

Modeling an outbreak of  
dolphin morbillivirus:  
US east coast  
(June 2013 – 2014)

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# Outline

- Background
- Data preparation
- Developing the model
- Results
- Conclusions

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# Background

Dolphin morbillivirus (DMV) : same virus genus as measles



Characteristics: highly contagious, respiratory transmission, lifelong immunity  
(i.e. similar to SIR assumptions)

Severe epidemics observed around the world



???

Marine mammals are  
challenging to study



Population movements?

Missed cases?

# US outbreak 2013-2014

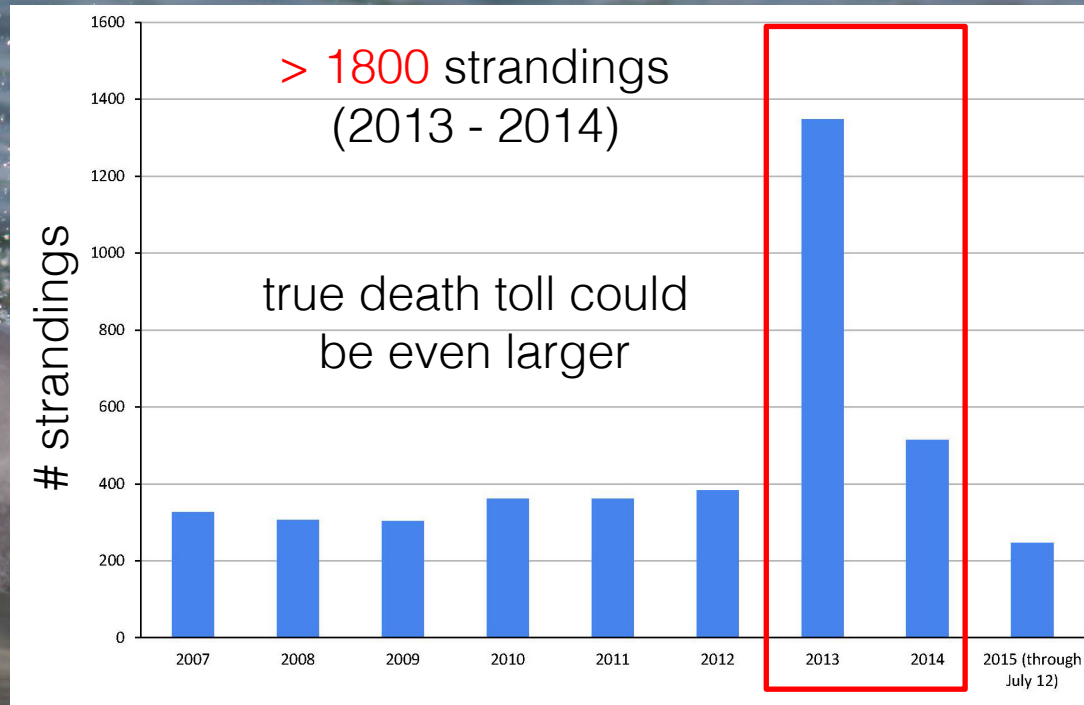


LATEST STORIES

PHOTO OF THE DAY

GENDER REVOLUTION

## What's Killing Bottlenose Dolphins?



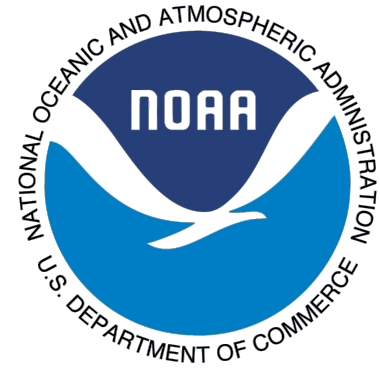
Source: NOAA

Last outbreak was 25 years ago... Why now?

# Epidemic progression



Rapidly  
spread from  
NY - FL



# Modeling aims

Specific questions to answer:

How transmissible is the disease?

How long is an individual infectious for?

How far can an infected individual travel?

Which areas are at greatest risk?

General idea:

$$\frac{dS}{dt} = -\frac{\beta SI}{N}$$

.....→ infectious period  $\frac{1}{\gamma}$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I$$

.....→ reproductive ratio  $R_0 \sim \frac{\beta}{\gamma}$

$$\frac{dR}{dt} = \gamma I$$

+ spatial component .....→ dolphin movement

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# Data

Data = **stranding** events i.e. animals that wash up on shore:

latitude, longitude, date, condition, sex, ...

Region	County	State	Latitude	Latitude Units	Longitude	Longitude Units	Observation Date	Year of Observation	Month of Observation	Day of Observation	Observation Status	Sex
NE	Sussex	DE	38.8031	decimal degrees	-75.18532	decimal degrees	2014-APR-08	2014	APR	8	MUMMIFIED/SKELETAL	UNKNOWN
NE	Sussex	DE	38.85588	decimal degrees	-75.24261	decimal degrees	2014-MAY-05	2014	MAY	5	ADVANCED DECOMPOSITION	FEMALE
NE	Sussex	DE	38.67672	decimal degrees	-75.06885	decimal degrees	2014-MAY-17	2014	MAY	17	ADVANCED DECOMPOSITION	MALE
NE	Sussex	DE	38.91356	decimal degrees	-75.30406	decimal degrees	2014-MAY-29	2014	MAY	29	MODERATE DECOMPOSITION	MALE
NE	Sussex	DE	38.66297	decimal degrees	-75.06713	decimal degrees	2014-JUN-13	2014	JUN	13	MODERATE DECOMPOSITION	MALE
SE	Brevard	FL	28.02498	decimal degrees	-80.536507	decimal degrees	2014-JAN-15	2014	JAN	15	MUMMIFIED/SKELETAL	UNKNOWN

But: cause of death could be DMV



OR

something else



e.g. injury, natural causes...



We want only **disease-induced** strandings in our model






**Challenge:** how to separate DMV strandings from everything else?



# Data Preparation

What we **have**:

1. Strandings from 2013 - 2014 outbreak  
'disease' + 'background' strandings  
2. Strandings from years **before the outbreak** (1996 – 2012)  
only 'background' strandings 

What we **need**:

1. Only 'disease' strandings from outbreak

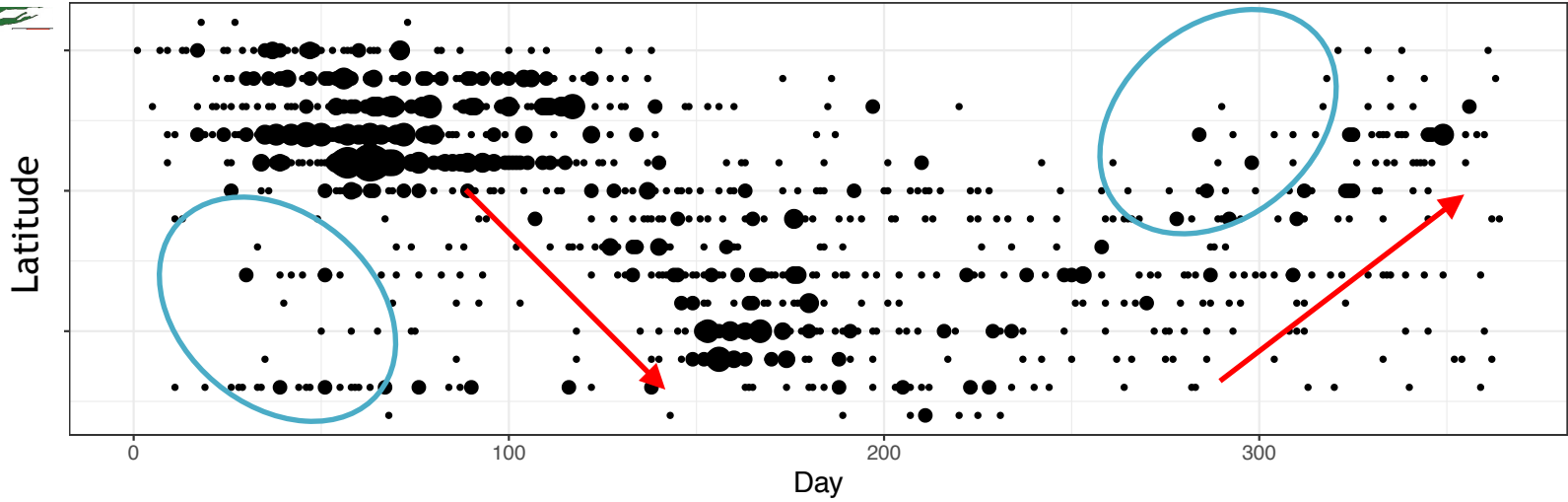
Basic idea:

$$\begin{array}{ccccccc} \text{disease} & = & \text{outbreak strandings} & - & \text{average rate of strandings before outbreak} \\ \img alt="skull and crossbones icon" data-bbox="65 825 105 900" & & \img alt="skull and crossbones icon" data-bbox="255 825 295 900" \img alt="sailboat icon" data-bbox="320 825 365 900" & & - & & \img alt="sailboat icon" data-bbox="565 820 615 895" \end{array}$$

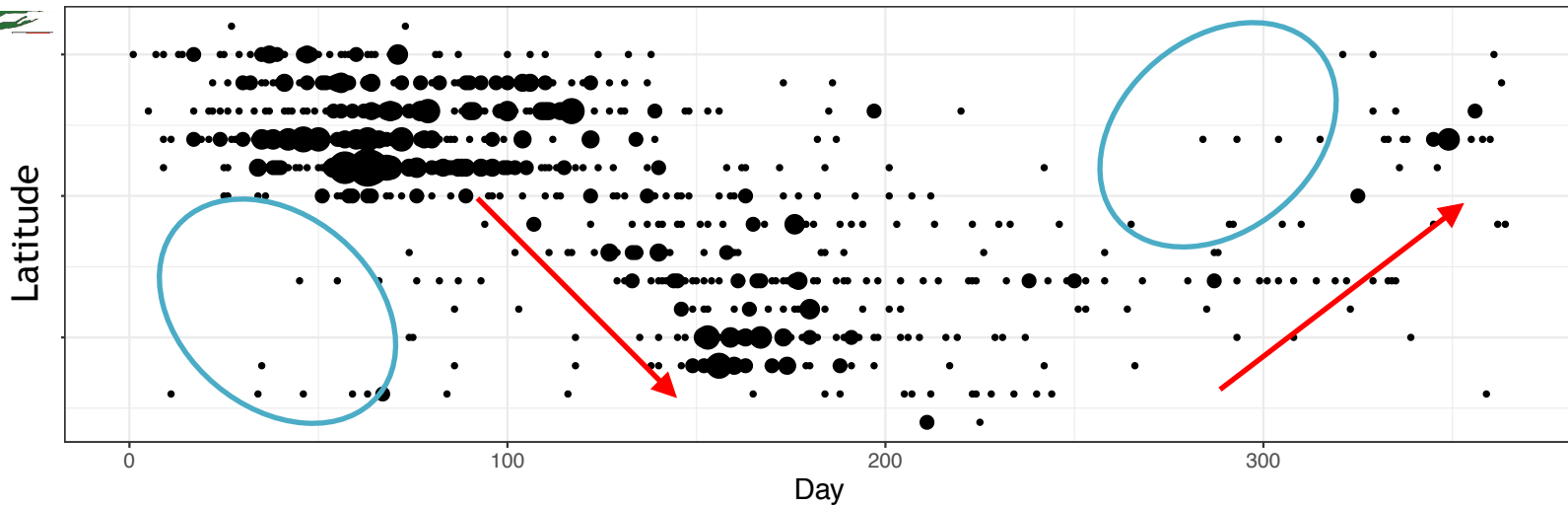
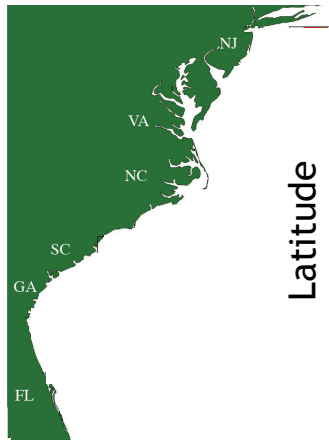
# Data Preparation



original outbreak strandings






disease-only strandings



# Data Preparation

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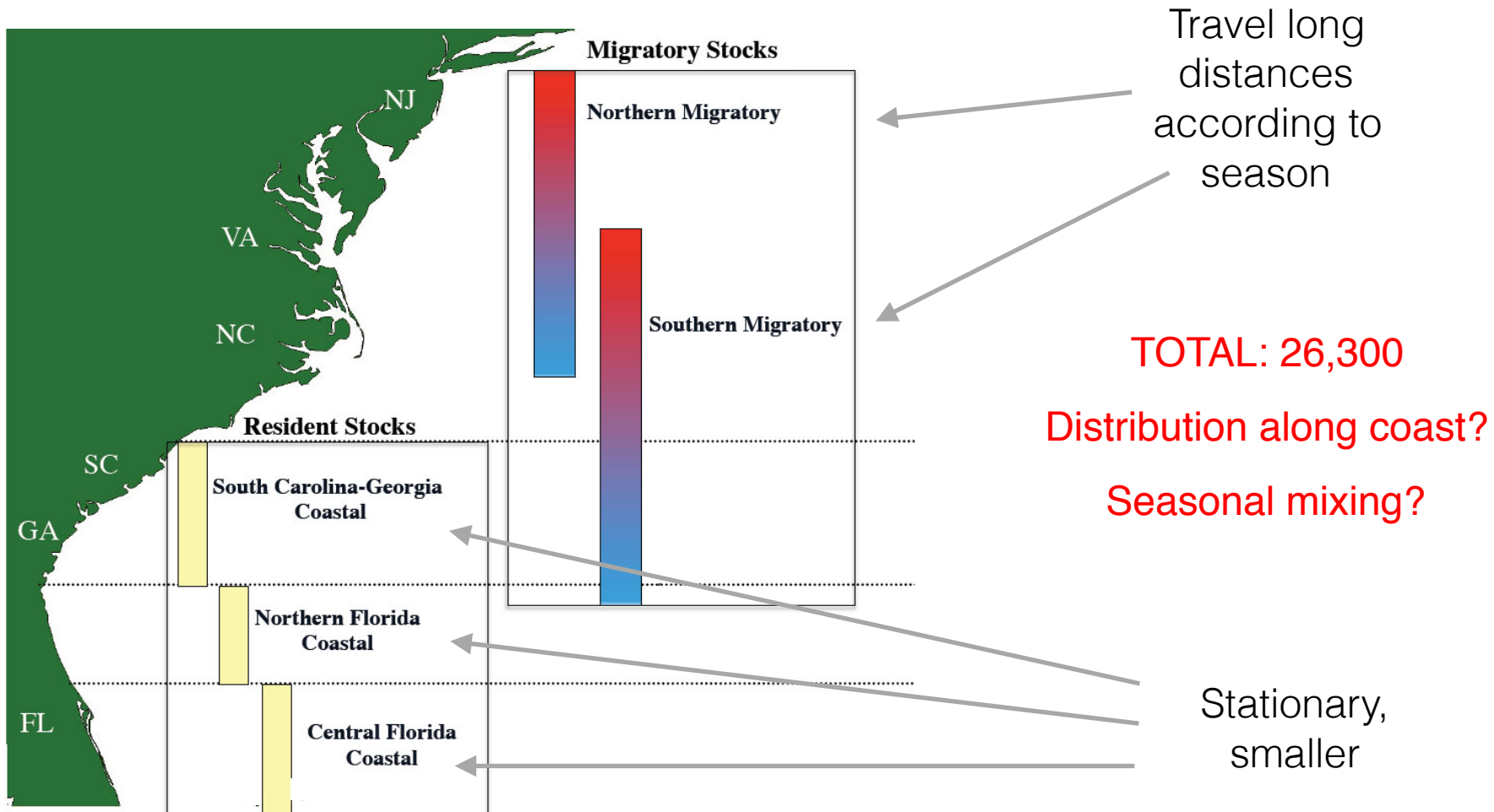
**AND...**



2. Population distribution  **estimate movement of susceptibles**

# Population distribution

Bottlenose dolphin population: 5 main groups



Source: NOAA

**Challenge:** how is the total population size (26,300) distributed along the coast?

# Population distribution

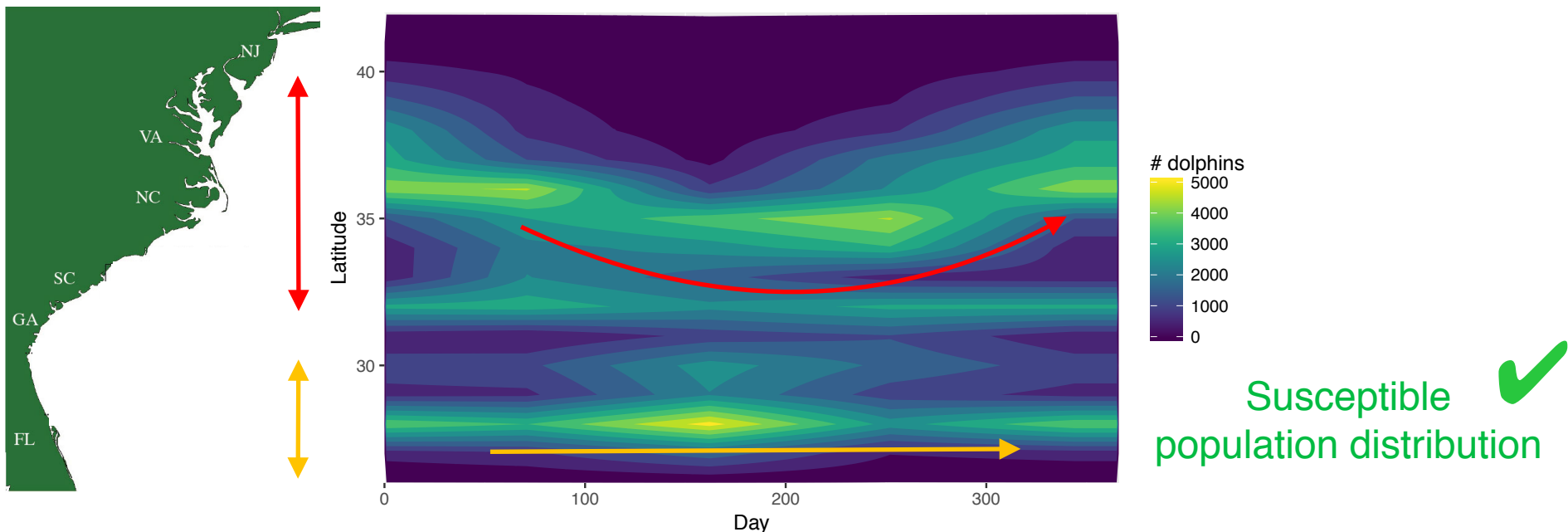
Assume: strandings  $\propto$  population size i.e.  $\uparrow$  strandings  $\rightarrow$   $\uparrow$  dolphins

Use: strandings from before outbreak ( no virus  $\Rightarrow$  susceptible )

For each time,  $t$ , and latitude,  $l$ :

$$\# \text{ dolphins}_{t,l} = \text{total population size} \times \frac{\# \text{ strandings}_{t,l}}{\text{total \# strandings}}$$

(26,300)



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# General idea

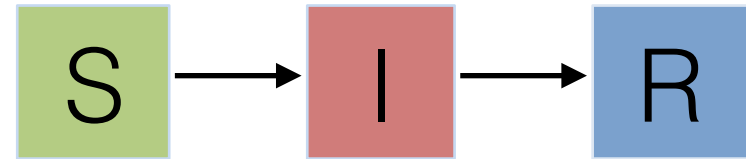
Disease dynamics:

How transmissible is the disease?

reproductive ratio,  $R_0$

How long is an individual infectious for?

infectious period



Spatial component:

Which areas are at greatest risk?

How far can an infected individual travel?

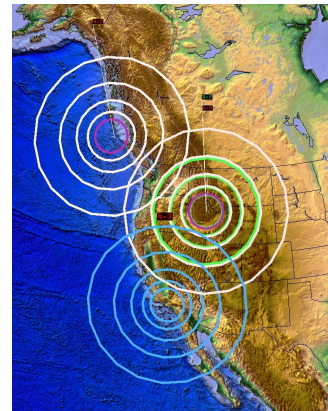


Model from seismology

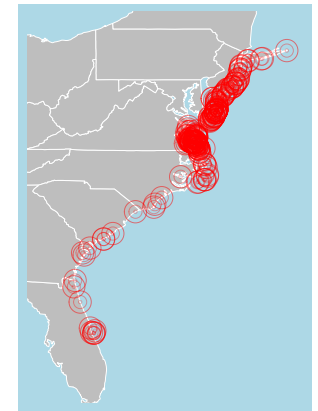
Ogata (1998)  
Ann. Inst. Stat. Math

Earthquakes, meningococcal disease,  
predicting crime rates, ...

clustering of aftershocks



clustering of strandings

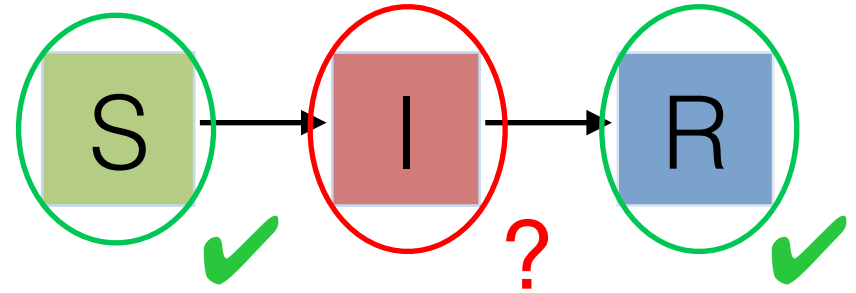




# General idea

We have estimates of:

1. population distribution
2. strandings due to disease



But:

Noisy & sparse



SIR model + spatial component + random noise

Solution:

SIR assumption: individuals have **constant** rate of infecting others

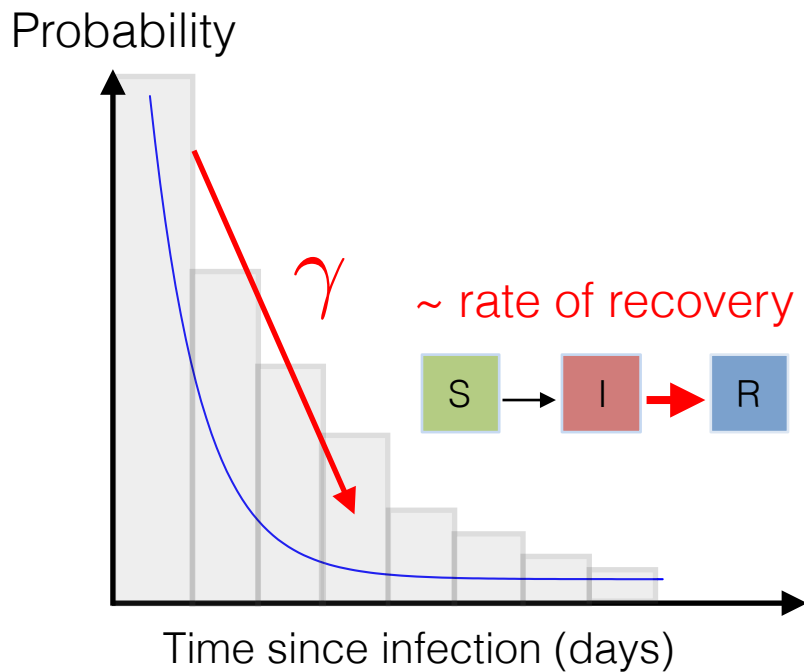


*Our* assumption: transmission is a **probability** that changes over **time** and **space**

# Developing the model

Assume individual probability of infecting others changes over time:

$$g(t) = \gamma \exp^{-\gamma t}$$

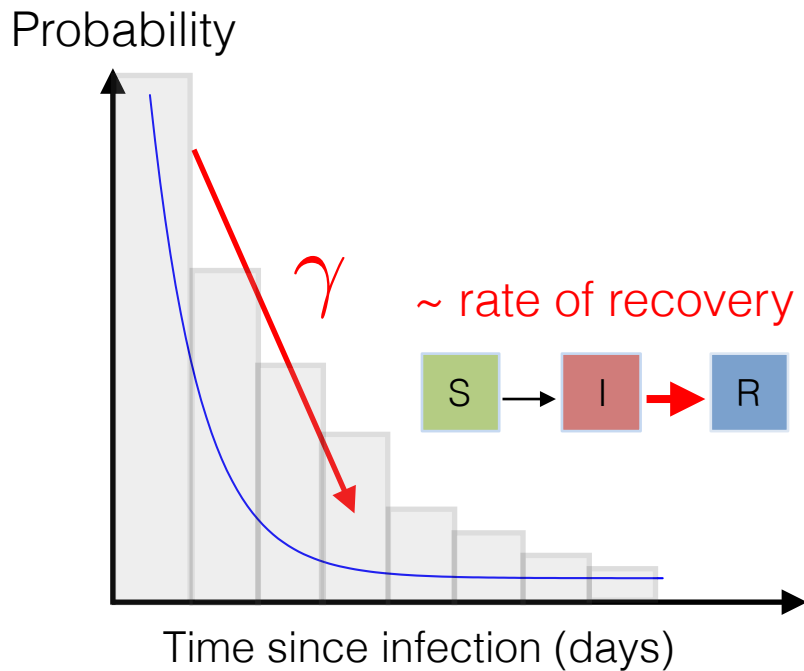


$$\frac{1}{\gamma} \sim \text{mean infectious period}$$

# Developing the model

Assume individual probability of infecting others changes  
over time:

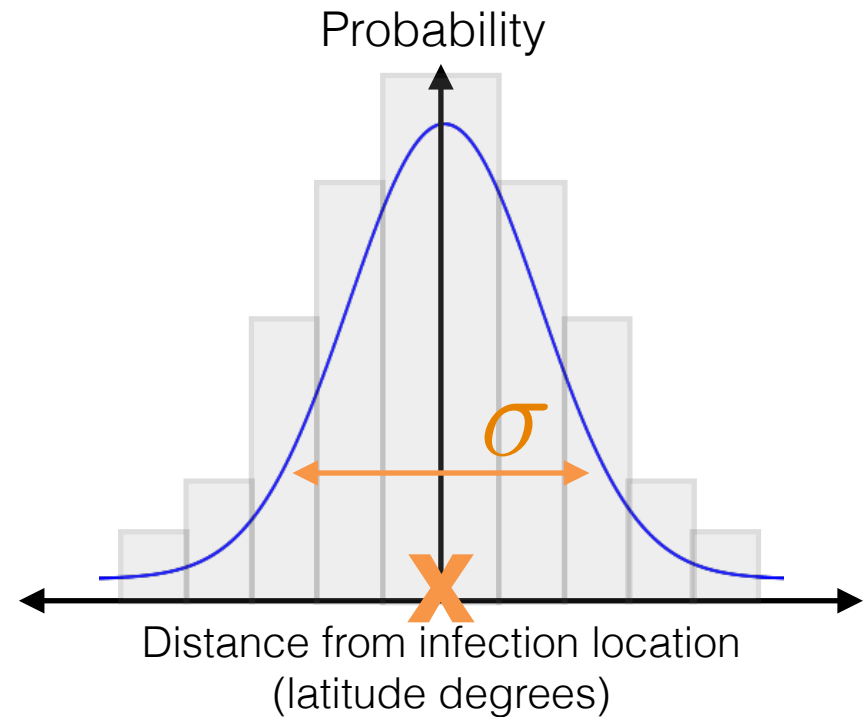
$$g(t) = \gamma \exp^{-\gamma t}$$



$$\frac{1}{\gamma} \sim \text{mean infectious period}$$

over space:

$$f(l) = \frac{1}{\sigma\sqrt{2\pi}} \exp -\frac{l^2}{2\sigma^2}$$

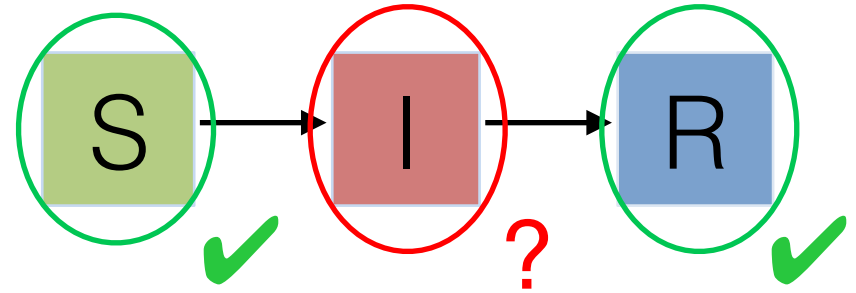


$$\sigma \sim \text{mean distance travelled}$$

# Developing the model

We have an approximation of:

1. population distribution
2. strandings due to disease



But:

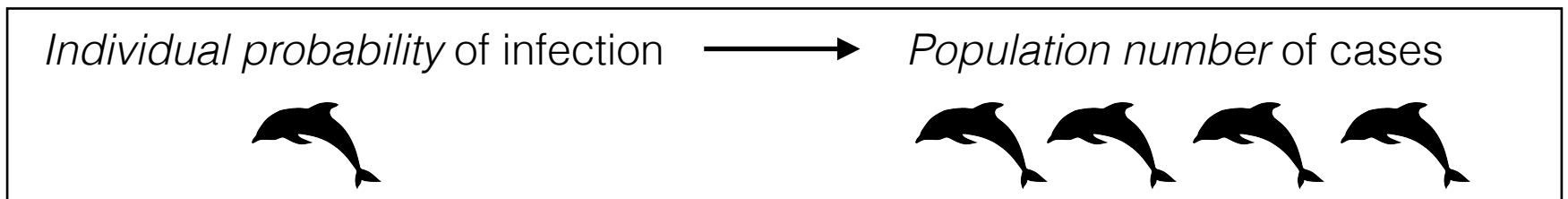
Noisy & sparse



SIR model + spatial component + random noise



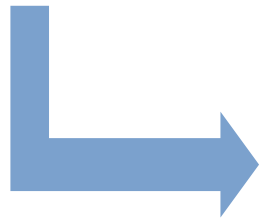
And finally...



# Developing the model

Total # new cases at time  $t$  and latitude  $l$ :

$$= \sum \text{# cases from each infected dolphin at } (t, l) \quad \img alt="dolphin icon" data-bbox="765 248 840 318"/>$$



$$= \sum R_0 \times g(t) \times f(l)$$

# infections  
over **all** time  
& space

**current**  
probability of  
infection at  $t$

**current**  
probability of  
infection at  $l$

Total # new cases at  $(t, l)$

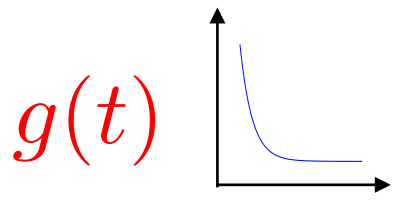
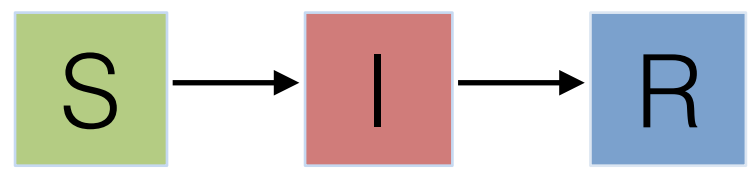


Repeat for every  $(t, l)$

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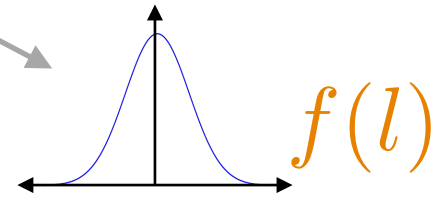
# Results



mean infectious period ~ 8 days

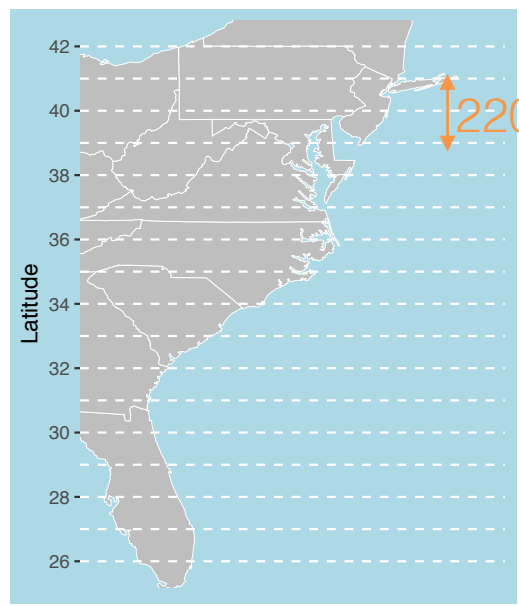
measles ~ 7 days  
PDV ~ 11 days

$R_0$

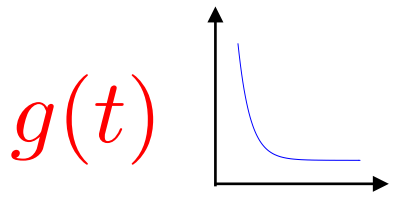
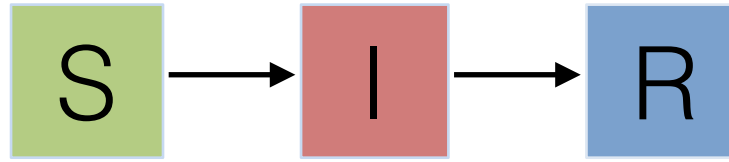


distance travelled ~ 2 latitude degrees

previous work ~ 120 - 350km



# Results

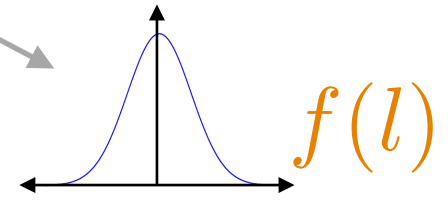


mean infectious  
period  $\sim 8$  days

measles  $\sim 7$  days  
PDV  $\sim 11$  days

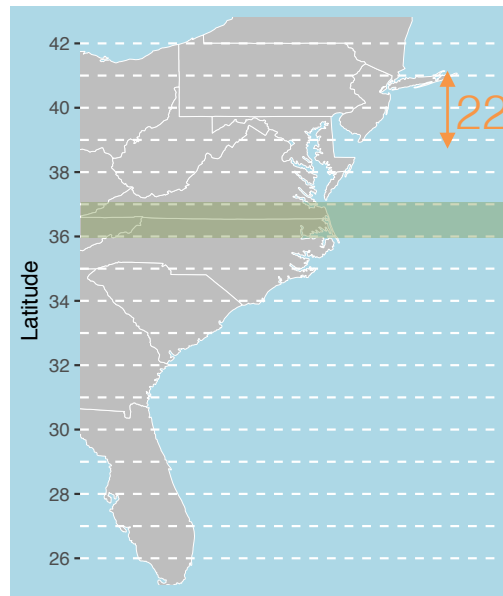
$$R_0 \sim 0.95 < 1$$

$\sim 3$



distance travelled  $\sim$   
2 latitude degrees

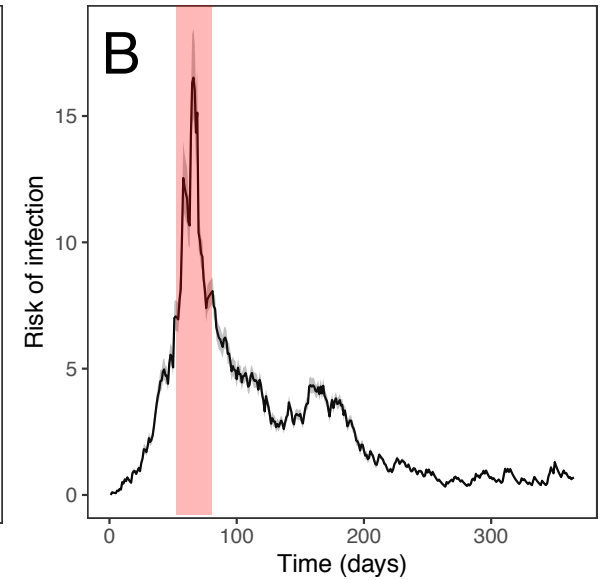
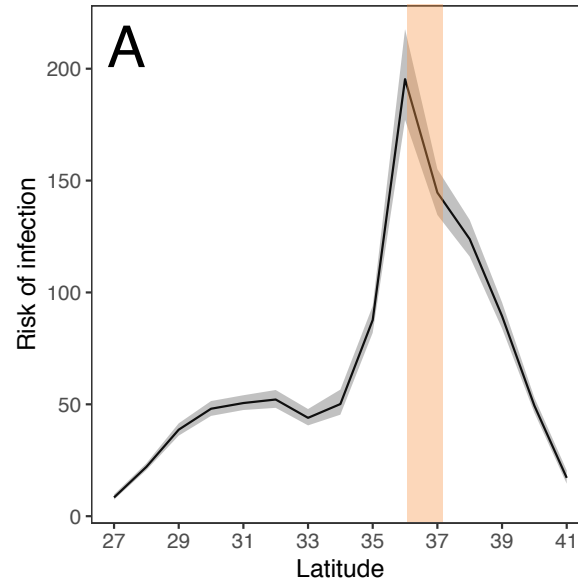
previous work  $\sim$   
120 - 350km





# Results

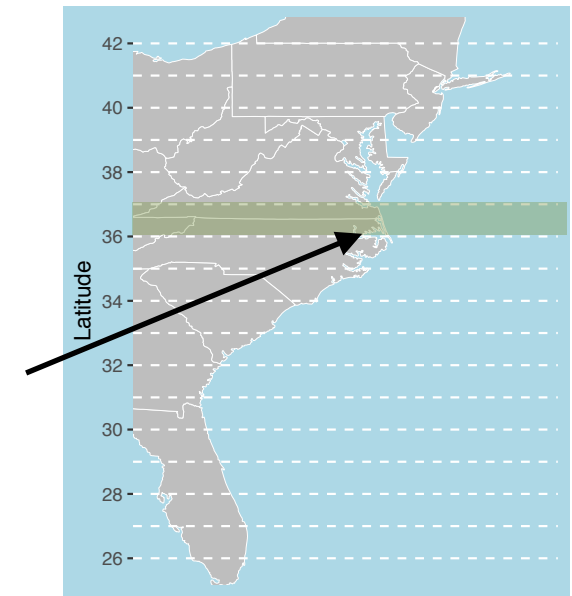
How does the risk of infection change in **space** and **time**?



Monitor this location during future outbreaks

↓  
 $R_0 \sim 3$

Virginia beach



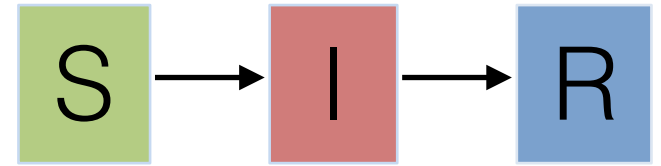
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# Conclusions

How long is an individual infectious for?

~ 8 days



How transmissible is the disease?

$R_0 < 1$  in general, but can reach as high as ~ 3

How far can an infected individual travel?

up to 2 latitude degrees

Which areas are at greatest risk?

Virginia beach, during summer migrations



Adapted SIR model can provide new insight into a poorly understood disease like DMV

# Ongoing research

What triggers new outbreaks?

How widespread is the virus?

Why 25 years?



Want to find out more?

Data (.csv file) available at:

<https://github.com/SineadMorris/Dolphin-morbillivirus>



Full details of model, analysis etc:

<http://rsif.royalsocietypublishing.org/content/12/112/20150676>

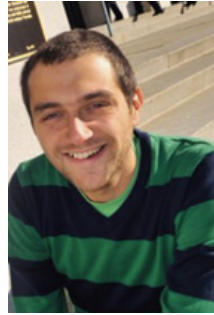
Partially observed epidemics in wildlife hosts: modelling an outbreak of dolphin morbillivirus in the northwestern Atlantic, June 2013–2014

Sinead E. Morris<sup>1,†</sup>, Jonathan L. Zelnert<sup>2,†</sup>, Deborah A. Fauquier<sup>3</sup>,  
Teresa K. Rowles<sup>3</sup>, Patricia E. Rosel<sup>4</sup>, Frances Gulland<sup>5,6</sup>  
and Bryan T. Grenfell<sup>1,7</sup>

# Thanks



Bryan Grenfell  
Princeton University



Jon Zelner  
University of Michigan



Deborah Fauquier  
NOAA

And many others...

**DMV project:**

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William MacLellan, NOAA  
Lance Garrison, NOAA  
Frances Gulland, The Marine Mammal Center  
The Marine Mammal Stranding Network  
RAPIDD

**PhD committee:**

Jessica Metcalf, Princeton University  
Cecile Viboud, NIH  
Andrea Graham, Princeton University

