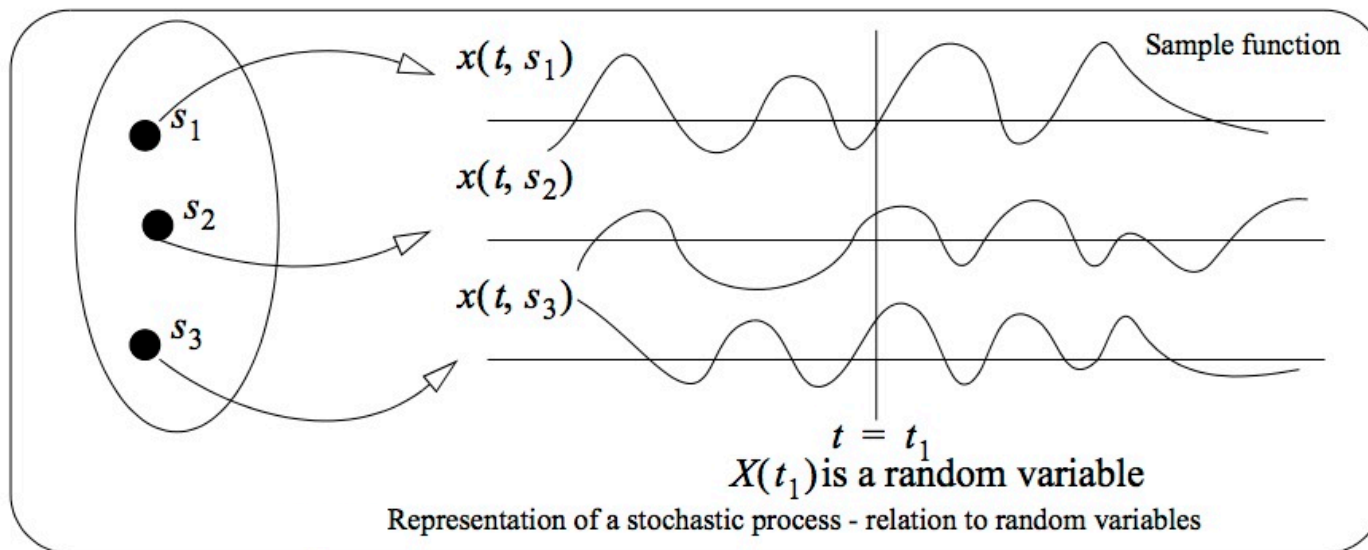


Is there a zombicidal maniac near you?

You'd better hope so!



Creatures of terror

- They are pale, pasty emaciated soulless creatures of horror
- From behind sunken eyes, their slow, feeble minds struggle to process anything but the most basic of data
- Despite this, they are capable of devastation and terror on an overwhelming scale
- That's right: supermodels!
- No, wait: zombies.



Individual-based modelling

- Also called agent-based modelling
- A simulation comprised of several entities or agents
- Each entity can be given a particular behaviour and act in a specific way
- This kind of modelling is useful for scenarios where behaviour plays a key role
- We can use it to examine the effects of introducing armed and trained zombie hunters as a control mechanism
- This is not recommended for most diseases.

Why zombie hunters?

- Most data on zombie behaviour patterns exist merely as conjecture and speculation from people who have never even seen a zombie
- Let alone killed one
- Thus, there is a growing gap between the readiness of the general population and that of certain private individuals
- Unchecked, a small zombie infestation can consume a large city in a matter of days
- Thus, controls are urgently needed.

Data collection

- Video games provide an excellent source of data
- Eg Half-Life 2
 - a first-person shooter video game
 - the player's presence affects everything around them
 - from the physical environment to the behaviours and even emotions of both friends and enemies
- The model is developed using Garry's Mod, using the Source game engine
 - www.garrysmode.com.

The players

- There are three classes of individual
 - humans
 - zombies
 - zombie hunters
- Humans are unarmed and unable to resist a zombie attack
 - when confronted with a zombie they will either run for their lives or cower in fear
- Hunters are equipped with a combat Acme shotgun
 - capable of firing six rounds before reloading.



Human behaviour

- When not faced with a zombie threat, unarmed humans will either wander randomly or stand idle
- Hunters will fire on a zombie if within range and only reload their weapons when there are no zombies nearby
- If they run out of ammo, they will attempt to run away to a safe distance before reloading
- When no zombies are present, they will wander randomly about the map.



Zombie behaviour

- Without any humans in sensory range, the zombie will wander aimlessly, independent of other zombies around
- When a human enters their range, the zombie will chase them down
- We assume these are fast zombies that can outrun a human
- Zombies will always pursue the nearest human
- All humans run at the same speed
- Once caught, a human is converted.

The code is available

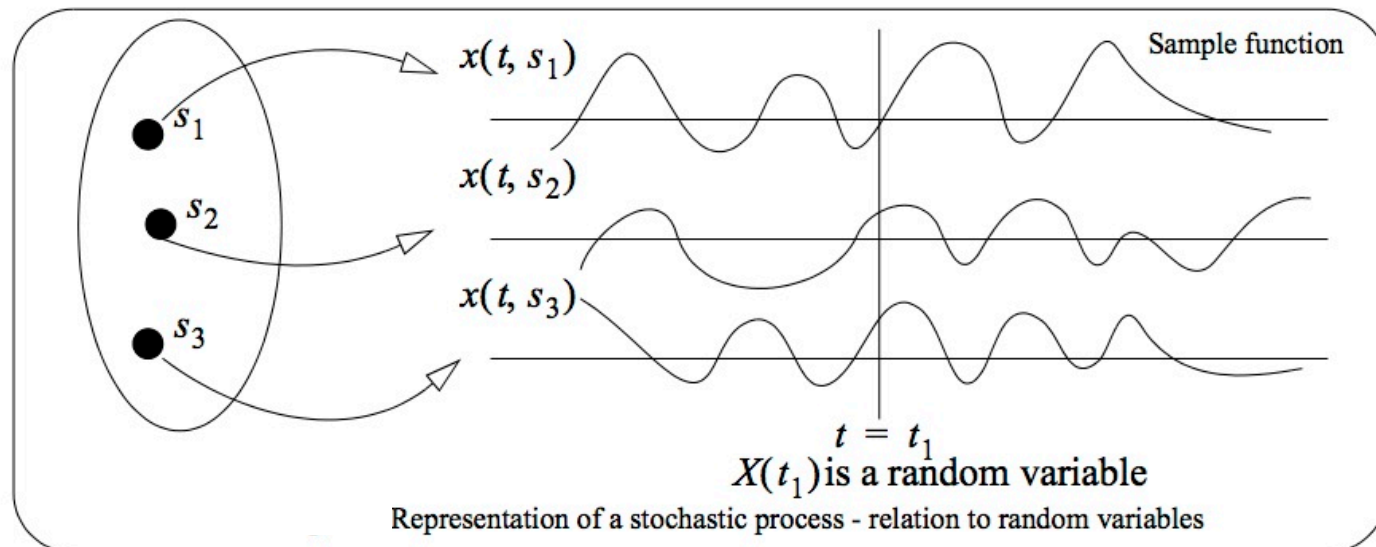
- A sample simulation:
<http://tinyurl.com/gmodzombiemodel>
- The code to replicate the experiments is freely available from the authors
 - nick.beeton@gmail.com
 - alexander.hoare@unsw.edu.au
 - brody.bear@gmail.com.

Stochastic model

- We can use a stochastic model in order to compare the individual-based model
- A stochastic model is one in which variation or noise in the parameters is included
- Time may be continuous or discrete
- This approximates the inherent randomness in the real world.

Random variables

- The random variables are defined on a given probability space
- A stochastic process assigns a sample function $x(t,s)$ to each outcome s
- A sample function is the time function associated with an outcome s .



A simple infection model

- The infection model is given by

$$\begin{aligned}\frac{dS}{dt} &= -f(S, Z) \\ \frac{dZ}{dt} &= f(S, Z)\end{aligned}$$

where

- S represents susceptible humans
 - Z represents zombies
 - $f(S, Z)$ is the transmission function
- The transmission function may take a number of forms, depending on the interactions.

Conversion to stochasticity

- Differential equations are deterministic
- This means that, given an initial condition, the same outcome will always result
- To convert a deterministic ODE into a stochastic form, we assume strong mixing
- This results in an exponential distribution between reaction events
- The probability density function is then

$$P(X \rightarrow X', \tau) = f(S, Z) e^{-f(S, Z)\tau} d\tau$$

where X is the state (S, Z) and X' is the state $(S-1, Z+1)$.

*S: susceptibles Z: zombies
f(S,Z): transmission function
 τ : time*

Our major question

- Is it feasible that the individual-based model has an underlying transmission function related to those found in the disease-modelling literature?
- To determine this, we need a measure of how well our individual-based model fits a particular transmission function
- We also need to measure how well the stochastic model fits
- Due to randomness, it will not be a perfect fit to any data.

Transmission dynamics

- For the individual-based model, 10 runs each were made
- Each pitted one zombie against 24, 49, 74 and 99 humans
- The humans were placed randomly
- Simulations were run until the zombies completely overran the human population
- These simulations give diverse data about S, Z, N and dZ/dt in order to compare functions
- Linear regression, via R^2 values, was used to determine coefficients.

*S: susceptibles Z: zombies
N: population t: time*

Comparison

- The stochastic model was run using the same initial conditions
- It was also sampled in the same way, for purposes of direct comparison
- Values for dZ/dt were then calculated from the sampled data, in the same way
- Agent-based modelling is a way of approximating situations where we do not have real data
- In this case, because collecting it is too dangerous.

Four transmission functions

- Mass-action transmission
 - rate is directly proportional to the density of both susceptibles and infecteds
 - assumes population is well-mixed
- Frequency-dependent transmission
 - host contact is independent of population density
 - reasonable when populations are large
- Power relationship
 - generalises mass action to powers of S and Z
- Asymptotic contact function
 - contact can also depend on the population.

S: susceptibles
Z: zombies

AICc

- Akaike Information Criterion (with correction)
- A measure of the relative goodness of fit of a statistical model
- This measures the amount of information lost when a given model is used to describe reality
- Candidate models can be ranked by AIC values to determine which best fit the data
- However, it is only a way of comparing models, not an absolute measure of accuracy
- It cannot evaluate wholly different model types.

Determining AICc

$$\text{AICc} = 2k - 2 \ln(L) + \frac{2k(k + 1)}{n - k - 1}$$

where

- k is the number of parameters
- L is the maximised value of the likelihood function for the estimated model
- n is the sample size
- The correction is a penalty for extra parameters
- The AICc value with the lowest score is the best fit to the data.

Possible transmission functions

		β (with 95% CI)	p (with 95% CI)	q (with 95% CI)	ϵ (with 95% CI)	AICc
Mass action	βSZ	0.000624 (0.00601-0.000646)				-5.333
Frequency-dependent	$\frac{\beta SZ}{N}$	0.0537 (0.0519-0.0555)				-104.711
Power relationship	$\beta S^p Z^q$	0.0103 (0.00772-0.0129)	0.473 (0.435-0.511)	0.762 (0.719-0.806)		-291.142
Asymptotic contact function	$\frac{\beta S^p Z^q}{1 - \epsilon + \epsilon N}$	0.00962 (0.00702-0.01221)	0.499 (0.446-0.552)	0.793 (0.730-0.855)	0.00168 (-0.00092-0.00428)	-291.125

- Note that the parameters such as β are different in each function
- The power relationship function is the best choice.

S: susceptibles Z: zombies
N: total population
 β : transmissibility p, q : powers
 ϵ : population dependency

Stochastic regression

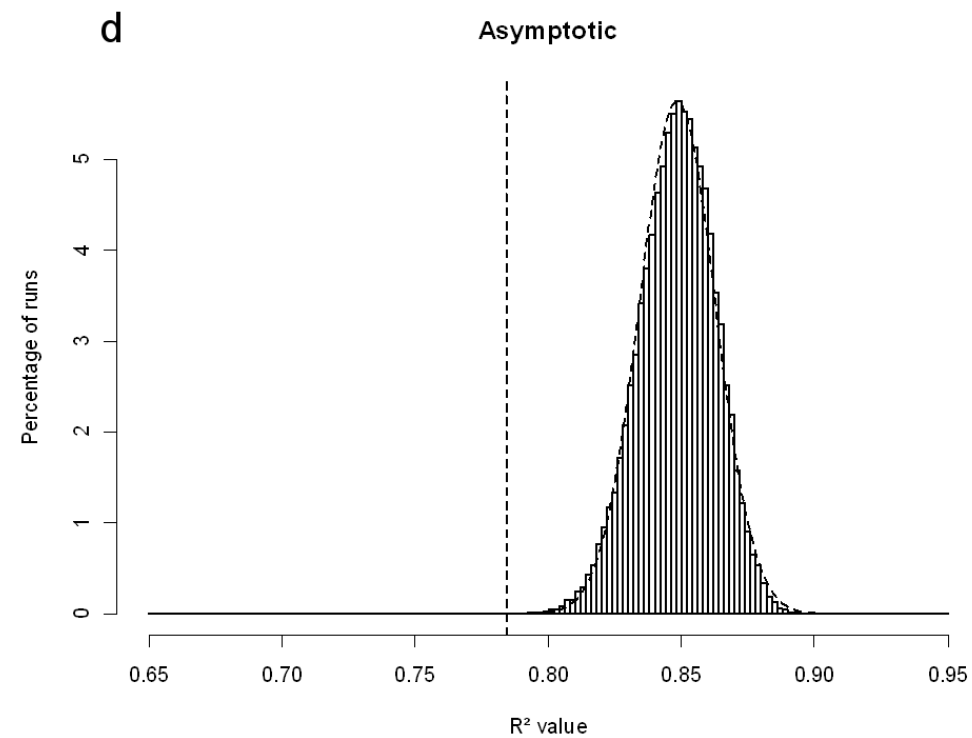
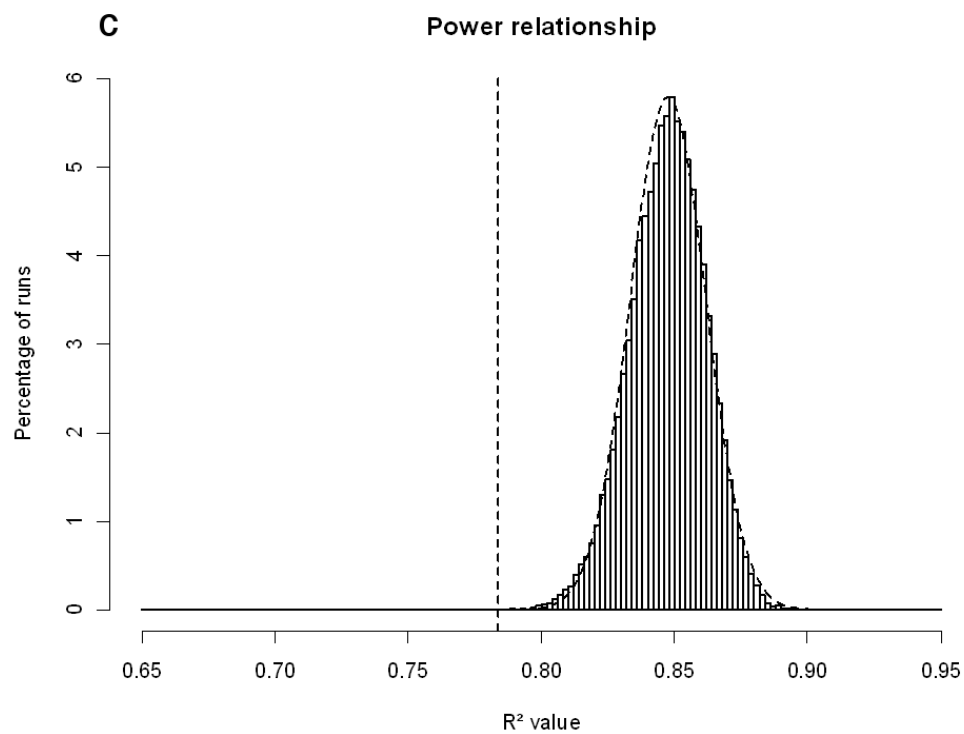
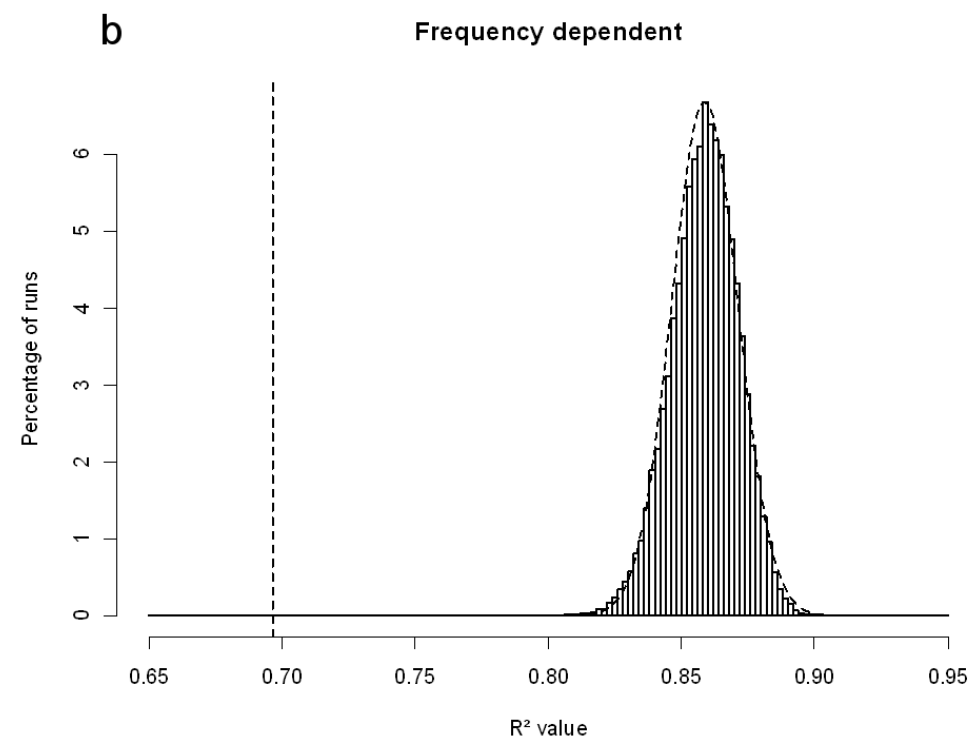
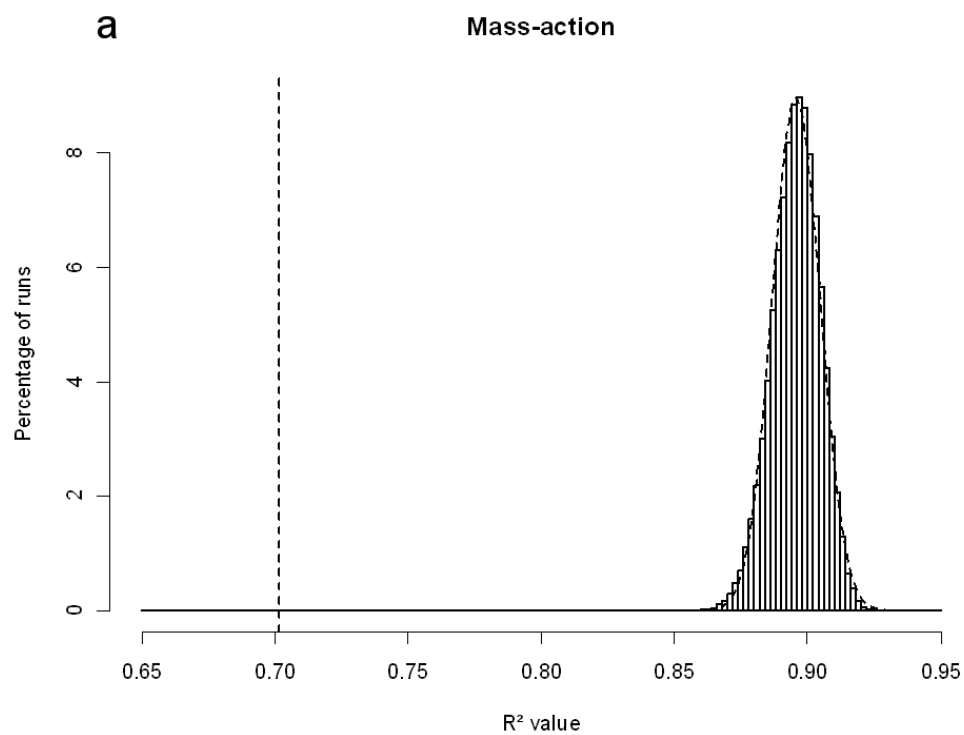
- For the stochastic model, we performed linear regression of the sampled dZ/dt data against the transmission function $f(S,Z)$
- The R^2 of this regression is a measure of goodness-of-fit
- This is exactly what we want from the data
- We want to know how closely the rate of infection for any pairing of S and Z matches the theoretical transmission function
- ie how well dZ/dt matches $f(S,Z)$.

*S: susceptibles Z: zombies
f(S,Z): transmission function
t: time R^2 : regression coefficient*

Histograms of R^2 values

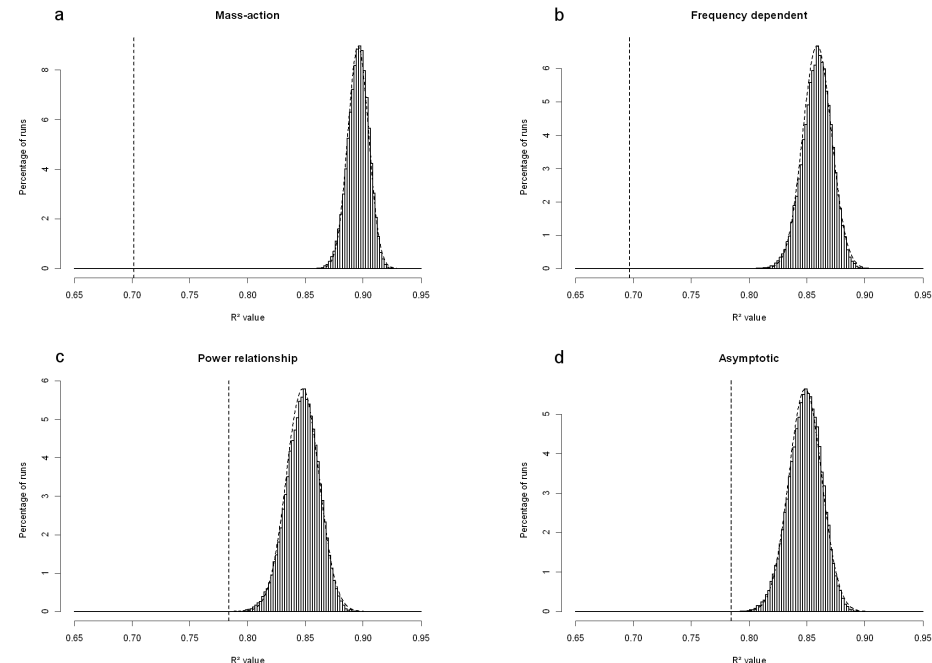
- The simulation was repeated 50,000 times for each function
- This gives a histogram of R^2 values
- Each histogram demonstrates a high correlation between each model's dZ/dt value and the respective transmission functions of around 0.8-0.9
- This is expected, as the only sources of error are from stochasticity and errors caused by the sampling process

*Z: zombies t: time
 R^2 : regression coefficient*



Comparing the individual-based model

- Fits from the individual-based model are also shown (vertical lines)
- These look quite different, but how can we be sure?
- After all, there are variations in the simulations, errors in sampling and so forth
- To answer this, we can construct and test a null hypothesis.



Null hypothesis

- If two models are identical, any measure of the output of one should lie within the distribution of the same measure in another
- Our goodness-of-fit value μ is such a measure
- It's calculated in the same way for the individual-based model and the stochastic model
- Thus, our null hypothesis H_0 is that the individual-based model gives the same goodness-of-fit value as the stochastic model:

$$H_0 : \mu_{\text{IBM}} = \mu_{\text{stoc}}.$$

Rejecting the null hypothesis

- If the null hypothesis is rejected, it means the stochastic model with a particular transmission function does not describe the data from the individual based model
- This suggests the individual-based model is not governed by the transmission function
- If it is not rejected, the stochastic model may describe this data
- Note that if the null hypothesis is not rejected, this is not a sufficient condition to accept a particular transmission function.

p-values

Transmission Function	p-value estimate from 50,000 runs	p-value estimate from normal curve
Mass action	0	4.49×10^{-105}
Frequency dependent	0	7.30×10^{-39}
Power relationship	0.00010	3.69×10^{-6}
Asymptotic contact	0.00008	3.52×10^{-6}

- Estimates of the probability of the individual-based model being a better fit than any given run of the stochastic model
- Uses 50,000 runs of the stochastic model and a Gaussian estimate of the probability distribution of the R^2 value of the stochastic model.

R^2 : regression coefficient

Power relationship is the winner

- The probability of the transmission function being mass action or frequency dependent is vanishingly small
- A power relationship is designed to fit less easily described transmission functions
- This is a better estimate, but the probability is still small
- However, adding an asymptotic contact function to it does nothing to improve its performance
- These confirm the AICc results from before.

Complexity of models

- Thus, due to the complex interactions between humans and zombies, both spatially and dynamically, their interactions are not easily explainable by a simple random-motion-based model
- Thus, more complex models such as individual-based models, are useful when studying zombie epidemics
- With some faith in the individual-based model, can we control epidemic using zombie hunters?

Adding zombie hunters

- We added hunters to the simulation in different numbers
- We started with either 50 or 100 human agents
- The game map has an approximate area of 4000m²
- Thus, our two scenarios represent human density of 12,500 and 25,000 people per km², respectively
- These model a sparse human population and a dense one.

A spontaneous outbreak

- Humans and hunters were randomly distributed across the map
- To simulate a spontaneous outbreak, five zombies were randomly distributed among the population
- The simulation was run until there were either no humans or no zombies left.

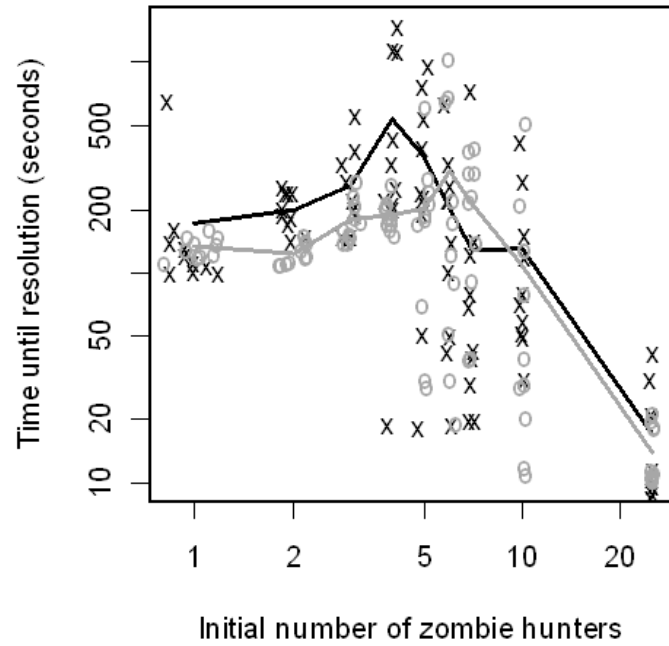
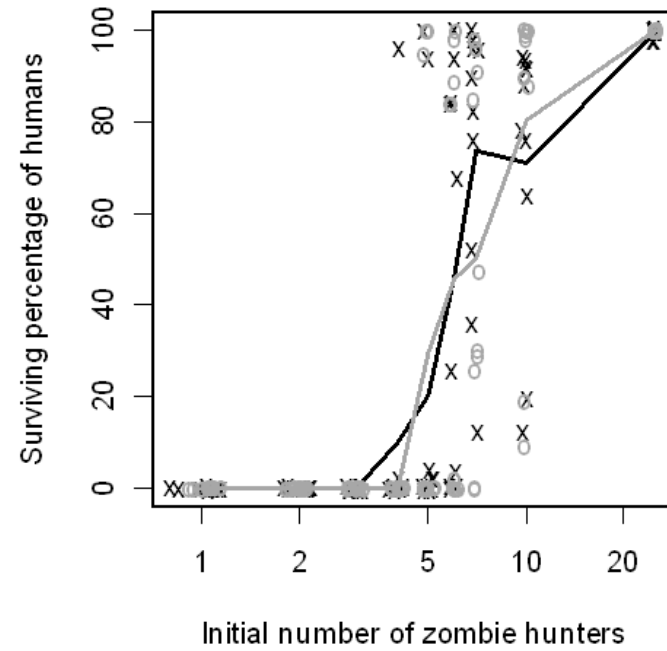
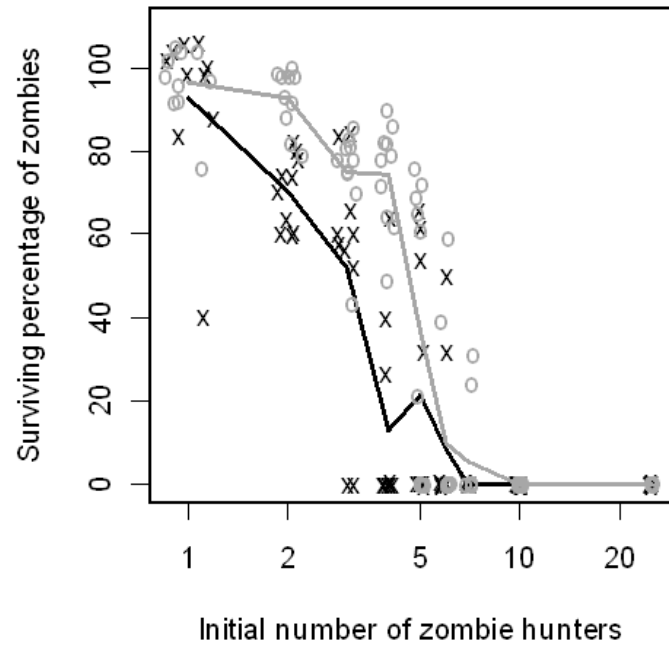
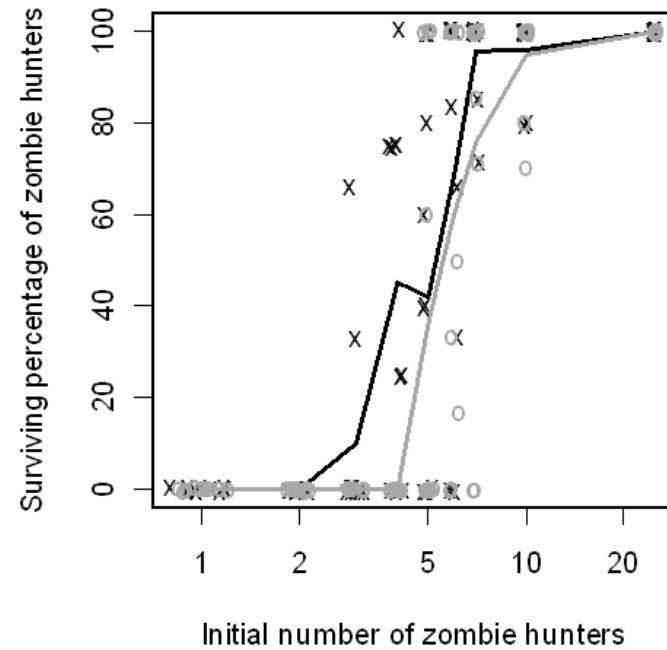
Final outcomes of each run

	50 humans			100 humans		
Number of hunters	Zombies win	Zombies lose		Zombies win	Zombies lose	
		Hunters survive	Hunters and humans survive		Hunters survive	Hunters and humans survive
1	10	0	0	10	0	0
2	10	0	0	10	0	0
3	8	2	0	10	0	0
4	3	5	2	10	0	0
5	4	1	5	6	1	3
6	2	1	7	2	2	6
7	0	0	10	2	0	8
10	0	0	10	0	0	10
25	0	0	10	0	0	10

- Either zombies take over entirely, hunters survive without any humans or both humans and hunters manage to survive.

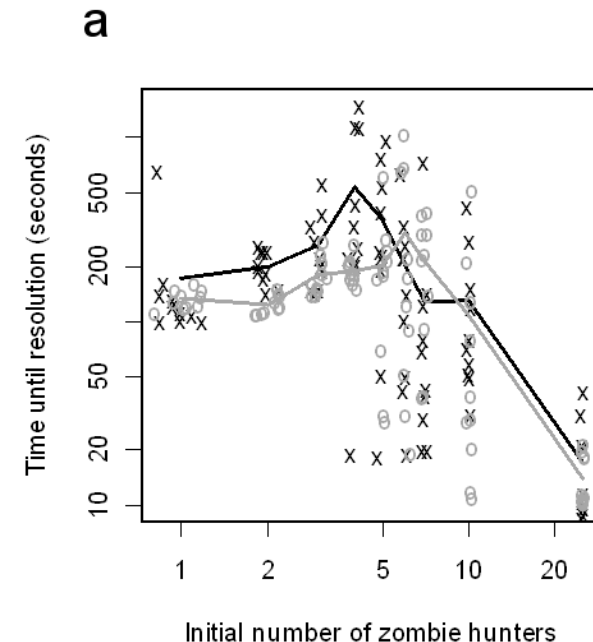
Expanding the results

- As expected, as more hunters are introduced, more scenarios occur in which humans and/or hunters survive
- We can also look at the results in more detail
- Not just the final outcome, but the extent of survival of each population
- There is some noise, as we're only running 10 simulations, but the trends are clear

a**b****c****d**

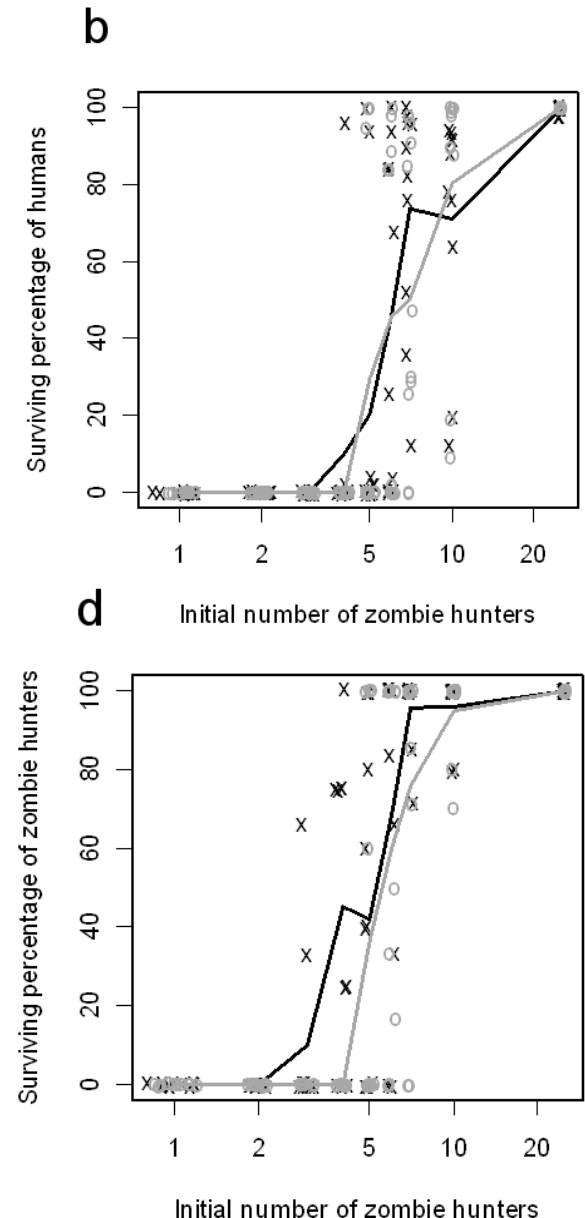
Maximum resolution time

- The time taken for a zombie-human conflict to result itself has a maximum at around 4 zombie hunters for 50 humans and 6 hunters for 100 humans
- Less than this and the zombies quickly take over
- Much more and the hunters make short work of the zombie plague.



Minimum number of zombie hunters

- The number of surviving humans and proportion of surviving hunters increases with the number of hunters
- At least 4 or 5 hunters seem to be required for any human survival
- With 7 or more, we are very likely to keep at least some humans alive.

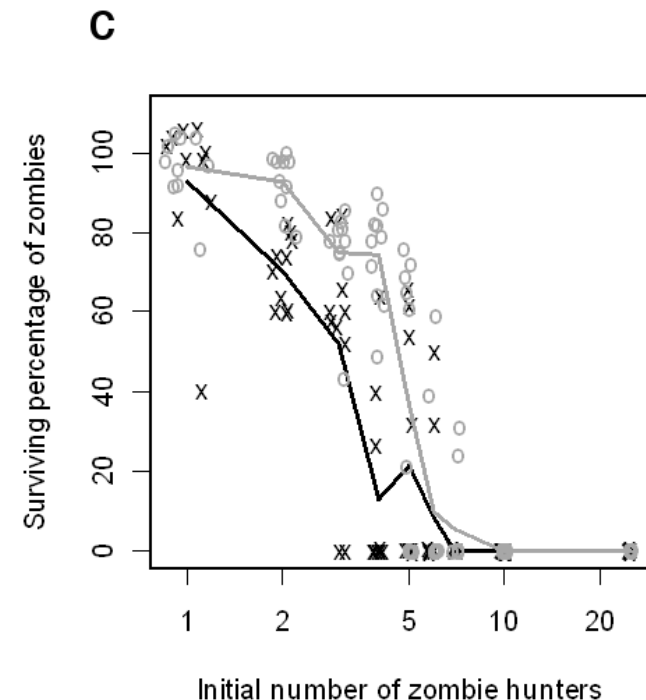


Emergent behaviour

- The actual number of human survivors varies from run to run, even with 10 hunters
- Also, either only a few humans survive or nearly all of them do
- This is likely due to emergent behaviour in the agent-based model
 - either the zombies are eradicated quickly
 - or else they have a chance to establish themselves and cause massive casualties
- This is supported by the bimodal resolution time around the 5 hunter mark.

Zombie survival

- Zombie survival decreases with an increasing number of hunters, unsurprisingly
- However, eradication cannot be guaranteed with any level of confidence until at least 7 hunters are present per 50 humans
(or 10 per 100 humans)
- Thus, a few hunters can make all the difference.



Observations on behaviour

- An agent-based model is no substitute for a live experimental trial
- However, we can gain some insights into zombie incursions by merely observing the simulations
- Zombies require critical mass to take down a hunter
 - if each zombie begins near a hunter, the hunters quickly finish off the zombies
 - if zombies begin in an area free of hunters, they can infect enough humans to form a mob which may survive a hunter encounter.

Zombie organisation

- Zombies require organisation to take down a hunter
 - even a large number of zombies who are wandering aimlessly can be picked off one by one
- The initial positioning of zombies, hunters and humans plays a vital role
 - if zombies are initially near hunters, they will be quickly destroyed
 - even if only one zombie survives, if it is near enough humans, it can start an epidemic on its own before detection by hunters.

Summary

- An effective way to protect a population is to distribute trained shotgun-armed hunters among the population
- A spontaneous zombie outbreak can be quickly quelled before gaining a foothold
- In a sparsely populated community, a ratio of 7 hunters to 50 humans is needed
- When human density is doubled, the lower ratio of 10 hunters to 100 humans is sufficient
- Thus, the number of hunters is not directly proportional to the density of humans.

An unexpected result

- A dense population does not necessarily accelerate the spread of zombie-ism
- This is because the dense setting forces more humans to stay within the “protection zones” of the hunters
- This enables each hunter to cover more humans, making them more efficient

Authors

- Nick Beeton (University of Tasmania)
- Alex Hoare (University of New South Wales)
- Brody Walker (University of Tasmania)

N. Beeton, A. Hoare, B. Walker. Is there a zombicidal maniac near you? You'd better hope so! (In: R. Smith? (ed) Mathematical Modelling of Zombies, University of Ottawa Press, *in press.*)