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Modelling the spread of bovine brucellosis in Paraguay through the trade of cows

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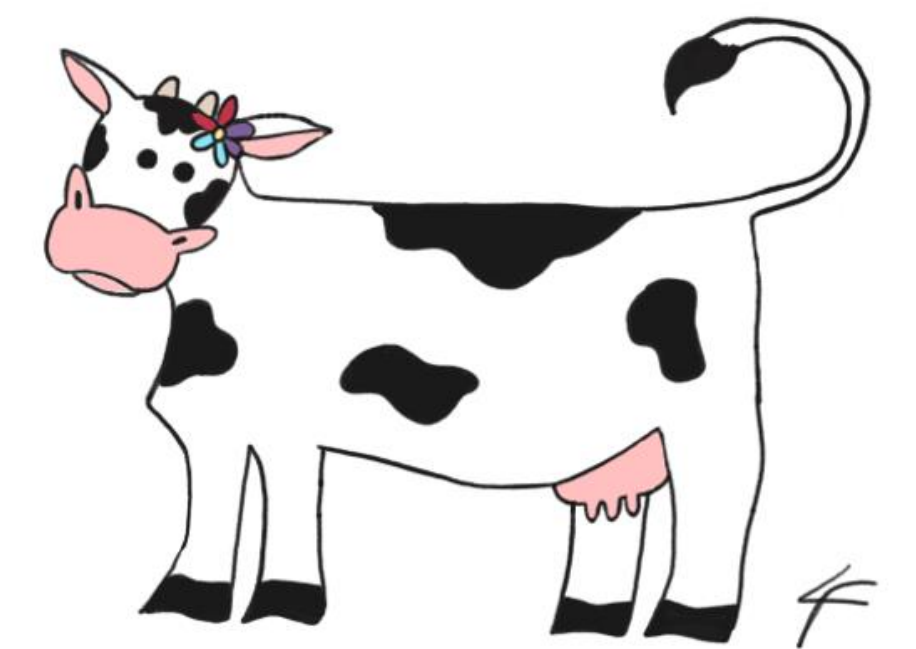


BACKGROUND



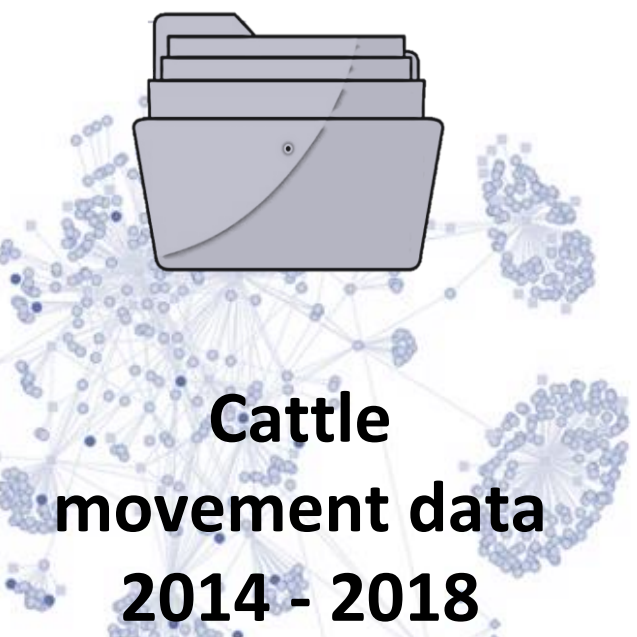
- Bovine brucellosis (BB), mainly caused by *Brucella abortus*, causes significant economic losses in the bovine sector
- In Paraguay, where livestock farming is the main economic activity, bovine brucellosis is an endemic disease and one of the main cattle diseases
- Paraguay is divided into 2 regions:
 - Eastern region:** large cattle population, extensive production
 - Western region:** large number of cattle farms, intensive production
- 3 categories of farm size according to the number of cows:
 - Small family farms with <20 cows
 - Medium commercial farms with 20-80 cows
 - Large commercial farms with >80 cows

The general objective of this work was to develop a bovine brucellosis transmission model to test different disease control scenarios.



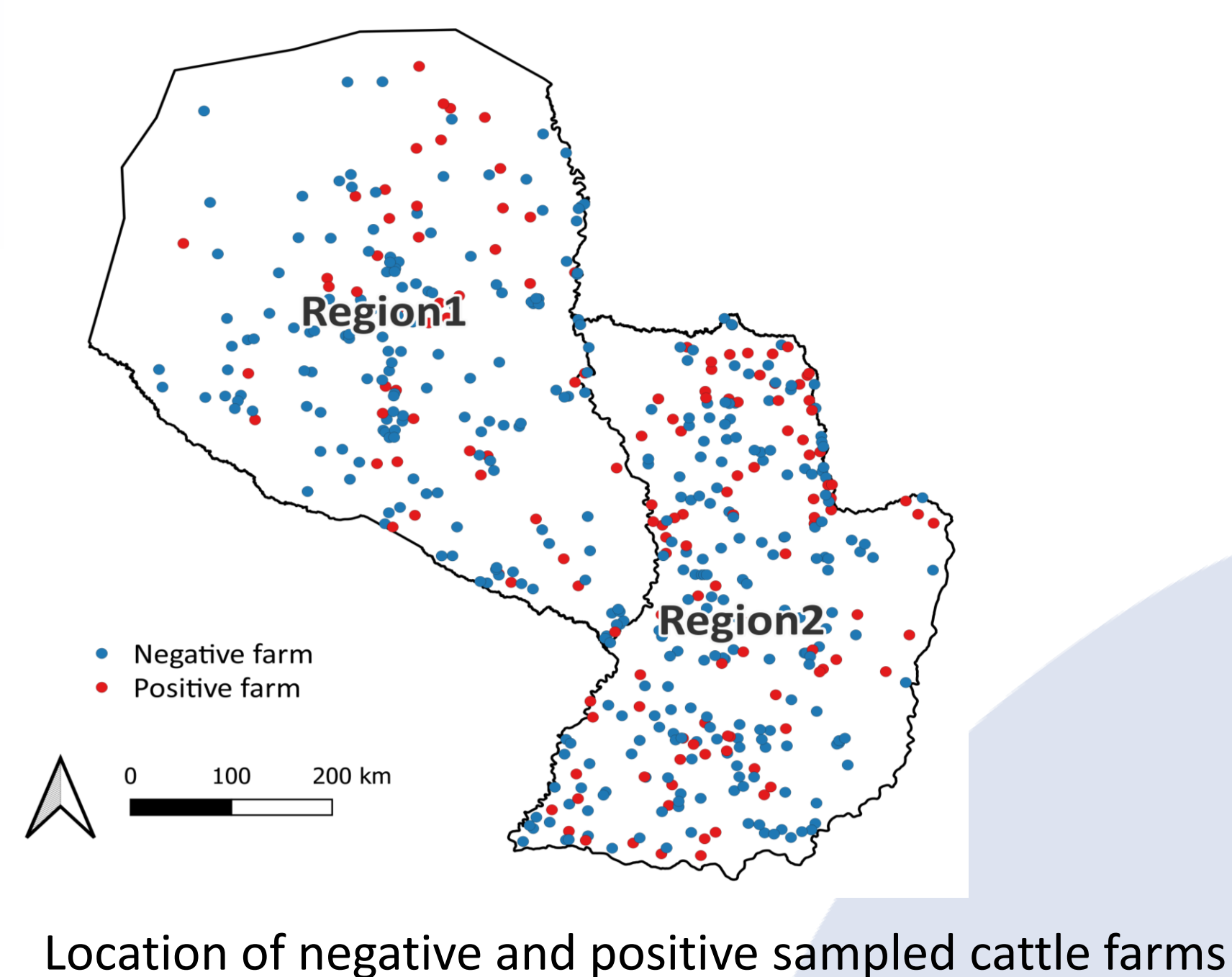
PRELIMINARY RESULTS

Database



Cattle movement data 2014 - 2018

National seroprevalence of bovine brucellosis in Paraguay in 2019



Model formulation:

We developed a deterministic model for the transmission of brucellosis by the trade of cows, based on a database of cattle movements between farms. Epidemiological units were farms. Time step was annual.

$$S_{x,y} \xrightarrow{1 - \left[\prod_{a \in X} (1 - \pi_{a,b})^{n_{ab}^{xy}} \cdot \prod_{b \in X} (1 - \psi_b)^{n_b^{x,y}} \right]} I_{x,y}$$

$$I_{x,y} \xrightarrow{\rho_{xy} \pi_{x,y} m_{x,y}} S_{x,y}$$

State variables: $S_{x,y}$ and $I_{x,y}$, number of susceptible/infected farms in region $x \in X$ of size $y \in Y$

Data: n_u^v number of animals sold by u to v , with $u = x, y$ for a farm of region x and size y , and $u = x$ for a market of region x

$m_{x,y}$ median size for a farm of region x and size category y

Calculated variable: Ψ_y proportion of infected animals in market of region y

Parameter estimation by minimizing the log-likelihood of seroprevalence data at the simulated epidemiological equilibrium

$\pi_{x,y}$ within-farm prevalence in farms of region x and size y

$\rho_{x,y}$ yearly culling probability of an infected animal in farms of region x and size y

When fitting the model we took into account the 2 regions and the 3 farm sizes

Region	Farm size	No. of farms	Median size
Region 1	≤20 cows	1,736	7
	21-80 cows	2,515	47
	>80 cows	3,992	204
Region 2	≤20 cows	33,564	7
	21-80 cows	11,030	35
	>80 cows	5,033	182

Summary of national brucellosis seroprevalence data

Region	Farm size	No. of farms	No. of positive animals	No. of sampled animals	Between-farm seroprevalence (%)	Animal seroprevalence (%)
Region 1	≤20 cows	11	1	173	9	0.5
	21-80 cows	59	13	1,016	22	13
	>80 cows	128	35	2,515	27	12
Region 2	≤20 cows	21	4	270	19	14
	21-80 cows	91	22	1,435	24	15
	>80 cows	157	68	2,969	43	22

Model choice: a total of 16 comparative models were compared that combined 4 possible parameterizations of $\pi_{x,y}$ and $\rho_{x,y}$: same value for all regions and farm sizes, farm size-specific values, region-specific values, both farm size and region-specific values. The model with **region-specific values of $\pi_{x,y}$** and **farm size-specific values of $\rho_{x,y}$** was selected based on AIC (1,138).

Model fit: in 96% of farms, the observed number of positive animals was within the 95% confidence interval of the prediction

Estimated parameters values:

Estimated parameters specific	value	(95% CI)
Within-farm prevalence: region 1	0.10	0.09 - 0.11
Within-farm prevalence: region 2	0.15	0.14 - 0.17
Yearly culling probability of an infected animal: ≤20 cows	0.08	0.04 - 0.14
Yearly culling probability of an infected animal: 21-80 cows	0.62	0.58 - 0.68
Yearly culling probability of an infected animal: >80 cows	0.89	0.88 - 0.90

Slight variation of $\pi_{x,y}$ according to region

Strong variation of $\rho_{x,y}$ according to farm size

Predicted between-farm prevalence

Region	Farm size	Prevalence (%)	(95% CI)
Region 1	≤20 cows	18	11-29
	21-80 cows	28	20-39
	>80 cows	30	24-37
Region 2	≤20 cows	22	10-43
	21-80 cows	25	18-35
	>80 cows	46	38-53

DISCUSSION AND PERSPECTIVES

Data on animal movement and the resulting contacts between farms can be represented in the form of networks. Several studies have shown how the spread of diseases follows the structure of these commercial networks. Our model shows a balance between the bovine brucellosis transmission between farms through cow trade, and an increasing yearly culling probability of infected animals according to farm size. This could be explained by differences in the professionalization of breeders and in the production types (e.g. fattening of cull cows in largest farms). In the future, this work could help predict results of the implementation of bovine brucellosis control methods in Paraguay.

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