

Bayesian coalescent inference of population size history

Alexei Drummond
University of Auckland

Workshop on Population and Speciation Genomics
Cesky Krumlov, 2016

1st February 2016

Population inference methods using BEAST2 we will cover

1. Extended Bayesian skyline plot (EBSP)
2. Structured coalescent (MultiTypeTree)
3. SNP-based species coalescent inference (SNAPP)

Not being covered

- ▶ Divergence time estimation
- ▶ relaxed molecular clocks
- ▶ multi-locus species coalescent inference (*BEAST)
- ▶ Epidemiological phylodynamic models
- ▶ Fossilized Birth-death model, sampled ancestors
- ▶ Programming new models in BEAST

Coalescent theory

Data: a **small genetic sample** from a **large background population**.

The coalescent

- ▶ is a model of the ancestral relationships of a sample of individuals taken from a larger population.
- ▶ describes a probability distribution on ancestral genealogies (trees) given a population history, $N(t)$.
 - ▶ Therefore the coalescent can convert information from ancestral genealogies into information about population history and vice versa.
- ▶ a model of ancestral genealogies, not sequences, and its simplest form assumes neutral evolution.
- ▶ can be thought of as a prior on the tree, in a Bayesian setting.

Coalescent theory

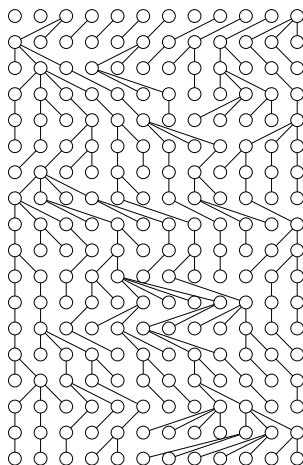
Hepatitis C in Egypt

Bayesian skyline plot

Most of theoretical population genetics is based on the idealized Wright-Fisher model of population which assumes

- ▶ Constant population size N
- ▶ Discrete generations
- ▶ Complete mixing

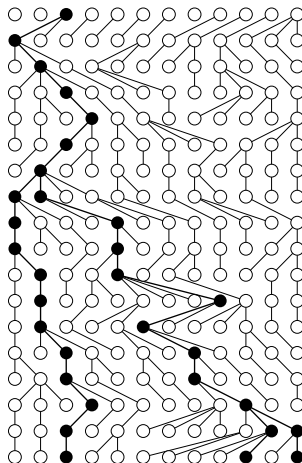
For the purposes of this presentation the population will be assumed to be haploid, as is the case for many pathogens.



Consider tracing the ancestry of a sample of k individuals from the present, back into the past.

This process eventually *coalesces* to a single common ancestor (*concestor*) of the sample of individuals.

Kingman's n -coalescent describes the statistical properties of such an ancestry when k is small compared to the total population size N .

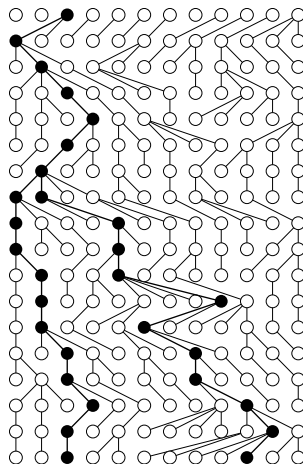


The coalescence of two ancestral lineages

- ▶ First, consider two random members from a population of fixed size N .
- ▶ By perfect mixing, the probability they share a *concestor* in the previous generation is $1/N$.
- ▶ The probability the concestor is t generations back is

$$\Pr\{t\} = \frac{1}{N} \left(1 - \frac{1}{N}\right)^{t-1}.$$

- ▶ It follows that $g = t - 1$, has a geometric distribution with a success rate of $\lambda = 1/N$, and so has mean N and variance of $N^3/(N - 1)$.



Coalescent theory

Hepatitis C in Egypt

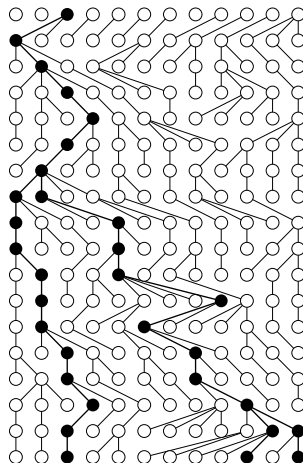
Bayesian skyline plot

The coalescence of k lineages

With k lineages the time to the first coalescence is derived in the same way, only now there are $\binom{k}{2}$ possible pairs that may coalesce, resulting in a success rate of $\lambda = \binom{k}{2}/N$ and mean time to first coalescence (t_k) of

$$E[t_k] = \frac{N}{\binom{k}{2}}.$$

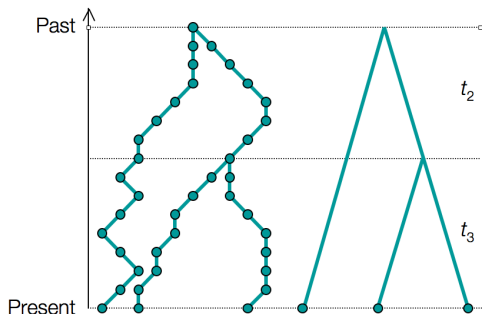
This implicitly assumes that N is much larger than $O(k^2)$, so that the probability of two coalescent events in the same generation is small.



The coalescent likelihood for a genealogy

For a genealogy with known coalescent times $\mathbf{t} = \{t_2, t_3, \dots, t_n\}$ we can write the likelihood:

$$f(\mathbf{t}|\mathbf{N}) = \frac{1}{N^{n-1}} \prod_{k=2}^n \exp\left(-\frac{\binom{k}{2} t_k}{N}\right).$$



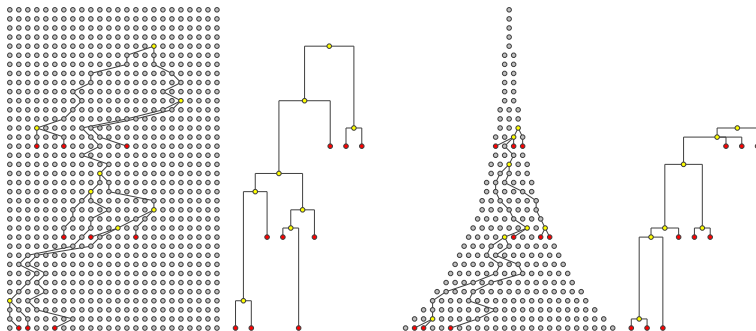
The coalescent with serial samples

Many epidemiological agents, like **RNA viruses**, evolve very rapidly, so that the effect of sampling the population at different times becomes important. **Ancient DNA** also requires careful handling of sampling times.

Coalescent theory

Hepatitis C in Egypt

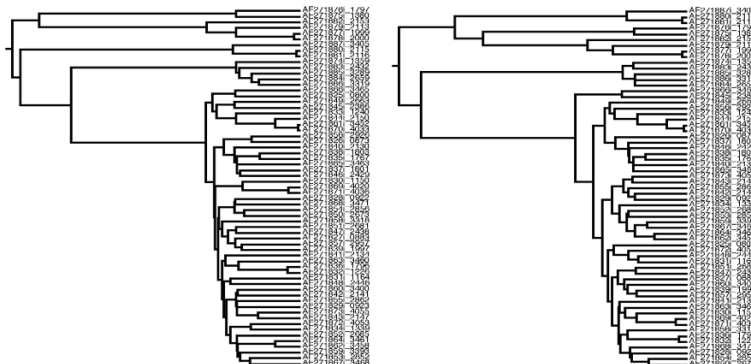
Bayesian skyline plot



Constant size

Exponential growth

Bayesian integration of uncertainty in genealogies



How similar are these two trees? Both of them are plausible given the data. We can use Bayesian Markov-chain Monte Carlo to average the coalescent over all plausible trees.

Hepatitis C in Egypt

Hepatitis C in Egypt

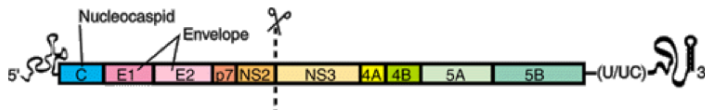
Cesky Krumlov

A case study of the coalescent approach to molecular epidemiology

Coalescent theory

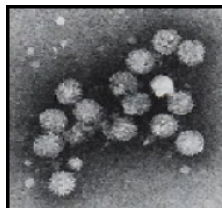
Hepatitis C in Egypt

Bayesian skyline plot



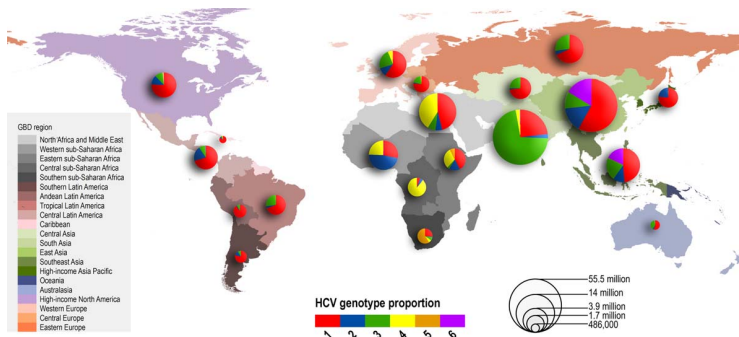
Hepatitis C (HCV)

- ▶ Identified in 1989
- ▶ 9.6kb single-stranded RNA genome
- ▶ Polyprotein cleaved by proteases
- ▶ Tissue culture system only recently developed



How important is Hepatitis C?

> 185 million people infected worldwide



- ▶ ~80% infections are chronic
- ▶ Liver cirrhosis and cancer risk
- ▶ 10,000 deaths per year in USA
- ▶ No protective immunity?

Coalescent theory

Hepatitis C in Egypt

Bayesian skyline plot

By percutaneous exposure to infected blood

- ▶ Blood transfusion / blood products
- ▶ Injecting and nasal drug use
- ▶ Sexual and vertical transmission
- ▶ Unsafe injections
- ▶ Unidentified routes



Coalescent population inference of HCV

Cesky Krumlov

Pybus *et al* (2003) *Molecular Biology and Evolution*

Coalescent theory

Hepatitis C in Egypt

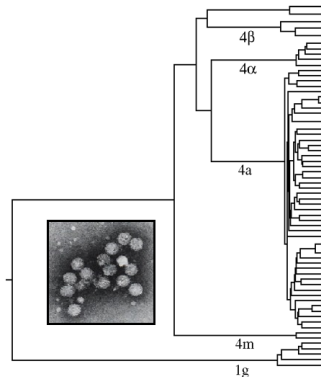
Bayesian skyline plot

Egyptian HCV gene sequences

n=61

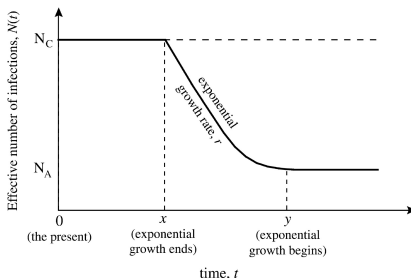
E1 gene, 411bp

- ▶ All sequence contemporaneous
- ▶ Egypt has highest prevalence of HCV worldwide (10-20%)
- ▶ But low prevalence in neighbouring states
- ▶ Why is Egypt so seriously affected?
- ▶ Parenteral antischistosomal therapy (PAT)?



- ▶ The coalescent can be extended to model any integrable function of varying population size.
- ▶ The model we used was a const-exp-const model.
- ▶ A Bayesian MCMC method was developed to sample the gene genealogy, the substitution model and demographic function simultaneously.

$$N(x) = \begin{cases} N_c & \text{if } t \leq x \\ N_c e^{-r(t-x)} & \text{if } x < t < y \\ N_A & \text{if } t \geq y \end{cases}$$



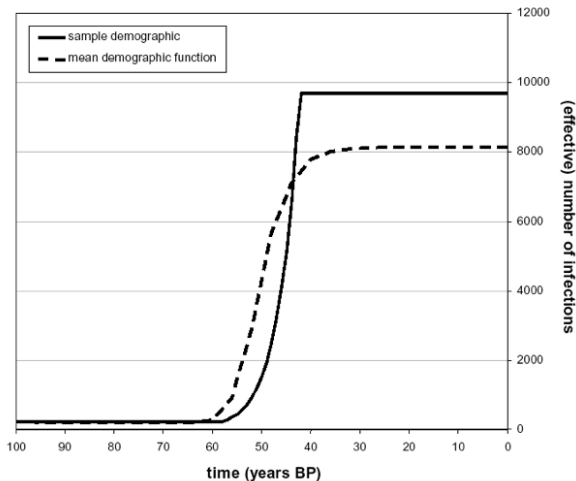
Estimated population history of HCV in Egypt

Cesky Krumlov

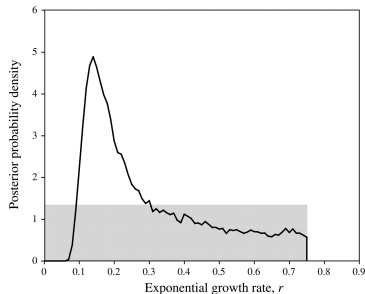
Coalescent theory

Hepatitis C in Egypt

Bayesian skyline plot

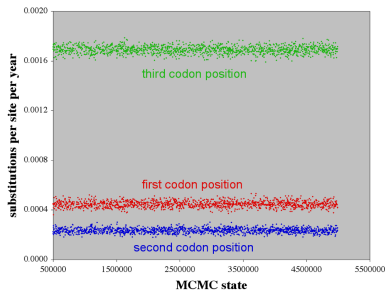


Demographic parameters

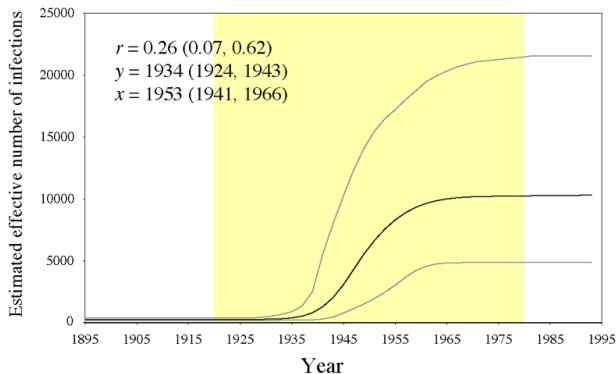


Growth rate of the growth phase
Grey box is the prior

Mutational parameters



Rates at different codon positions,
All significantly different



Coalescent theory

Hepatitis C in Egypt

Bayesian skyline plot

- Marginalized over uncertainty in genealogy and mutational processes
- Yellow band represents time over which PAT was employed in Egypt

Bayesian skyline plot

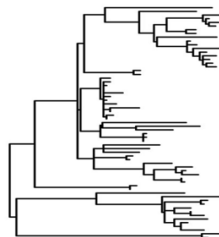
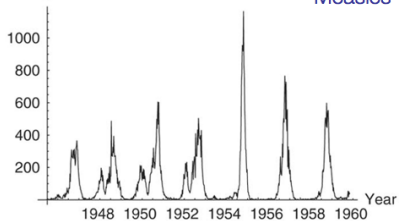
Coalescent theory

Hepatitis C in Egypt

Bayesian skyline plot

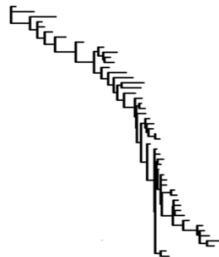
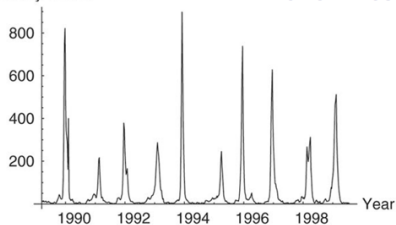
Weekly Cases

Measles virus



Weekly Cases

Human influenza virus

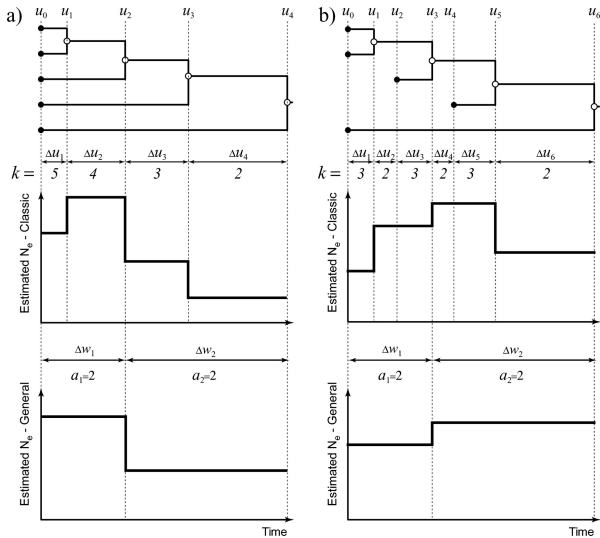


“Skyline” coalescent model

Coalescent theory

Hepatitis C in Egypt

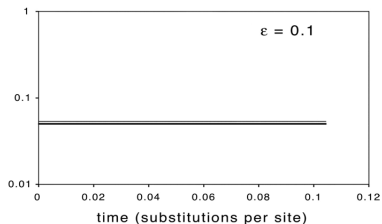
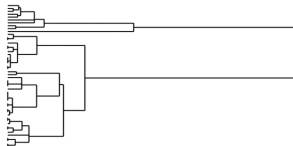
Bayesian skyline plot



The generalized skyline plot - simulated data

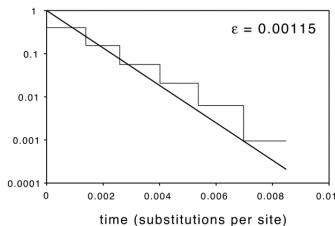
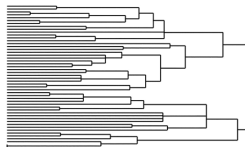
Constant population size,

$$N(t) = N_0$$



Exponential growth,

$$N(t) = N_0 e^{-rt}$$

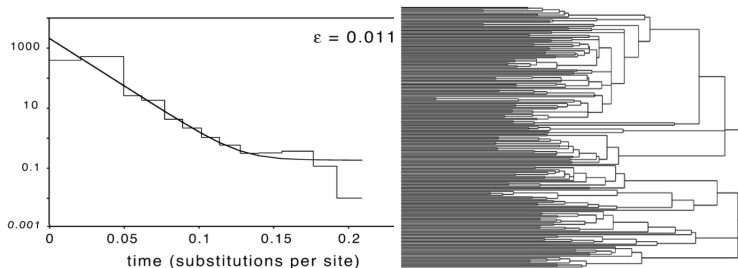


The generalized skyline plot - HIV-1 group M

The tree used here was estimated in Yusim *et al* (2001) *Phil. Trans. Roy. Soc. Lond. B* **356**:855-866.

The black curve is a parametric coalescent estimate obtained from the same data under the expansion model,

$$N(t) = (N_0 - N_A)e^{-rt} + N_A$$



The Bayesian skyline plot

Drummond *et al* (2005) *Molecular Biology and Evolution*

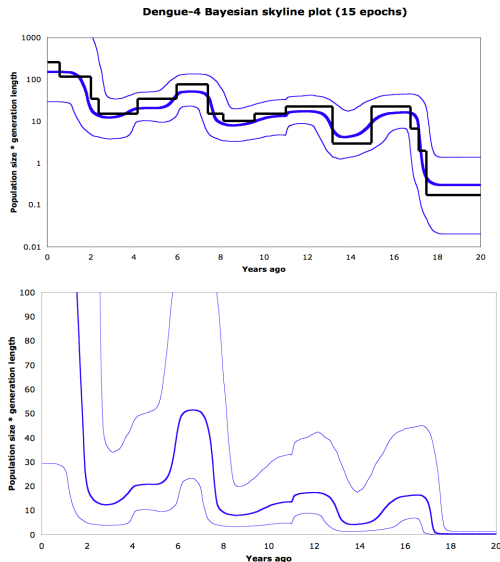
Cesky Krumlov

Coalescent theory

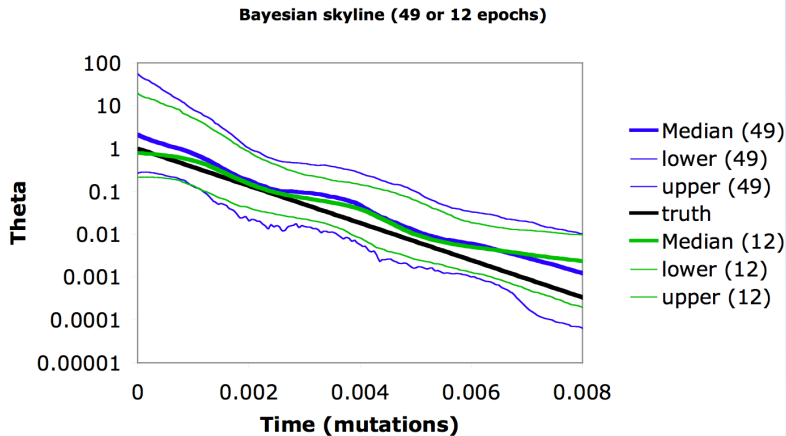
Hepatitis C in Egypt

Bayesian skyline plot

The Bayesian skyline plot estimates a demographic function that has a certain fixed number of steps (in this example 15) and then integrates over all possible positions of the break points, and population sizes within each epoch.



Validating the Bayesian skyline plot



Comparison of BSP to parametric coalescent

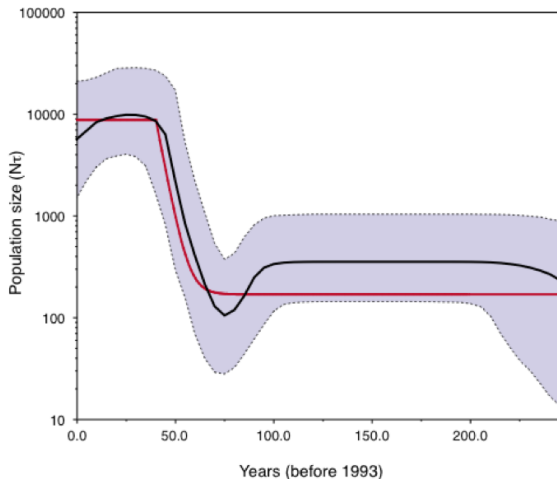
Hepatitis C in Egypt

Cesky Krumlov

Coalescent theory

Hepatitis C in Egypt

Bayesian skyline plot



Modeling complex demographic history

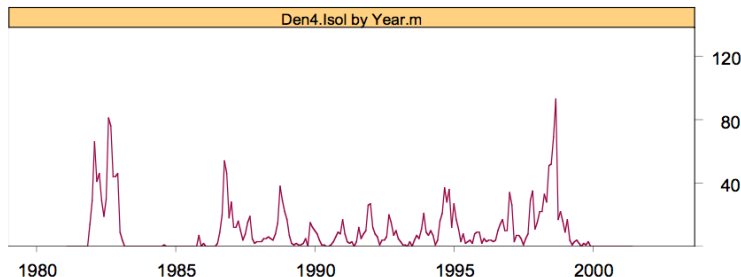
Cesky Krumlov

Dengue 4 in Puerto Rico

Coalescent theory

Hepatitis C in Egypt

Bayesian skyline plot



- ▶ $N(t) = N_0 \exp(-rt)$
 - ▶ log marginal likelihood = -10566.421
- ▶ $N(t)$ = scaled-translated case data
 - ▶ log marginal likelihood = -10478.572

Comparing BSP to incidence data

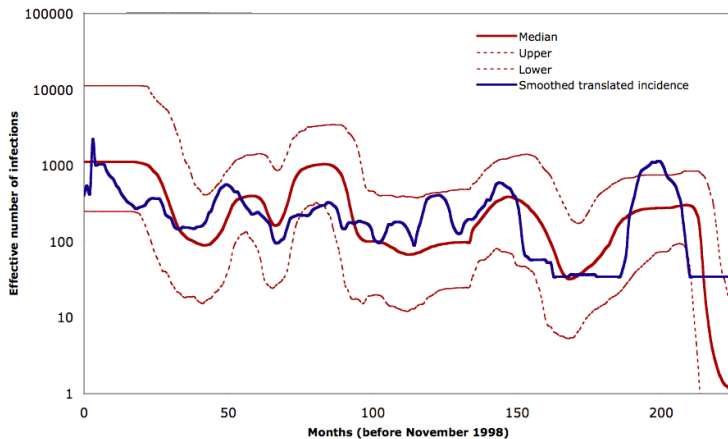
Dengue 4 in Puerto Rico

Cesky Krumlov

Coalescent theory

Hepatitis C in Egypt

Bayesian skyline plot



Extended BSP: Stochastic Variable Selection

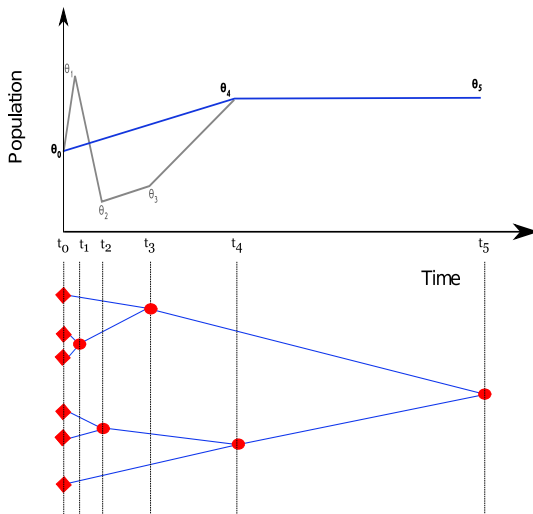
Heled and Drummond (2008)

Cesky Krumlov

Coalescent theory

Hepatitis C in Egypt

Bayesian skyline plot



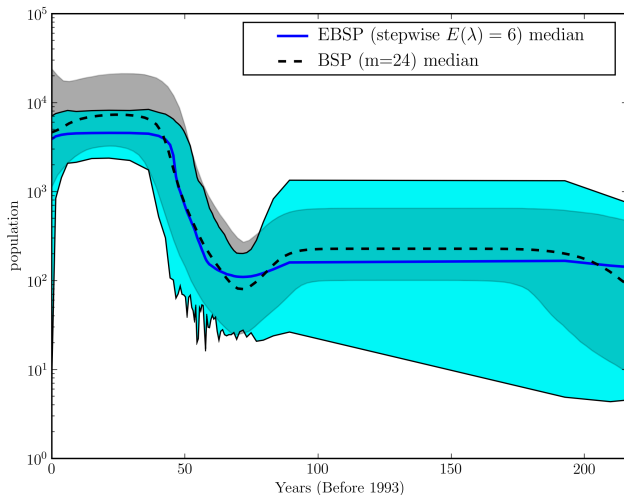
Comparison of EBSP with BSP on Egypt HCV

Cesky Krumlov

Coalescent theory

Hepatitis C in Egypt

Bayesian skyline plot



Detecting evolutionary bottlenecks using EBSP

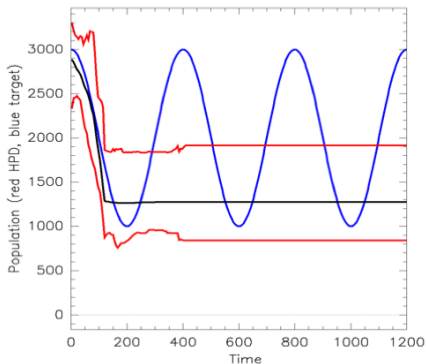
Cesky Krumlov

Coalescent theory

Hepatitis C in Egypt

Bayesian skyline plot

480 contemporaneous samples from a single locus



Detecting evolutionary bottlenecks using EBSP

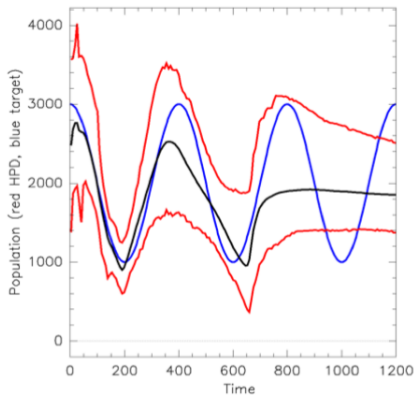
Cesky Krumlov

Coalescent theory

Hepatitis C in Egypt

Bayesian skyline plot

16 contemporaneous samples from each of 32 loci



Detecting evolutionary bottlenecks using EBSP

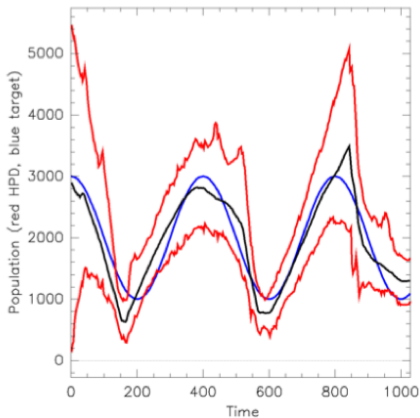
Cesky Krumlov

Coalescent theory

Hepatitis C in Egypt

Bayesian skyline plot

480 samples sampled through time from a single locus



The population genetic dynamics of Influenza A

Rambaut *et al* (2008) *Nature* 453:615-620

Cesky Krumlov

Coalescent theory

Hepatitis C in Egypt

Bayesian skyline plot

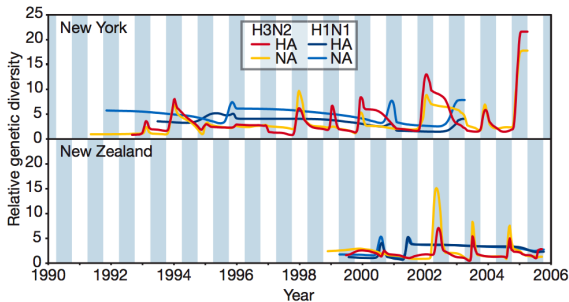
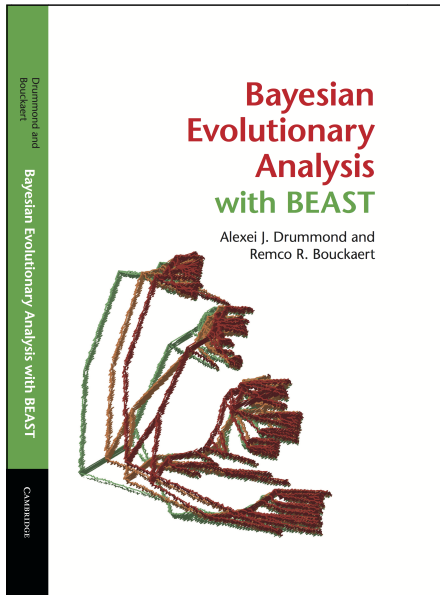


Figure 1 | Population dynamics of genetic diversity in influenza A virus. Bayesian skyline plots of the HA and NA segments for the A/H3N2 and A/H1N1 subtypes in New York state (top) and New Zealand (bottom). The horizontal shaded blocks represent the winter seasons. The y-axes represent a measure of relative genetic diversity (see Methods for details). The shorter timescale of New Zealand skyline plot is due to the shorter sampling period.

- ▶ Coalescent theory provides a mathematical framework for accurately modelling small genetic samples and the stochastic outcomes of genetic drift due to random mating.
- ▶ Coalescent theory provides backward probabilities for population parameters.
- ▶ In most implementations the coalescent does not directly model small populations or stochastically fluctuating populations.
- ▶ Coalescent theory can be extended to:
 - ▶ non-parametric fluctuating populations
 - ▶ structured populations
 - ▶ gene conversion



Taming the BEAST



Bayesian evolutionary analysis by sampling trees

A summer school on Bayesian phylogenetic and phylodynamic analyses in BEAST2 with invited talks, lectures and tutorials by leading and renowned experts in the field.

Alexei Drummond University of Auckland

Tracy Heath Iowa State University

Oliver Pybus University of Oxford

Tanja Stadler ETH Zürich

Tim Vaughan University of Auckland

26 June - 1 July 2016
Engelberg, Switzerland



Computational Evolution

For further information and to apply:
<http://www.bsse.ethz.ch/cevo/taming-the-beast.html>



D-BSSE
Department of Biosystems
Science and Engineering