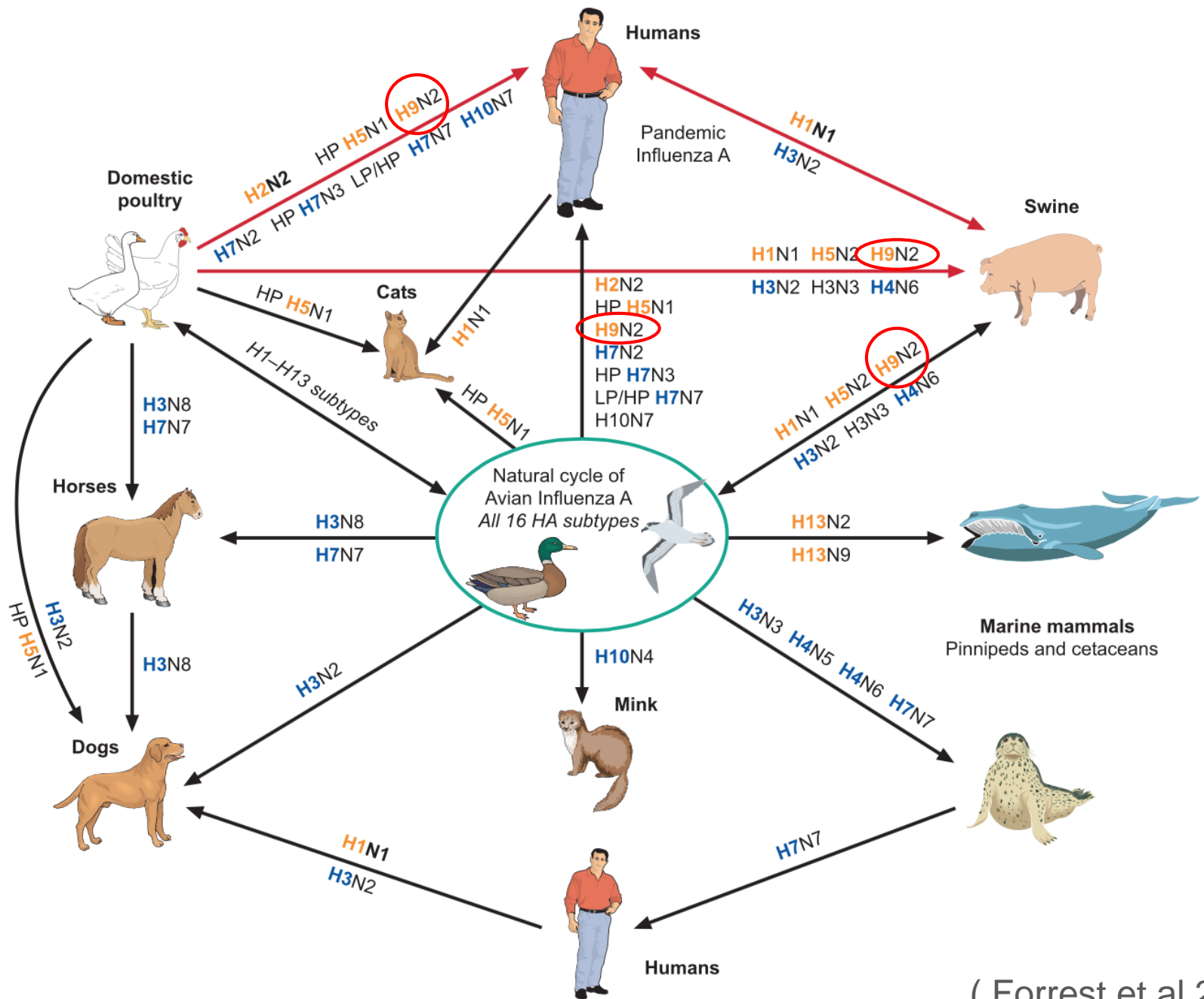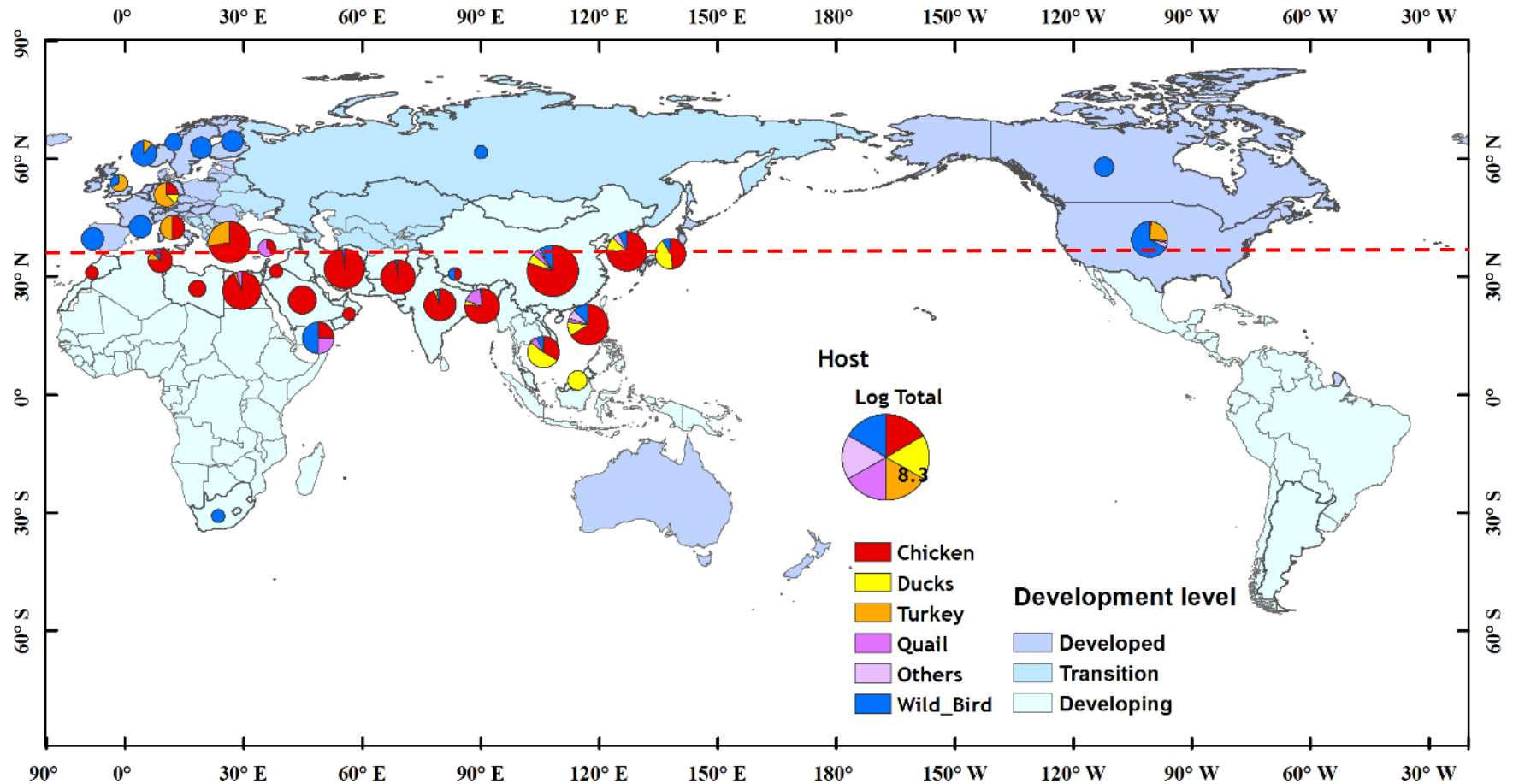# Modeling the global dynamics of avian influenza H9N2

Jing Yang and Alexei Drummond
Center for Computational Evolution,
University of Auckland
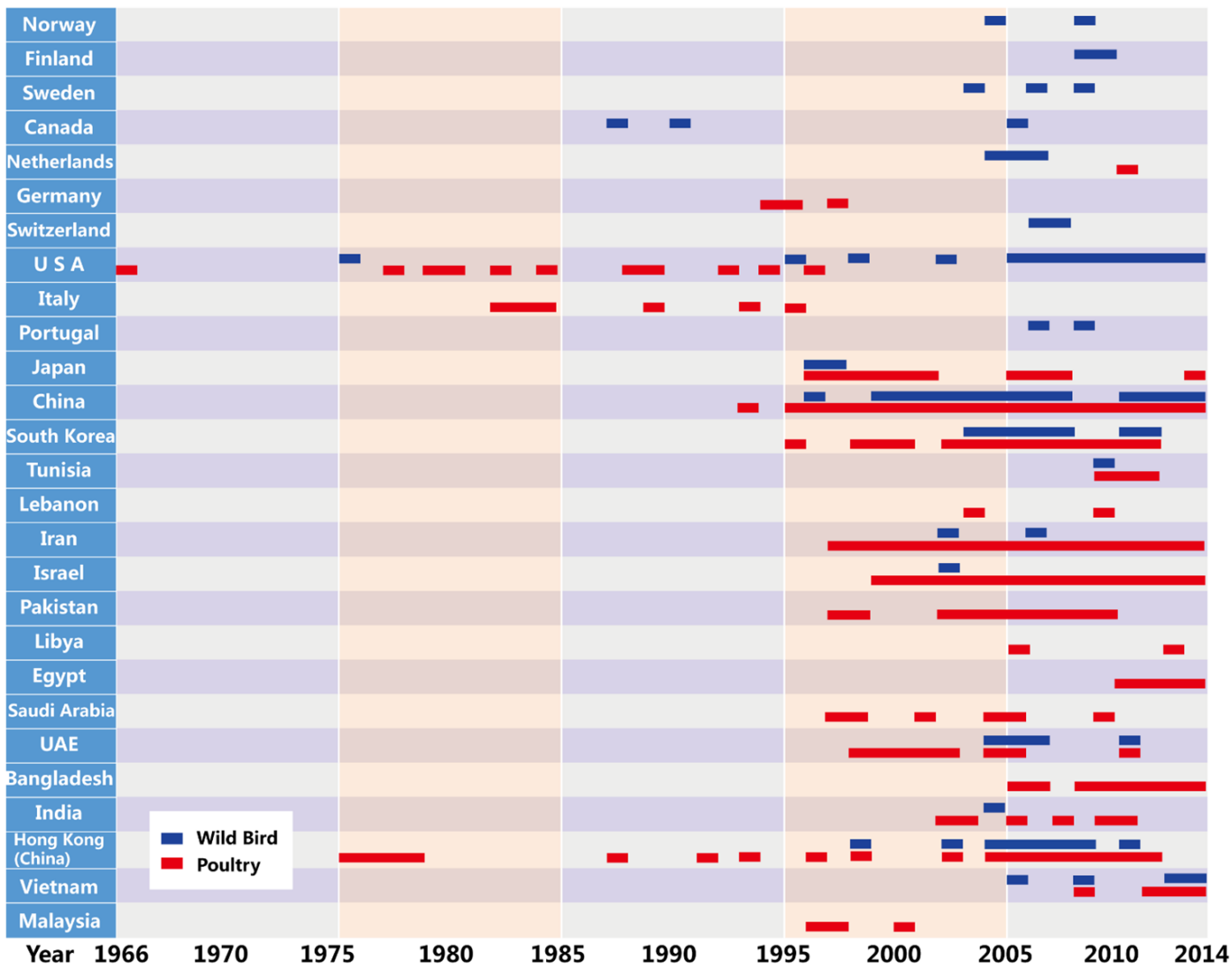
(Forrest et al 2010)

Spatial patterns

Spatial patterns

1. Since the mid 1990s, H9N2 began to spread into multiple countries, especially in Asia.
2. Latitude with different hosts

(y axis – countries were listed from high to low latitude in north hemisphere)

BEAST: Bayesian evolutionary analysis by sampling trees

Alexei J Drummond[*,1,2] and Andrew Rambaut[3]

Bayesian Phylogenetics with BEAUti and the BEAST 1.7

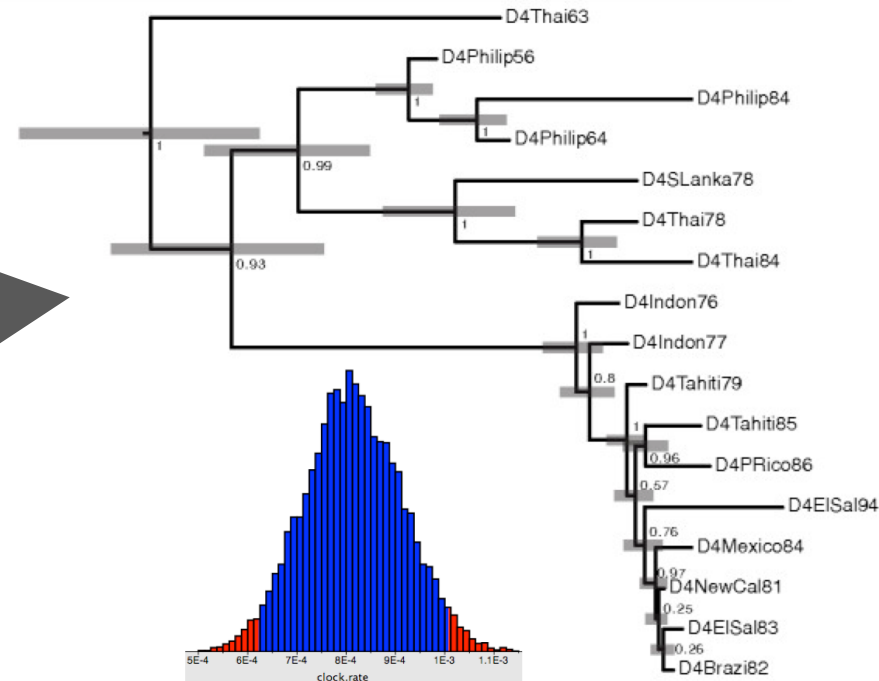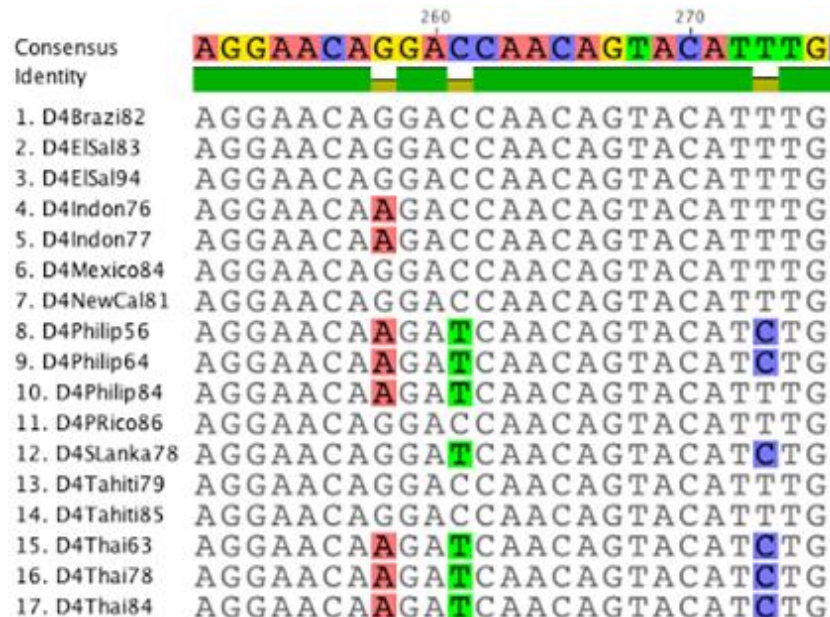Alexei J. Drummond,[*,1,2] Marc A. Suchard,[*,3,4] Dong Xie,[1,2] and Andrew Rambaut[*,5]

BEAST 2: A Software Platform for Bayesian Evolutionary Analysis

Remco Bouckaert[1*], Joseph Heled[1], Denise Kühnert[1,2], Tim Vaughan[1,3], Chieh-Hsi Wu[1], Dong Xie[1], Marc A. Suchard[4,5], Andrew Rambaut[6], Alexei J. Drummond[1,7*]
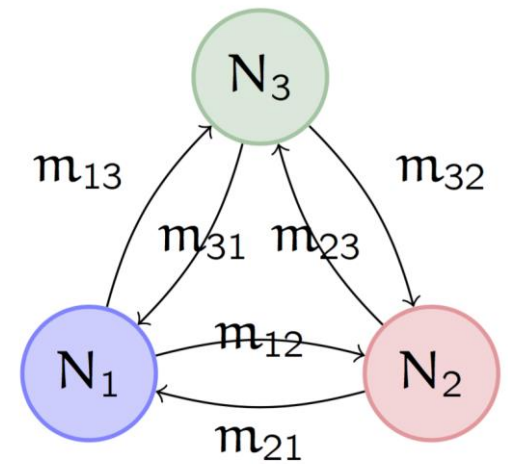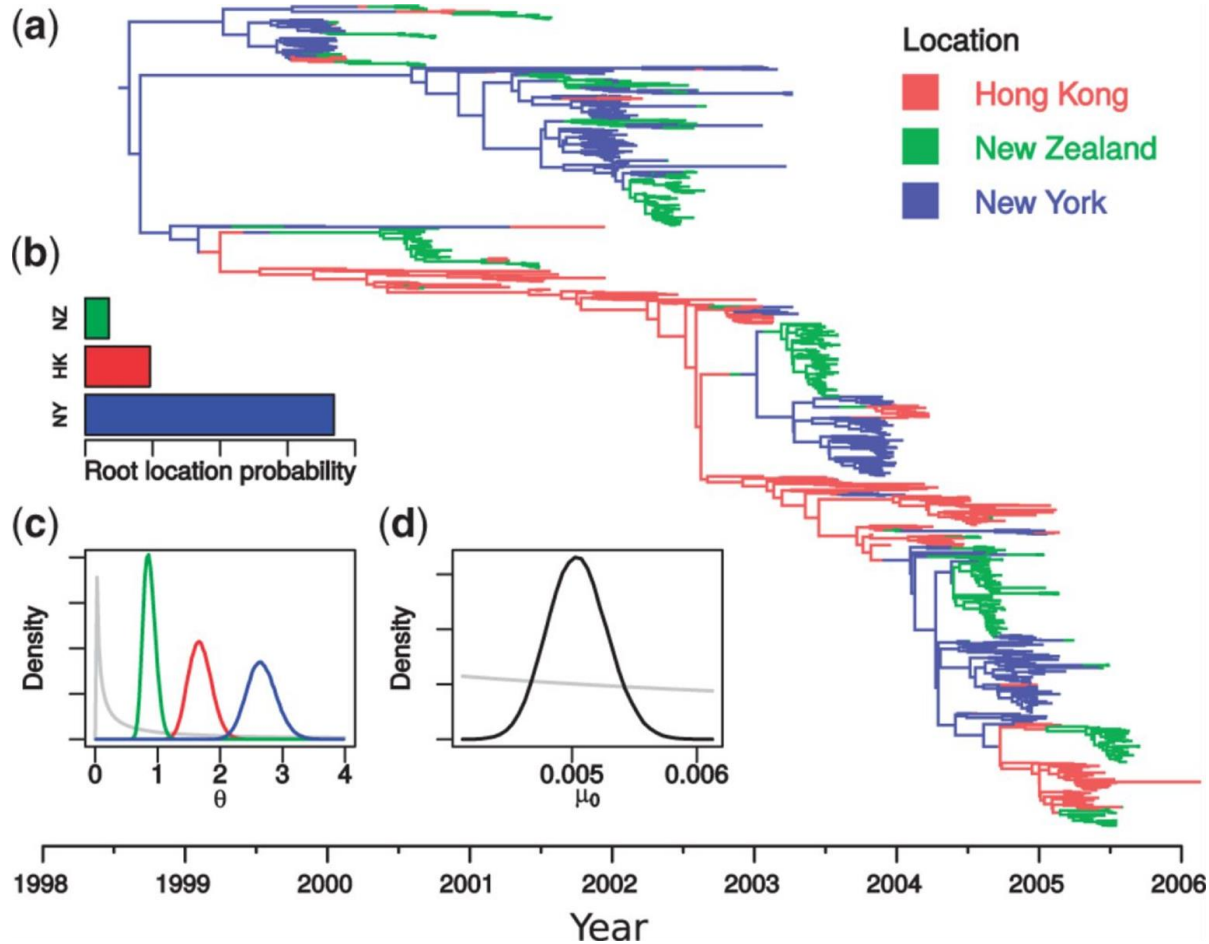

>15,000 scientific studies have used this software since 2007;
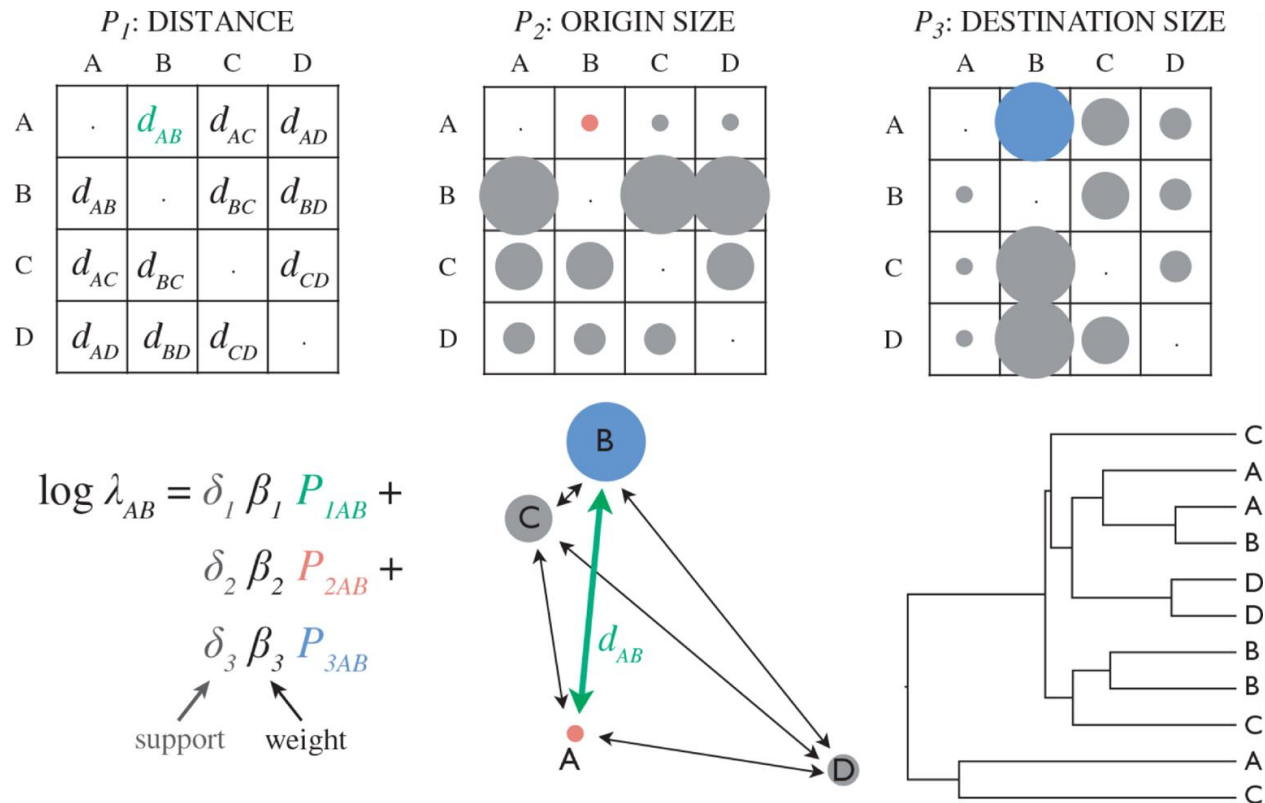> 2,500 studies this year alone (2017)

Evolution is happening right now!

2015   2016   2017

Structured coalescent model
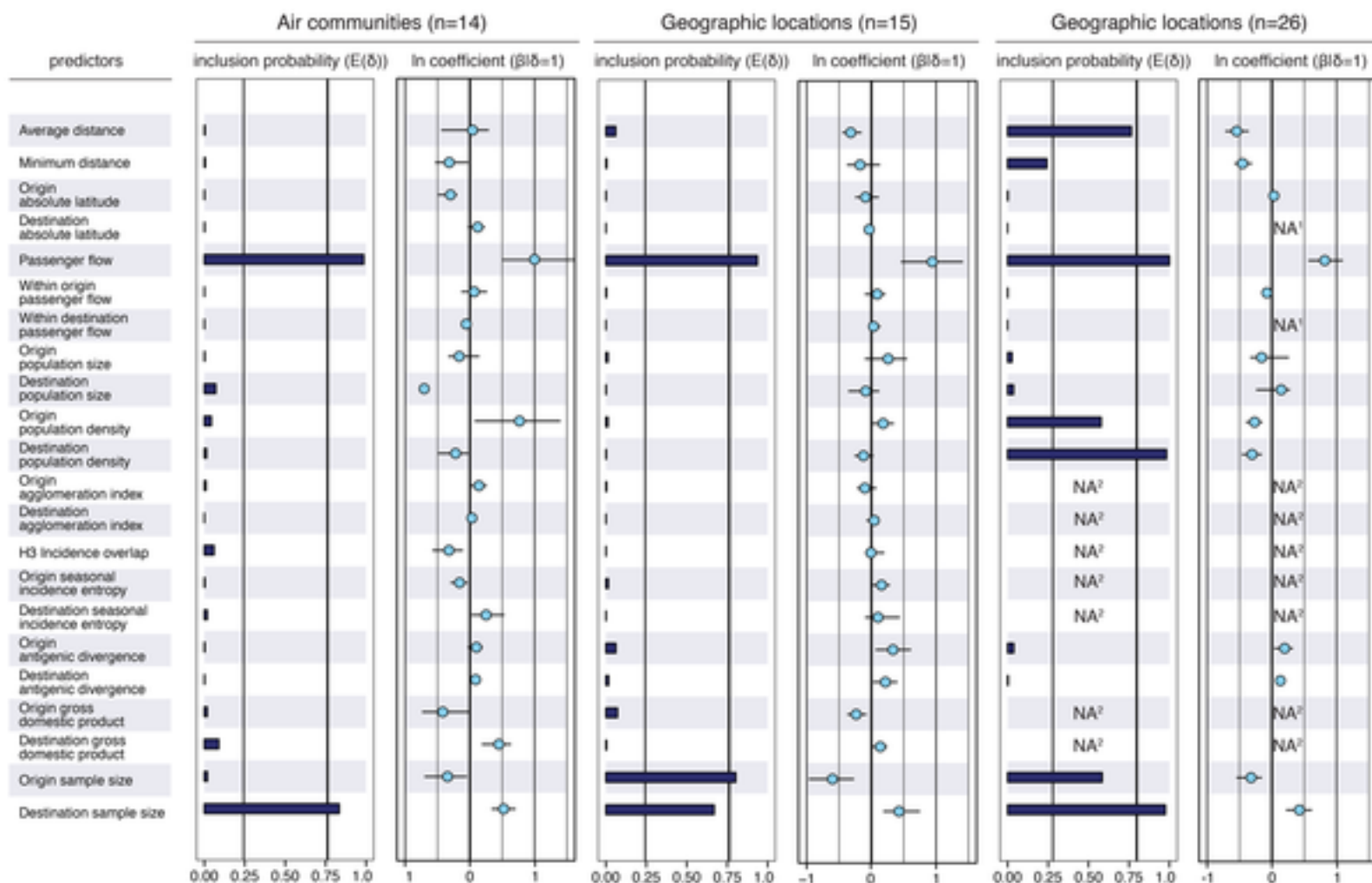
General linear models for molecular evolutionary data

Figure 2. Predictors of global H3N2 diffusion among the 14 air communities and the 15 & 26 geographic locations.
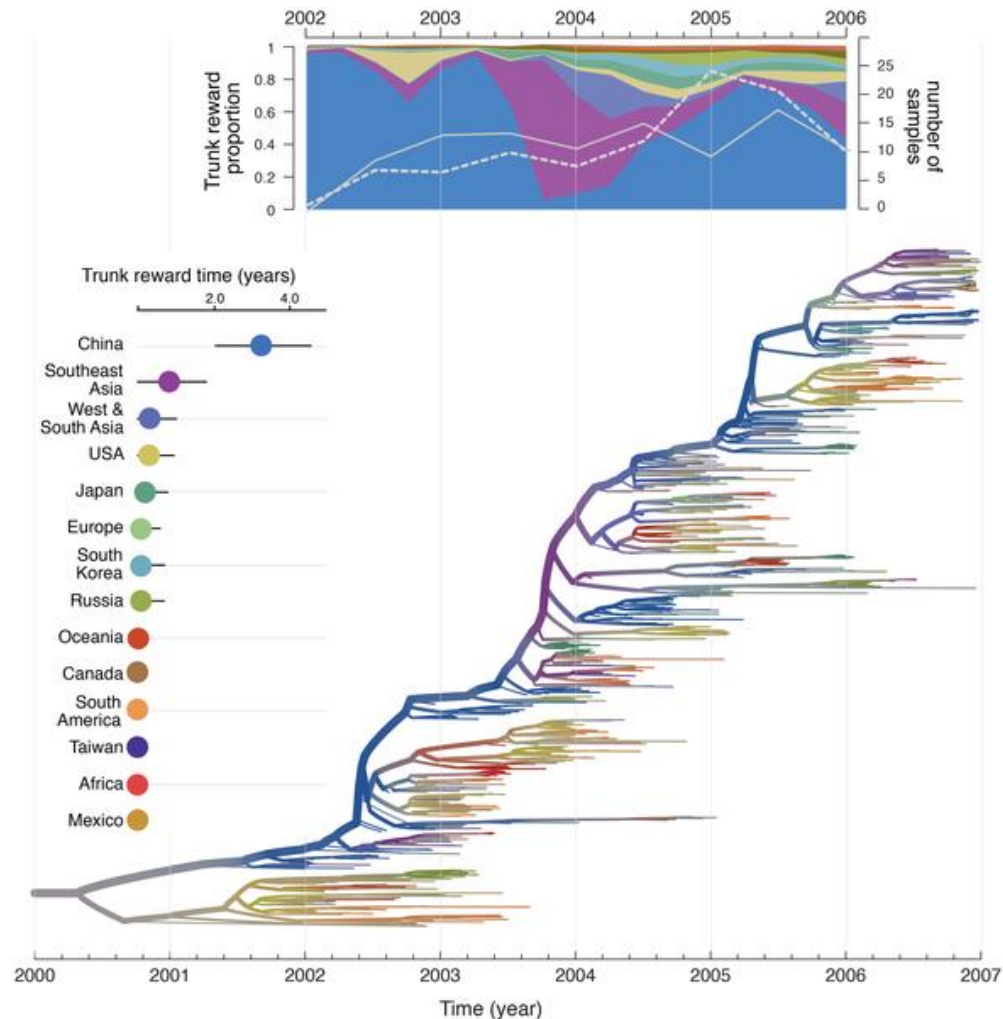
Lemey P, Rambaut A, Bedford T, Faria N, Bielejec F, et al. (2014) Unifying Viral Genetics and Human Transportation Data to Predict the Global Transmission Dynamics of Human Influenza H3N2. PLOS Pathogens 10(2): e1003932.
https://doi.org/10.1371/journal.ppat.1003932
http://journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1003932

Figure 3. Phylogeographic reconstruction and spatial history of the trunk lineage.

PLOS | PATHOGENS

Hypothesis

Poultry trade and poultry production will be predictive of the spatial population dynamics of avian influenza H9N2

Data

Global avian-origin H9N2 AIV full length HA genes:

        n: curated 647 sequences
        L: 1683 nucleotides
        (East Asia: 288; South Asia: 75; Southeast Asia: 23; West Asia: 149; Europe:34; North America:47; Africa: 31)

Asian avian-origin H9N2 AIV HA genes: Total: 535 sequences
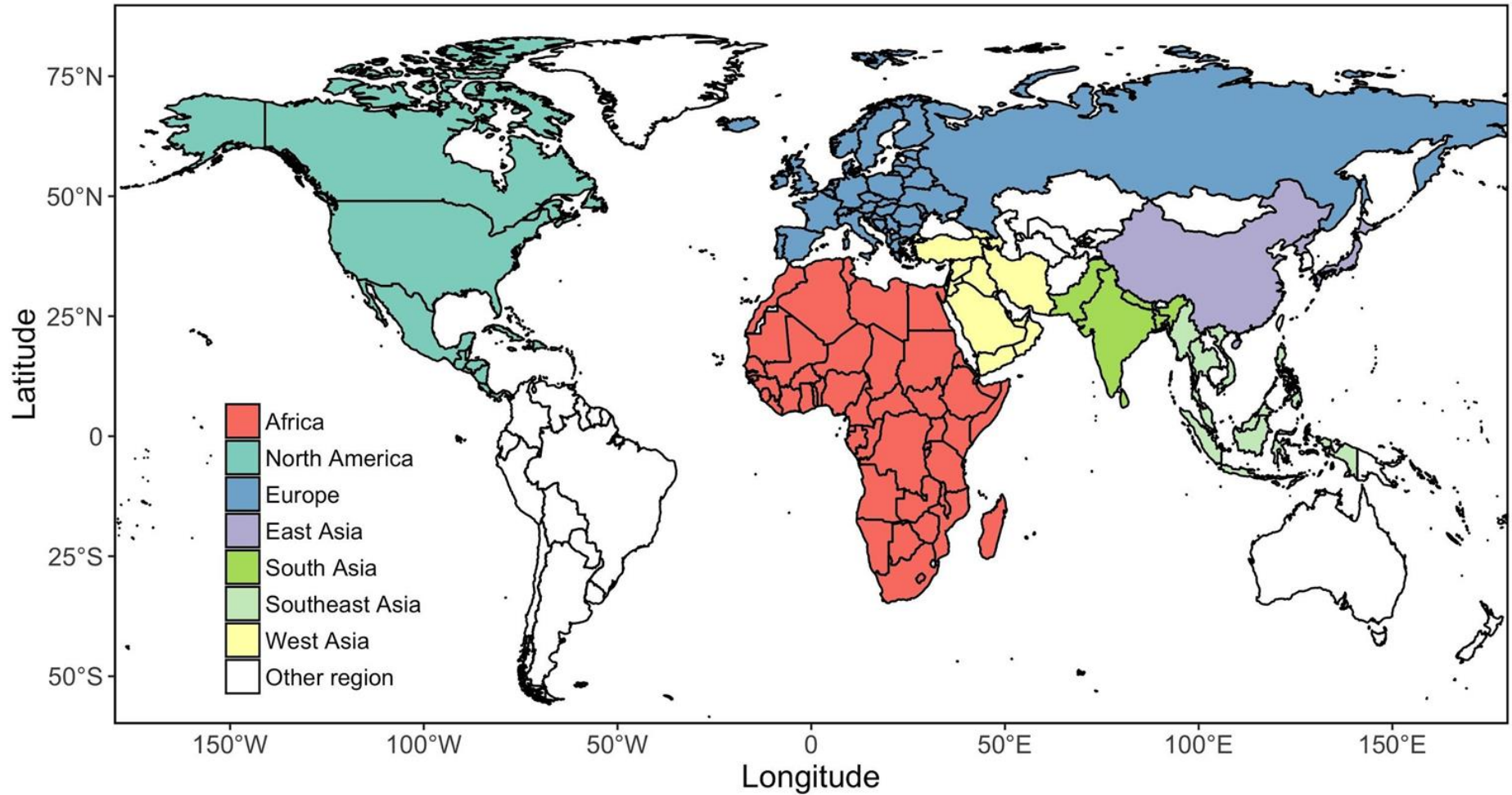
GenBank Influenza Virus Database
(http://www.ncbi.nlm.nih.gov/genomes/FLU/FLU.html)

Poultry production and trade data:

    Poultry production: 1986-2013
    Poultry trade: 1986-2013
    FAOSTAT (http://faostat3.fao.org)

Regions

Poultry trade around the world
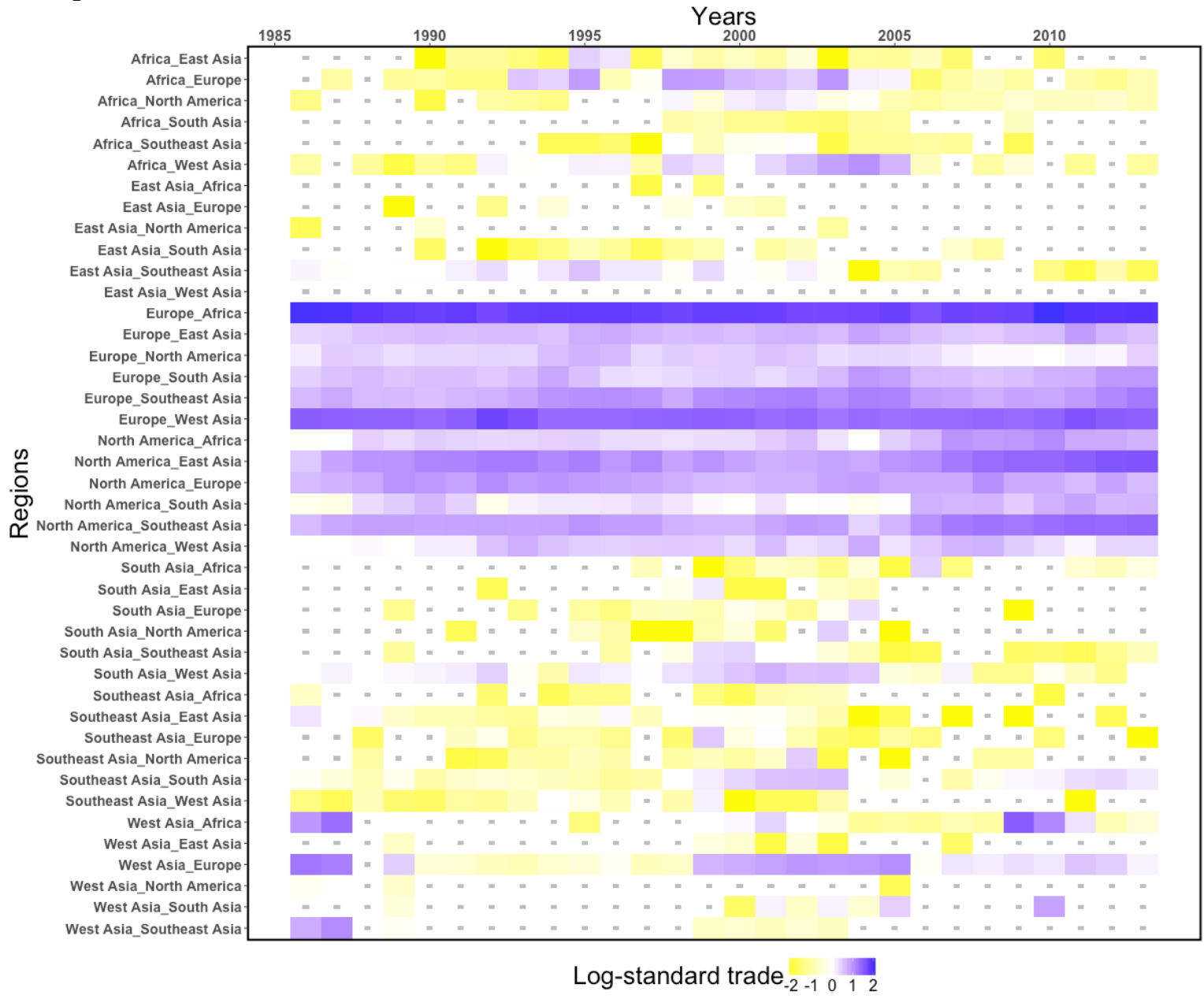
Poultry production around the world

average poultry trade over 28 years on global and asian scale.

Time-scaled tree of global

(Inferred by)

Poultry trade in Asia
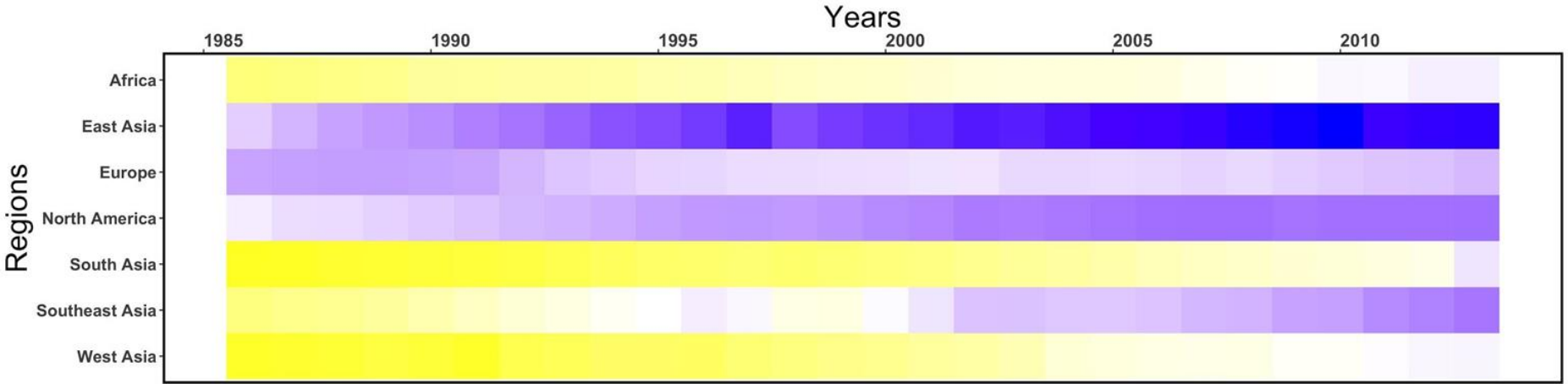
Log-standard trade

Log-standard production
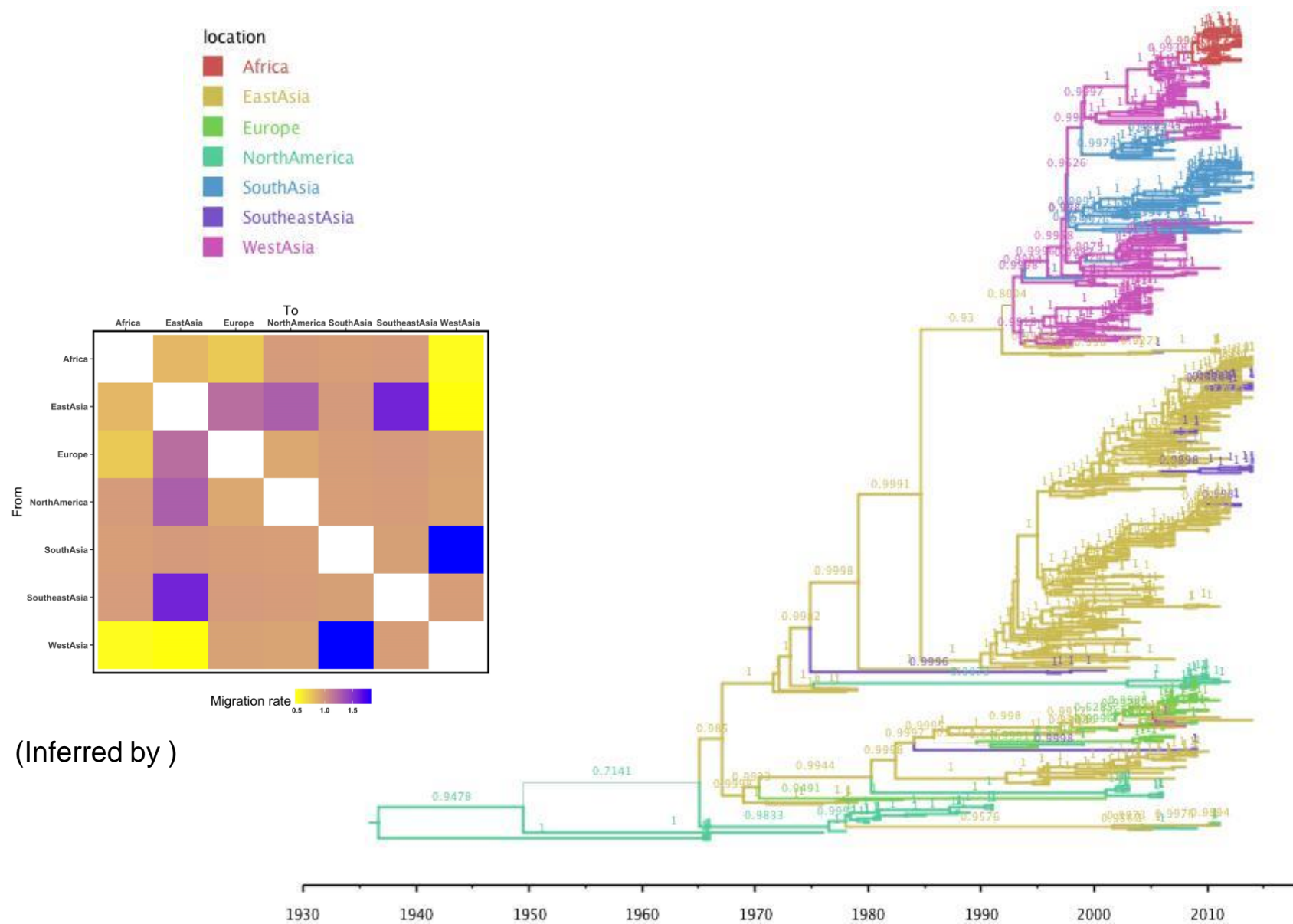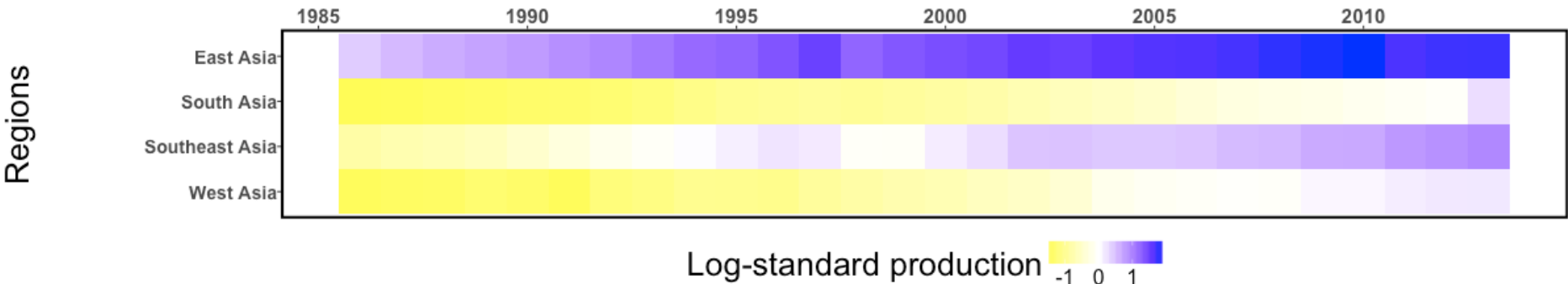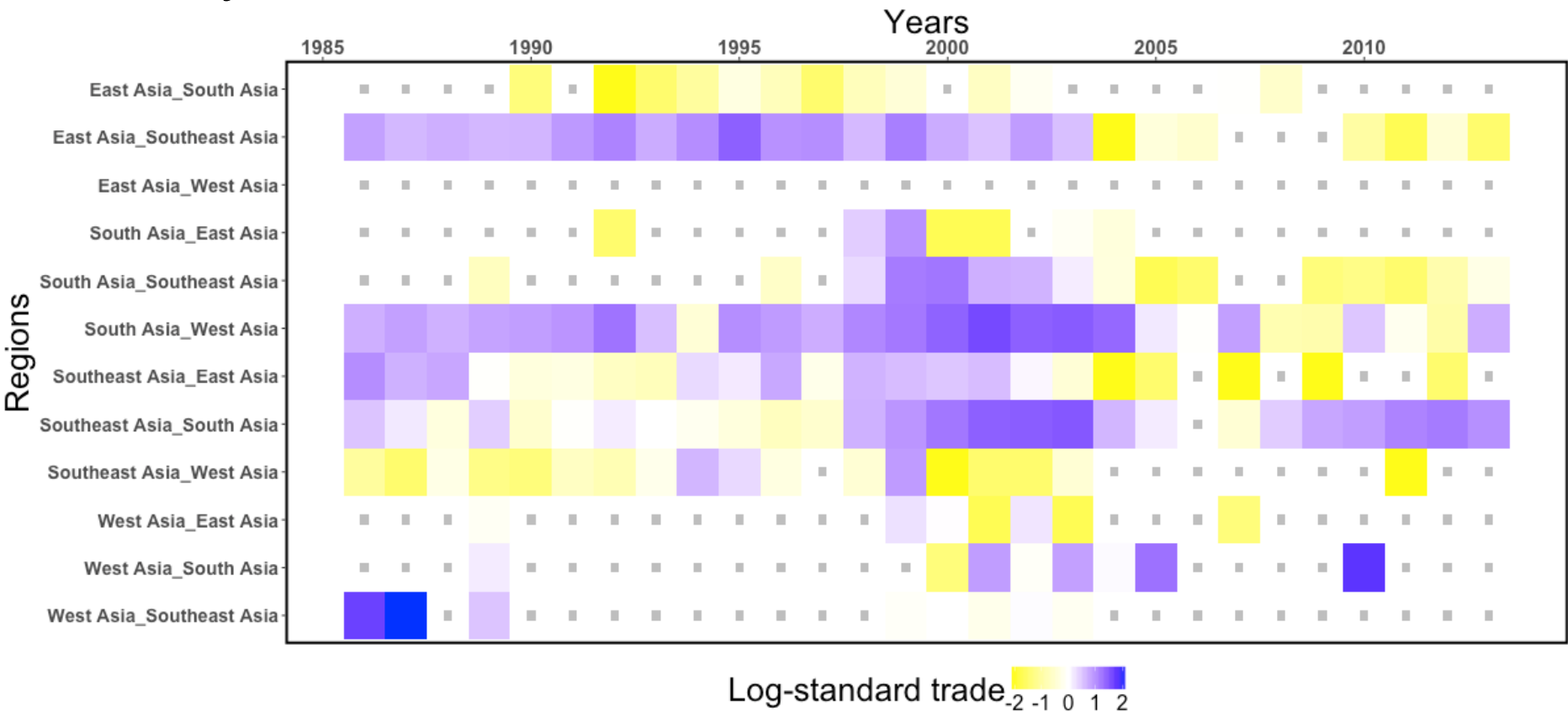
Time-scaled tree in Asia
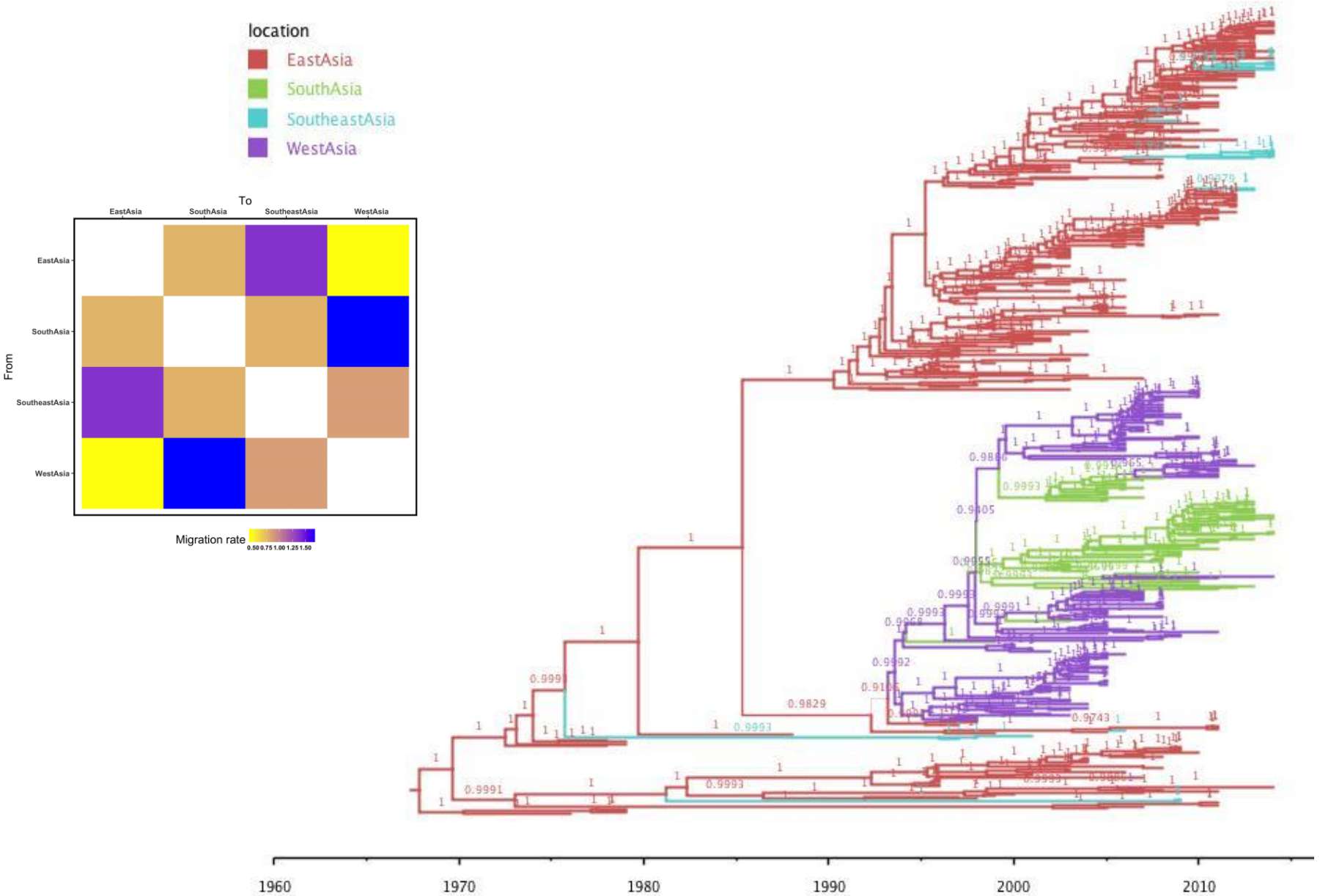
Statistical support for poultry trade as explanatory variable

Model	Asia	
	Poultry trade	Poultry production
No covariates / non-structured	No formal test	N/A
Time-averaged covariates / **non-structured** population model	++	N/A
Time-averaged covariates / **structured** population model	--	++
Full temporal covariates / **structured** population model	++	++

Conclusions

- There is weak direct statistical support for poultry trade as a driver for the spread of H9N2 avian influenza.

- Expanding the data set from 600 -> 4000 sequences will improve power but is computationally challenging

- Model granularity in time and space can have a decisive effect on hypothesis testing.

- New methods for molecular epidemiology will increasingly be characterized by data integration efforts.

- Integration of detailed covariate data with molecular epidemiological analyses will allow formal testing of drivers.