


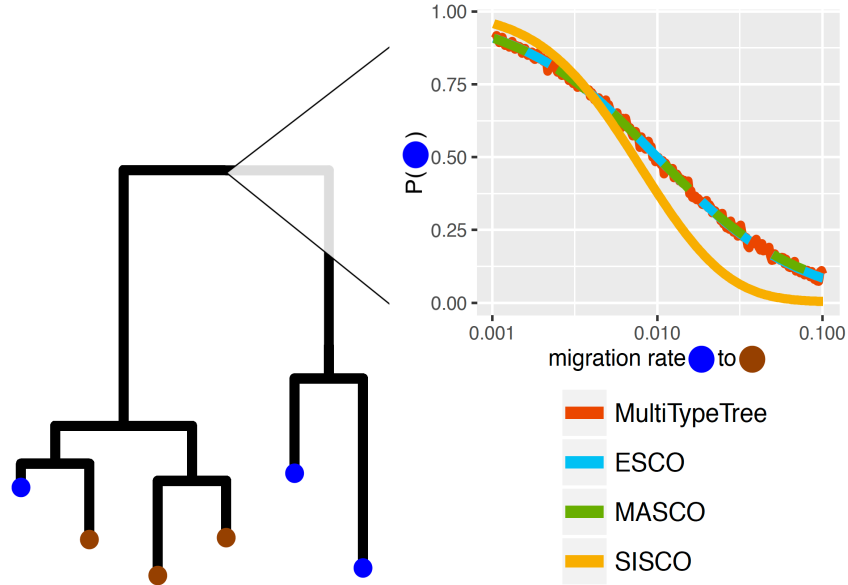
Viral genomic
epidemiology at
human-animal
interface

Debapriyo Chakraborty
Postdoc, Roche group

Viral genomic sequences: advantages

- Carries info on
 - spatial dynamics
 - changes in viral population size
 - immune selection
 - Increasingly cheaper and faster tech
 - For few viruses, already large data
- Links viral genetic variation changes to epidemiological and evolutionary change
- 

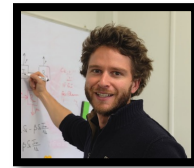
Phylogeography—tracking viral spatial spread



(Müller *et al.* 2017)

Phylogeography of HPAI H5N8 spread in French poultry

Chakraborty *et al.* 2022. *Transboundary and Emerging Diseases*

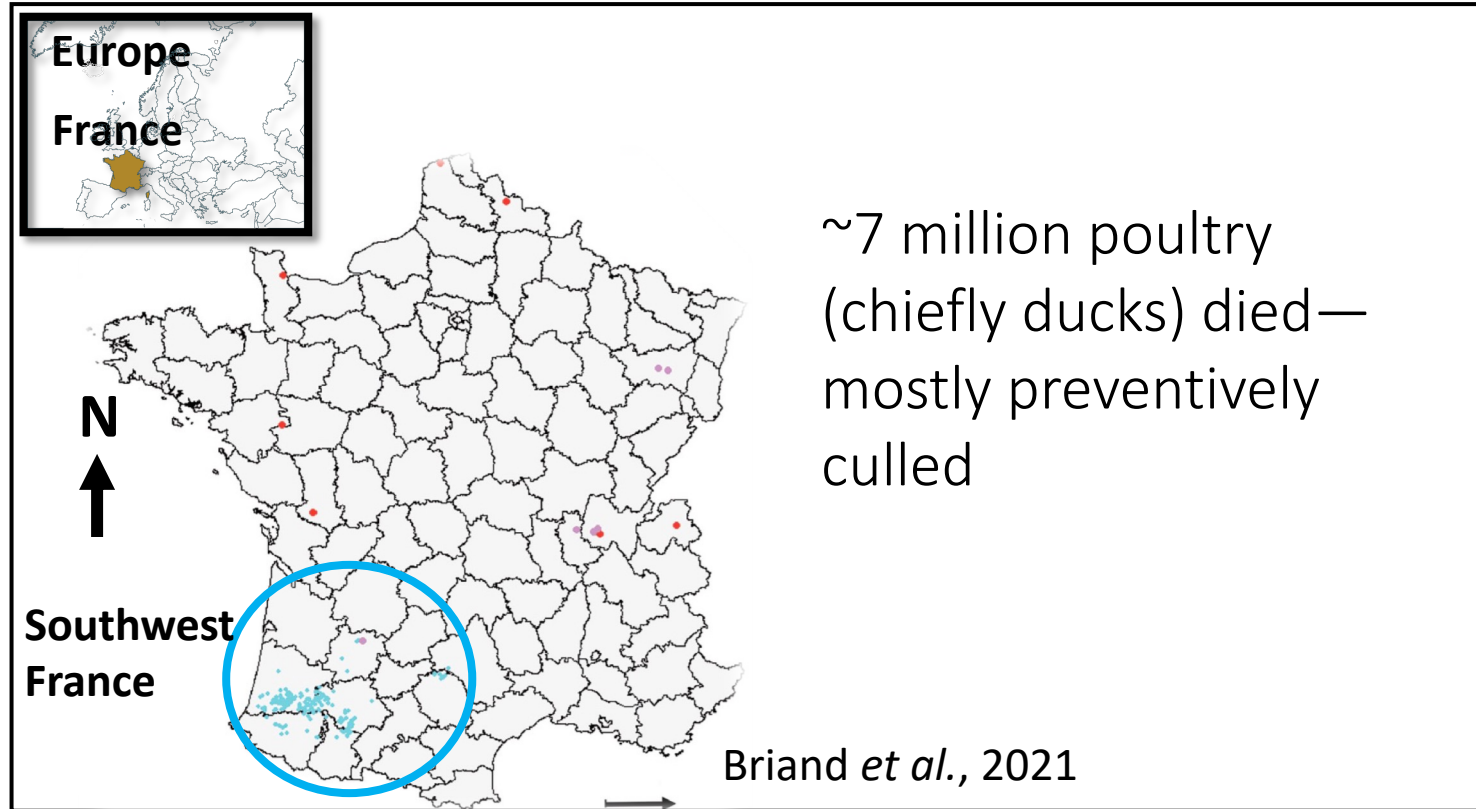


Timothée Vergne, IHAP, Toulouse



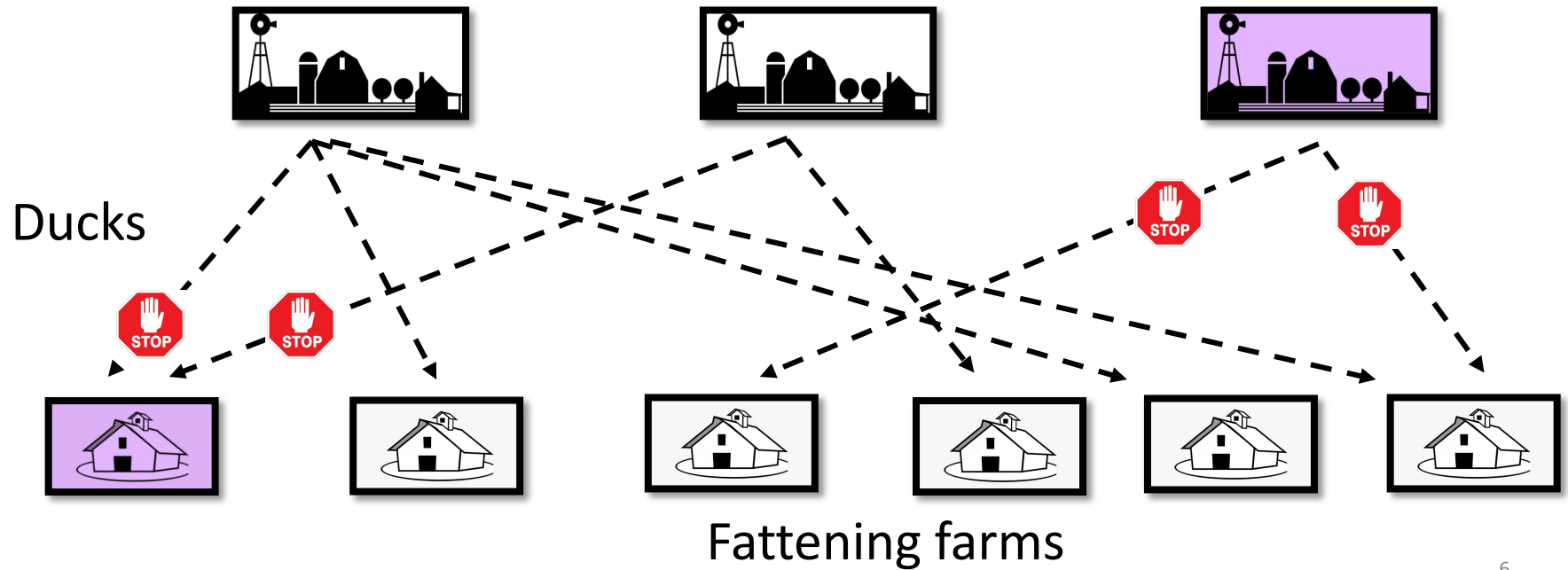
Mathilde Paul, IHAP, Toulouse

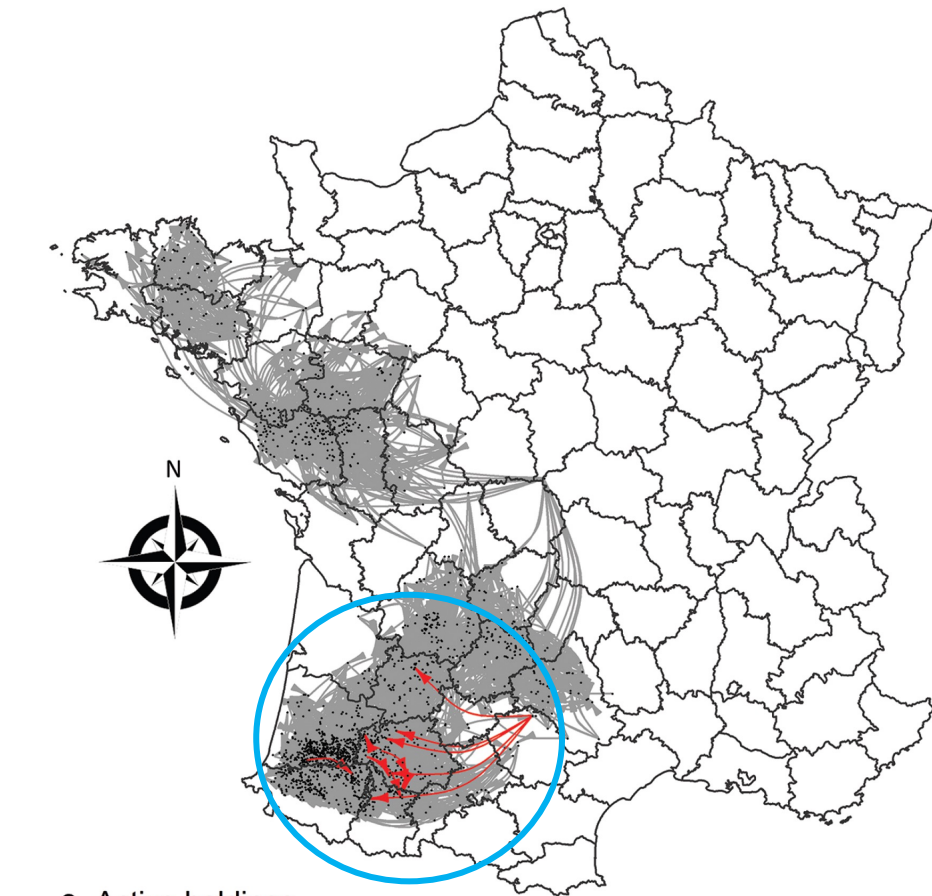
First major HPAI H5N8 epidemic in 2016-17



Duck movement and control measure to stop viral spread

Duck breeding farms





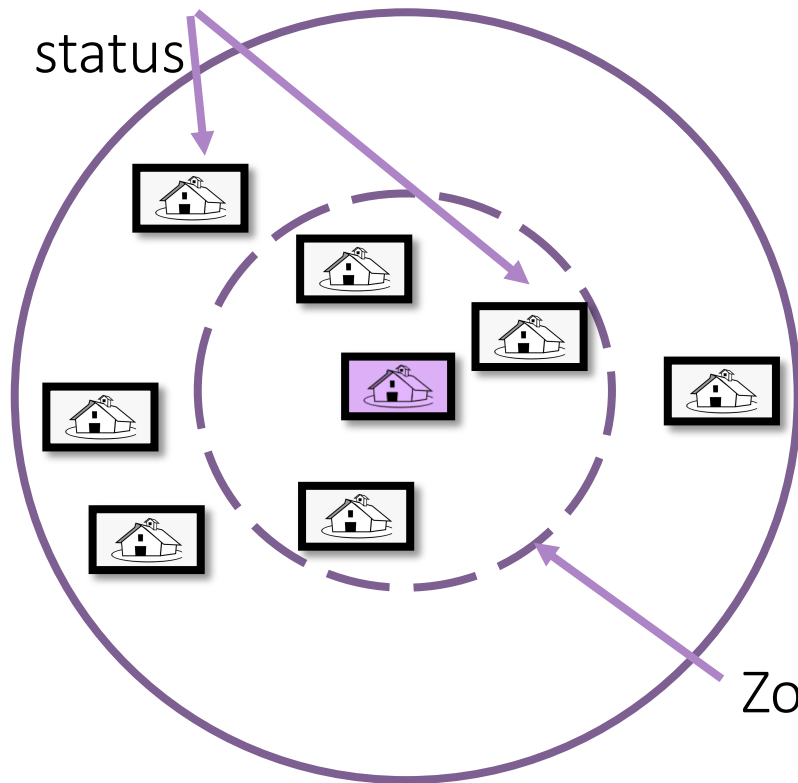
- Active holdings
- Movements of duck flocks between holdings
- At-risk movements of duck flocks between holdings

Movement network models:
HPAI H5N8 spread mainly by local transmission

Guinat *et al.*, 2020

Preventive culling (3 phases) of farms to stop viral spread

Unknown infection status

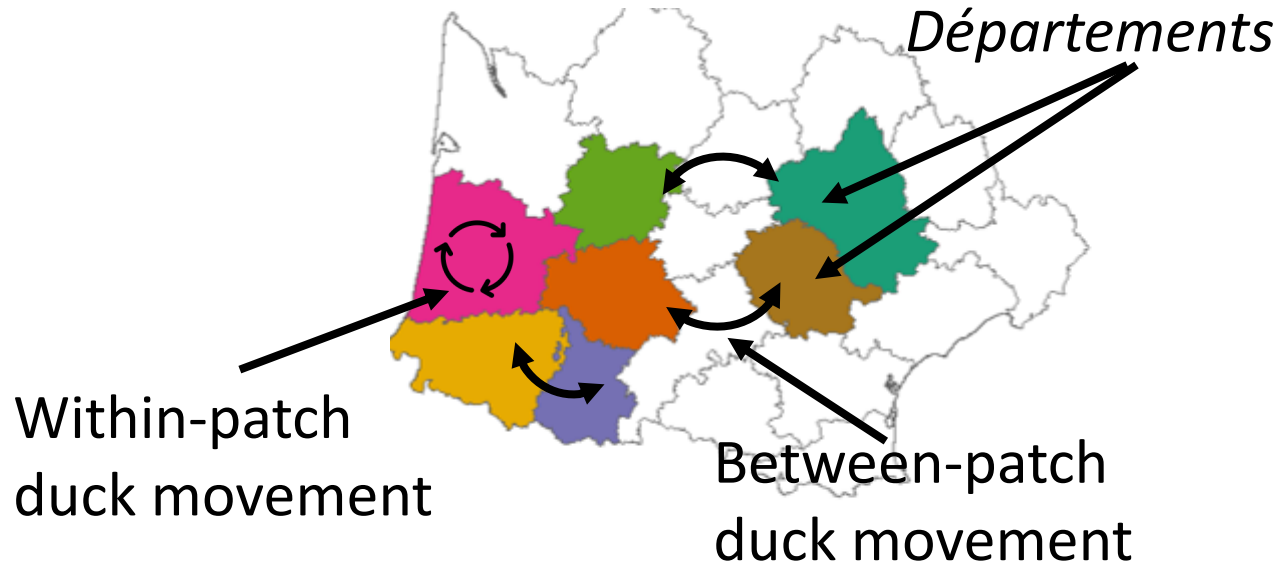


Epi simulations—modest impact of delay between detection and preventive culling

Andronico *et al.* 2019

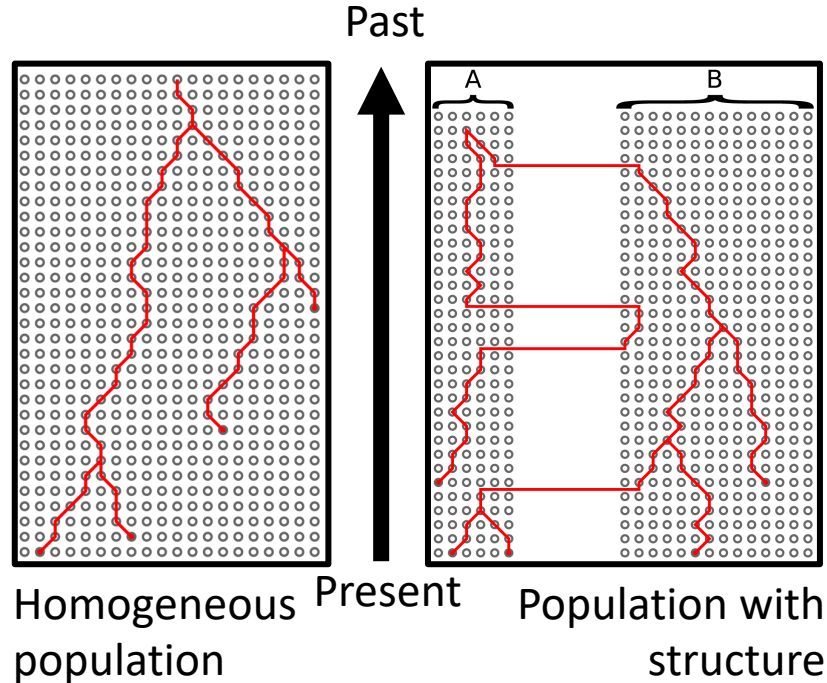
Did the control measures impact viral spread?

H5N8 spread spatial structure



Generalised island model

Structured coalescent = Tree prior



Inferred parameters:

Effective population size (N_e ; patch viral genetic variation)

Viral migration rates (m ; spread between patches)

Marginal approximation of the structured COalescenT (**MASCOT**)

- A recent approximation
- More efficient than exact inference
- Ne dynamic (piecewise constant) when predictor available
- Implemented in BEAST2

(Müller *et al.* 2017)

Hypothesis testing by data integration:

Use predictor data to inform temporal change across patches

m and $N_e \sim \text{Covariate 1} + \text{Covariate 2} + \dots$

(Müller *et al.* 2017, 2019)

Data

Genomic data—196 viral genomes
(one seq/farm) across seven
départements

Epi. and culling data—No. of
infected farms and their location

Livestock movement data—dates of
culling and number of duck
shipments within and between
départements

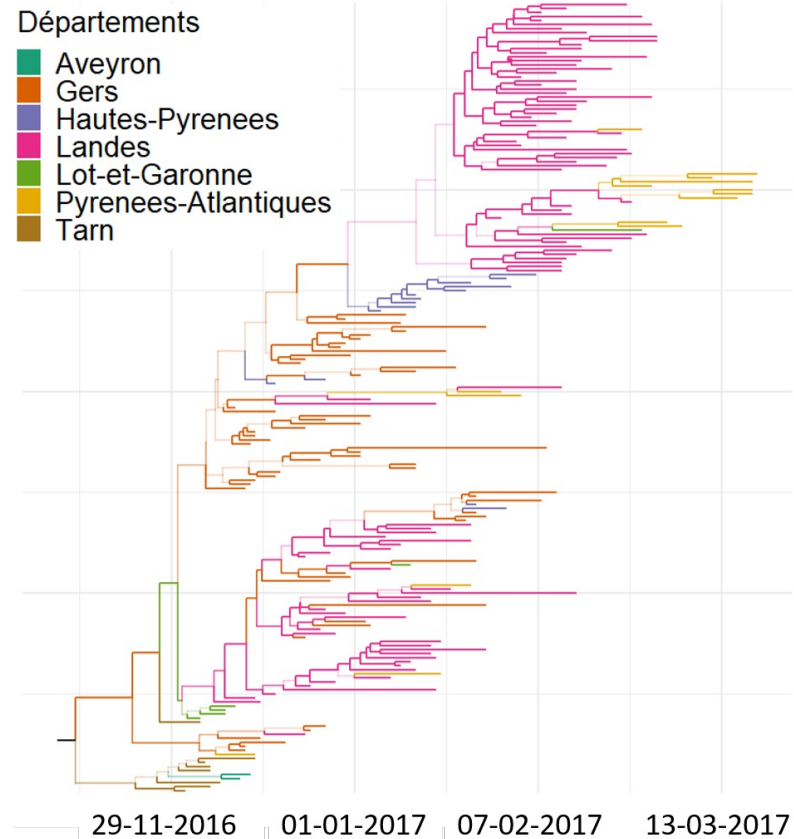


Virology lab, ANSES, Ploufragan

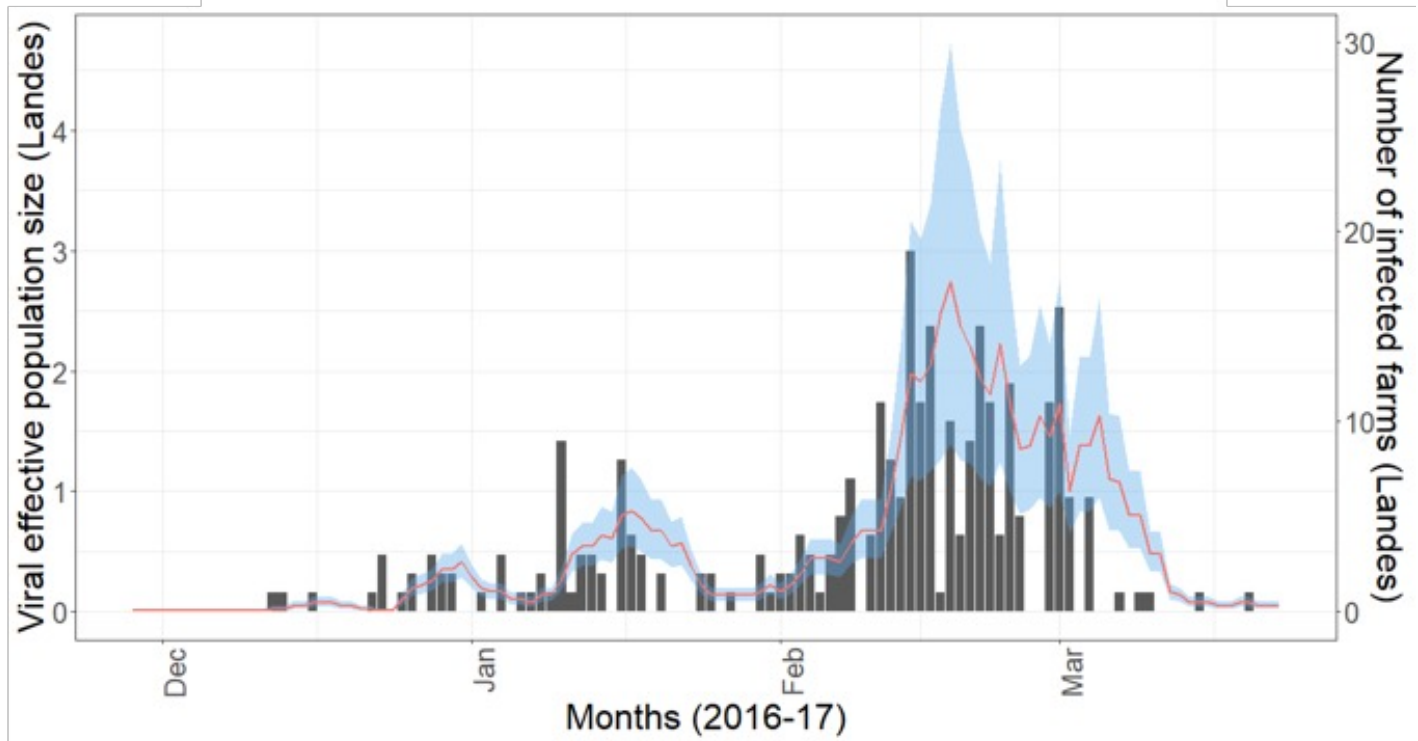


Claire Guinat
IHAP ENVT, Toulouse

Virus spread between neighbouring depts.

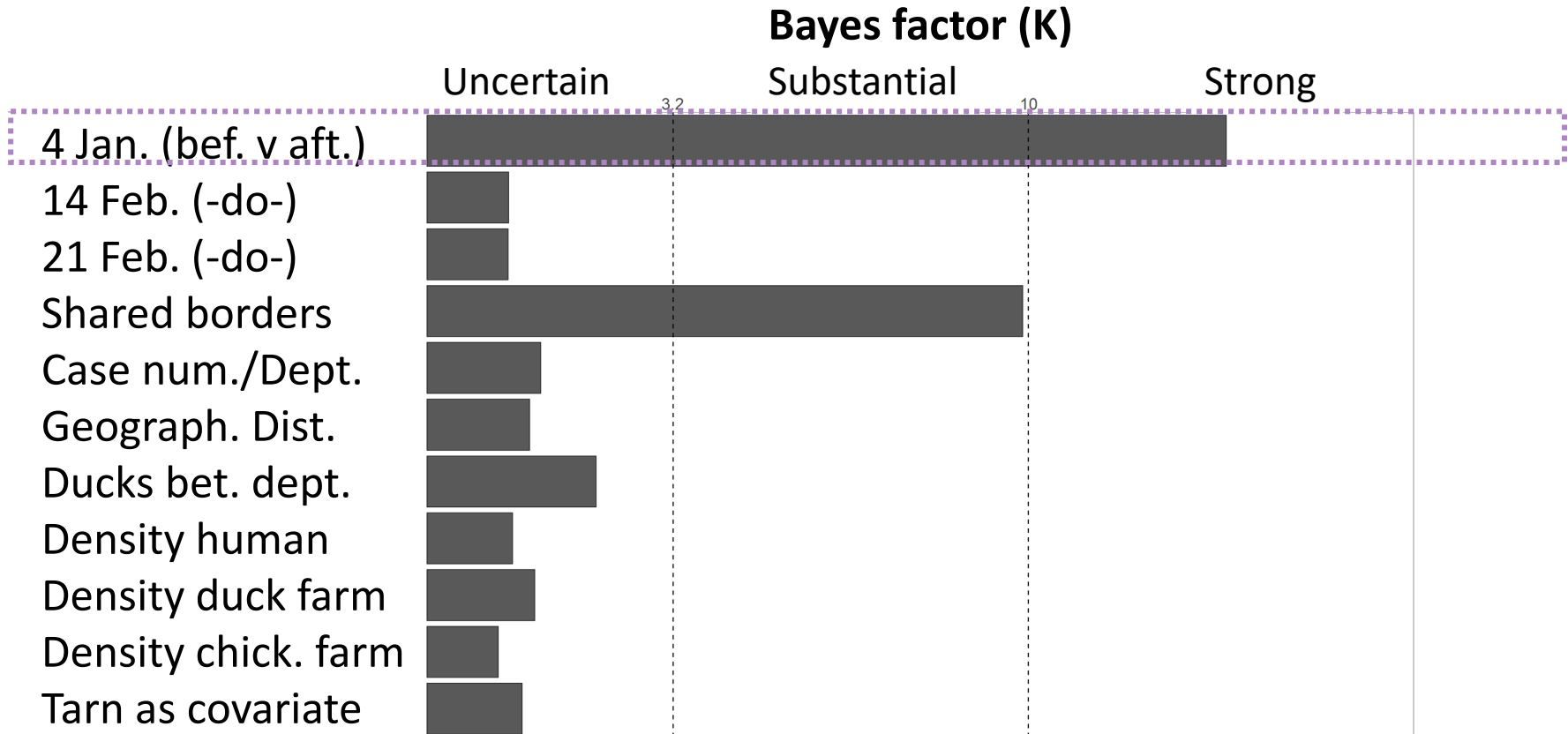


Ne tracks within-patch case count (Landes; as an example)

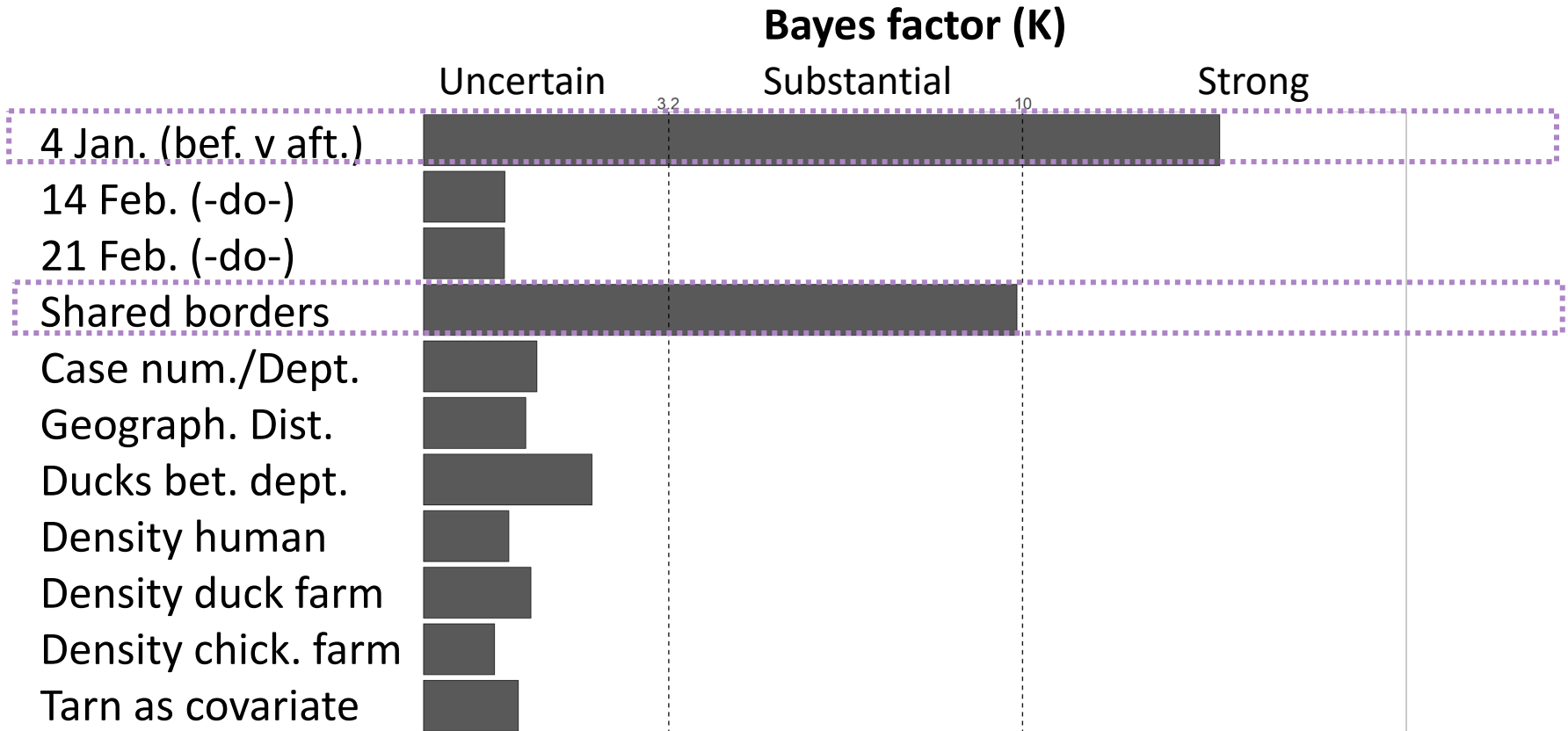


Hypothesis testing I — Predictors of viral migration rate

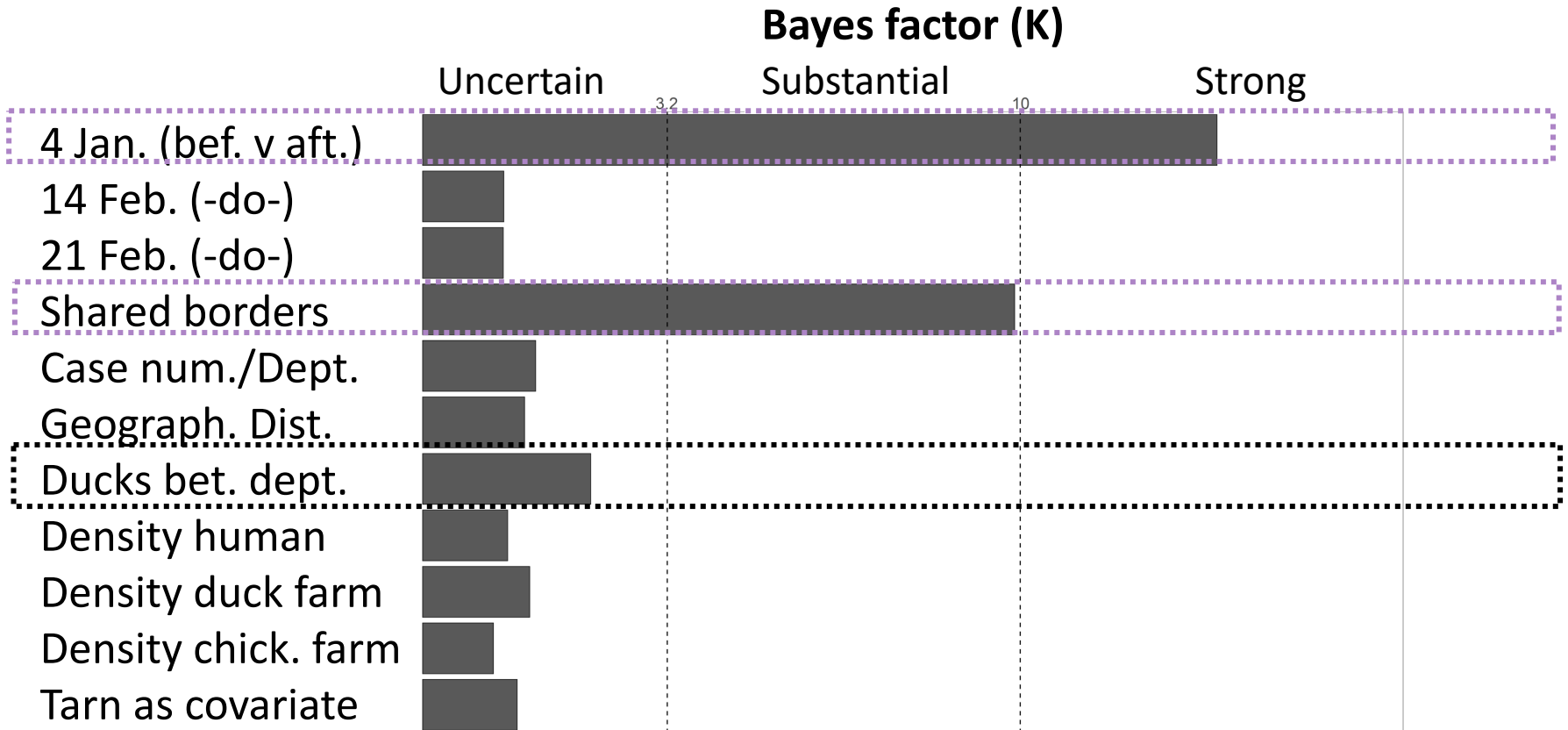
Viral spread reduced following preventive culling



Virus spread between adjacent departments

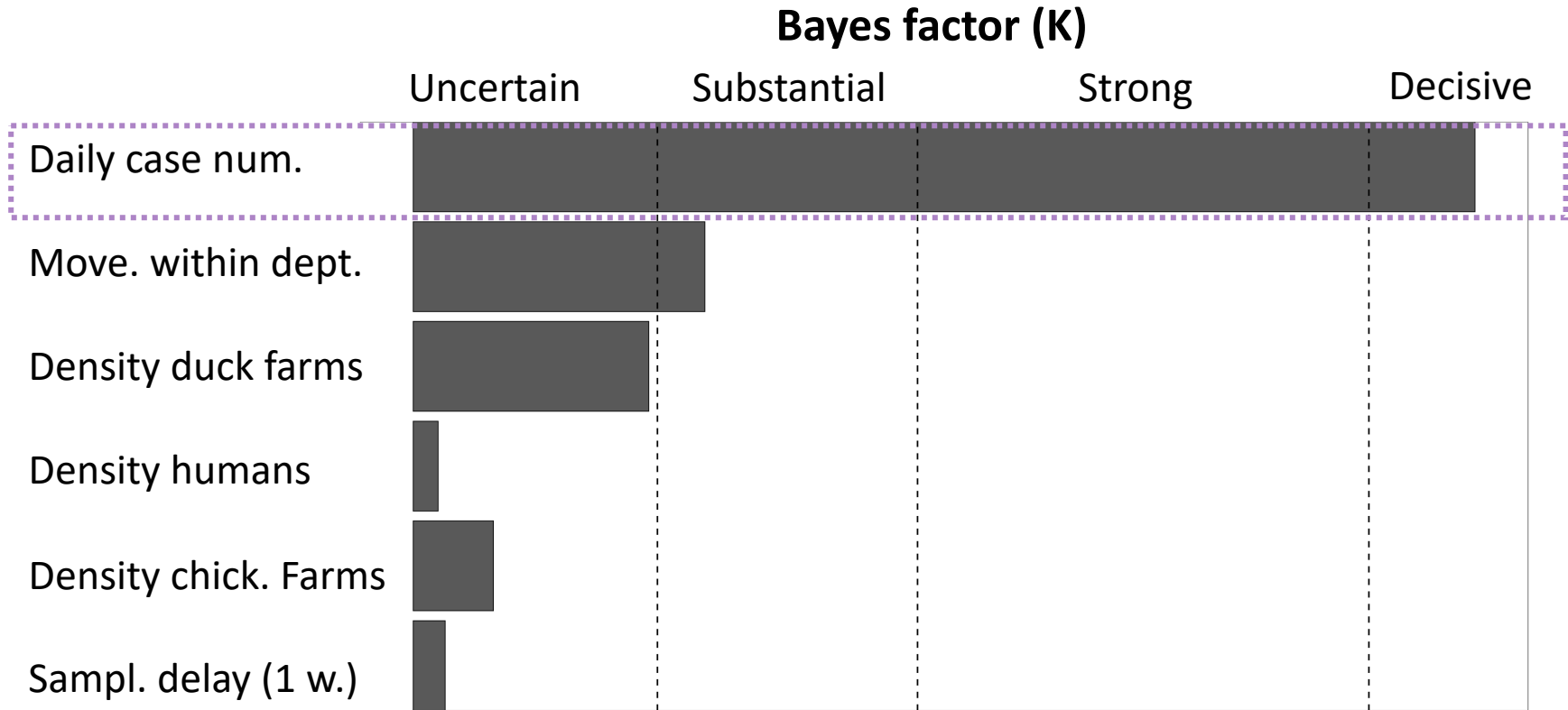


Virus spread not associated with duck movement



Hypothesis testing II —Predictors of viral Ne

Increased daily cases predicted increased N_e



Within *dept*, increased duck movement (weakly) increased epidemic size

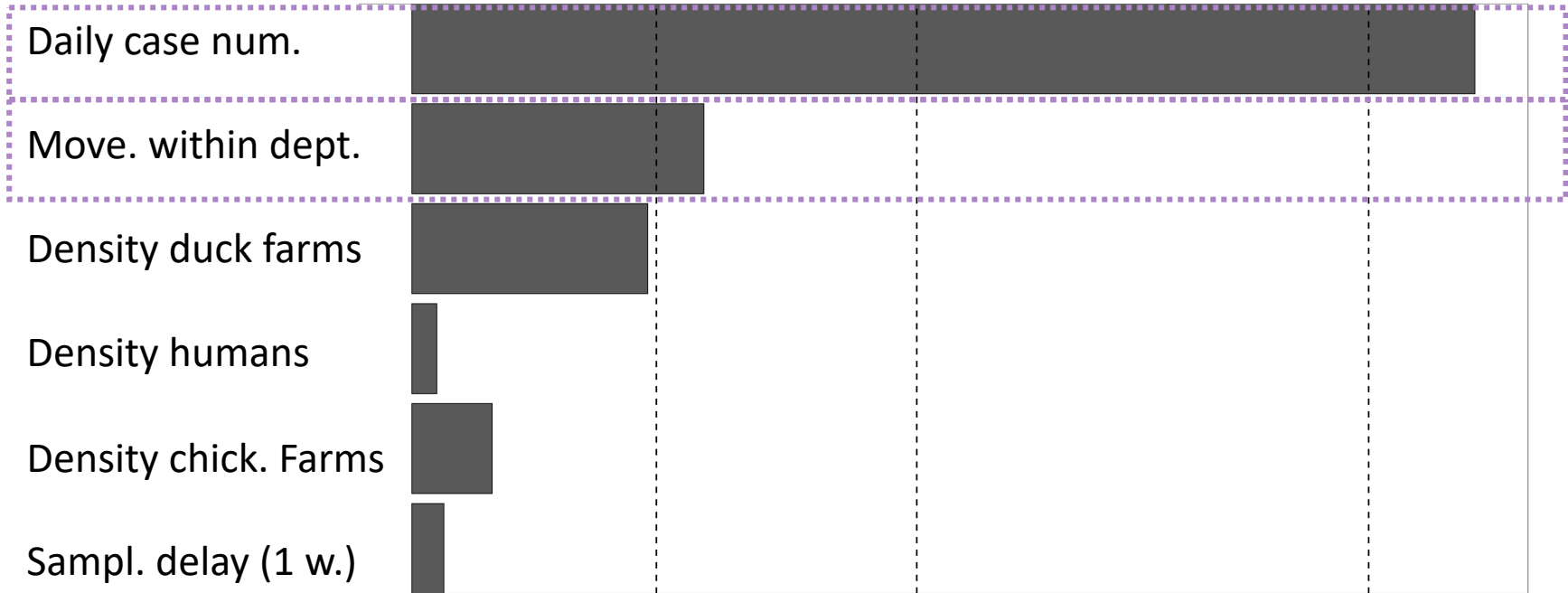
Bayes factor (K)

Uncertain

Substantial

Strong

Decisive

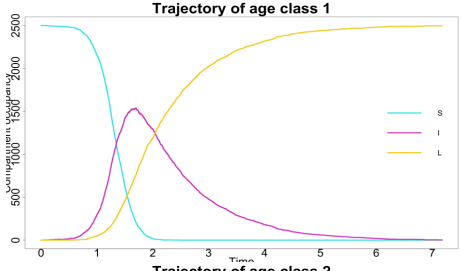
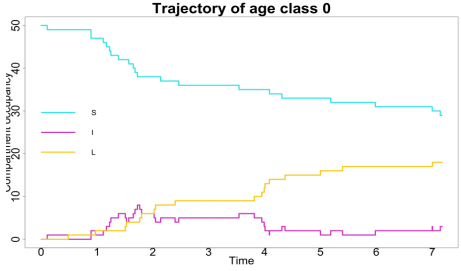


Major takeaways

- 1) Early preventive culling effective in slowing down between-patch spread
- 2) Duck movement increased spread locally (within-patch)
- 3) Virus spread across adjacent patches—but not by duck movement (Fomites? Wind?)
- 4) Farm density not linked to epidemic spread

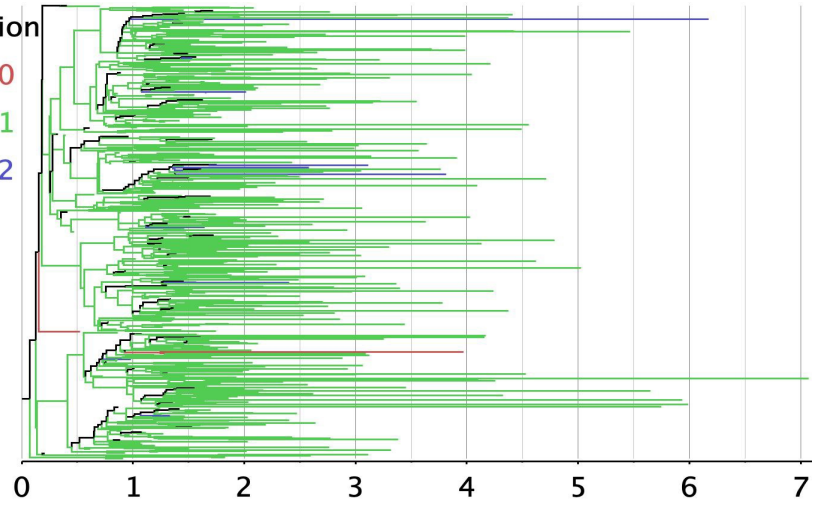
Current work at MIVEGEC

Simulation-based inference of transmission dynamics



location

- 0 (red)
- 1 (green)
- 2 (blue)



Population traj. of diff. sub-pops.

Phylogeny of lineages across sub-pops.

Thank you!



debapriyo.chakraborty@ird.fr



debapriyoc@gmail.com



@debapriyo81



<https://github.com/dc27708>