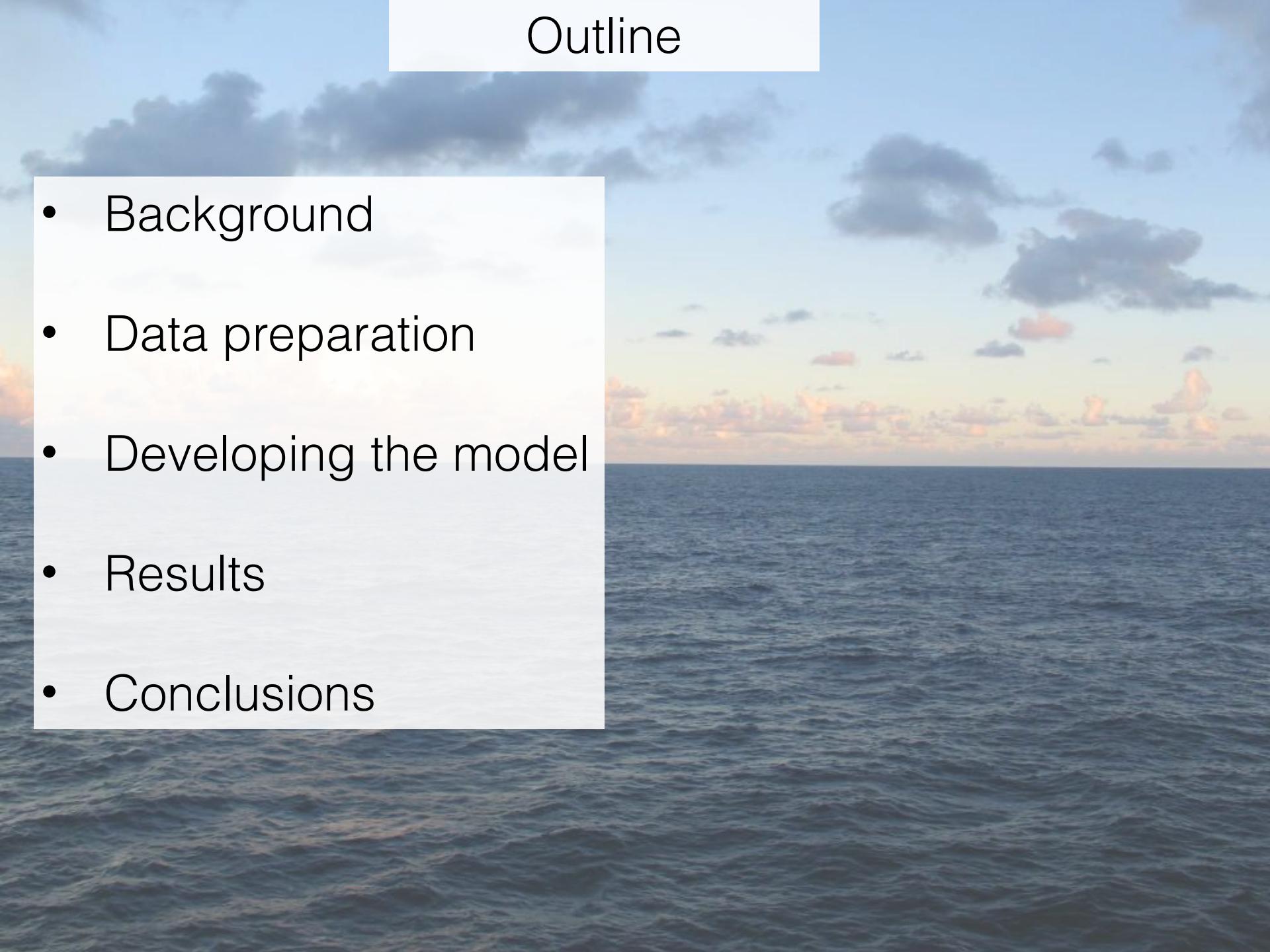


Modeling an outbreak of dolphin morbillivirus: US east coast (June 2013 – 2014)

Sinead Morris
Princeton University
semorris@princeton.edu

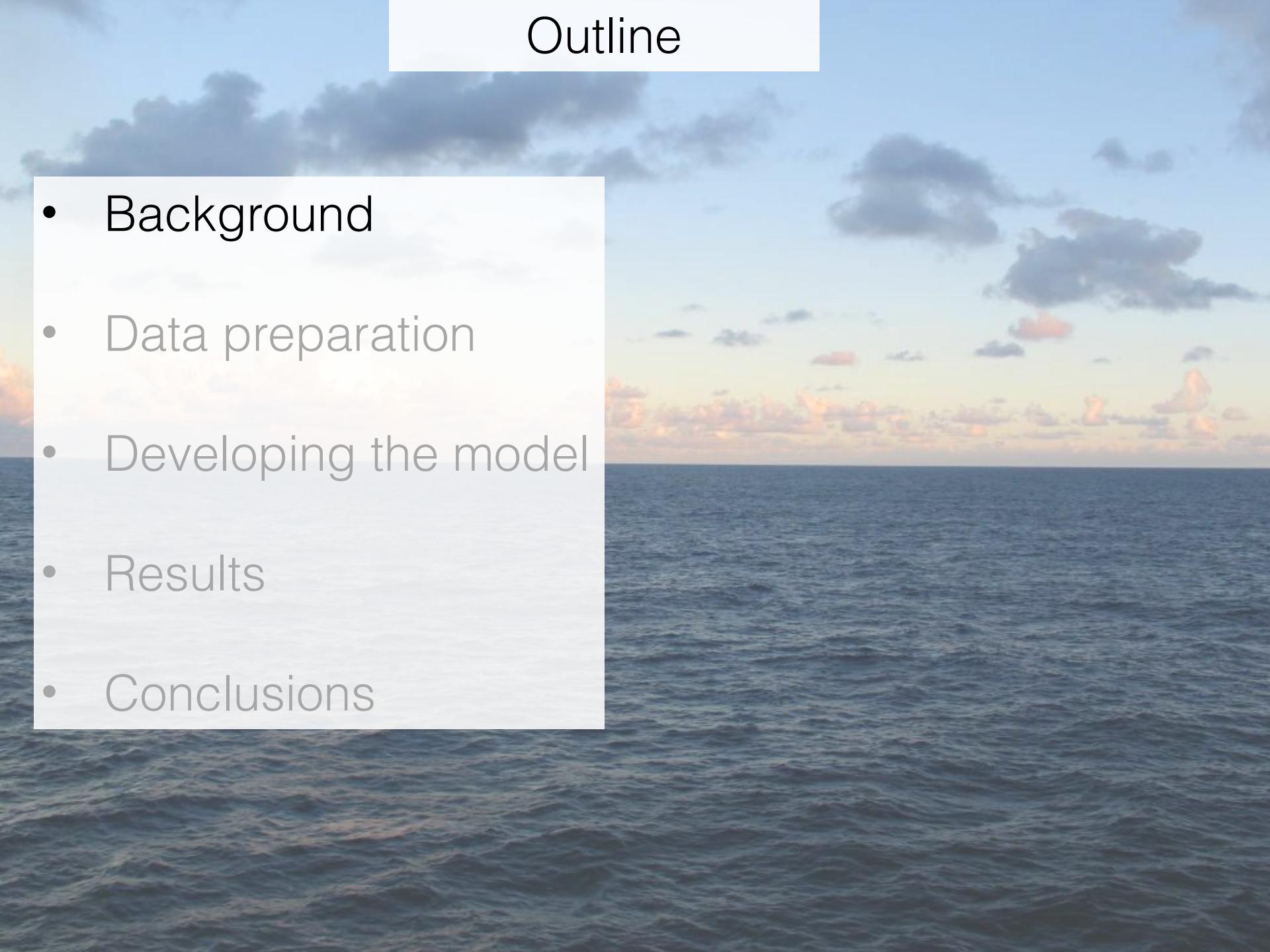
Outline

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



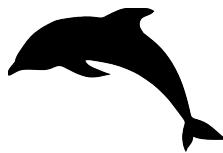
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Background

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

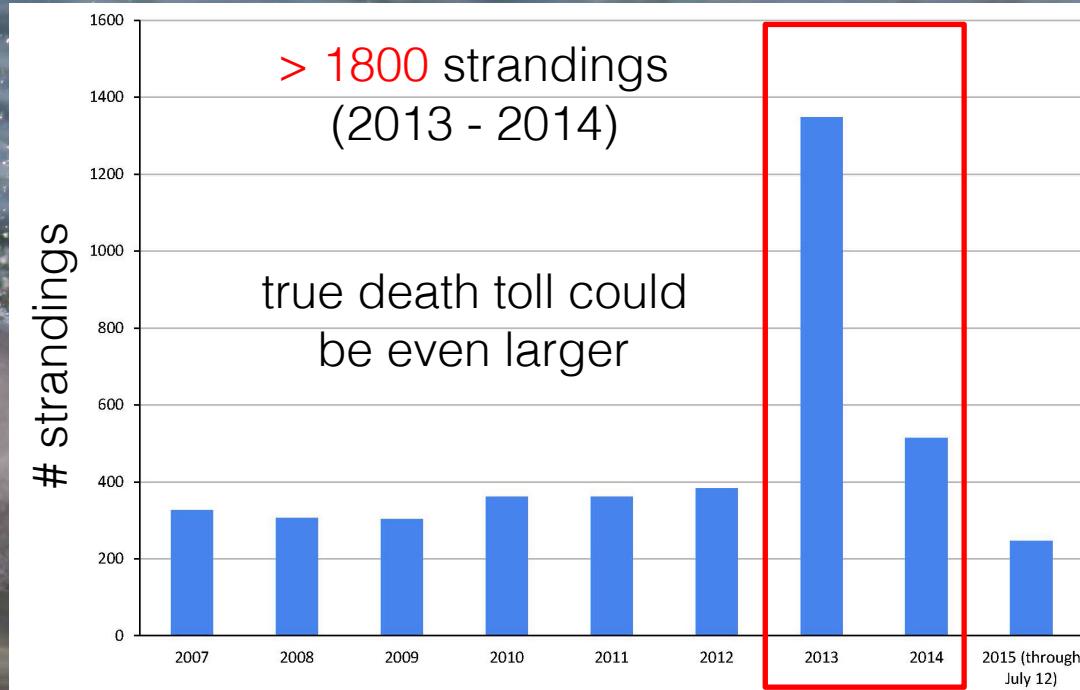


LATEST STORIES

PHOTO OF THE DAY

GENDER REVOLUTION

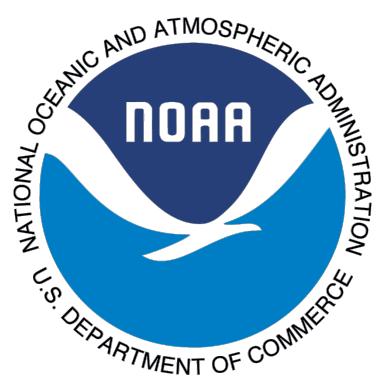
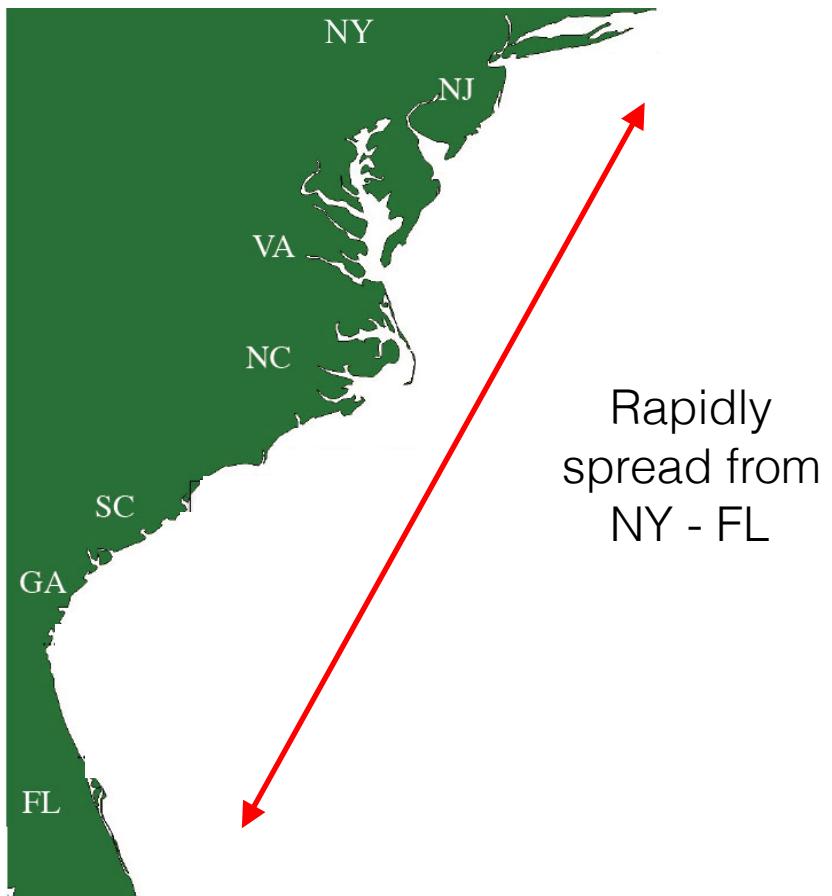
What's Killing Bottlenose Dolphins?



Source: NOAA

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

Epidemic progression



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:

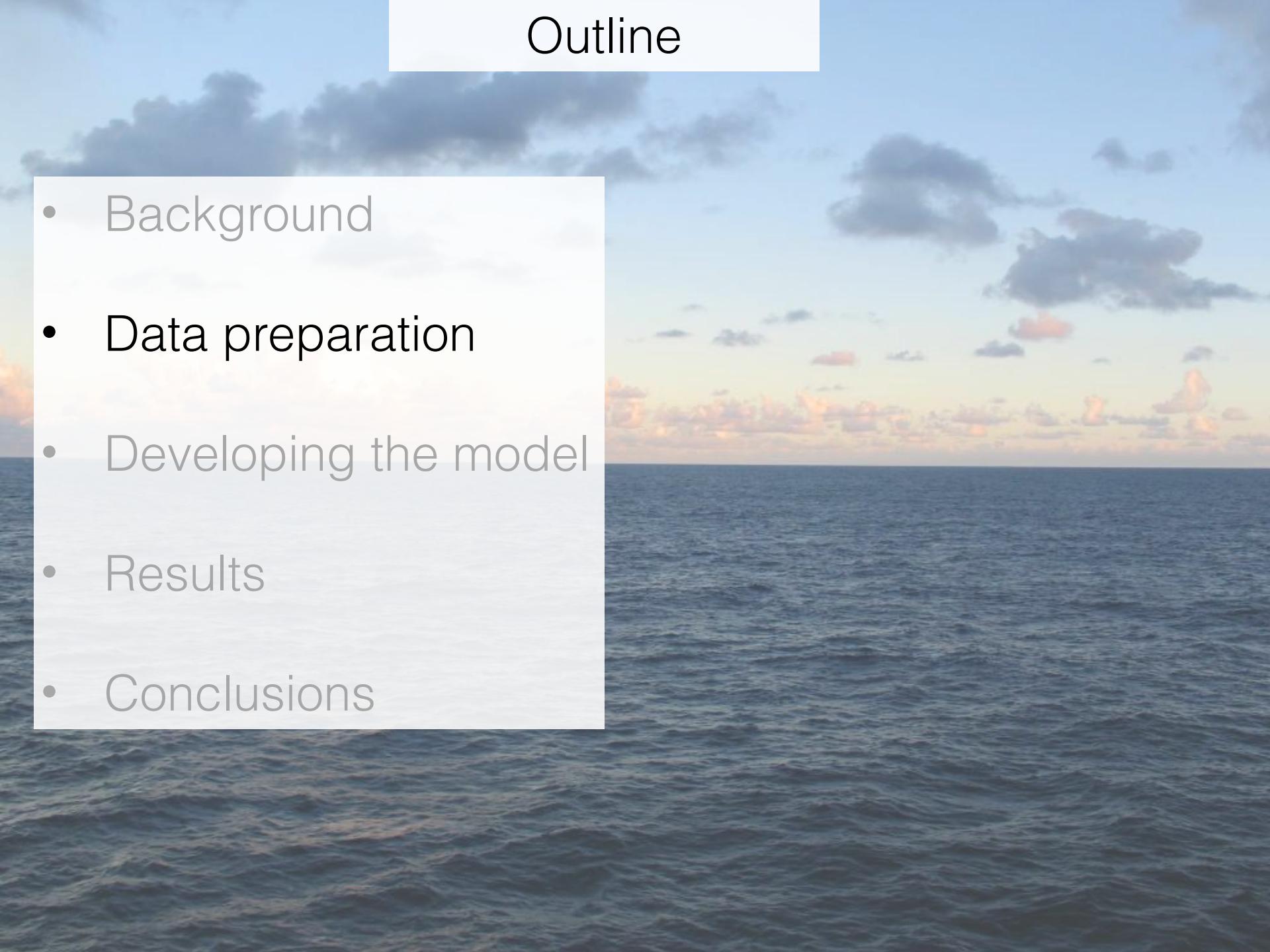
$$\frac{dS}{dt} = -\frac{\beta SI}{N} \quad \dots \rightarrow \text{infectious period} \quad \frac{1}{\gamma}$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I \quad \dots \rightarrow \text{reproductive ratio} \quad R_0 \sim \frac{\beta}{\gamma}$$

$$\frac{dR}{dt} = \gamma I \quad + \text{spatial component} \dots \rightarrow \text{dolphin movement}$$

Outline

- Background
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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:

$$\text{disease} = \text{outbreak strandings} - \text{average rate of strandings before outbreak}$$



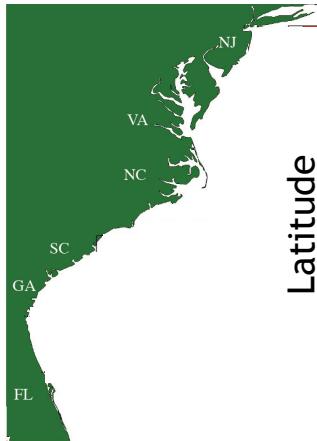
-



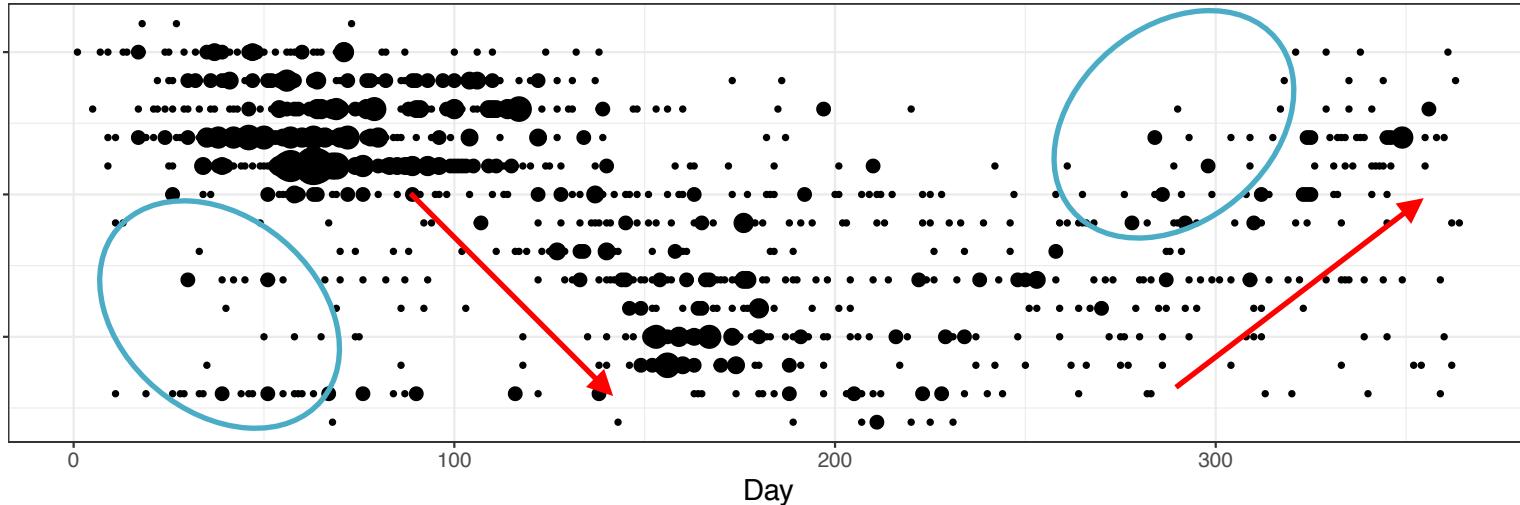
Data Preparation



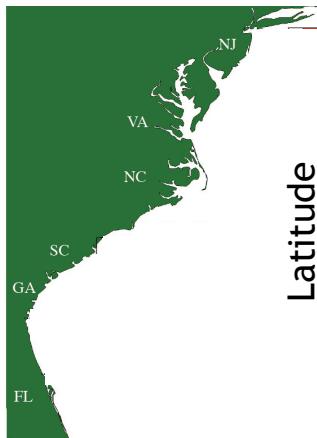
original outbreak strandings



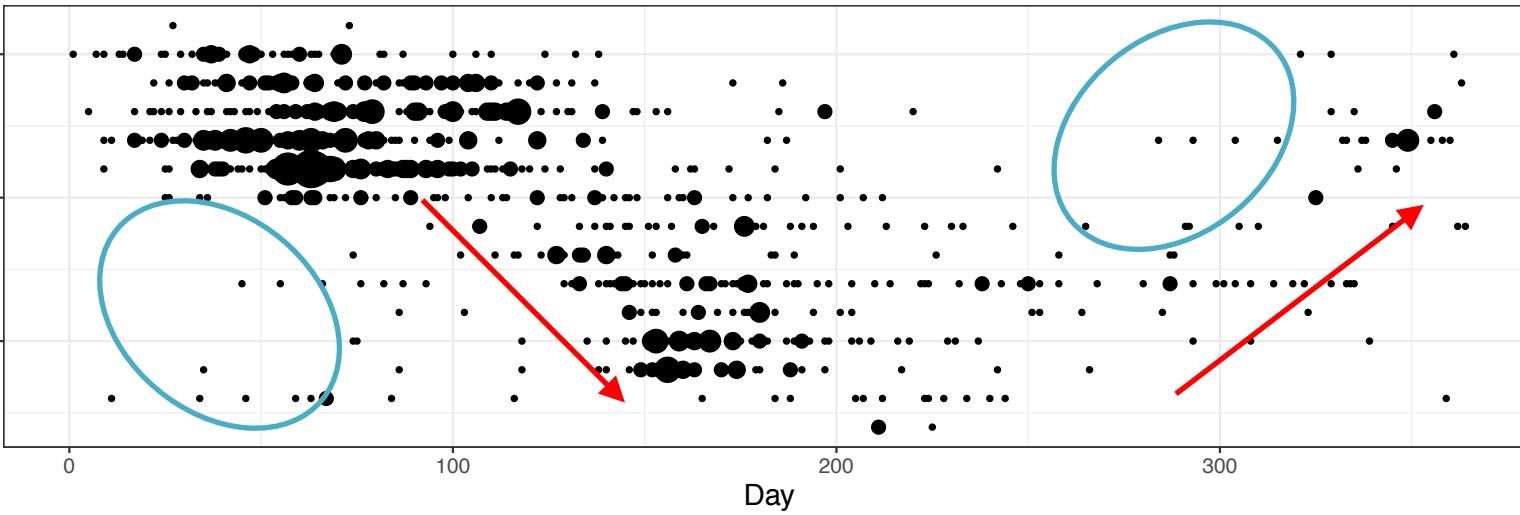
Latitude



disease-only strandings



Latitude



Data Preparation

What we **have**:

1. Strandings from 2013-2014 outbreak
'disease' + 'background' strandings



2. Strandings from years **before the outbreak** (1996 – 2012)
'background' strandings



What we **need**:

1. Only 'disease' strandings from outbreak



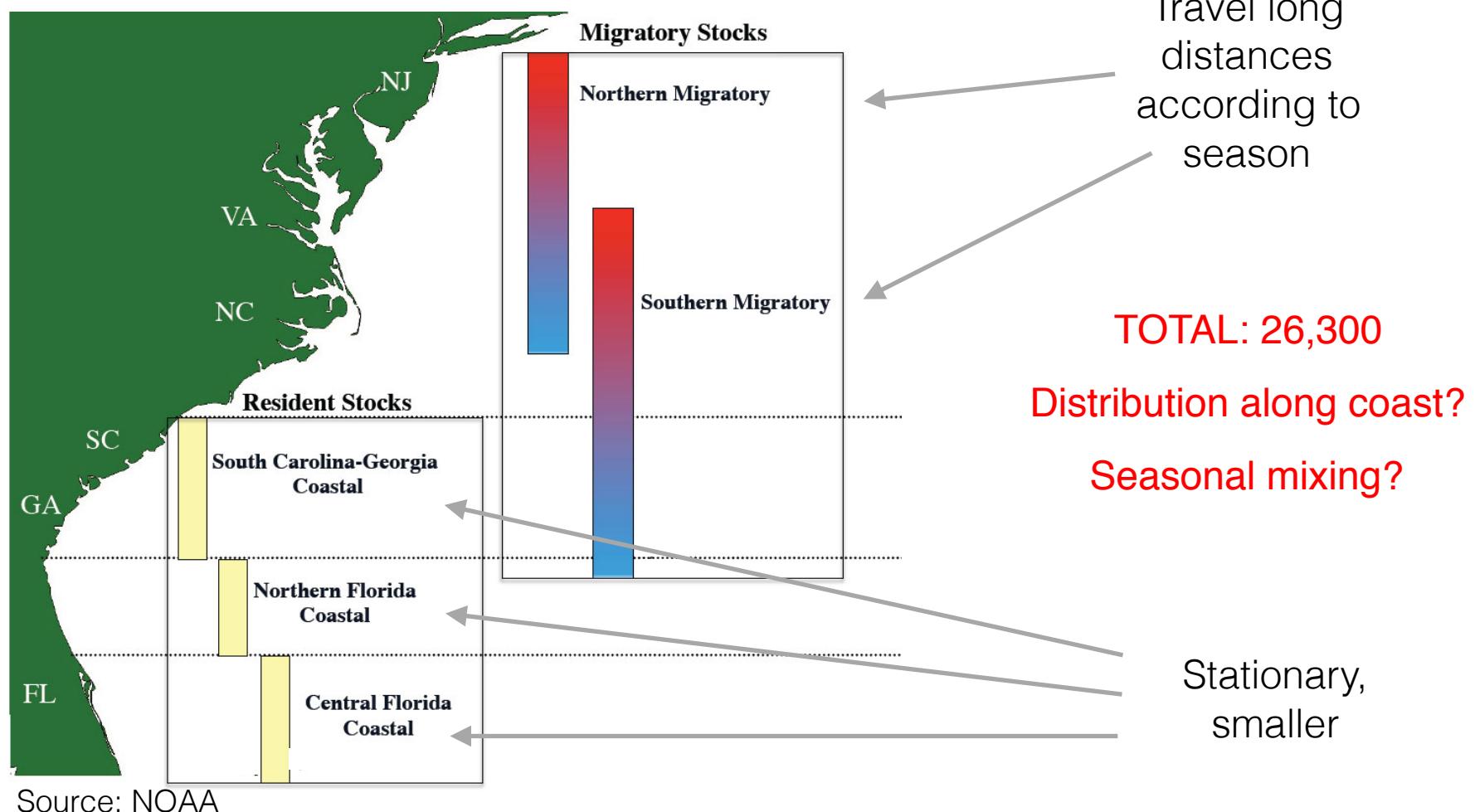
AND...



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

Population distribution

Bottlenose dolphin population: 5 main groups



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

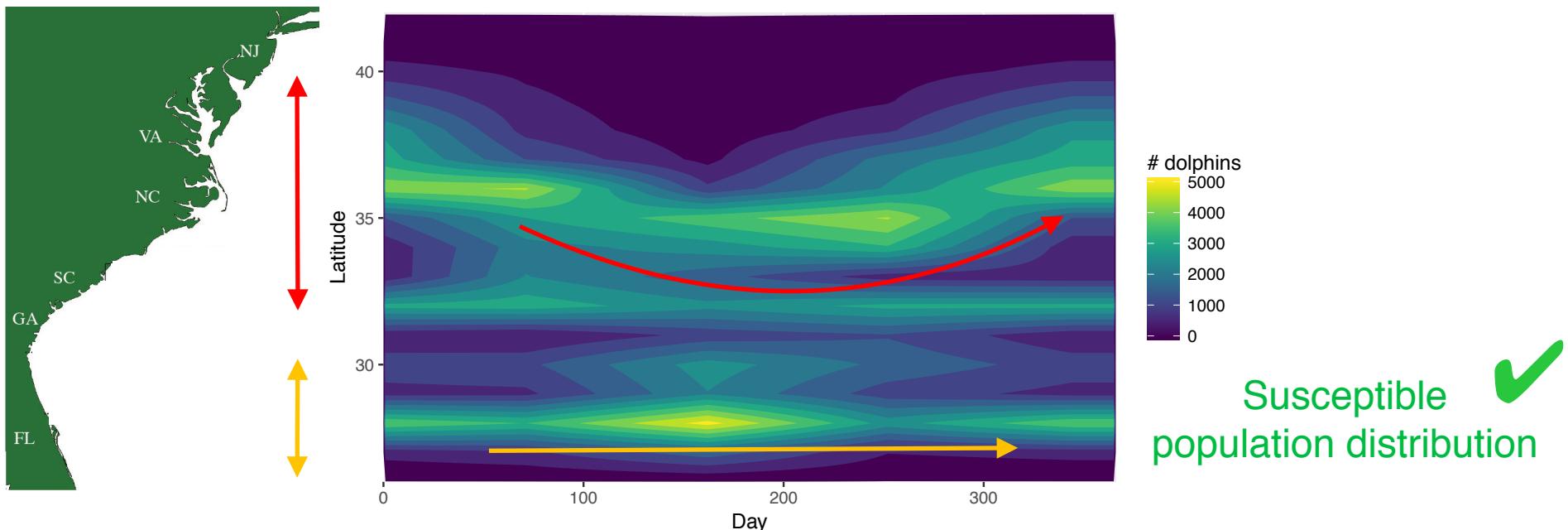
Population distribution

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

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

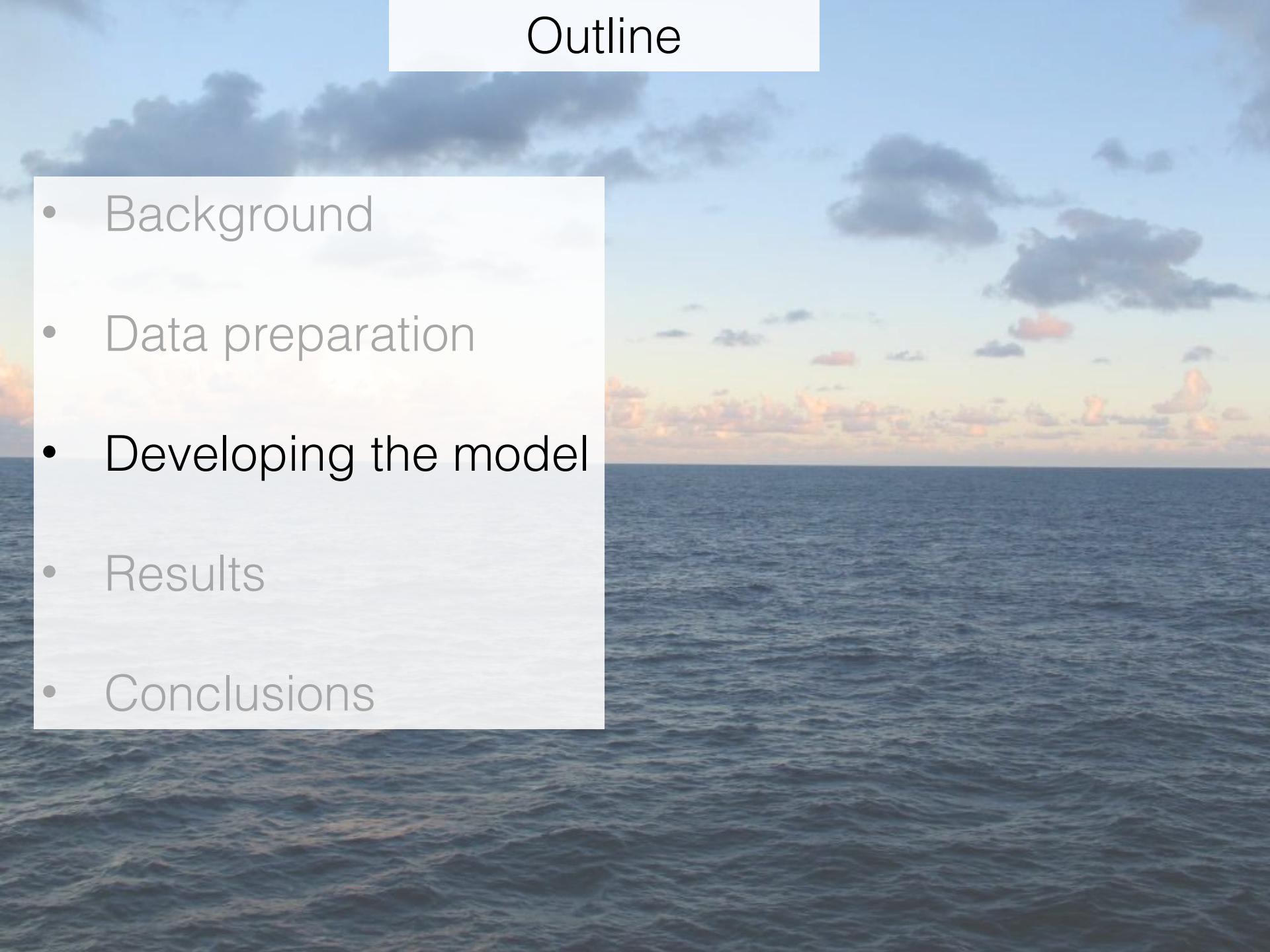
For each time, t , and latitude, l :

$$\# \text{ dolphins}_{t,l} = \frac{\text{total population size}}{(26,300)} \times \frac{\# \text{ strandings}_{t,l}}{\text{total } \# \text{ strandings}}$$



Outline

- Background
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General idea

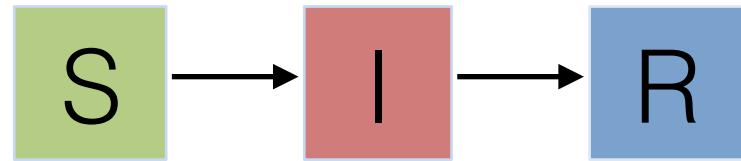
Disease dynamics:

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?

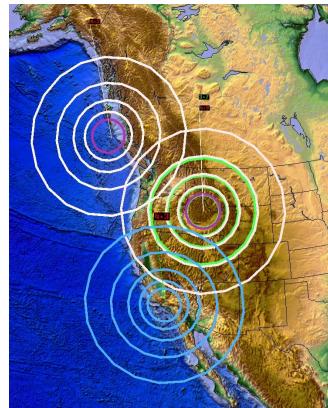


Model from seismology

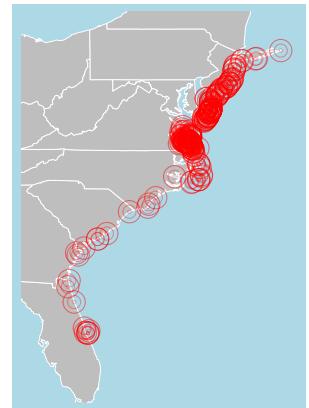
Ogata (1998)
Ann. Inst. Stat. Math

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

clustering of aftershocks



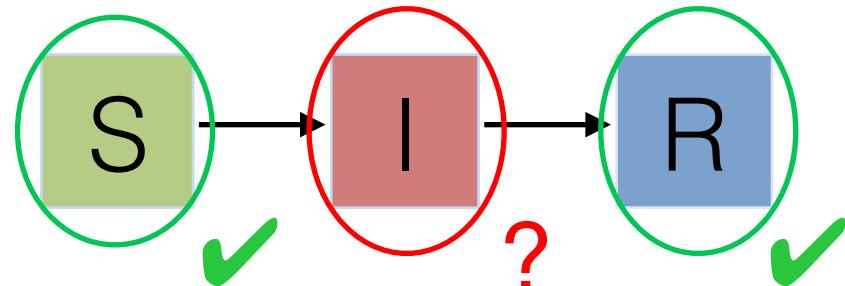
clustering of strandings



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

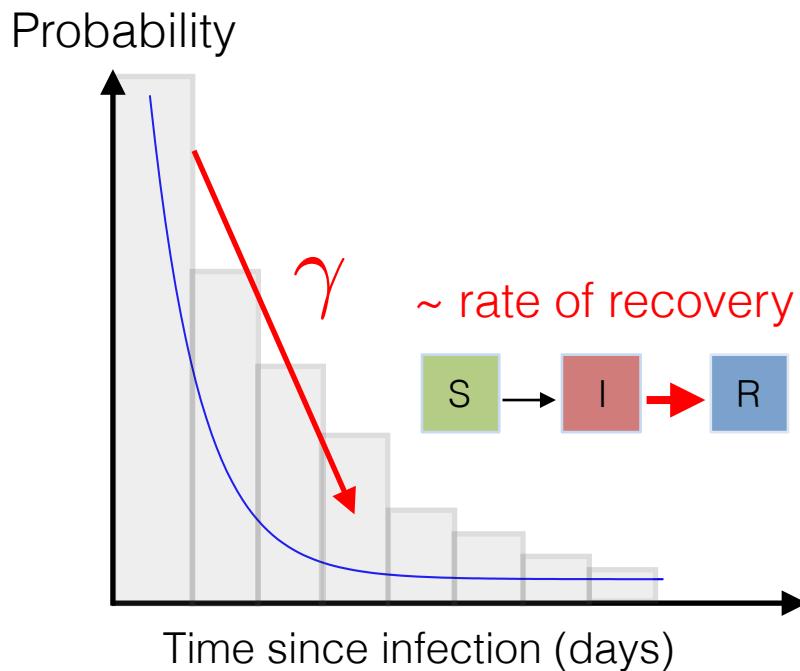


Our assumption: transmission is a **probability** that changes over **time** and **space**

Developing the model

Assume individual probability of infecting others changes over time:

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

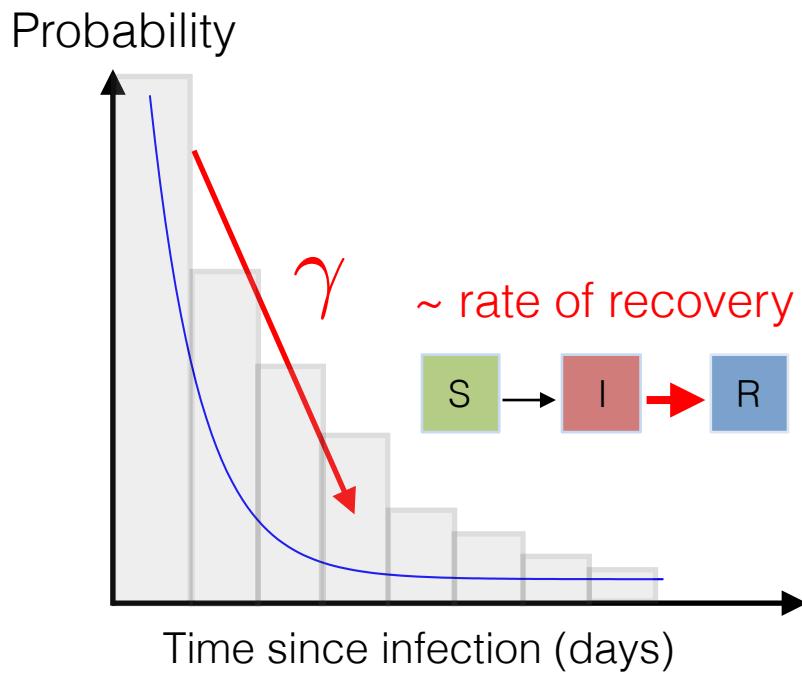


$$\frac{1}{\gamma} \sim \text{mean infectious period}$$

Developing the model

Assume individual probability of infecting others changes over time:

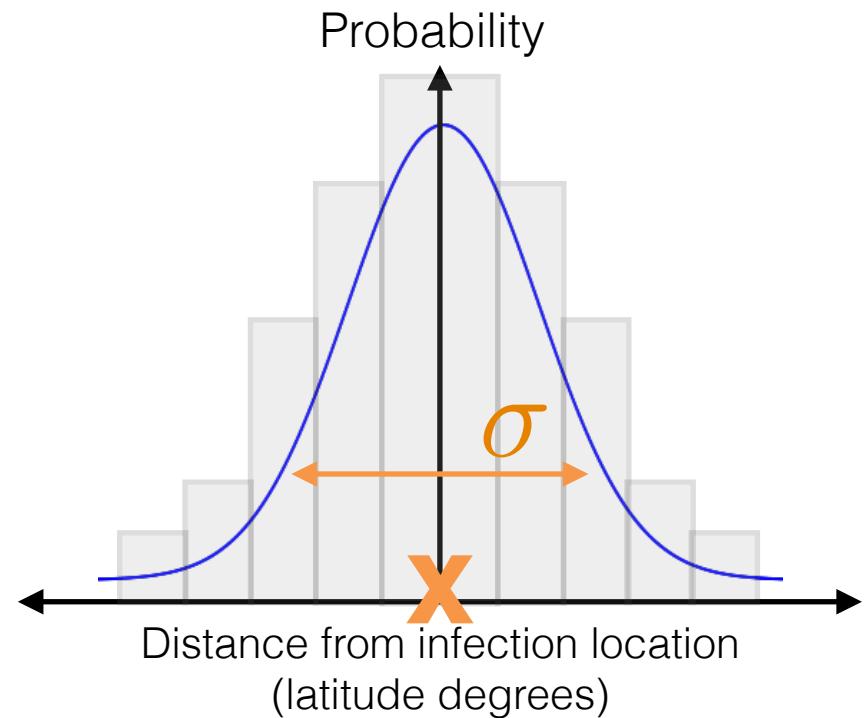
$$g(t) = \gamma \exp^{-\gamma t}$$



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

over space:

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

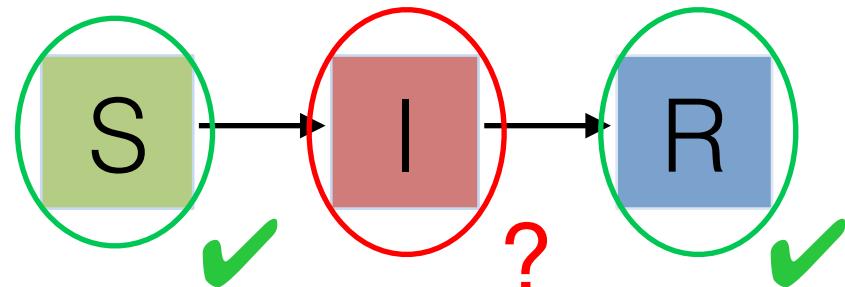


$$\sigma \sim \text{mean distance travelled}$$

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...

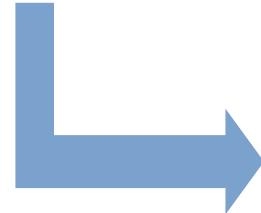
Individual probability of infection ————— *Population number of cases*



Developing the model

Total # new cases at time t and latitude l :

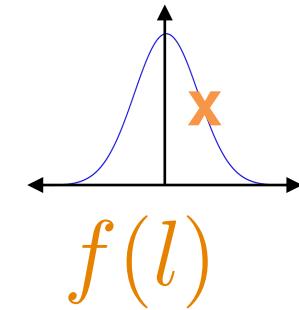
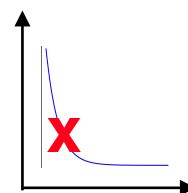
$$= \sum \text{# cases from each infected dolphin at } (t, l)$$



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

infections
over **all** time
& space

current
probability of
infection at t



current
probability of
infection at l

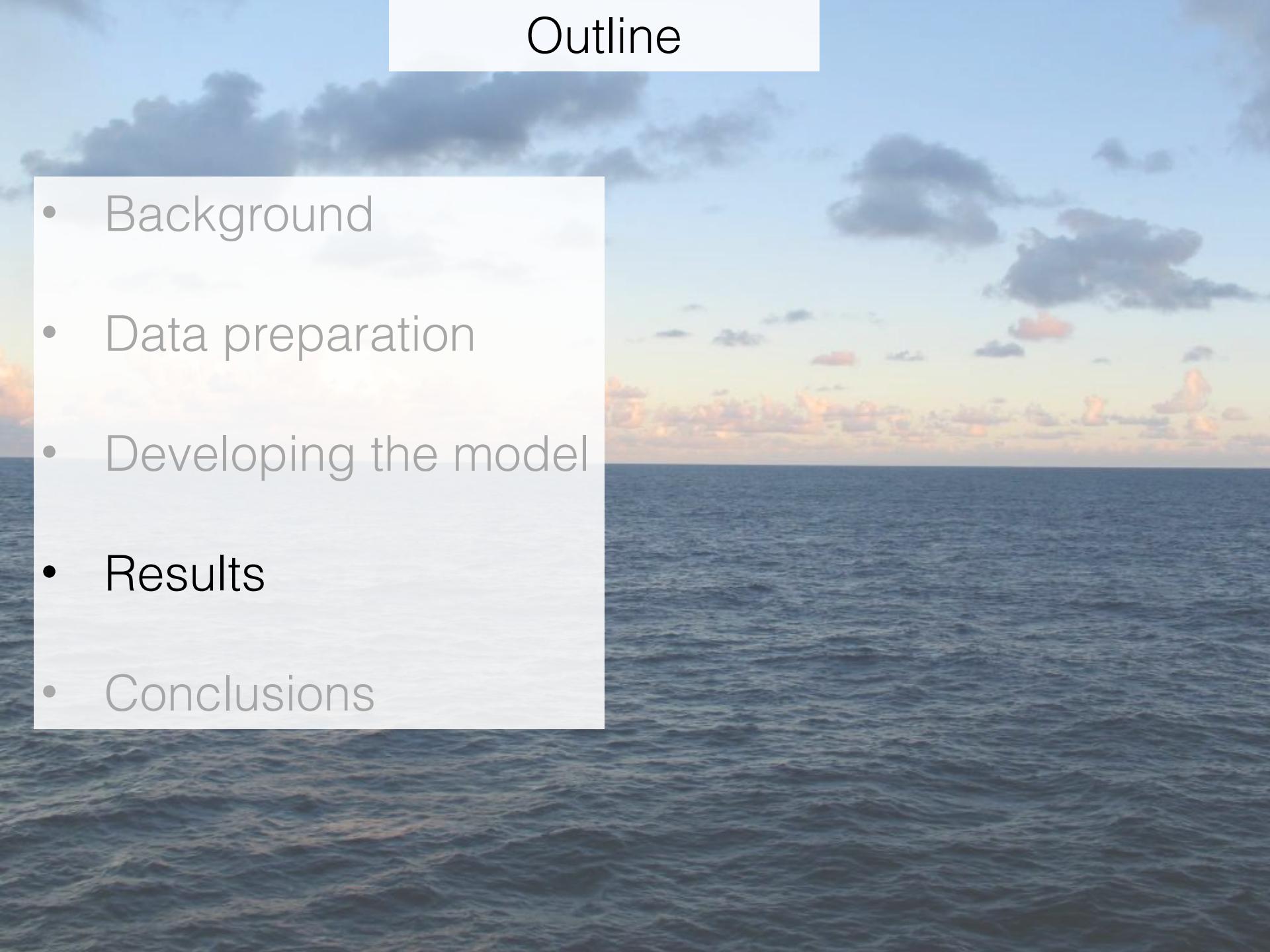
Total # new cases at (t, l)



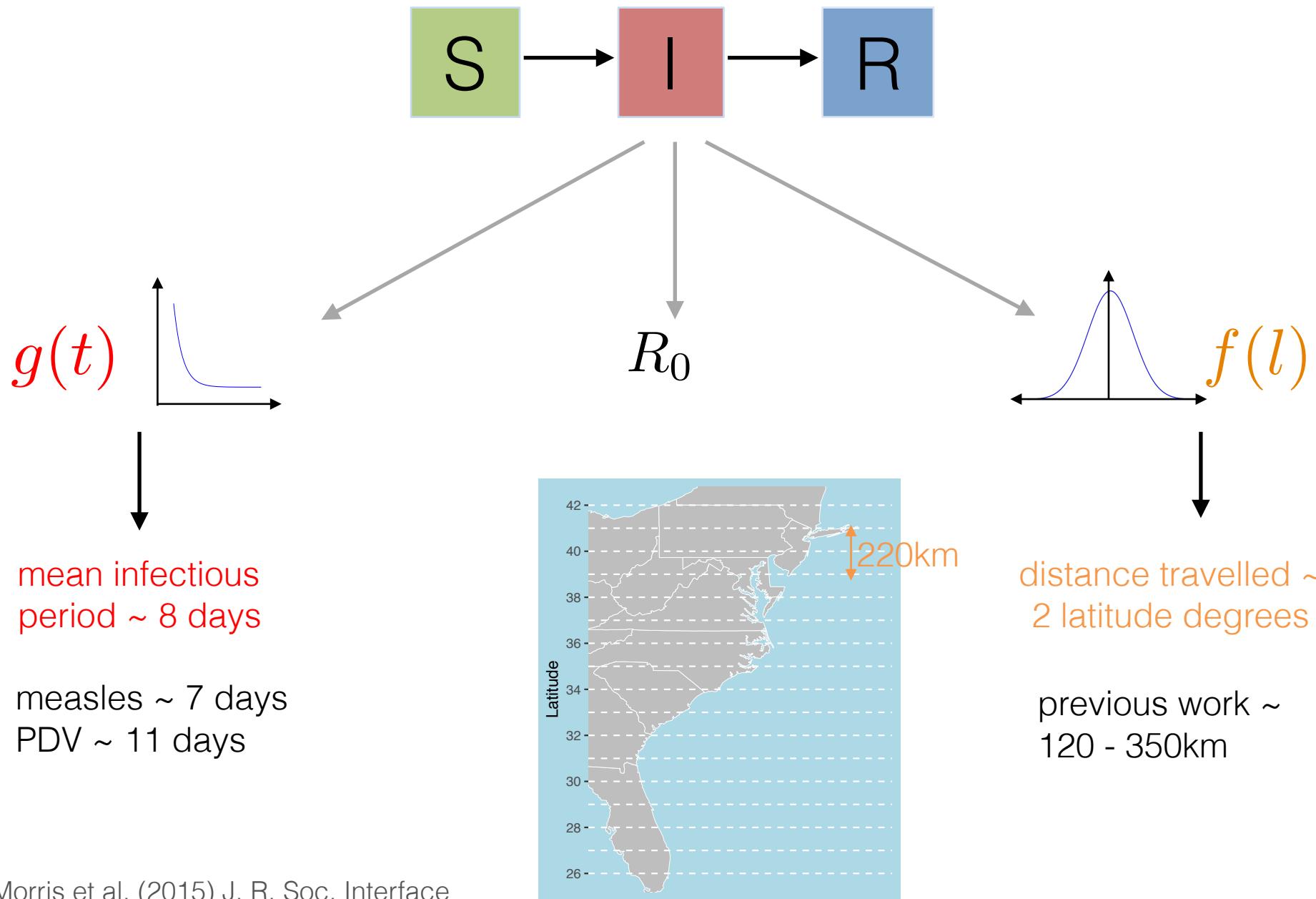
Repeat for every (t, l)

Outline

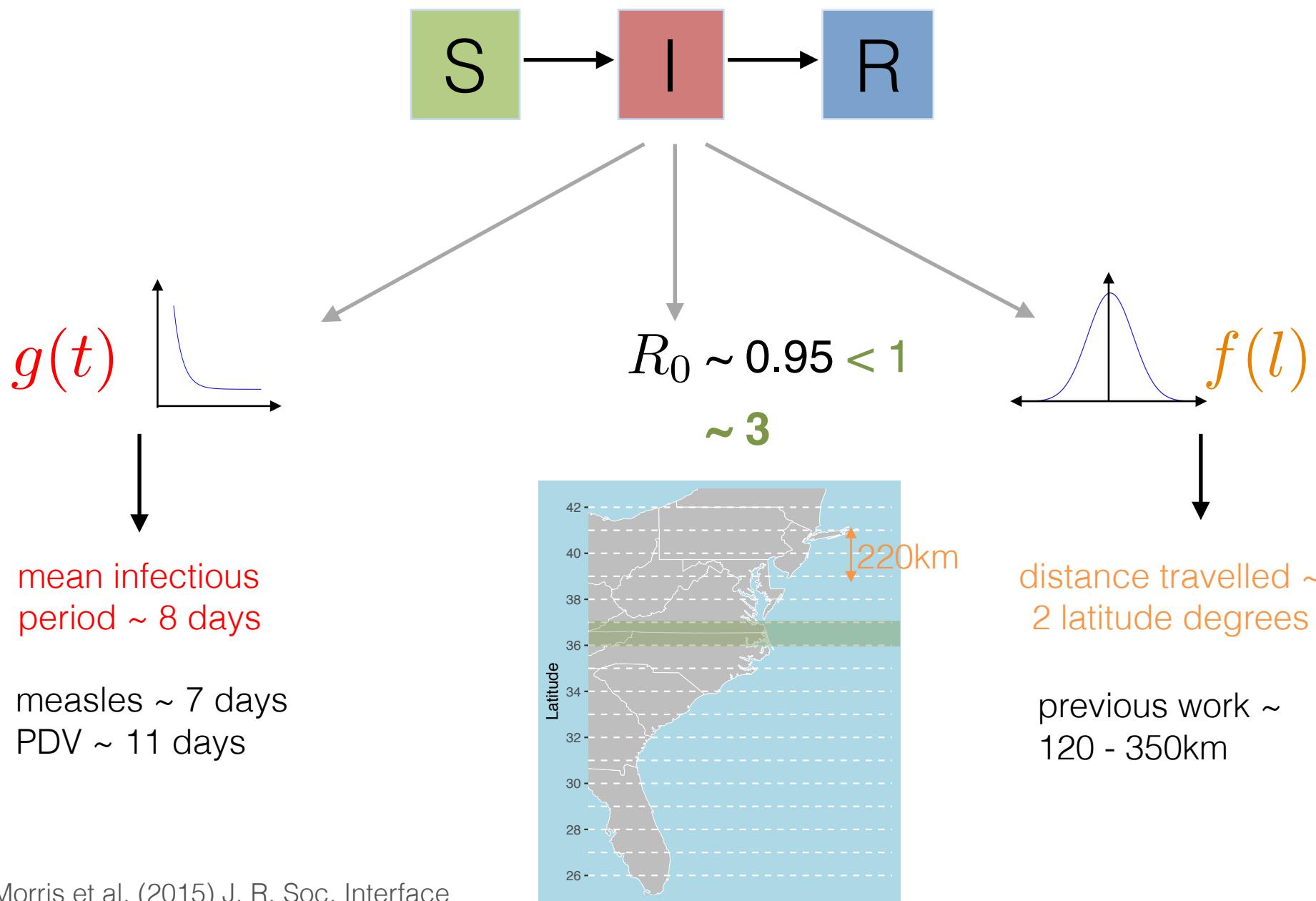
- Background
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Results

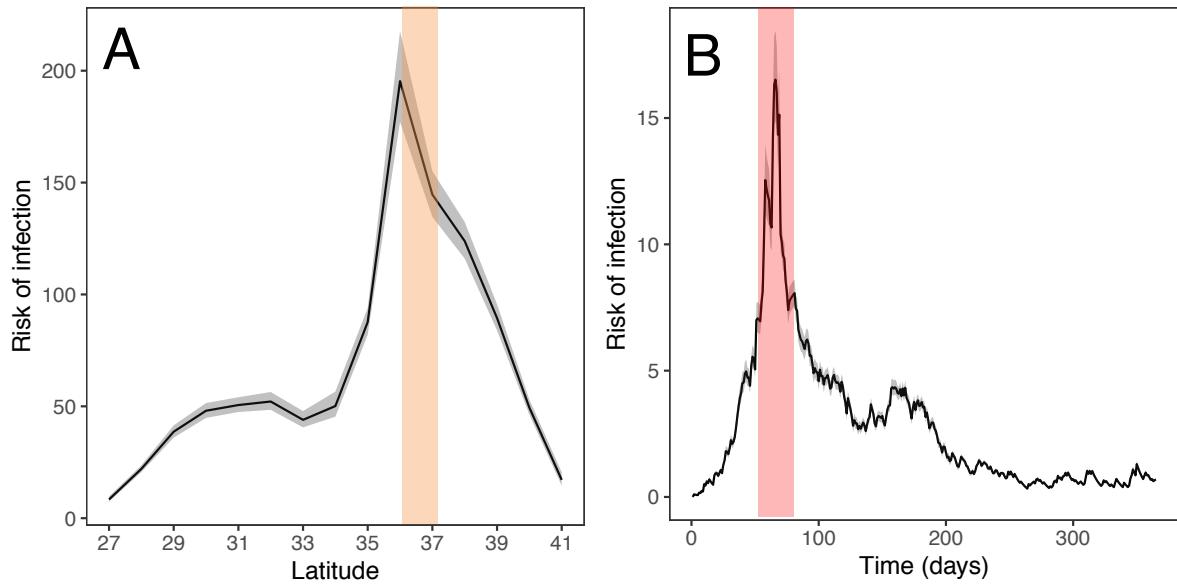


Results



Results

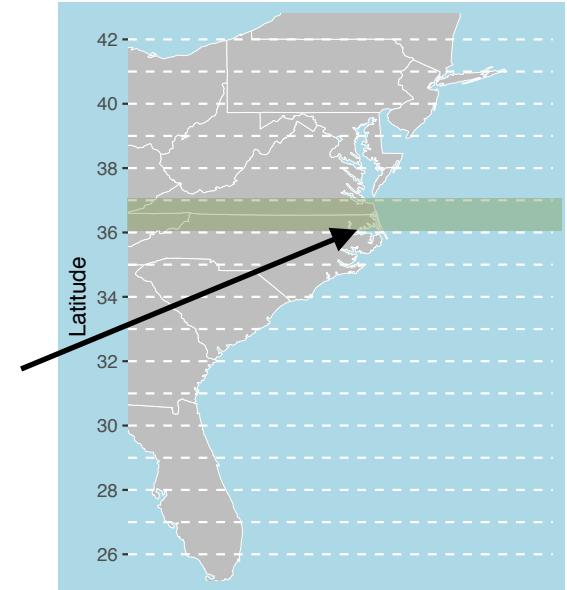
How does the risk
of infection change
in **space** and **time**?



Monitor this location during future
outbreaks

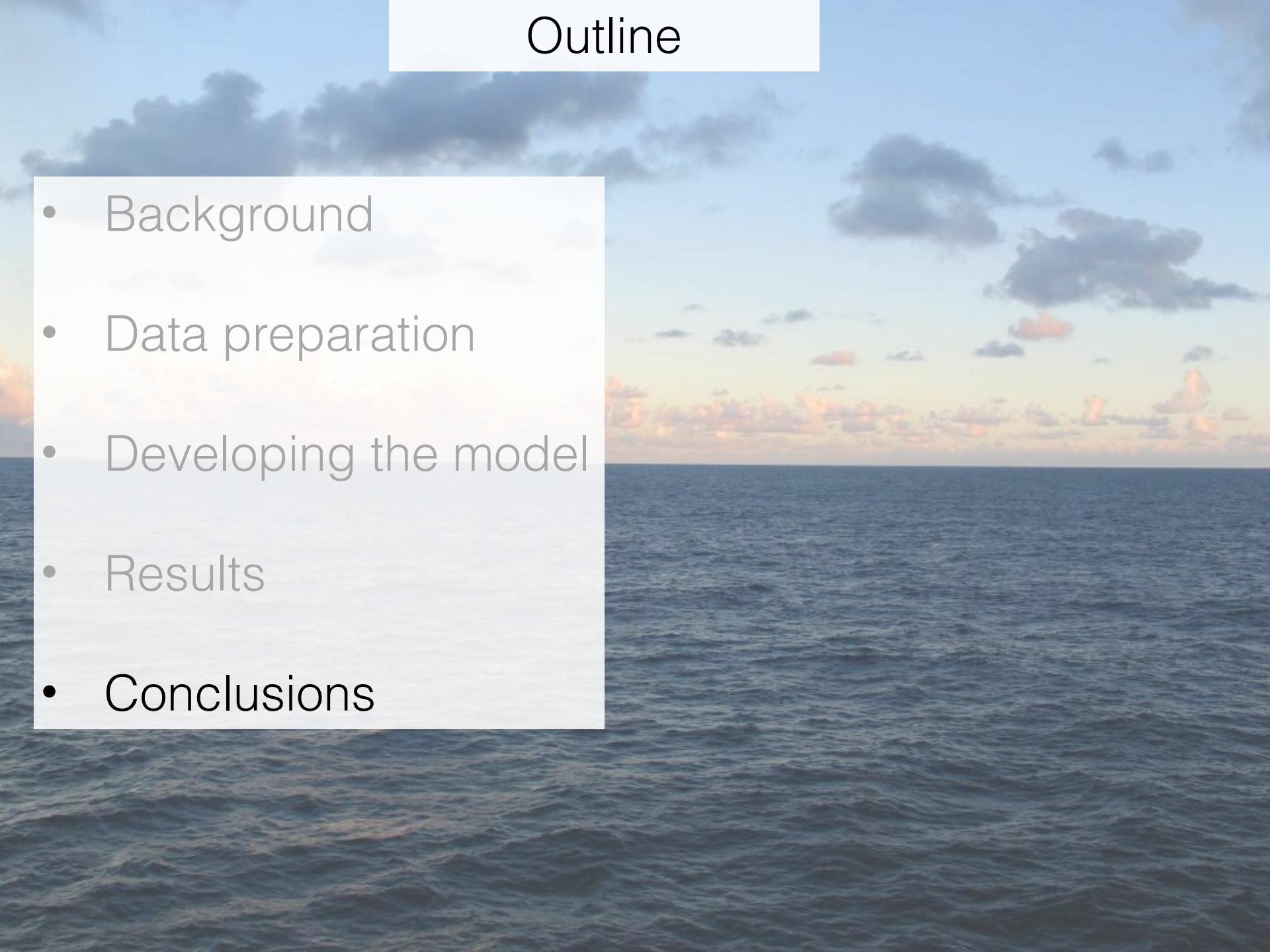
$$R_0 \sim 3$$

Virginia beach



Outline

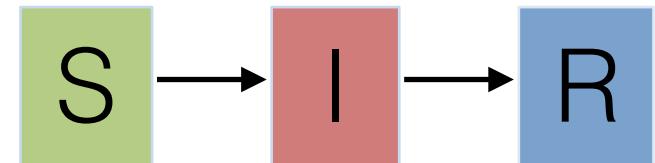
- Background
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Conclusions

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?

Why 25 years?

How widespread is the virus?



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>

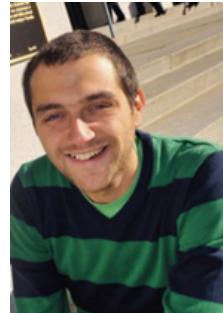
Partially observed epidemics in wildlife hosts: modelling an outbreak of dolphin morbillivirus in the northwestern Atlantic, June 2013–2014

Sinead E. Morris^{1,†}, Jonathan L. Zelner^{2,†}, Deborah A. Fauquier³, Teresa K. Rowles³, Patricia E. Rosel⁴, Frances Gulland^{5,6} and Bryan T. Grenfell^{1,7}

Thanks



Bryan Grenfell
Princeton University



Jon Zelner
University of Michigan



Deborah Fauquier
NOAA

And many others...

DMV project:

Teresa Rowles, NOAA
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Aleta Hohn, NOAA
William MacLellan, NOAA
Lance Garrison, NOAA
Frances Gulland, The Marine Mammal Center
The Marine Mammal Stranding Network
RAPIDD

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