

# A Multi-Agent System for Modelling the Spread of Lethal Wilt in Oil-Palm Plantations

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## Importance of oil palm:

- Cooking products
- Cleaning products
- Special greases and lubricants
- Personal hygiene and cosmetics
- Production of biodiesel and electrical energy
- Pharmaceutical

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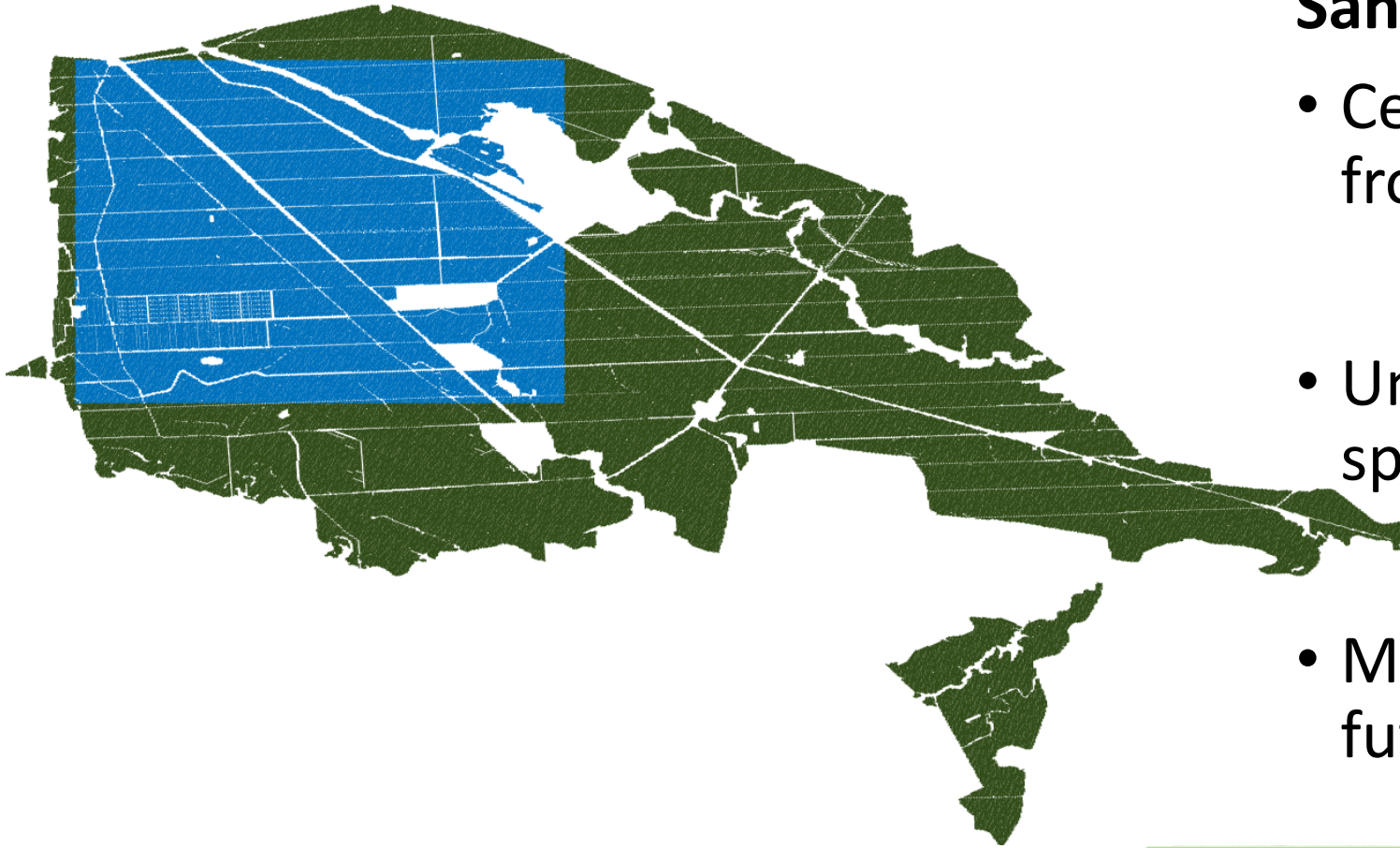
# What is the issue with Lethal Wilt ?

- Infectious vector not fully determined yet
- Loss and delay of production and increased insurance premiums
- Detrimental to sustainable production



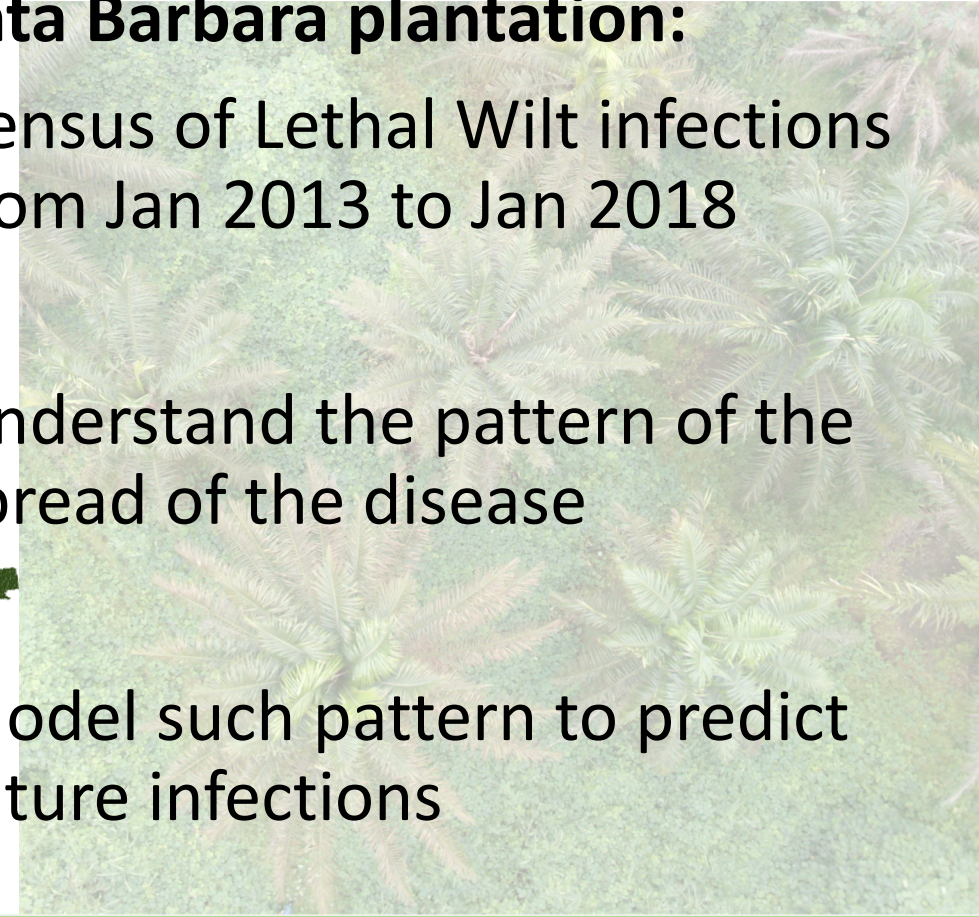
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# Data used and Objectives



## Santa Barbara plantation:

- Census of Lethal Wilt infections from Jan 2013 to Jan 2018
- Understand the pattern of the spread of the disease
- Model such pattern to predict future infections



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# Sustainable agriculture



- The plantation is on land used previously for other crops, no deforestation
- Maximizing the production of the plantation allows for sustainable growth with no deforestation or increasing more land used
- Modelling enables this

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# Related work

Modelling in agriculture has increased significantly in applications that support sustainability and efficiency:

- Work has been done to model biodiversity vs. income to small producers studying synergies between development and conservation
- Remote sensing supports optimisation of crop management
- Many works use agents to model epidemiological processes.

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# Collating and organising the data

- We chose a square section of the plantation's census data, and organised it in a grid of NxN cells
- We performed the analysis of different granularities to determine if a consistent pattern could be identified
- We analysed the frequency of reinfection in each cell and in its neighbours
- The result are consistent at each granularity level thus confirming the spread is local

TABLE I  
CELL RISK OF INFECTION AT VARYING GRANULARITIES (WINDOWS = 6)

Grid	RI	PNI	ANI	NI	NNI
$8^2$	0.94	0.83	0.99	0.56	0.04
$16^2$	0.67	0.64	0.95	0.33	0.14
$32^2$	0.4	0.38	0.71	0.15	0.08
$64^2$	0.1	0.1	0.28	0.05	0.03

TABLE II  
CELL RISK OF INFECTION AT VARYING WINDOWS (GRANULARITY =  $32^2$ )

Window	RI	PNI	ANI	NI	NNI
1	0.15	0.13	0.14	0.06	0.05
3	0.28	0.27	0.54	0.11	0.07
6	0.4	0.38	0.71	0.15	0.08
12	0.57	0.53	0.86	0.02	0.08

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# Modelling the infection path

We propose a multi-agent based approach

- Agents take a directed walk from all newly infected cells, and predict the spread based on the cells where these agents end and the number of times each cell is visited
- There are two stages to the proposed model:
- With Kernel Density Estimation (KDE) areas with more infections have a higher density, directing agent's walk
- Subsequently, each agent is biased to walk 'uphill' towards denser areas

$$\hat{f}(x) = \frac{1}{N} \sum_{i=1}^n K\left(\frac{x - x(i)}{h}\right)$$

$$P_{cn_i} = \frac{d_i}{\sum_{j=1}^8 d_j}$$

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# Metrics

We evaluate the performance in terms of True Positives (TP), True Negatives (TN), False Positives (FP), and False Negatives (FN)

- We evaluate the precision **P** of the model:
- The model's recall score **R**:
- And the *Rand Index* **RI** which is essentially the overall accuracy of the model:

$$P = \frac{TP}{TP + FP}$$

$$R = \frac{TP}{TP + FN}$$

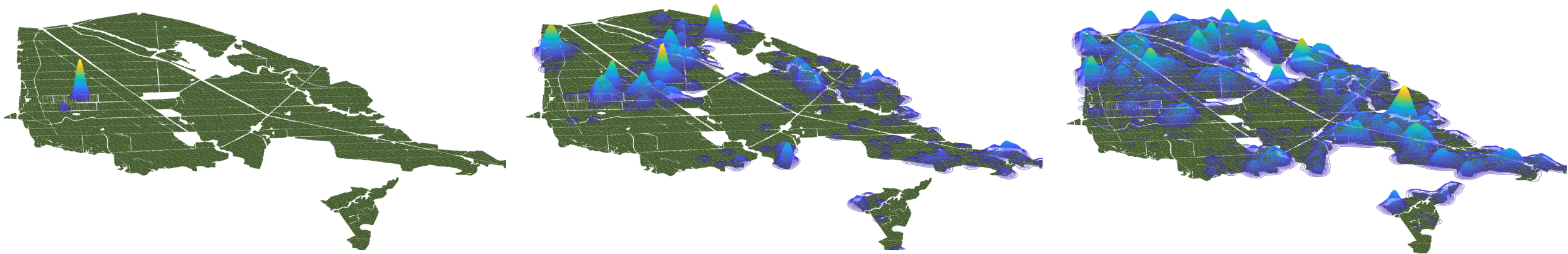
$$RI = \frac{TP + TN}{TP + FN + TN + FP}$$

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# Results

The modelling is done comparing to the ground truth distribution from the census of infection densities, estimated to the final time-step as below

Due to the stochastic nature of the model, for each experiment we present the mean (and deviation) of 100 runs

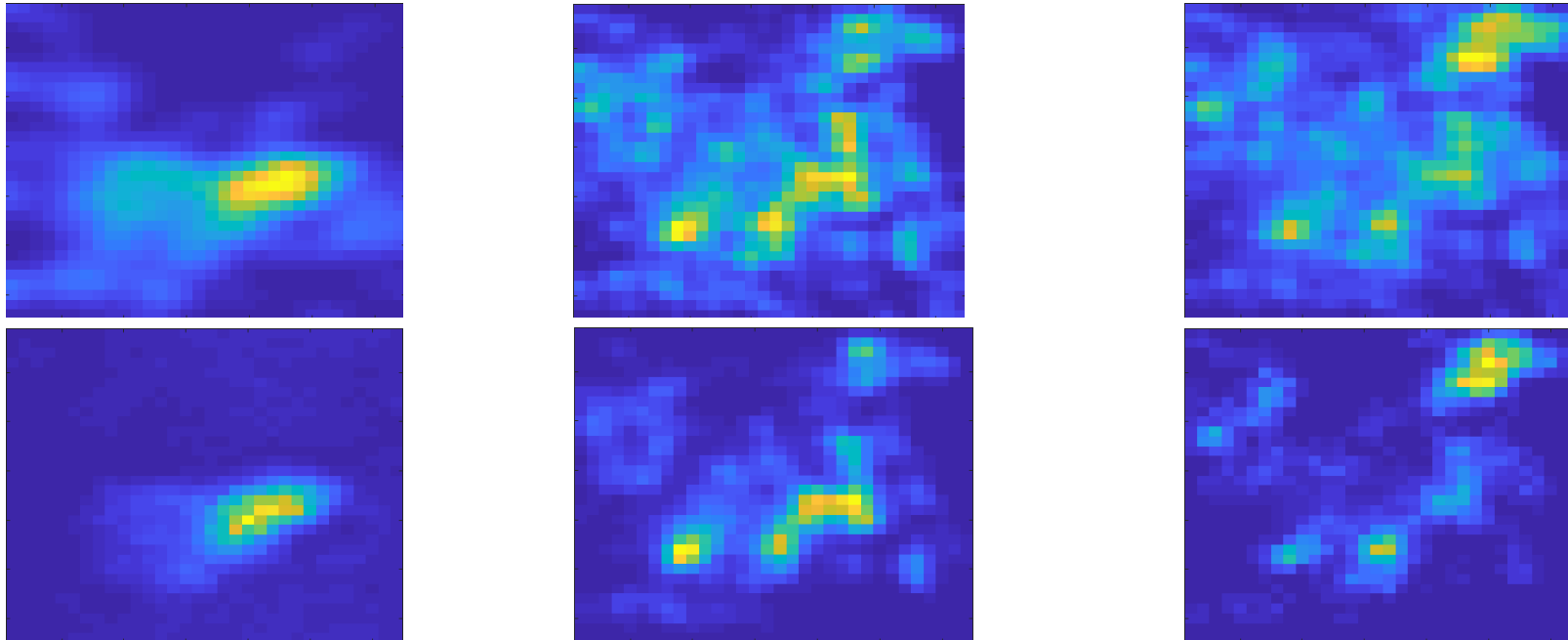


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# Results

For 60 agents taking 3 steps and a threshold value of 1.5 the model achieves 69% precision ( $\pm 0.002$ ), 75% Recall ( $\pm 0.001$ ) and a Rand Index of 74% ( $\pm 0.001$ ).

The month to month accuracy compared visually, actuals above and models below



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# Conclusions

- Our analysis shows that the disease is much more likely to spread to a local area (for example through insect vectors) rather than a far-way area (for example, via an airborne vector)
- The direction and severity of the spread is an emergent consequence, a result of a local 'build-up' of infections, forming isolated clusters
- The data confirms the intuition, though modelling this process is difficult due to the frequently stochastic behaviour of the process
- In the future we will try other agent-based models, e.g. agents that can learn from previous decisions as opposed to a biased-walk directed only

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# Thank you!



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**Project “Lethal Wilt Evolution” data and simulation:**

[https://dmu.figshare.com/articles/Lethal\\_Wilt\\_Evolution/8283944](https://dmu.figshare.com/articles/Lethal_Wilt_Evolution/8283944)

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## Q&A

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