

Regional spread of BVDV

Contribution of between-herd trade movements & geographical proximity

Ezanno P., Qi L., Vergu E.

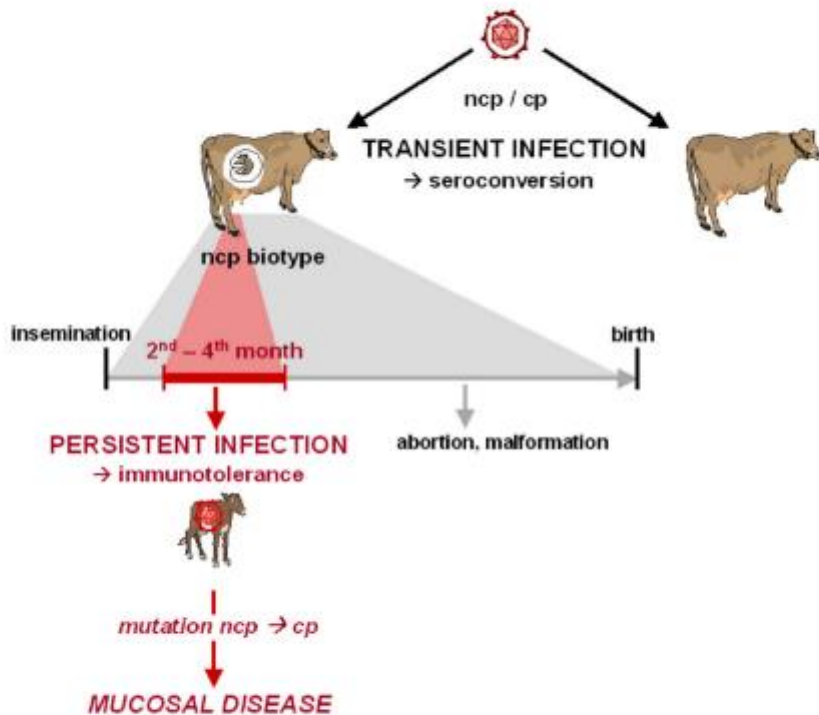
pauline.ezanno@oniris-nantes.fr



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Bovine Viral Diarrhea



- worldwide endemic disease
- welfare and productivity (reproduction, milk production,...)
- permanently infected (PI) animals (50% chance of dying per year)

Control strategies at herd level:

- vaccination
- test and cull of calves
- hygiene

Regional spread

- Trade movements
- Proximity contacts



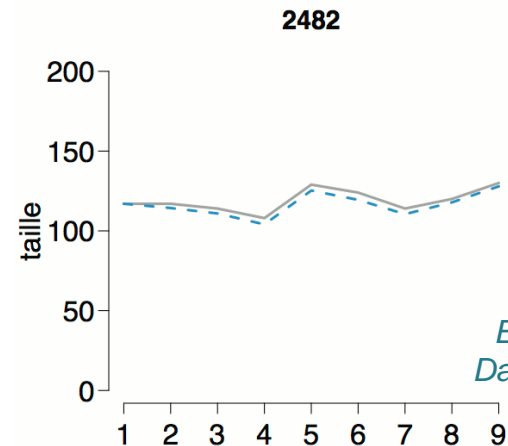
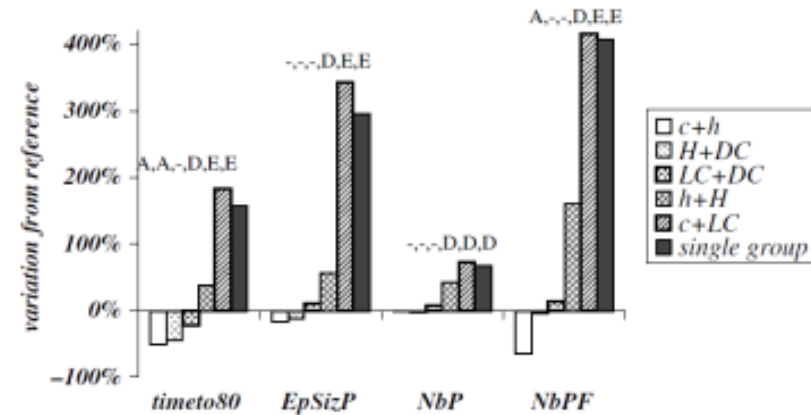
➔ **Fade-out at farm scale & regional control but still circulating: contribution of trade / proximity contacts?**

Peterhans E, Bachofen C, Stalder H, et al. Cytopathic bovine viral diarrhea viruses (BVDV): emerging pestiviruses doomed to extinction. Vet Res. 2010;41(6):44.

Flexible and realistic within-herd models

Coupling herd dynamics & BVDV transmission

- Vertical transmission & PI
- Horizontal transmission
- Contact structure & seasons
- Herd size, management & location calibrated on data (births, culling, etc per age per herd)



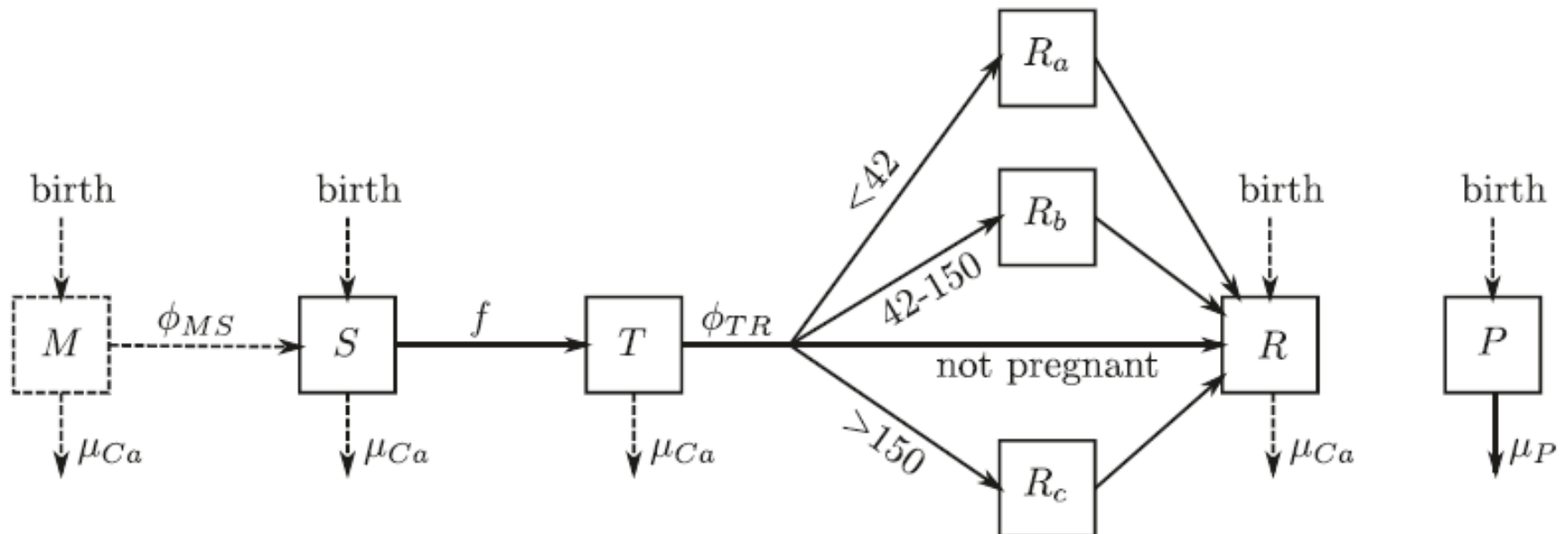
Viet et al., PVM 2004
Ezanno et al., PVM 2008
Ezanno et al., Vet Res 2009
Damman et al., Vet Res 2015
Qi et al., Epidemics subm.

Flexible and realistic within-herd models

Health states

Horizontal transmission in groupe g

$$p_{\text{inf}}^{\text{herd}}(g, t) = \beta_w^P \frac{P(g, t)}{N(g, t)} + \beta_w^T \frac{T(g, t)}{N(g, t)} + \sum_{a \neq g} \beta_b^P \frac{P(a, t)}{N(a, t)N(g, t)}$$



A data-based regional model

Couples within dairy herd dynamics through observed trade movements & proximity contacts

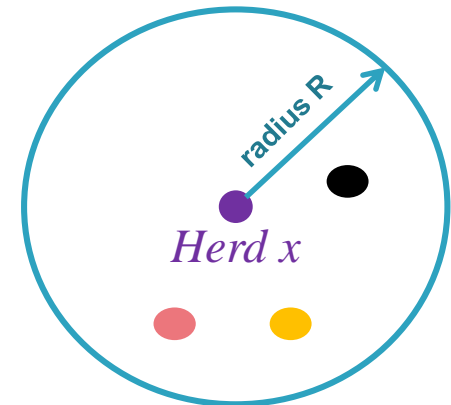
Trade movements

- Date, source, destination, age → data
- Infection → $f(\text{prevalence in source herd})$

Proximity contacts

$$p_{inf}^{neigh}(g, t) = \frac{\beta_{BN}^P}{N(g, t)} \frac{PI \text{ animals in neighborhood}}{\text{Total animals in neighbourhood}}$$

$$prob_{inf}(g, t) = 1 - e^{-\Delta \{p_{inf}^{herd}(g, t) + p_{inf}^{neigh}(g, t)\}}$$

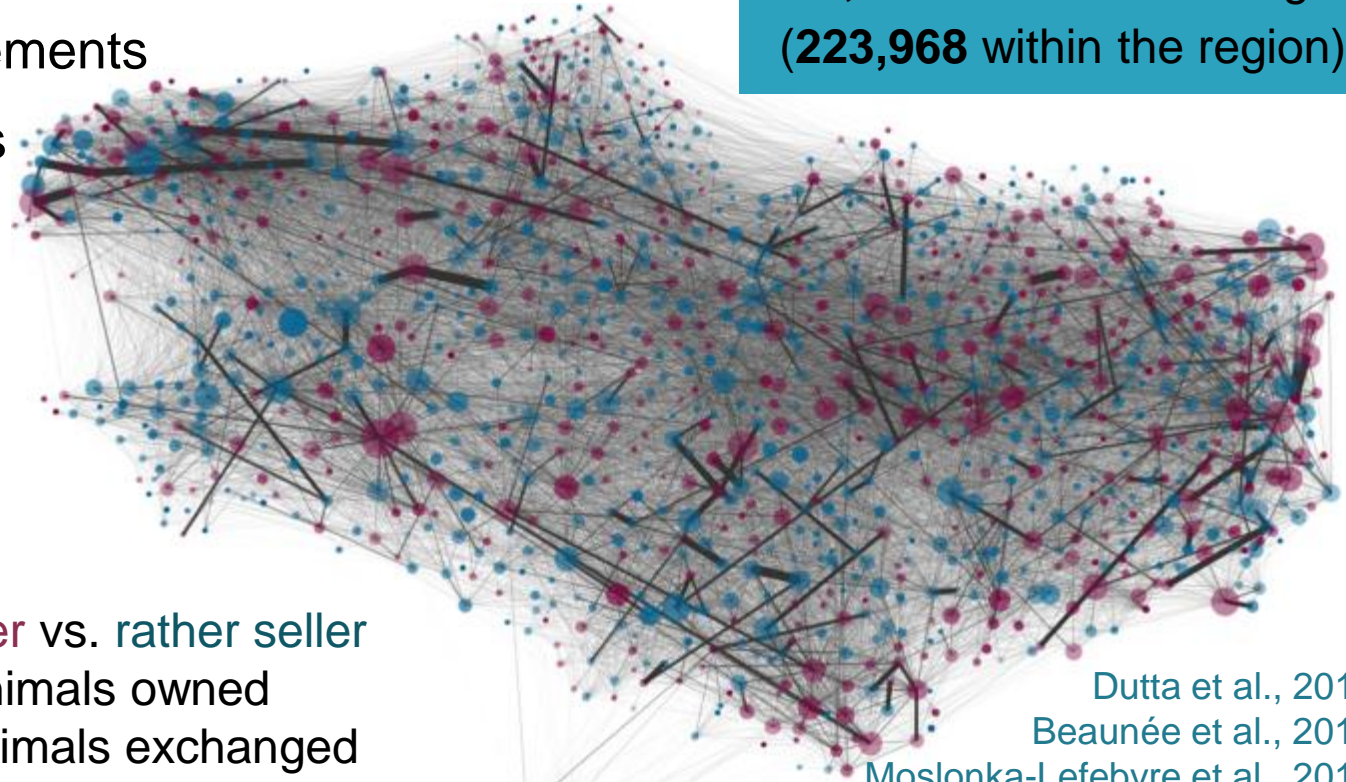
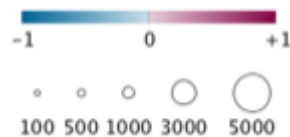


Neighbors of herd x

Cattle trade movement data & herd location

- French cattle identification database
 - ID, type & age of animals exchanged
 - ID and type of holdings in contact
 - Date of movements
 - Town borders

Brittany (France)
2005-2013
12,857 active farms
919,304 animals exchanged
(223,968 within the region)



Nodes = rather buyer vs. rather seller
Size ~ number of animals owned
Link ~ number of animals exchanged

Dutta et al., 2014
Beaunée et al., 2015
Moslonka-Lefebvre et al., 2016

Simulation setting

Parameters

- ^a Calibrated using data
- ^b Experts knowledge
- ^c Publications
- ^d Assumptions

	Description	Value	Ref.
$r^*(g)$	Outgoing rate per age group:death, consumption, cull		a
rb	Birth rate per age group per year		a
rs	Sex-ratio	0.5	b
rm	rate of mortality of PI animals	0.026	c
rmPI	rate of mortality of PI calves at birth:	0.01	c
β_W^P	Within-group transmission rate for PI animals	0.5	c
β_W^T	Within-group transmission rate for T Ianimals	0.03	c
β_B^P	Between-group transmission rate for PI animals	0.1	d
β_B^T	Between-group transmission rate for T Ianimals	0	d
β_{BN}^P	Between-neighbor transmission rate for PI animals	0,03	d
R	Neighborhood circle radius	2km	d

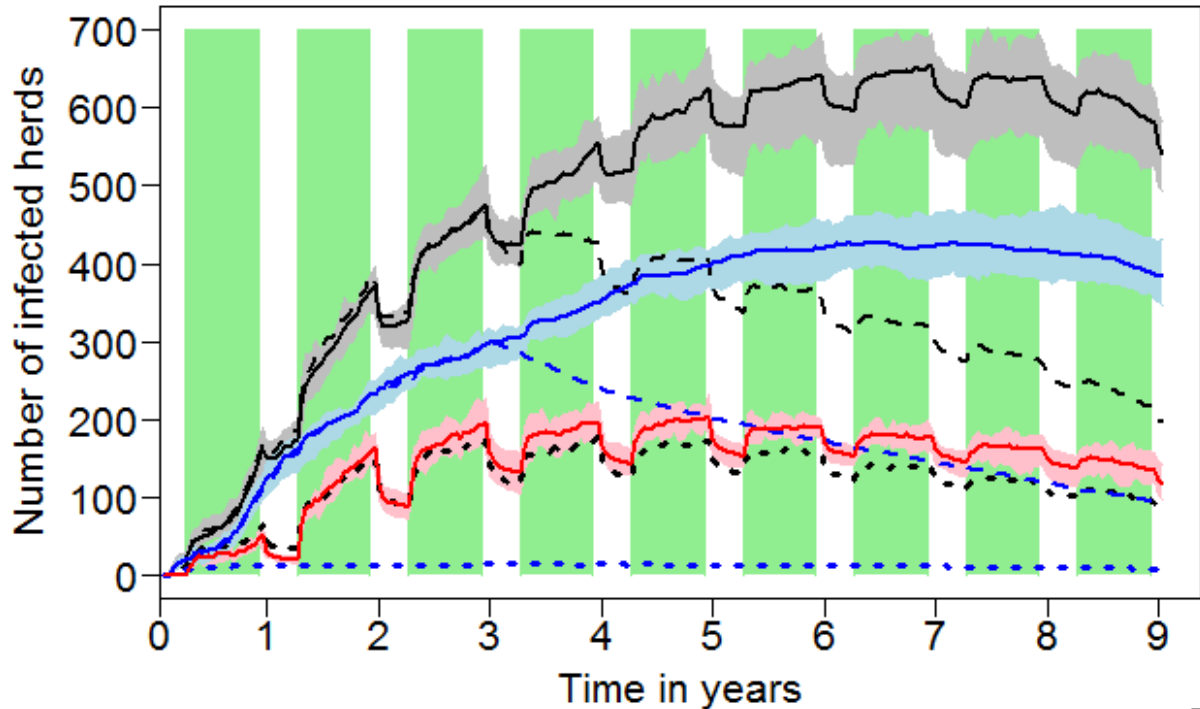
Simulated farms

- Herds active over 9 years (2005-13), ≥ 10 heifers + cows \rightarrow 12,750 herds

Initial conditions : 2 situations

- 10% randomly chosen farms, each with 1 PI cow, all others free
- Endemic situation (i.e. 9 years after the previous case)

BVDV spread at a regional scale

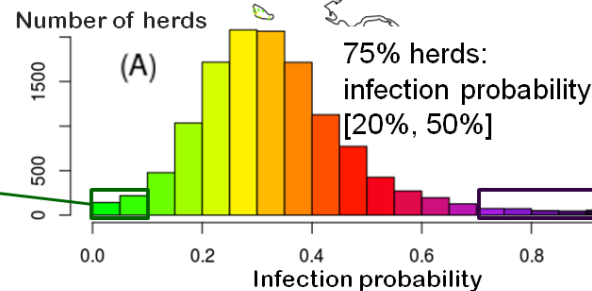
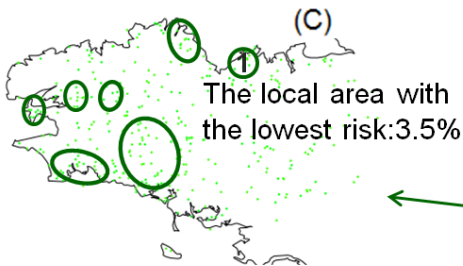
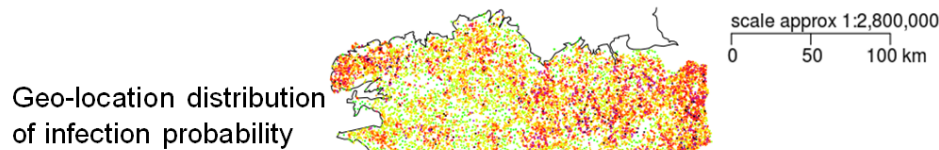


- NB and MV both increase infected herds in the metapopulation
- Perfect test & cull of traded PIs NOT enough to eradicate BVDV

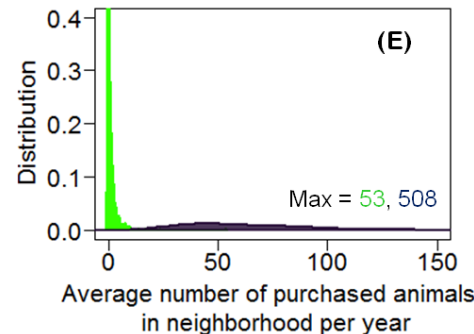
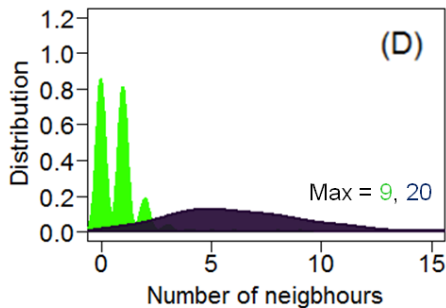
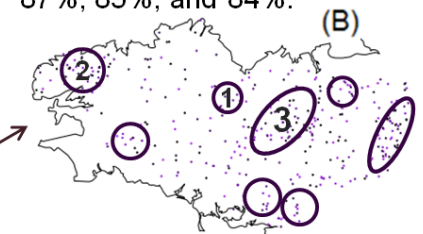
- - - Control starts at the end of the 3rd year
 Control starts at the beginning of the 1st year

— NB+MV
 — NB
 — MV

Herd infection probability: spatial distribution & contribution of NB and MV

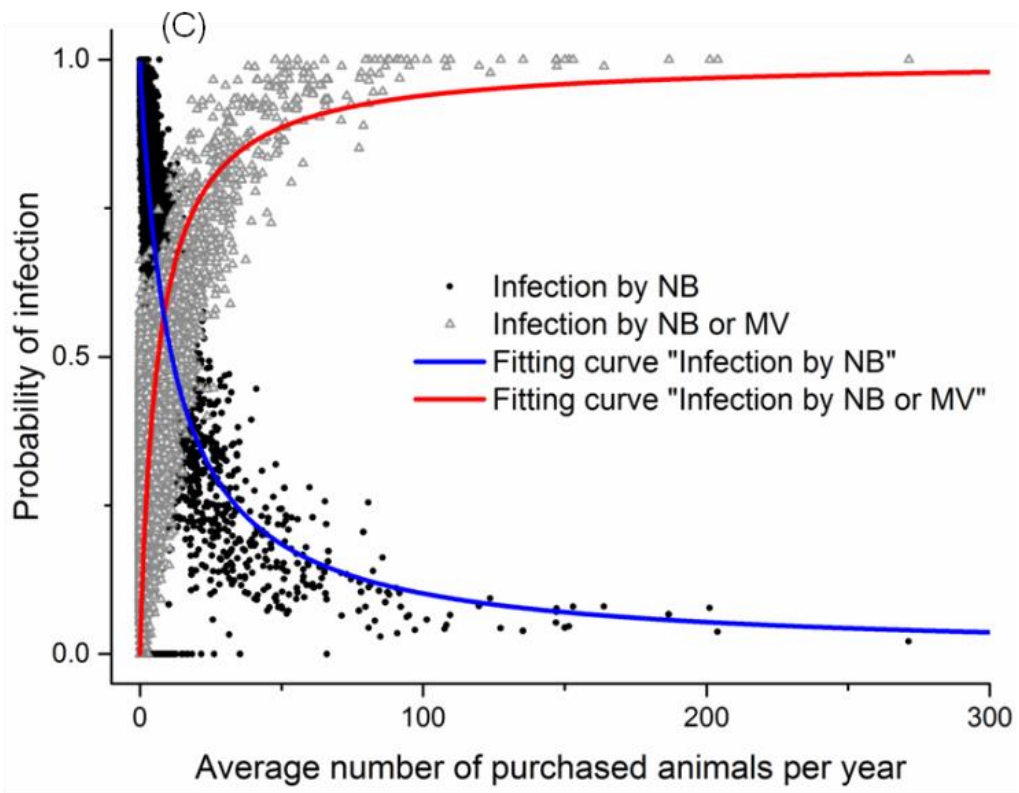
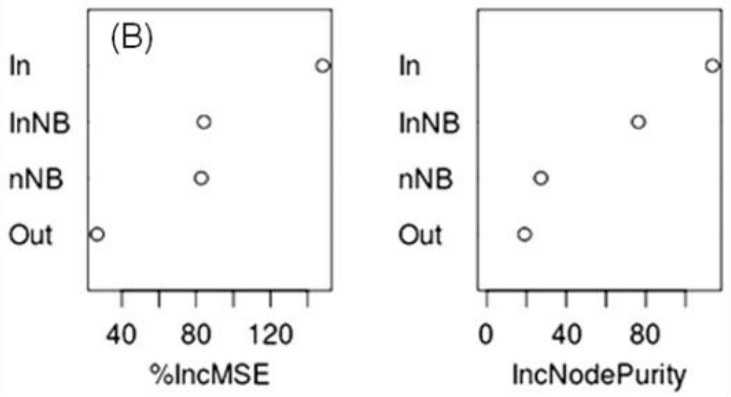
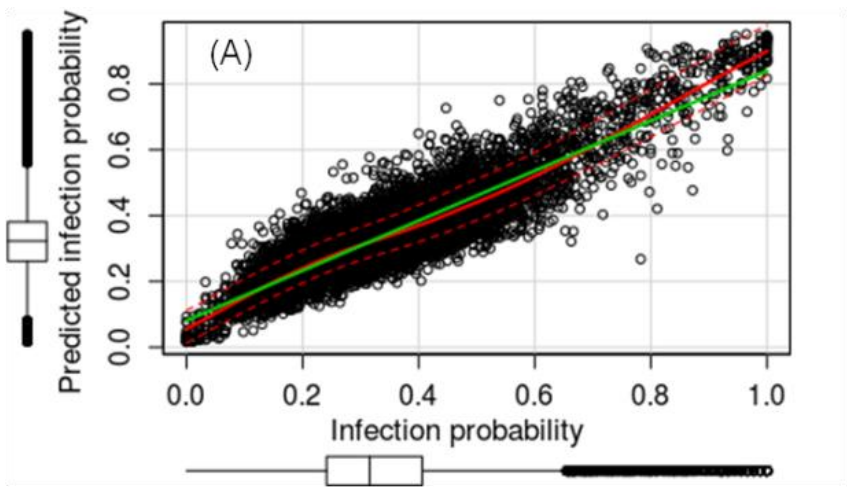


The local areas with top 3 highest risk 87%, 85%, and 84%.



■ Infection Probability < 10%
■ Infection Probability > 70%

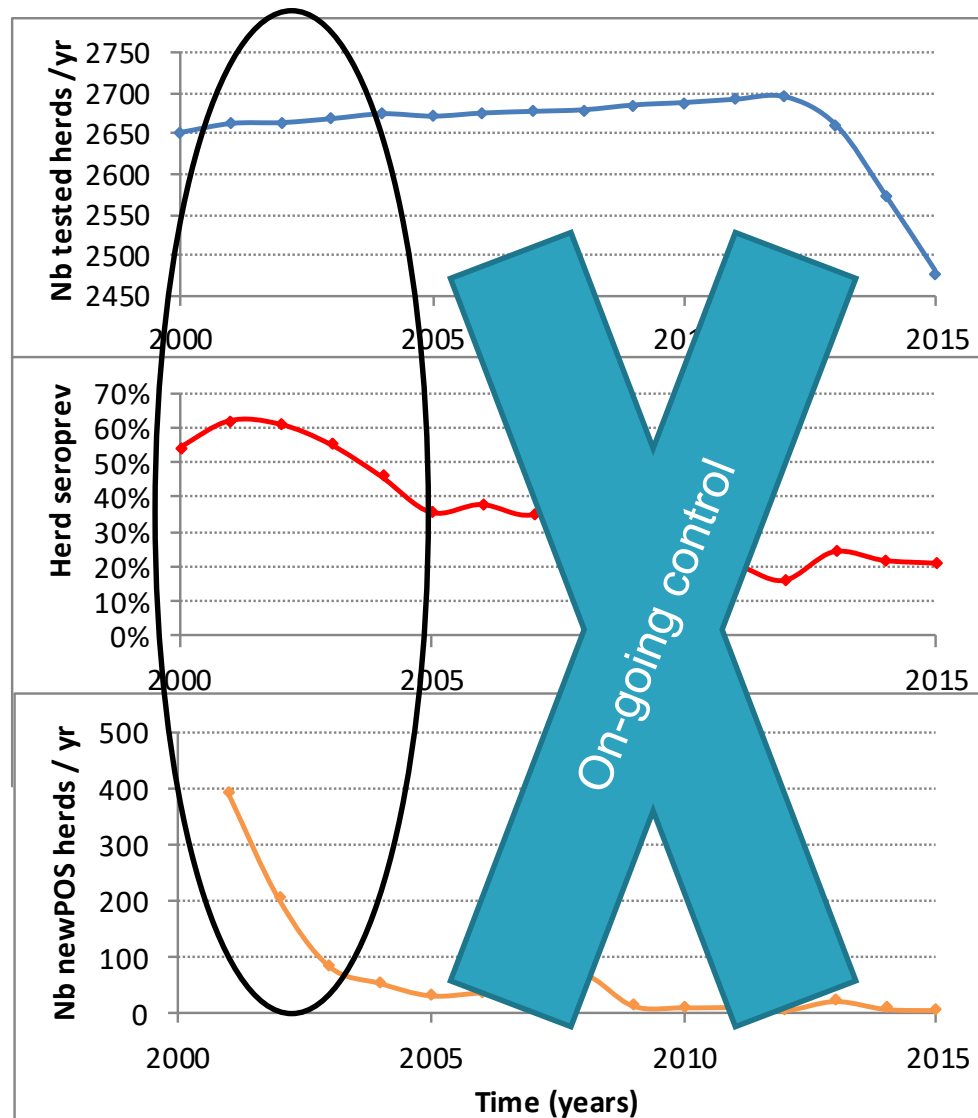
Herd infection probability



Comparison to observed data

Finistere (Brittany)

- Observations
 - ~2650 herds / ~3000 herds
 - ~50-60% seroprevalence
 - ~100-400 newly infected herds



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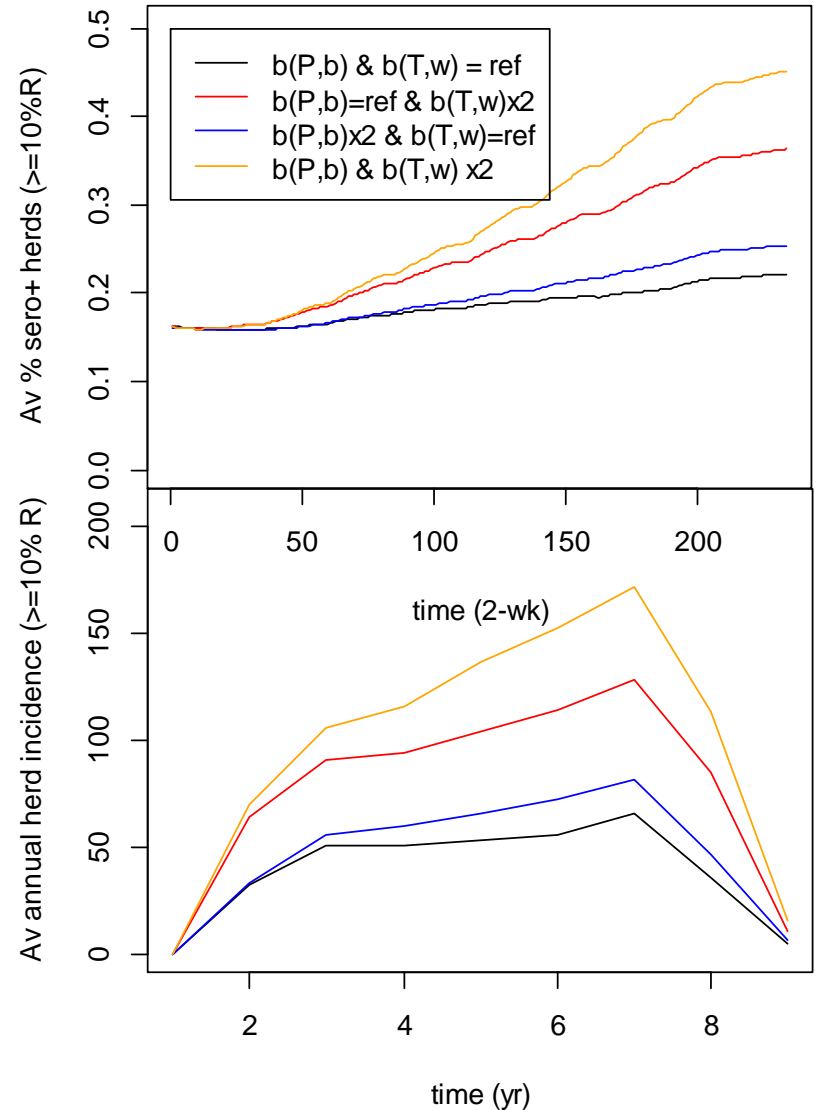
- Simulations

- ~20% seroprevalence
- ~50 newly infected herds

To reach 50-60% seroprev & 100-400 incidence

➔ increase transmission rates

b(P,nb) & Radius x2



Take-home message & discussion

A data-driven multiscale model to better understand regional BVDV spread

- Realistic framework, flexible & efficient
- Lacks fattening unit and beef herds & needs calibrations
- Accounting for territorial specificities → A tool for managers to evaluate control strategies

Perspectives

- Model simplification: vertical transmission using calf-dam data
- Better structure for input data
- Inclusion of beef herds & fattening units
- Inclusion of control measures other than tests at purchase



E. Vergu



L. Qi



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