Plant Epidemics: data analysis and parameter estimation

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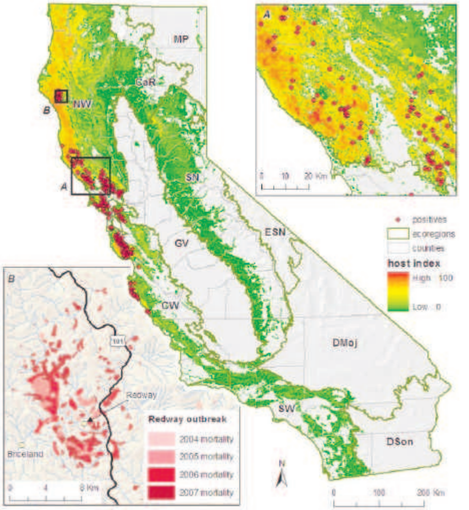
Some glimpses of:

- some of the systems and problems we study
- why they are economically and/or ecologically important
- the sort of datasets we deal with
- some of the methods we use

Example: Sudden Oak Death

- since 1990 killed millions of oak trees in forests of Western U.S coast (Oregon; California)
- alters structure of plant and microbial communities, and ecosystem function
- risk of forest fire hazards increased
- both short- and long-range transmission
- since 2002 also in England (esp. SW)



Meentemeyer, R. K., N. J. Cunniffe, A. R. Cook, J. A. N. Filipe, R. D. Hunter, D. M. Rizzo, and C. A. Gilligan. 2011. Epidemiological modeling of invasion in heterogeneous landscapes: spread of sudden oak death in California (1990 2030). Ecosphere 2(2)

Example: HLB (Citrus Greening)

- the most devastating disease of citrus worldwide
- insect-vectored, carried from Asia into Brazil (2004), South Florida (2005)
- huge economical losses and continue decline of affected commercial citrus industries
- need for a short-term managing solution

Orange groves, Florida, end 2004 (appr. 2×10^5 trees)

Orange groves, Florida, end 2010

What we can do and why

- build models for the disease
- estimate model parameters from the data (how fast the disease spreads, how far away...)
- use estimates and numerical simulations to:
  - predict future course of the epidemic
  - find most likely future outbreak locations
  - assess possible management strategies
- inform policy makers, suggest control strategies

Example dataset: Citrus Canker in Florida

Citrus Canker:

- affects fruit, with severe losses in quality and quantity of yield
- spores mainly spread by wind-blown rain
- re-introduced in Florida in 1995
- eradication programme (until 2006): compulsory removal of millions of trees (incl. residential trees)
- dataset: monthly snapshots from surveys in the field

Suburban Miami (1997-1999)

Data courtesy of Tim Gottwald

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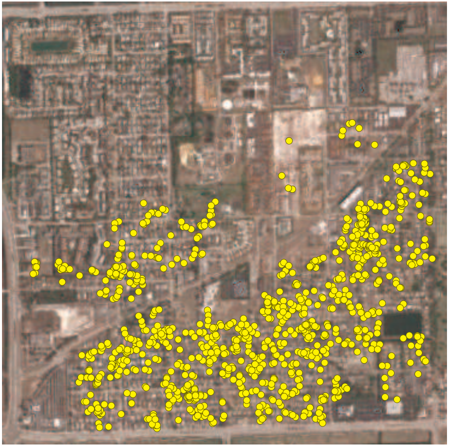
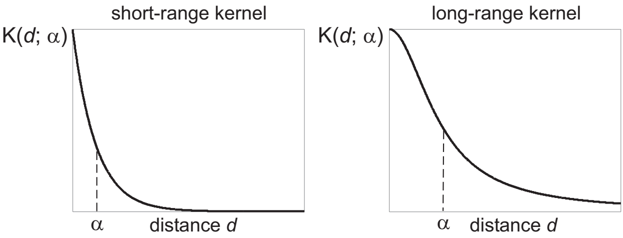


Data courtesy of Tim Gottwald

- Stochastic process
- rate of transmission infected→susceptible depending on relative distance d: proportional to a "dispersal kernel" $K\,(d;\,\alpha)$
- need to choose the function $K\,(d;\,\alpha)$
- then estimate the parameter α (i.e., typical dispersal distance in the case of a short-range kernel)

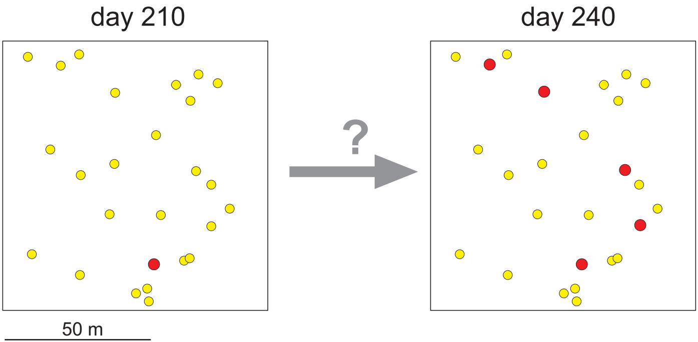


Citrus canker: model (simplified) and parameter estimation

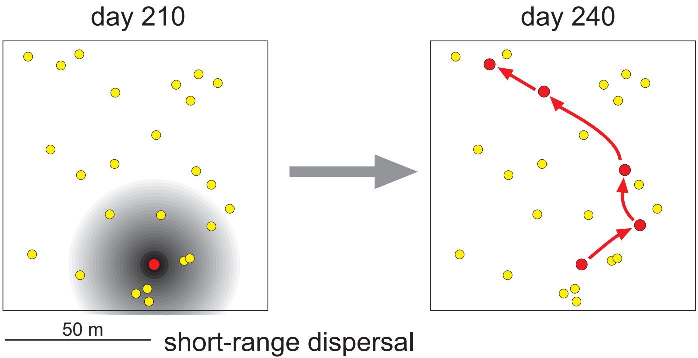
Why is dispersal length important?

- Control measures (here, culling around infected trees) need to match the spatial spread of disease

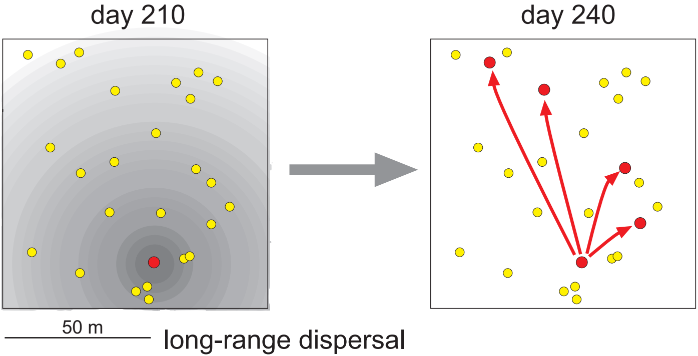
Estimating dispersal



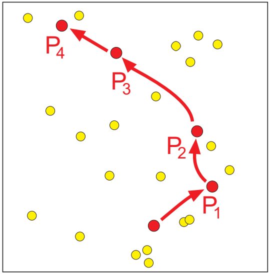
Dispersal function: short-range?



Dispersal function: long-range?



Parameter estimation: estimate infection paths



- Chosen a value for α, sum the probabilities of *all* the possible infection paths: $P = P_1 \times P_2 \times P_3 \times P_4 \times \dots$

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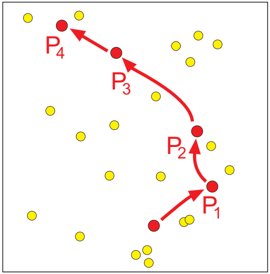

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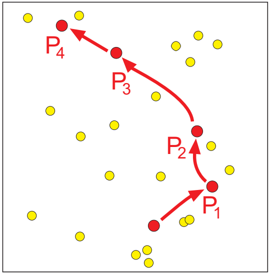

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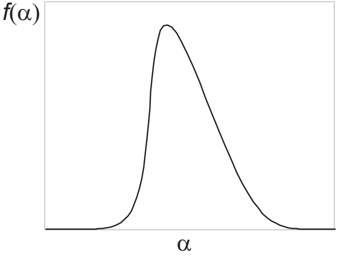

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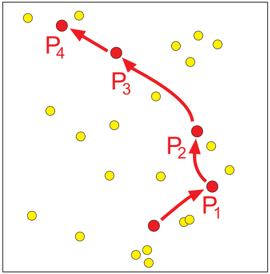

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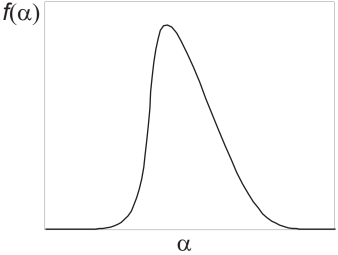

- A possible alternative: approximate, simulation-based, fully numerical computational methods (work in progress)...

Thanks to:

- Christopher Gilligan (head of Epidemiology and Modelling Group)

For Sudden Oak Death:

- João Filipe (Epidemology and Modelling Group)
- Nik Cunniffe (Epidemology and Modelling Group)
- Ross Meentemeyer (University of North Carolina)
- Alex Cook (National University of Singapore)

For Citrus Canker:

- Tim Gottwald (U.S. Department of Agriculture)
- Alex Cook (National University of Singapore)