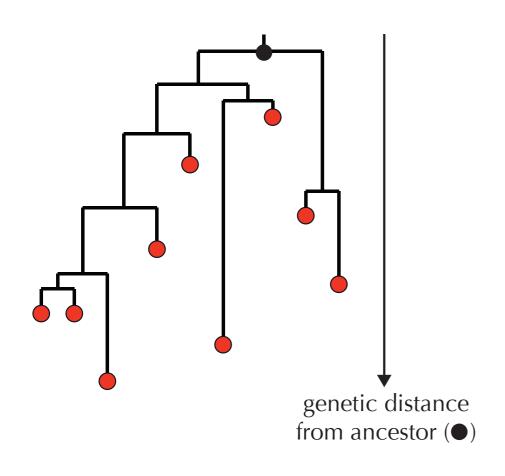
- How genetically diverse is a pathogen population?
- How do pathogen genomes change through time?
- How does pathogen genetic diversity vary through space?
- What processes or events determine these changes?

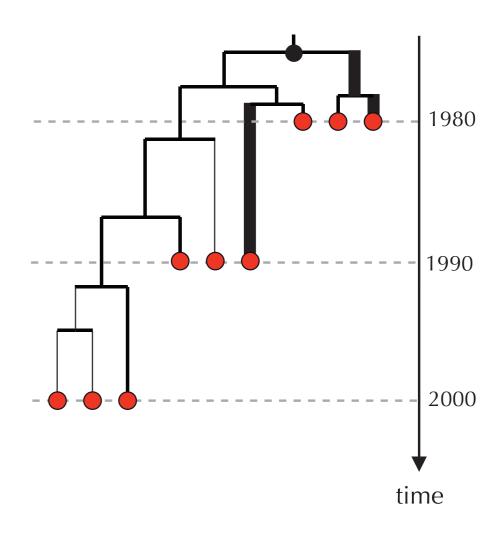
- When did an epidemic start?
- Where did it come from?
- How fast is it transmitting?
- In what direction is it spreading?
- Are hosts X,Y & Z epidemiologically linked?

Commonly-used methods for the evolutionary analysis of rapidly-evolving pathogens

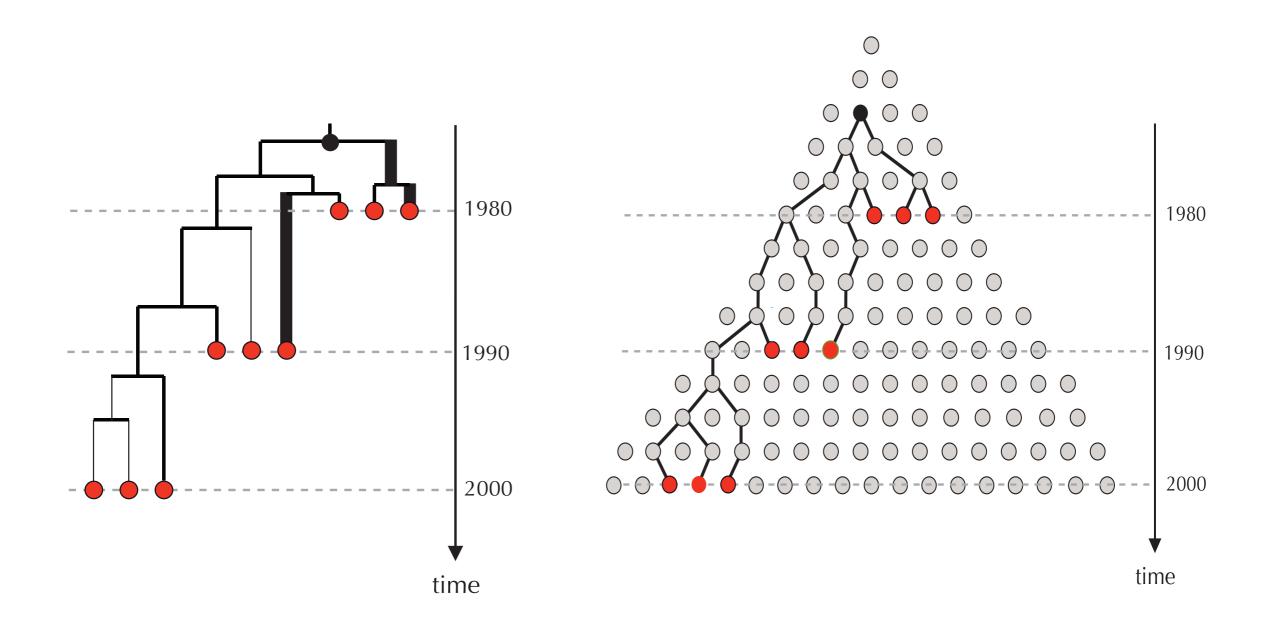
- Molecular clocks
- Coalescent theory
- Phylogeography
- Selection analysis
- Recombination analysis

(I) The Molecular Clock

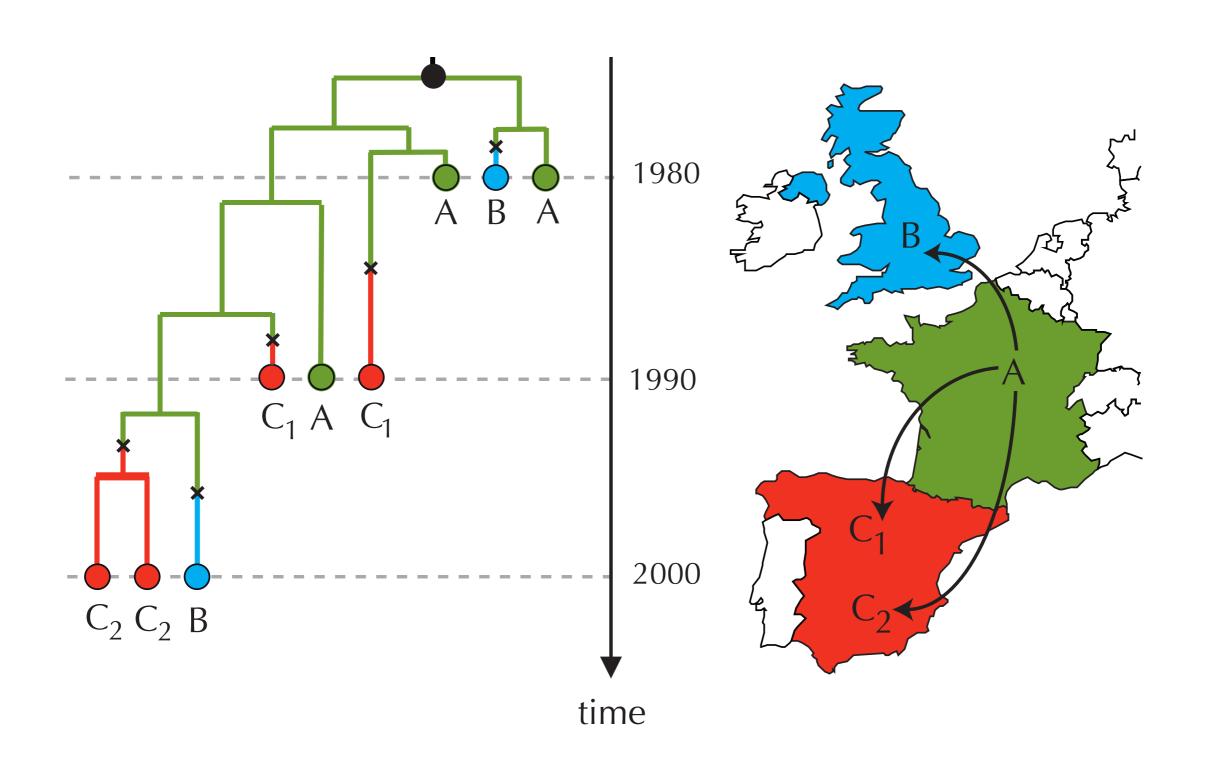




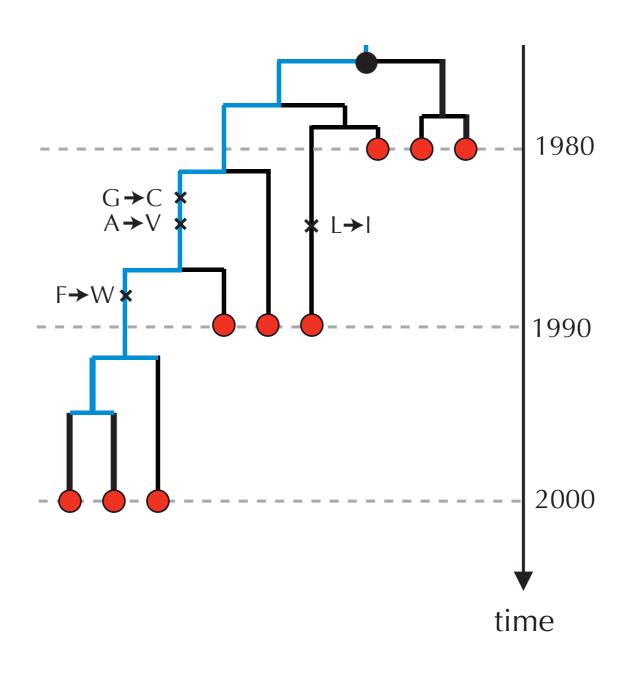
(2) Coalescent Theory / Birth Death Models



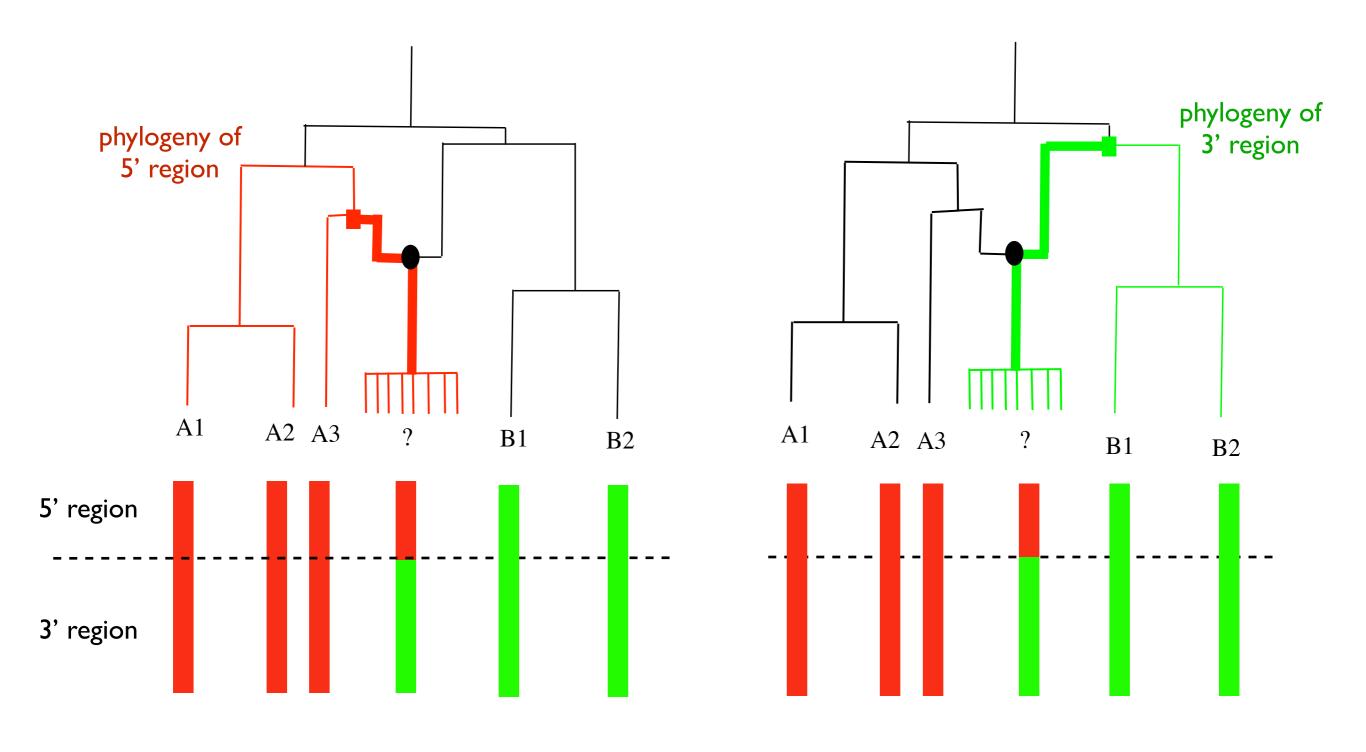
(3) Trait evolution



(4) Selection Analysis



(5) Recombination Analysis



SAMPLES FROM INFECTED INDIVIDUALS

Clinical Virology Genomics



PATHOGEN GENOME SEQUENCES

Alignment Methods Sequence Evolution Models



GENETIC DISTANCES



Recombination **Analysis**

Phylogenetic Methods

PHYLOGENY

(time scale = genetic distance)

TempEst Molecular Clocks



PHYLOGENY

(time scale = years)





Trait evolution models

Coalescent Theory Birth/Death Models

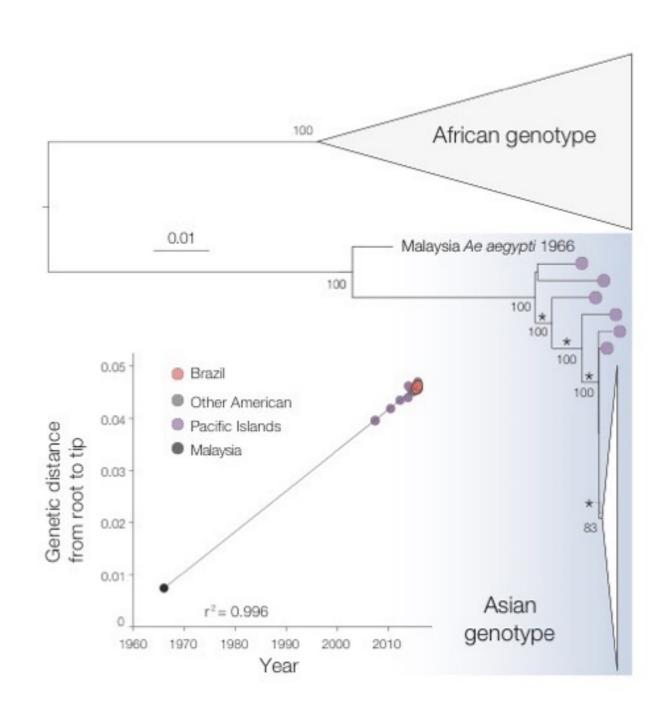


PHENOTYPE ADAPTATION EVOLUTION DYNAMICS

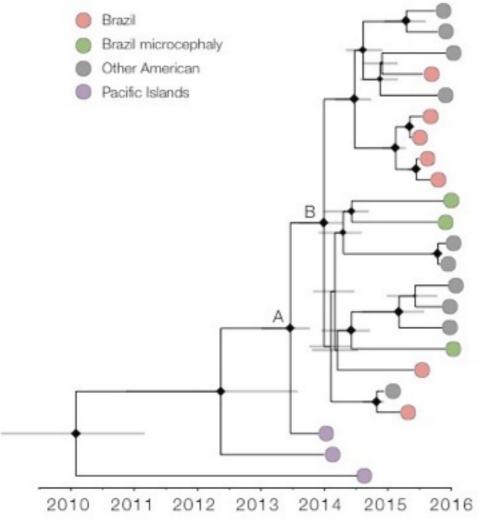
POPULATION DYNAMICS

Zika virus in the Americas

- Zika virus isolated in Uganda in 1947
- Transmitted via Aedes aegypti that is also the main vector of DENV, CHIKV and YFV
- Flavivirus with single stranded RNA genome of 11kb
- Two phylogenetic genotypes: African and Asian
- Yap Islands (2007), French Polynesia
 (2013-14), New Caledonia (2014), Easter
 Island (2014), Samoa (2015)
- Circulation of the ZIKV Asian genotype in Bahia, northeast Brazil confirmed in March 2015
- Increase in microcephaly cases noted in October 2015



Single introduction of Zika into the Americas



KU312312, Suriname, 02-10-2015 KU312313, Suriname, 15-10-2015 KU501215, Puerto Rico, 01-12-2015 KU365778, Brazil_Belem, 23-07-2015 KU312314, Suriname, 15-10-2015 KU365777, Brazil_Belem, 21-07-2015 KU365780, Brazil Paralba, 18-05-2015 KU707826, Brazil Salvador, 01-07-2015 KU365779, Brazil Belem, 02-09-2015 BeH823343, Brazil Ceara, 18-11-2015 KU527068, Brazil Natal, 15-10-2015 KU501216, Guatemala, 01-12-2015 KU501217, Guatemala, 01-11-2015 KU647676, Martinique, 15-12-2015 KU646828, Colombia, 10-11-2015 KU646827, Colombia, 10-11-2015 KU497555, Brazil Paraiba, 30-11-2015 BeH818305, Brazil Maranhao, 02-06-2015 KU509998, Haiti, 12-12-2014 KJ776791, French Polynesia, 28-11-2013 KJ634273, Cook Islands, 2014 KU681081, Thailand, 09-07-2014

Large scale mobility patterns and the arrival of ZIKV in Brazil

