



Developing surveillance strategies for *Xylella fastidiosa* in the Mediterranean region



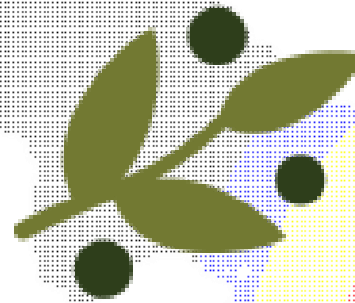
University of
Salford
MANCHESTER

1967 • 2017 50 YEARS



Centre for
Ecology & Hydrology

NATURAL ENVIRONMENT RESEARCH COUNCIL



XF ACTORS

Alexander Mastin (University of Salford)
Steven White (CEH Wallingford)
Daniel Chapman (CEH Edinburgh)
Stephen Parnell (University of Salford)

A decorative green geometric pattern consisting of various triangles and polygons in shades of green and yellow, located in the top-left corner.

PLAN OF TALK

- 1) Surveillance for *Xylella fastidiosa* in Apulia, Italy.
- 2) Optimising surveillance strategies.
- 3) Applying the method to *X. fastidiosa* in Apulia.
- 4) Preliminary conclusions.

1) SURVEILLANCE FOR *XYLELLA FASTIDIOSA* IN APULIA, ITALY

***XYLELLA FASTIDIOSA* IN APULIA**

ruzzo

Molise

Campania

Basilicata

Apulia

**Eradication from southern
Apulia is no longer
considered possible.**

Strona, G., Carstens, C. J., &
Beck, P. S. (2017). *Scientific
Reports*, 7.





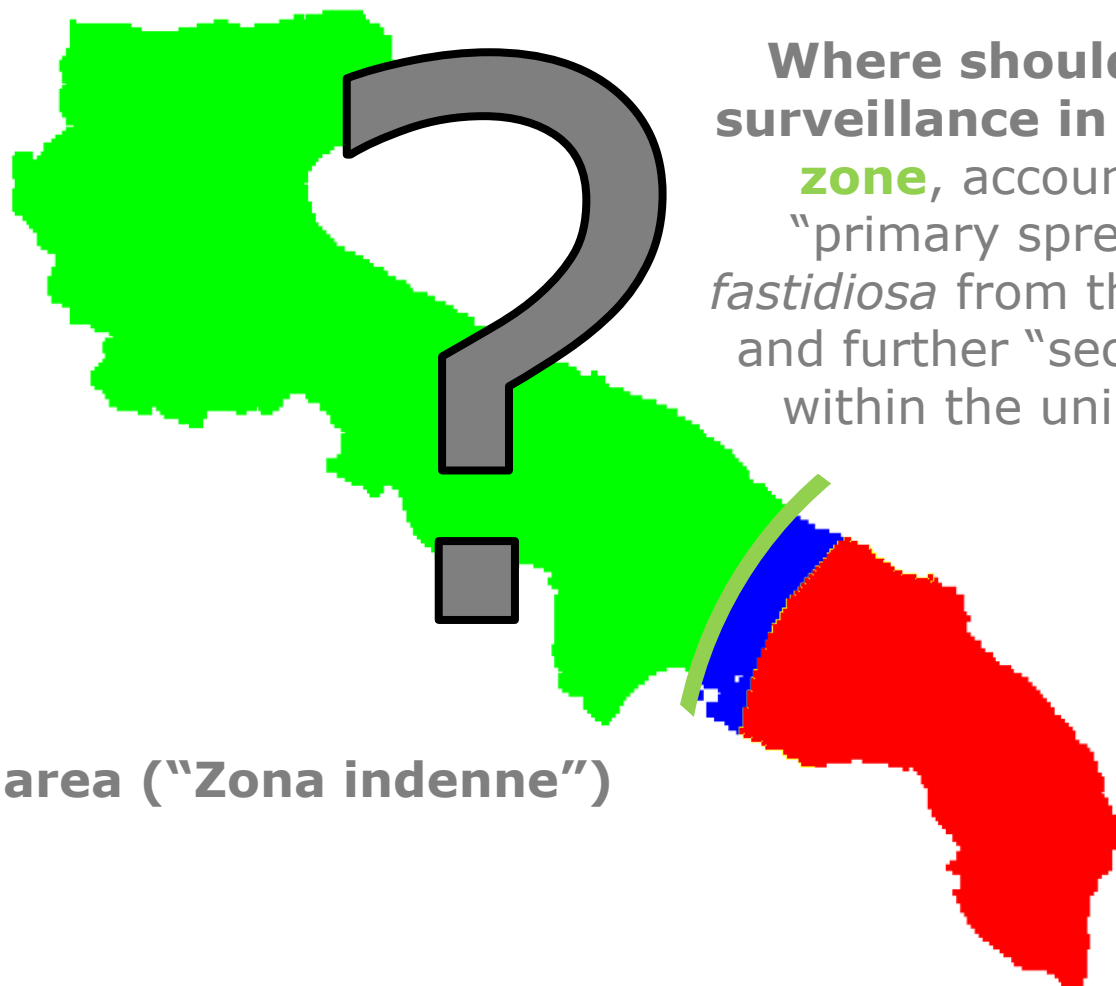
XYLELLA FASTIDIOSA IN APULIA

A large amount of surveillance effort is focussed on the region around the **border of the known infected and uninfected areas.**



Containment area ("Zona contenimento")
30km wide

XYLELLA FASTIDIOSA IN APULIA



Where should we conduct surveillance in the **uninfected zone**, accounting for both “primary spread” of *Xylella fastidiosa* from the infected zone, and further “secondary spread” within the uninfected zone?

Uninfected area (“Zona indenne”)

2) OPTIMISING SURVEILLANCE STRATEGIES

A cluster of green and yellow geometric shapes, resembling leaves or abstract foliage, located in the top-left corner.

XYLELLA FASTIDIOSA IN APULIA

- **Surveillance strategies** are needed to detect **further spread beyond the buffer zone** so that appropriate control and containment measures can be implemented.
- These measures should account for the **biology of the pathogen**.

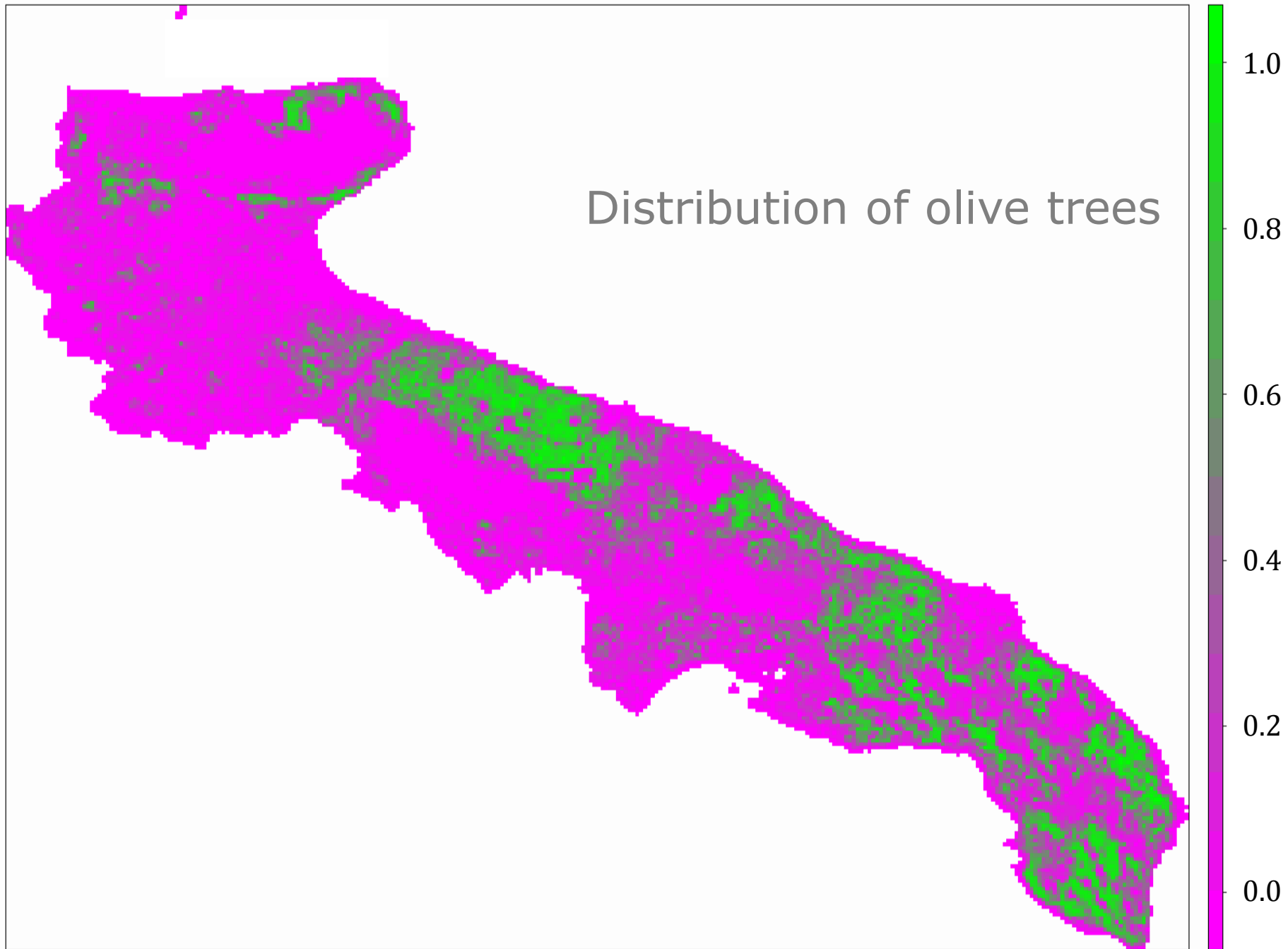
MODELLING SPREAD

Used a **grid-based, stochastic model**
(White, S. M., Bullock, J. M., Hooftman, D. A.,
& Chapman, D. S. (2017). *Biological Invasions*
19(6) 1825-1837):

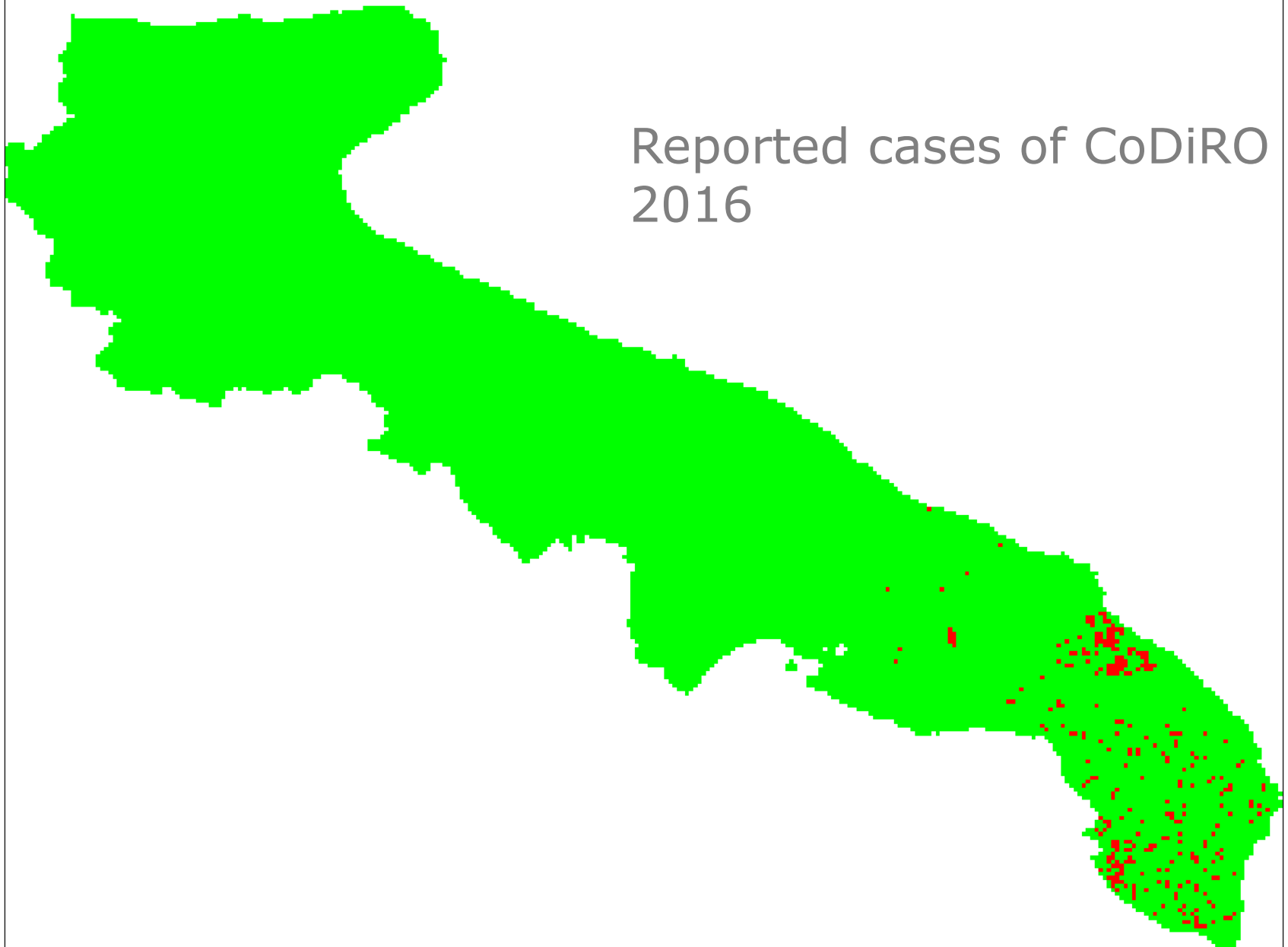
- Deterministic growth in incidence within infected cells
- “Stratified dispersal”:
 - Deterministic shorter-distance, “local”, spread
 - Stochastic longer-distance “jumps”



Distribution of olive trees



Reported cases of CoDiRO 2016



MODELLING LONG DISTANCE SPREAD

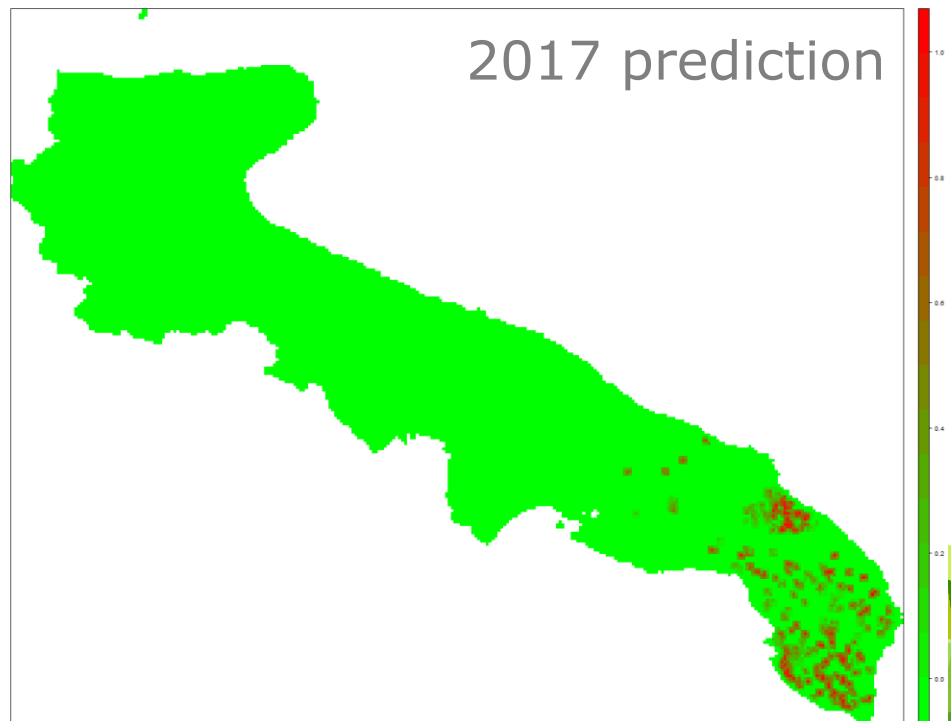
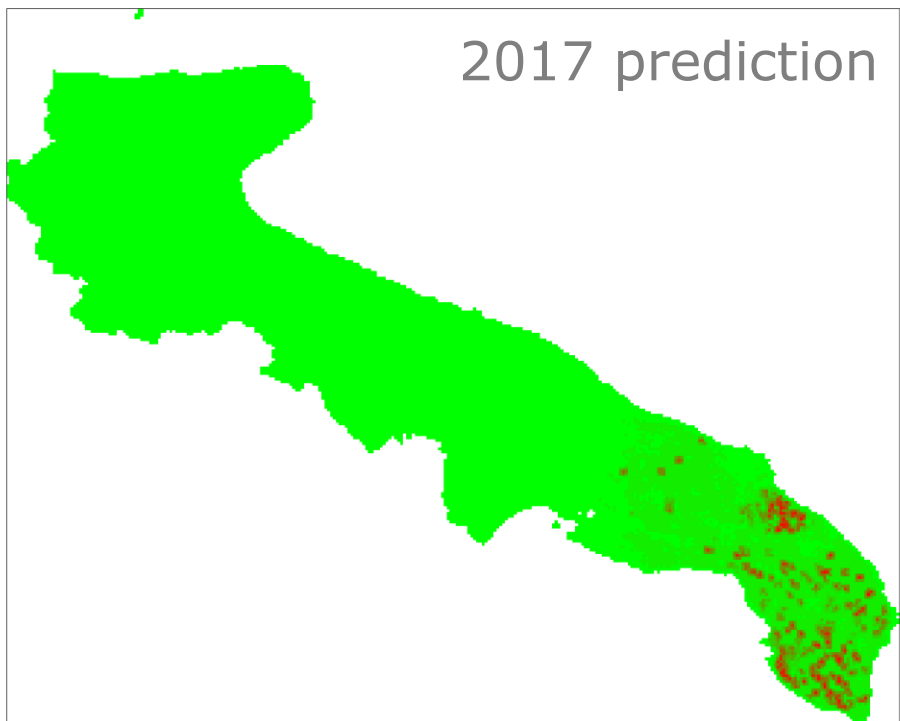
Mean incidence of infection (10,000 realisations)

Default parameters
(Gaussian long distance dispersal)

More long range spread
(Uniform long distance dispersal)

2017 prediction

2017 prediction



MODELLING SPREAD

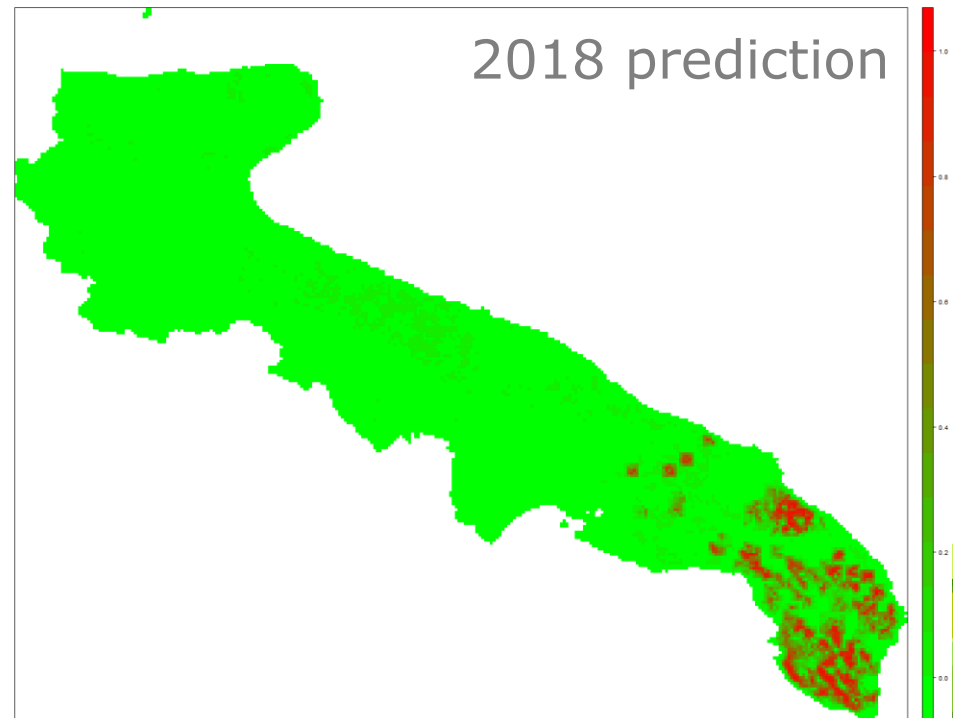
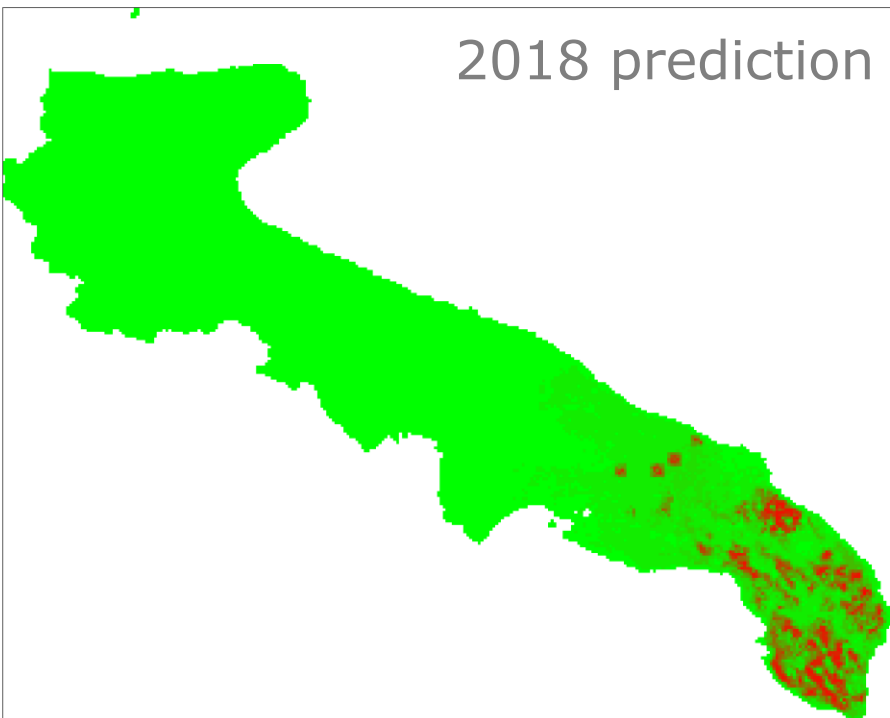
Mean incidence of infection (10,000 realisations)

Default parameters
(Gaussian long distance dispersal)

2018 prediction

More long range spread
(Uniform long distance dispersal)

2018 prediction

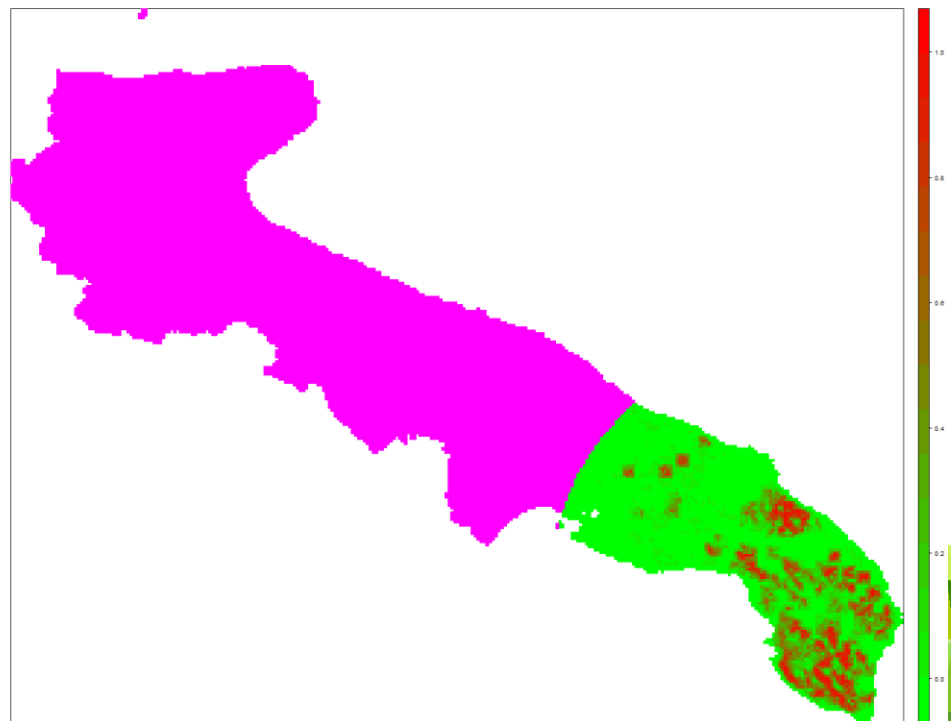
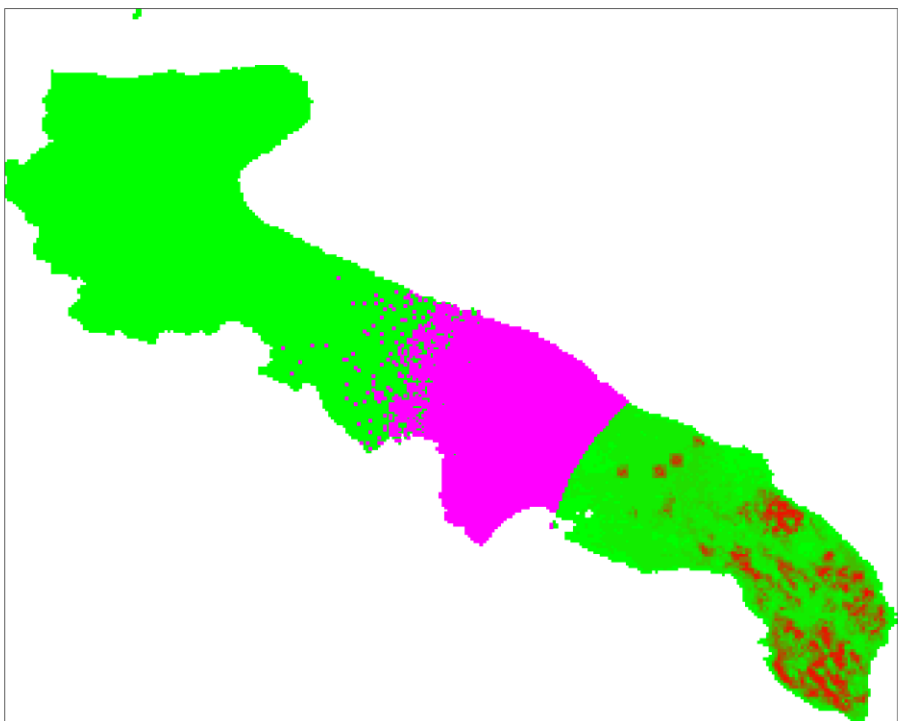


MODELLING SPREAD

Area of Apulian uninfected zone with **at least one predicted incursion** (from 10,000 model realisations, over two years) in the absence of any control/surveillance measures.

Default parameters

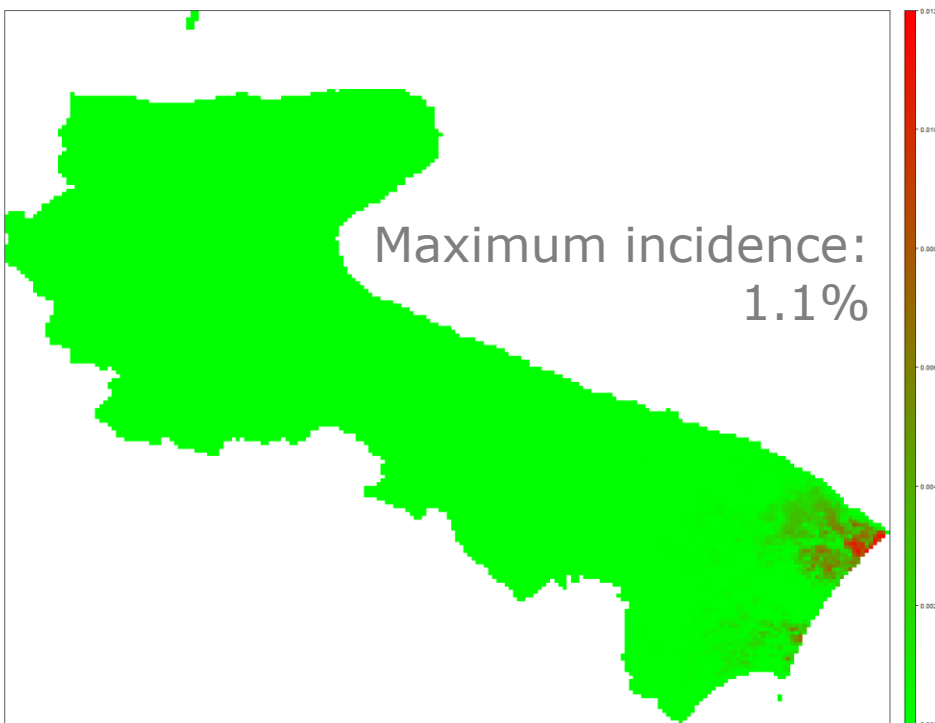
More long range spread



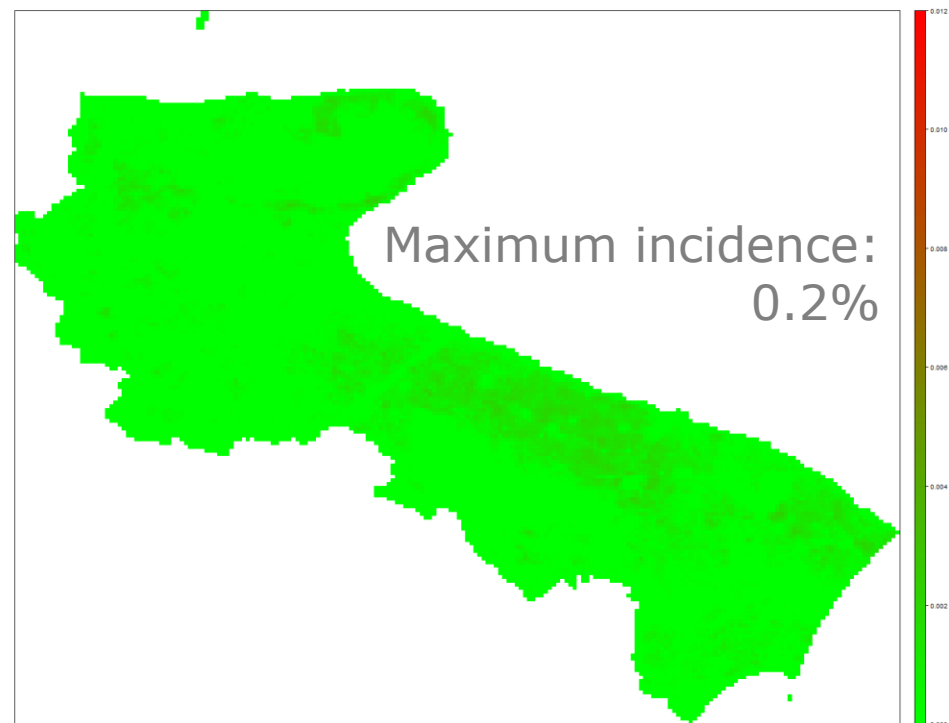
MODELLING SPREAD

Mean incidence in the uninfected zone
(10,000 model realisations).

Gaussian spread



Uniform spread



OPTIMISING SURVEILLANCE

- We want our surveillance strategy to **minimise the probability of failing to detect infection.**
- We can calculate this probability when we inspect:
 - N locations
 - x trees per location

When the incidence in each location is p_n

$$P(\text{no det}) = \prod_{n=1}^N (1 - p_n)^x$$

OPTIMISING SURVEILLANCE

- We want our surveillance strategy to **minimise the probability of failing to detect infection.**
- We can calculate this probability when we inspect:
 - N locations
 - x trees per location

When the incidence in each location is p_n

$$P(\text{no det}) = \prod_{n=1}^N (1 - p_n)^x$$

Probability of not selecting an infected tree, **if we took one sample from site n**

OPTIMISING SURVEILLANCE

- We want our surveillance strategy to **minimise the probability of failing to detect infection.**
- We can calculate this probability when we inspect:
 - N locations
 - x trees per location

When the incidence in each location is p_n

$$P(\text{no det}) = \prod_{n=1}^N (1 - p_n)^x$$

Probability of not selecting **any** infected trees, **when we sample x trees from site n**

OPTIMISING SURVEILLANCE

- We want our surveillance strategy to **minimise the probability of failing to detect infection.**
- We can calculate this probability when we inspect:
 - N locations
 - x trees per location

When the incidence in each location is p_n

$$P(\text{no det}) = \prod_{n=1}^N (1 - p_n)^x$$

Probability of not selecting any infected trees, **when we sample all N sites, with x trees from each**

OPTIMISING SURVEILLANCE

- *X. fastidiosa* CoDiRO is characterised predominantly by “secondary spread” (i.e. within olive groves)
- To account for this, we used two consecutive years' incidence predictions (p_{n_1} and p_{n_2}):

$$P(\text{no det}) = \prod_{n=1}^N (1 - p_{n_1})^x (1 - p_{n_2})^x$$

OPTIMISING SURVEILLANCE

- *X. fastidiosa* CoDiRO is characterised predominantly by “secondary spread” (i.e. **within** olive groves)
- To account for this, we used two consecutive years' incidence predictions (p_{n_1} and p_{n_2}):

$$P(\text{no det}) = \prod_{n=1}^N (1 - p_{n_1})^x (1 - p_{n_2})^x$$

Probability of not selecting any infected trees **in either year 1 or 2,** when we sample all N sites, with x trees from each

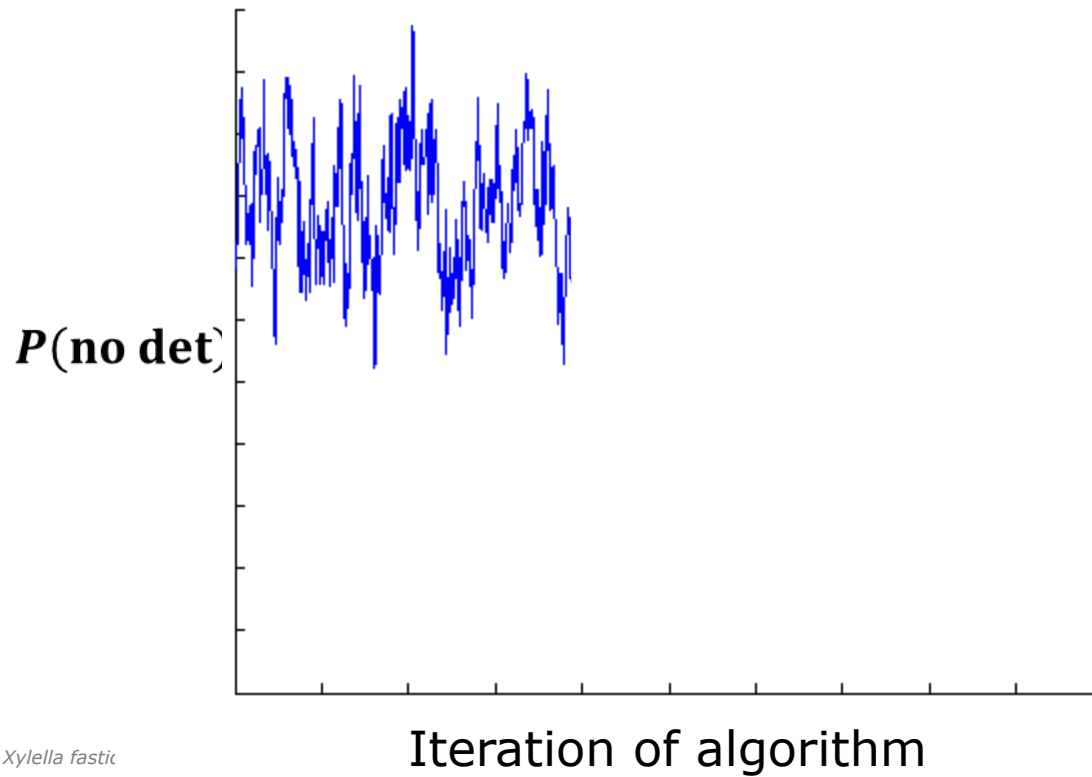
A decorative green geometric pattern in the top-left corner, composed of various shades of green triangles and polygons.

OPTIMISING SURVEILLANCE

- For **any** set of N sites, we can estimate the probability of failing to detect infection.
- We need a way of finding the combination of sites which **minimises** this probability.
- However, the number of combinations of sites is too great to evaluate all possible combinations.
- We can use **algorithmic optimisation routines** (such as **simulated annealing**) to identify the best combination without having to evaluate all combinations.

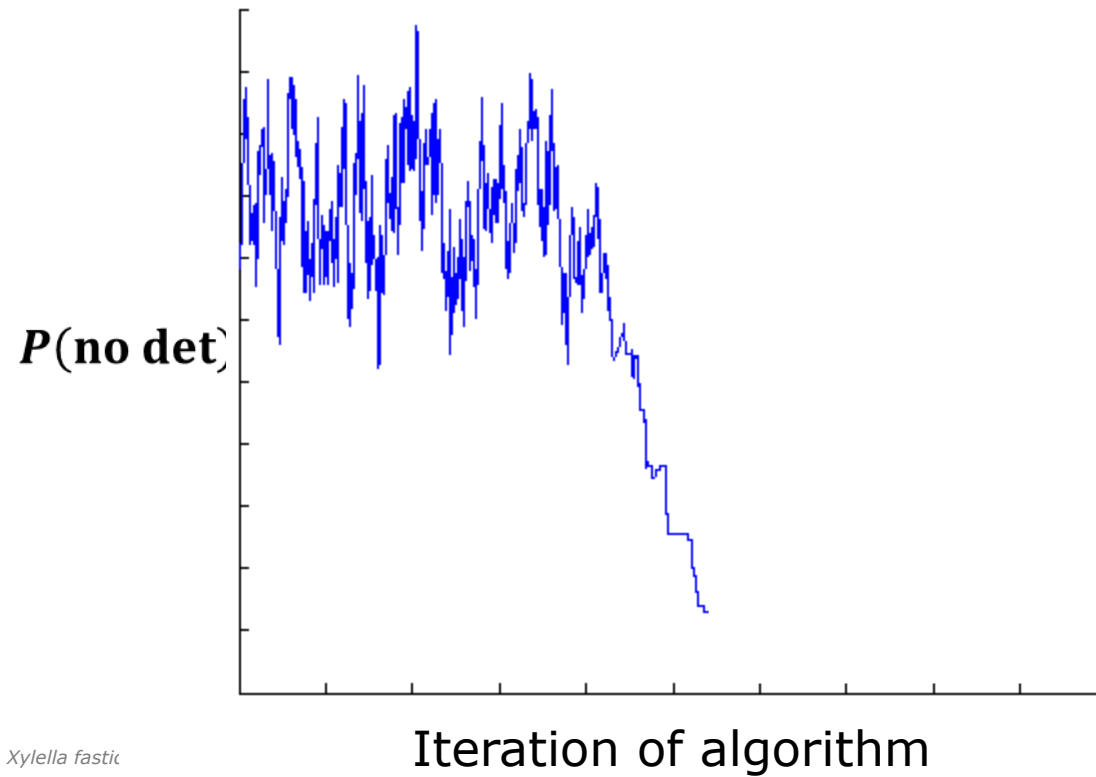
SIMULATED ANNEALING

Exploring the parameter space



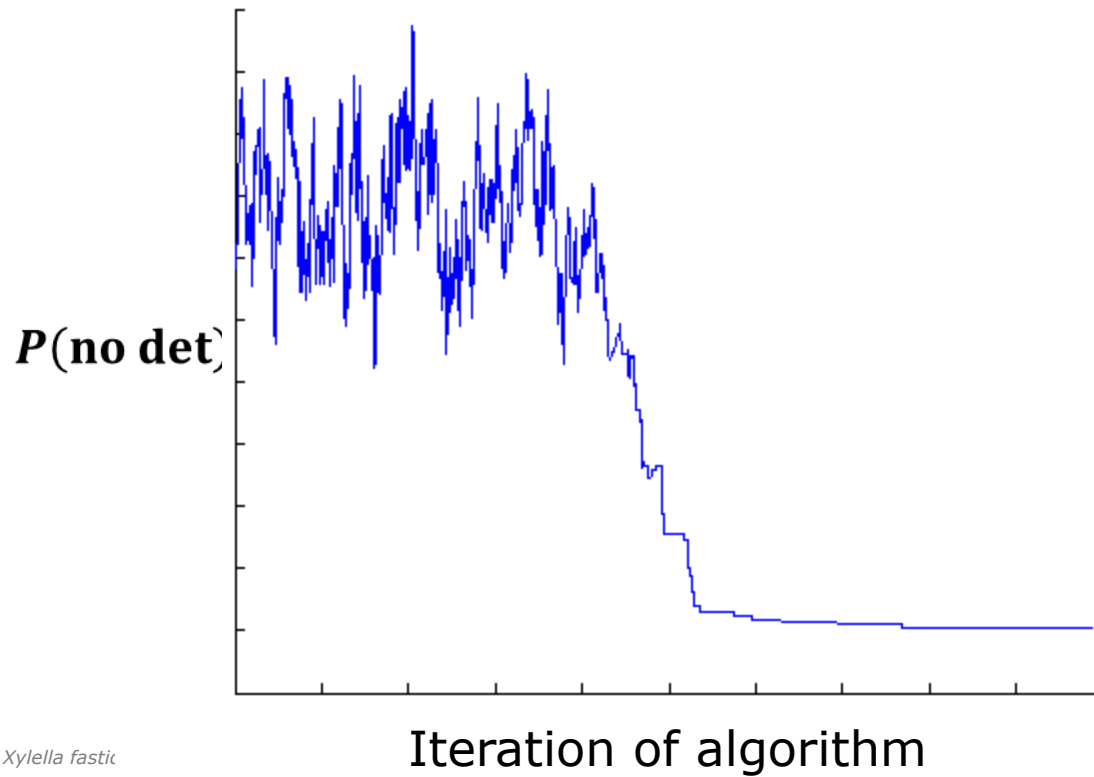
SIMULATED ANNEALING

Rejecting poor selections



SIMULATED ANNEALING

Identifying optimal locations



A decorative graphic in the top-left corner consisting of overlapping green and yellow triangles of various sizes.

SIMULATED ANNEALING

- We used simulated annealing to identify **which locations should be sampled in order to minimise the probability that we fail to detect infection.**
- We assumed that an average of **1 tree per hectare** was inspected (100 trees per km² grid cell).
- We repeated this approach for **different numbers of sample locations** – from 50 to 500.

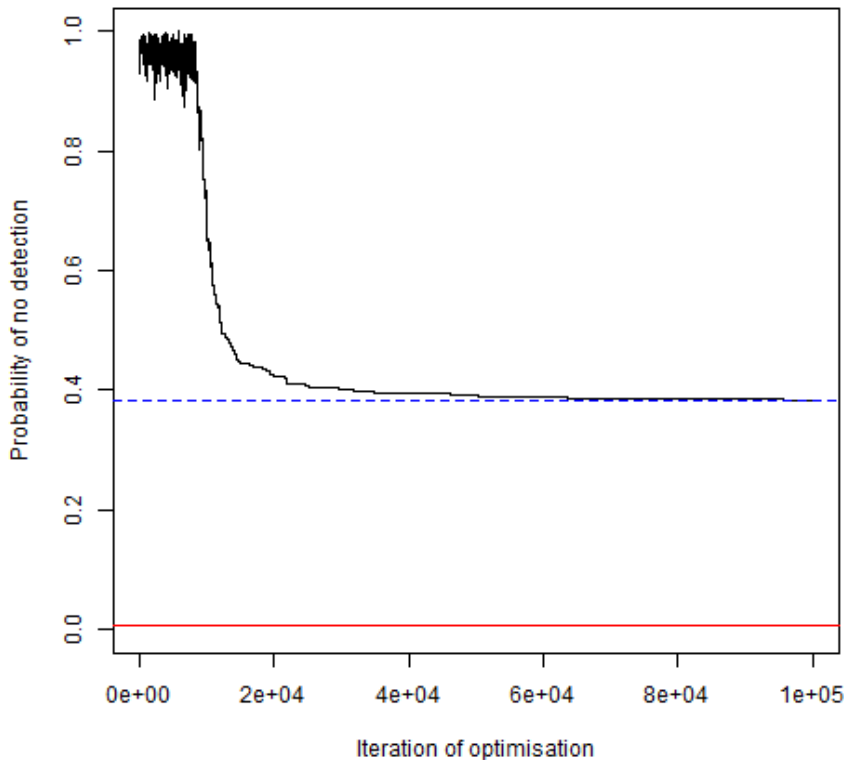
APPLYING THE METHOD TO *X. FASTIDIOSA* IN APULIA: PRELIMINARY RESULTS

PRELIMINARY RESULTS

Probability of no detection when sampling 100 trees in each of a specified number of sites:

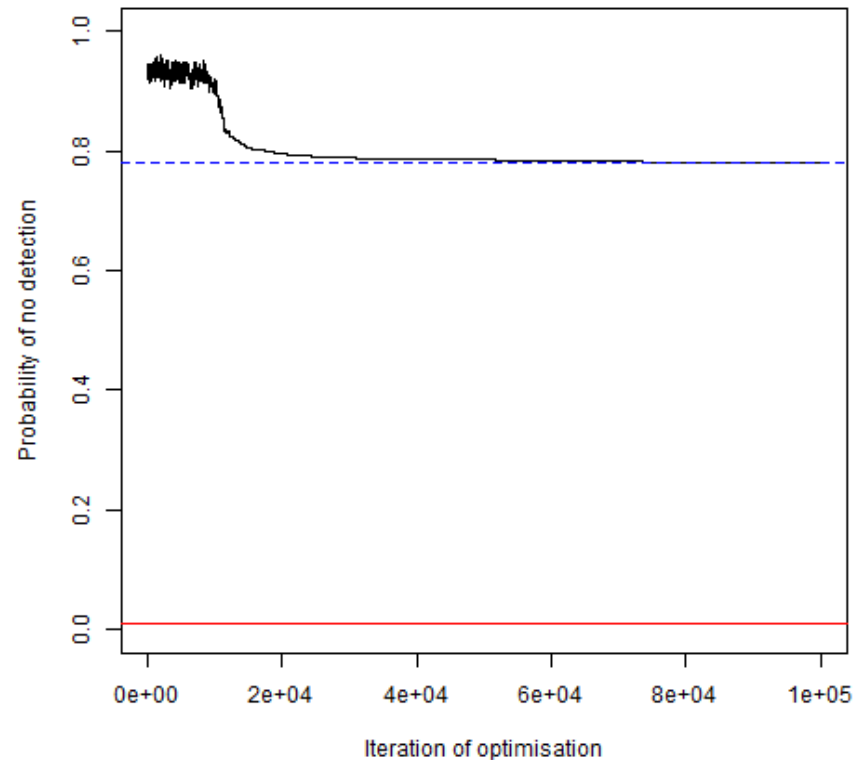
Default parameters

50 sites. Final probability of no detection: 0.38

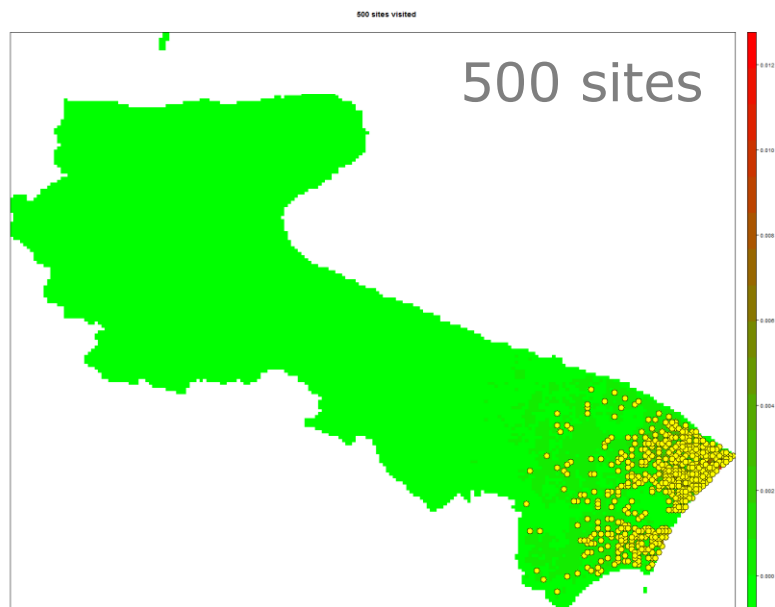
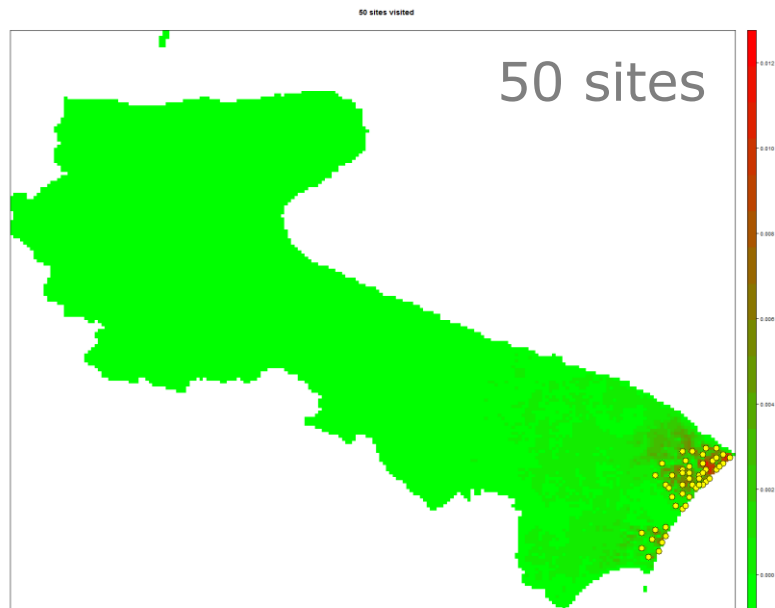


More long range spread

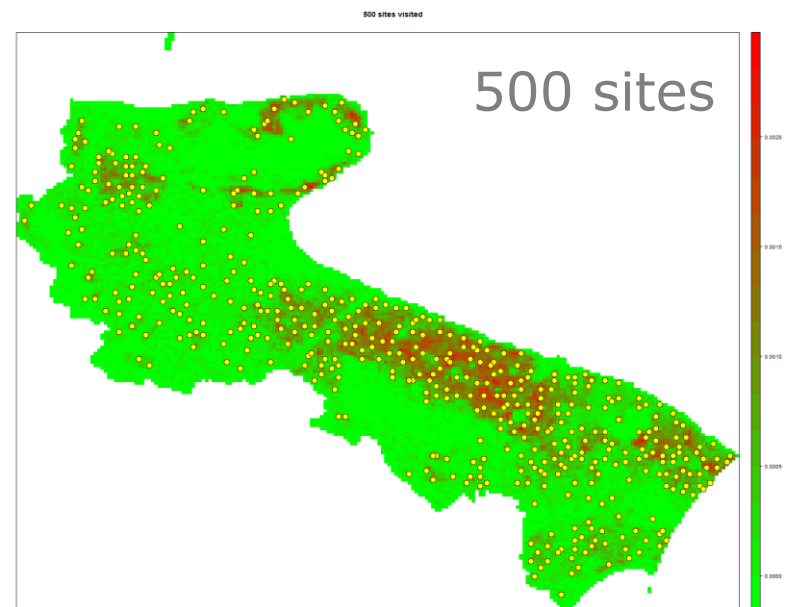
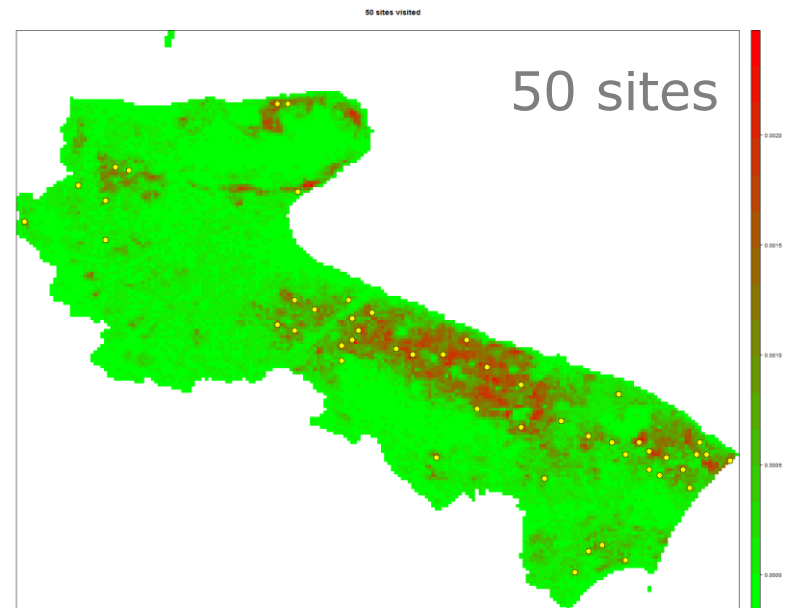
50 sites. Final probability of no detection: 0.78



Default parameters



More long range spread

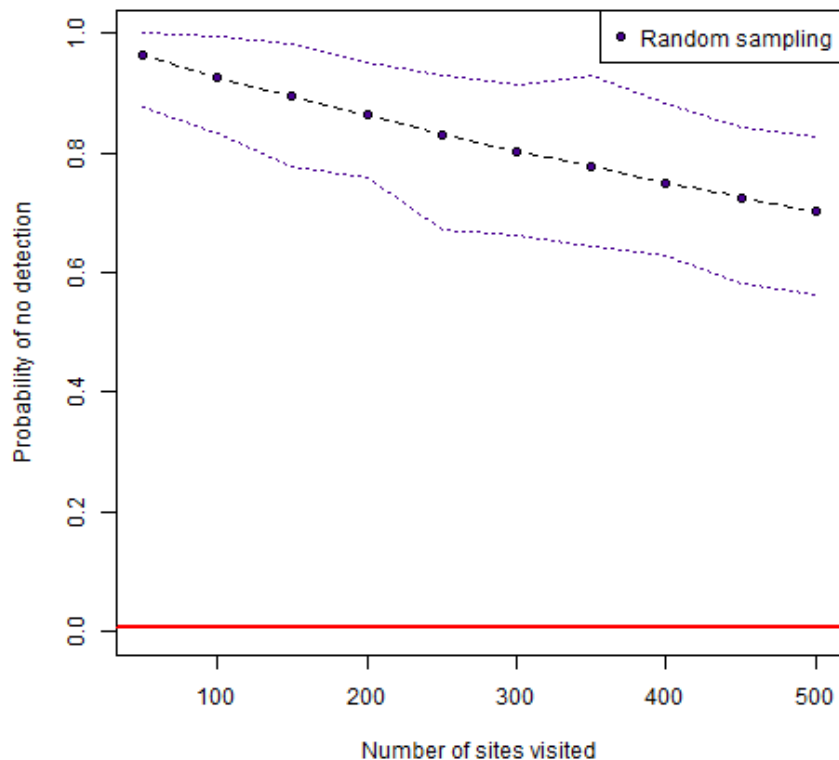


PRELIMINARY RESULTS

Probability of no detection when visiting a specified number of sites **randomly** from the population:

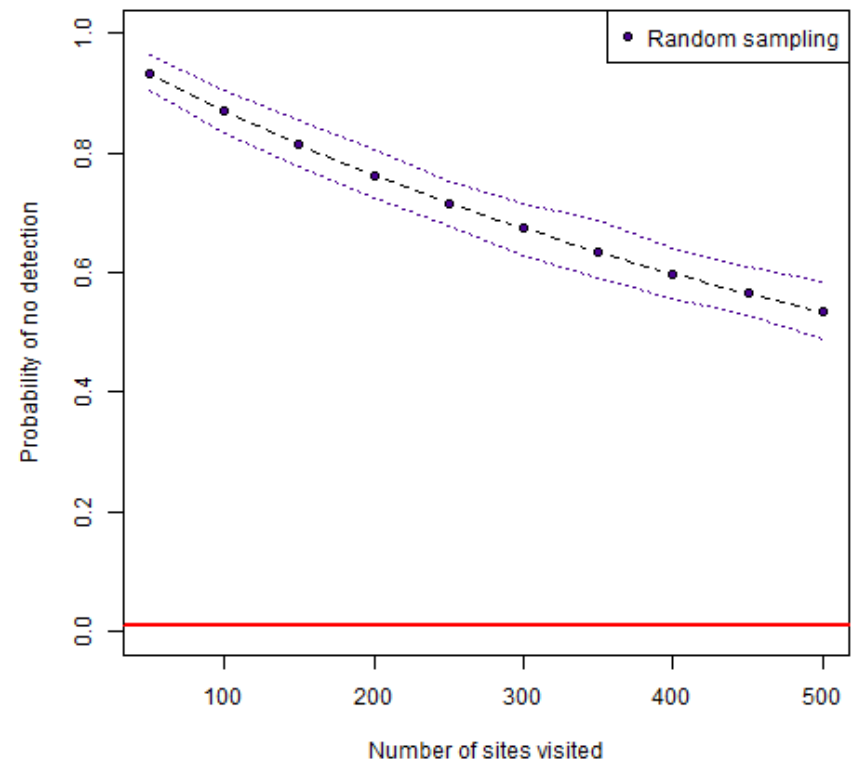
Default parameters

Probability of no detection when 100 samples collected per site



More long range spread

Probability of no detection when 100 samples collected per site

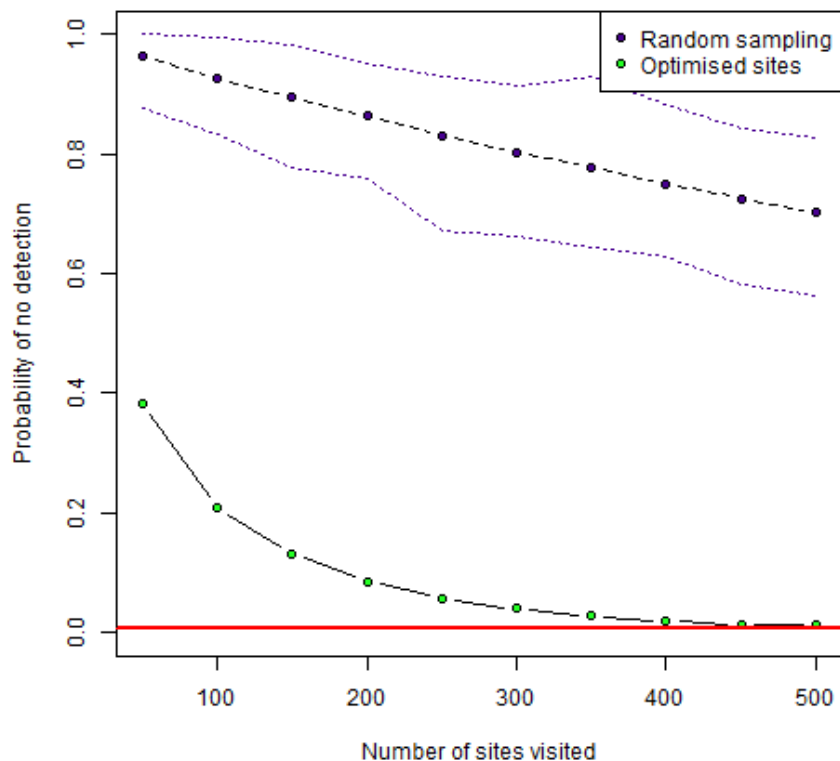


PRELIMINARY RESULTS

Probability of no detection when visiting the specified number of **optimal sites**:

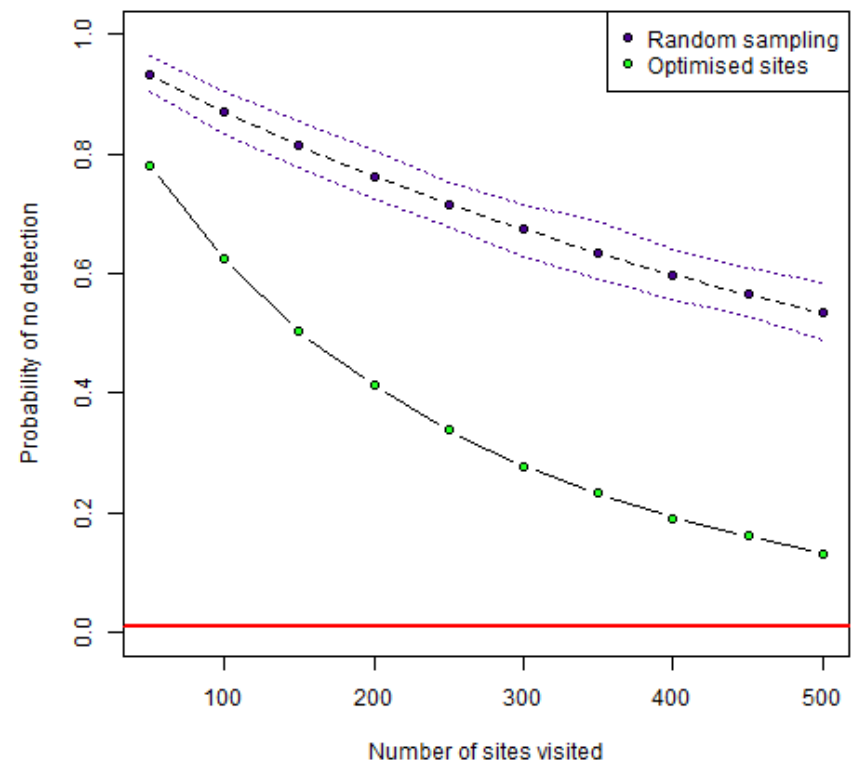
Default parameters

Probability of no detection when 100 samples collected per site



More long range spread

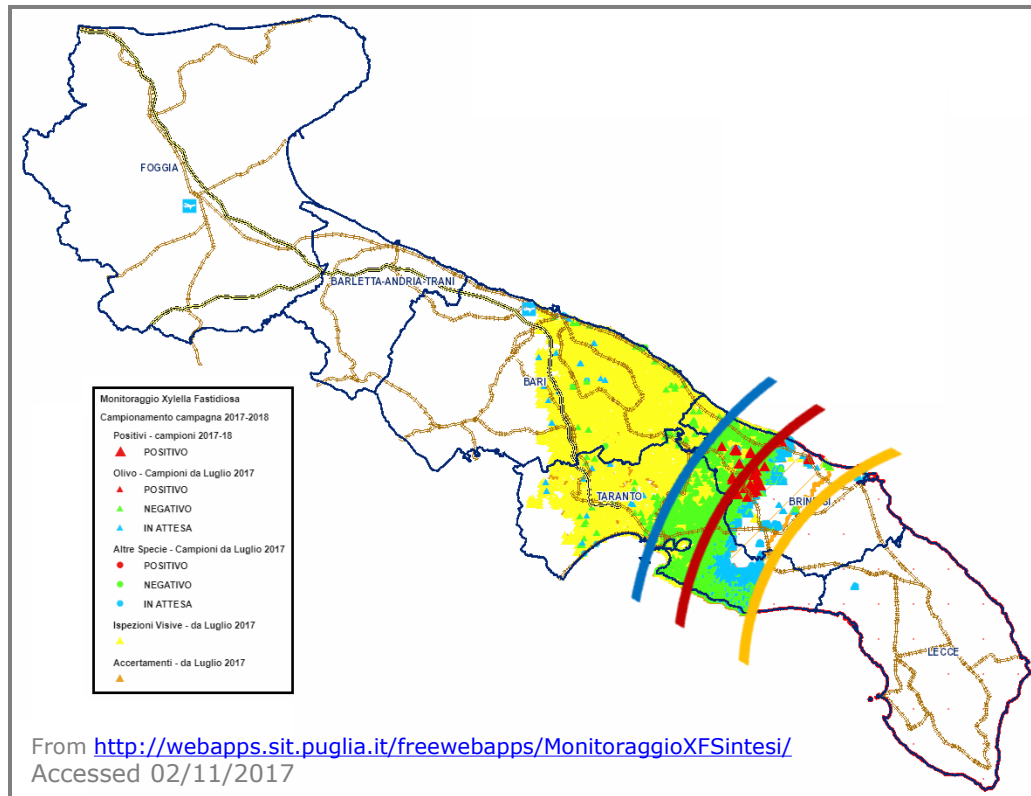
Probability of no detection when 100 samples collected per site



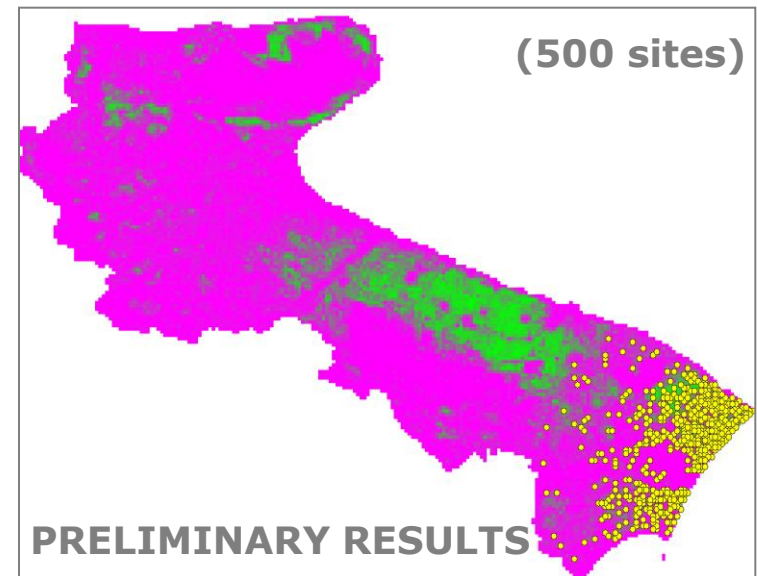
PRELIMINARY CONCLUSIONS

SURVEILLANCE COMPARISON: DEFAULT PARAMETERS

Actual surveillance, 2017

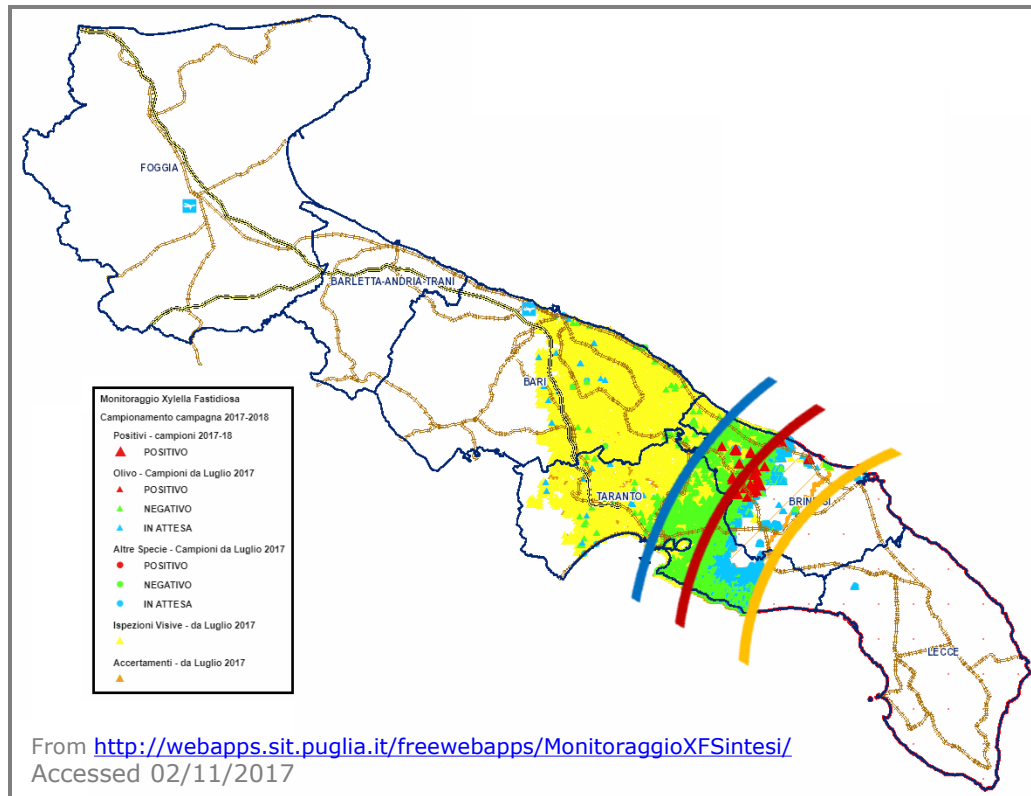


Optimal surveillance

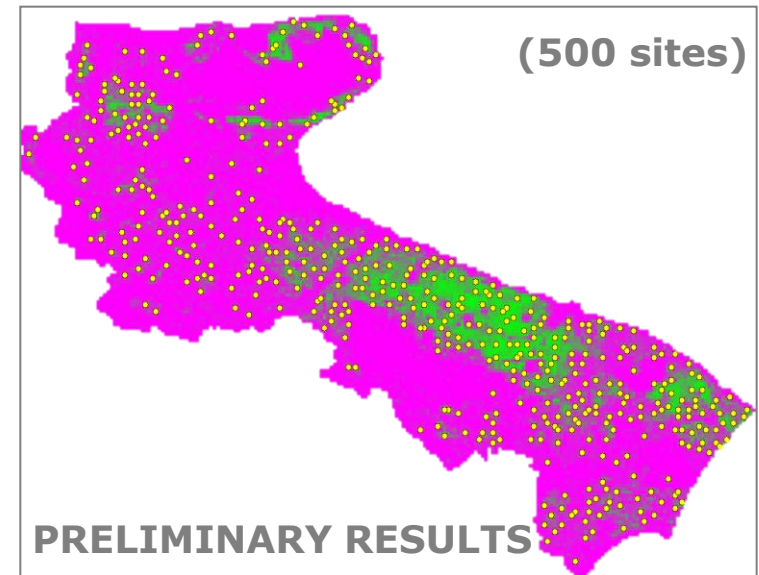


SURVEILLANCE COMPARISON: LONG DISTANCE SPREAD

Actual surveillance, 2017



Optimal surveillance



PRELIMINARY CONCLUSIONS

- **Simulation models** of *Xylella fastidiosa* spread can be used to identify **where best to conduct surveillance** in the uninfected zone of Apulia.
- The best place to conduct surveillance depends on the **nature of pathogen spread** from the infected zone – and may not always be close to the buffer zone boundary.
- Correctly **characterising this long-distance spread is crucial**, this is now the focus of work with the CEH to improve upon our current (provisional) findings.

Thank you!



European
Commission

Horizon 2020
European Union funding
for Research & Innovation



University of
Salford
MANCHESTER

1967 • 2017 50 YEARS



**Centre for
Ecology & Hydrology**

NATURAL ENVIRONMENT RESEARCH COUNCIL



Steven White (CEH Wallingford)



Daniel Chapman (CEH Edinburgh)



Stephen Parnell (University of Salford)

**This project is funded by the European Commission
as part of the Horizon 2020 program**

(SFS-09-2016, XF-ACTORS, grant agreement 727987)