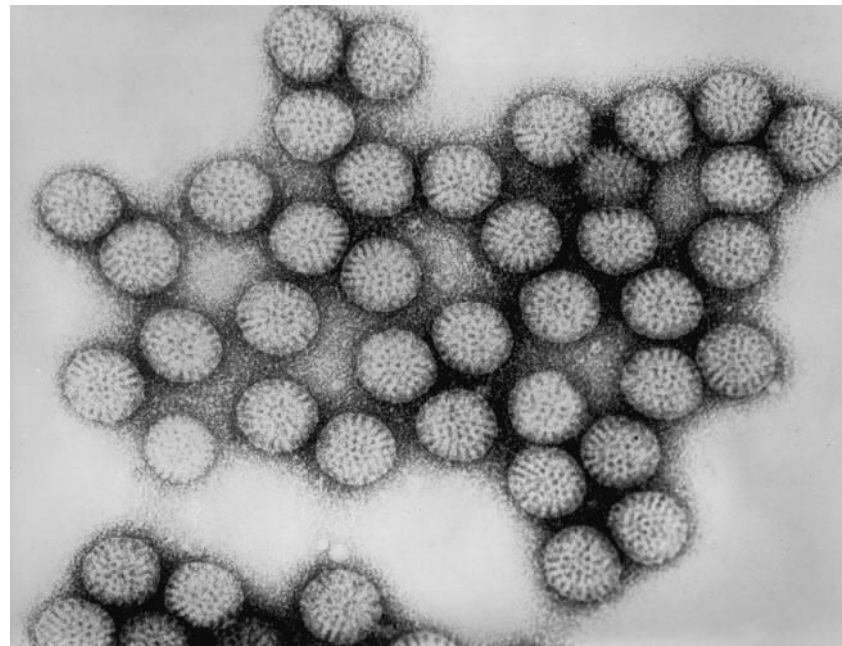
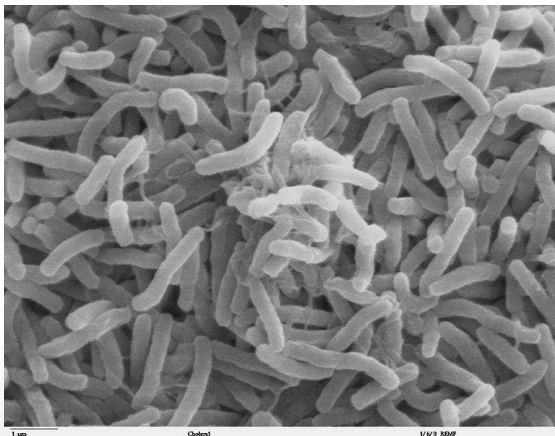


# Dose-response relationships for transmission modeling

Andrew Brouwer  
University of Michigan



# Acknowledgements

- Funding: Models of Infectious Disease Agent Study (MIDAS)
- Collaborators:
  - Joseph Eisenberg, University of Michigan
  - Mark Weir, The Ohio State University
  - Marisa Eisenberg, University of Michigan
  - Rafael Meza, University of Michigan

# The role of the environment

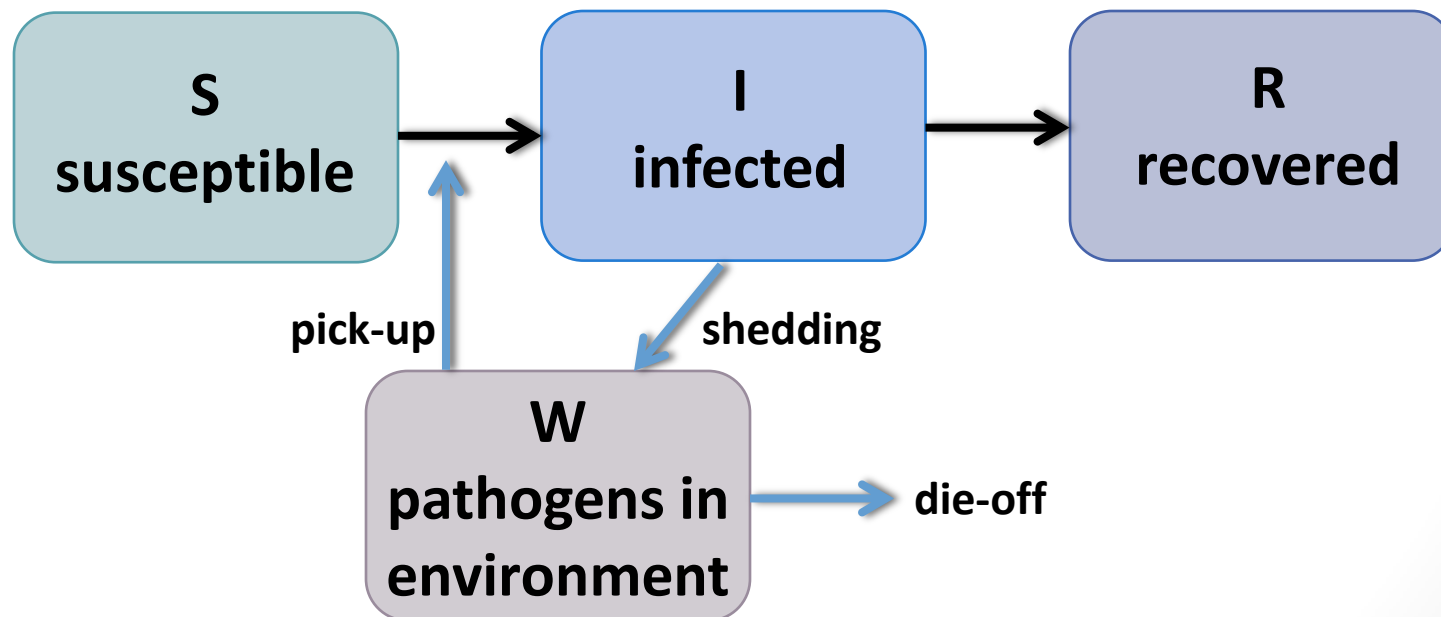
- Historically, classical SIR dynamics, which do not explicitly model the environment, have been very successful at modeling outbreaks.
- However, the environment mediates transmission for many pathogens, which can impact dynamics. This occurs in a variety of media: water, air, food, fomites, etc.

# The role of the environment

- Mitigation often uses environmental interventions: water treatment, hand-washing, surface decontamination, etc.
- Explicitly modeling the environment allows us to consider environmental interventions, pathogen persistence and transport, and the variability of pathogen dose.

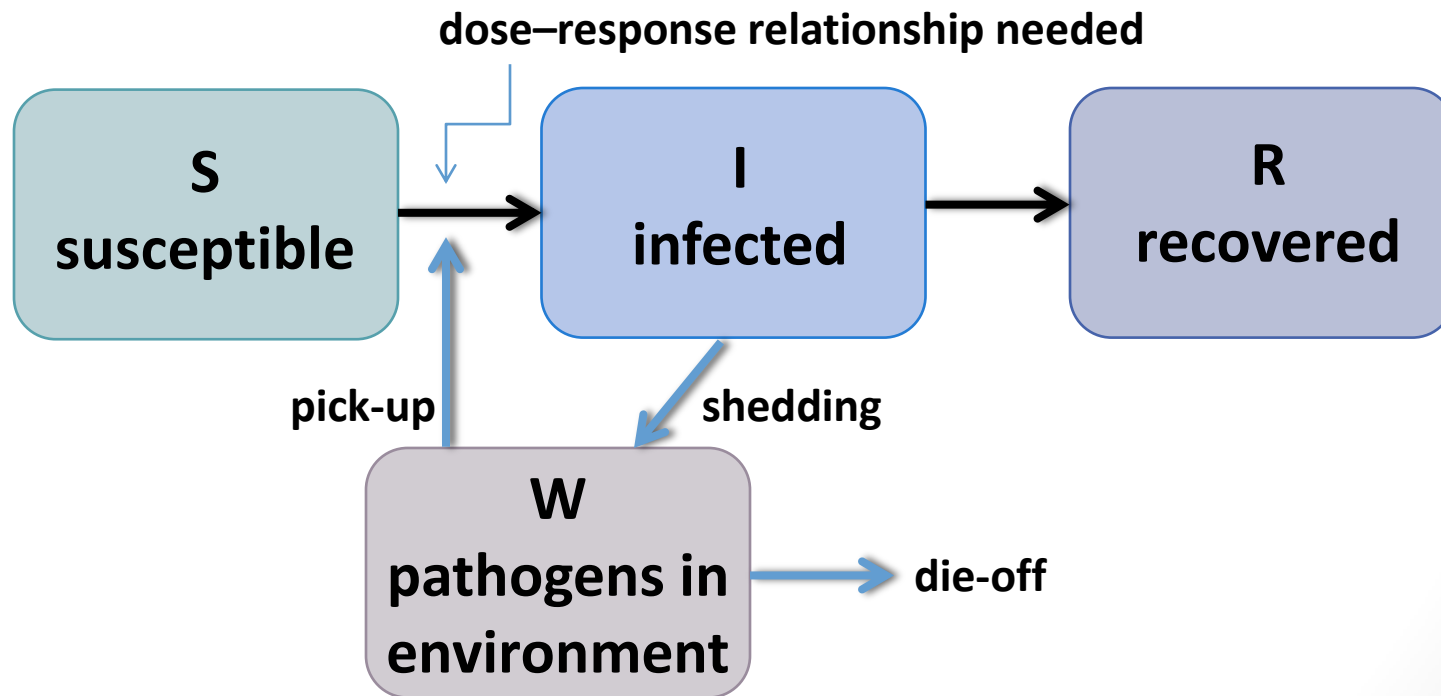
# Framework

- EITS (Li, 2009) and SIWR (Tien and Earn, 2010) are two models that explicitly considers the role of the environment.



# Framework

- We need to model the relationship between the number of pathogens someone is exposed to and the corresponding probability of infection



# Dose-response relationship

- The probability of becoming infected may not be linear with pathogen dose.
- Categories of DR functions
  - Biologically derived: exponential, exact beta-Poisson
  - Mathematically convenient: Hill functions, linear, approximate Beta-Poisson
  - Empirically derived: log-normal, Weibull

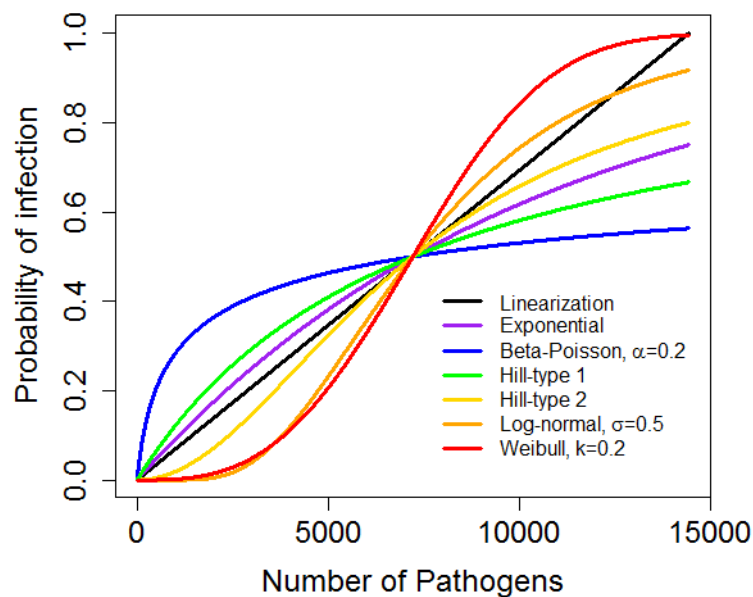


Figure: Example DR functions, with same  $ID_{50}$ .

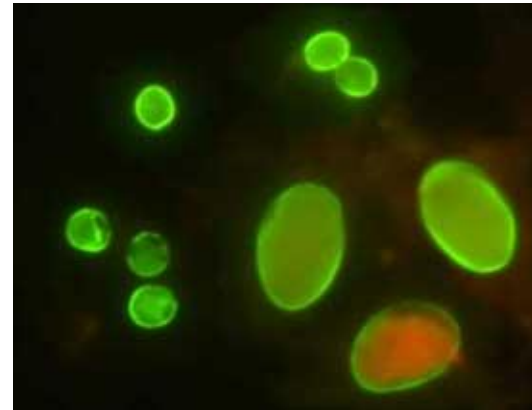
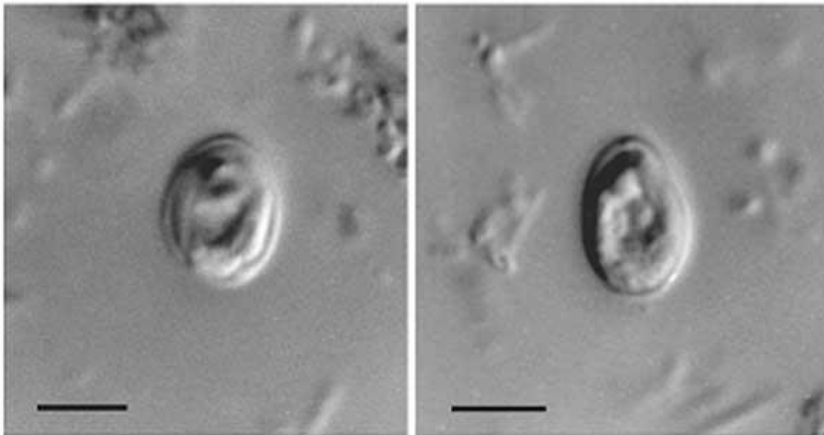
# State of the field

- The field of quantitative microbial risk assessment (QMRA) has developed much the experimental dose–response literature.
- Theoretical work for ODE transmission models has been agnostic to functional form.
- Implications of the choice of dose–response functional form have not previously been described.



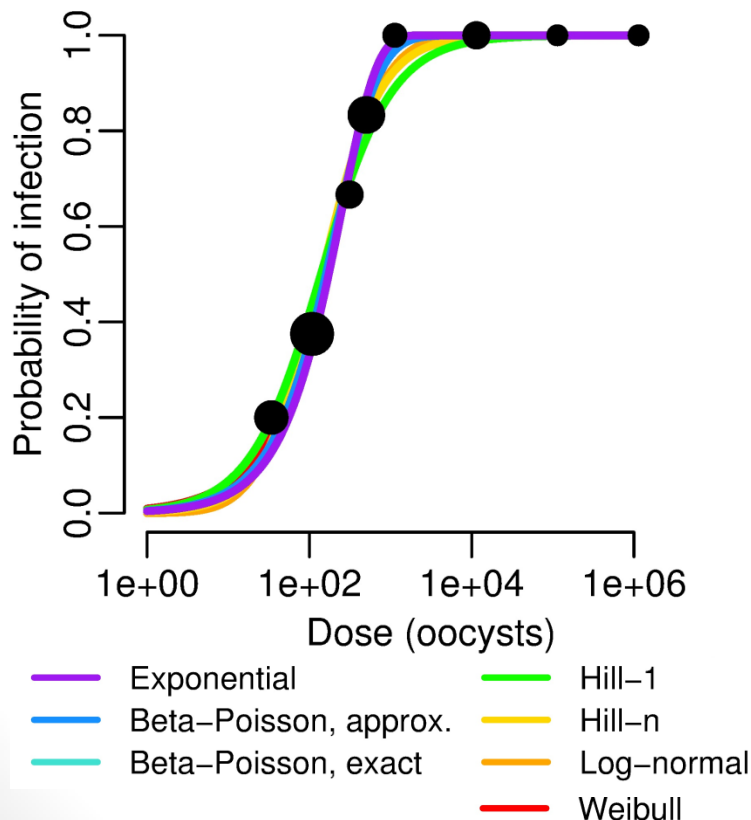
# Example: *Cryptosporidium*

- *Cryptosporidium* is a genus of parasitic protozoa that cause gastrointestinal illness (cryptosporidiosis).
- The spore form (oocyst) is environmentally hardy and resists chlorine disinfection.



# Example: *Cryptosporidium*

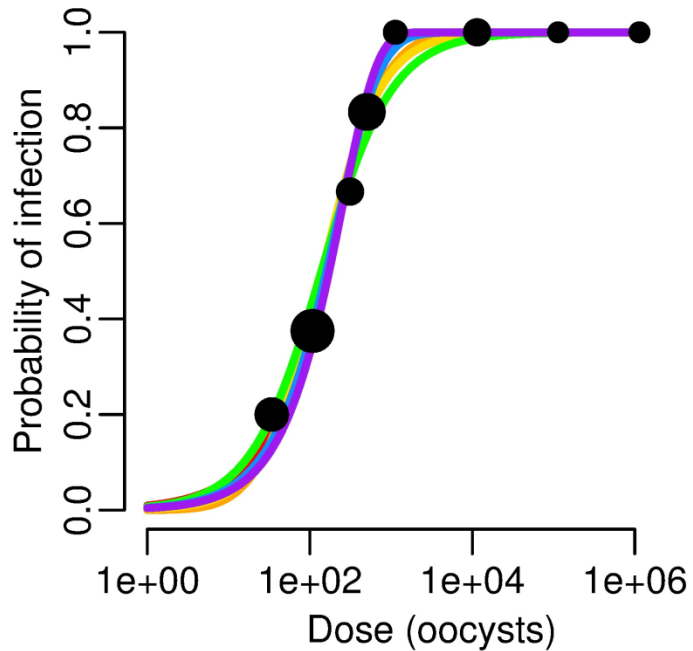
- Dose-response data is available for the Iowa strain of *C. parvum* in Dupont et al. 1995 (NEJM).



- We fit six dose-response functions to this data.
- We use the functions in an EITS model (with exposed compartment) parameterized to loosely represent *Cryptosporidium*.

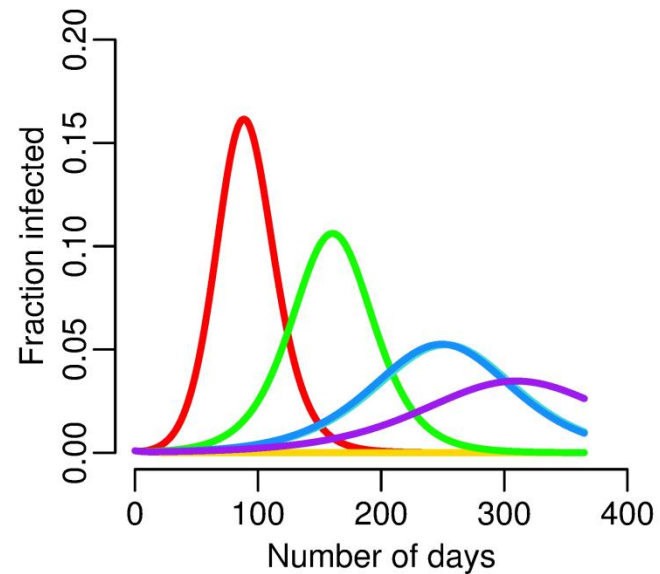
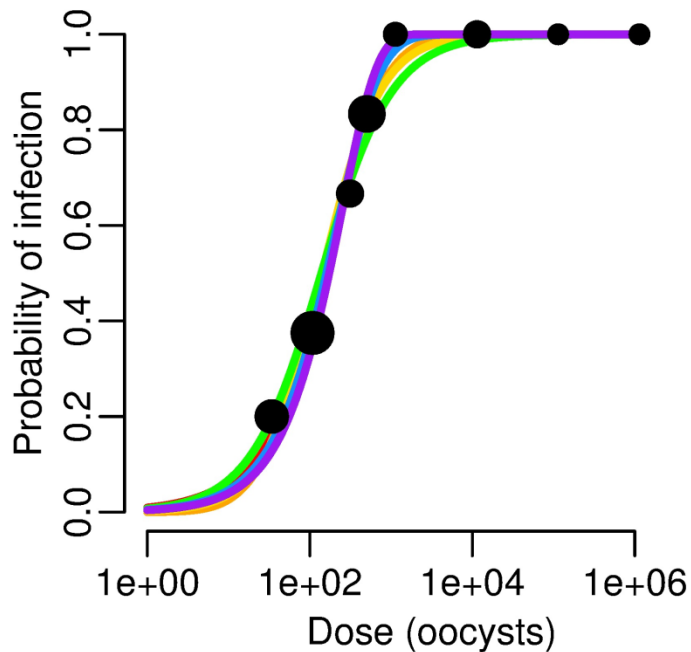
# Example: *Cryptosporidium*

$$\dot{S} = -S \times (\text{contact rate}) \times f(\text{dose})$$



# Example: *Cryptosporidium*

$$\dot{S} = -S \times (\text{contact rate}) \times f(\text{dose})$$



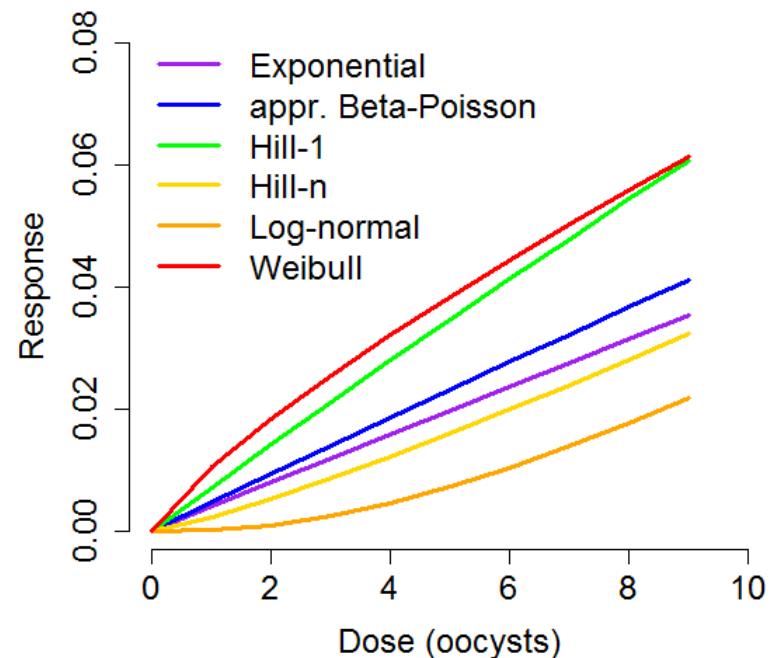
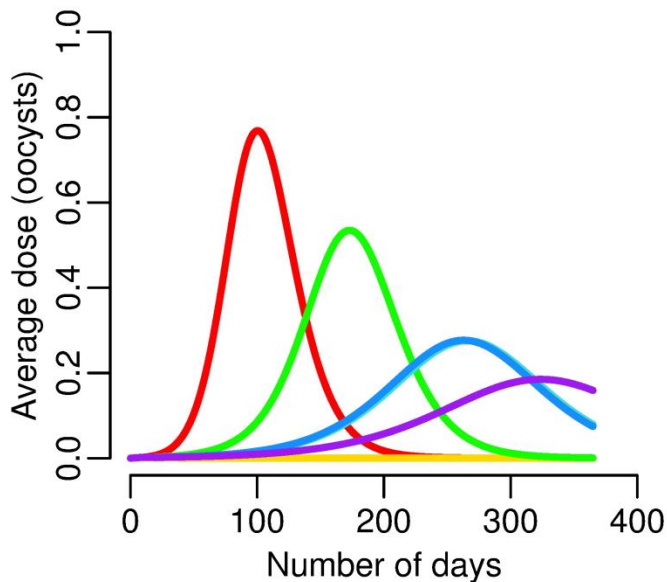
What appears to be good agreement in dose-response functions creates dramatically different dynamics!

# Example: *Cryptosporidium*

- Why are medium and high dose data so uninformative for disease dynamics?

# Example: *Cryptosporidium*

- Why are medium and high dose data so uninformative for disease dynamics?
- There is significant spread in the low-dose regime, where the dynamics are actually happening.



# This is a problem

- Experimental data is well-fit by many dose–response functions, but these all give very different dynamics.
- Dynamics are controlled by the low-dose regime, but we have little-to-no experimental data there.

Is this modeling approach futile?



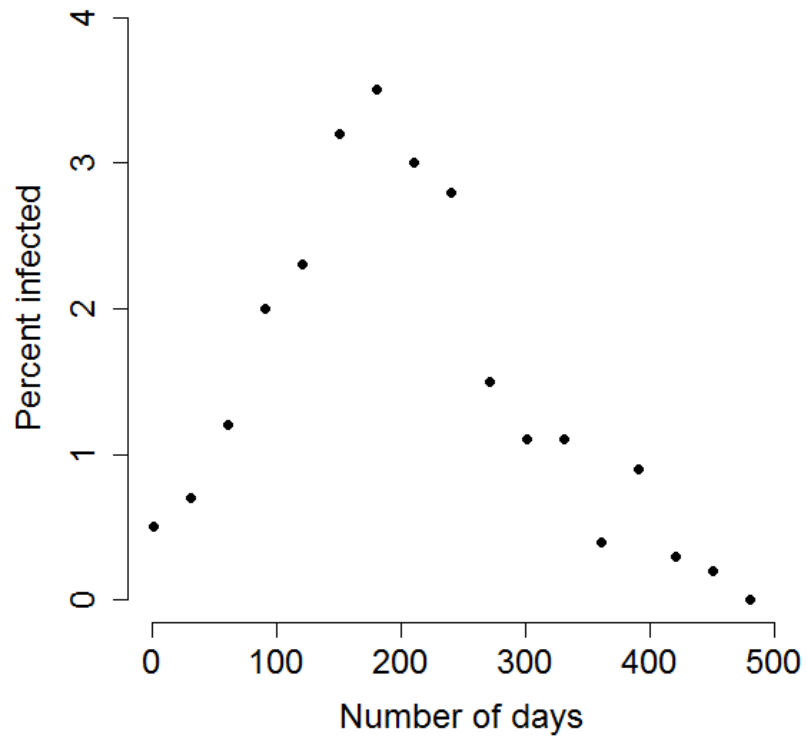
# Is this modeling approach futile?

- Not necessarily!

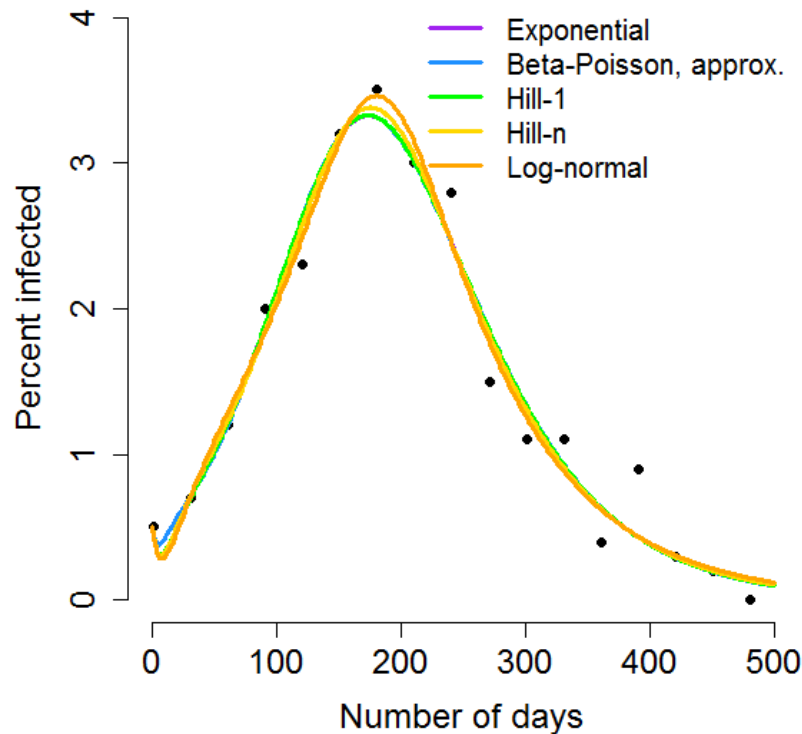
# Is this modeling approach futile?

- Not necessarily!
- The previous example assumes that we know all of the other parameters, like shedding and pick-up rate, but this is unrealistic.
- We can manage multiple sources of uncertainty with identifiability analysis, and environmental monitoring can provide additional information.

# Fitting to data

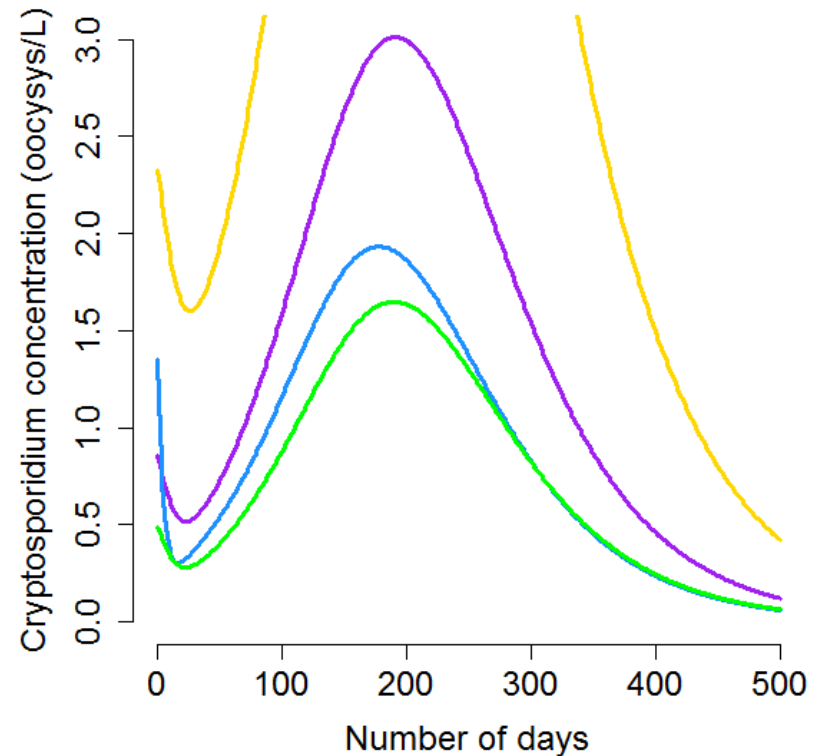
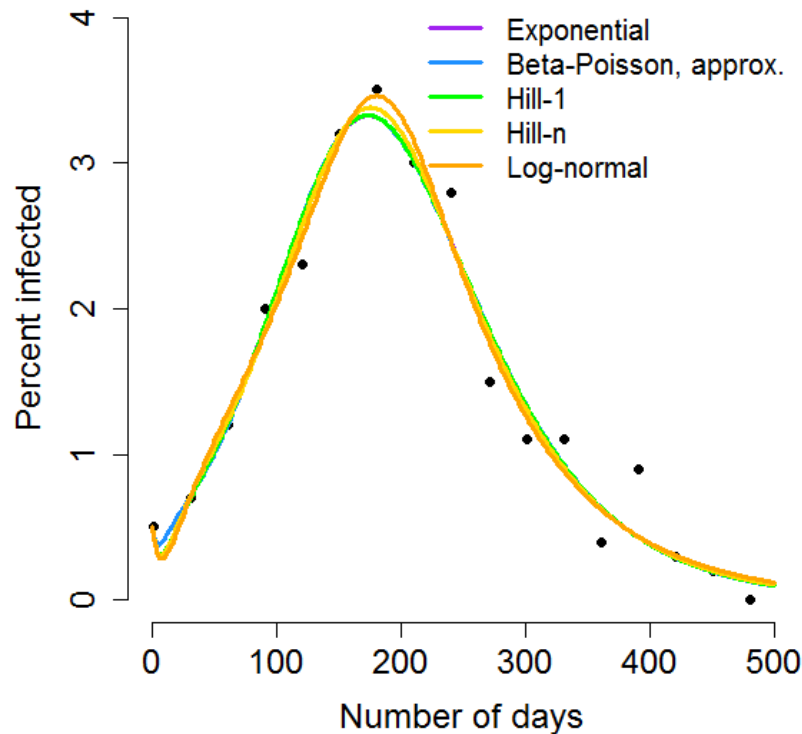


# Fitting to data



Different dose response models can fit the data equally well.

# Fitting to data



But the different models predict different pathogen concentrations.

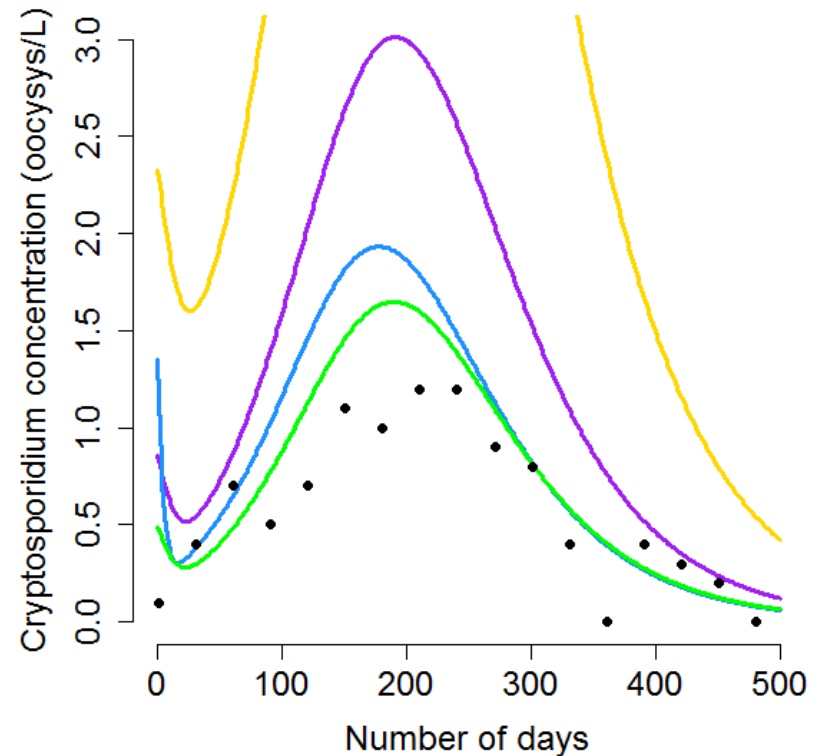
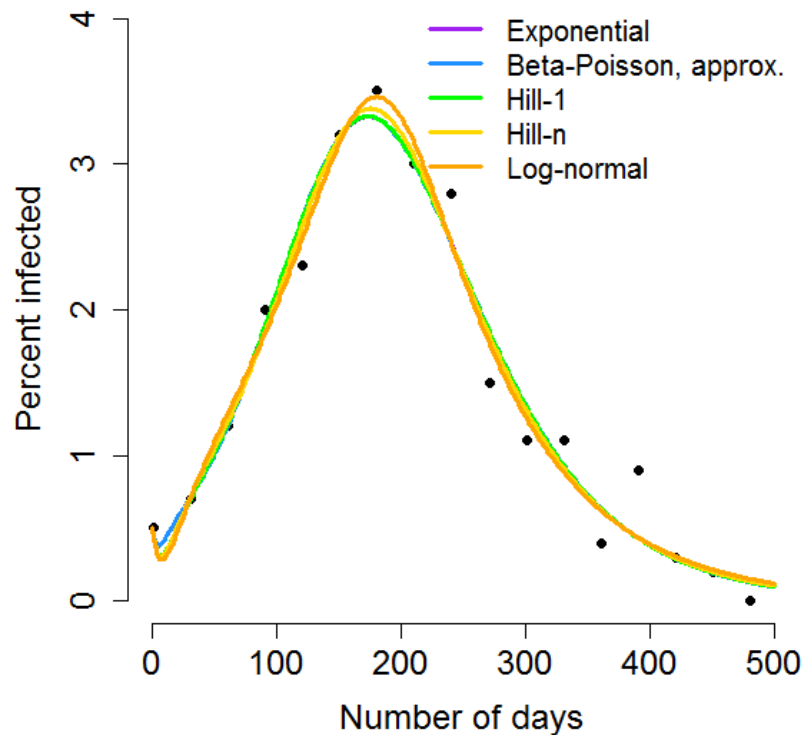
# Infectivity and shedding

- The low-dose infectivity and the shedding rate can trade-off (i.e. are in the same identifiable combination) to give the same case data.
  - Fewer, highly infectious pathogens
  - More, less infectious pathogens

# Infectivity and shedding

- The low-dose infectivity and the shedding rate can trade-off (i.e. are in the same identifiable combination) to give the same case data.
  - Fewer, highly infectious pathogens
  - More, less infectious pathogens
- Observing the concentration of pathogens in the environment could point us to the right place on the continuum.

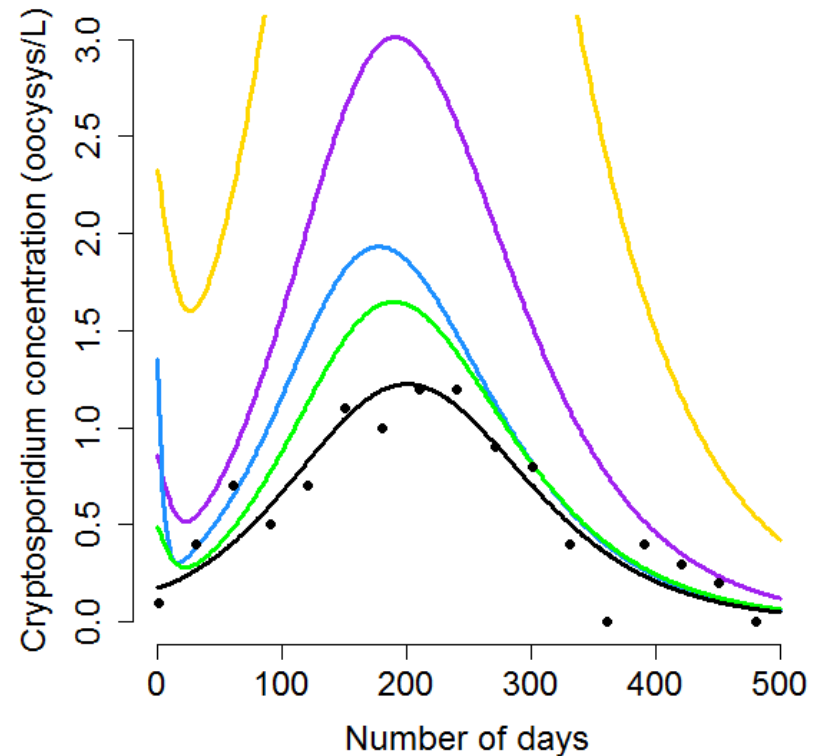
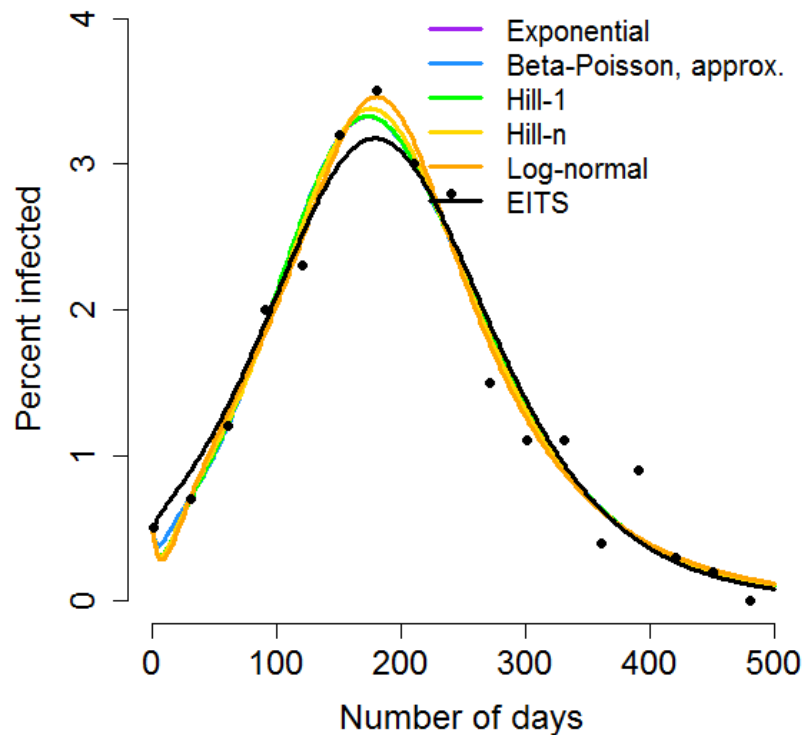
# Fitting to data



So, if we measure the environment...



# Fitting to data

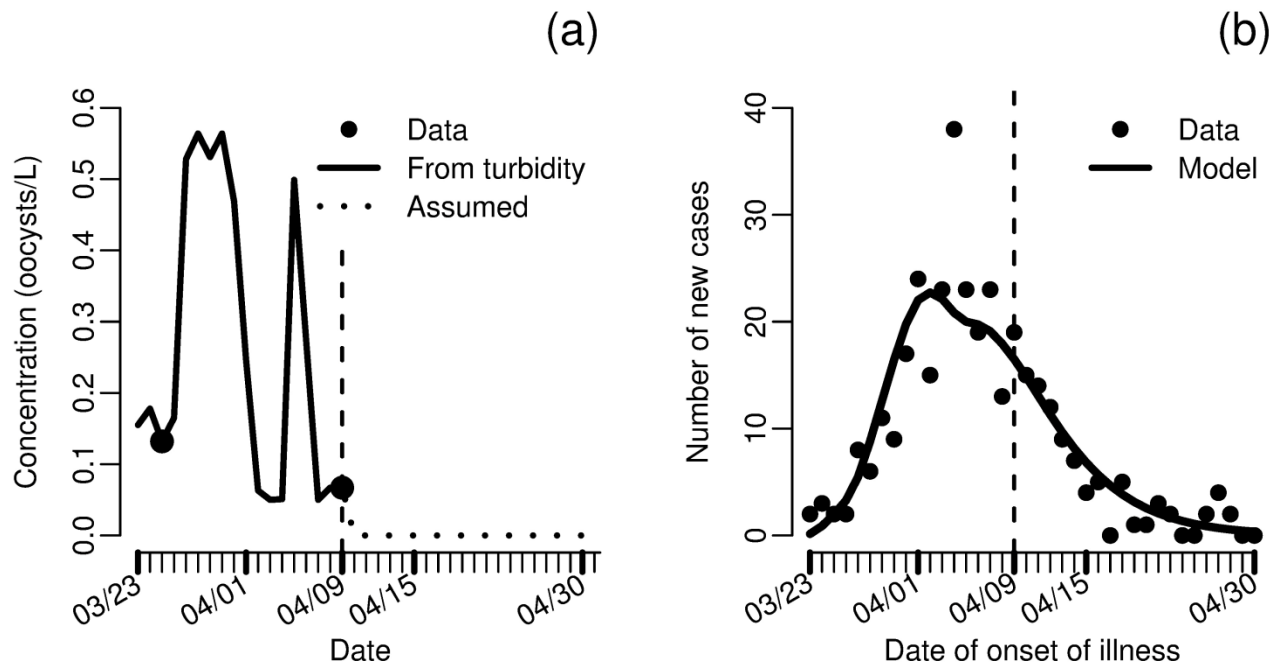


... we can fit to both data sets using a linear model. This approach allows us to estimate, not fix *a priori*, the infectivity.

# Milwaukee *Cryptosporidium* outbreak

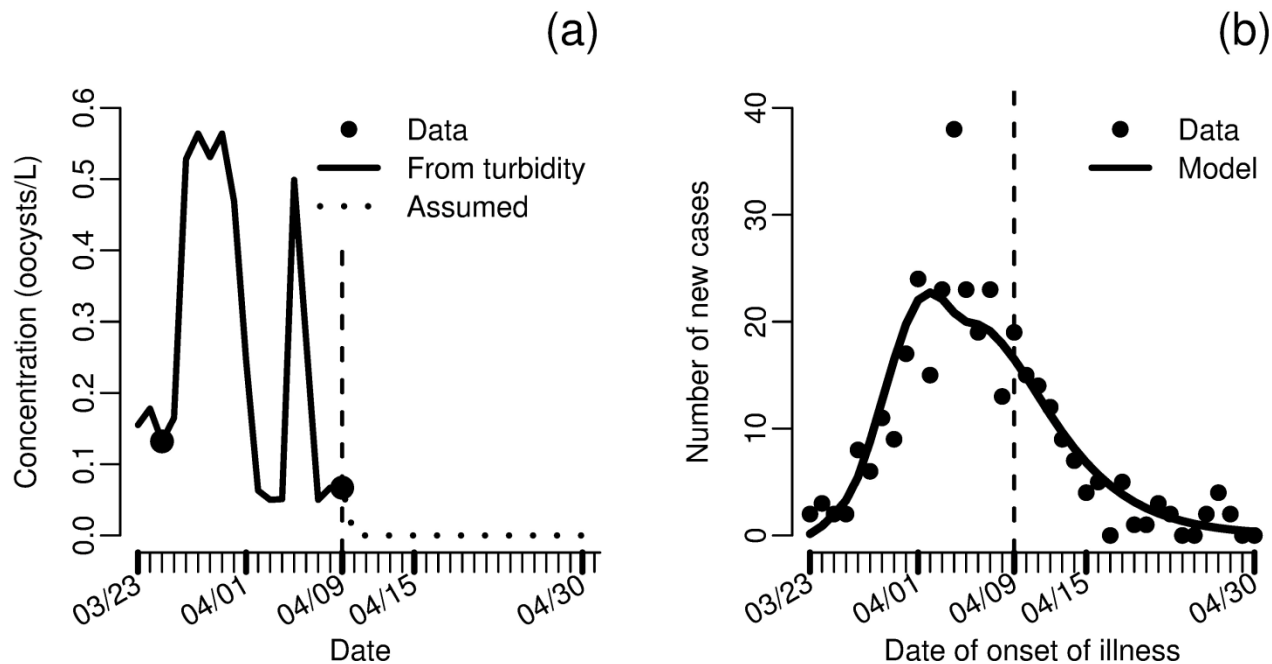
- In March of 1993, one of Milwaukee's two water treatment plants malfunctioned.
- Cases of watery diarrhea began shortly thereafter.
- *Cryptosporidium* was isolate from stool samples.
- Approximately 400,000 people were affected.
- Turbidity was recorded daily, but only two water samples were tested for *Cryptosporidium* concentration.

# Milwaukee Outbreak



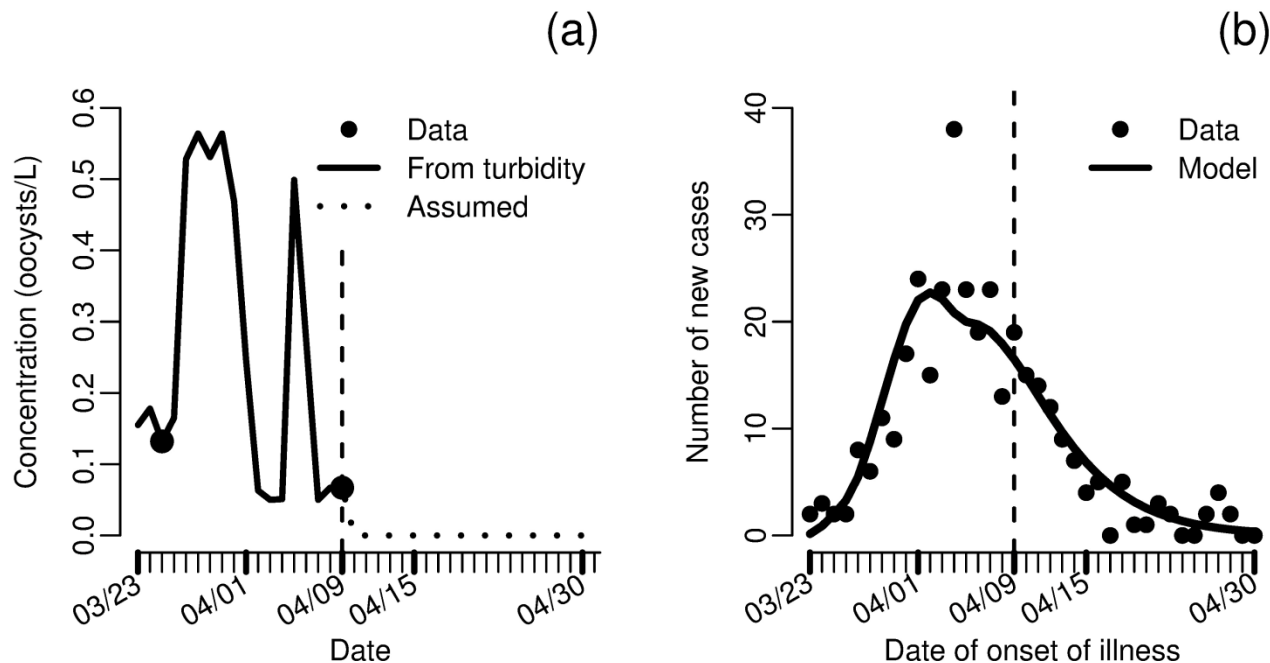
- Here, we use turbidity data as a proxy for exposure to the pathogen compartment, and fit the model to the case data.

# Milwaukee Outbreak



- We can estimate, under reasonable assumptions of water consumption rates, that the infectivity was an order of magnitude greater than the Iowa strain of *C. parvum*, much closer to the TAMU strain.

# Milwaukee Outbreak



- Environmental monitoring can help us estimate infectivity from data, instead of being forced to assume an infectivity from a dose–response form.

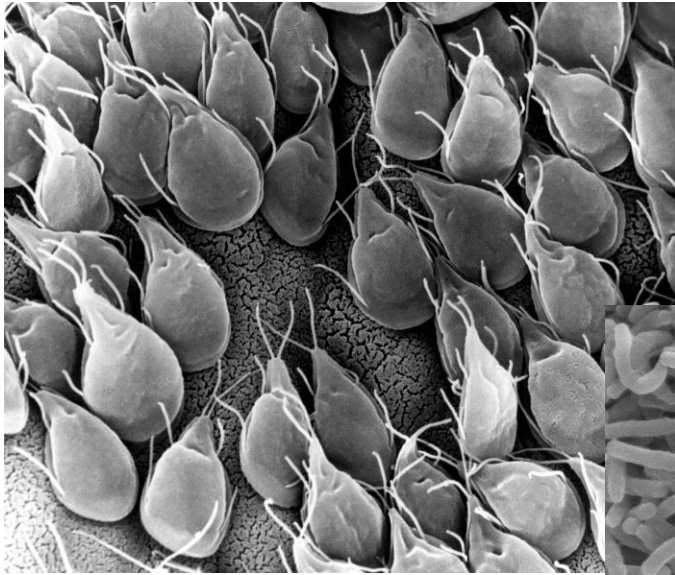
# Final thoughts

- Most dose-response data is in the middle and high dose regime, but it is the low dose regime that governs dynamics.
- Constraining functions at higher doses does not satisfactorily constrain behavior at low-doses.
- Statistical “best-fit” is only one of many criteria that should be taken into account. Biological mechanism and realism of the low-dose regime should be primary.

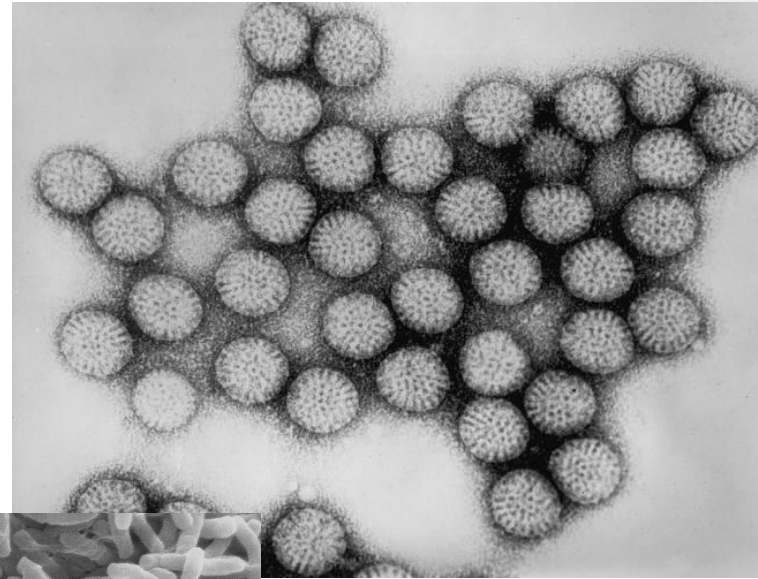
# Final thoughts

- Incorporating the environment into models:
  - better understanding of the role and importance of underlying environmental processes.
- Can assess potential interventions:
  - more effective intervention design and allocation of resources.
- Significant challenges remain.
  - Low-dose regime of dose-response functions

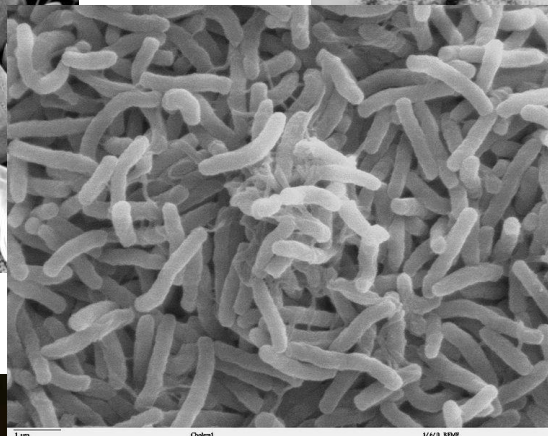
# Thank you!



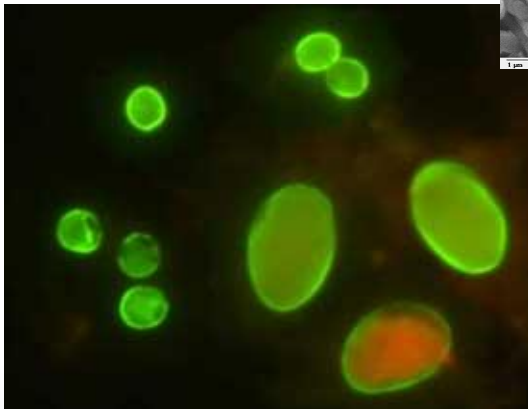
Giardia



Rotavirus



Cholera



Cryptosporidium



Influenza