



University of  
**Salford**  
MANCHESTER



3<sup>rd</sup> European Conference on  
*Xylella fastidiosa* and XF-ACTORS final meeting

# Improving early detection surveillance for *Xylella fastidiosa* in Apulia

**Alexander Mastin<sup>1</sup>, Frank van den Bosch<sup>1,2</sup>,  
Nik Cunniffe<sup>3</sup>, Stephen Parnell<sup>1</sup>**

<sup>1</sup>University of Salford, UK

<sup>2</sup>Curtin University, Australia

<sup>3</sup>University of Cambridge, UK

[a.mastin@salford.ac.uk](mailto:a.mastin@salford.ac.uk)  
@lexmastin





# OVERVIEW

- **Why do we want to conduct surveillance for *Xylella fastidiosa*?**
- **Where and how should we should conduct surveillance for *X. fastidiosa* in the uninfected zone of Apulia?**
- **Summary and conclusions**



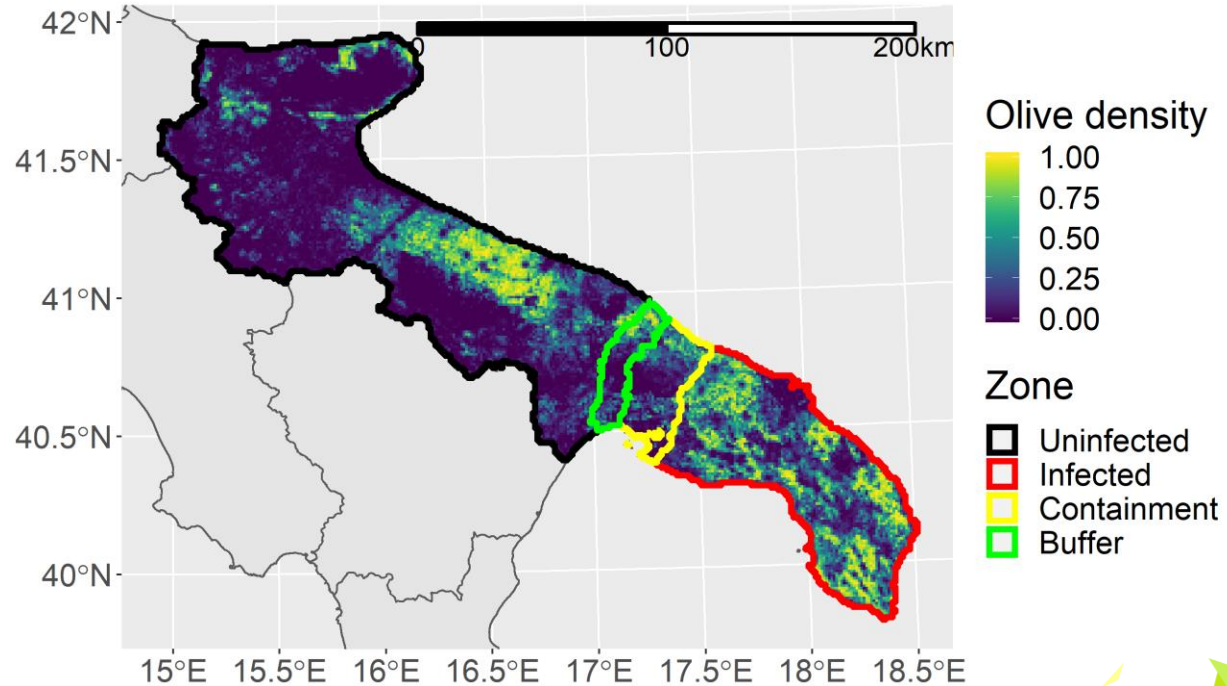
# OVERVIEW

- **Why do we want to conduct surveillance for *Xylella fastidiosa*?**
- Where and how should we should conduct surveillance for *X. fastidiosa* in the uninfected zone of Apulia?
- Summary and conclusions

# WHAT IS THE AIM OF SURVEILLANCE?

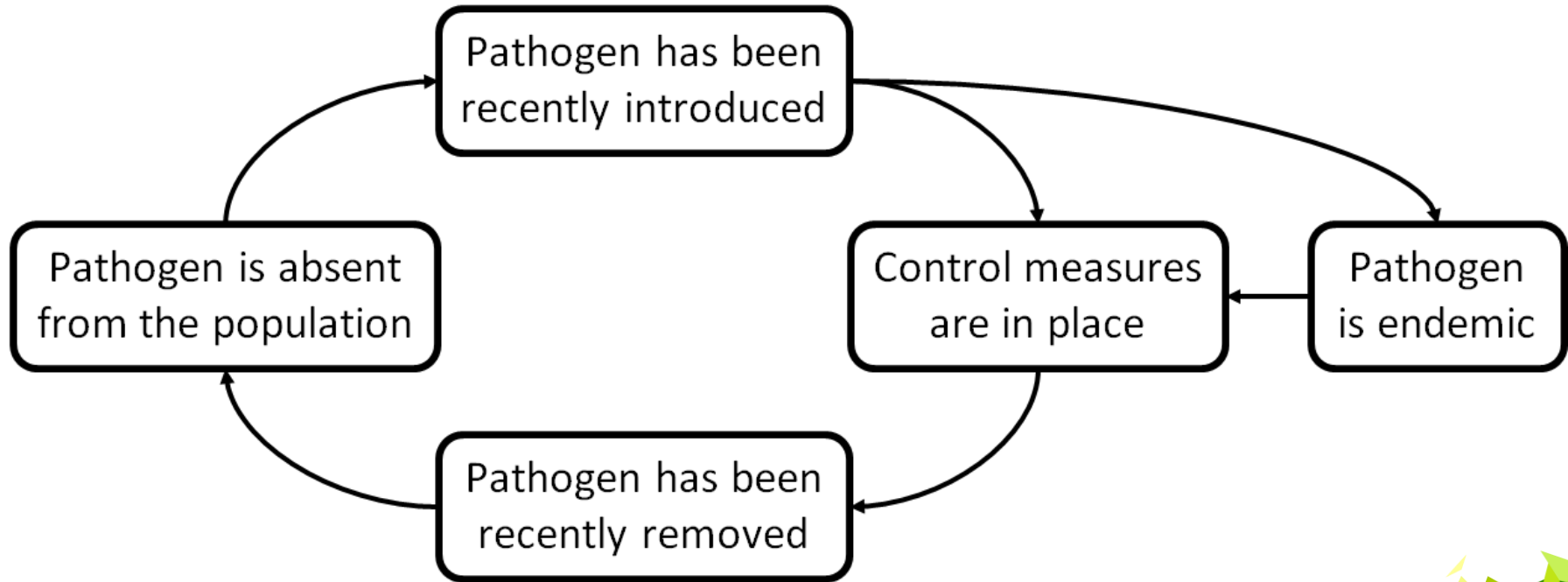
*X. fastidiosa* is not thought to be present within the **Uninfected** and **Buffer Zones** of Apulia.

We term these the **“Uninfected Area”**.

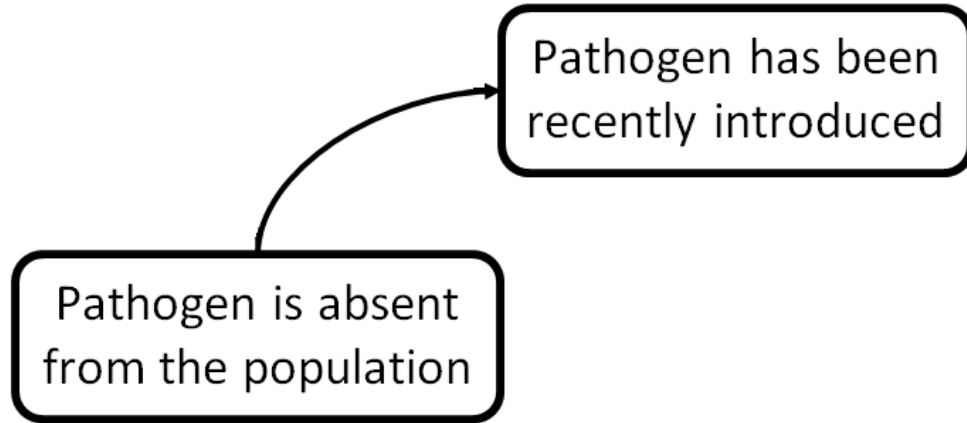


(Boundaries as of January 2020)

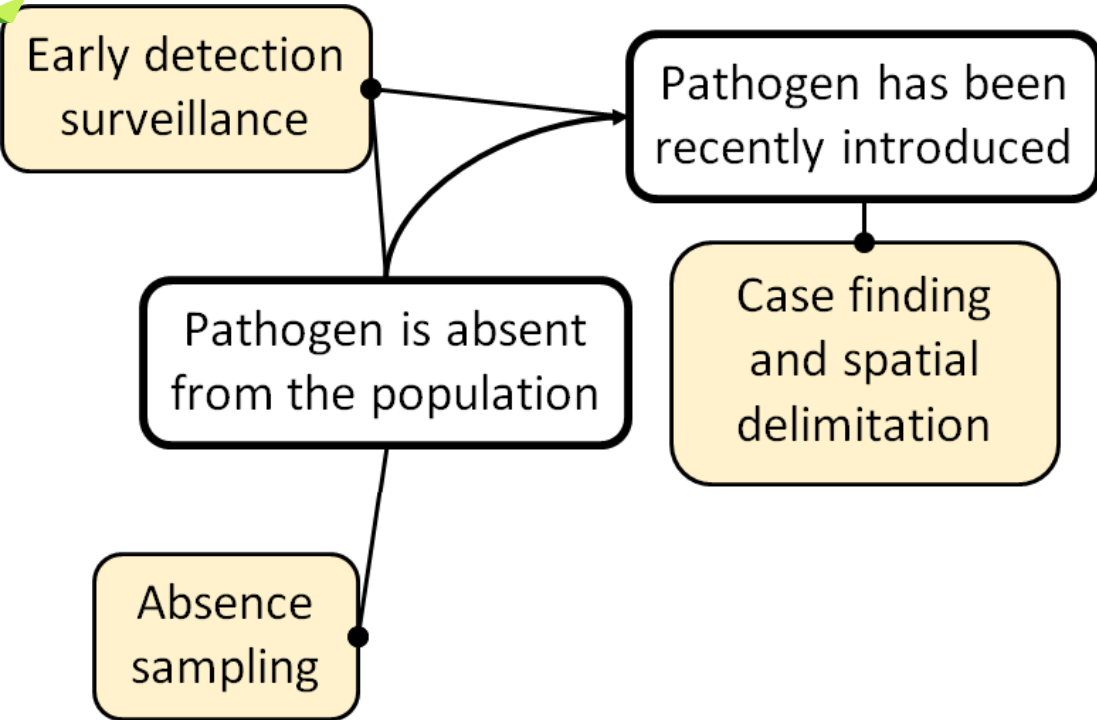
# WHAT IS THE AIM OF SURVEILLANCE?



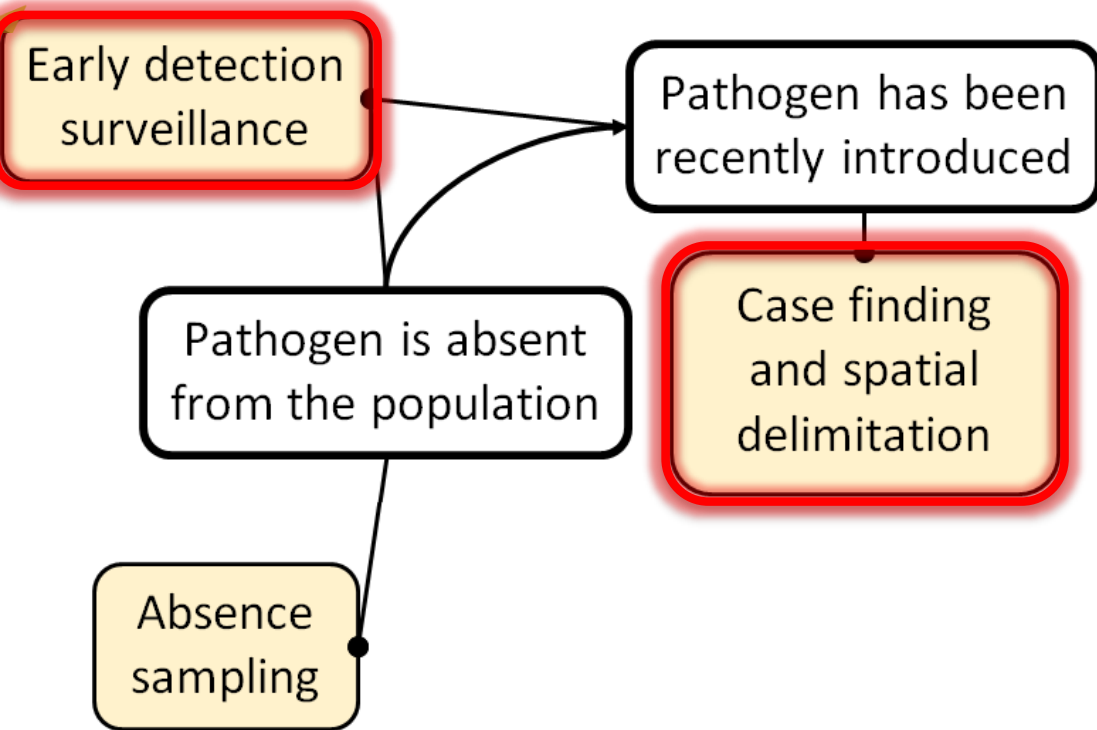
# WHAT IS THE AIM OF SURVEILLANCE?



# WHAT IS THE AIM OF SURVEILLANCE?



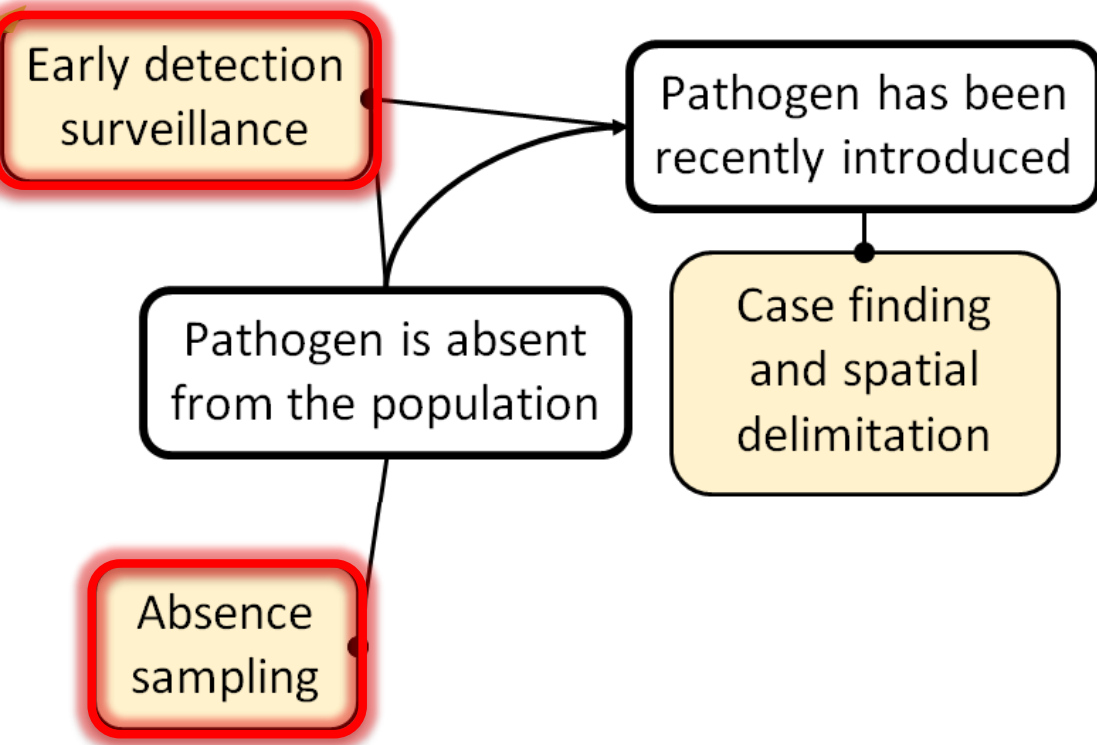
# WHAT IS THE AIM OF SURVEILLANCE?



**Where should we sample in the uninfected area of Apulia?**



# WHAT IS THE AIM OF SURVEILLANCE?



**How should we sample in the uninfected area of Apulia?**



# OVERVIEW

- Why do we want to conduct surveillance for *Xylella fastidiosa*?
- **Where and how should we should conduct surveillance for *X. fastidiosa* in the uninfected zone of Apulia?**
- Summary and conclusions

# OPTIMISING SURVEILLANCE

- We link a **stochastic spatial model of pathogen spread** with an **optimisation routine** to identify where best to look for *X. fastidiosa*.

## PLOS BIOLOGY

RESEARCH ARTICLE

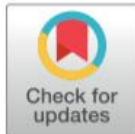
### Optimising risk-based surveillance for early detection of invasive plant pathogens

Alexander J. Mastin<sup>1\*</sup>, Timothy R. Gottwald<sup>2</sup>, Frank van den Bosch<sup>1,3</sup>, Nik J. Cunniffe<sup>4‡</sup>, Stephen Parnell<sup>1‡</sup>

**1** Ecosystems and Environment Research Centre, School of Science, Engineering and Environment, University of Salford, Greater Manchester, United Kingdom, **2** USDA Agricultural Research Service, Fort Pierce, Florida, United States of America, **3** Department of Environment and Agriculture, Centre for Crop and Disease Management, Curtin University, Bentley, Perth, Australia, **4** Department of Plant Sciences, Downing Street, Cambridge, United Kingdom

‡ These authors are joint senior authors on this work.

\* [a.mastin@salford.ac.uk](mailto:a.mastin@salford.ac.uk)



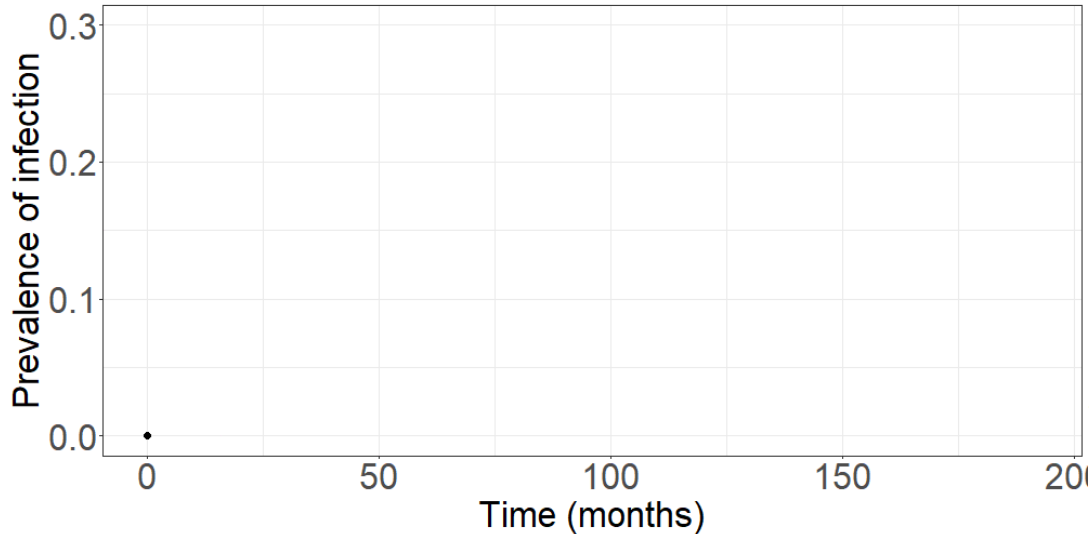
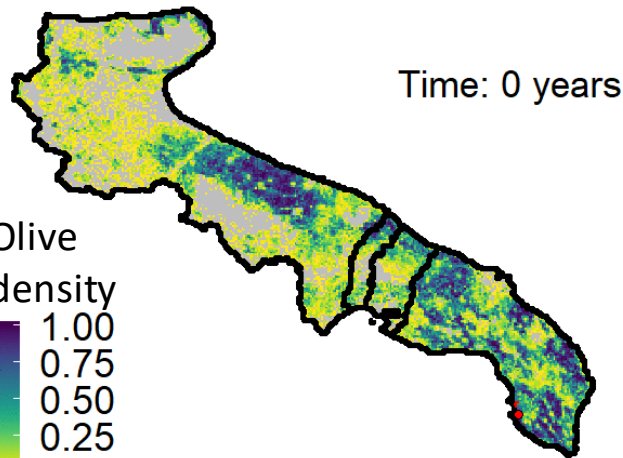
# SPREAD MODEL

**Short range spread**

**No long distance jumps**

For the simulations themselves, we ran **1000 model realisations** up to a **prevalence of 0.1%** in the uninfected areas.

Olive density  
1.00  
0.75  
0.50  
0.25

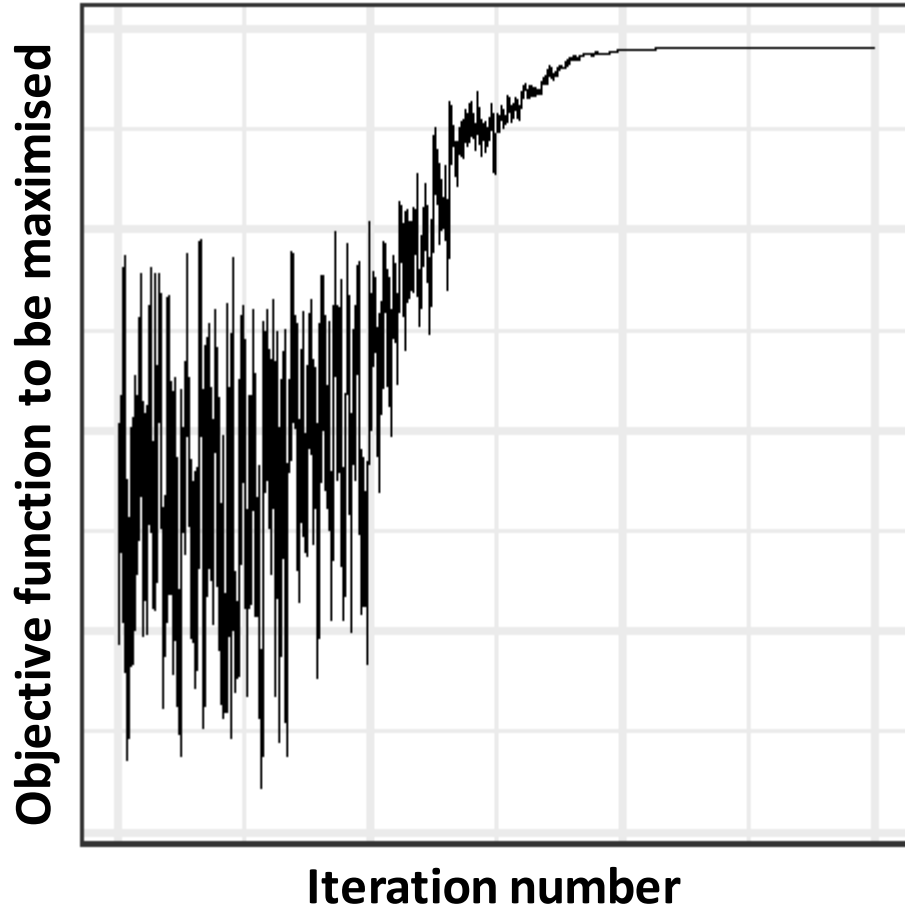




# OBJECTIVE FUNCTION

- This is a metric which **summarises our overall surveillance aim.**
- For **Case Finding**, it was the **mean number of positive detections** over all model realisations.
- For **Early Detection Surveillance**, it was the **mean probability of at least one positive detection** over all model realisations.

# SIMULATED ANNEALING



Randomly select sites.

Replace one site with another randomly selected.

Assess the **objective function** of the new and old arrangements.

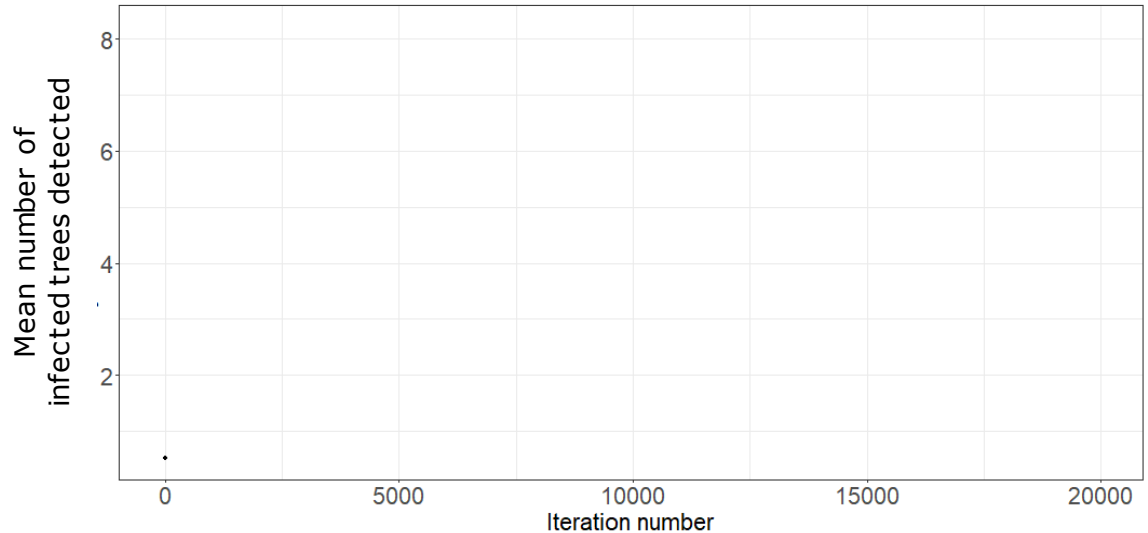
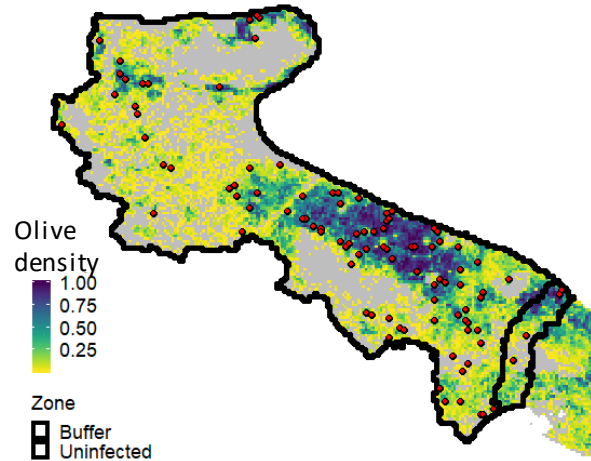
Accept all "better" arrangements. Accept a (declining) proportion of "worse" arrangements.

# OPTIMISATION

## Maximising the number of detections

### (Case finding)

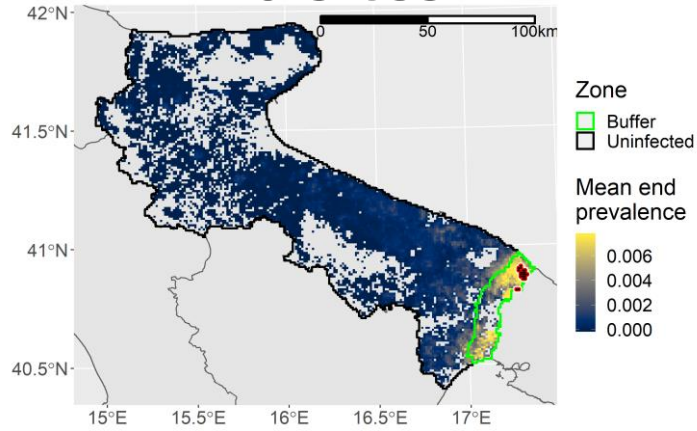
We assume **100 hosts** are inspected per  $1\text{km}^2$  cell, with a **one year detection lag**.



# OPTIMAL DISTRIBUTION OF SITES

Number of  
detections

## 20 sites

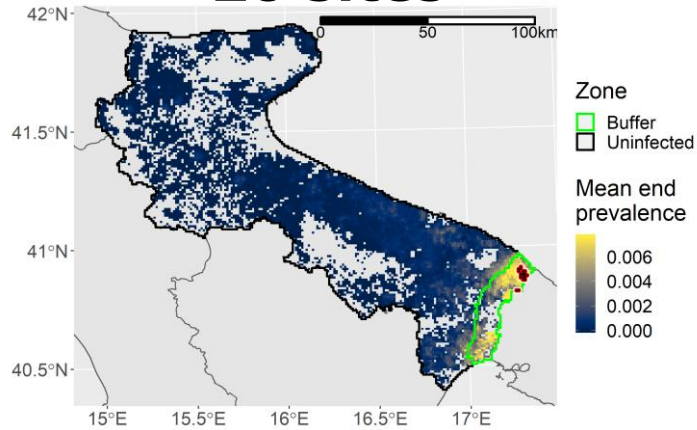




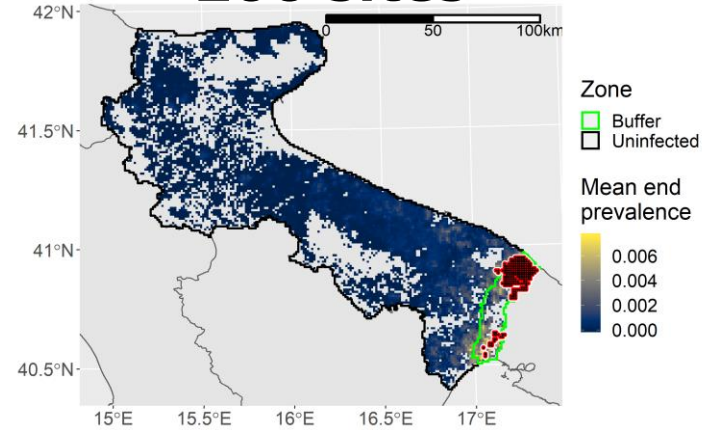
# OPTIMAL DISTRIBUTION OF SITES

Number of  
detections

## 20 sites



## 200 sites

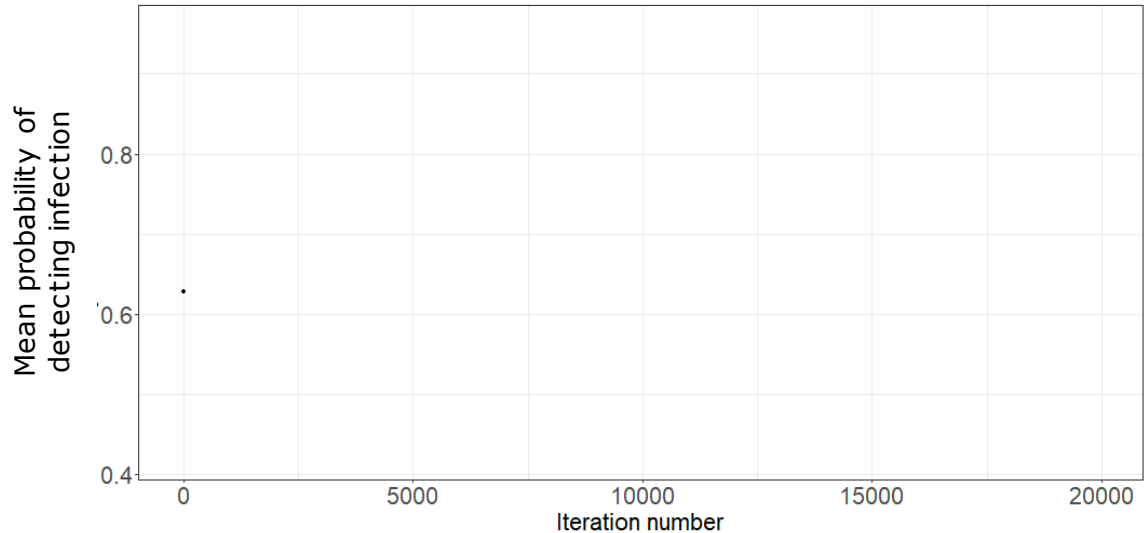
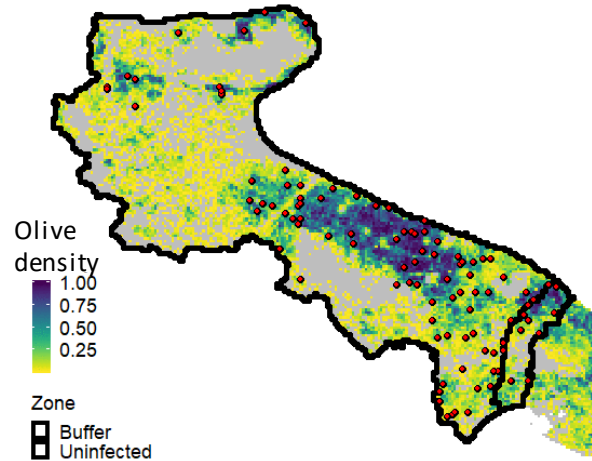


# OPTIMISATION

## Maximising the probability of detection

(Early detection)

We assume **100 hosts** are inspected per  $1\text{km}^2$  cell, with a **one year detection lag**.

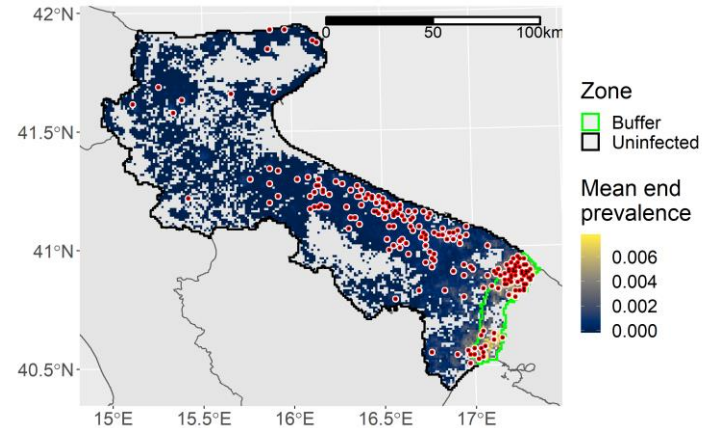
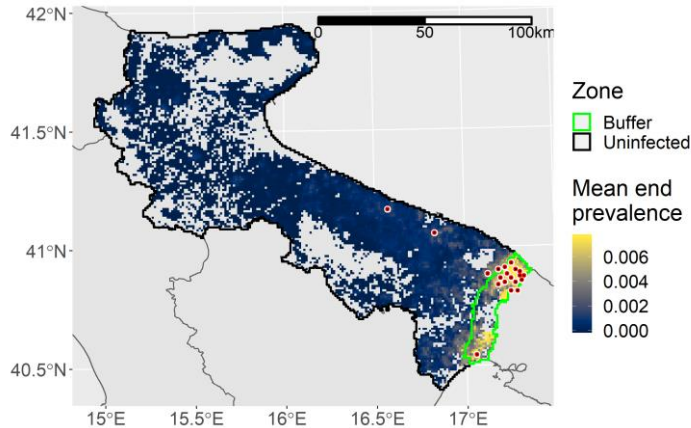


# OPTIMAL DISTRIBUTION OF SITES

## 20 sites

## 200 sites

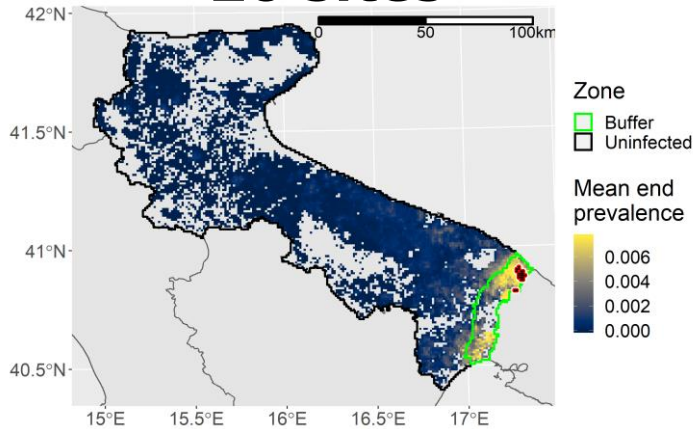
Probability  
of detection



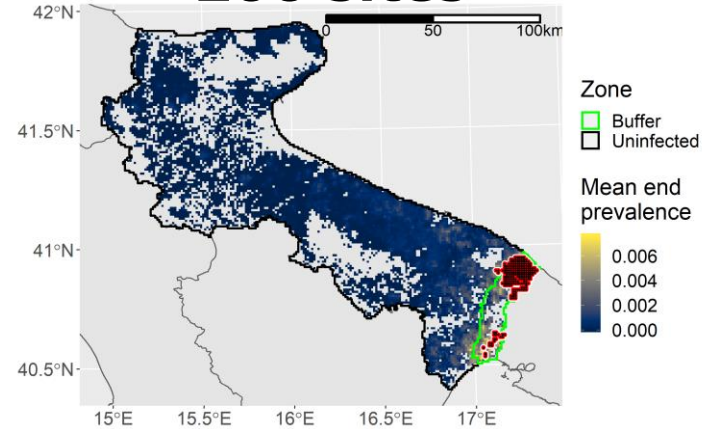
# OPTIMAL DISTRIBUTION OF SITES

Number of  
detections

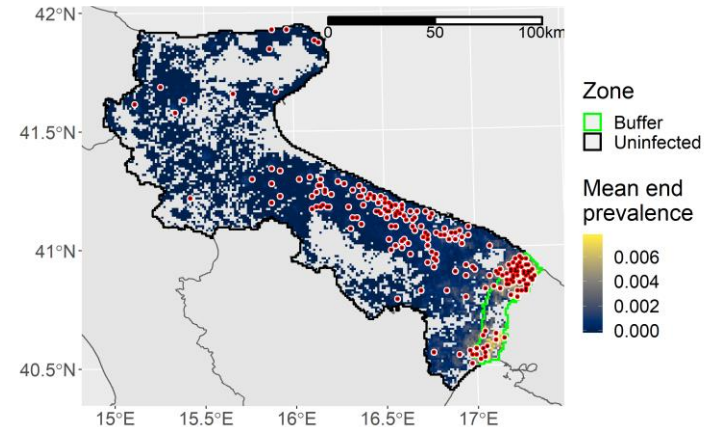
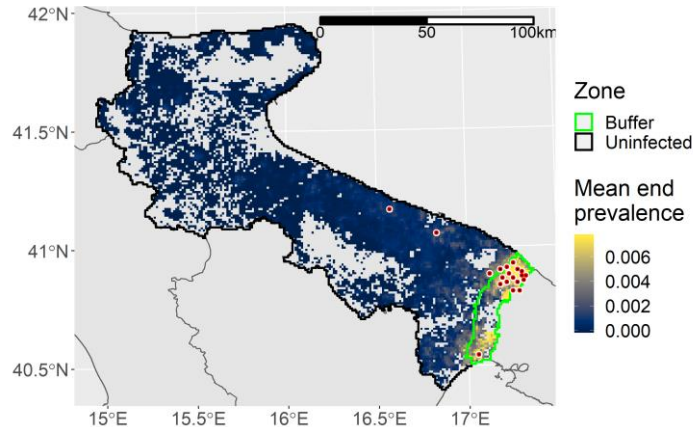
20 sites



200 sites

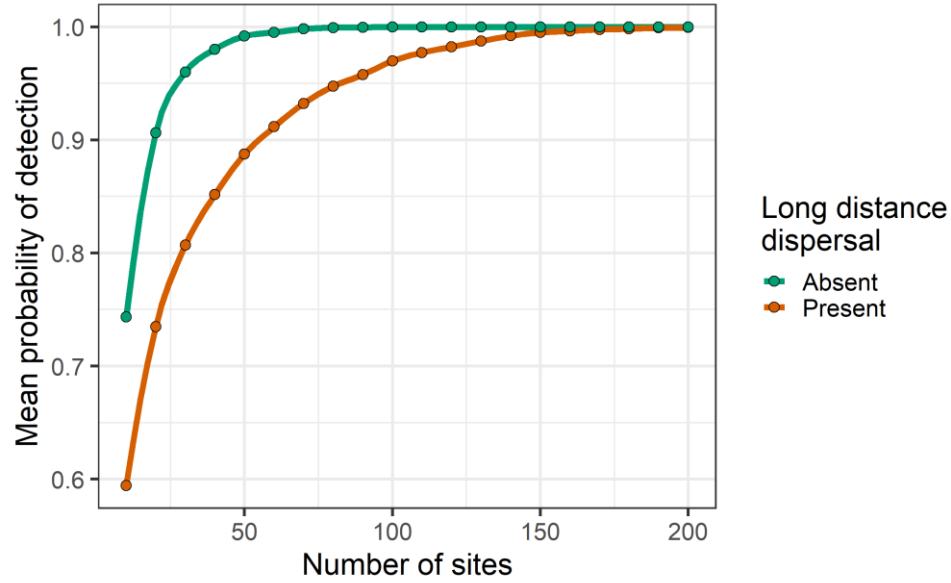


Probability  
of detection



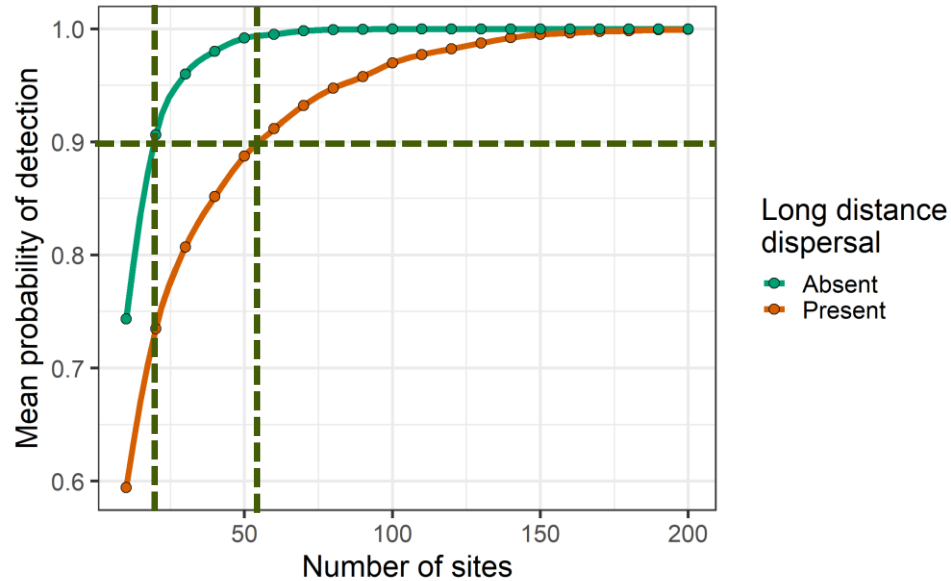
# IMPACT OF EPIDEMIOLOGY AND DETECTION METHOD ON DETECTION ABILITY

## Long distance dispersal



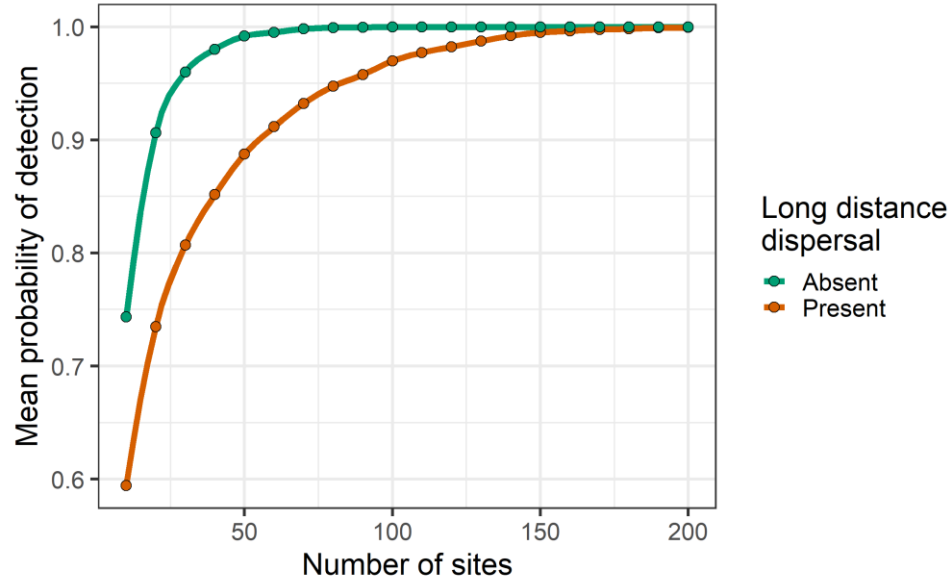
# IMPACT OF EPIDEMIOLOGY AND DETECTION METHOD ON DETECTION ABILITY

## Long distance dispersal

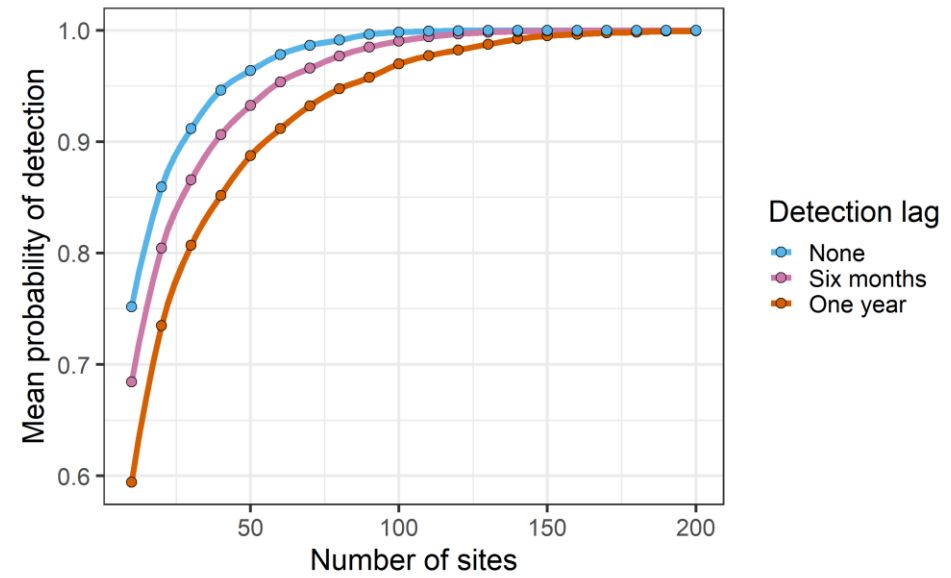


# IMPACT OF EPIDEMIOLOGY AND DETECTION METHOD ON DETECTION ABILITY

## Long distance dispersal

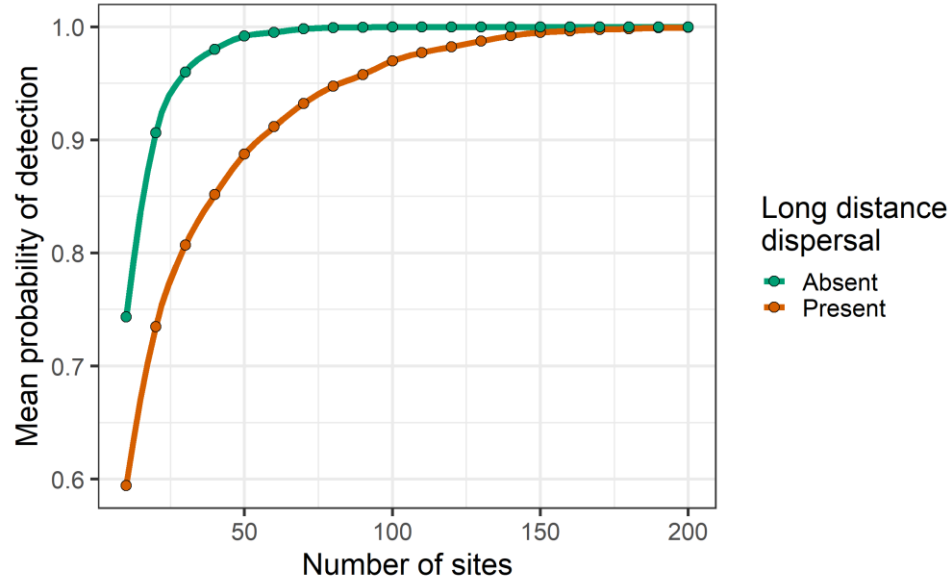


## Lag before detection

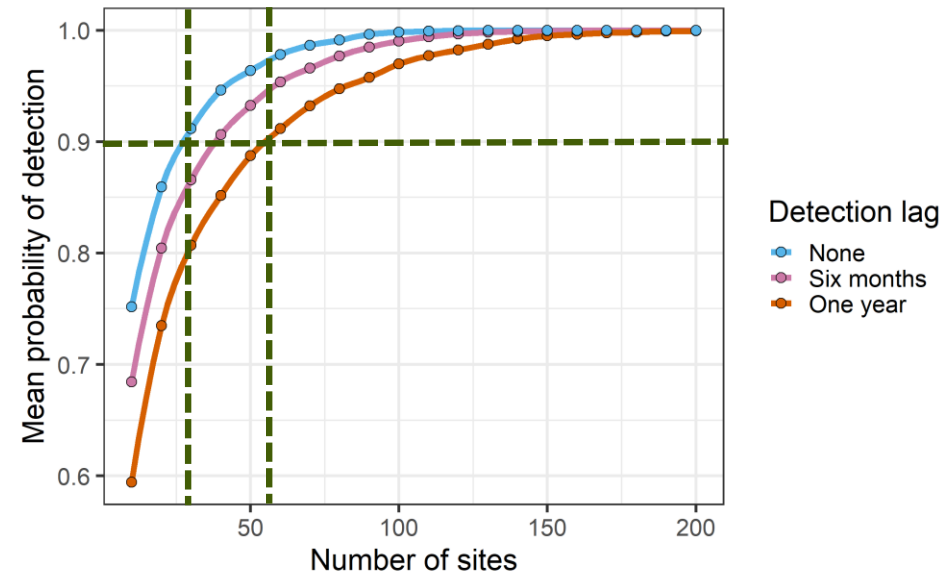


# IMPACT OF EPIDEMIOLOGY AND DETECTION METHOD ON DETECTION ABILITY

## Long distance dispersal



## Lag before detection





# CONSIDERING THE SURVEILLANCE STRATEGY

- We adapt our previous methods to find out **how different surveillance strategies affect our ability to confidently declare pathogen absence**. We consider **visual inspection of hosts, laboratory testing of hosts, and laboratory testing of insect vectors**.

PHILOSOPHICAL  
TRANSACTIONS B

royalsocietypublishing.org/journal/rstb

Research



**Cite this article:** Mastin AJ, van den Bosch F, van den Berg F, Parnell SR. 2019 Quantifying the hidden costs of imperfect detection for early detection surveillance. *Phil. Trans. R. Soc. B* **374**: 20180261. <http://dx.doi.org/10.1098/rstb.2018.0261>

Accepted: 15 January 2019

## Quantifying the hidden costs of imperfect detection for early detection surveillance

Alexander J. Mastin<sup>1</sup>, Frank van den Bosch<sup>2</sup>, Femke van den Berg<sup>3</sup> and Stephen R. Parnell<sup>1</sup>

<sup>1</sup>Ecosystems and Environment Research Centre, School of Environment and Life Sciences, University of Salford, Greater Manchester M5 4WT, UK

<sup>2</sup>Computational and Systems Biology, Rothamsted Research, Harpenden, Hertfordshire AL5 2JQ, UK

<sup>3</sup>Fera, National Agri-Food Innovation Campus, Sand Hutton, York YO41 1LZ, UK

AJM, 0000-0002-9536-3378

The global spread of pathogens poses an increasing threat to health, ecosystems and agriculture worldwide. As early detection of new incursions is key to effective control, new diagnostic tests that can detect pathogen presence shortly after initial infection hold great potential for detection of infection in individual hosts. However, these tests may be too expensive to be implemented at the sampling intensities required for early detection of a new epidemic at the population level. To evaluate the trade-off between earlier



ELSEVIER

Contents lists available at ScienceDirect

Journal of Theoretical Biology

journal homepage: [www.elsevier.com/locate/jtb](http://www.elsevier.com/locate/jtb)



Sampling for disease absence—deriving informed monitoring from epidemic traits

Yoann Bourhis<sup>a,\*</sup>, Timothy R. Gottwald<sup>b</sup>, Francisco J. Lopez-Ruiz<sup>c</sup>, Sujin Patarapuwadol<sup>d</sup>, Frank van den Bosch<sup>a</sup>

<sup>a</sup>Rothamsted Research, Department of Biointeraction and Crop Protection, Harpenden, Herts. AL5 2JQ, UK

<sup>b</sup>US Department of Agriculture, Agricultural Research Service, Ft. Pierce, Florida 34945, USA

<sup>c</sup>Centre for Crop and Disease Management, School of Molecular and Life Sciences, Curtin University, Bentley, WA, Australia

<sup>d</sup>Department of Plant pathology, Faculty of Agriculture at Kamphaeng Saen Kasetsart University, Kamphaeng Saen Campus Nakhon Pathom, 73140, Thailand

ARTICLE INFO

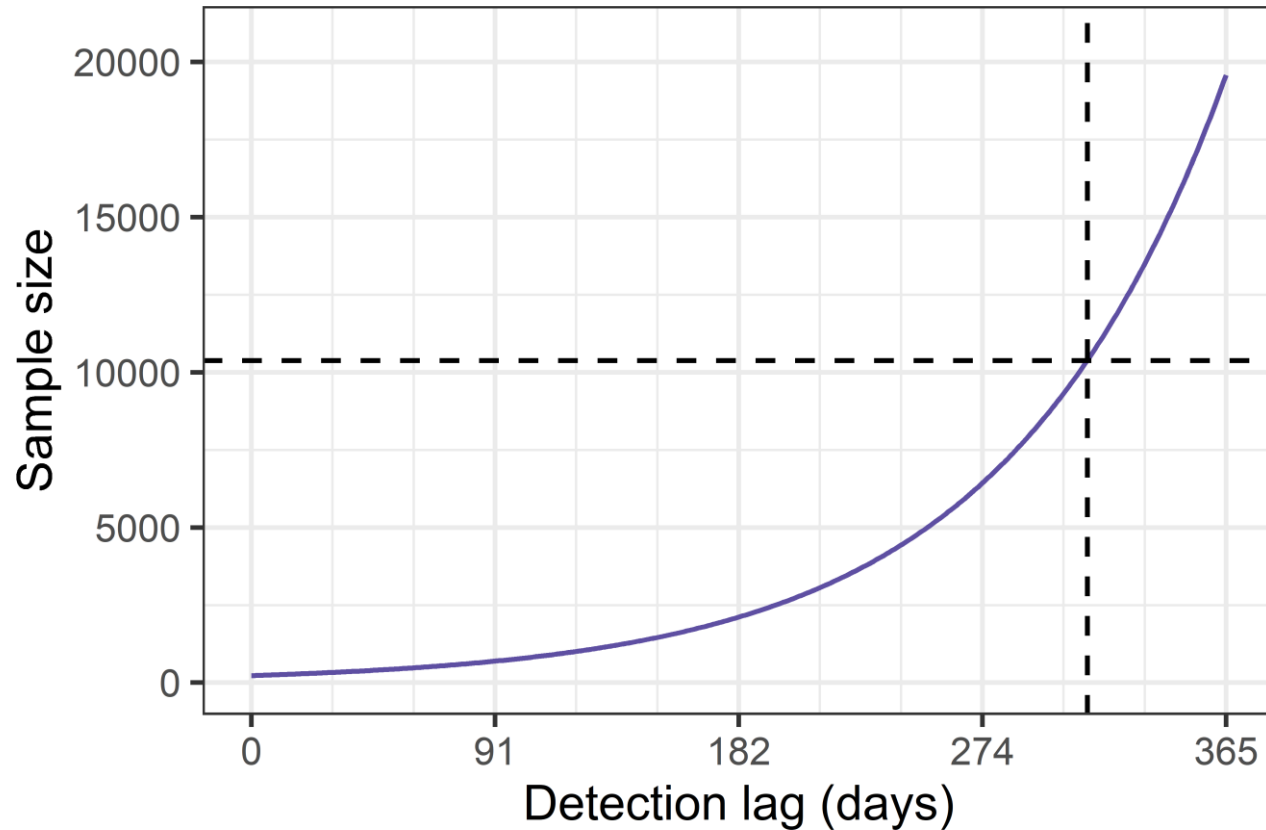
*Article history:*  
Received 17 May 2018  
Revised 13 July 2018  
Accepted 17 October 2018  
Available online 18 October 2018

ABSTRACT

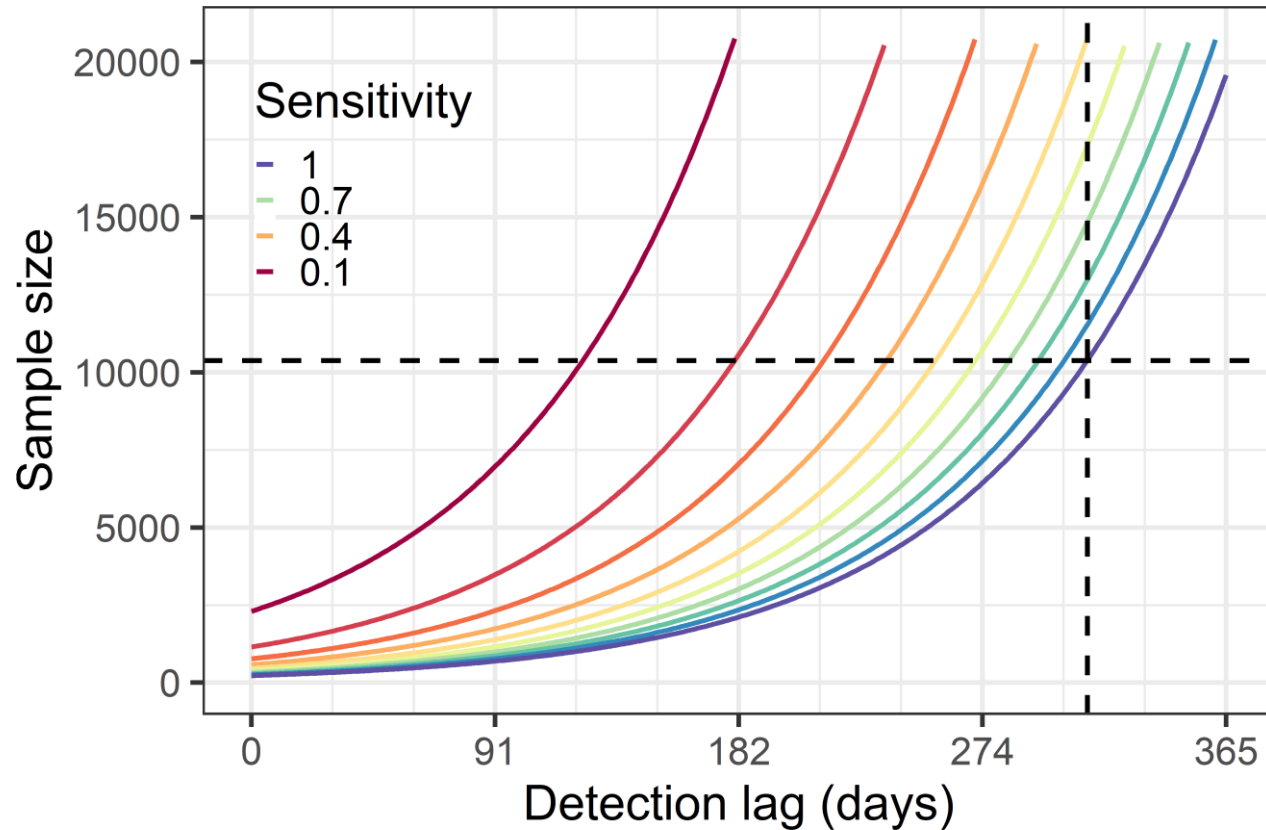
Monitoring for disease requires subsets of the host population to be sampled and tested. If all the samples return healthy, what are the chances the disease was present but missed? In this paper, we developed a statistical approach to solve this problem considering the fundamental infectious diseases: their growing incidence in the host population. The model gives



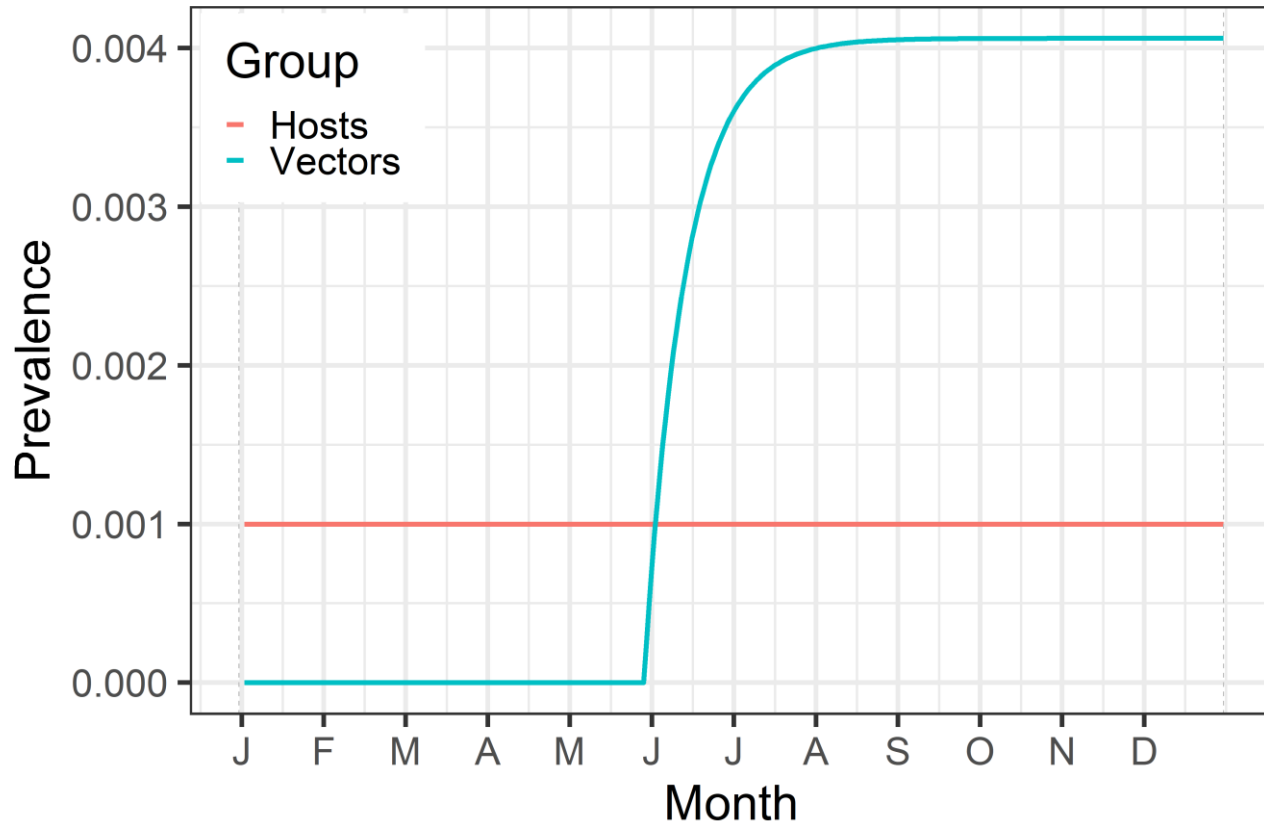
# IMPACT OF DETECTION LAG ON SAMPLE SIZE



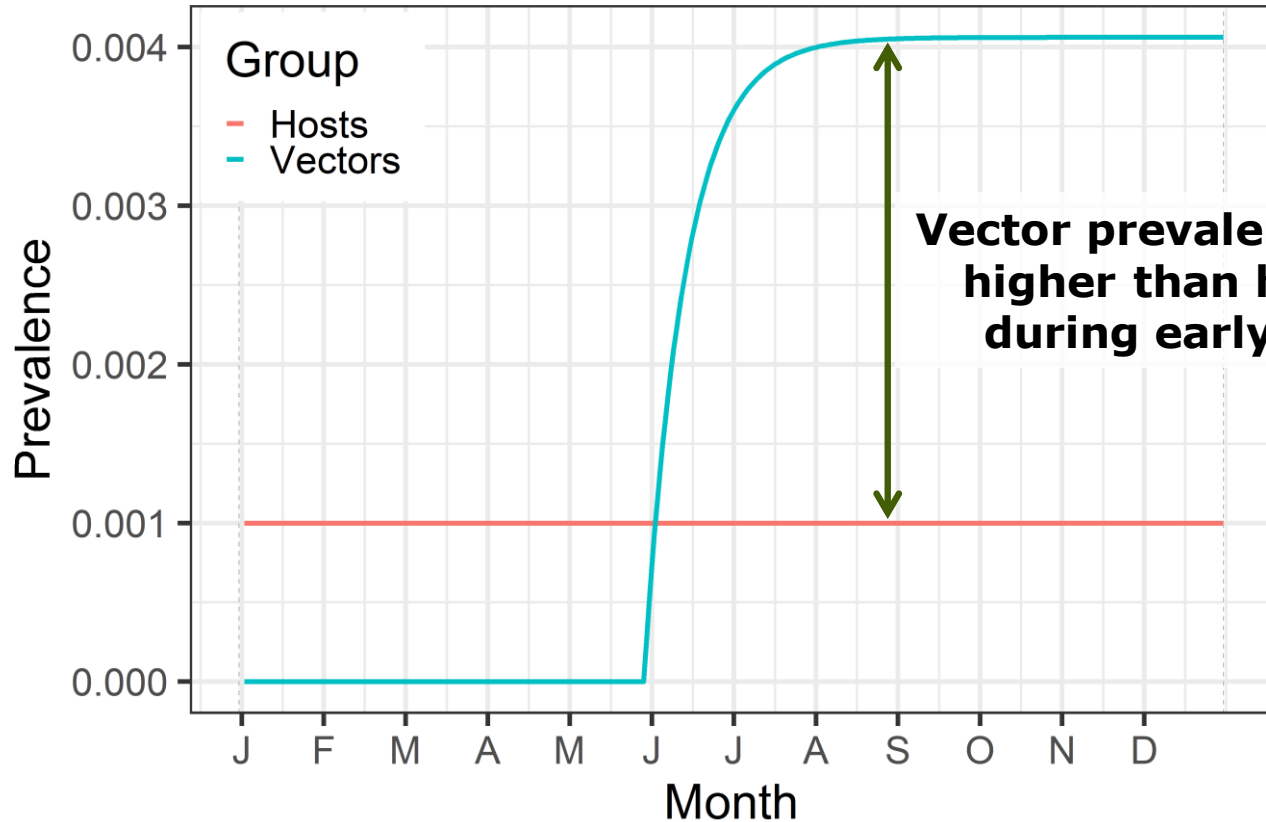
# IMPACT OF DETECTION METHOD ON SAMPLE SIZE



# DETECTABLE PREVALENCE IN HOSTS AND VECTORS



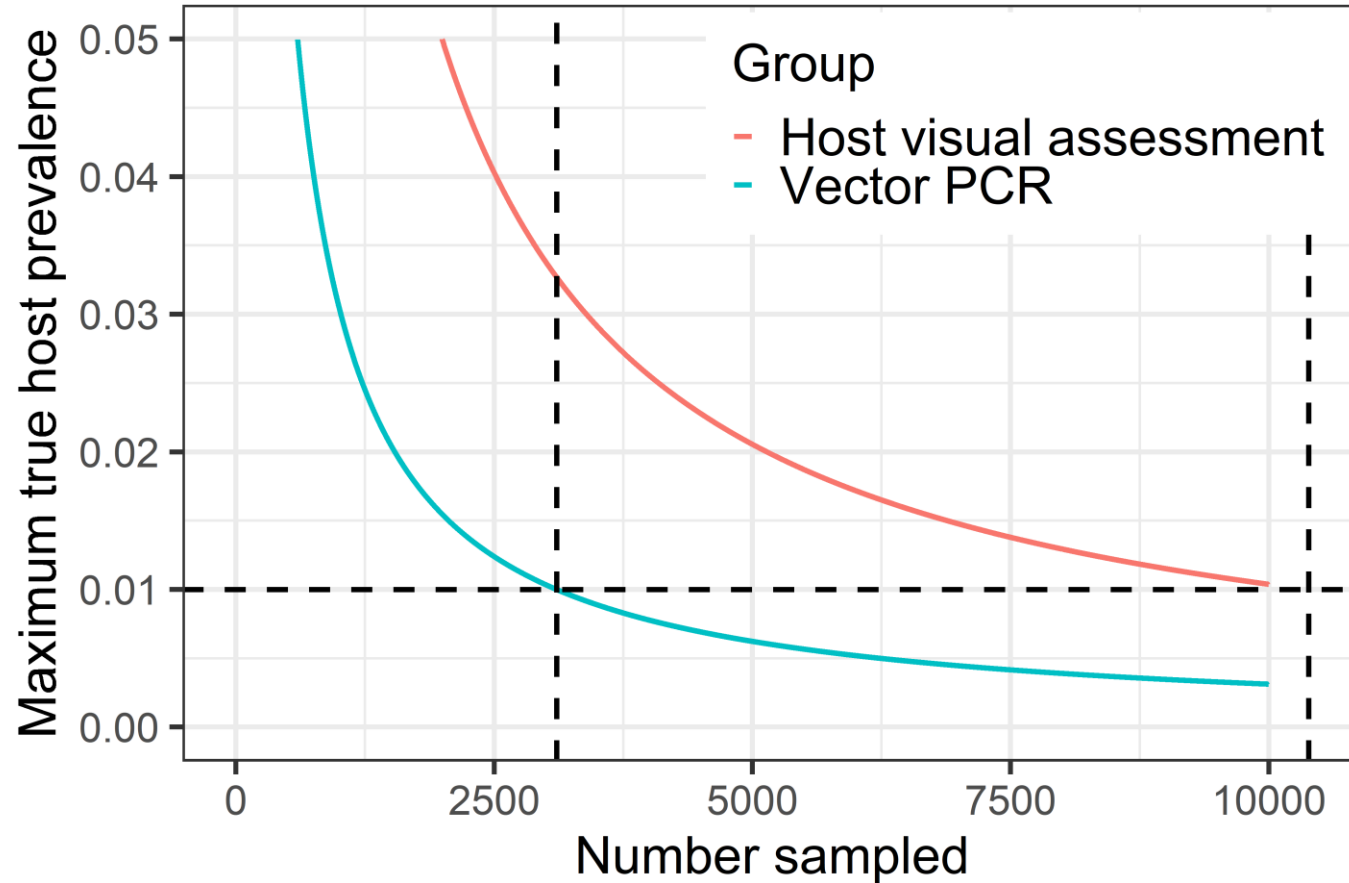
# DETECTABLE PREVALENCE IN HOSTS AND VECTORS



**Vector prevalence up to 4 times higher than host prevalence during early stage spread.**



# VALUE OF VECTOR SURVEILLANCE





# OVERVIEW

- Why do we want to conduct surveillance for *Xylella fastidiosa*?
- Where and how should we should conduct surveillance for *X. fastidiosa* in the uninfected zone of Apulia?
- **Summary and conclusions**



# SUMMARY AND CONCLUSIONS

- **The surveillance aim influences the optimal deployment of survey resources:**
  - Resources should be mainly placed towards the border of the known infected area to maximise the number of detections.
  - Resources should also be placed further from the infected area to maximise the probability of “early detection”.
- **Higher levels of surveillance are required** in order to reliably detect new incursions when:
  - The pathogen can move through **unpredictable, long distance “jumps”**.
  - There is a **detection lag** before infection can be identified.





# SUMMARY AND CONCLUSIONS

- **The rapid rate of spread of *X. fastidiosa* and the length of the presymptomatic period makes visual inspection challenging** when the prevalence threshold for detection is low (for example, when declaring absence of infection).
- **This problem is unlikely to be addressed through the use of host molecular tests**, which would be expected to have both low diagnostic sensitivities in presymptomatic hosts and high costs of deployment.
- **Collection and testing of vectors may solve these problems**, meaning that fewer vectors than hosts would need to be tested. Pooling of vectors for testing reduces the impact of testing costs and make this strategy cost effective.



# ACKNOWLEDGEMENTS

- Maria Saponari, IPSP-CNR, Bari, Italy
- Domenico Bosco, IPSP-CNR, Torino, Italy
- Emilio Guerrieri, IPSP-CNR, Portici, Italy
- Juan Navas-Cortés, IAS-CSIC, Córdoba, Spain
- Daniel Chapman, University of Stirling, UK
- Steven White, CEH Wallingford, UK
  
- Xf-Actors
- BRIGIT consortium

**Thank you all for listening!**