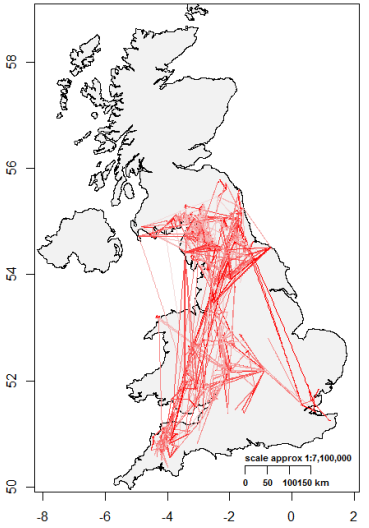
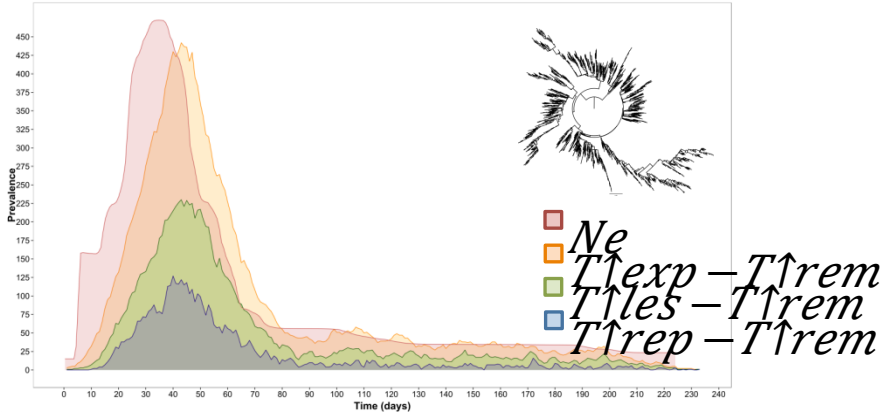
"Combine data based on epidemiological observations with phylogenetic inference in trying to establish a correlation between disease incidence and the demography of virus evolution and, therefore, in investigating the extent of sequence variability that is evident in disease outbreaks in the field."

- ✓ How can the 'effective viral population size' be scaled to some epidemiological relevant measure of incidence (*i.e.* effective number of infected epi-units)?
- ✓ How does the sampling design affect the estimation of virus evolution and population demography?
- ✓ Can sequence data be used to infer unobserved disease events and what is the likely current prevalence in the host population?





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