

# Estimating dynamic risk factors for pathogen transmission using community-level bird census data

## Can we follow pathogen movements?

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### Problematic: how to follow pathogen movements?

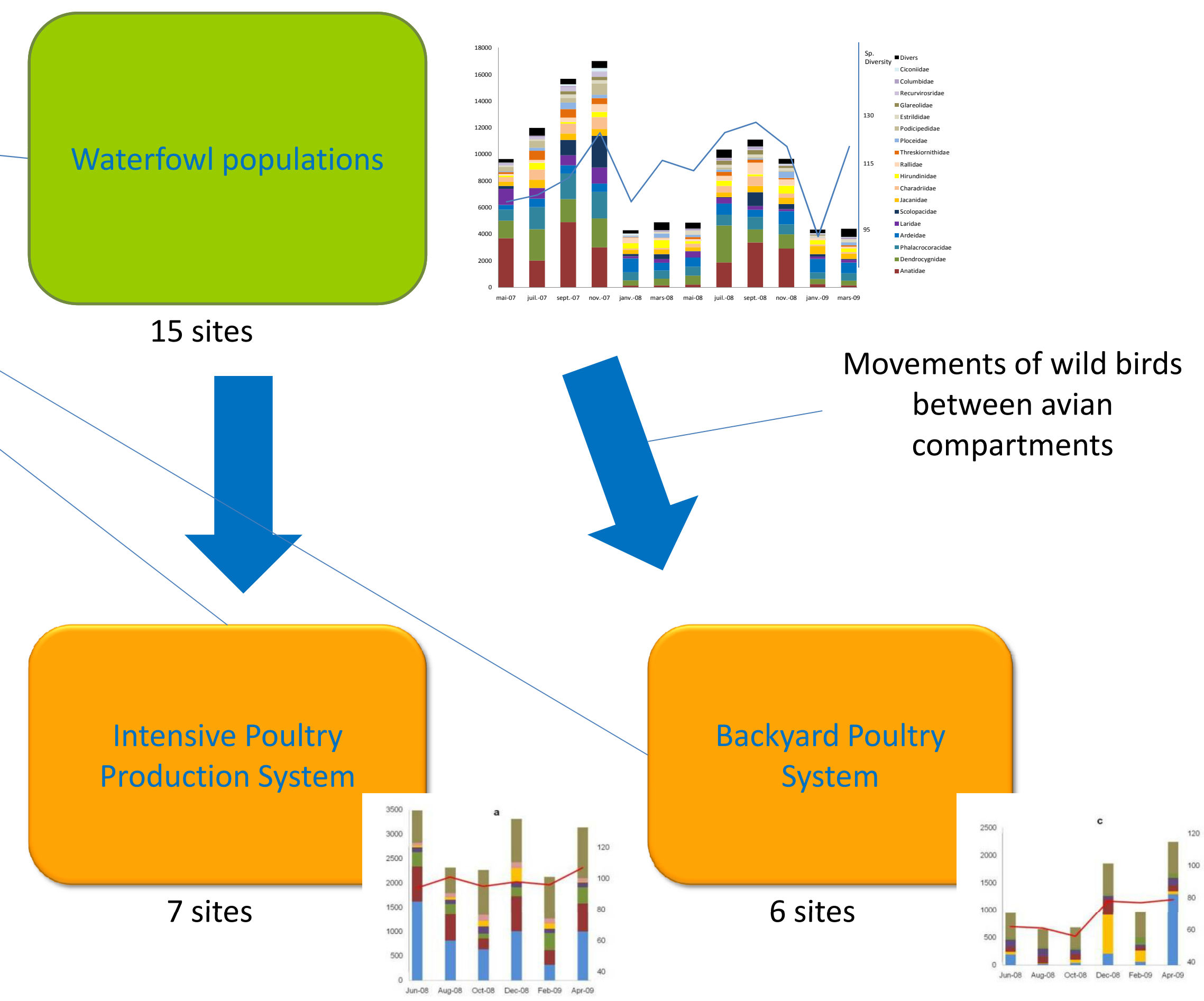
- Pathogens are dependent on the mobility of their hosts or their vectors
- You cannot « see » most of pathogens
- To track pathogen mobility:
  - Use host movements & contacts as an "a priori" estimator of movements
  - Use pathogen data in multiple host populations as an "a posteriori" estimator of movements

→ We present a framework to investigate and predict pathogen movements in a given ecosystem based on the estimated host contacts

### « What is the risk of Avian Influenza transmission from the waterfowl community to domestic bird populations ? »

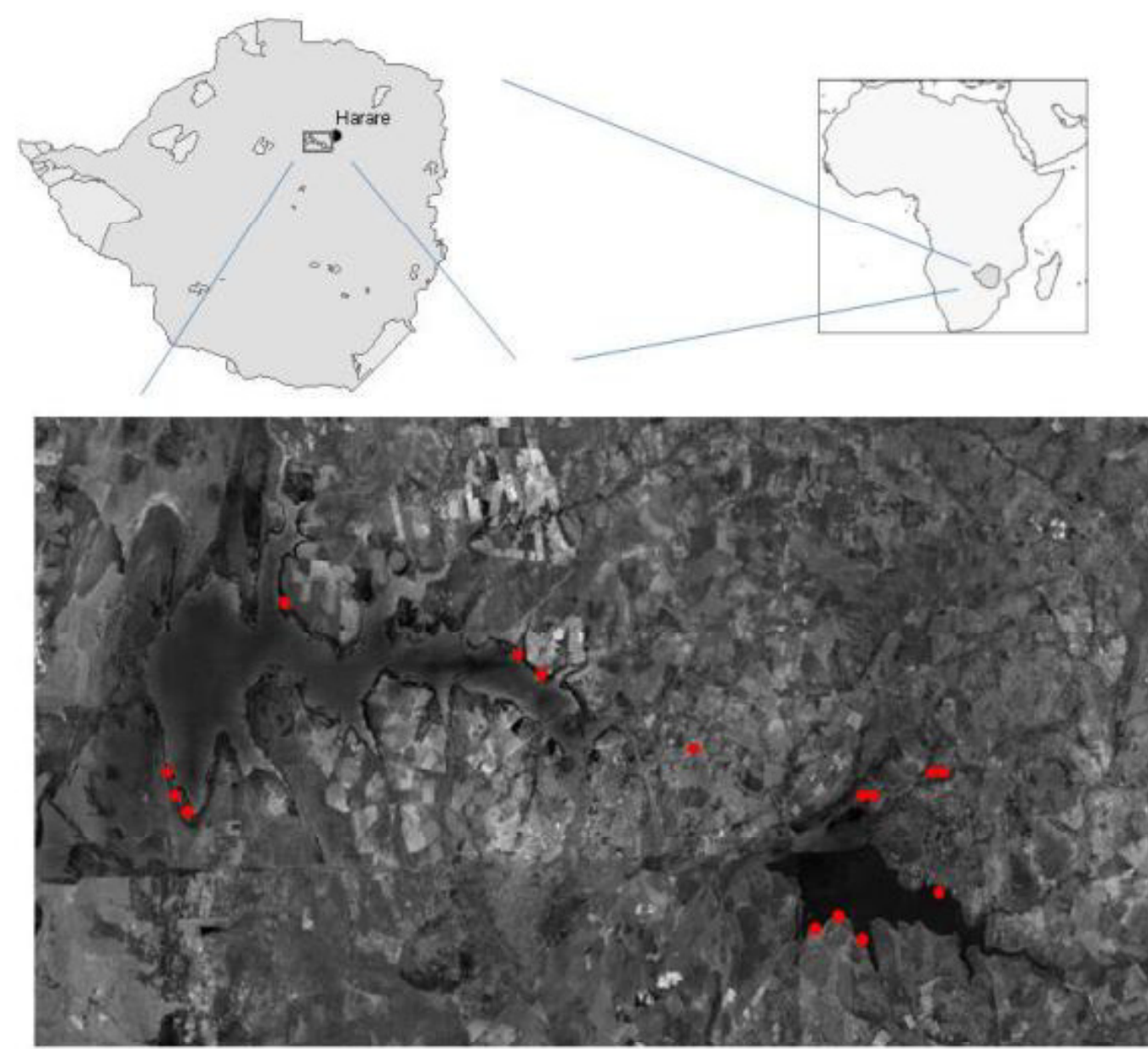
#### Description of wild bird communities (bird families)

Every 2 months for 1 year, regular focal counts of wild birds at 34 sites, 4 times per week



### Study Site

Lake Chivero & Manyame, 35kms West of Harare, Zimbabwe (red dots are waterfowl counting sites)



### Building of a risk factor model

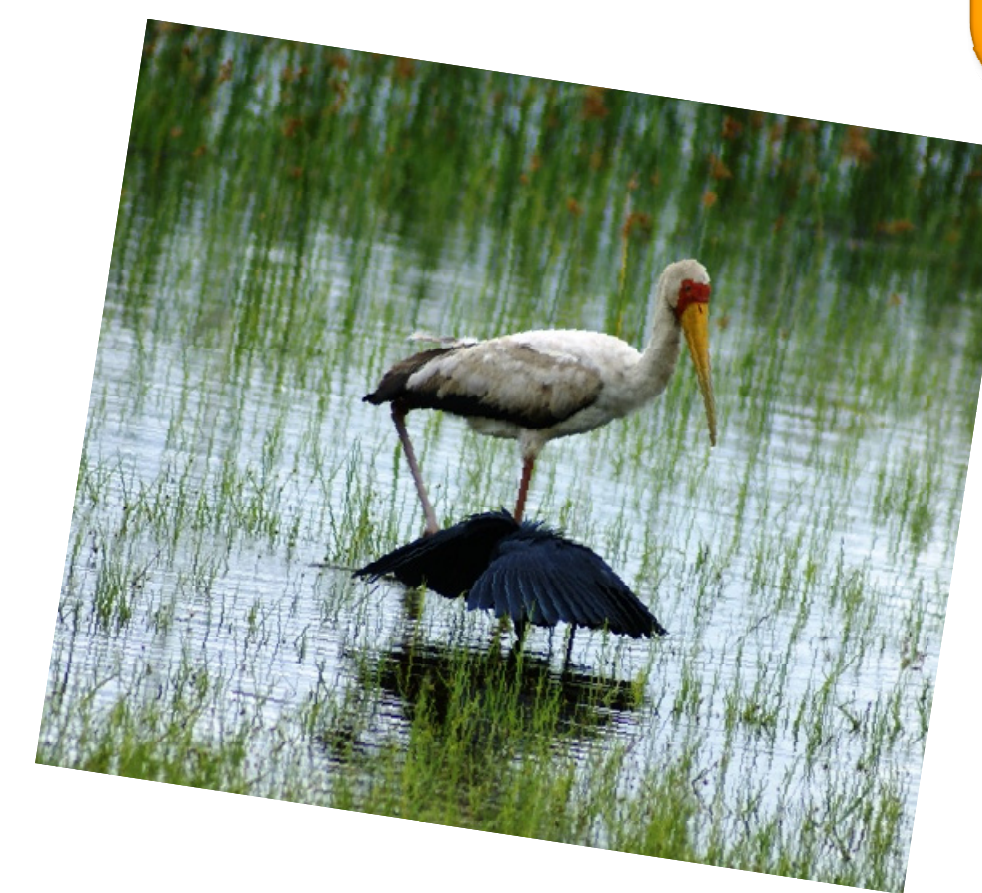
Based on Risk Factors for Avian Influenza (ecological and epidemiological knowledge)

#### Dynamic Risk Factors

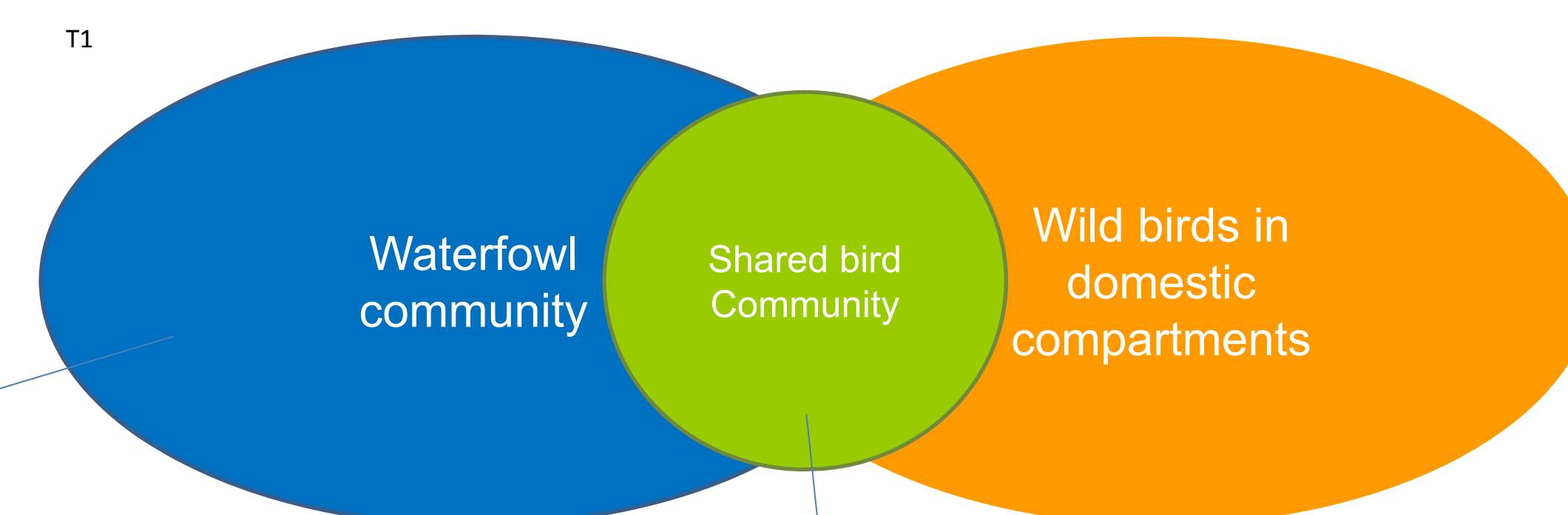
RF	Characteristic	Justification & Description
1	Abundance	Total number of bird observed per species
2	Gregariousness	Average group size
3	Mixing	The ratio of the number of species observed on the same sites and at the same time, divided by the total number of species counted during the 60 counts
4	Immigration	Difference between the number of birds observed in a count at time t and a count in the same location at time t-1.
5	Percentage of juveniles in the population	Using a simple population model

#### Non-Dynamic Risk Factors

6	Movement patterns	We defined four movement patterns and ranked them
7	Feeding habits	We identified four feeding behaviors that were ranked



### Building a model of Epidemiological Interaction between avian compartments based on the shared bird community

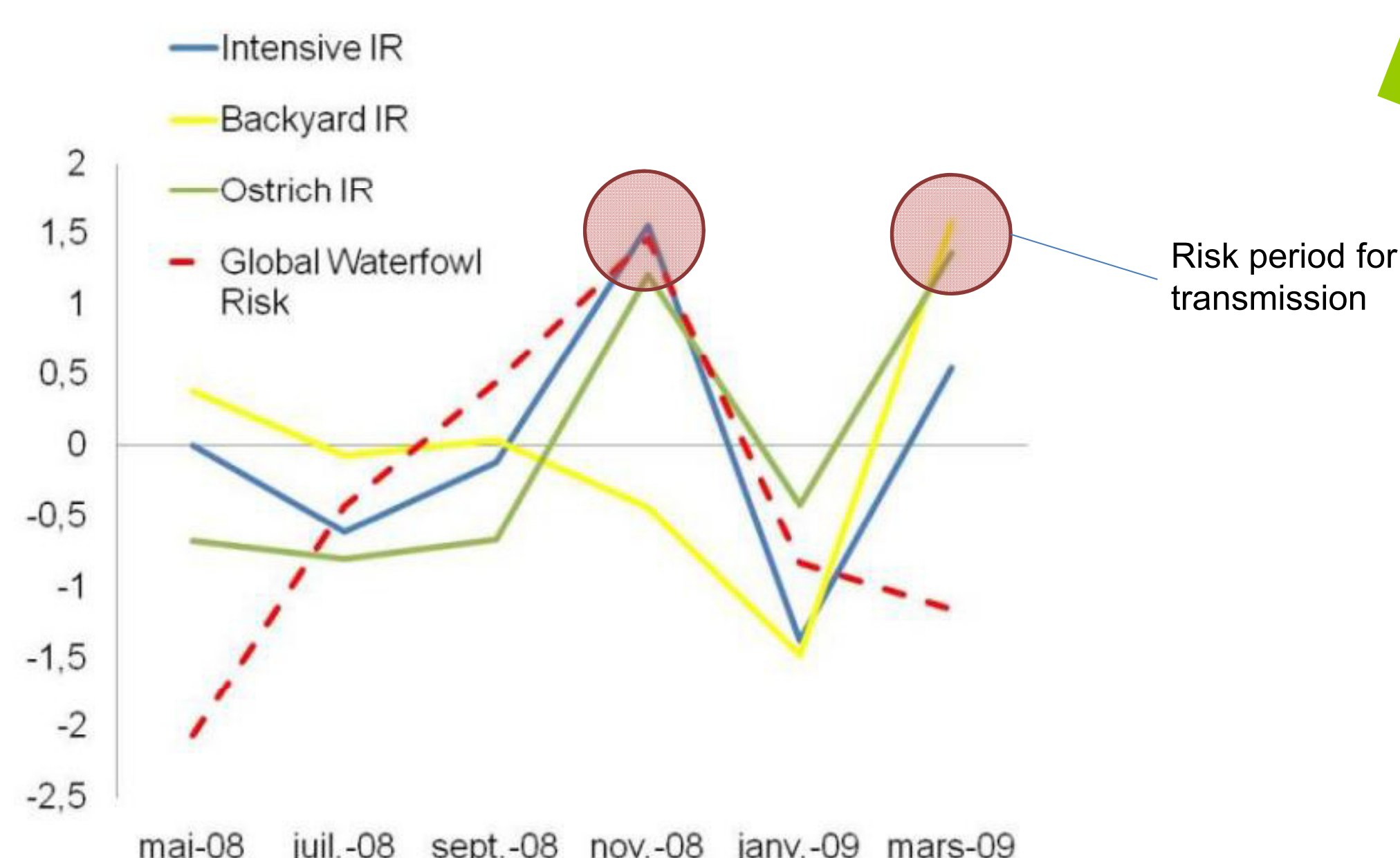


**Global waterfowl risk**  
= sum of risks across all species in the waterfowl community weighted by their abundance

**Interaction risk**  
between 2 avian compartments = Risk represented by the sum of risks across all species in the shared community weighted by their abundances



### Identifying risk season for pathogen transmission



Interaction Risk (IR) for each domestic compartment (calculated using the species risk calculated from the 7 Risk Factors and multiplied by the number of observations per species shared by the 2 compartments) and global waterfowl risk (using the 7 Risk Factors value per species and multiplied by 1 –presence – or 0 –absence – for each species).

### Identifying potential bridge species in each Risk period

Bird families most at risk of transmitting pathogen to domestic birds (here intensive poultry)

Intensive Poultry	November Peak	Mars Peak	Representative Species of each bird family
Ploceidae	30,30%	31,80%	Red-billed quelea (77%)
Estrilidae	21,80%	18,60%	Bronze mannikin (50%)
Hirundidae	8,50%	0,00%	Barn swallow (90%)
Ardeidae	0,00%	10,60%	Cattle egret (35%)
<b>Total</b>	<b>60,60%</b>	<b>61,00%</b>	

For each bird families, the most represented species can be used as potential bridge species

### References

Caron A., de Garine-Wichatitsky M., Gaidet N., Chiweshe N., Cumming G. S. Estimating dynamic risk factors for pathogen transmission using community-level bird census data. Ecology & Society, *in press*

### CONCLUSIONS

- Using only bird counts and risk factors, we can identify bird families and species most likely to spread pathogens from one host population to another
- This protocol could help targeting surveillance and control of pathogen spill-over at the wild/domestic interface
- Next step: targeted sampling of the potential bridge species



This work has been implemented in the framework of the RP-PCP (Research Platform « Production and Conservation in Partnership »)



Funded by the French Ministry of Foreign Affairs