

Post-Harvest Diseases of Apples: From Spore Dispersal to Epidemiology

Rebecca C. Tyson

Louise Nelson

Meghan Dutot, Katrina Williams

UBC Okanagan, Kelowna, BC

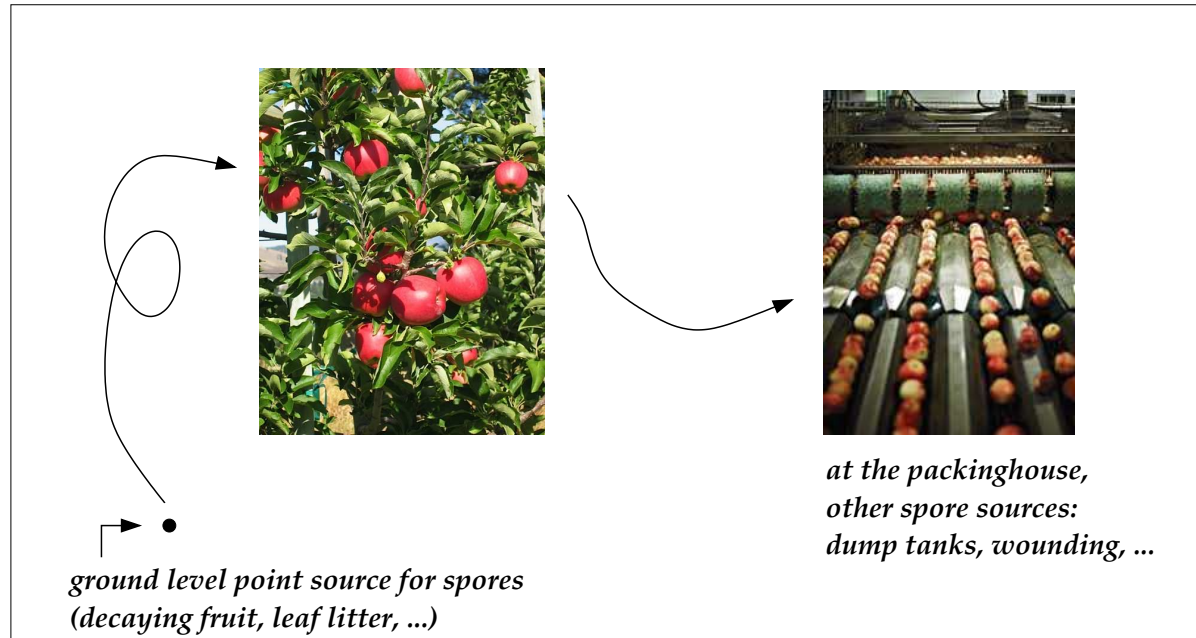
Post-Harvest Diseases



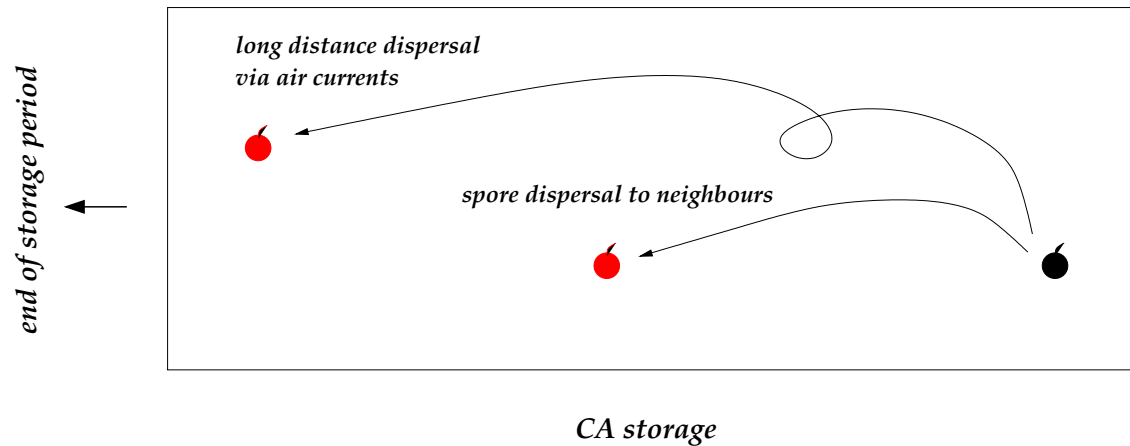
- Fungal infection causes severe decay of apples during storage

Spore Dispersal to Epidemiology

Primary Inoculation



Secondary Inoculation and Disease Spread



Disease Incidence and Orchard Management

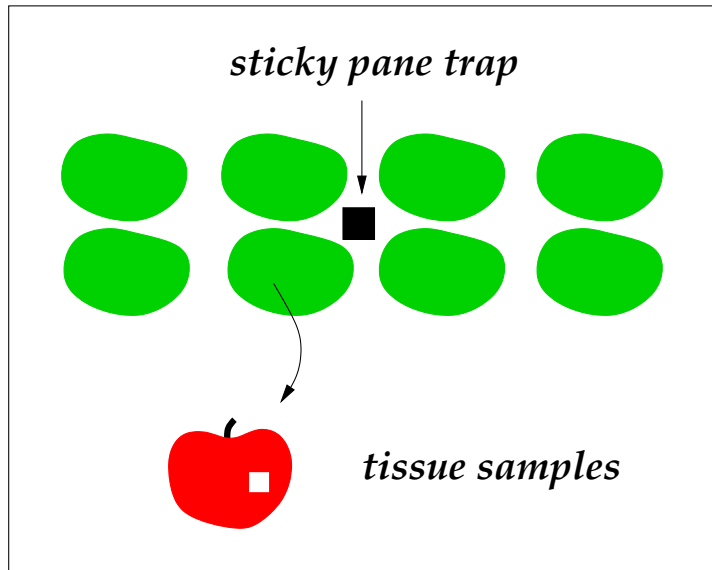
Assumption : There is a direct causal relationship between orchard management practices and disease incidence on stored fruit.

Evidence :

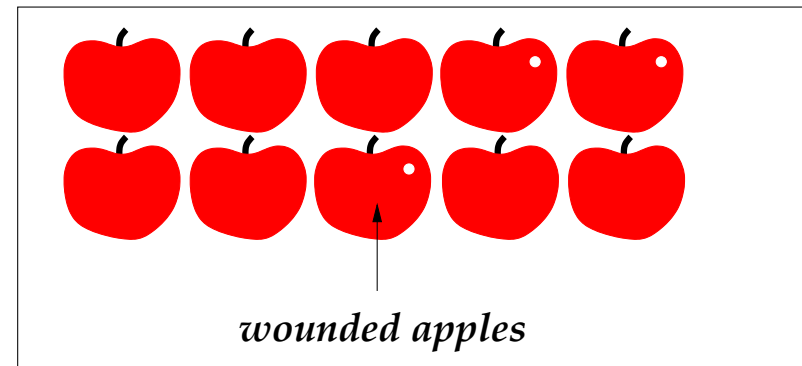
- Spotts et. al. (2009) At-harvest prediction of grey mould risk in pear fruit in long-term cold storage. *Crop Protection* 28(5):414–420.
- Spotts, R.A., Sanderson, P.G., Lennox, C.L., Sugar, D., and Cervantes, L.A. 1998. Wounding, wound healing and staining of mature pear fruit. *Postharvest Biology and Technology* 13:27-36.

Field Study

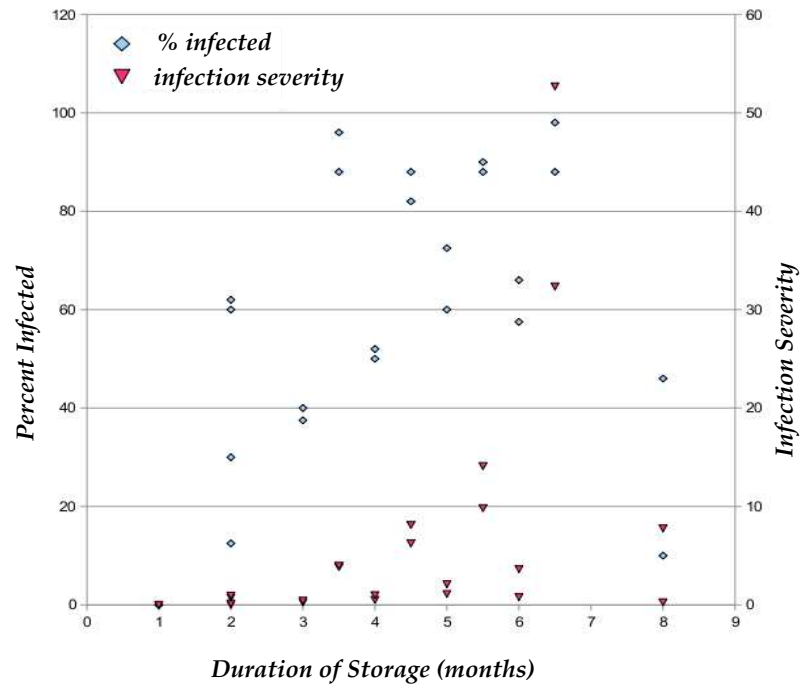
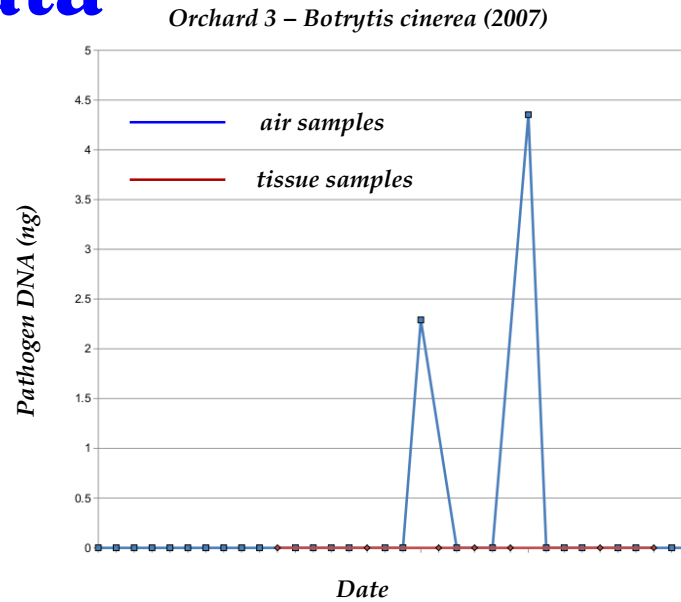
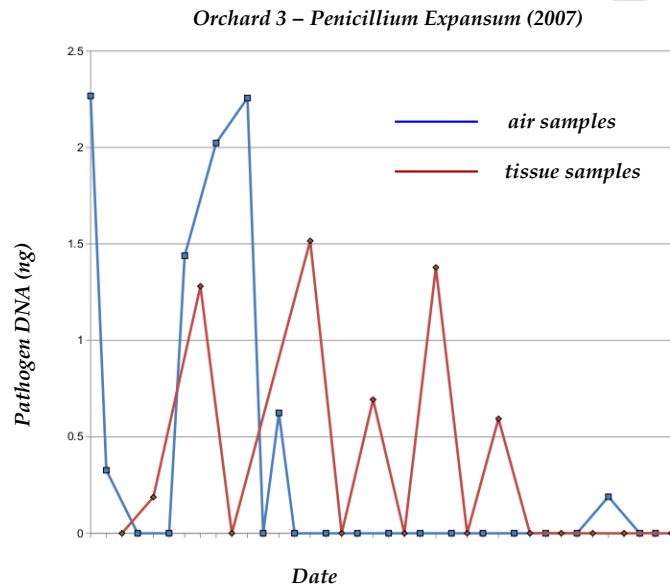
In the Orchard: Spore presence



In CA storage: Disease incidence



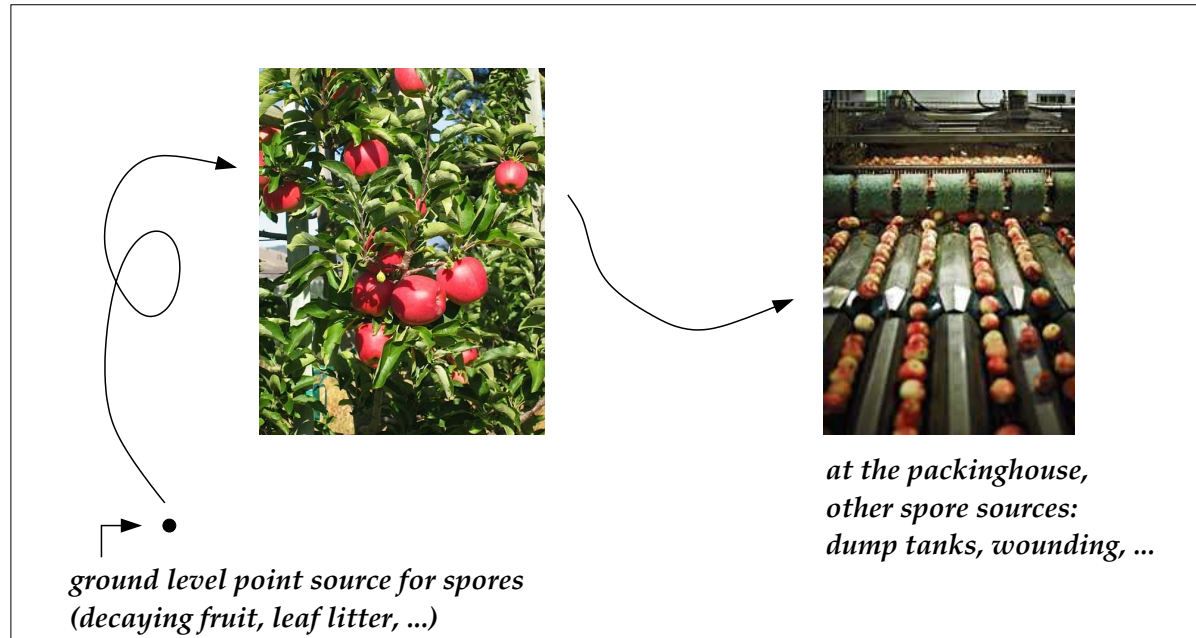
Data



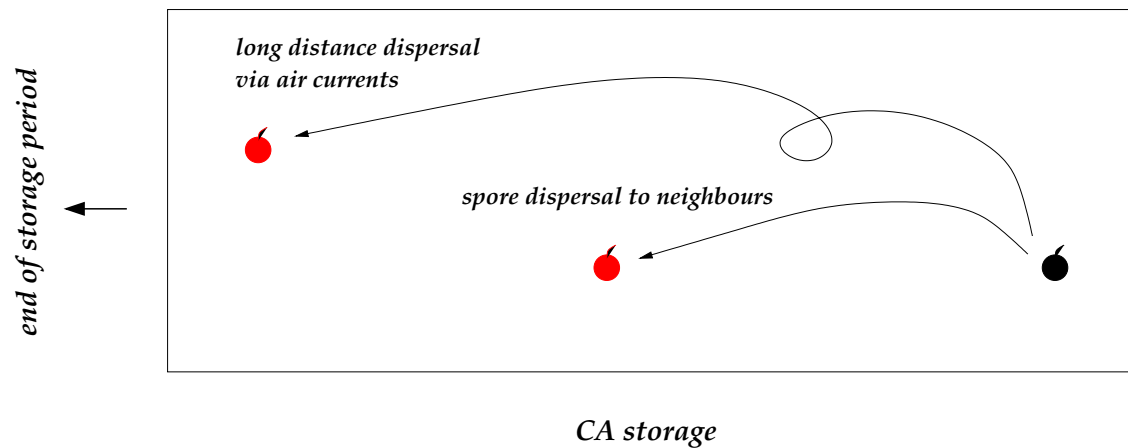
Spore presence data predicted very little.

Spore Dispersal to Epidemiology

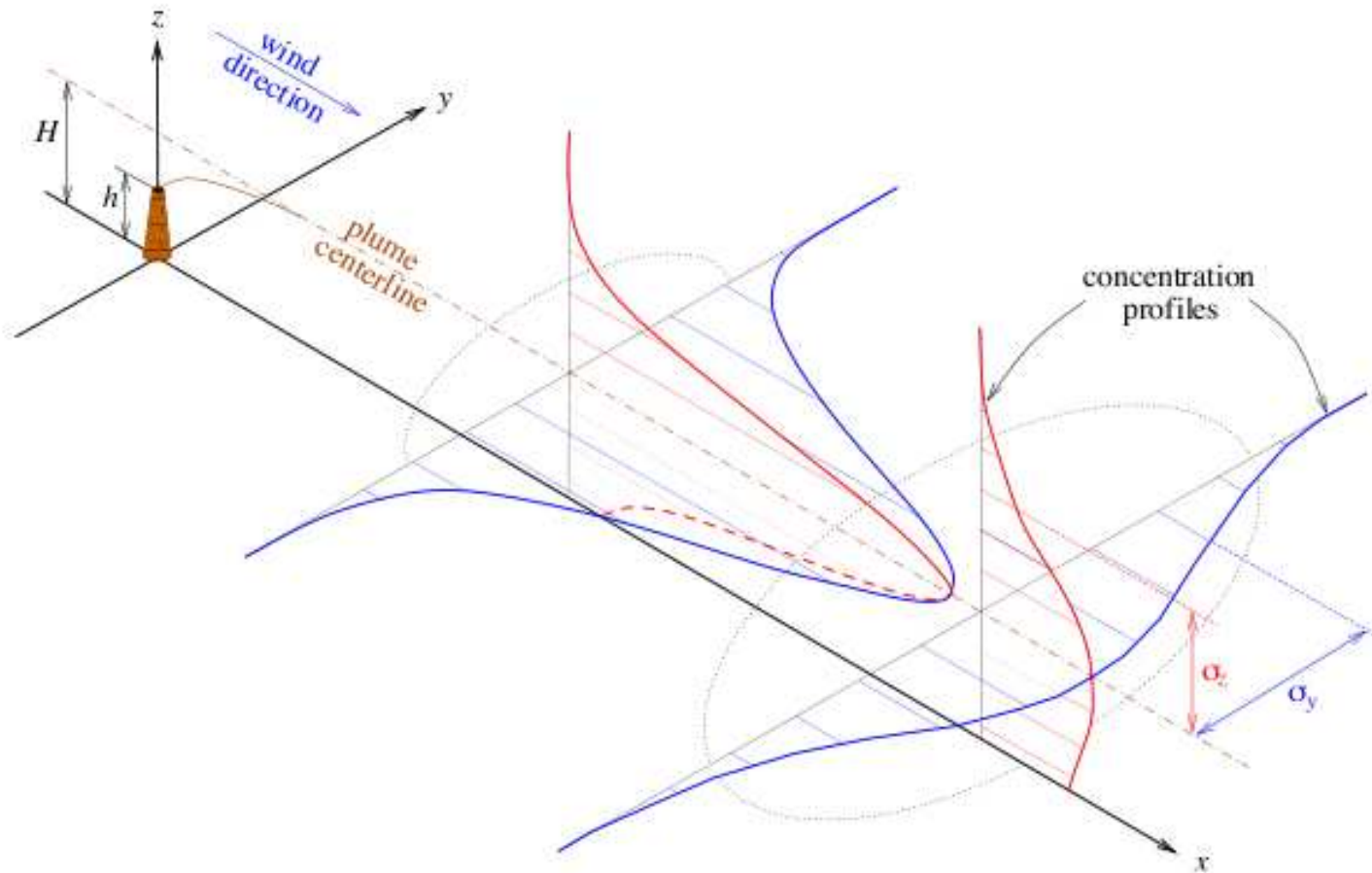
Primary Inoculation



Secondary Inoculation and Disease Spread



Model #1: Spore Dispersal



Source: Stockie, J.M. (2010) The mathematics of atmospheric dispersion modelling. *Atmospheric Environment* **44**:1097-1107

Gaussian Plume Model for a Point Source

Steady-State solution:

$$C(r, y, z) = \frac{Q}{4\pi ur} \exp\left(-\frac{y^2}{4r}\right) \left[\exp\left(-\frac{(z-H)^2}{4r}\right) + \exp\left(-\frac{(z+H)^2}{4r}\right) \right]$$

where

$$r = \frac{1}{u} \int_0^x K(\xi) d(\xi)$$

and where

C = concentration of contaminant

(x, y, z) = cartesian coordinates centred at the source

u = wind velocity

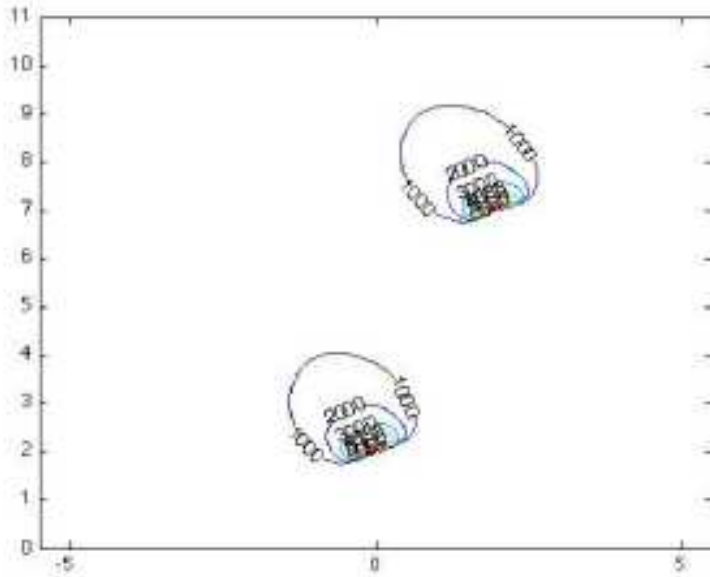
H = height of the source

Q = emission rate

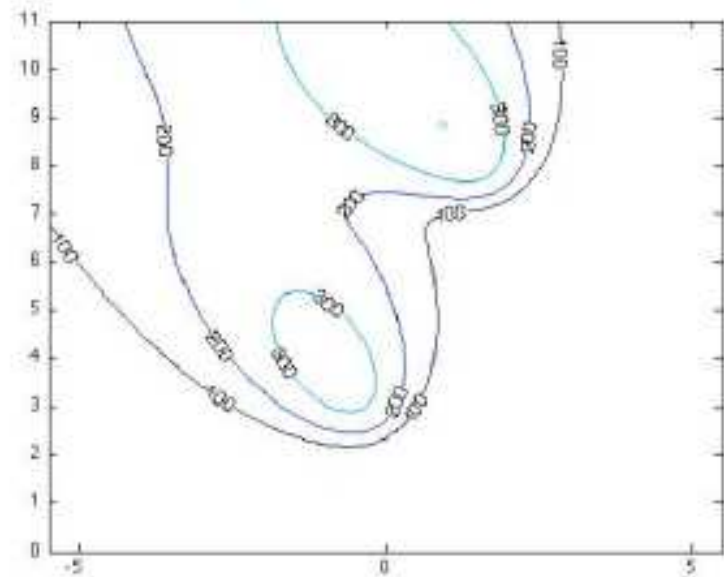
Assumptions

1. contaminant emitted at a constant rate and constant height
2. constant wind velocity aligned with positive x -axis
3. parameters are time-independant & the time scale is long
4. eddy diffusivities, K , functions of x only & diffusion is isotropic
5. wind velocity is sufficiently large so that diffusion in the x -direction is negligible
6. variations in topography are negligible
7. the contaminant does not penetrate the ground

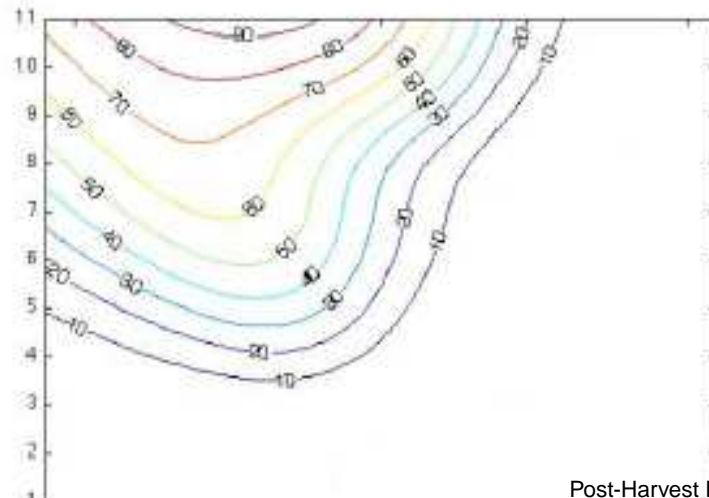
Concentration Profiles



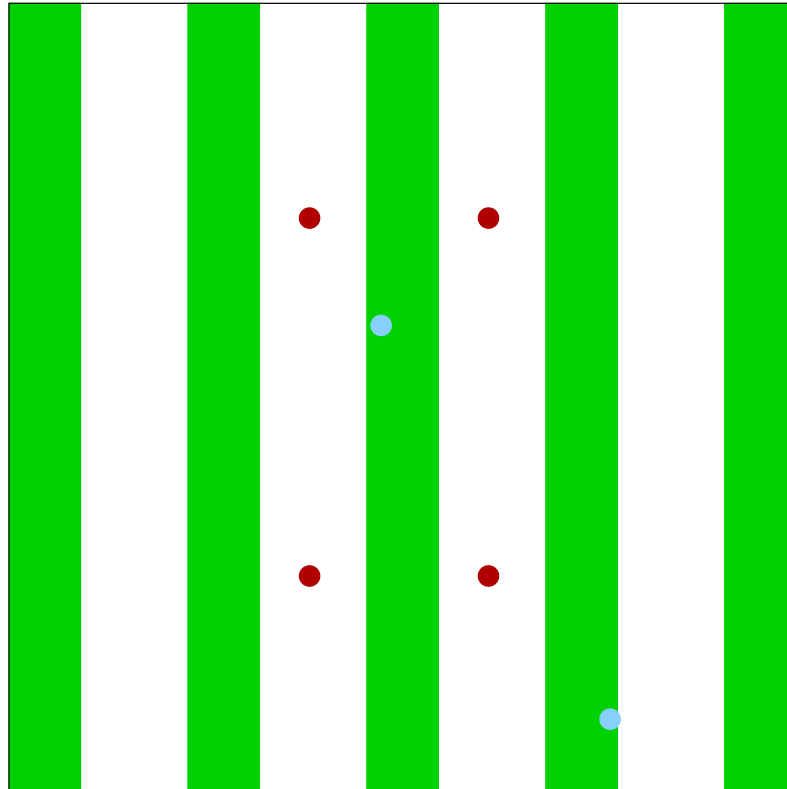
(a) Ground-level



(b) Mid-plume



Orchard & Receptor Layout



● *spore source (ground level)*

● *spore receptor (canopy level)*

■ *apple trees*

dimensions: 10m x 10m

How many spore receptors does it take to get an accurate measure of spore presence?

Simulation Experiments

Consider

$$\begin{aligned} S &= \text{measure of total spore presence detected by } t = T \\ &= S(C(\vec{X}_s), n_r, T, \vec{W}, n_s), \end{aligned}$$

where

$$n_r = \text{**number of spore receptors } (0 \leq n \leq 100),$$

$$T = \text{simulation time,}$$

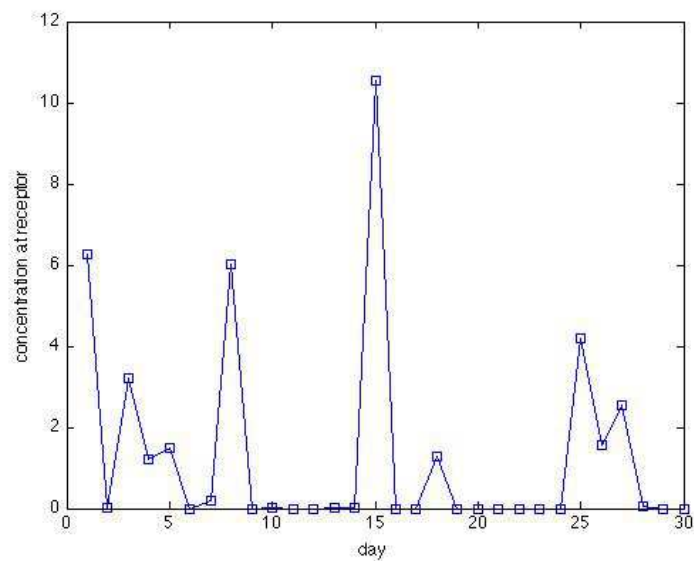
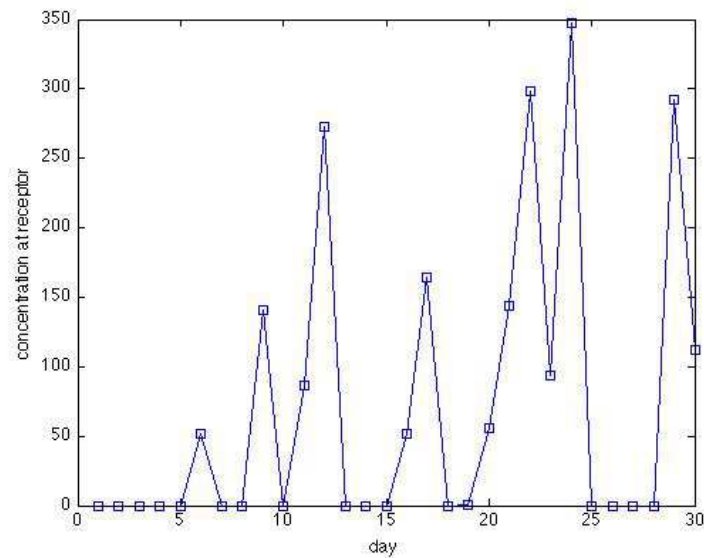
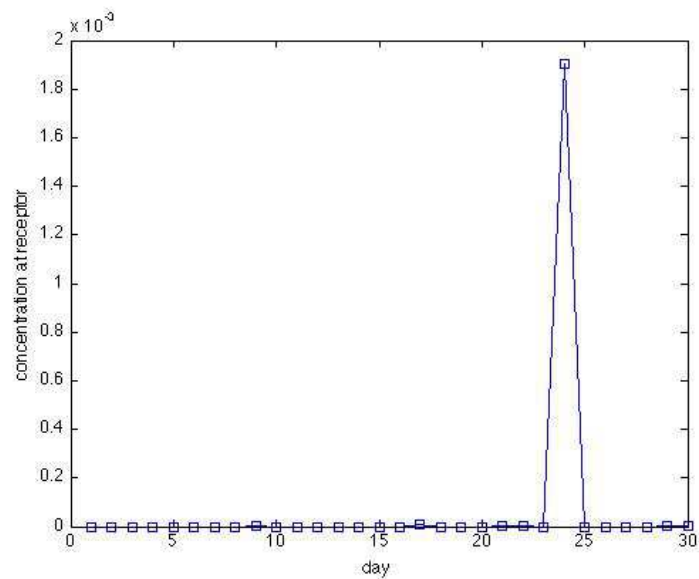
$$\vec{W} = \text{vector of wind data for } (0 \leq t \leq T),$$

$$n_s = \text{number of spore sources,}$$

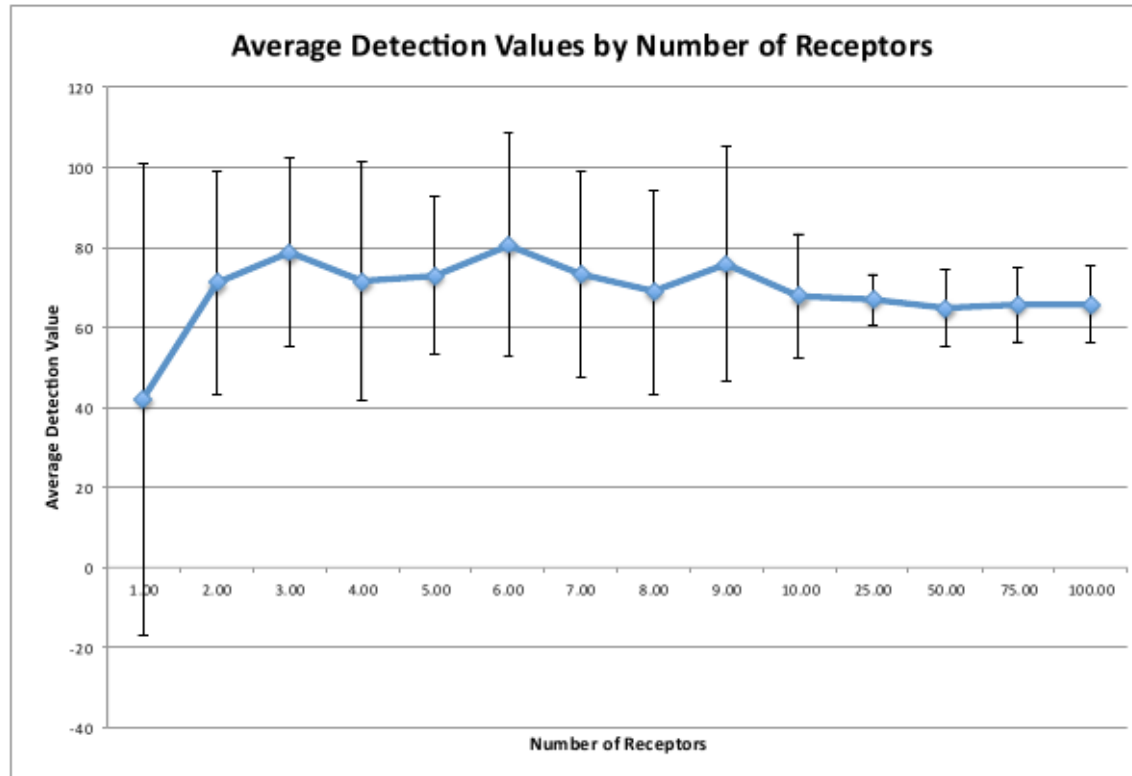
$$\vec{X}_s = \text{position of spore sources.}$$

- Test: optimal n_r
- Experiment: fix all parameters, Replicates (20): vary \vec{X}_s .

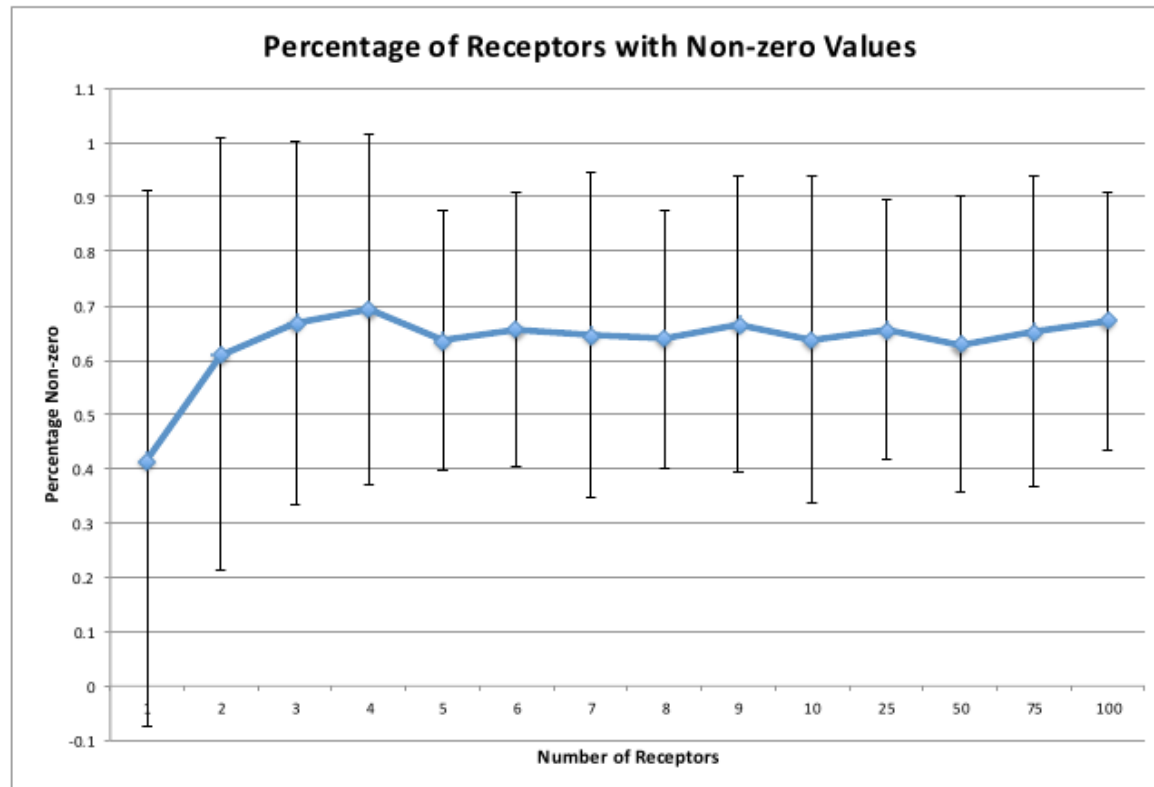
Simulation Results - Spore Detection



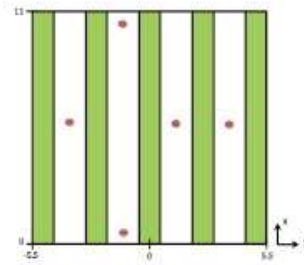
Simulation Results - Monthly Averages



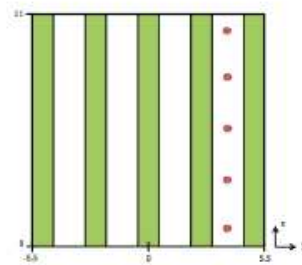
Simulation Results - Percent Nonzero Detection



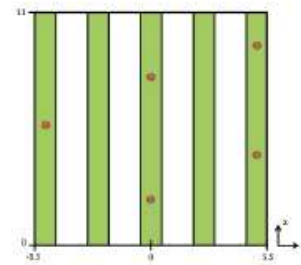
Simulation Results - Receptor Arrangement



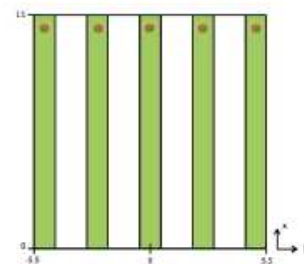
(a) Coordinates A



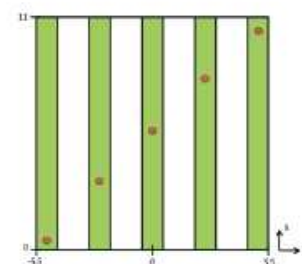
(b) Coordinates B



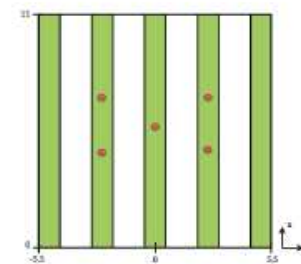
(c) Coordinates C



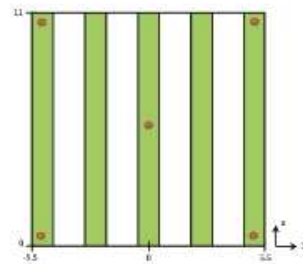
(d) Coordinates D



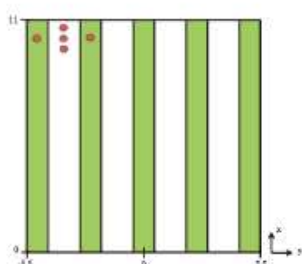
(e) Coordinates E



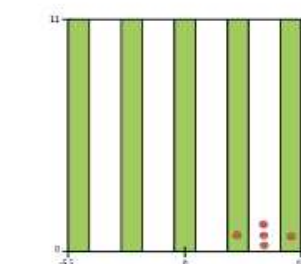
(f) Coordinates F



(g) Coordinates G

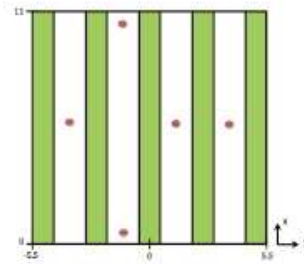


(h) Coordinates H

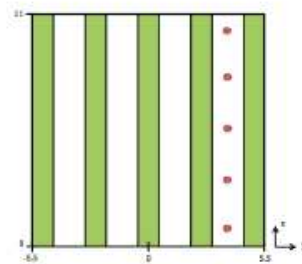


(i) Coordinates I

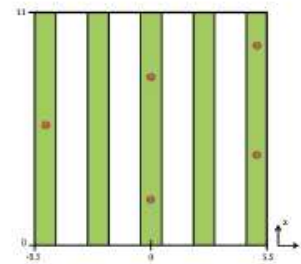
Simulation Results - Receptor Arrangement



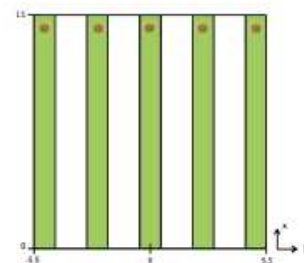
(a) Coordinates A



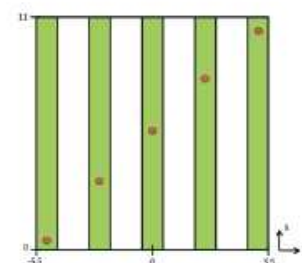
(b) Coordinates B



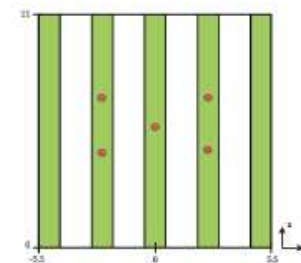
(c) Coordinates C



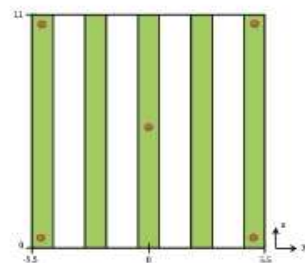
(d) Coordinates D



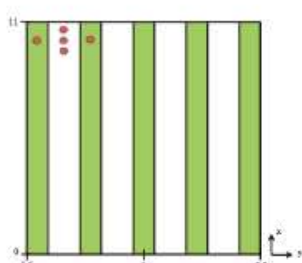
(e) Coordinates E



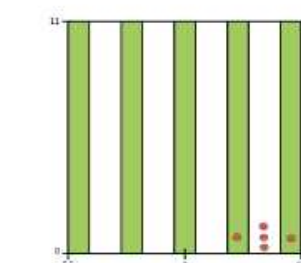
(f) Coordinates F



(g) Coordinates G

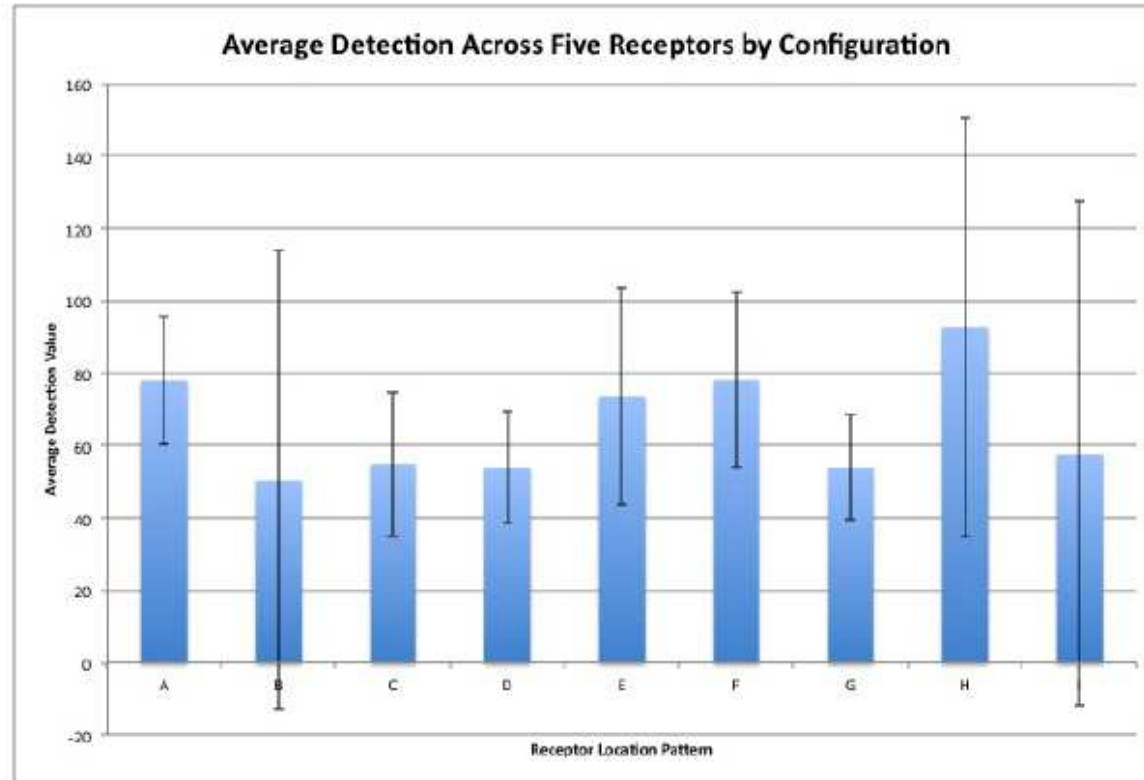


(h) Coordinates H



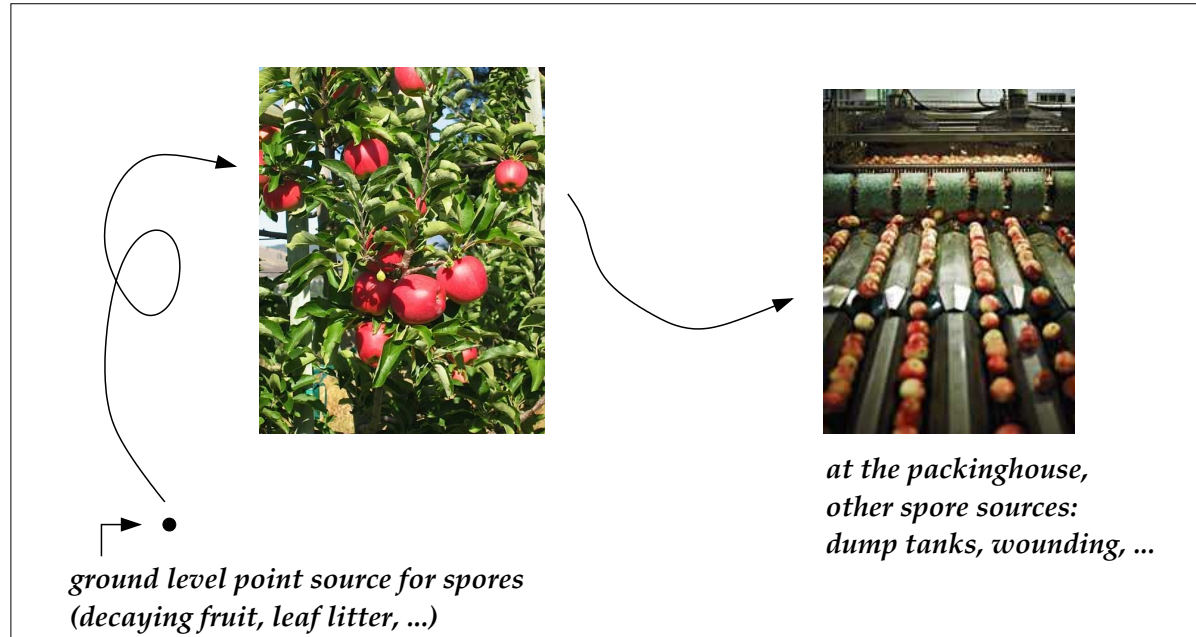
(i) Coordinates I

Simulation Results - Receptor Arrangement

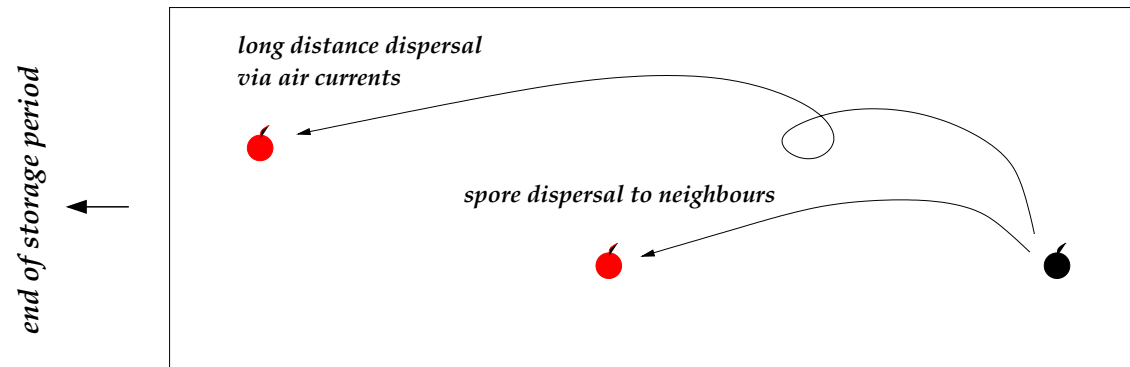


Spore Dispersal to Epidemiology

Primary Inoculation



Secondary Inoculation and Disease Spread



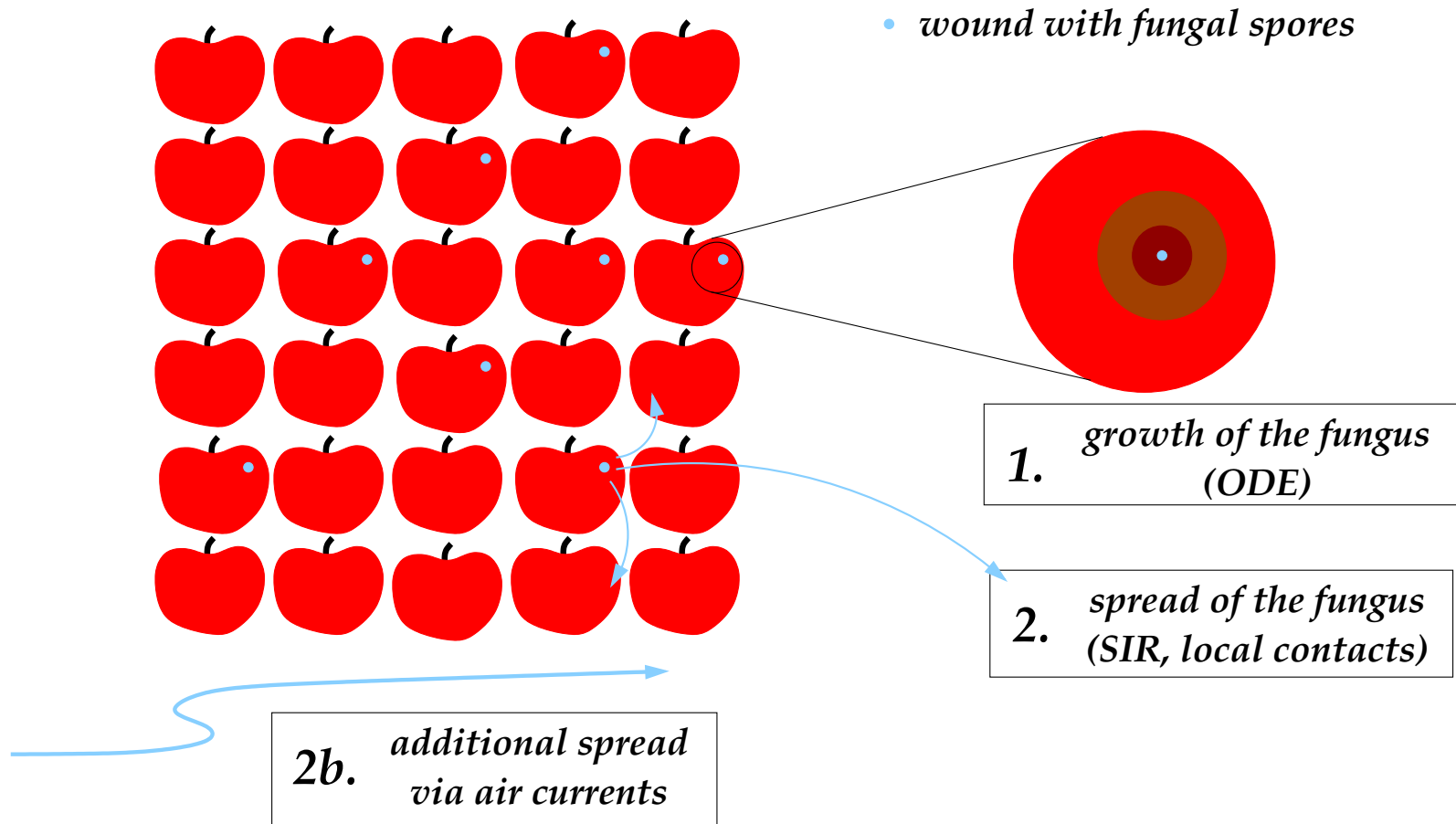
CA storage

Model #2: Epidemiology - Why?

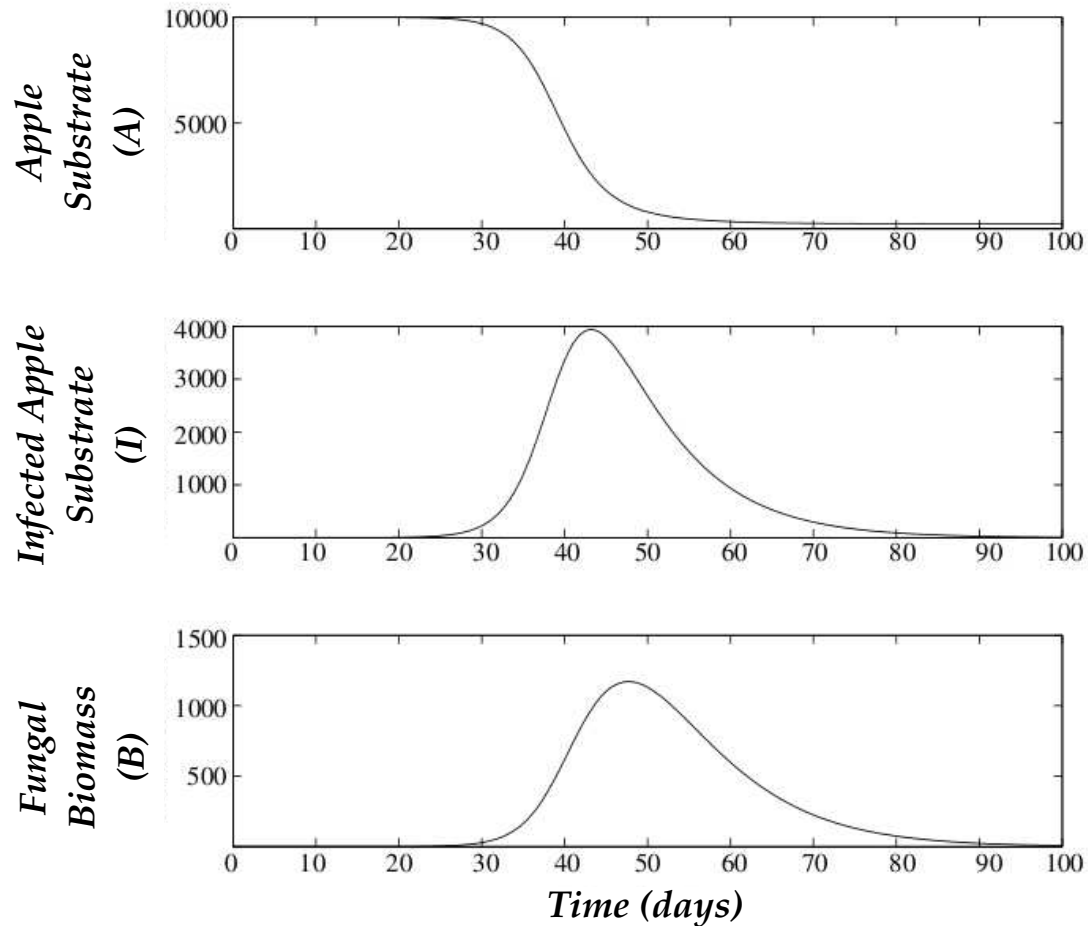
- It is expensive to open the storage rooms to assess the extent of disease.
- Accurate prediction of disease-free storage periods would prevent major crop losses.



Model #2: Epidemiology



Fungal Growth Model



$$\frac{dA}{dt} = -\alpha GIA$$

$$\frac{dI}{dt} = \alpha GIA - \beta I$$

$$\frac{dB}{dt} = GI - \mu B$$

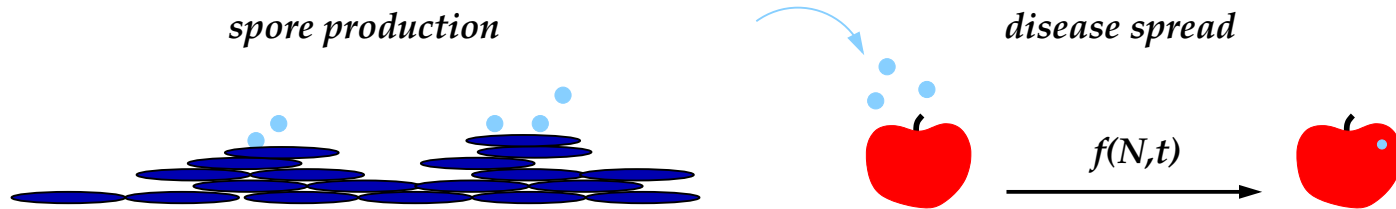
Adapted From: Lamour et.al. (2002) Quasi-steady state approximation to a fungal growth model *Journal of Mathematics Applied in Medicine and*

Biology **19**:163–183

Disease Spread



Disease Spread - SIR



Infection spread from one apple to another is given by

$$f(N, t) = \mathbf{1}(N) p \gamma(t),$$

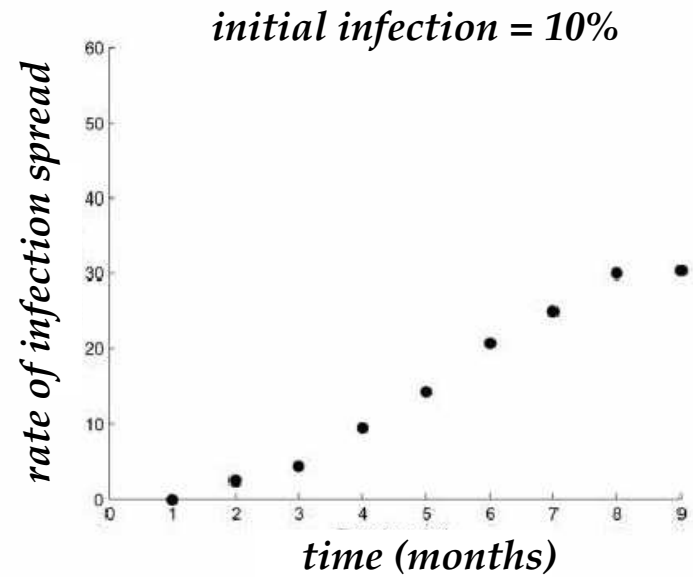
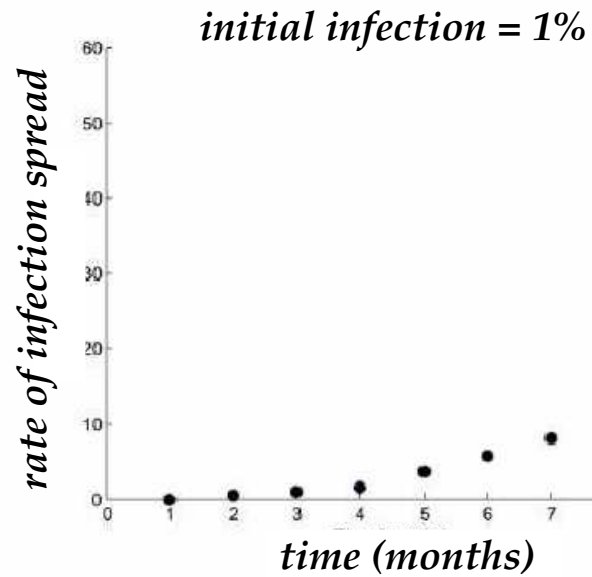
where

N = number of nearest neighbours that have $B(t) > B_{min}$

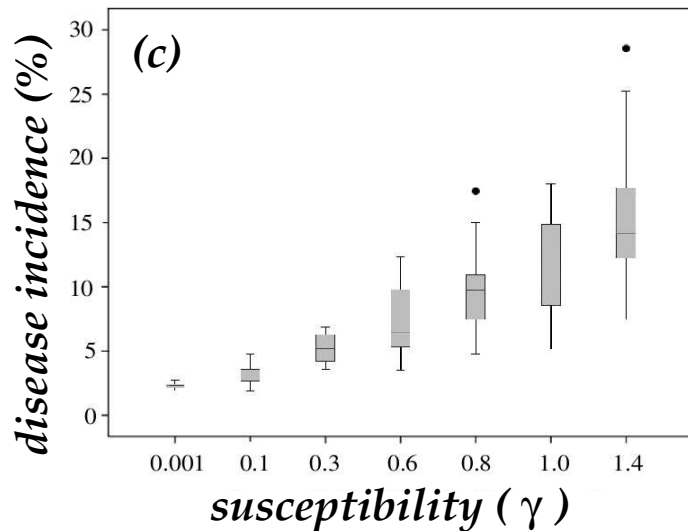
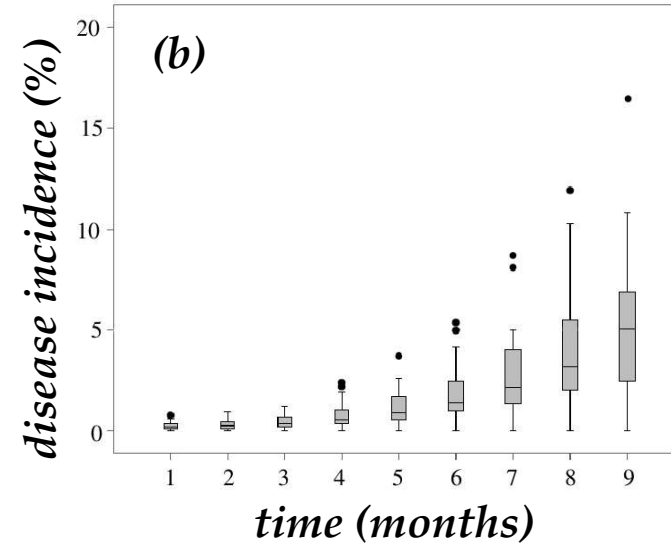
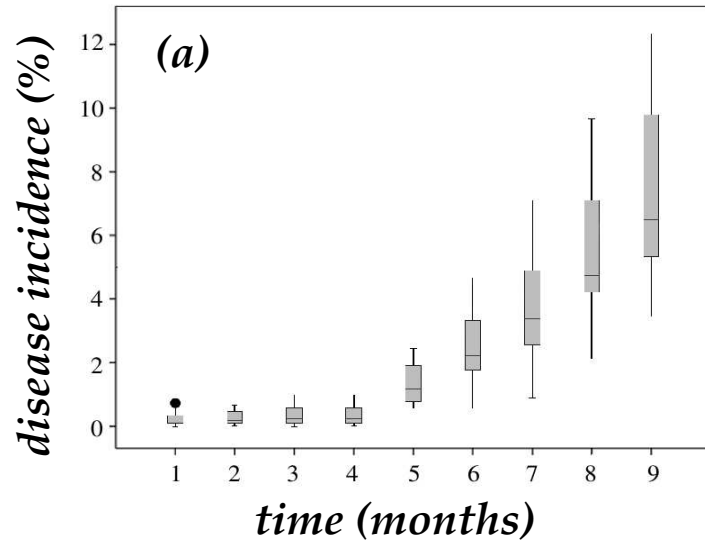
p = baseline infection rate

$\gamma(t)$ = susceptibility function, $\gamma'(t) > 0$

Results - Initial Infection

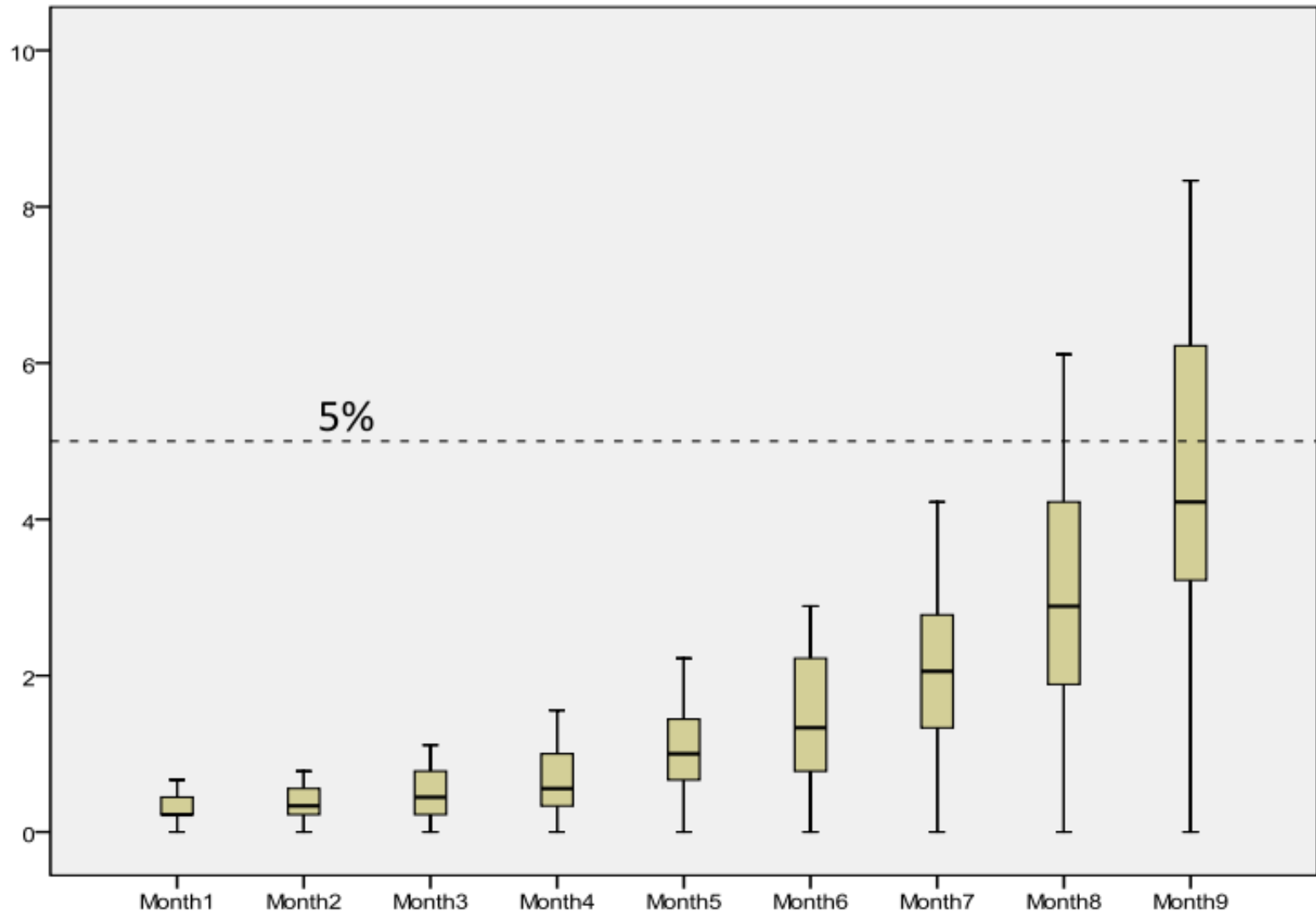


Results - Spread & Susceptibility



- (a) local spread only*
- (b) local & global spread*
- (c) increasing susceptibility*

Results - Storage Duration

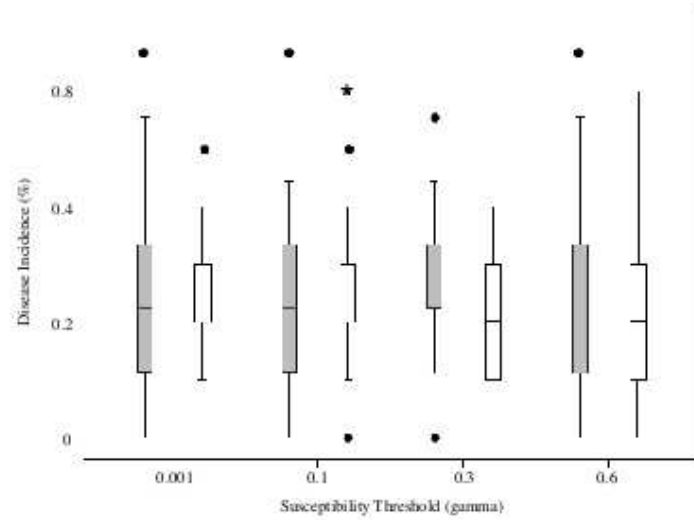


Results - Rate of Infection Spread

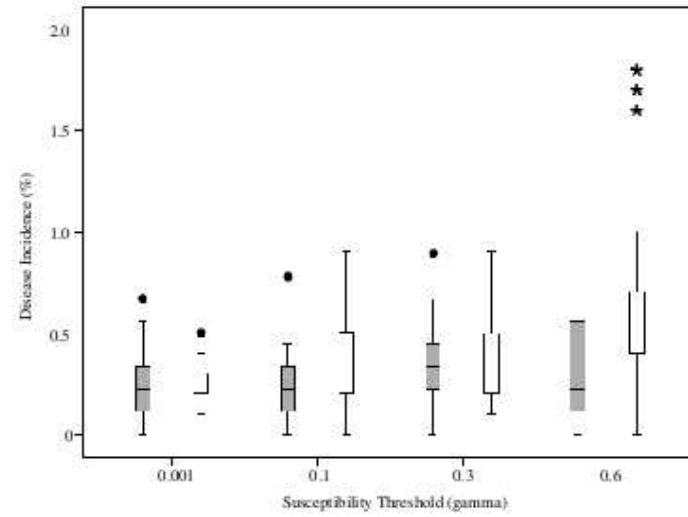
		Storage Duration (months)		
Factor	Treatment	2	5	9
Location	Center	0.47	2.20	10.23
	Side	0.23	1.33	5.20
	Corner	0.20	0.70	2.77
Aggregation	Clumped	0.50	3.20	13.17
	Dispersed	1.57	9.57	41.80

Results - 3D

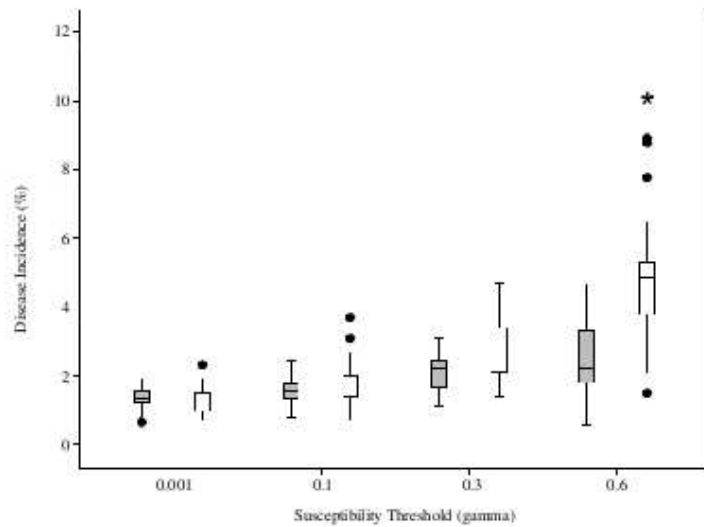
a)



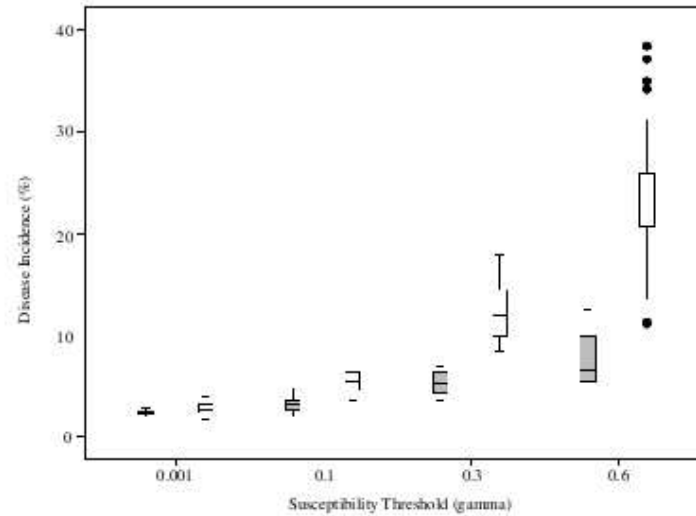
b)



c)



d)



Conclusions

The accumulation of rare events over a long period of time mean high variability in the outcome.

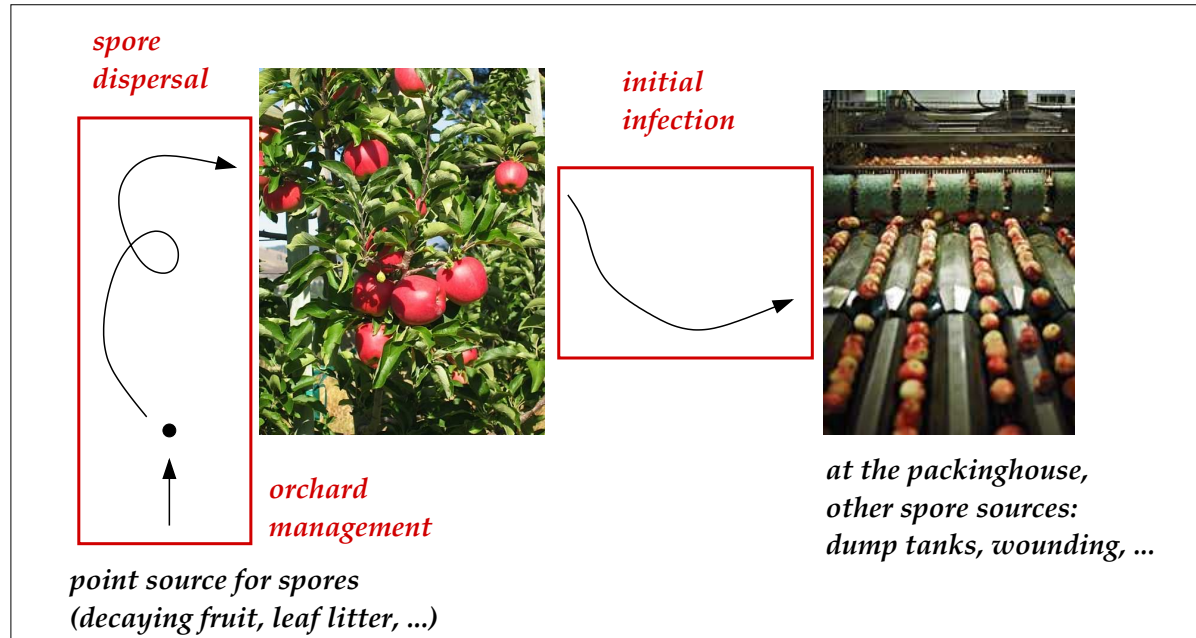
Predictable:

- number and placement of orchard receptors needed to obtain reliable measure of spore presence
- storage time for which risk of unacceptable crop loss is acceptable

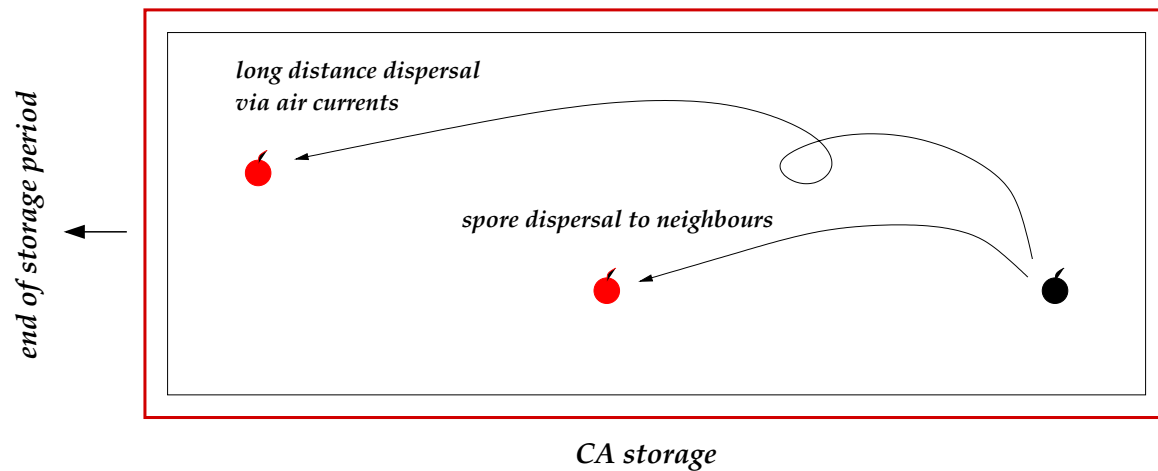


Hypothesis

Primary Inoculation



Secondary Inoculation and Disease Spread



Correlations with Spore Presence

Significant correlations between:

1. air DNA

- wind direction ($p = 0.01$)

2. tissue DNA

- average temp ($p = 0.017$)
- average temp day before measurement ($p = 0.028$)
- rainfall day before measurement ($p = 0.038$)
- maximum wind speed ($p = 0.014$)

Regression of (2) gives $R^2 = 0.023$ and $\sigma = 0.001$.

Correlations with Disease Incidence

Significant correlations between:

- percent infected
 - m , number of months in storage ($p = 0.000$)
 - C_i , average temp last i days ($p = 0.005, 0.000$ & 0.003)
 - R_i , rainfall during last i days ($p = 0.000$ & -0.032)
 - Sp_i , average tissue spore count last i days ($p = 0.0006$ & 0.000)
 - $i = 50, 14$ or 1

R^2	parameters included
0.325	R_{14}
0.416	R_{14} and m
0.491	R_{14} , m , and C_{14}
0.501	R_{14} , m , C_{14} , and Sp_{14}

Modified Model with Absorption

$$C(x, y, z) = \frac{Q}{2\pi u \sigma_z} \frac{1}{\sigma_y} \exp\left(\frac{-y^2}{2\sigma_y^2}\right) \times \frac{1}{\sigma_z} \left[\exp\left(\frac{-(H-z)^2}{2\sigma_z^2}\right) + R \exp\left(\frac{-(H+z)^2}{2\sigma_z^2}\right) \right]$$

where

$$\sigma_z = K(z_0)ax^b, \quad \sigma_y = K(z_0)10^p x^q$$

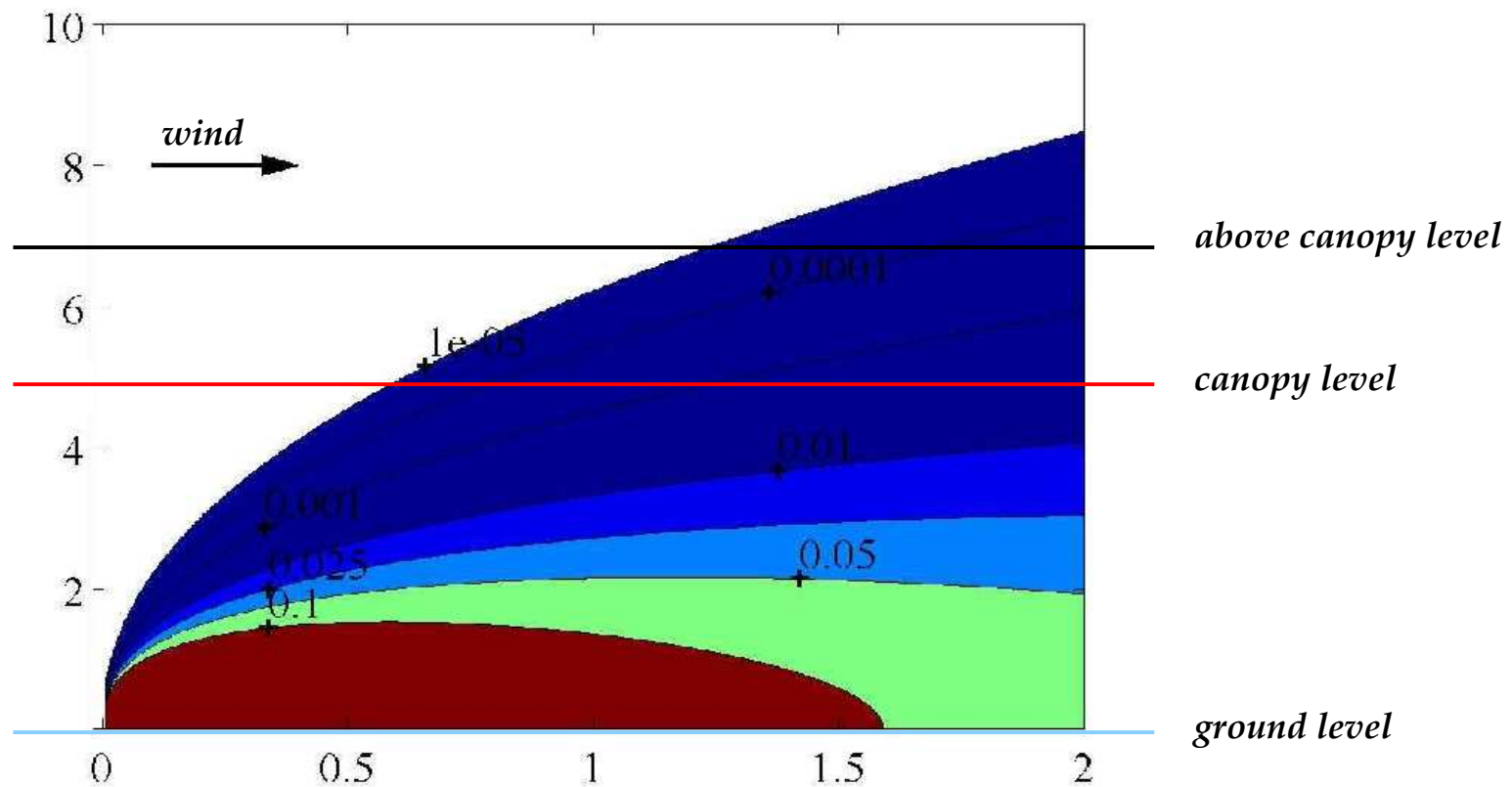
a, b, p, q = stability class constants, empirical

z_0 = roughness length

R = absorption at ground level (1 - reflection, 0 - absorption)

Source: Spijkerboer et. al. (2002) Ability of the Gaussian Plume Model to predict spore dispersal over a potato crop. *Ecological Modelling* 155:1-18

Vertical Plume



Source: Stockie, J.M. (2010) The mathematics of atmospheric dispersion modelling. *Atmospheric Environment* 44:1097-1107