

Learning from the uncertain: Modelling and forecasting infectious disease dynamics

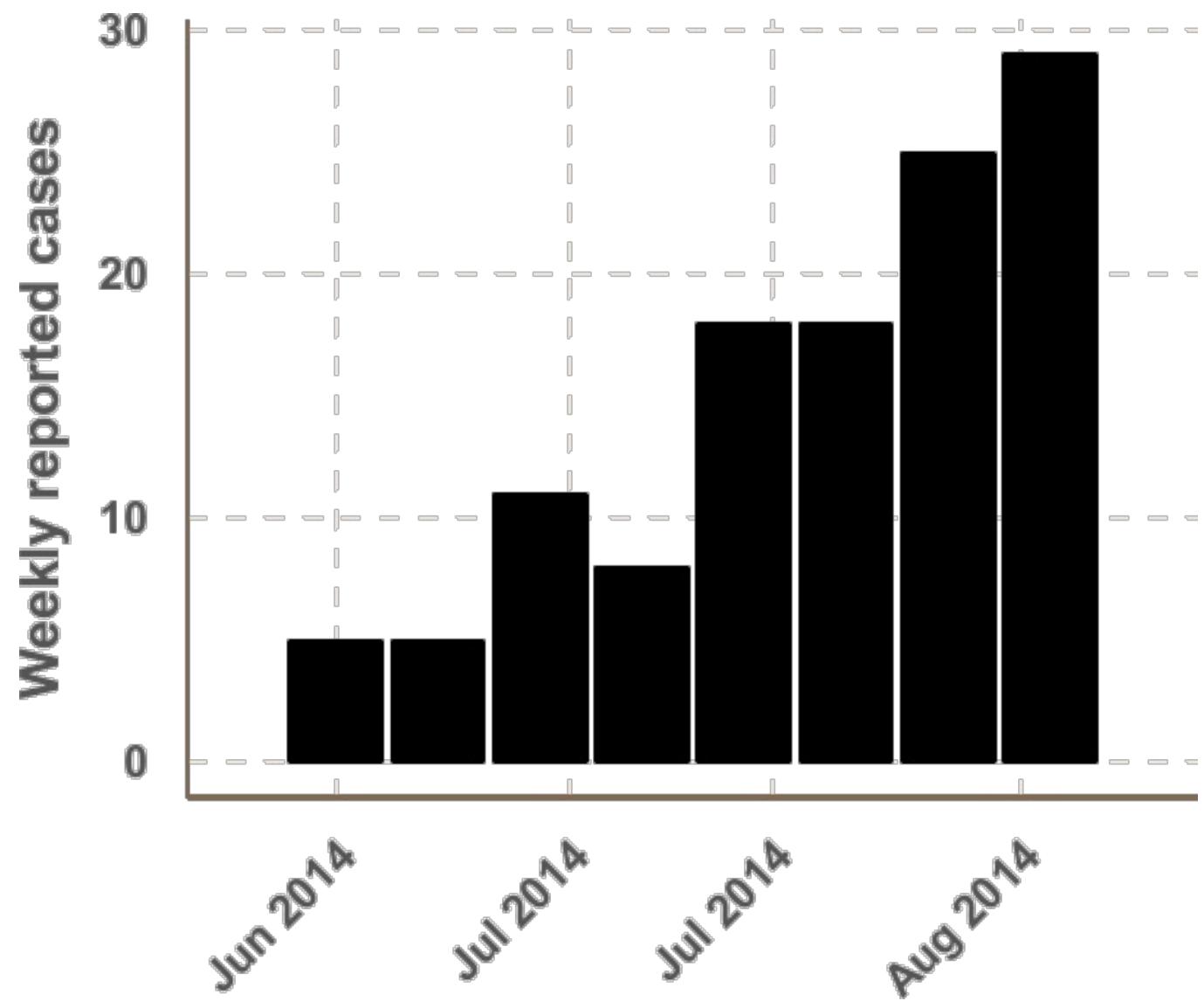
Sebastian Funk
10 January, 2017

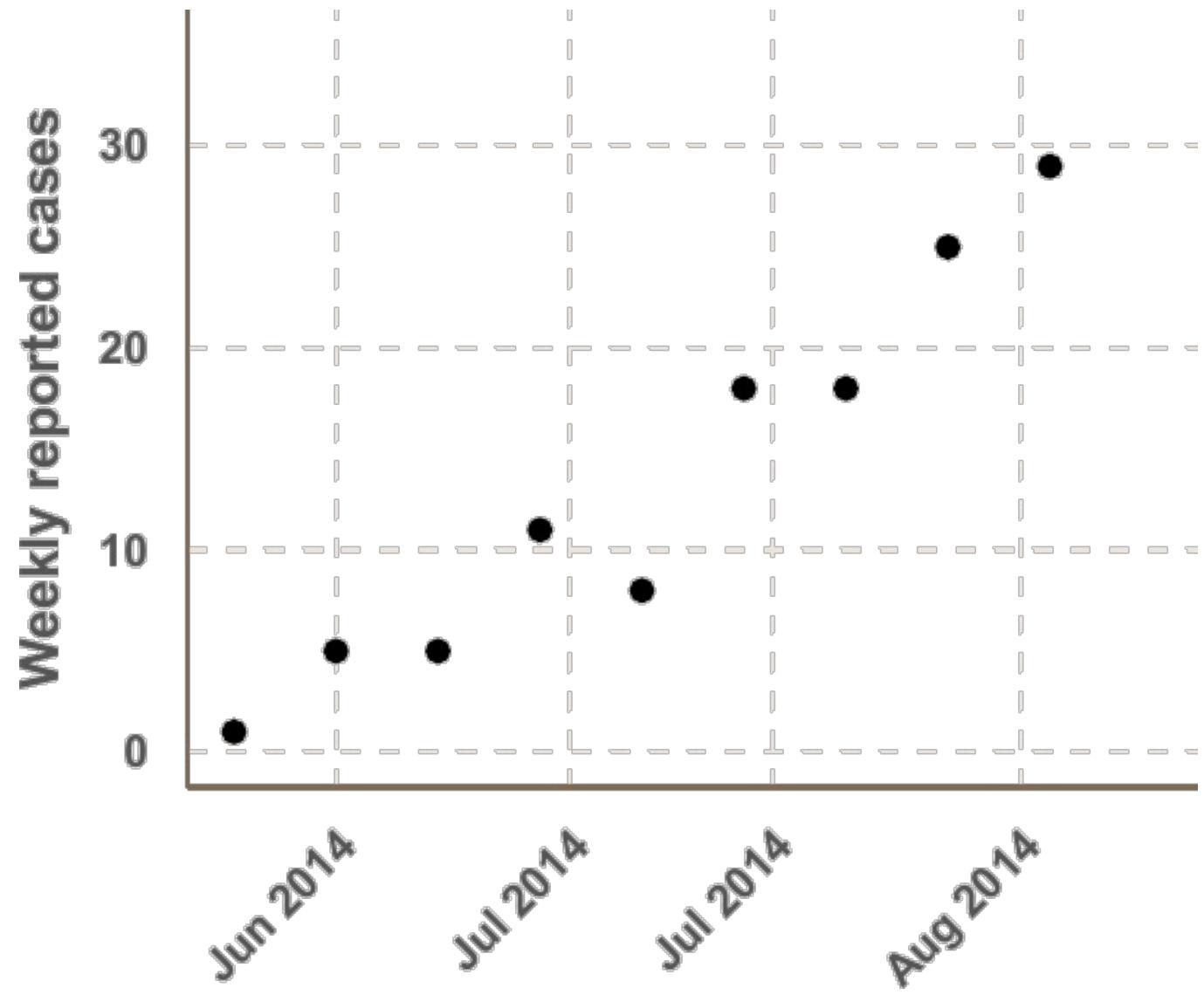
Wellcome Trust Centre for Human Genetics, Oxford

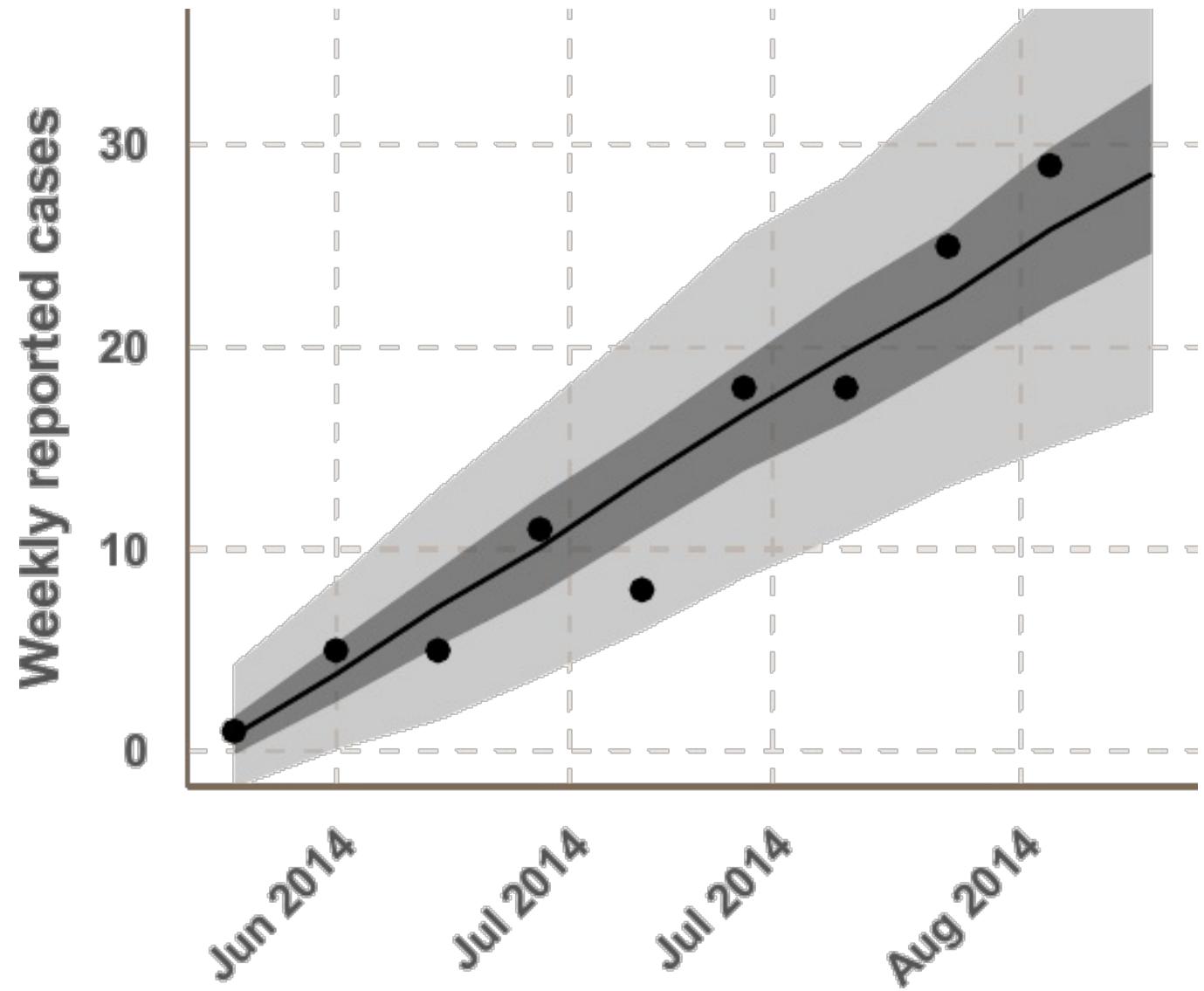
Summer 2014



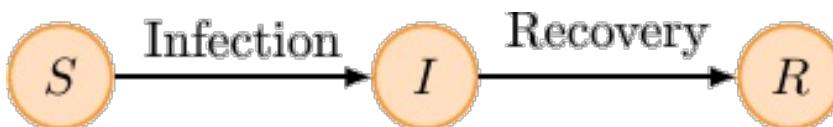
SUSPECT







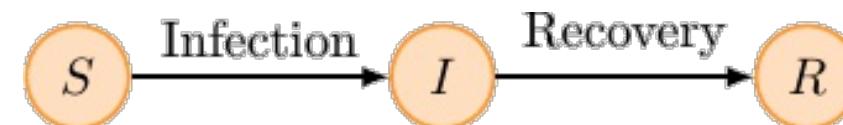
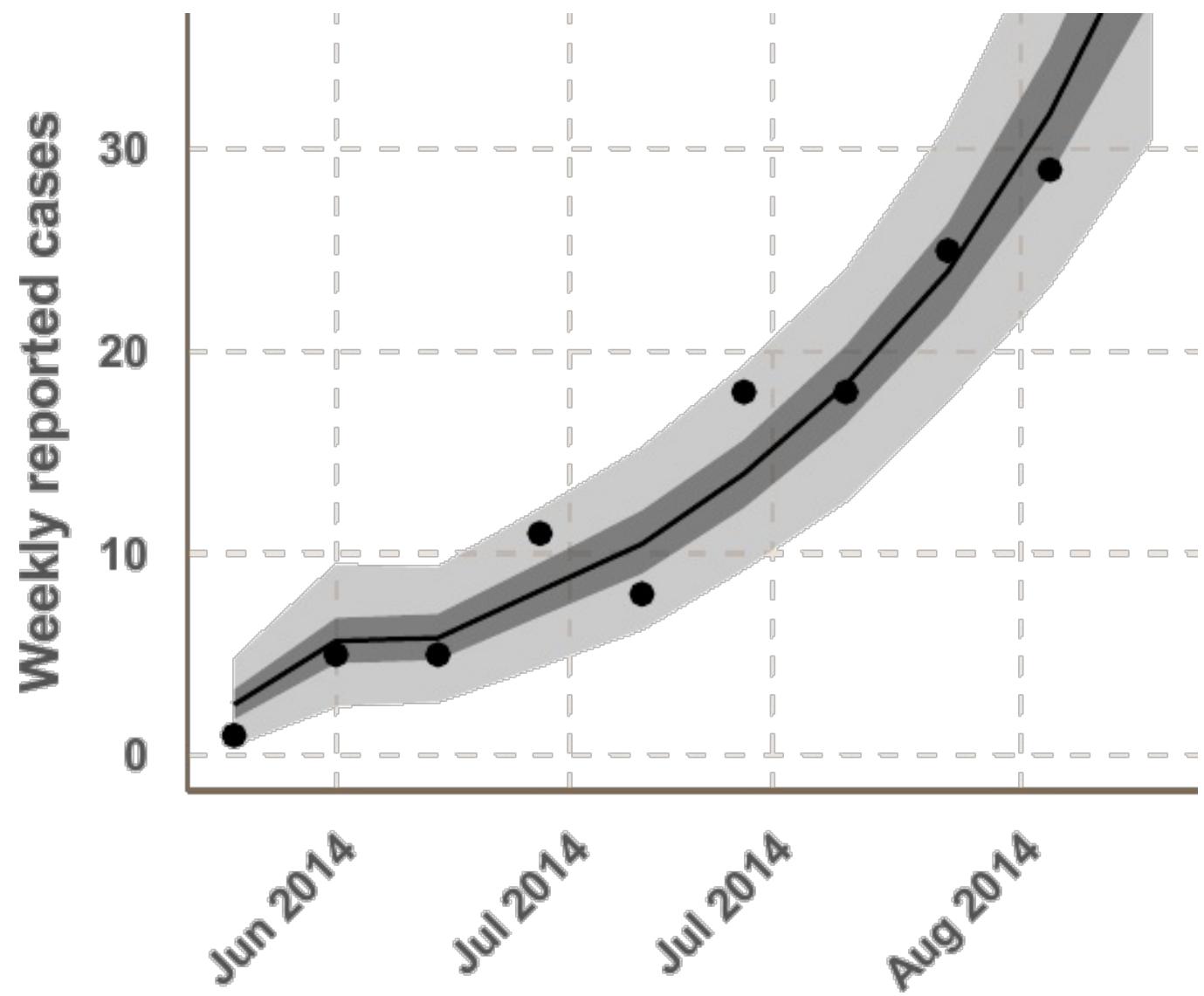
$$y = ax + b$$

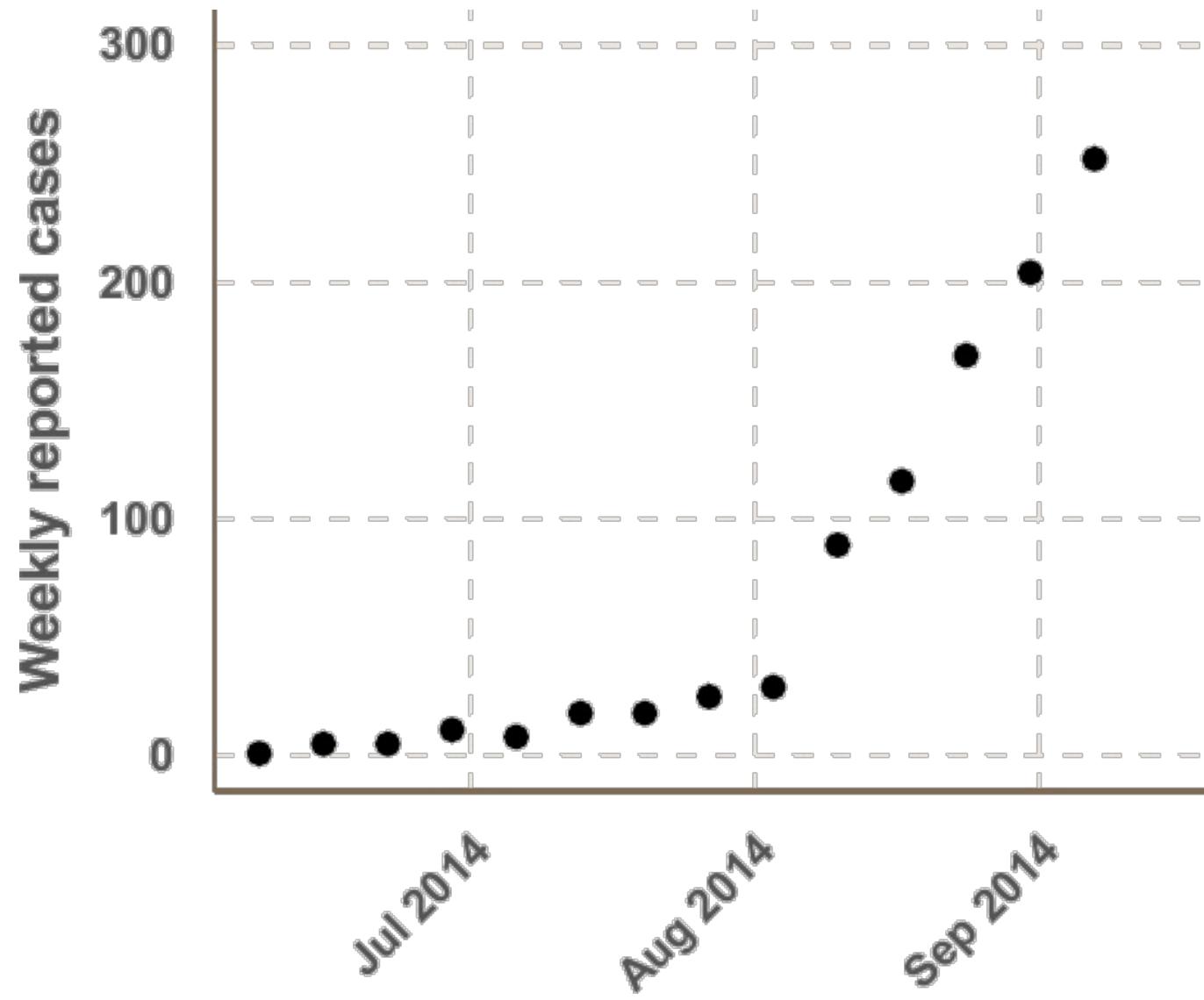


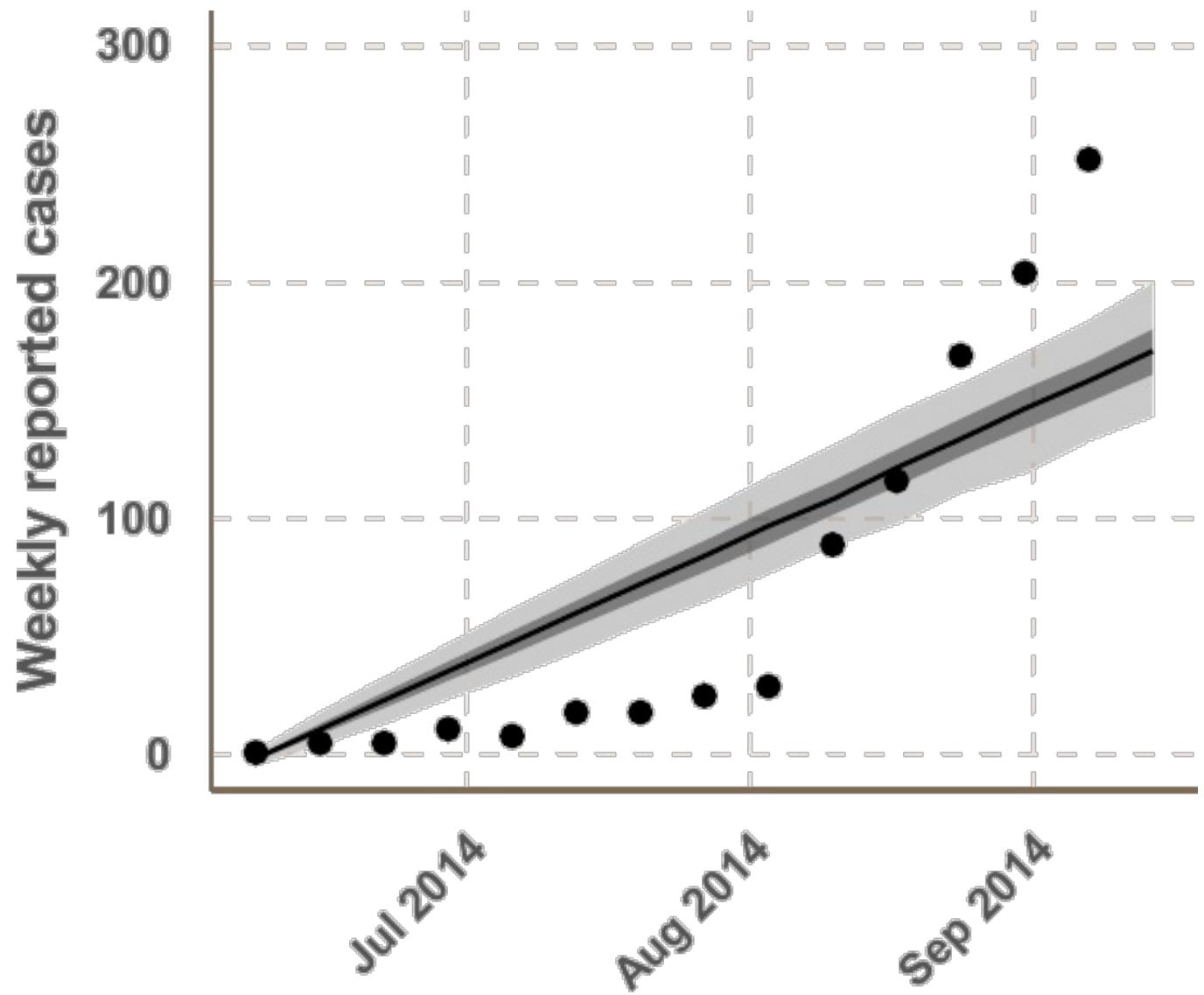
$$\dot{S} = - R_0 \gamma \frac{S}{N} I$$

$$\dot{I} = + R_0 \gamma \frac{S}{N} I - \gamma I$$

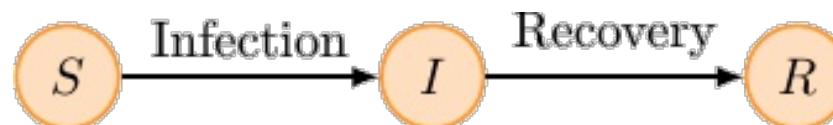
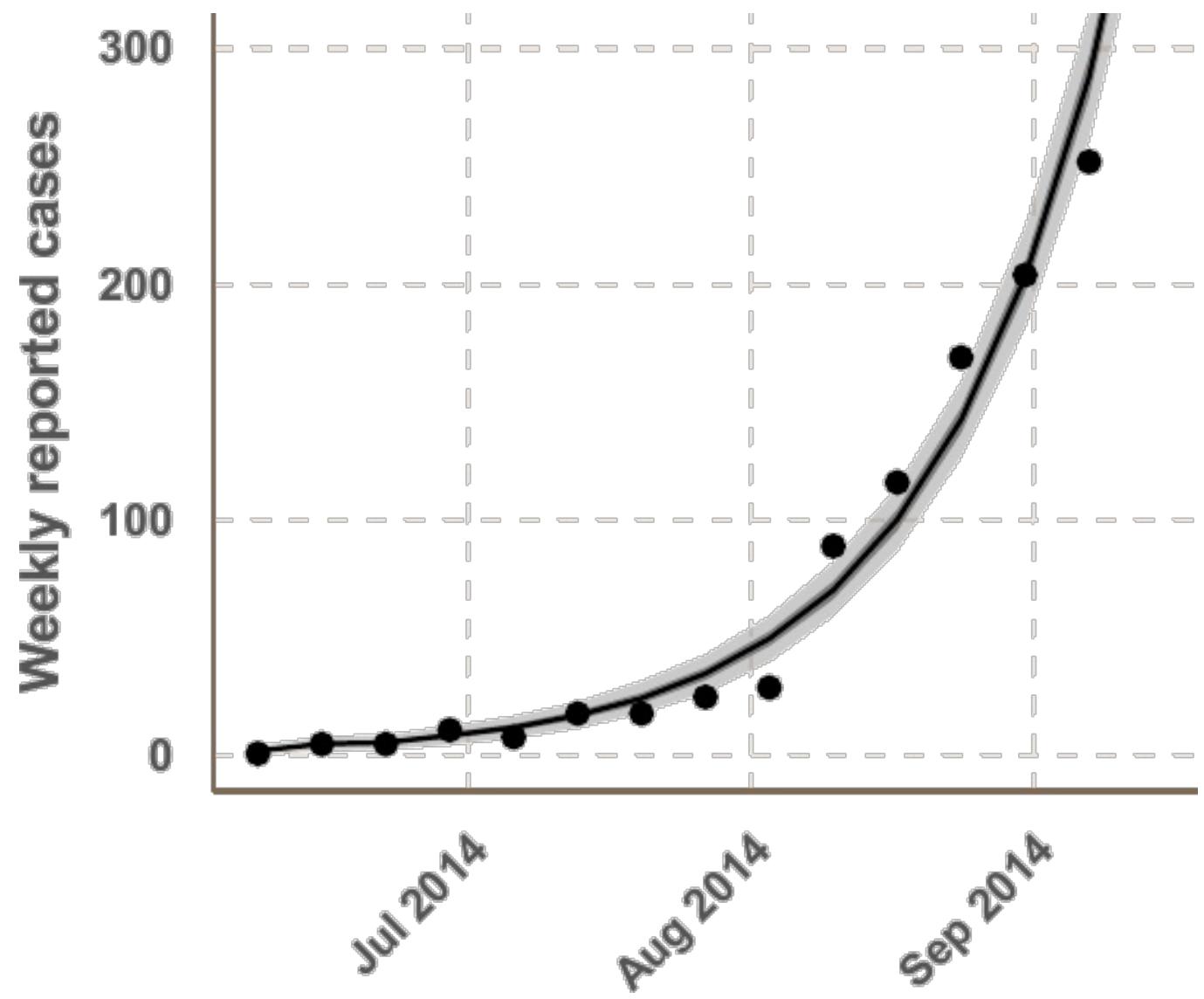
$$\dot{R} = + \gamma I$$

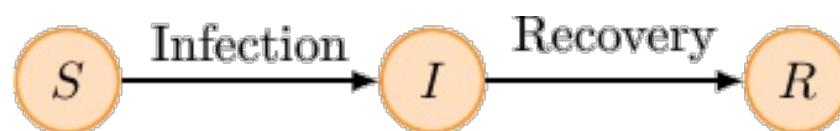
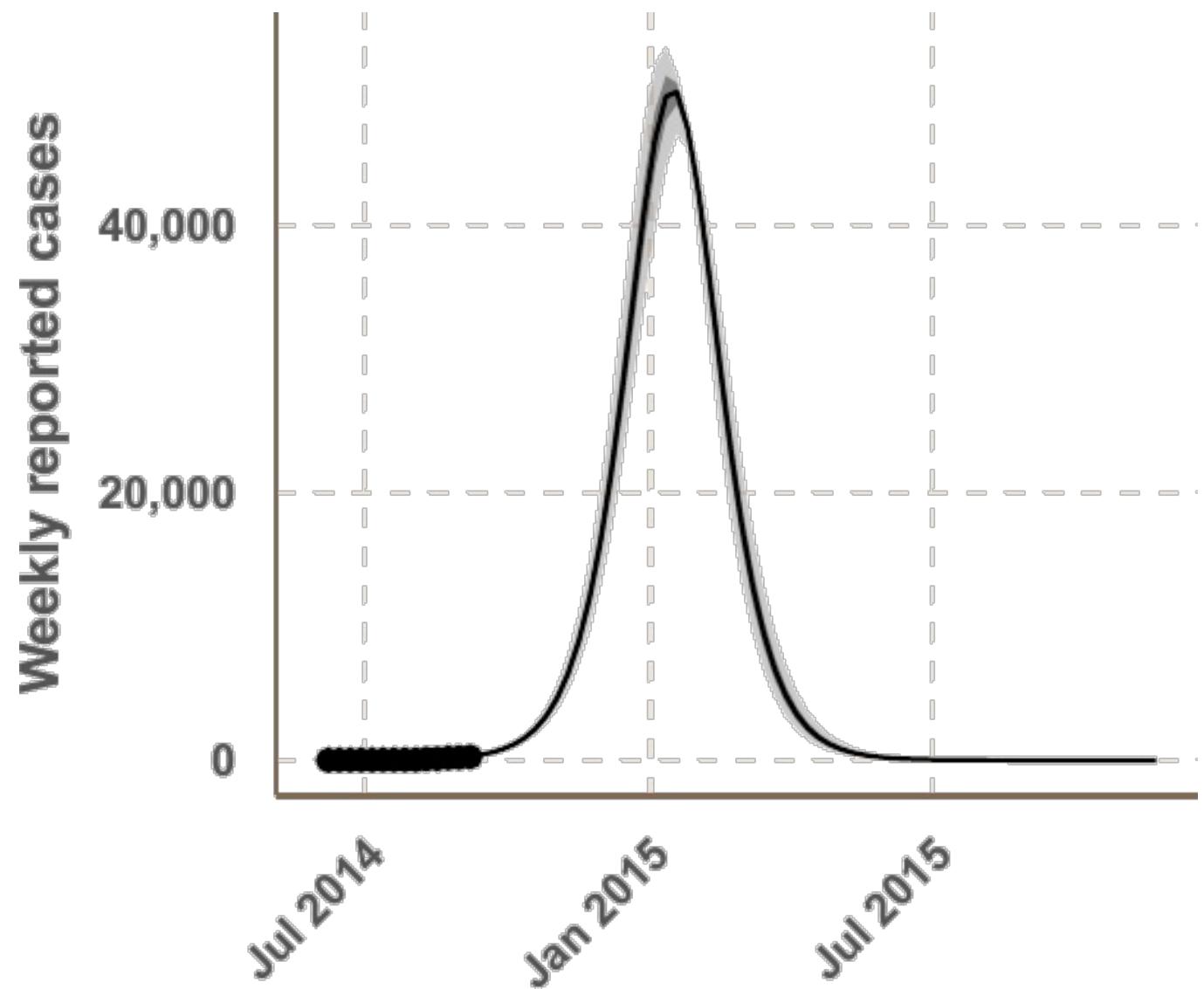


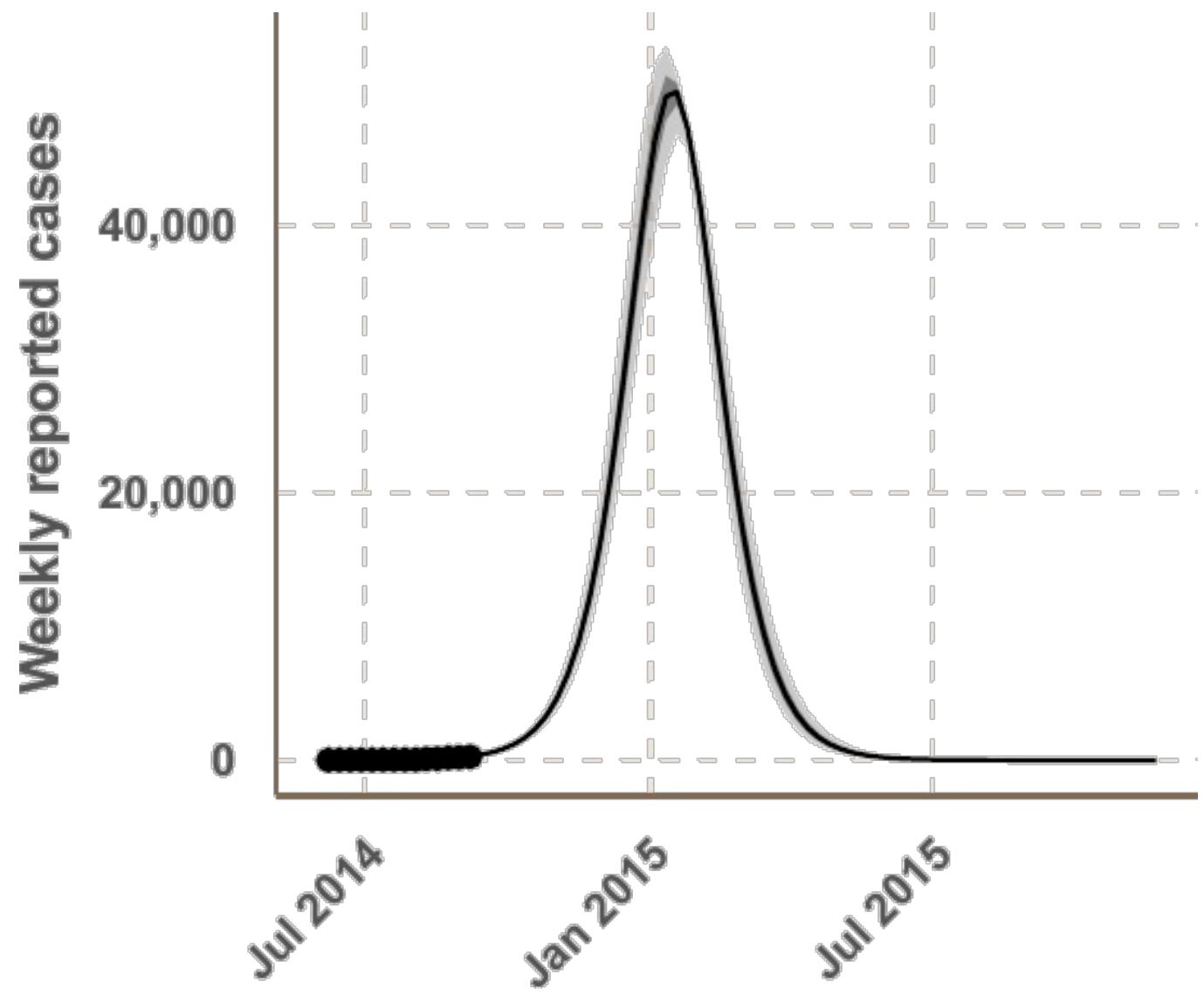


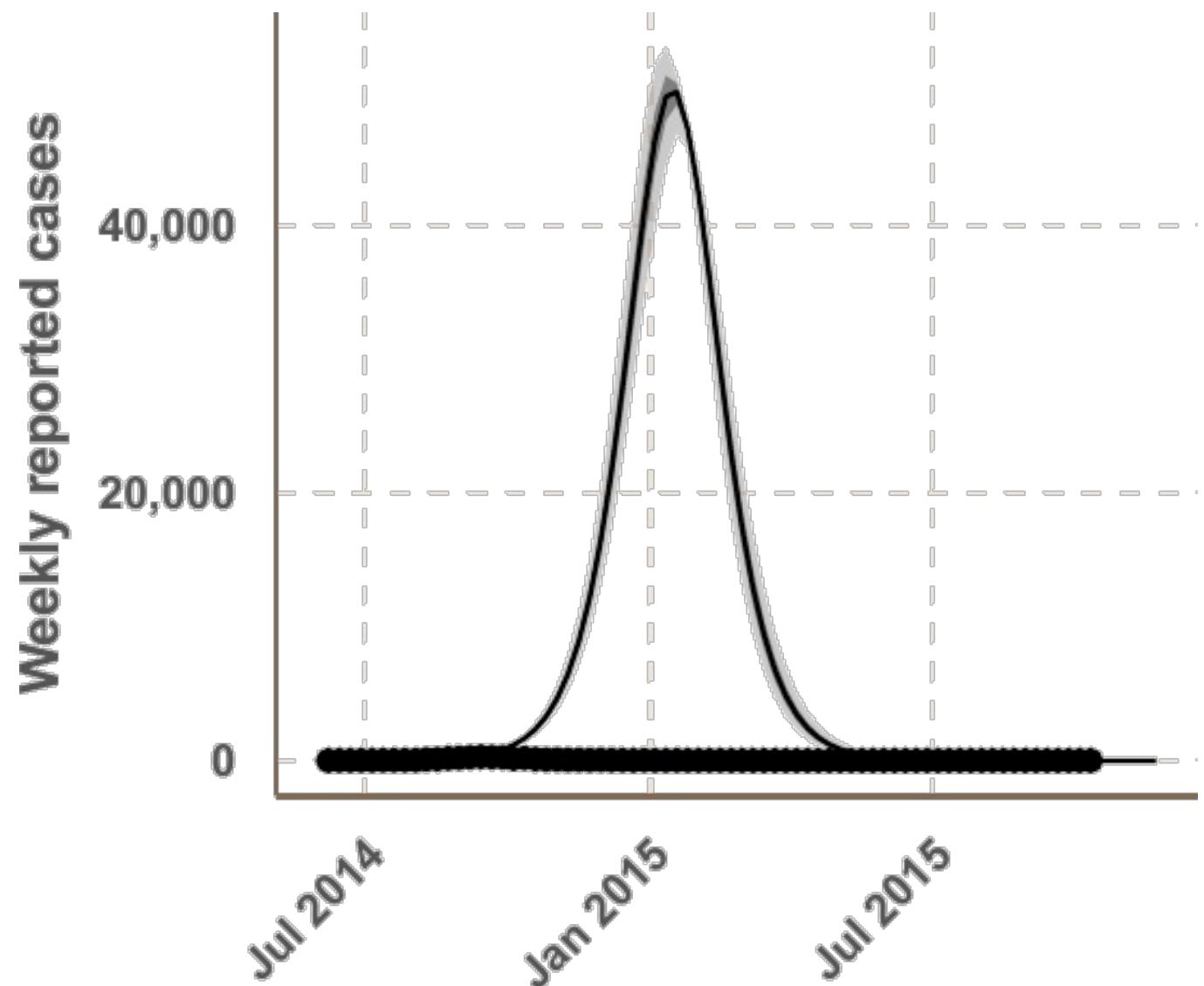


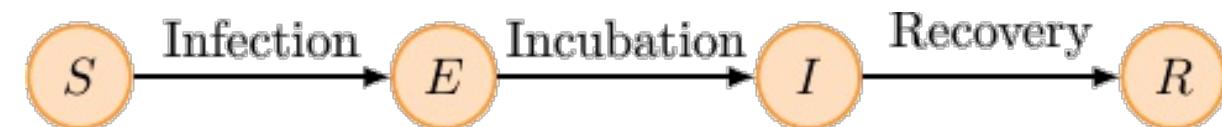
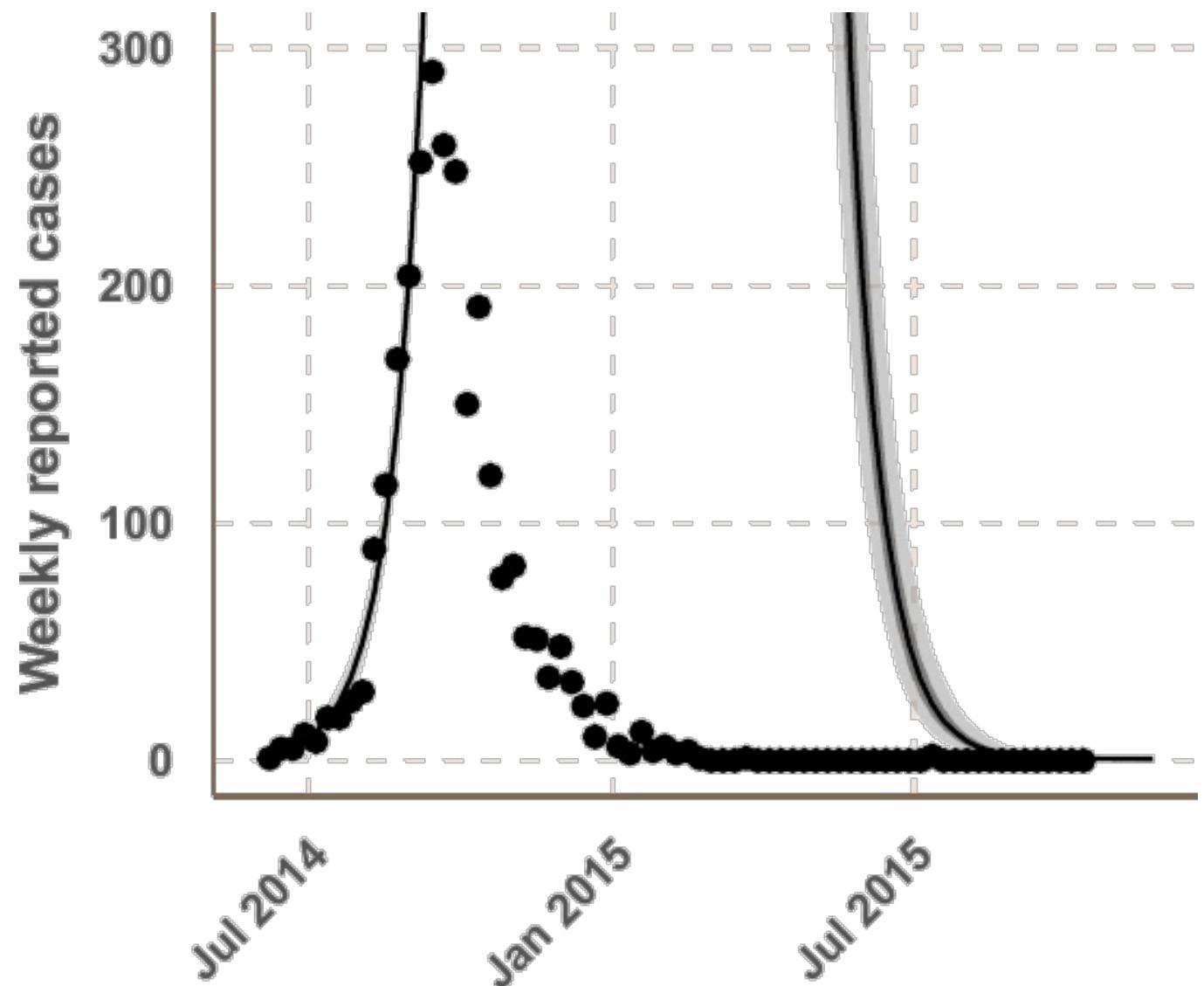
$$y = ax + b$$









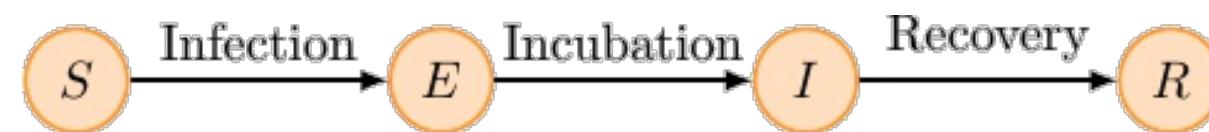


A semi-mechanistic model for real-time forecasting

The unknown

- Community/hospital/funeral transmission
- Spatial dynamics
- Changes in behaviour
- Changes in reporting
- Interventions
- Seasonality
- etc

The known



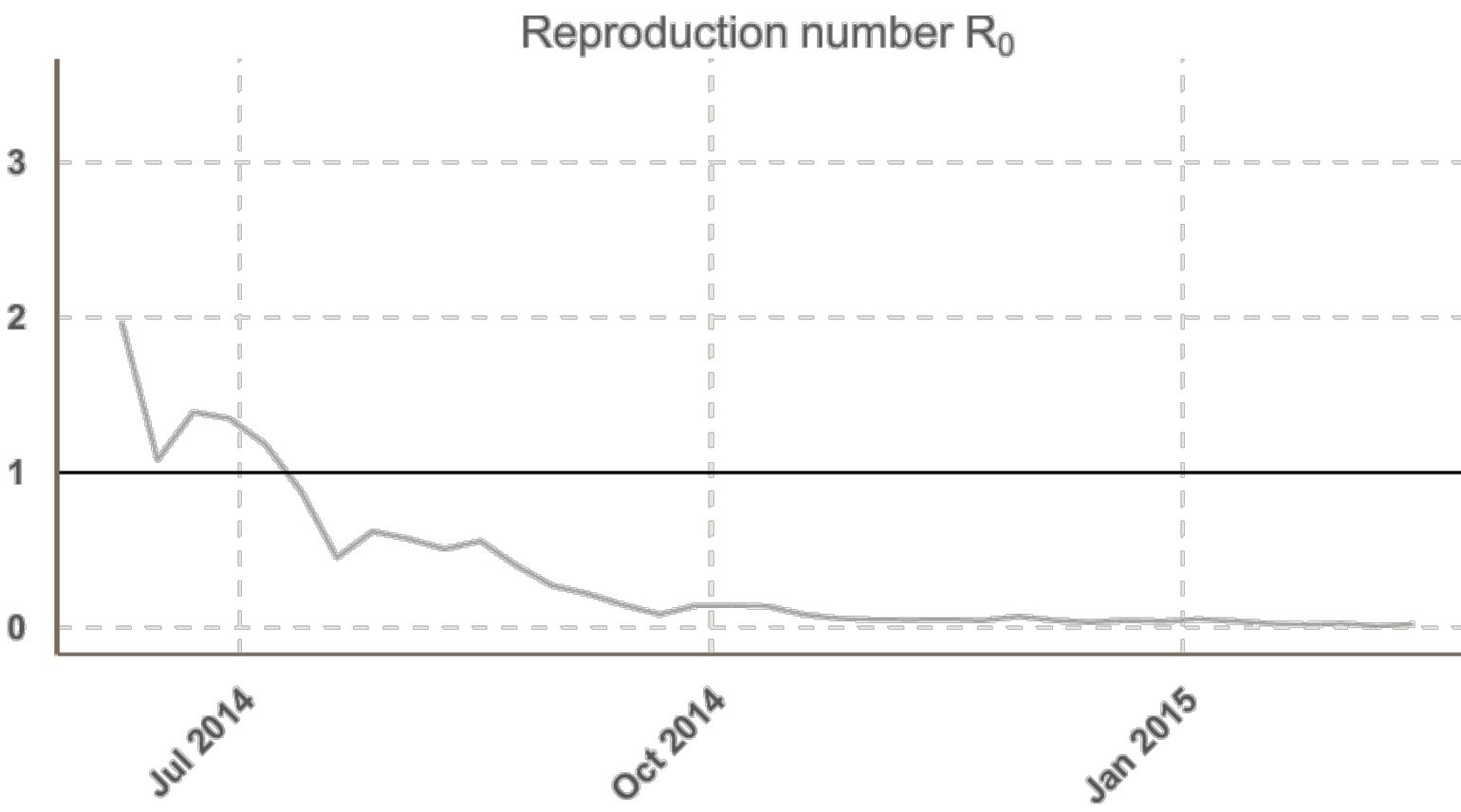
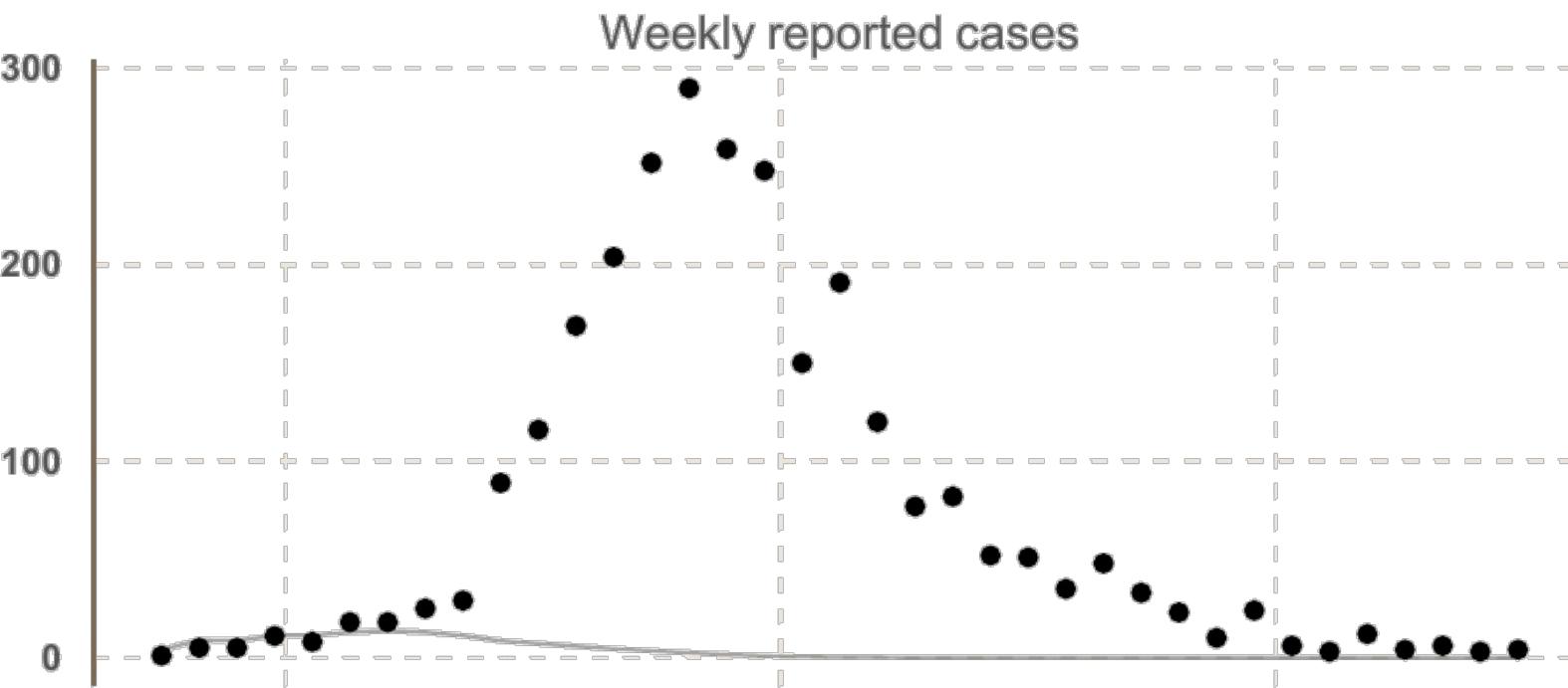
- Average incubation period (~9 days)
- Average infectious period (~11 days)
- Case-fatality rate (~70%)

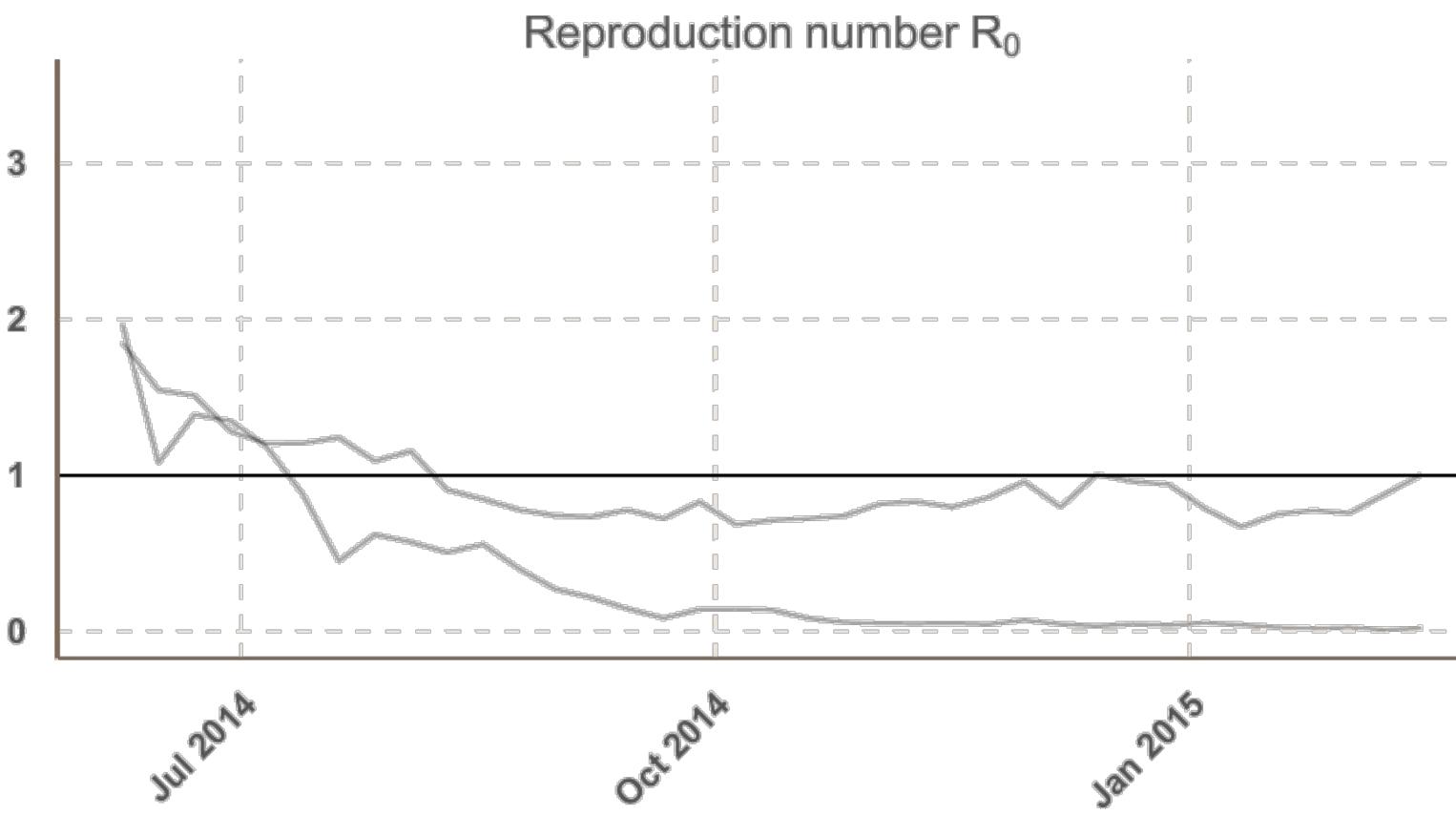
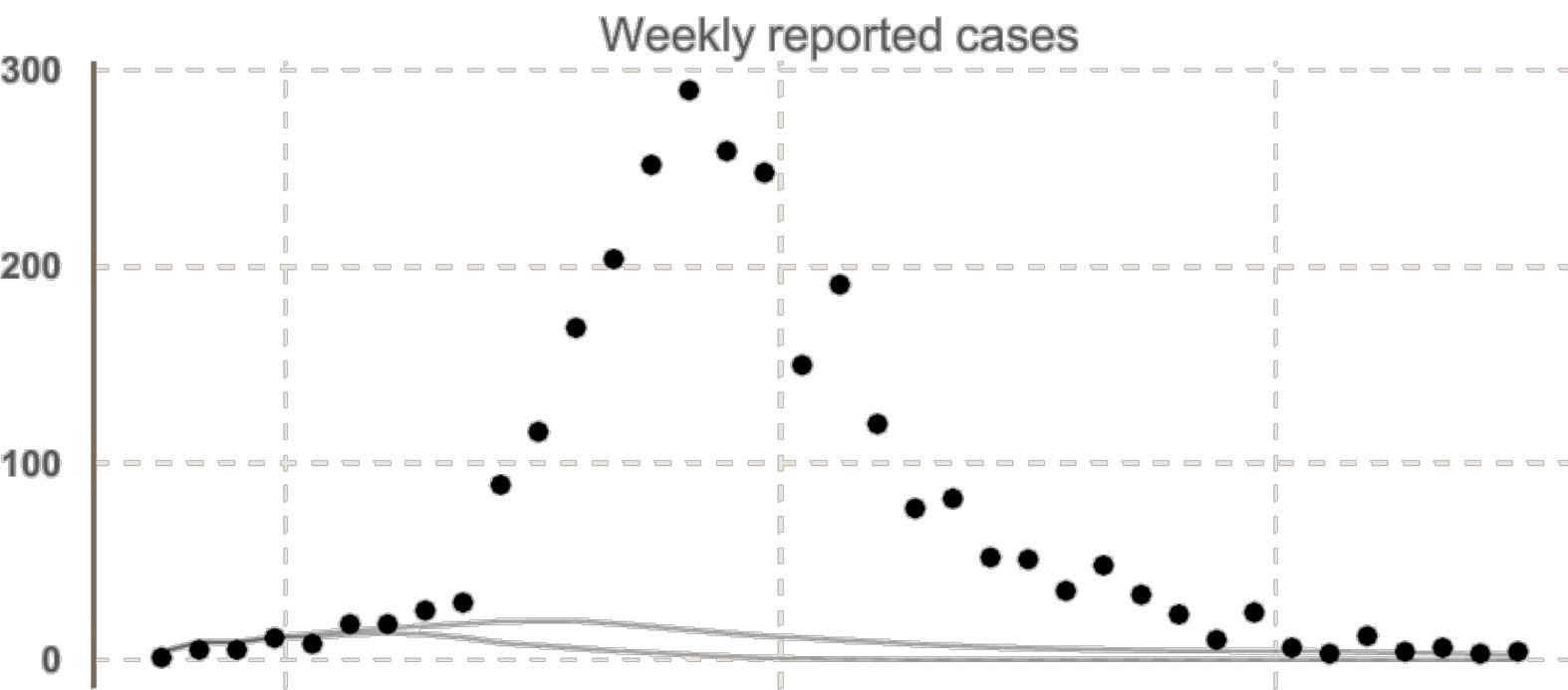
WHO Ebola response team (2014)

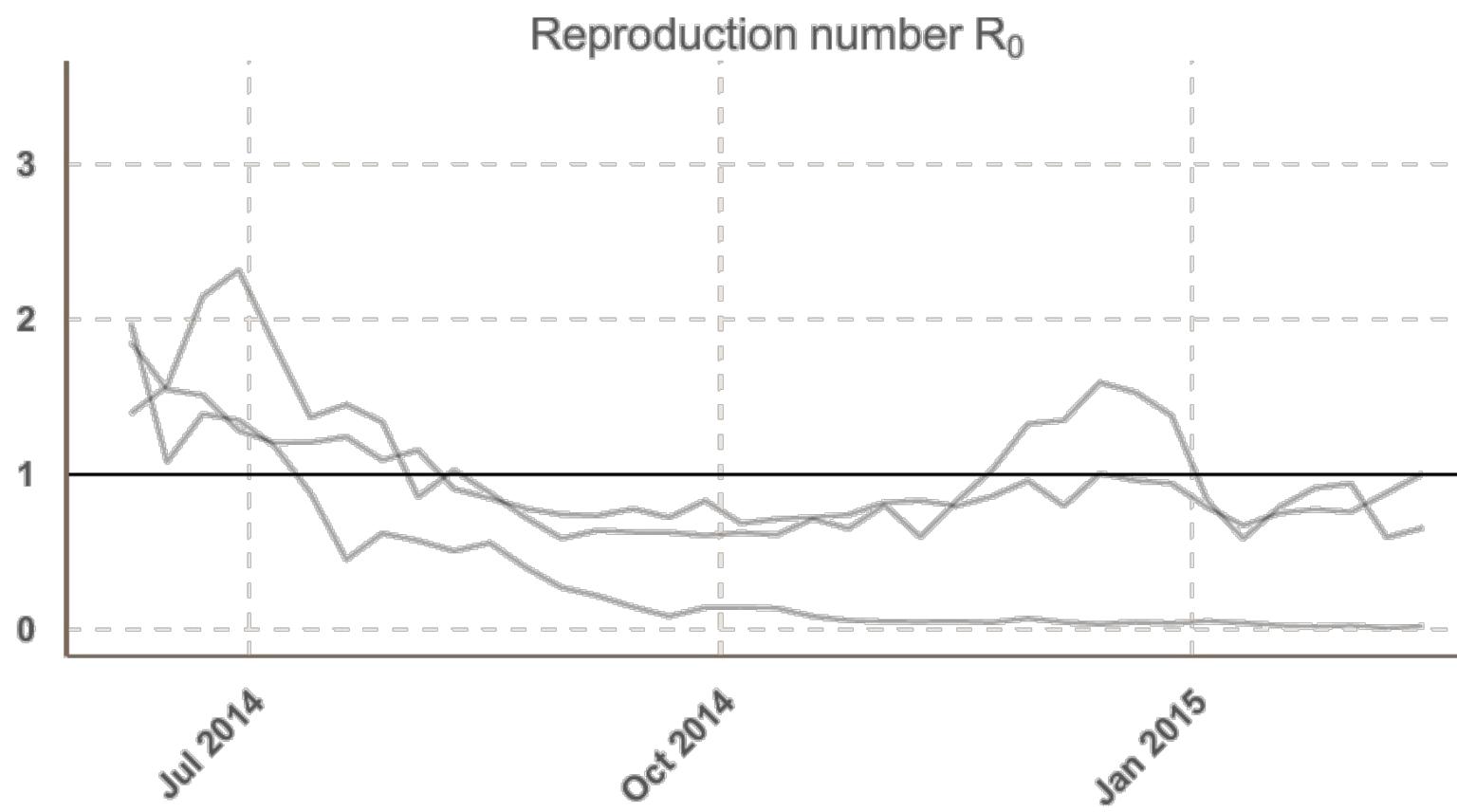
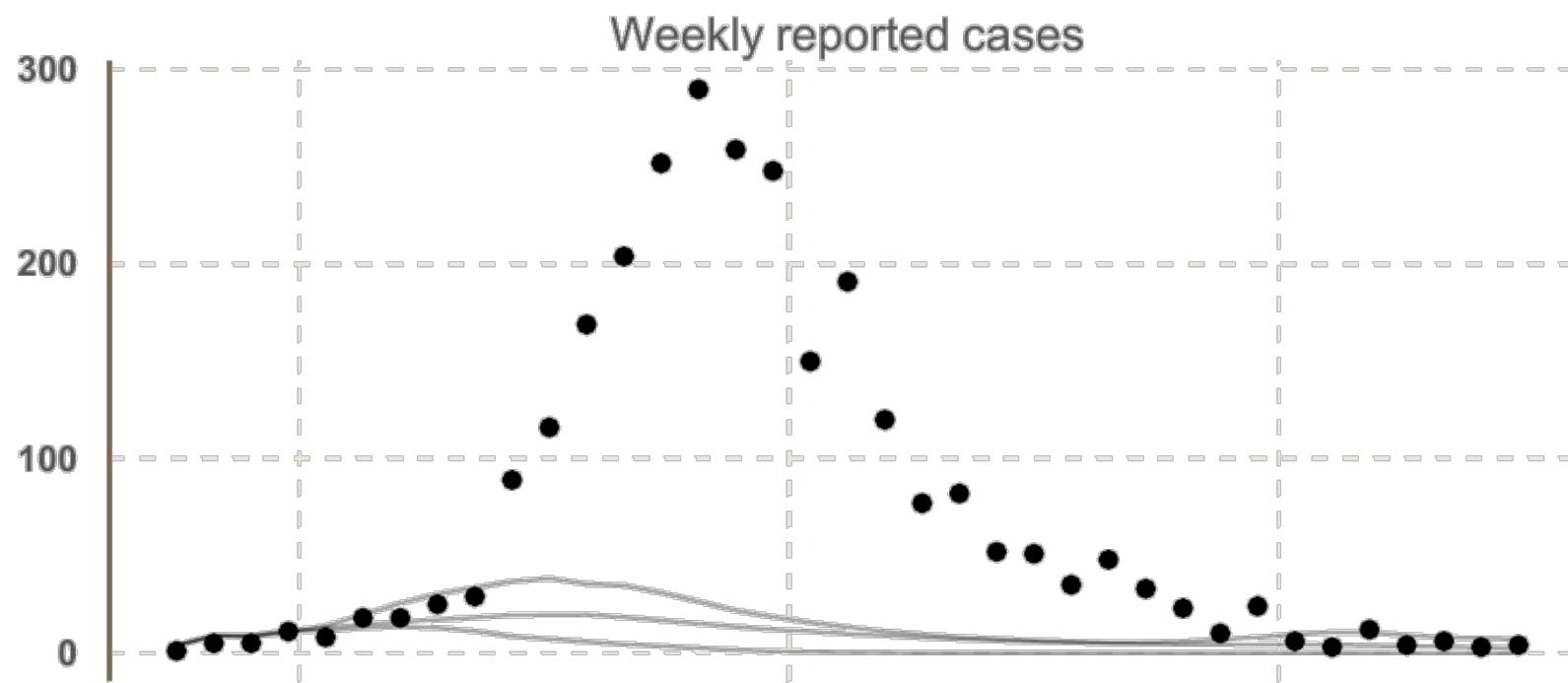
Transmission intensity as a stochastic process

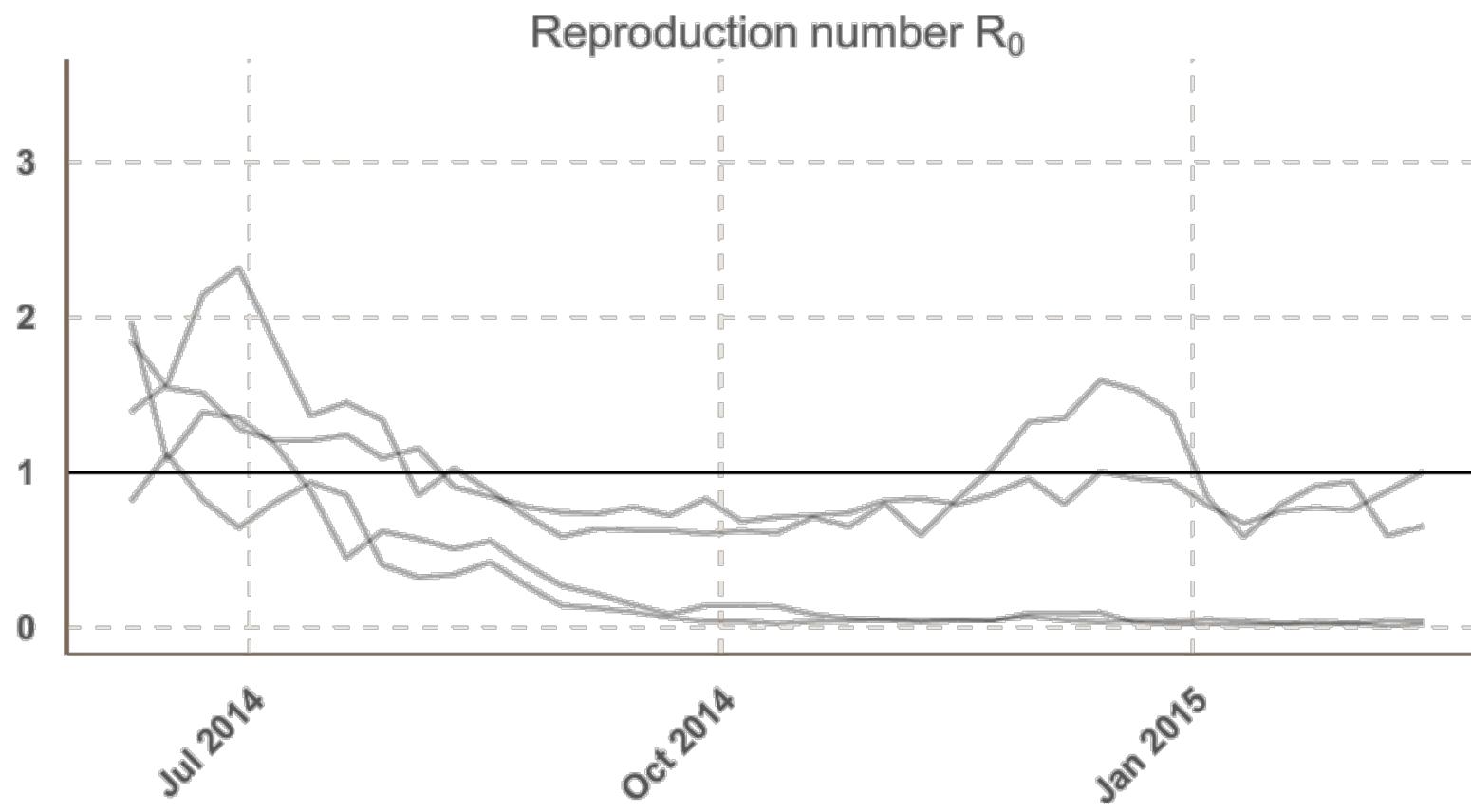
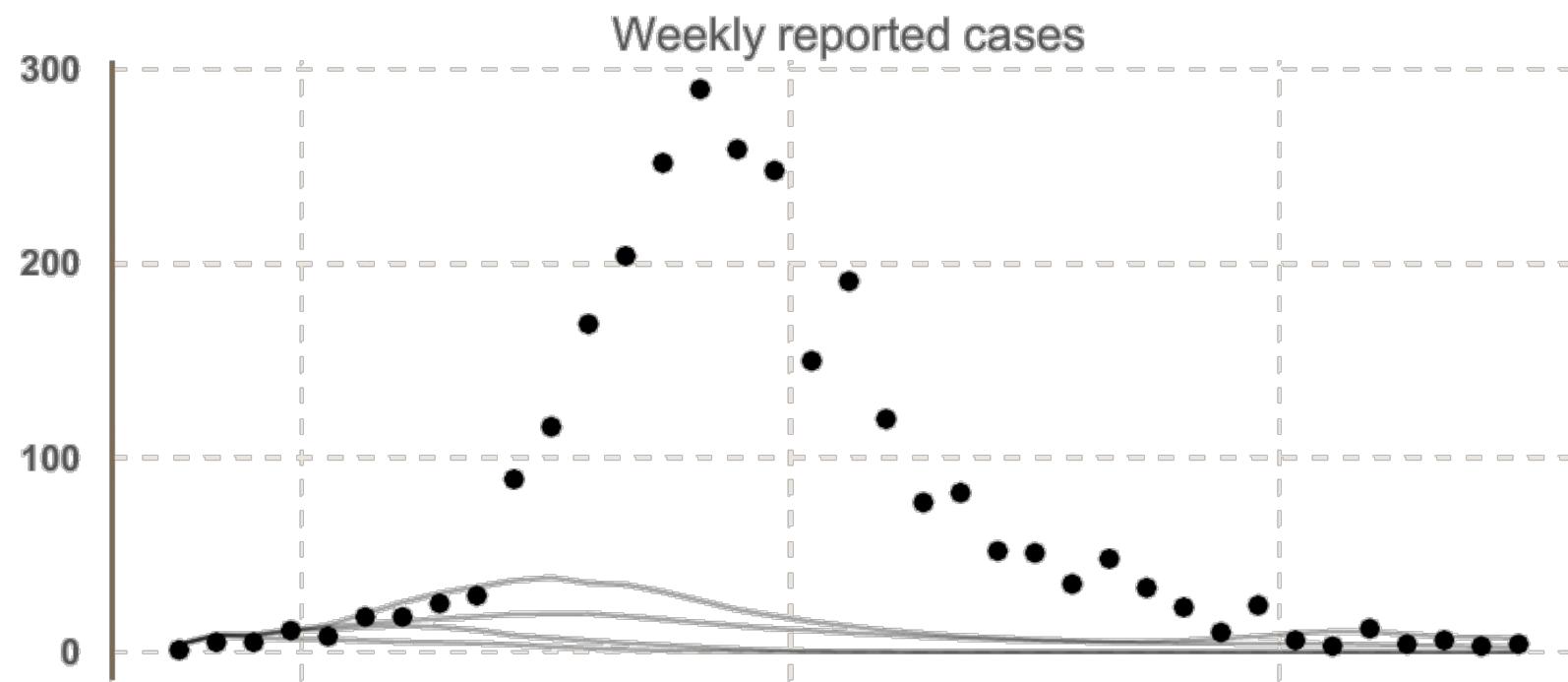
$$d \log(R_0(t)) = \sigma dW_t$$

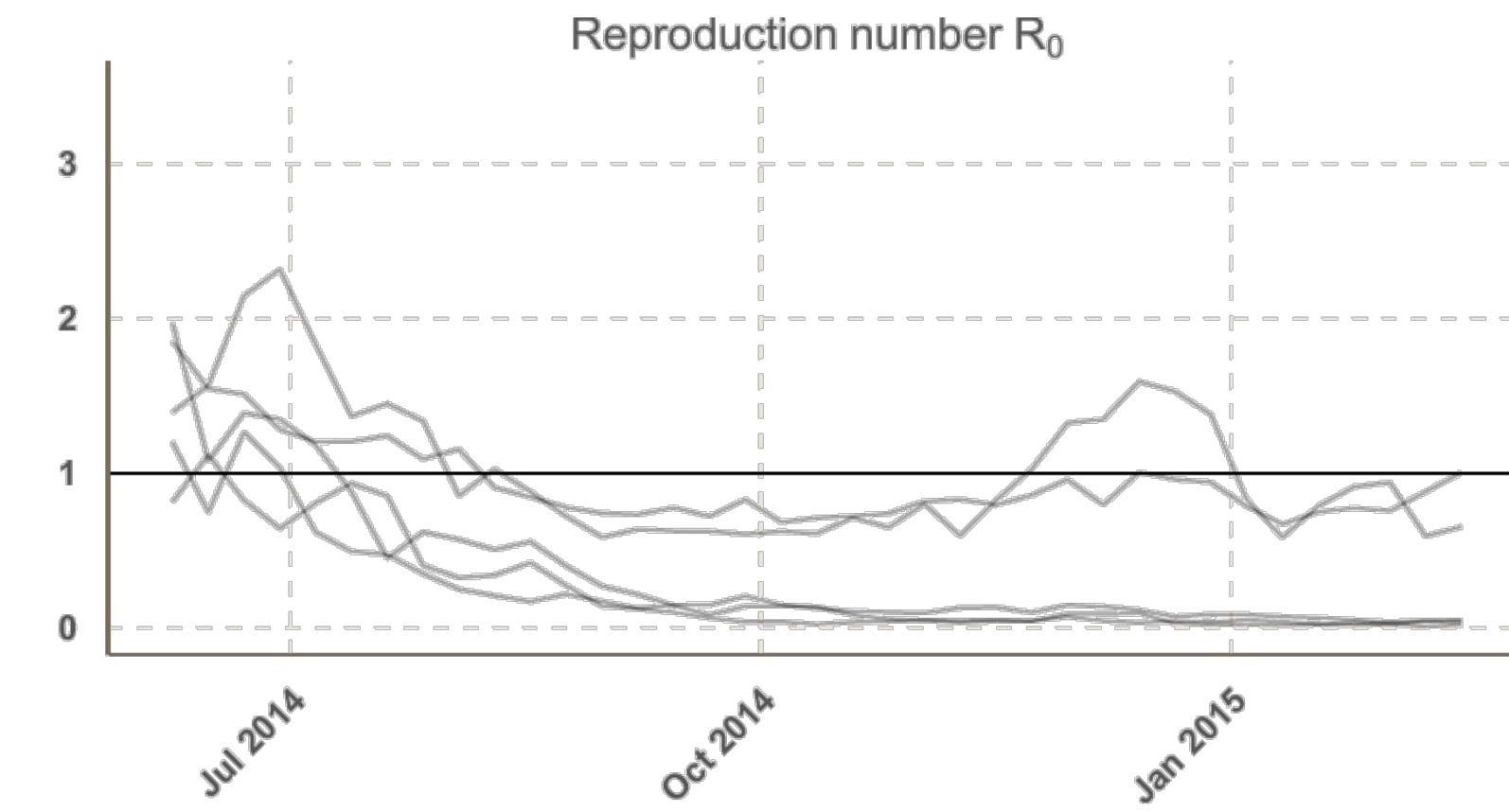
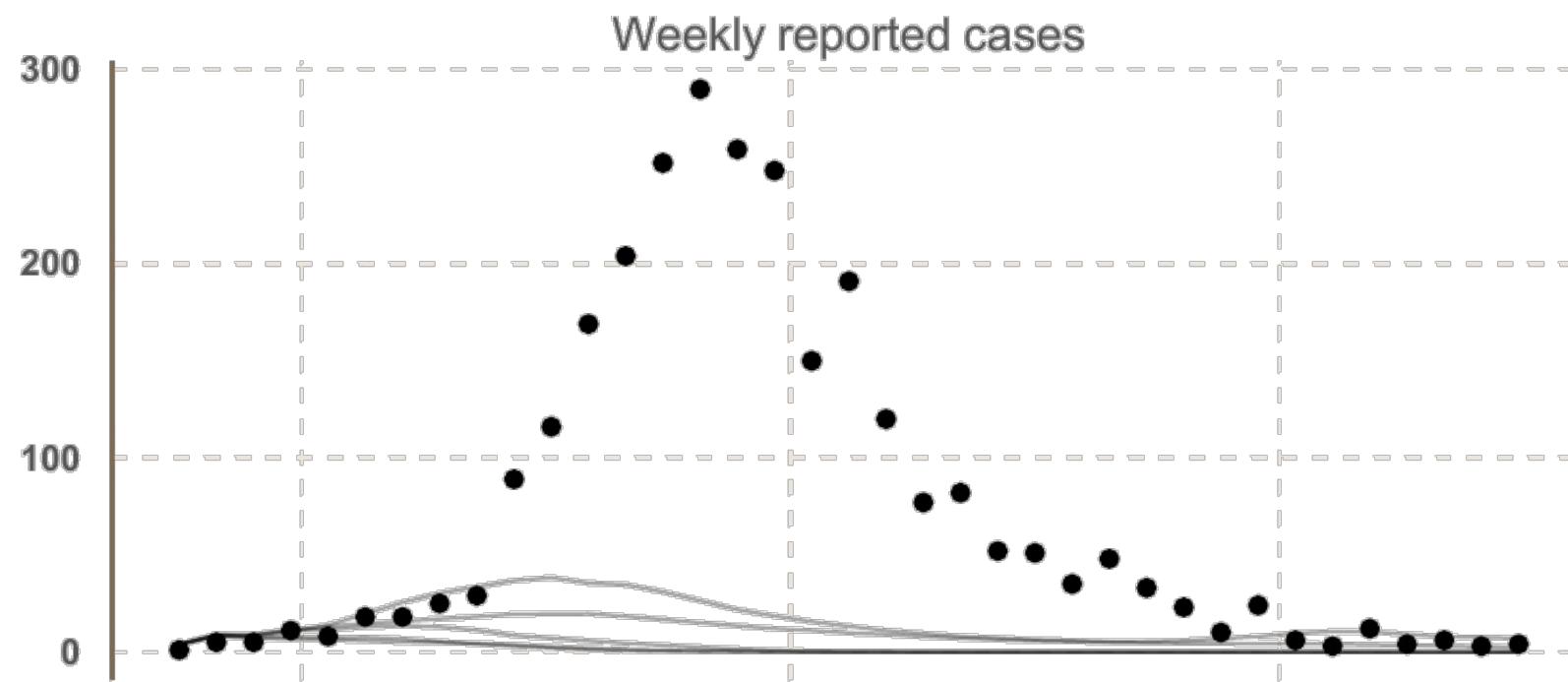
Dureau (2013)

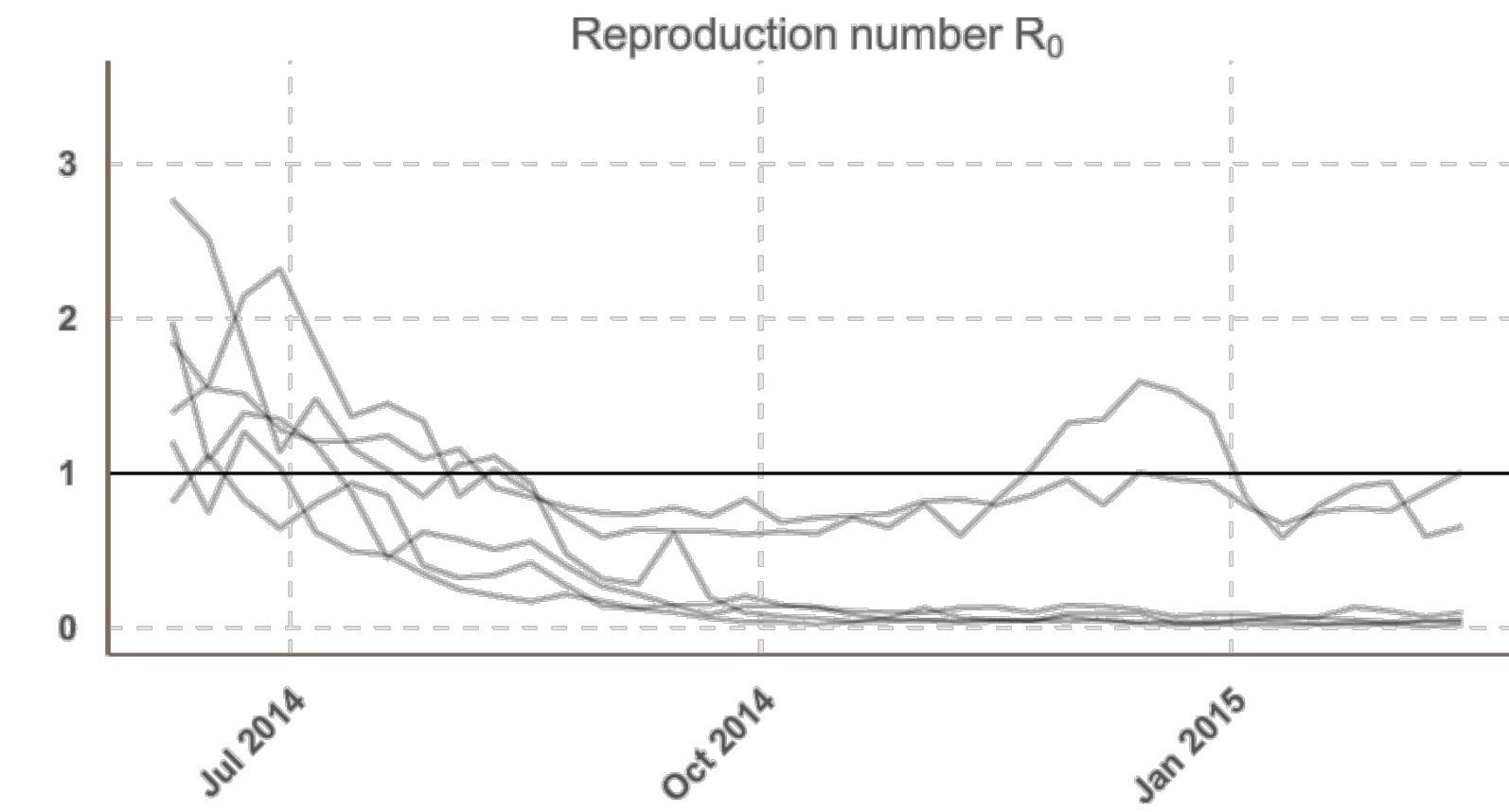
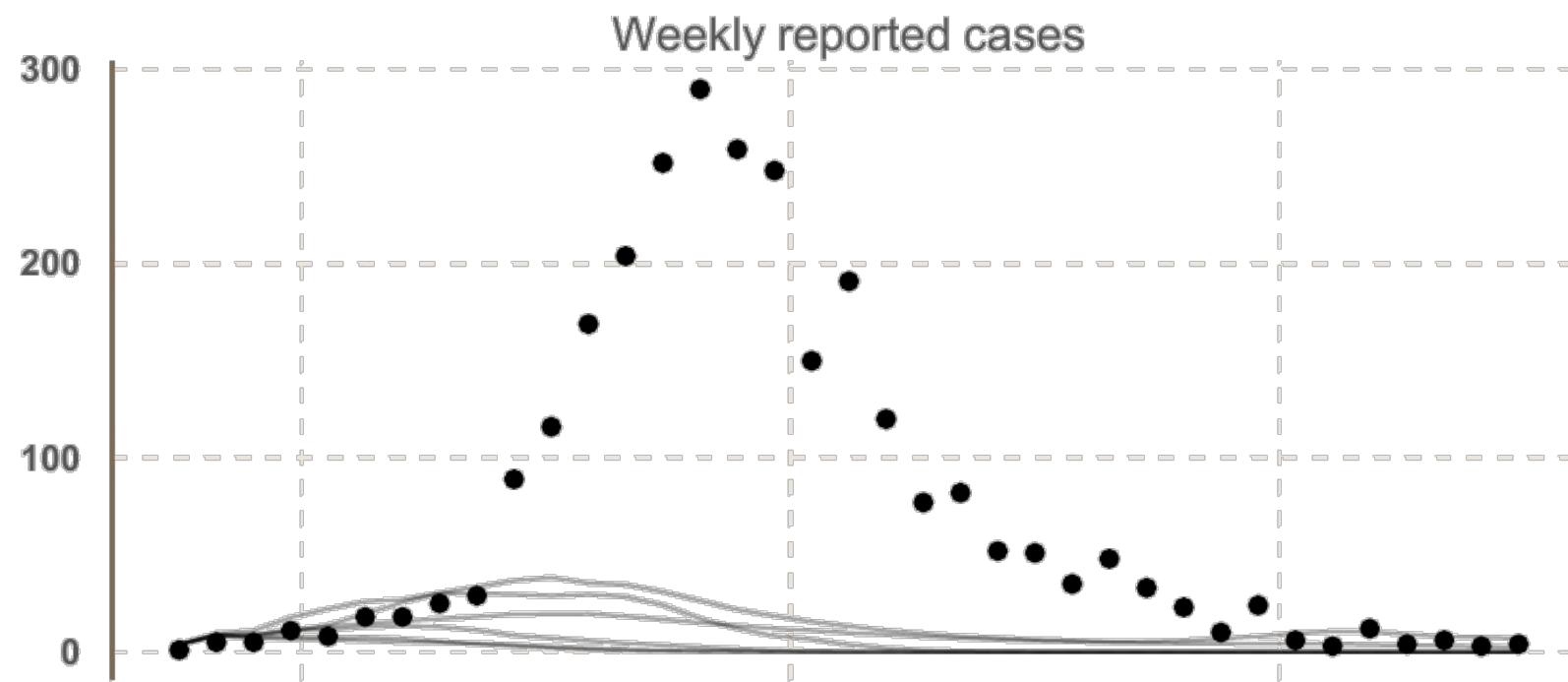


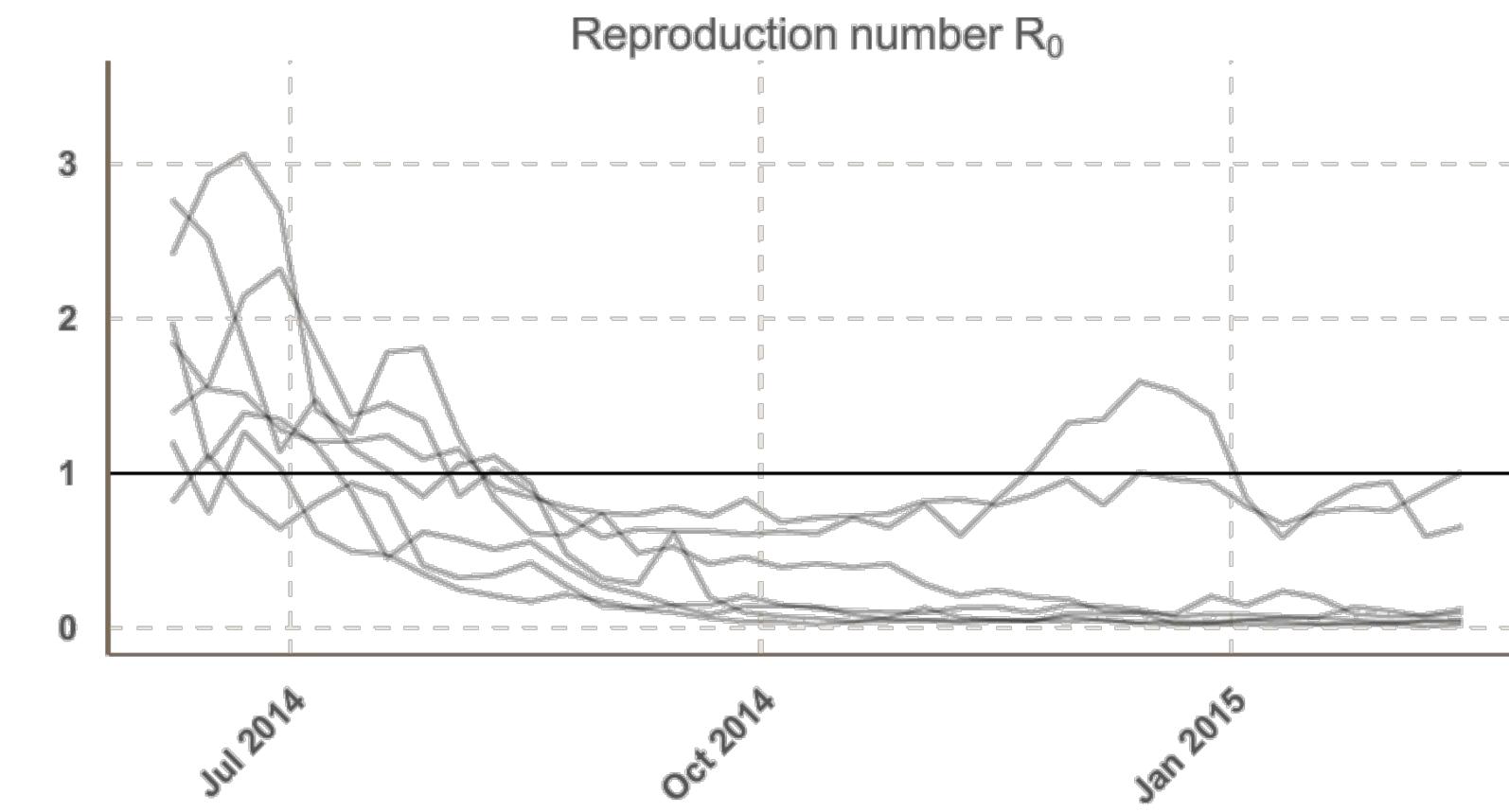
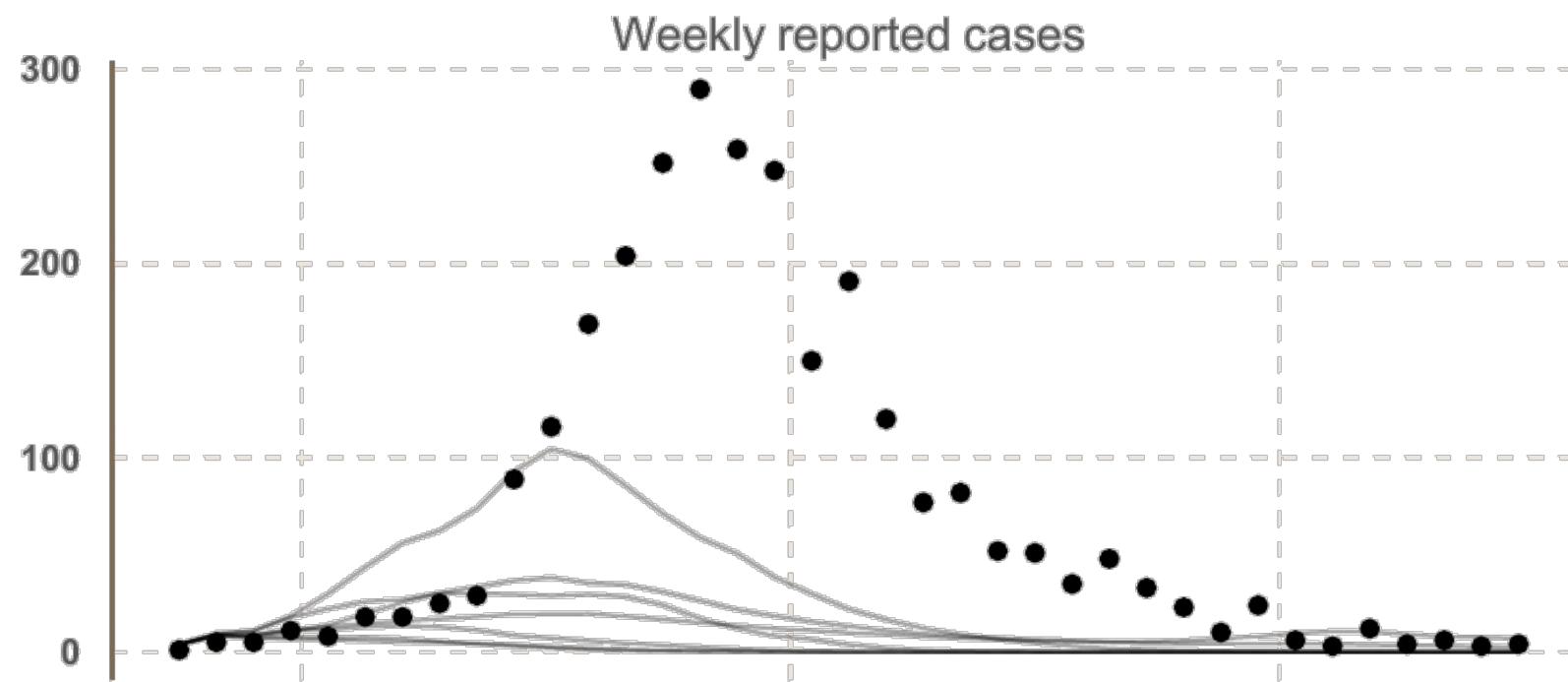


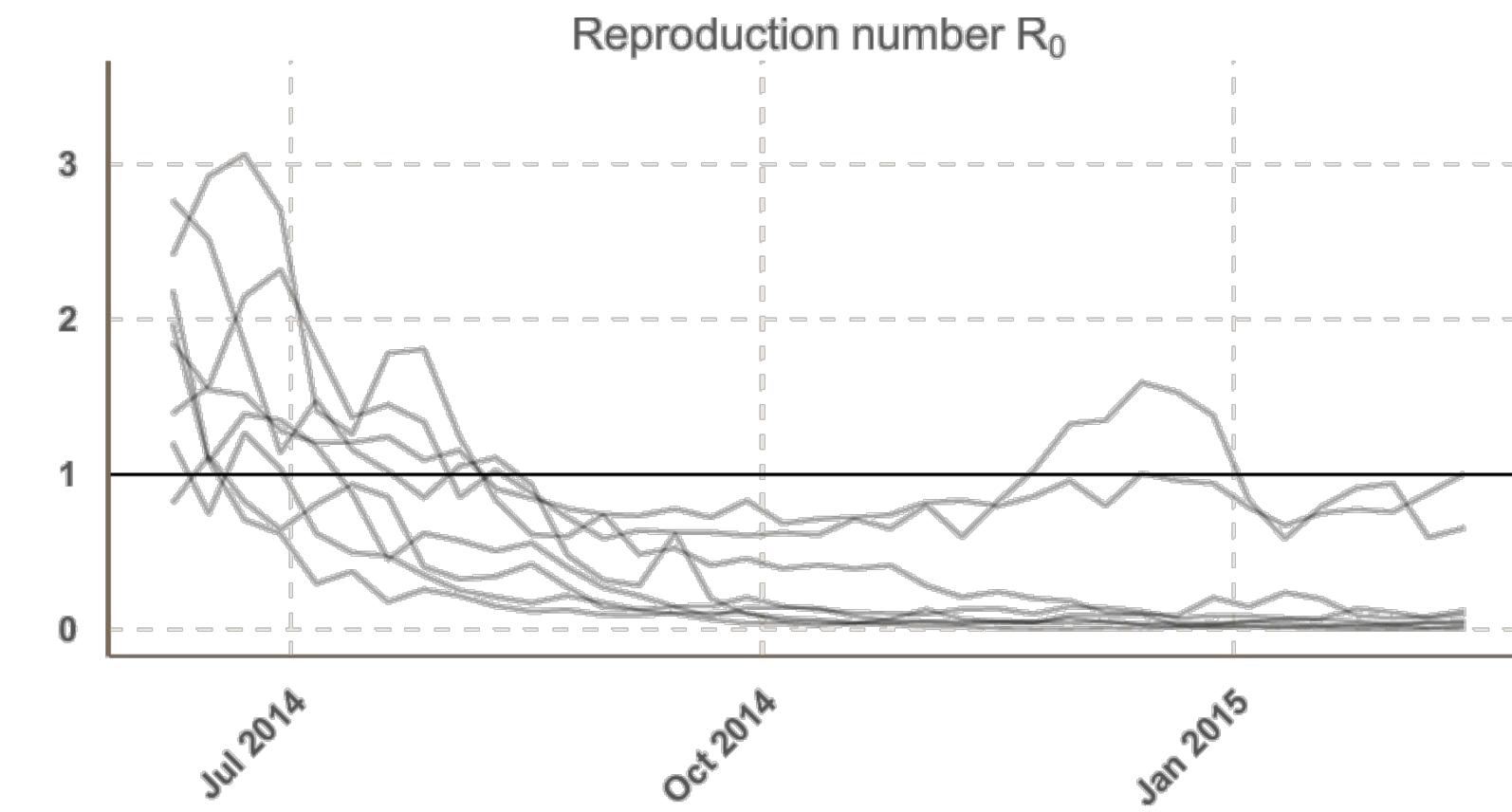
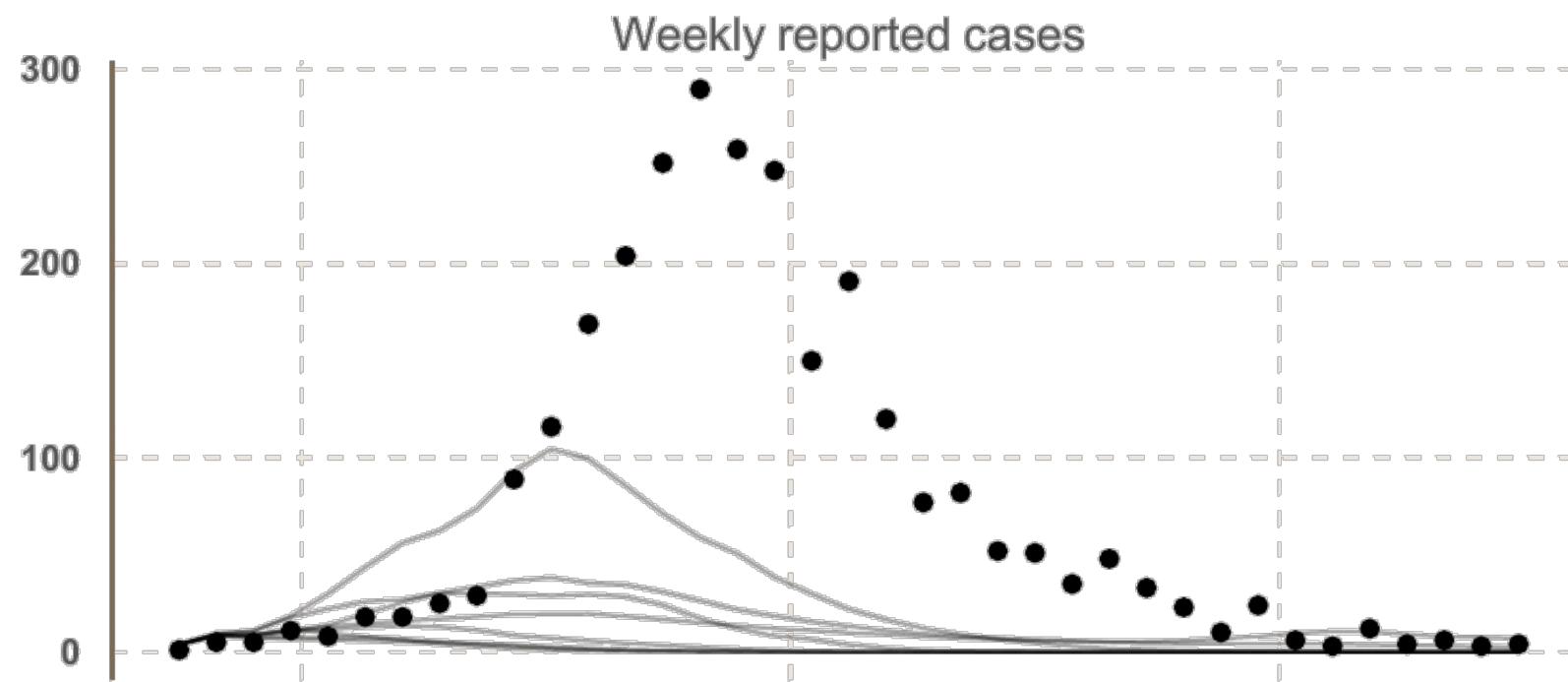


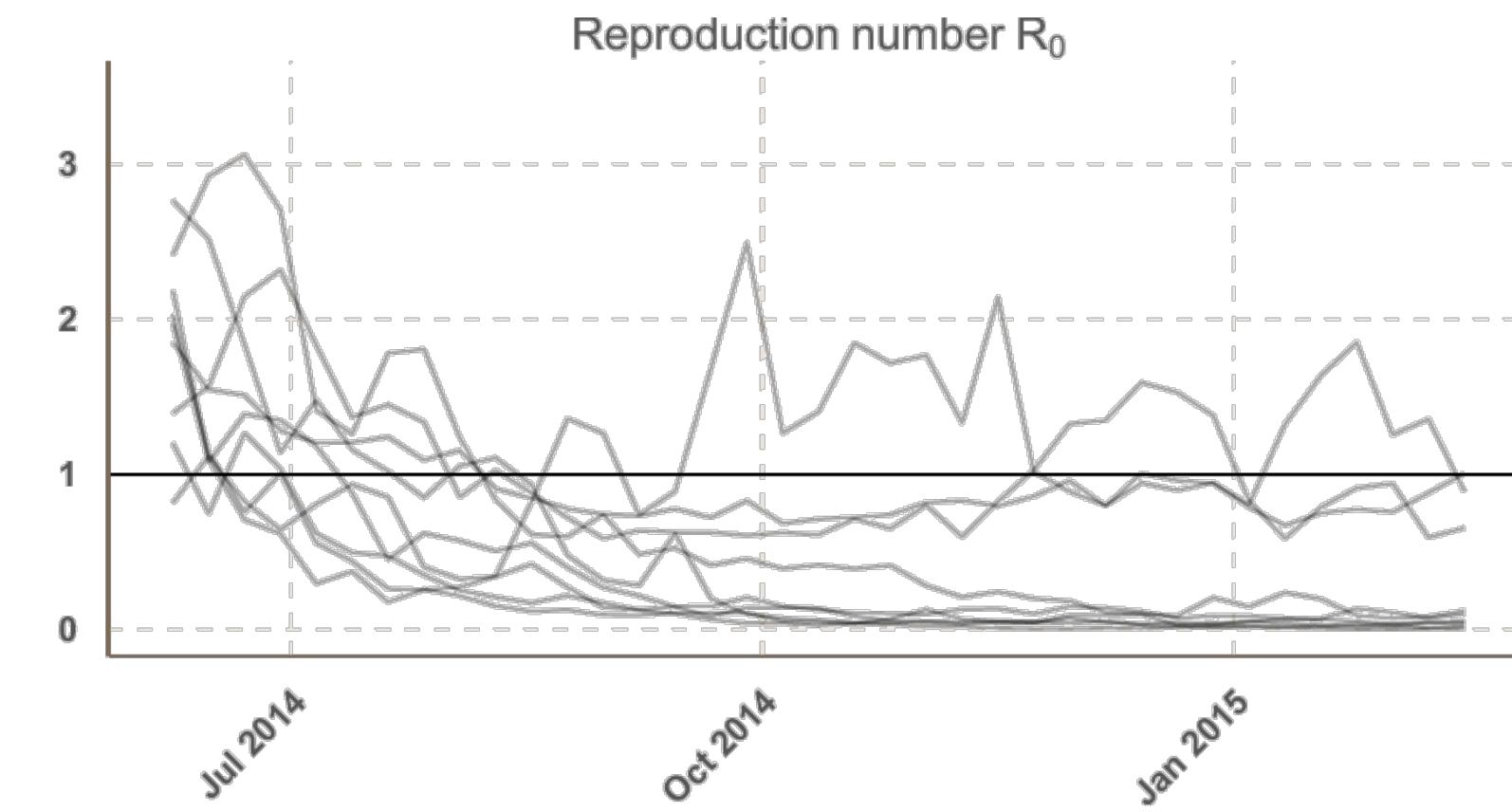
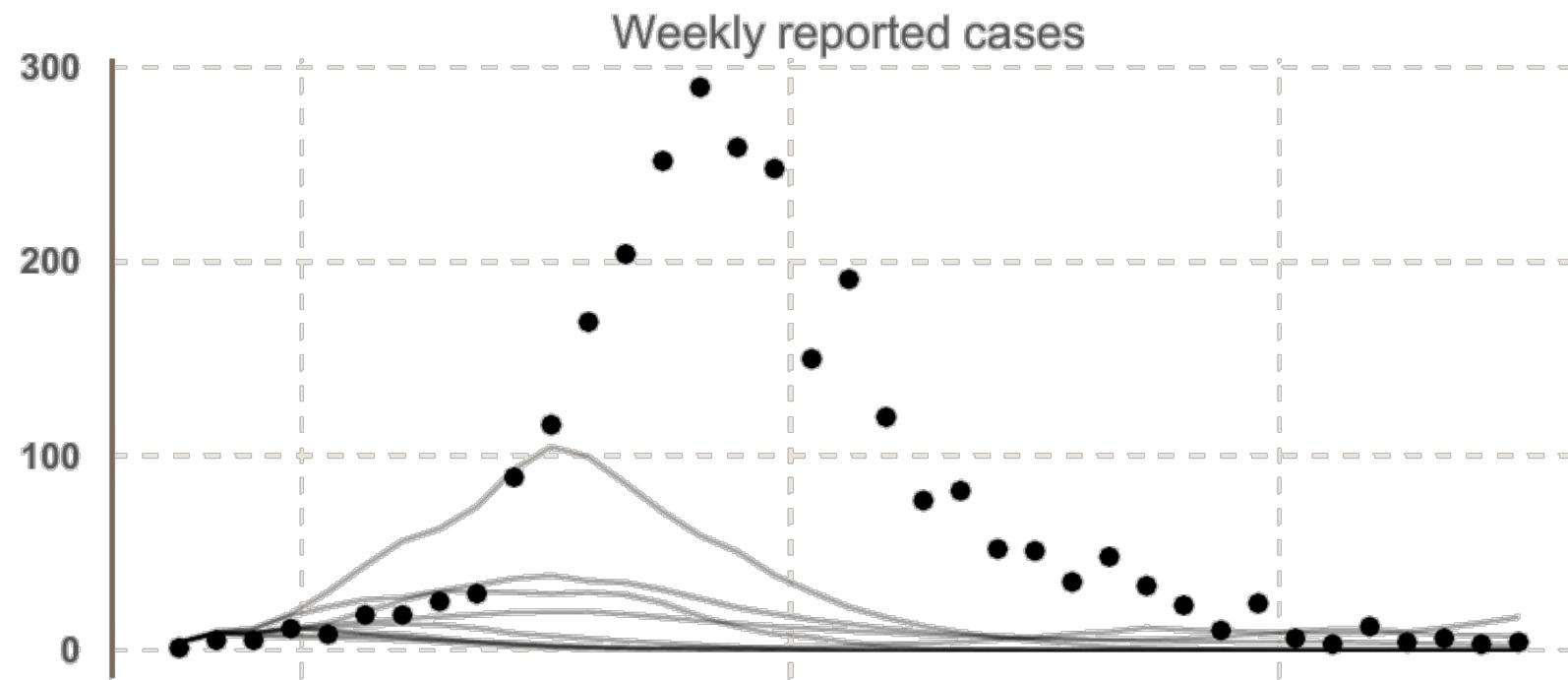


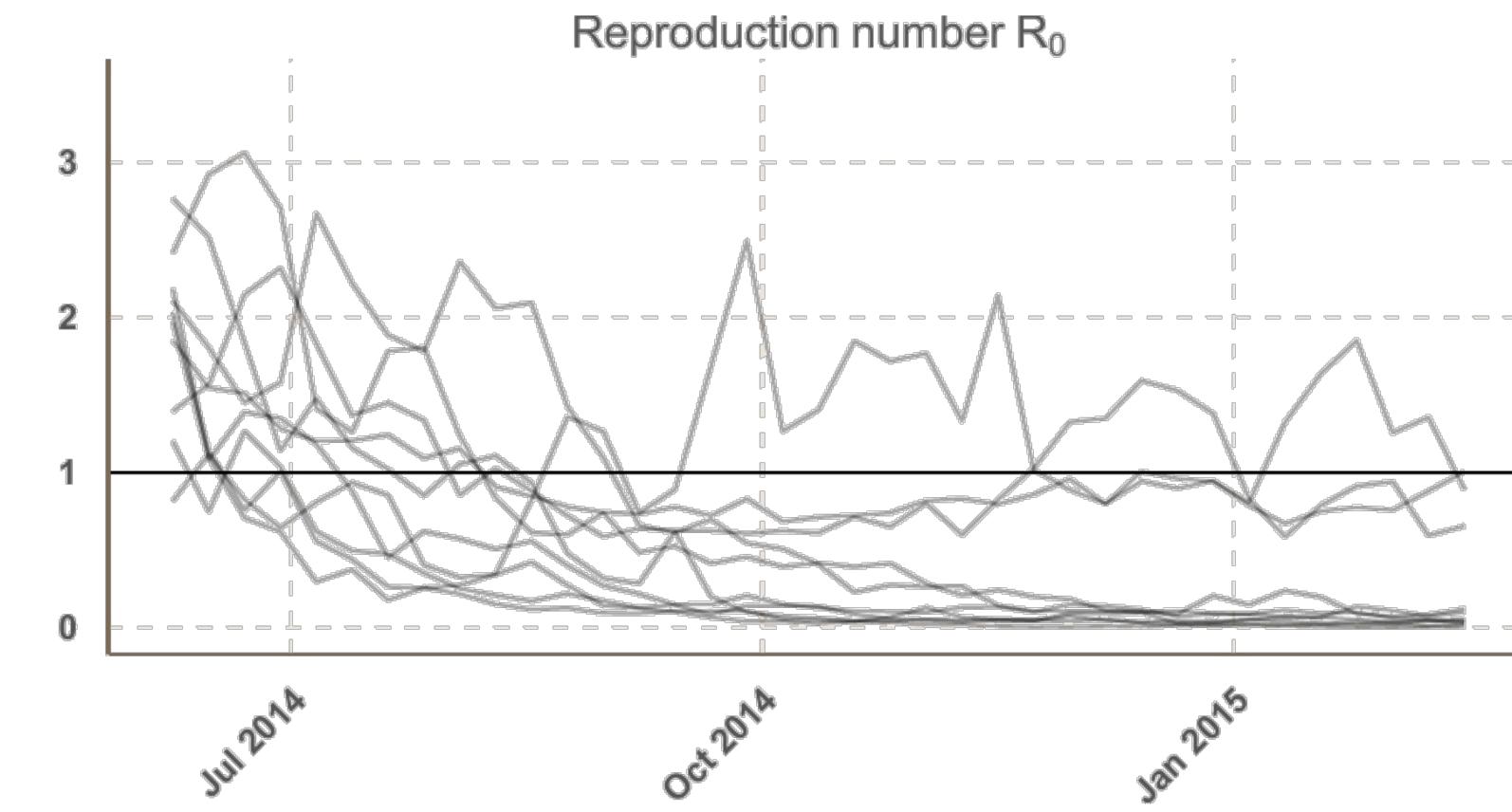
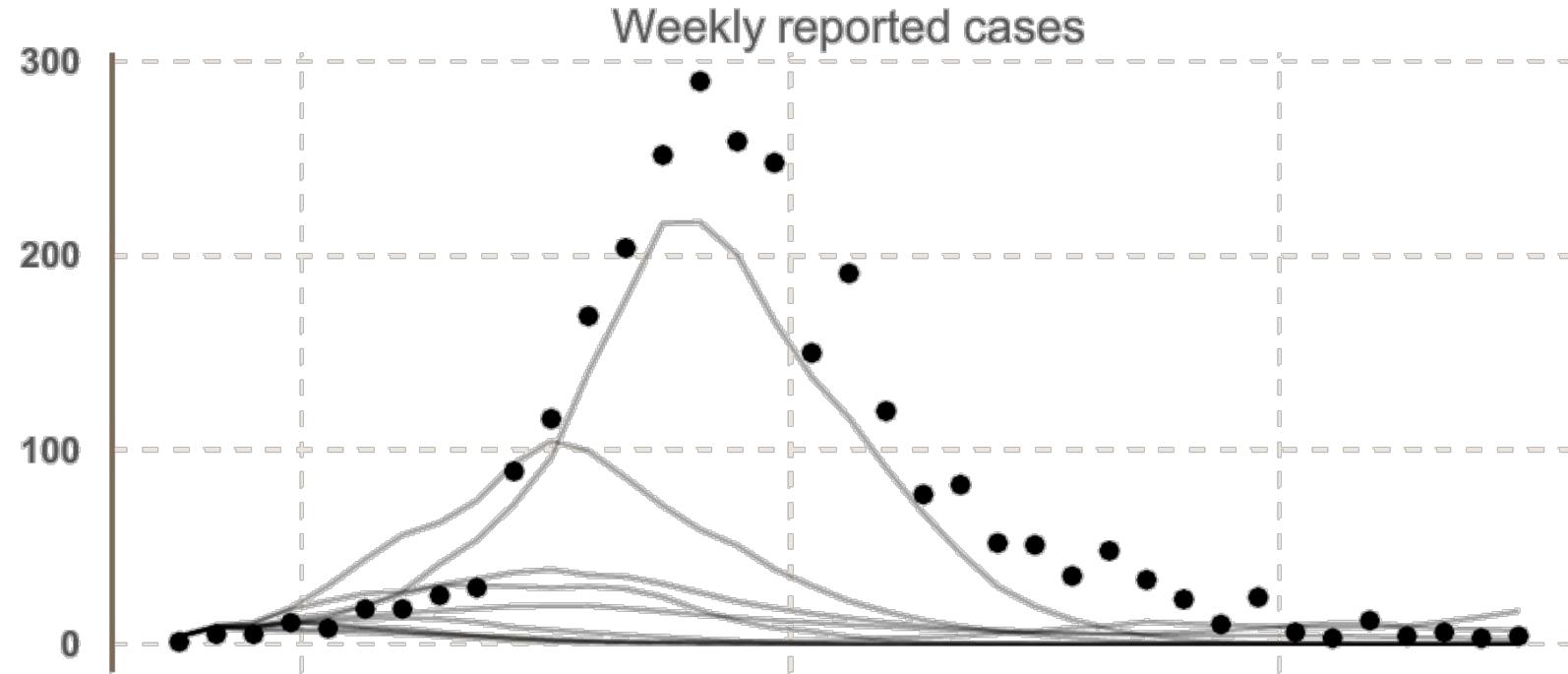




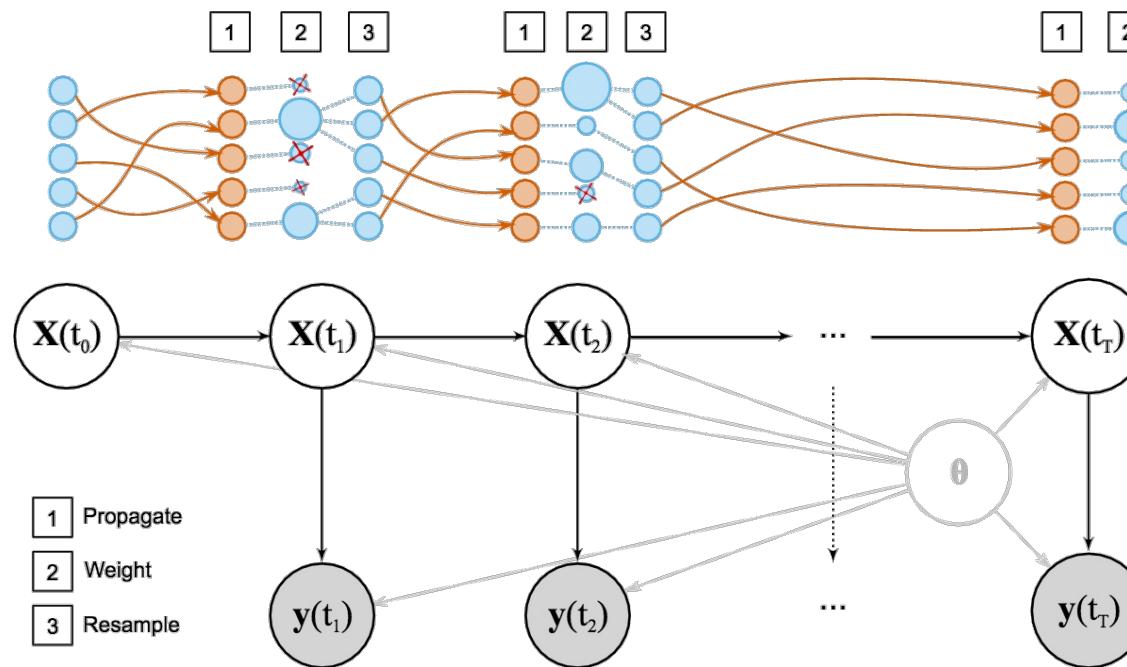








Particle MCMC



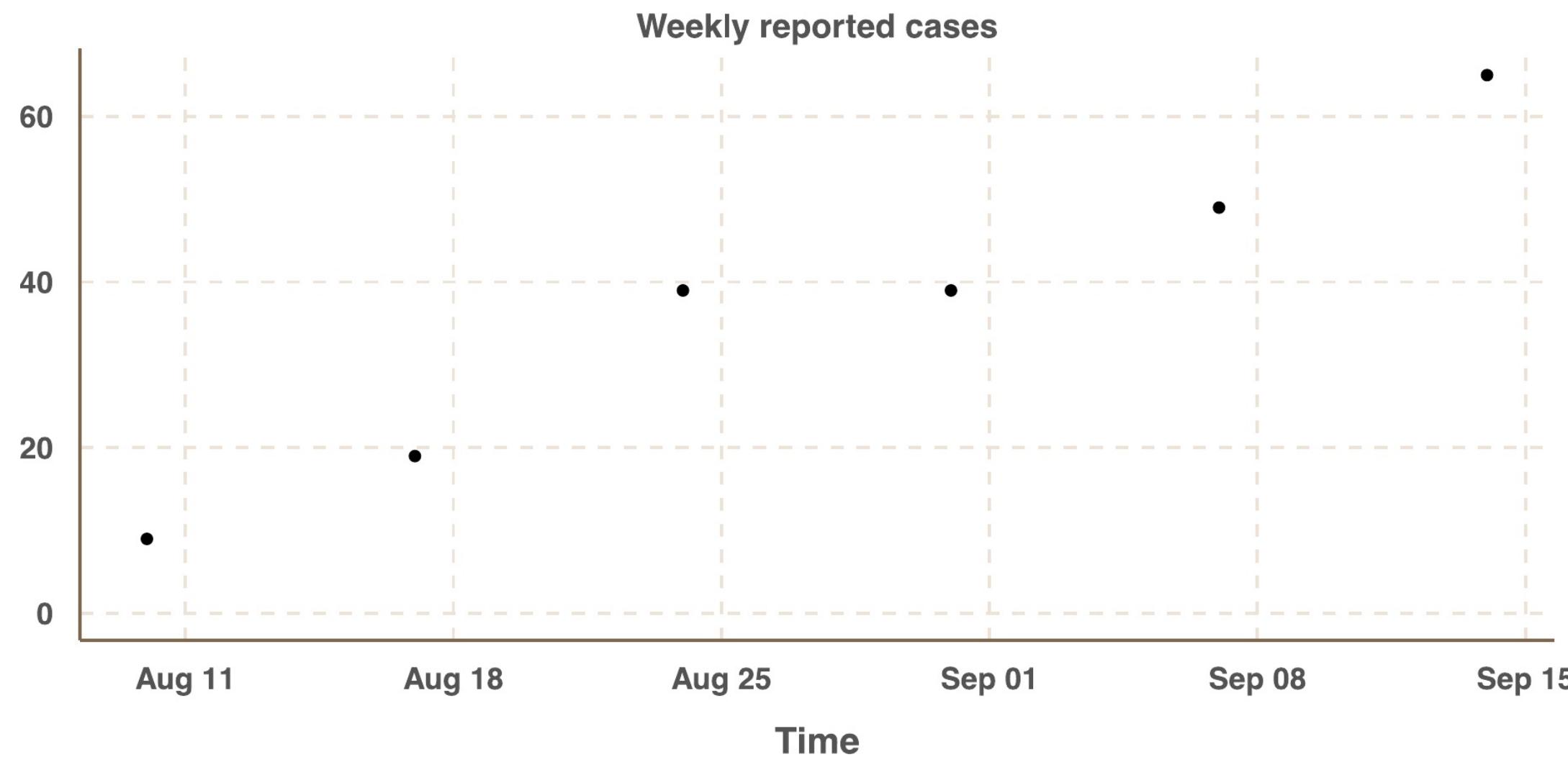
- Method for **filtering** trajectories consistent with data
- Highly parallelisable

Andrieu (2010), Murray (2013)

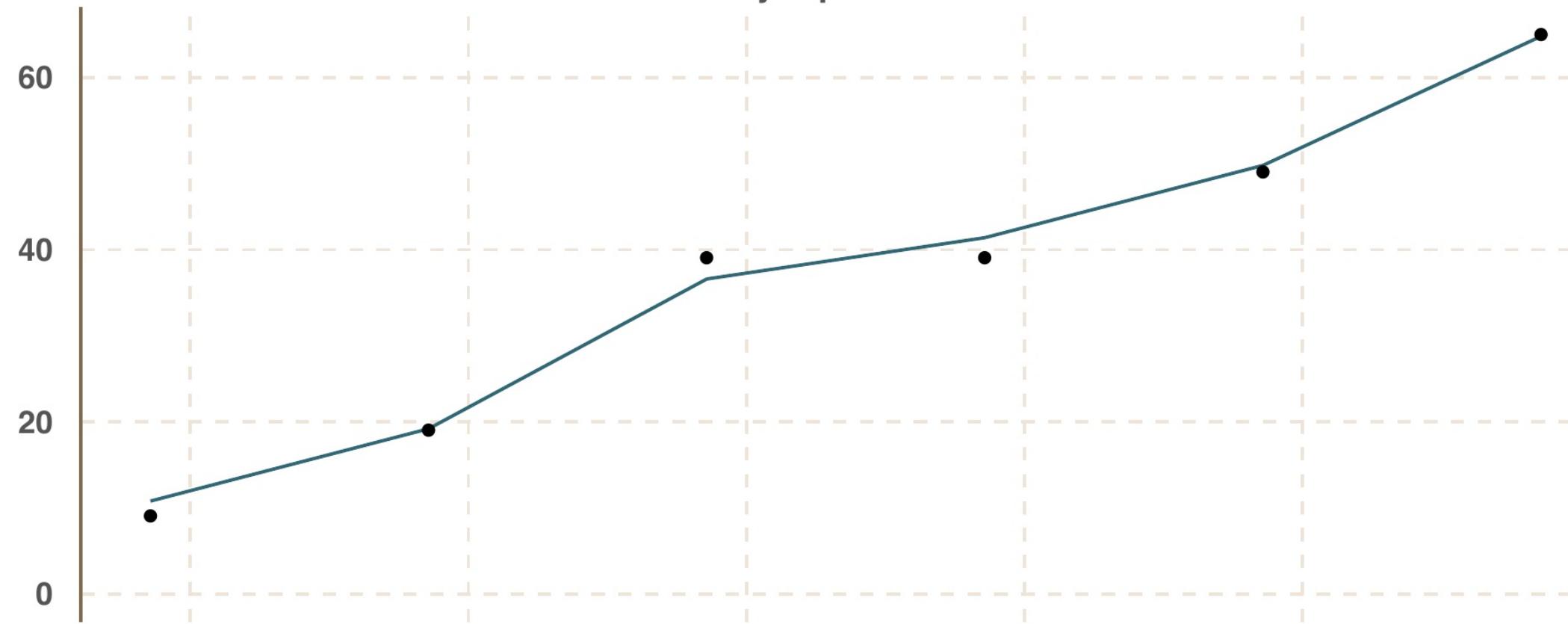
Forecasting the Ebola epidemic

"We were losing ourselves in details [...] all we needed to know is, are the number of cases rising, falling or levelling off?"

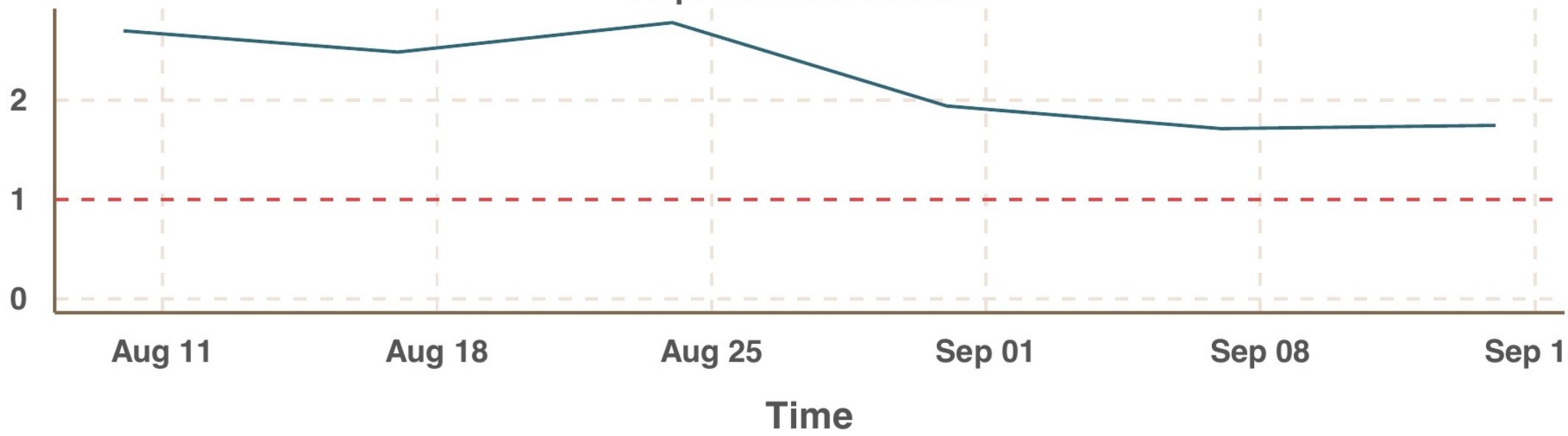
Hans Rosling



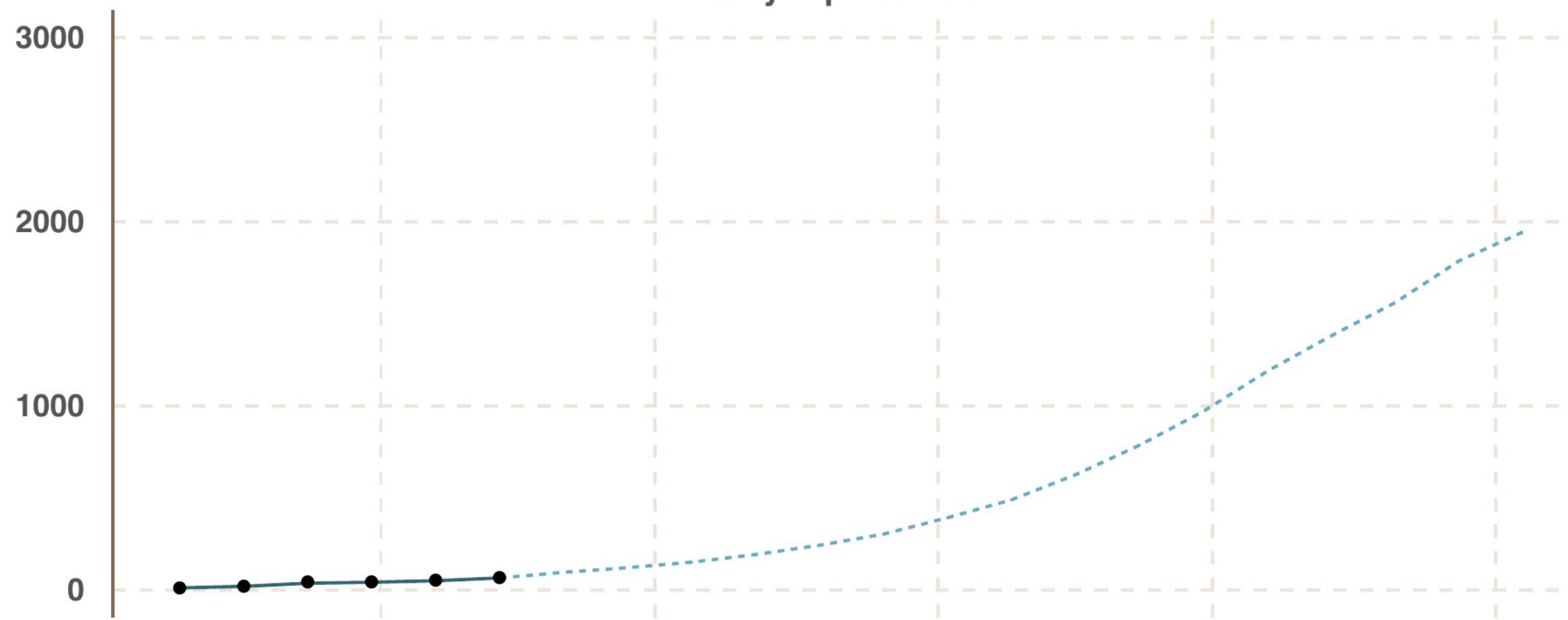
Weekly reported cases



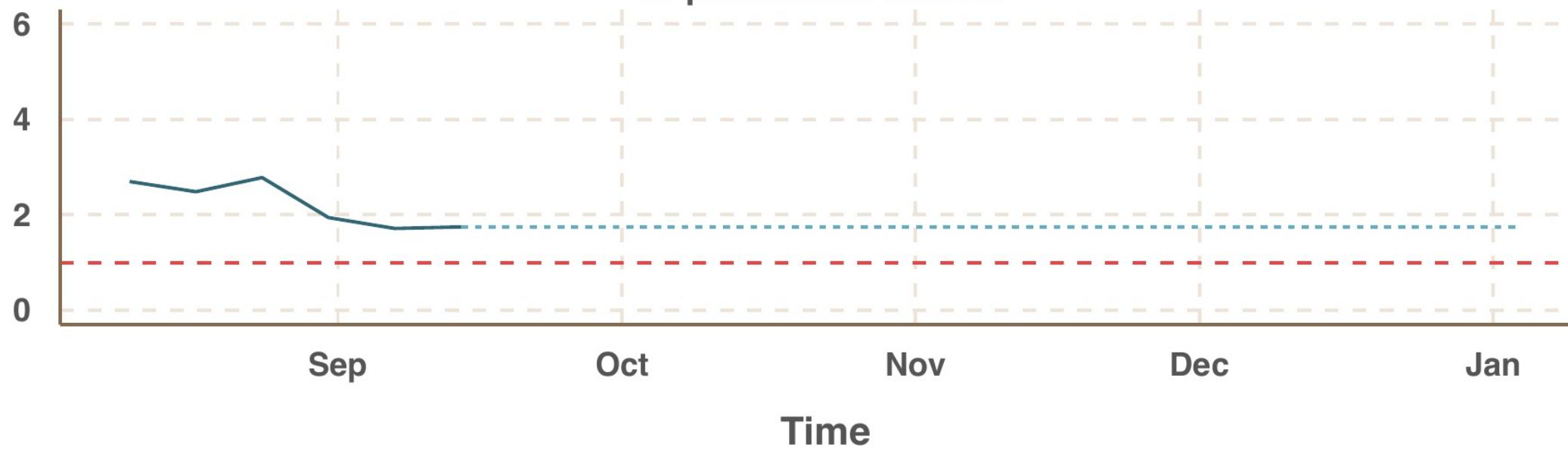
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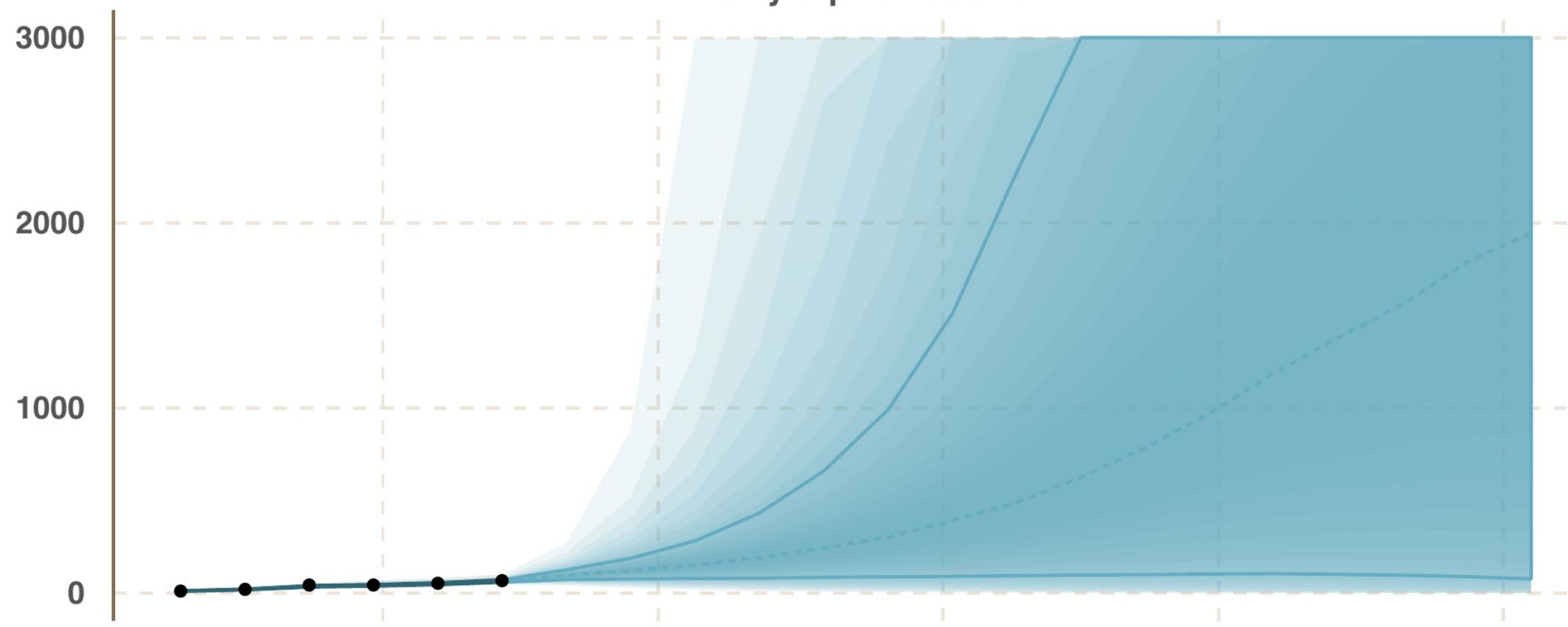
Weekly reported cases



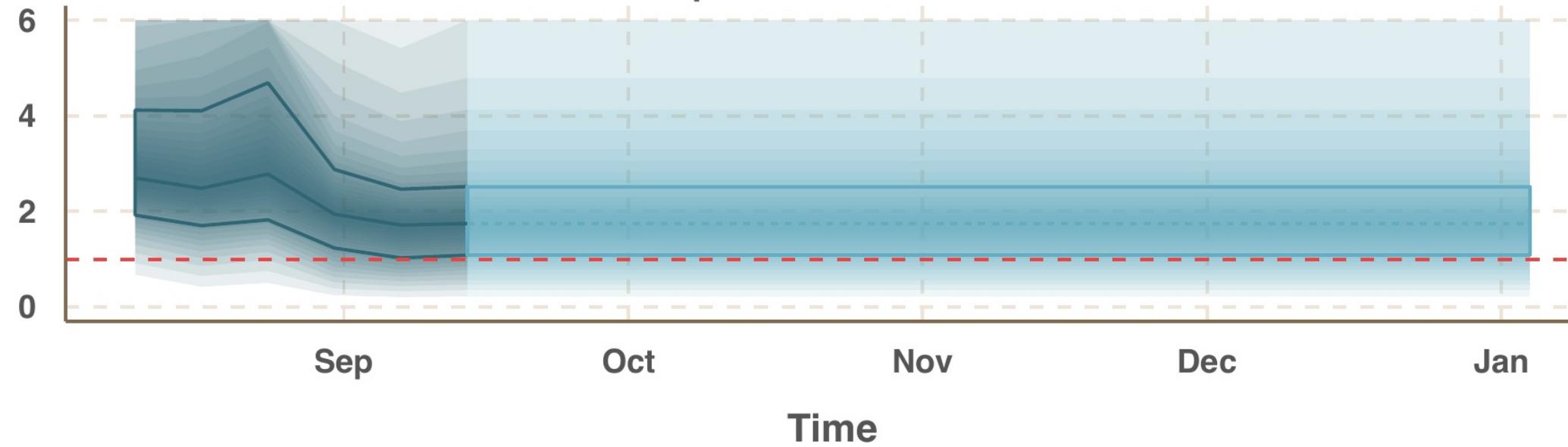
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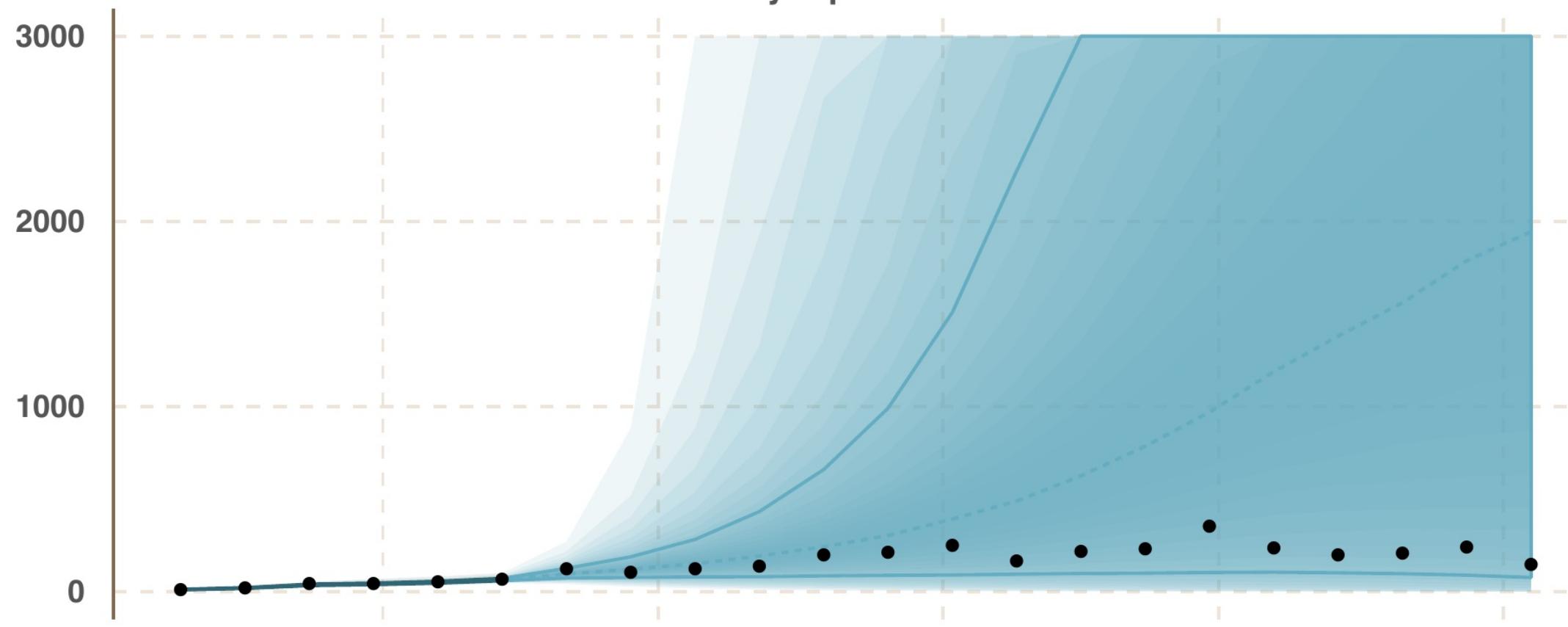
Weekly reported cases



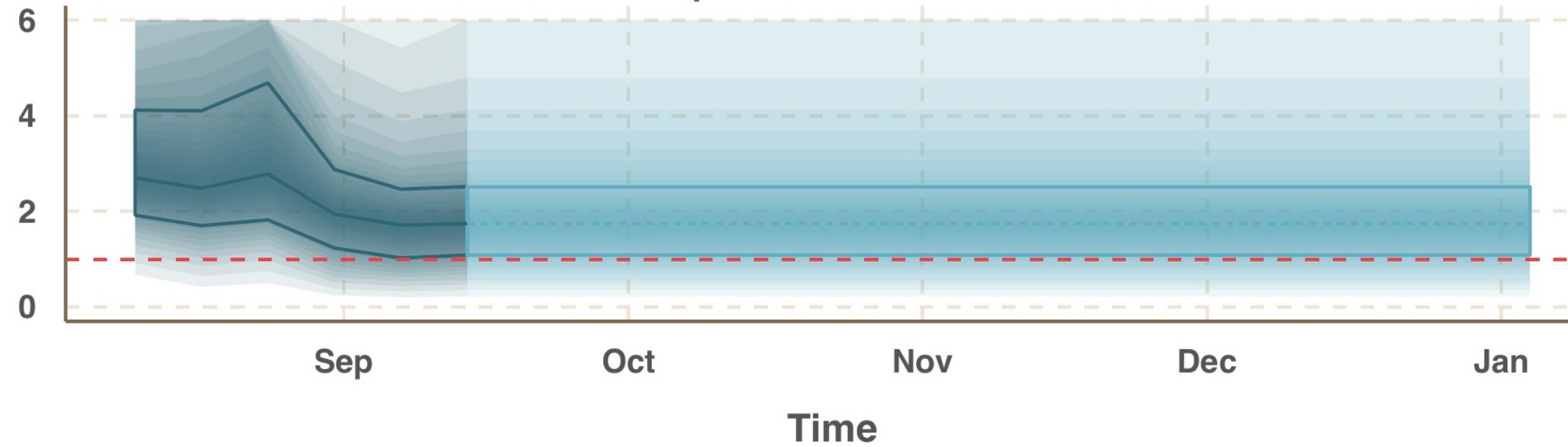
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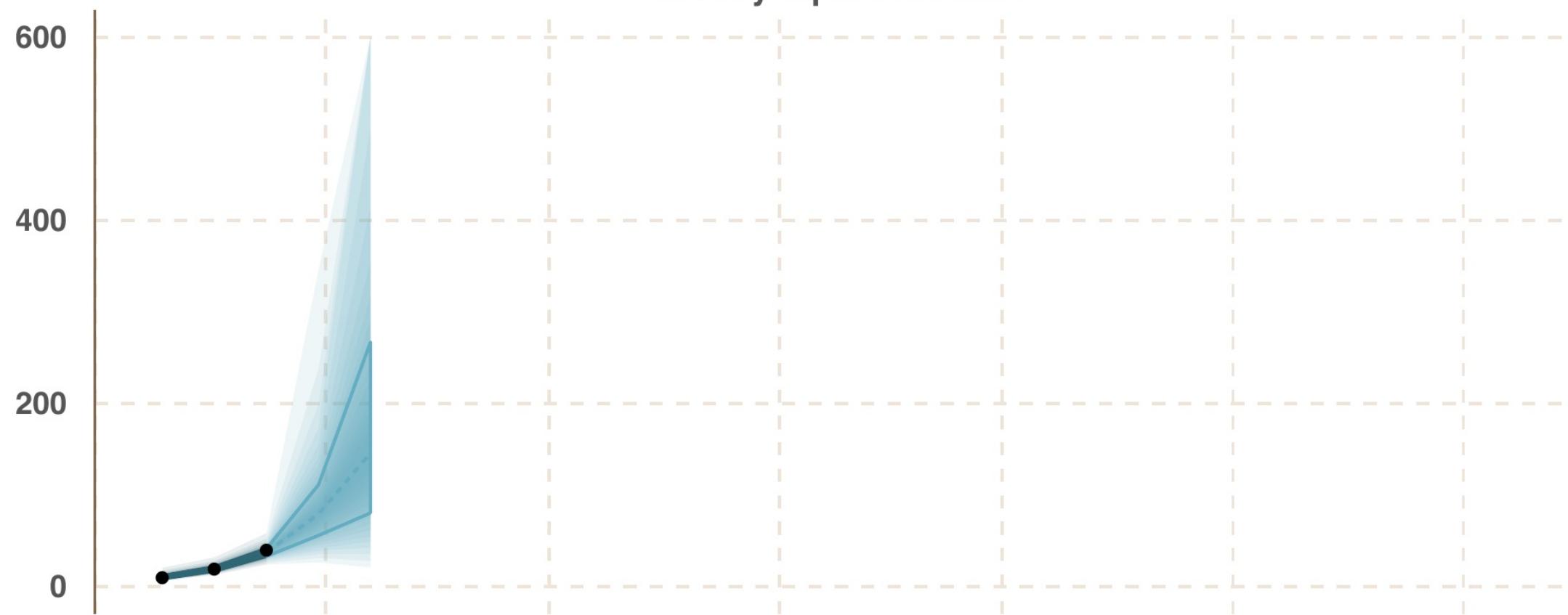
Weekly reported cases



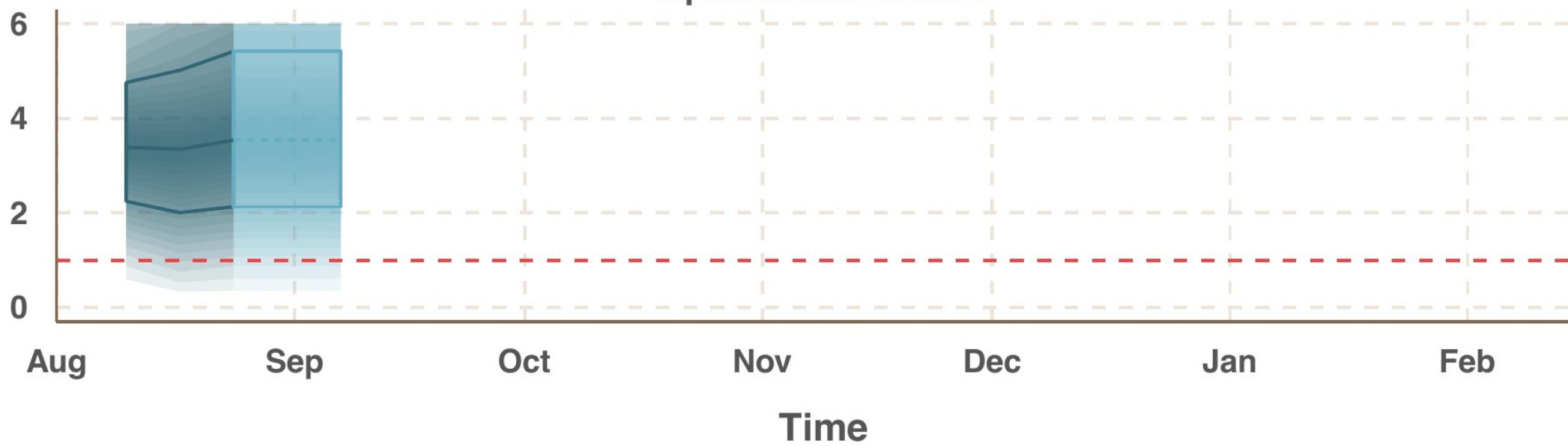
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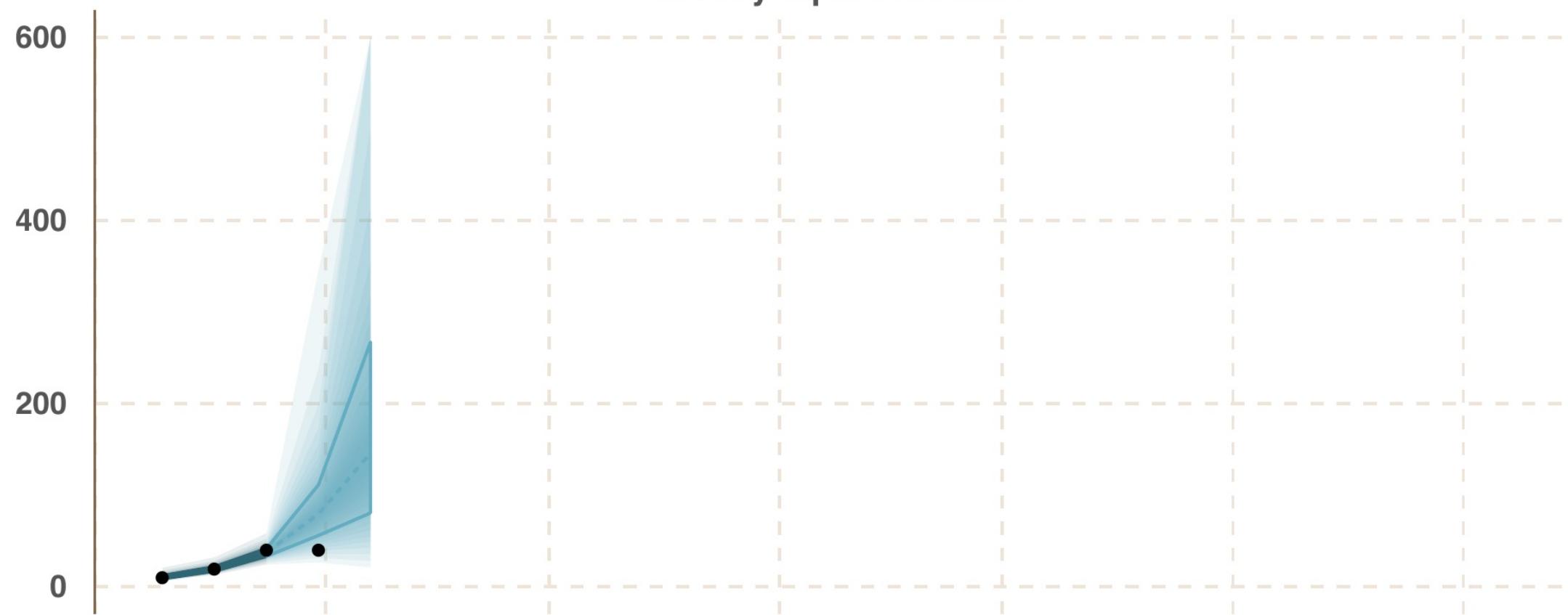
Weekly reported cases



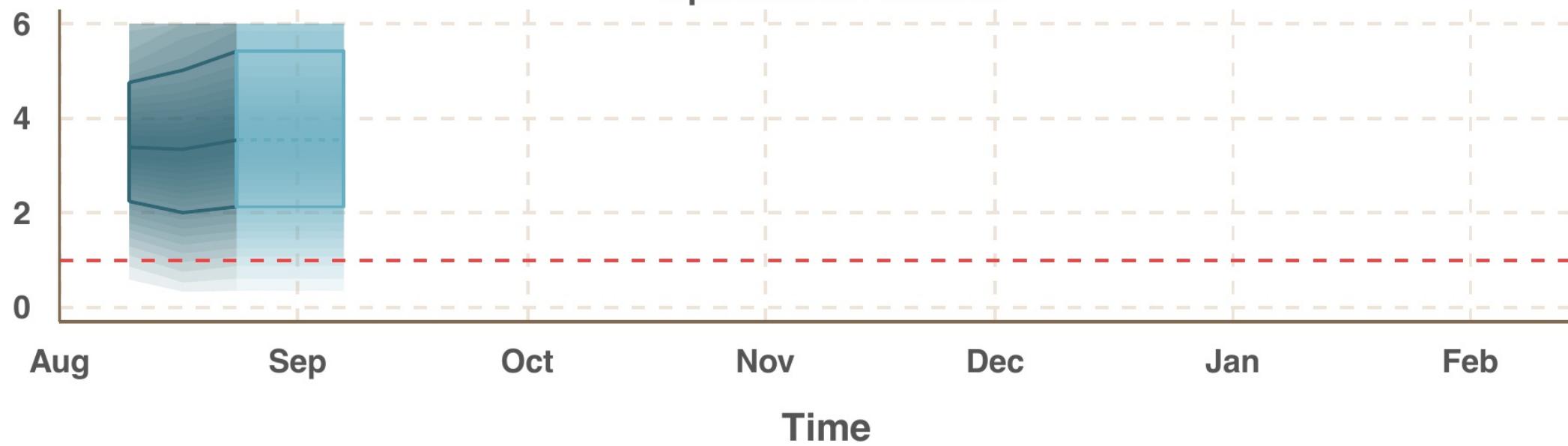
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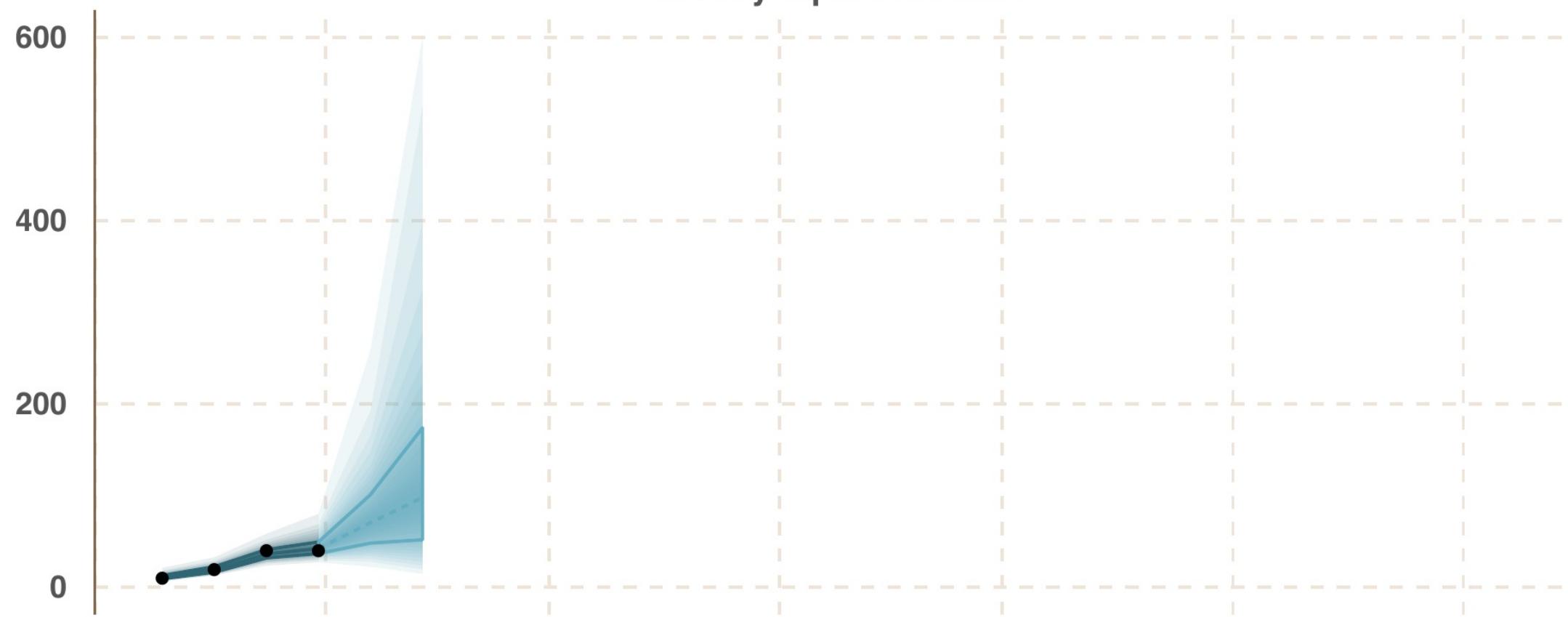
Weekly reported cases



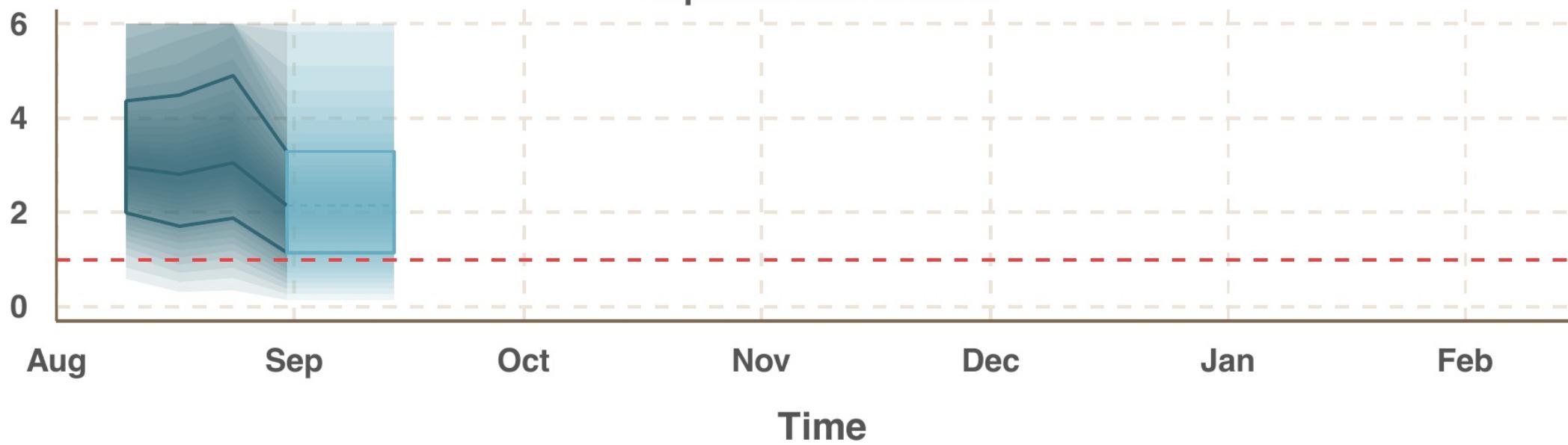
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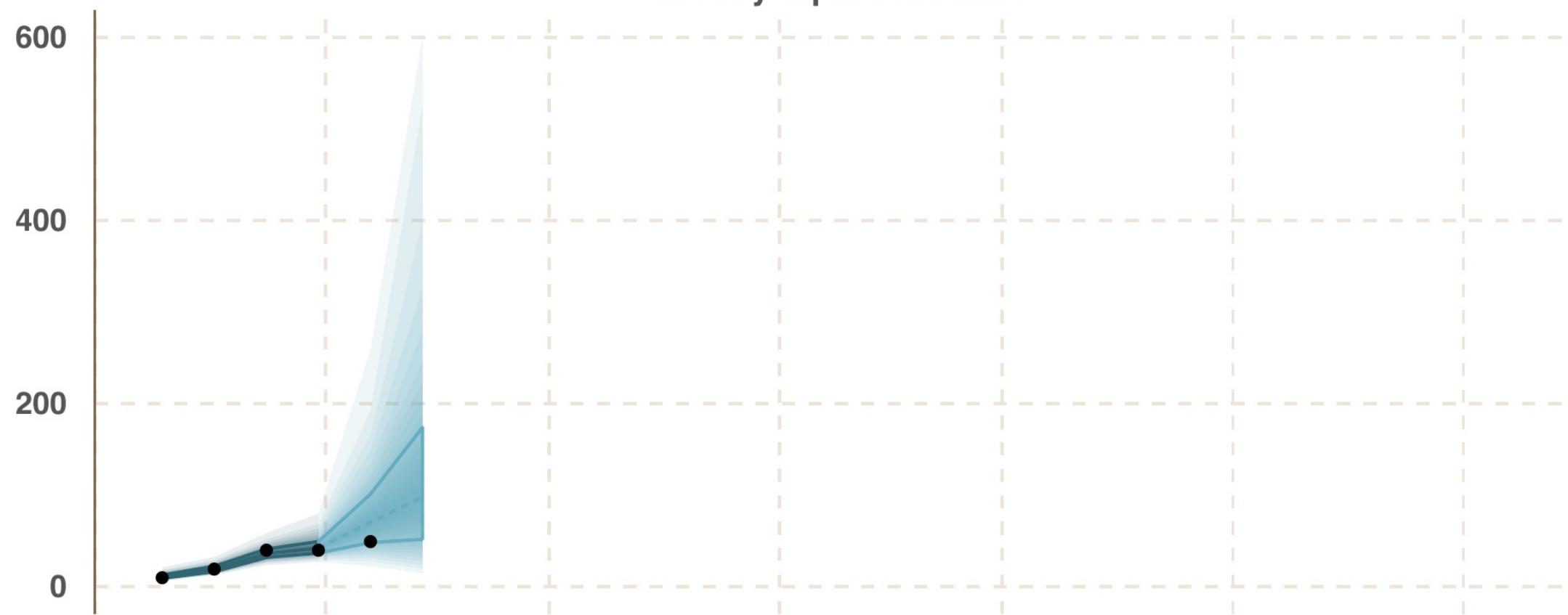
Weekly reported cases



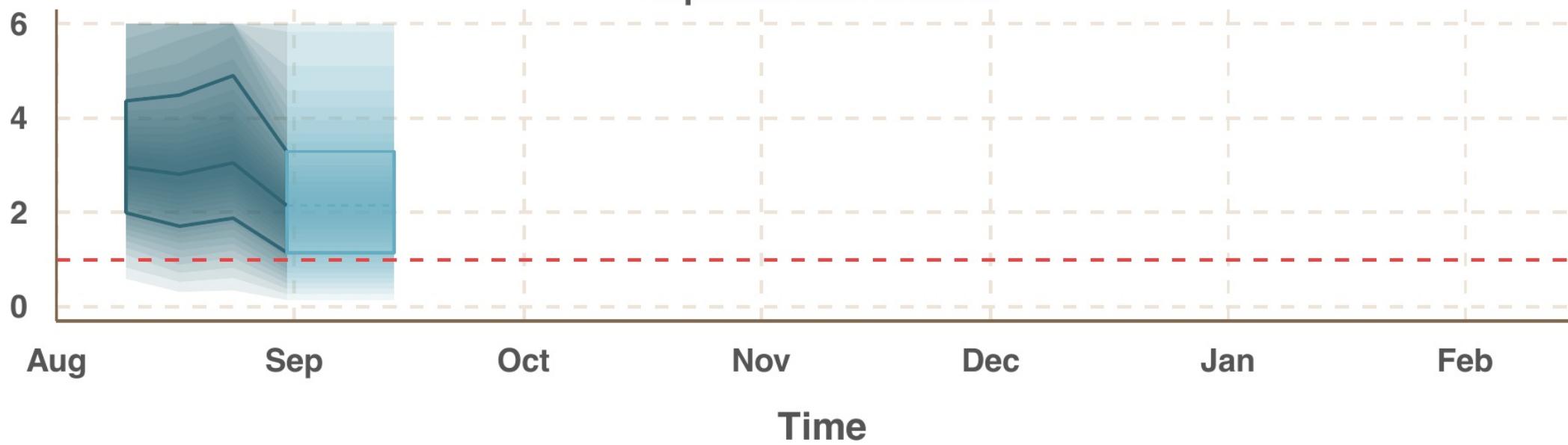
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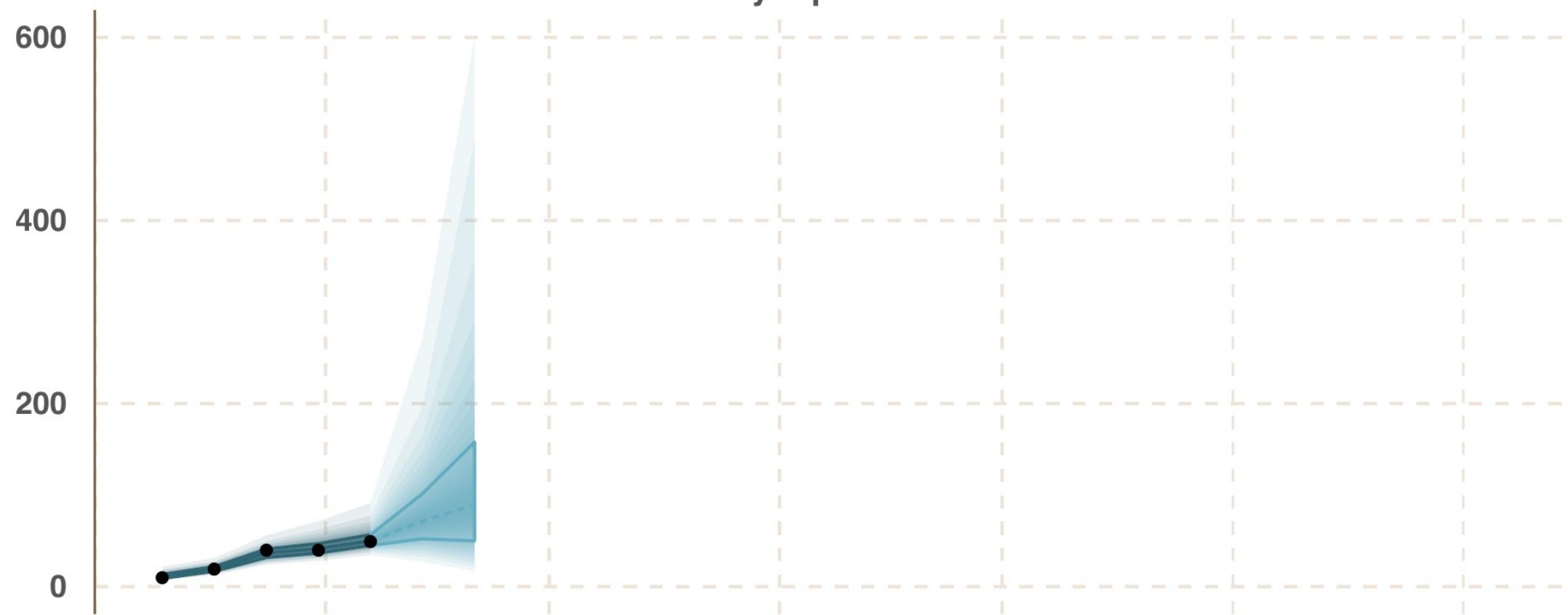
Weekly reported cases



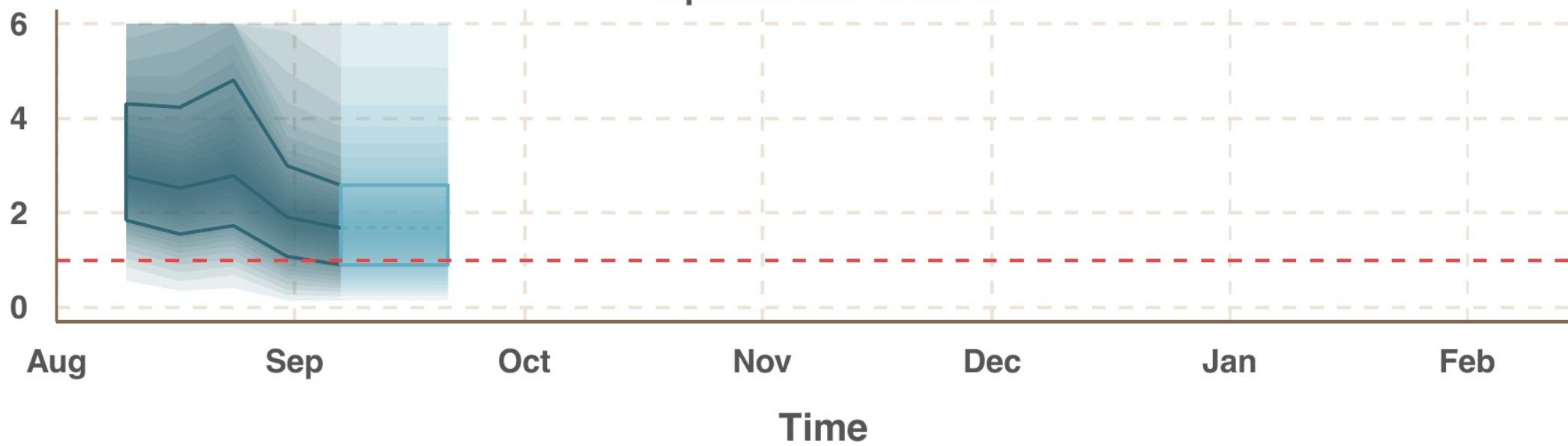
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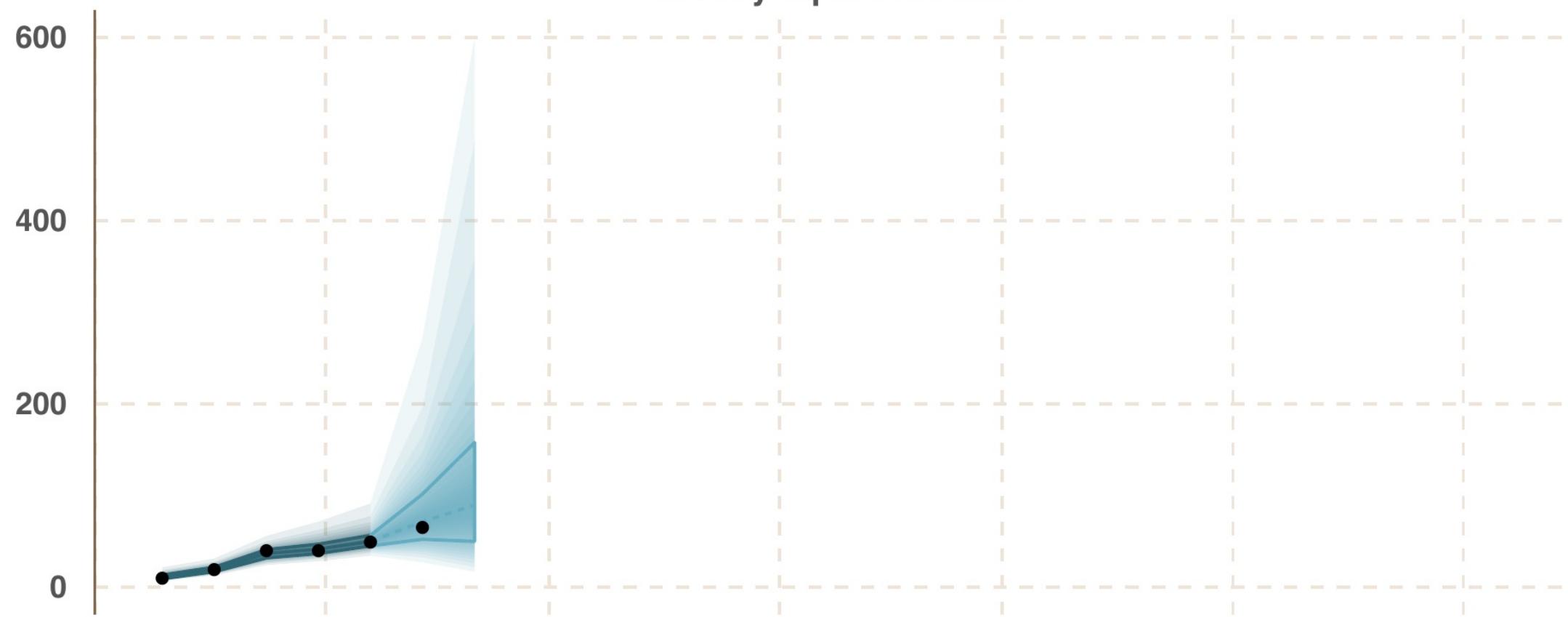
Weekly reported cases



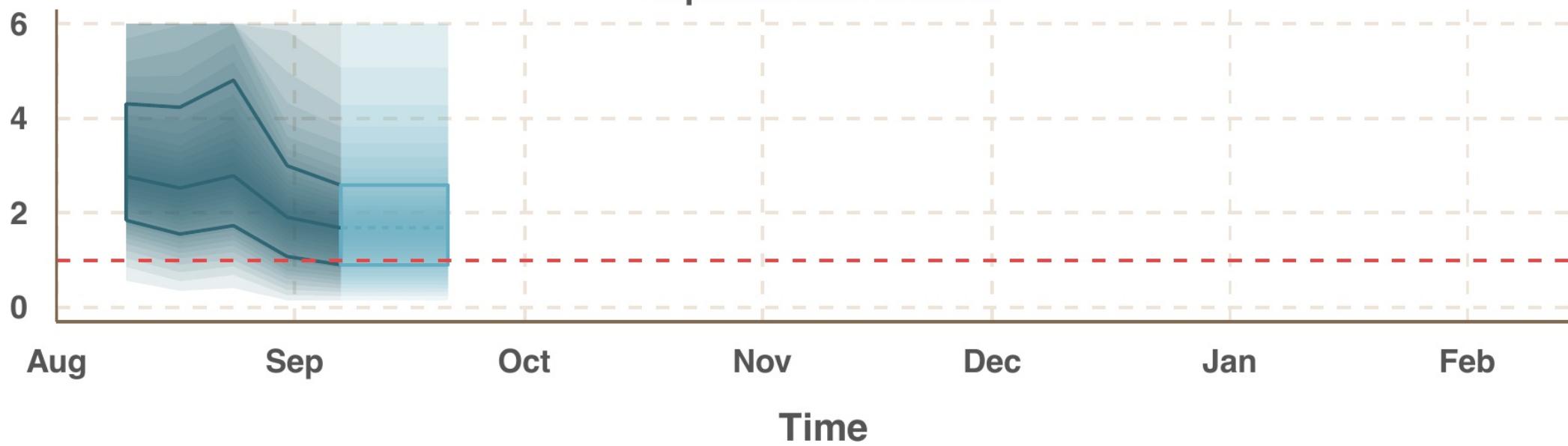
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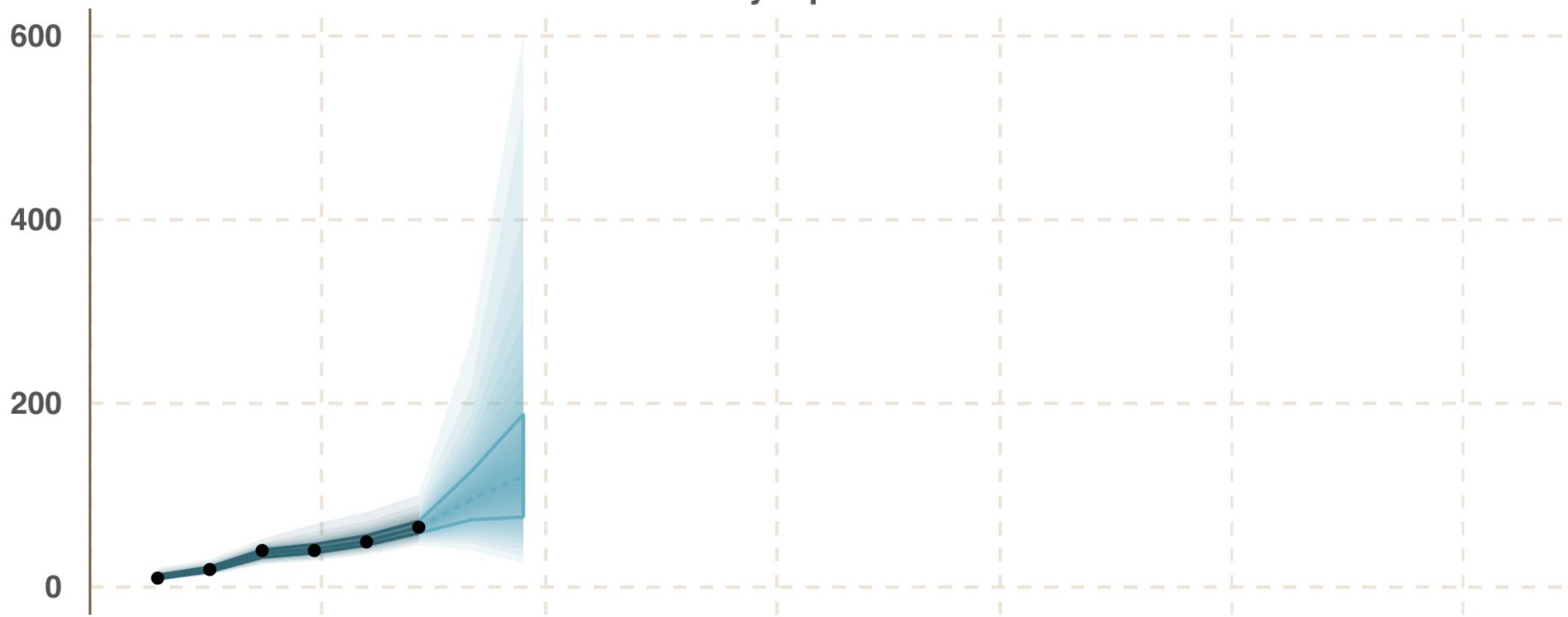
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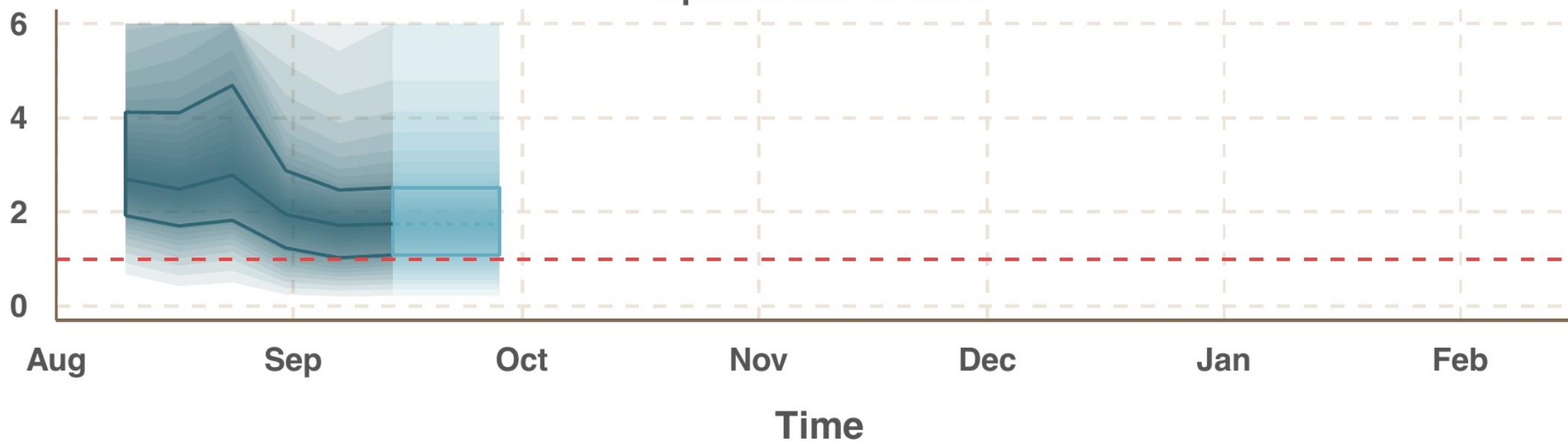
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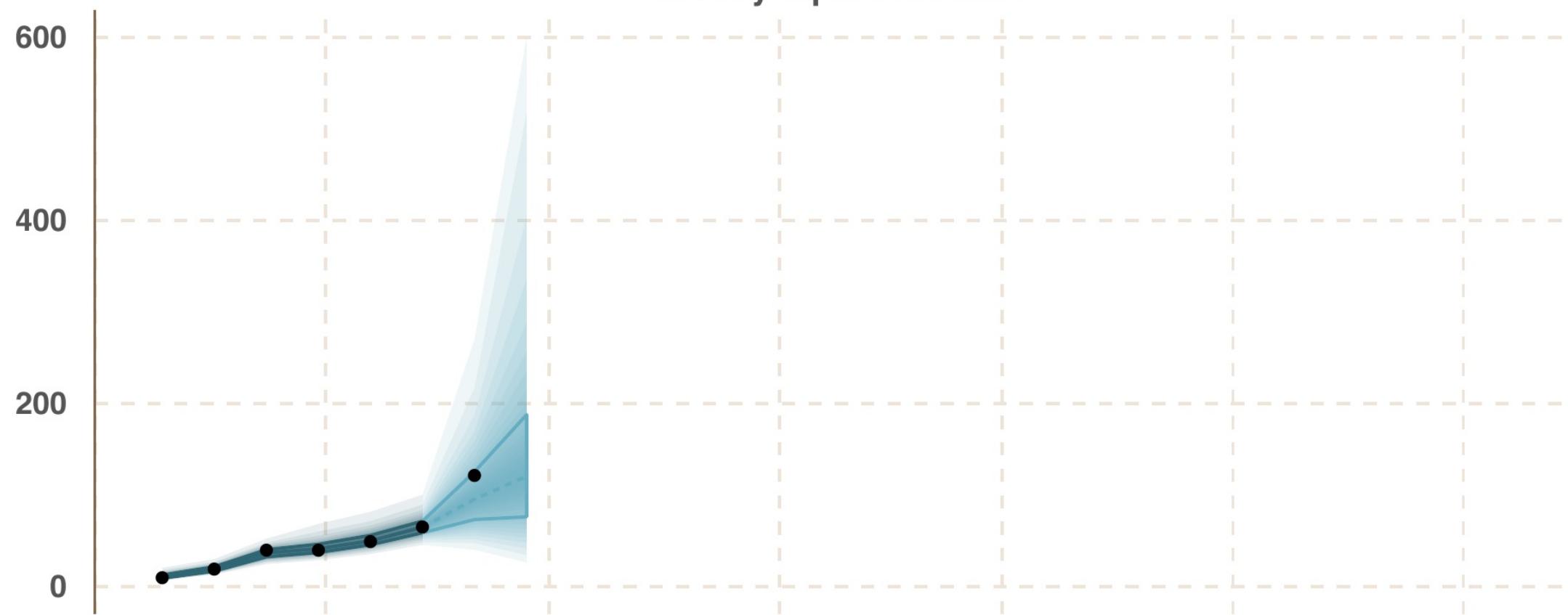
Weekly reported cases



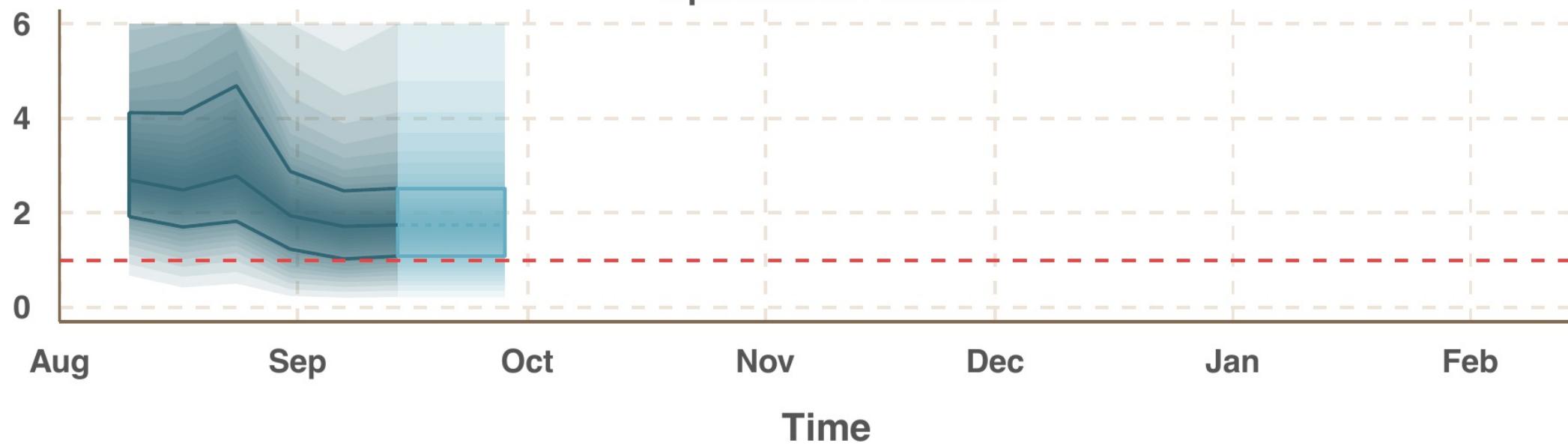
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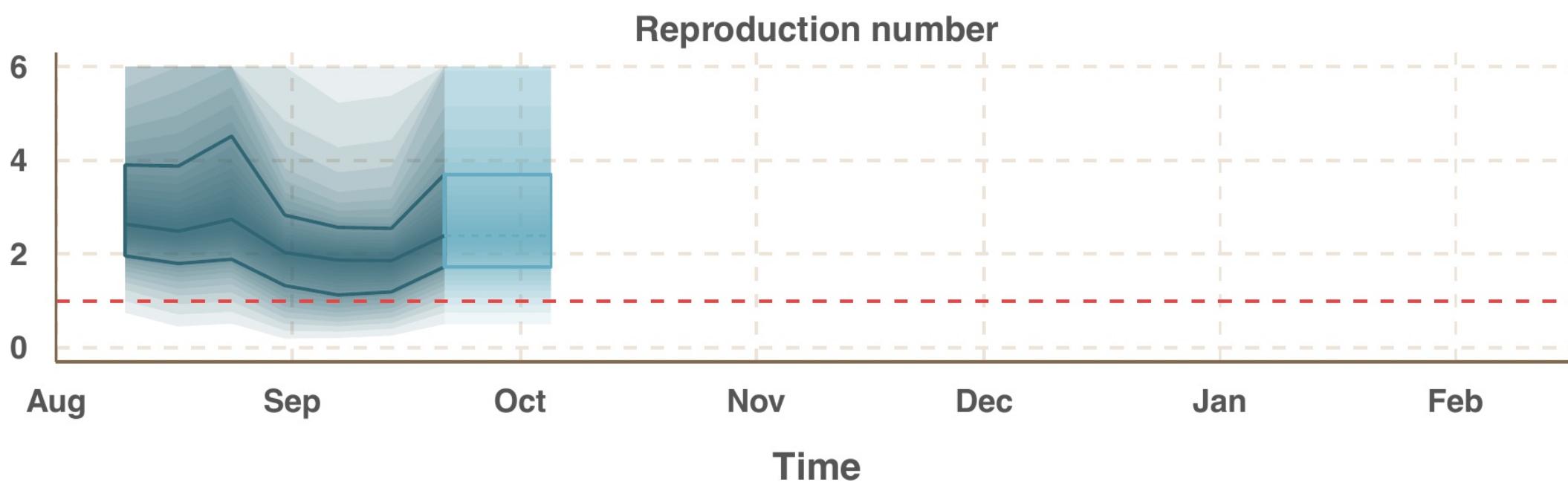
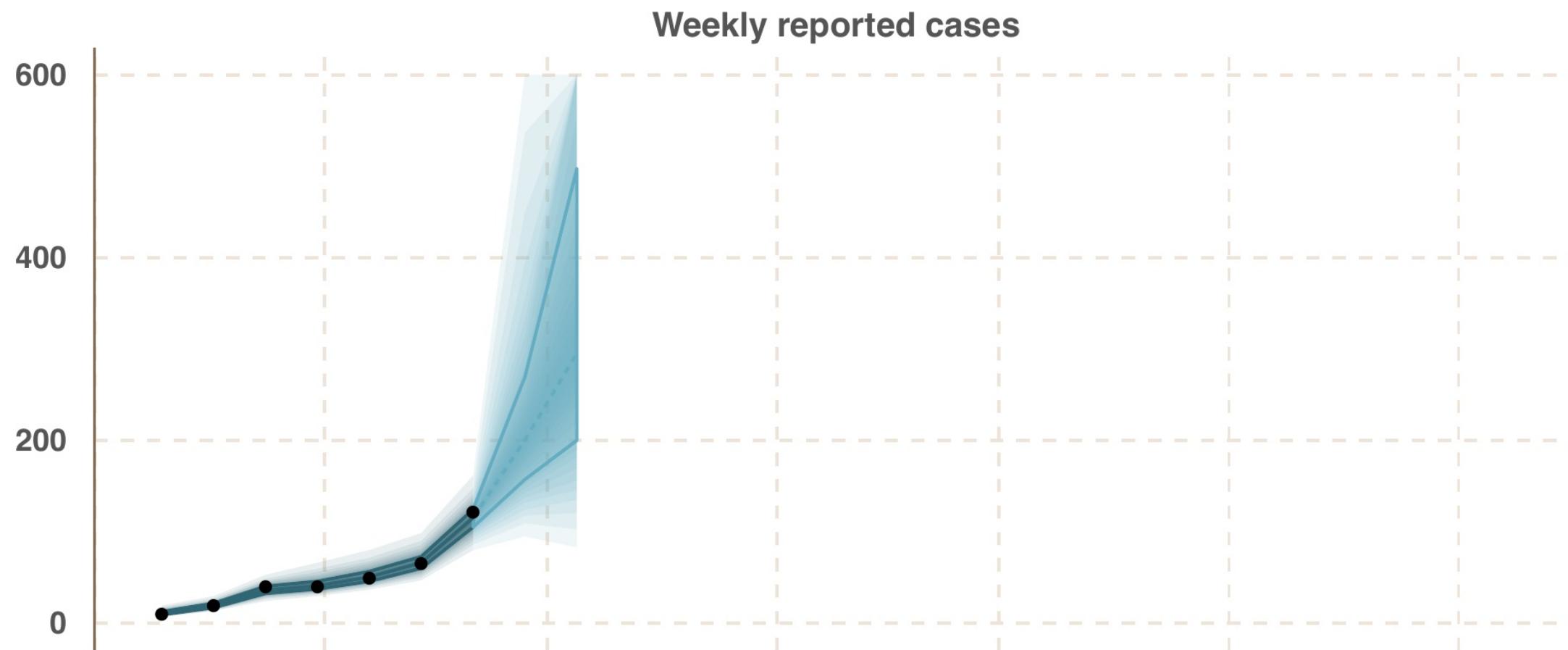


Weekly reported cases

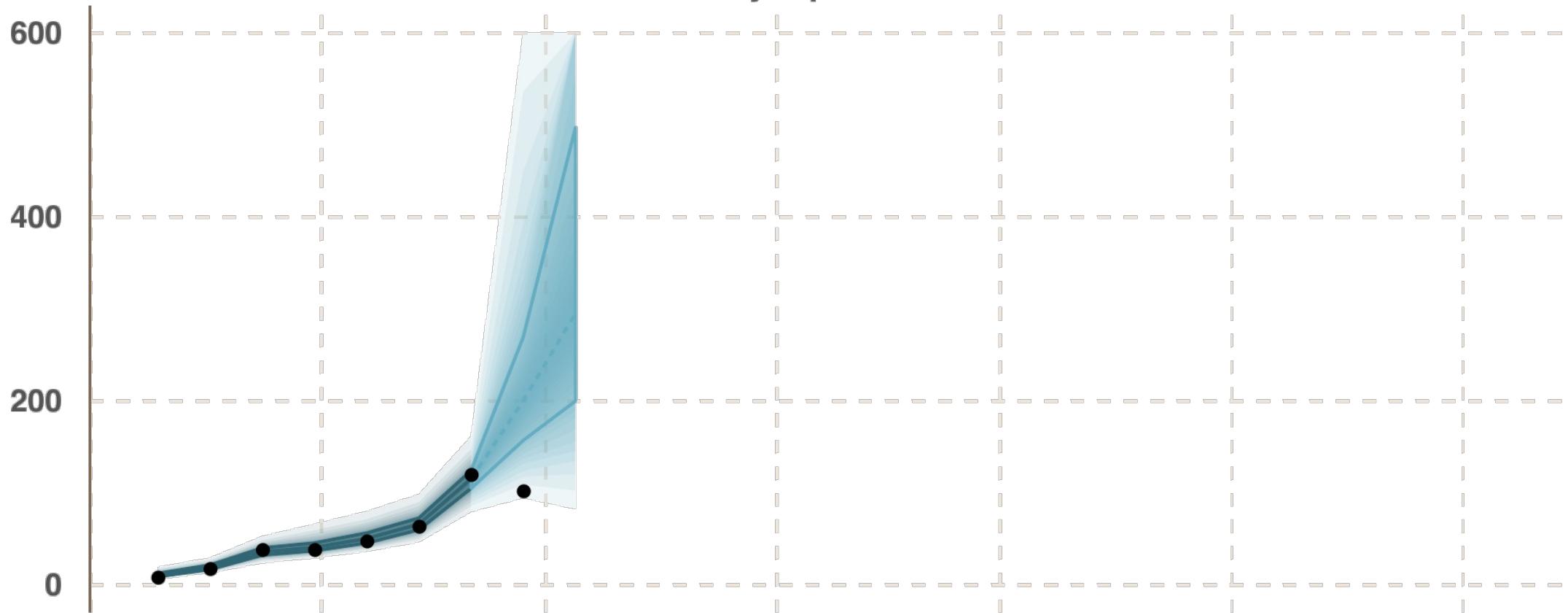


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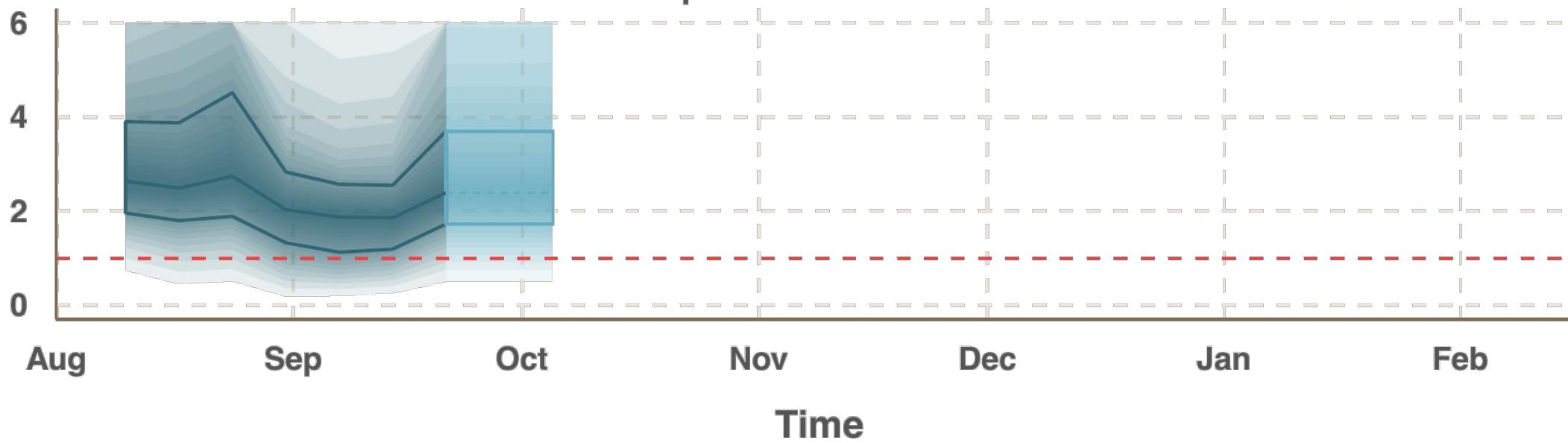




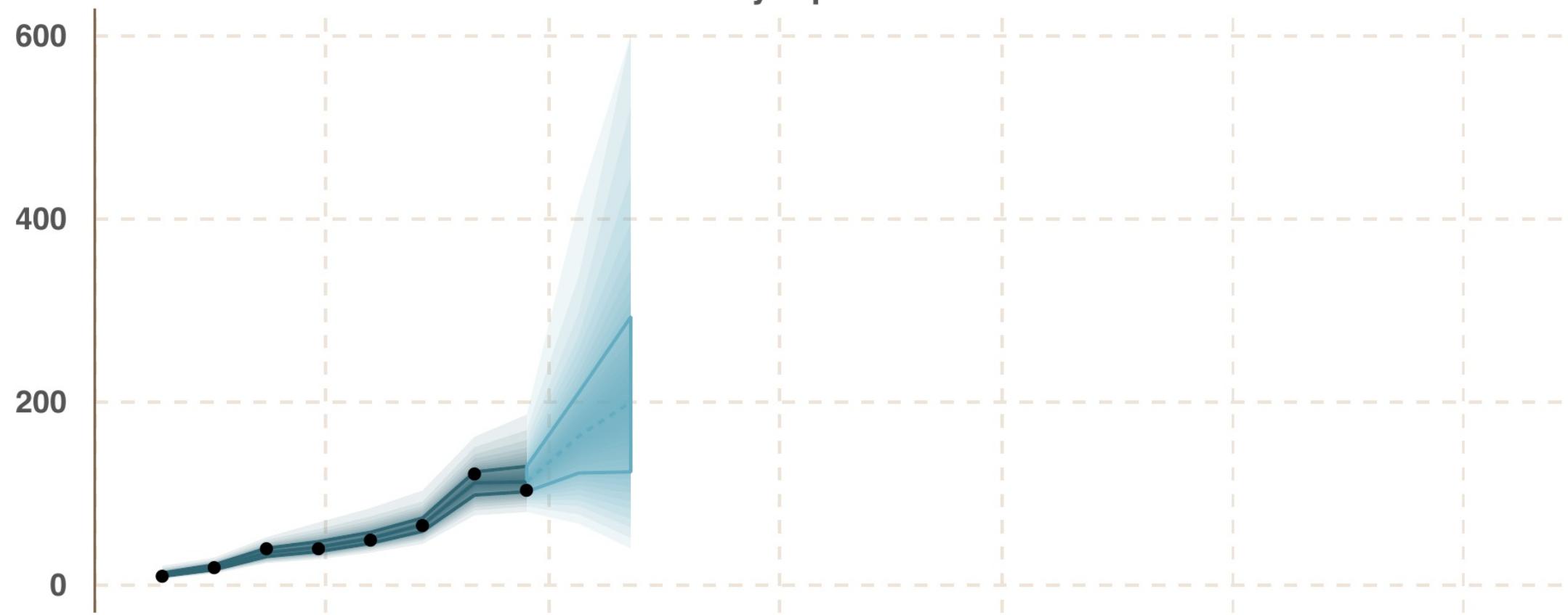
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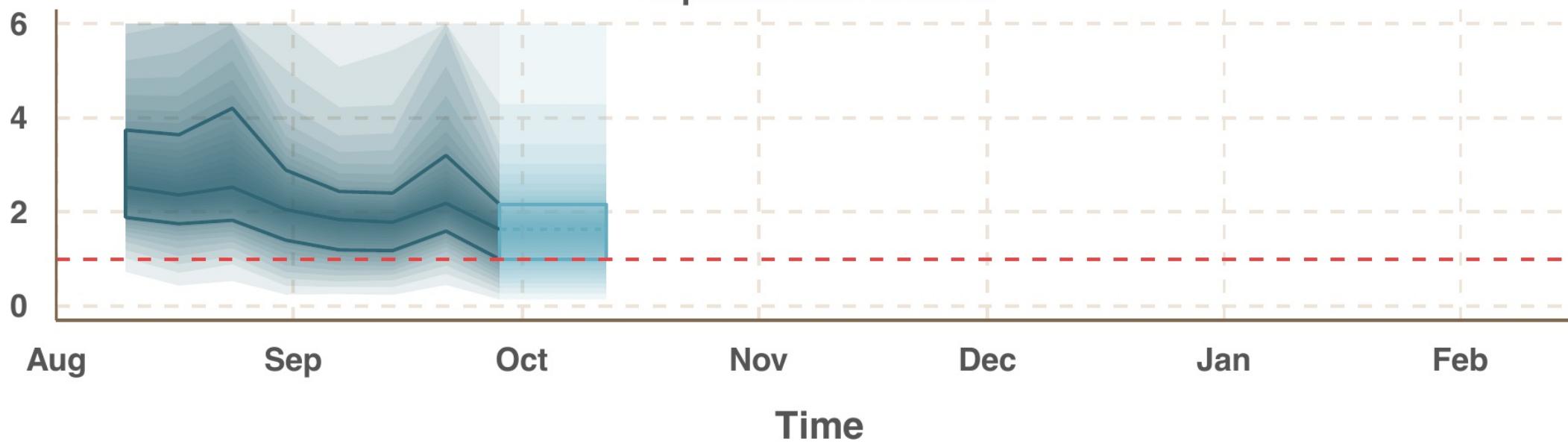
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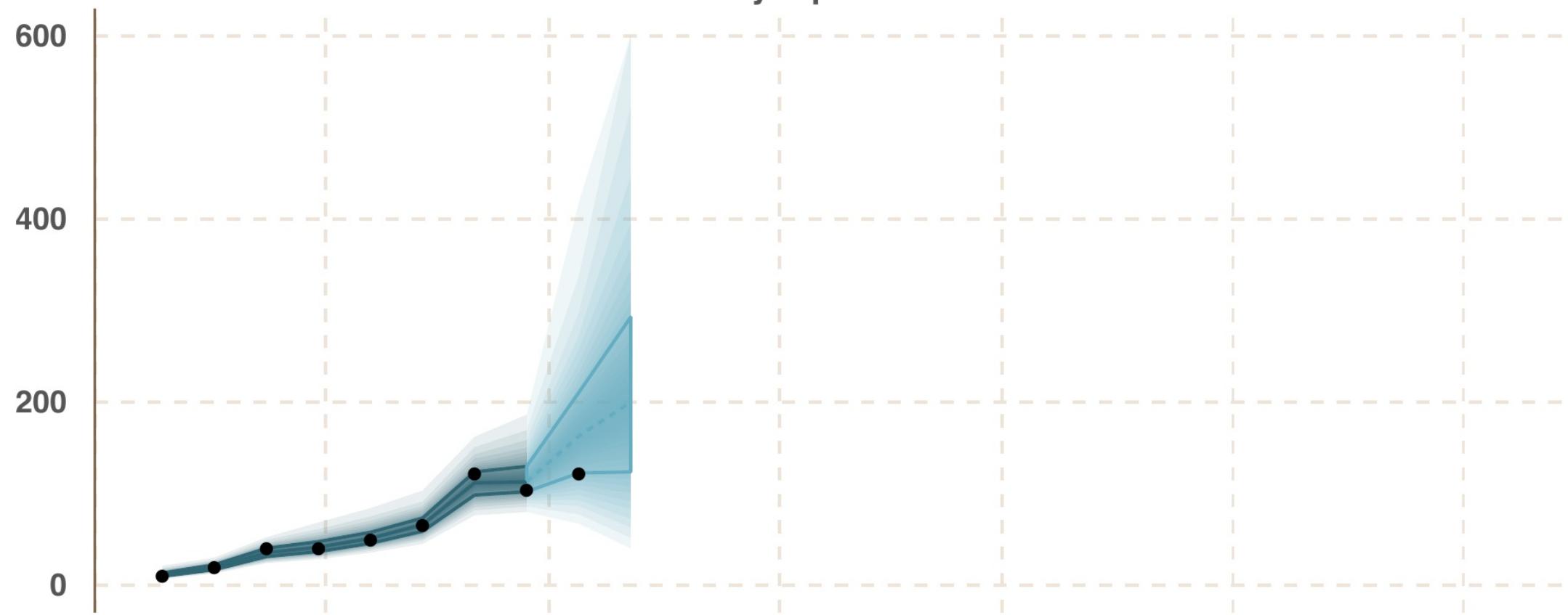
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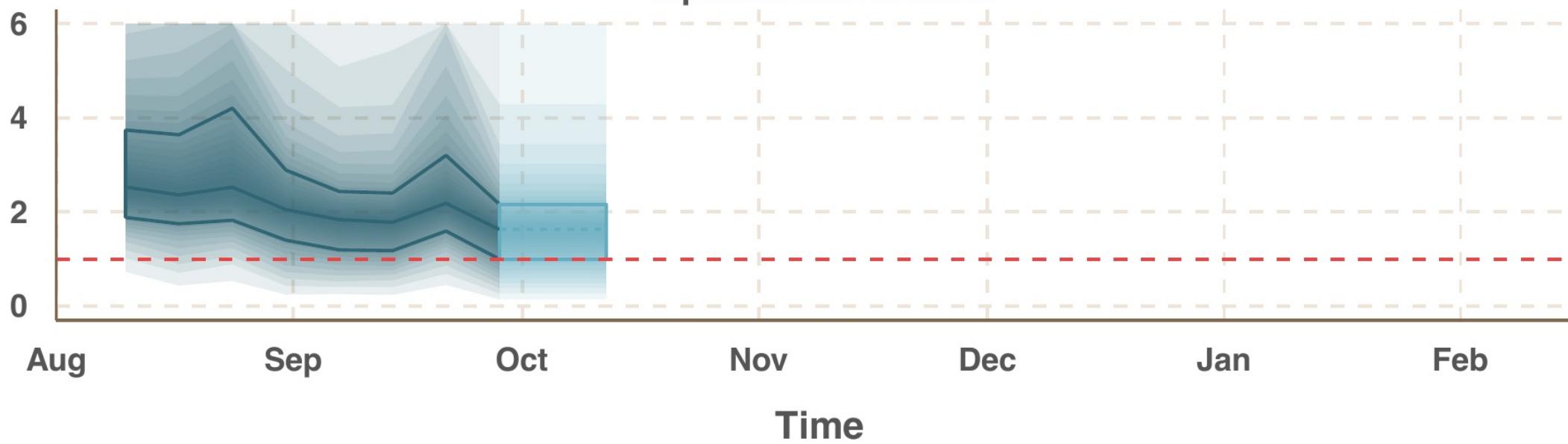
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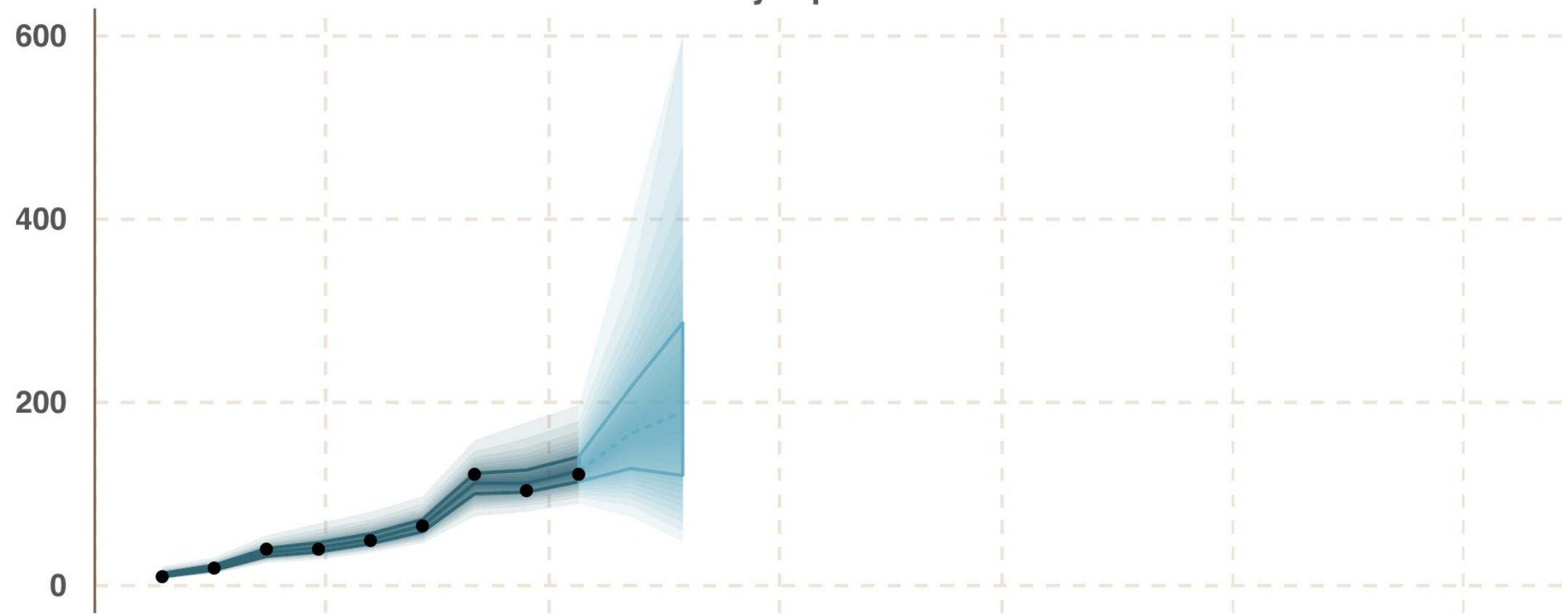
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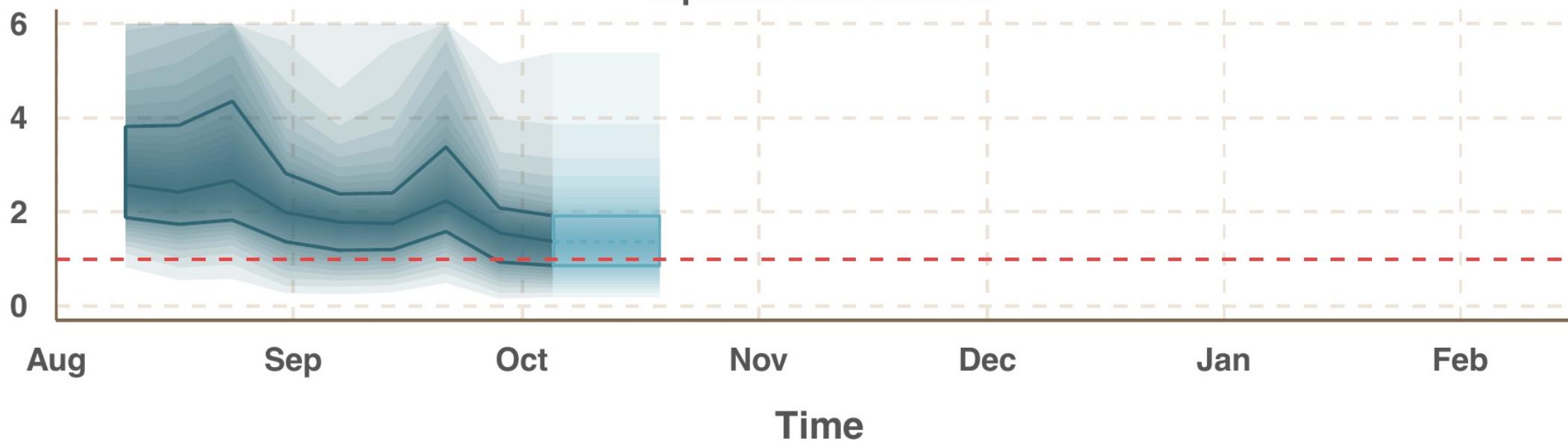
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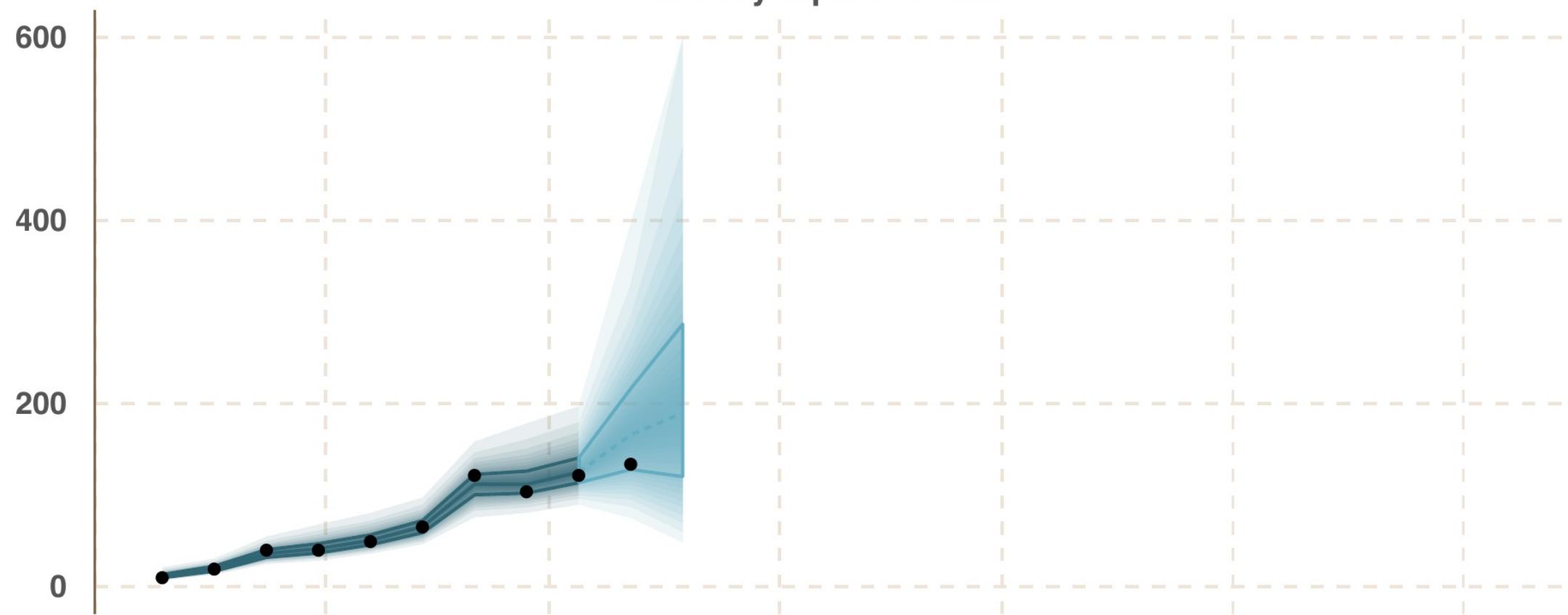
Weekly reported cases



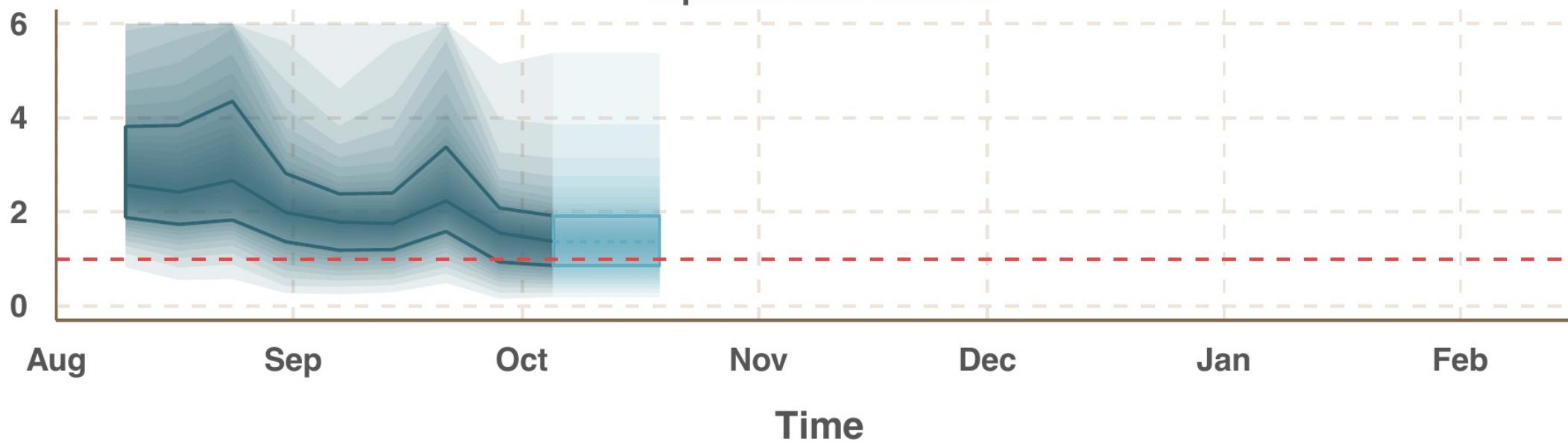
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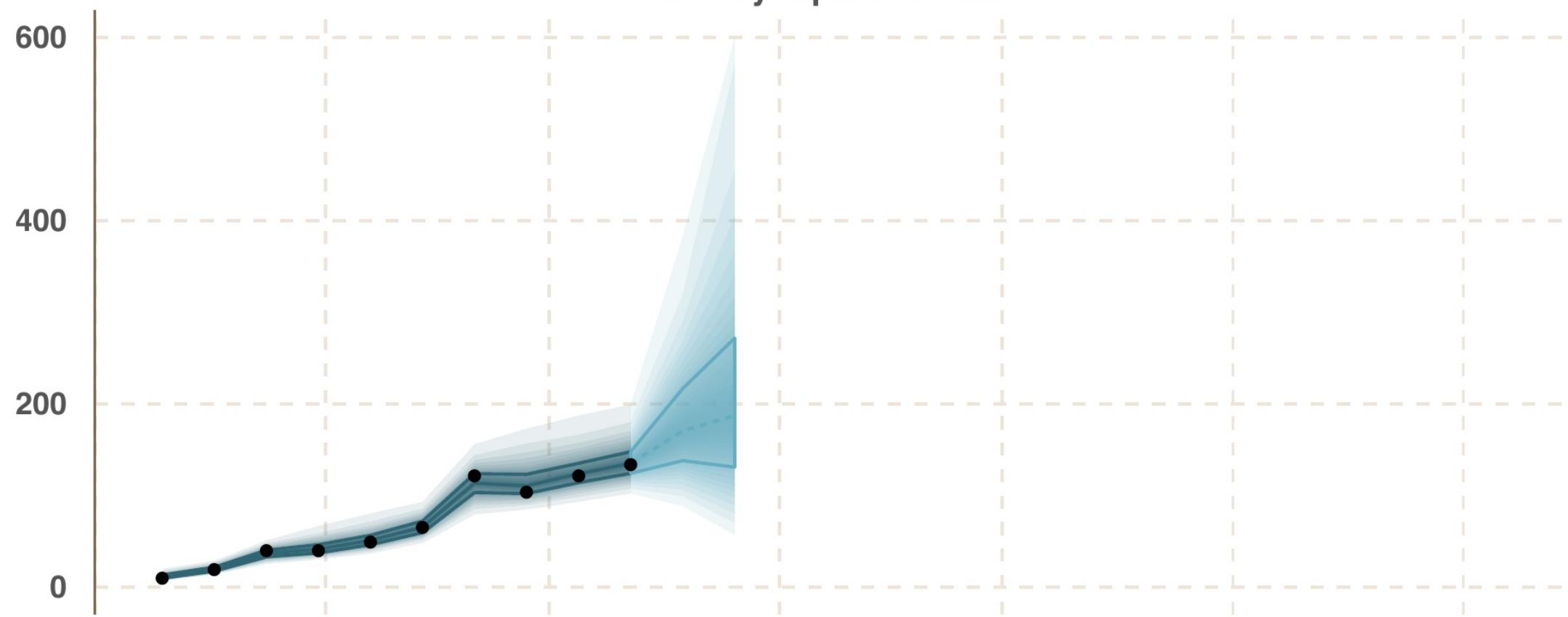
Weekly reported cases



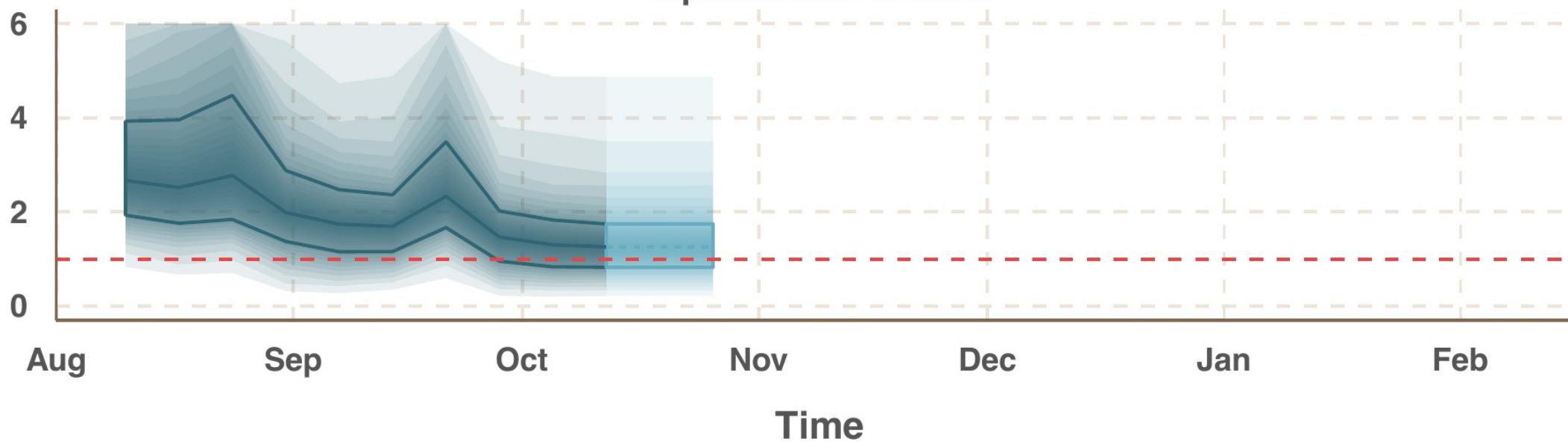
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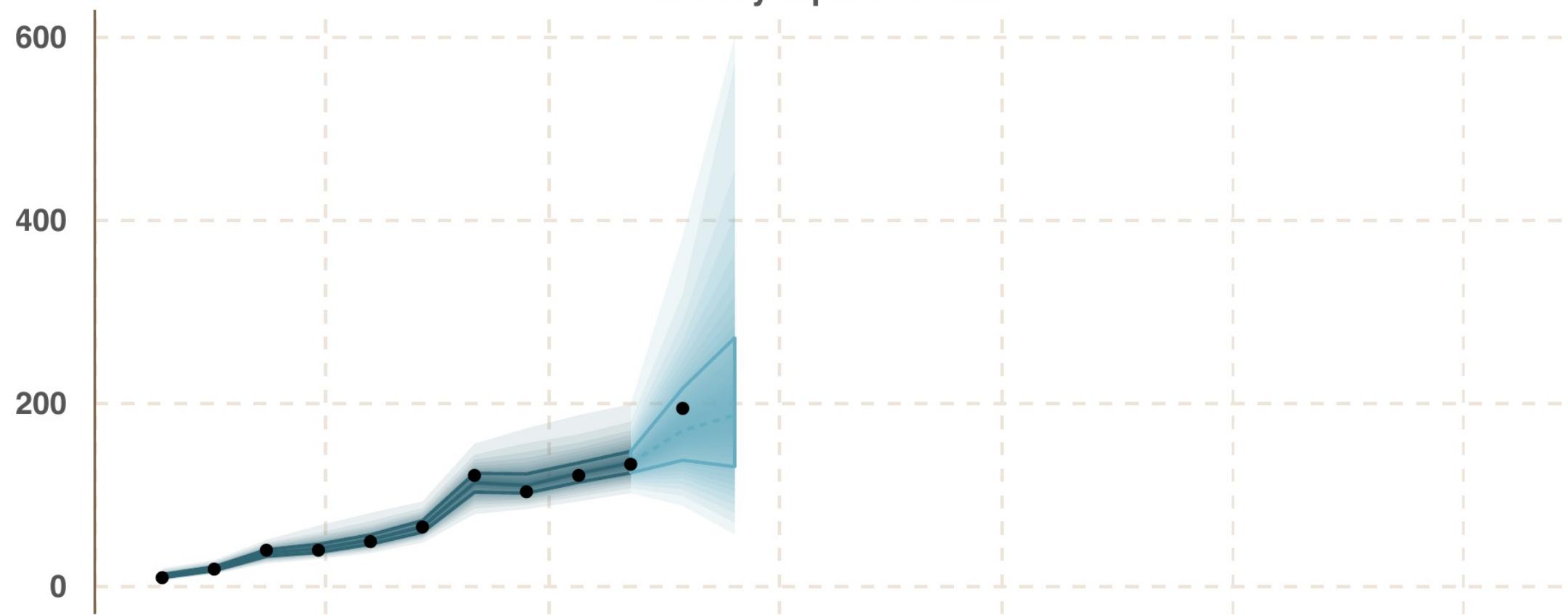
Weekly reported cases



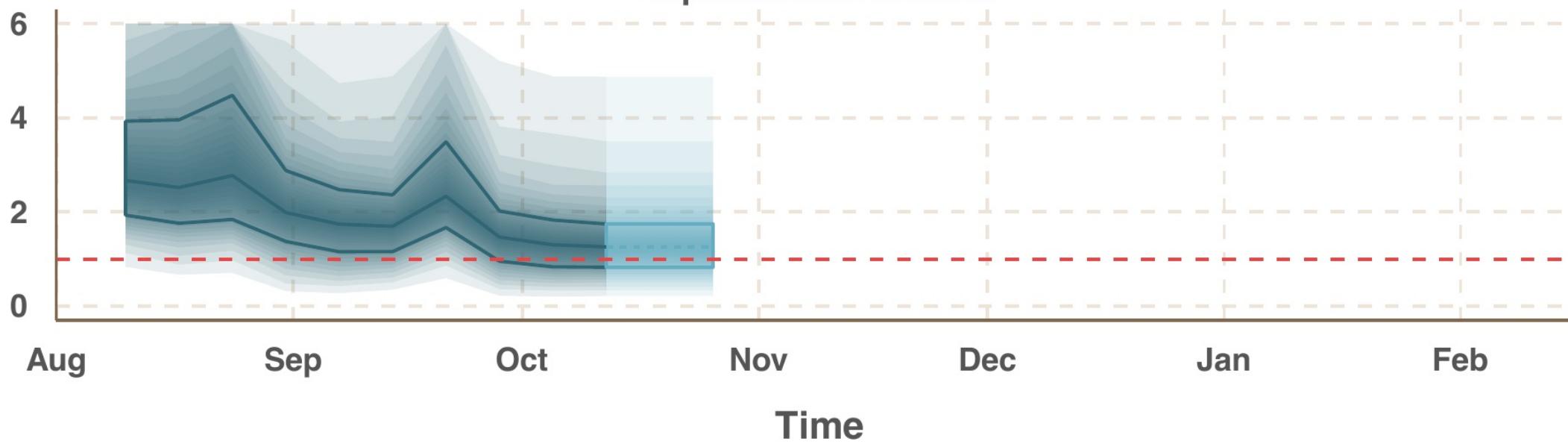
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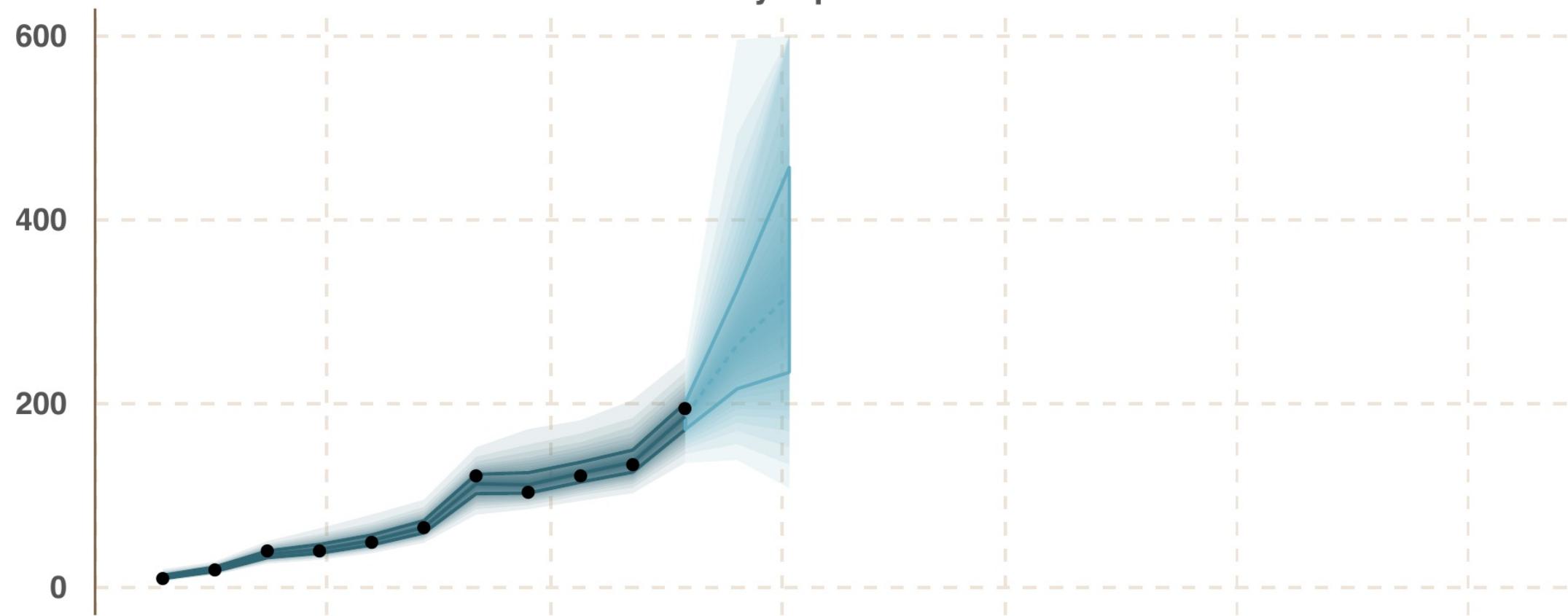
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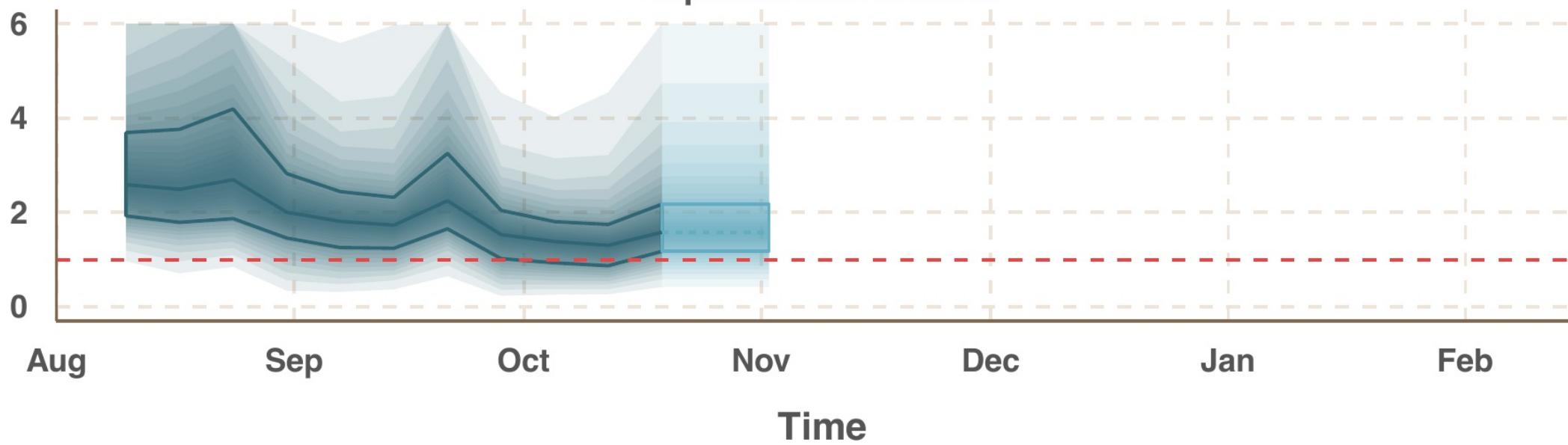
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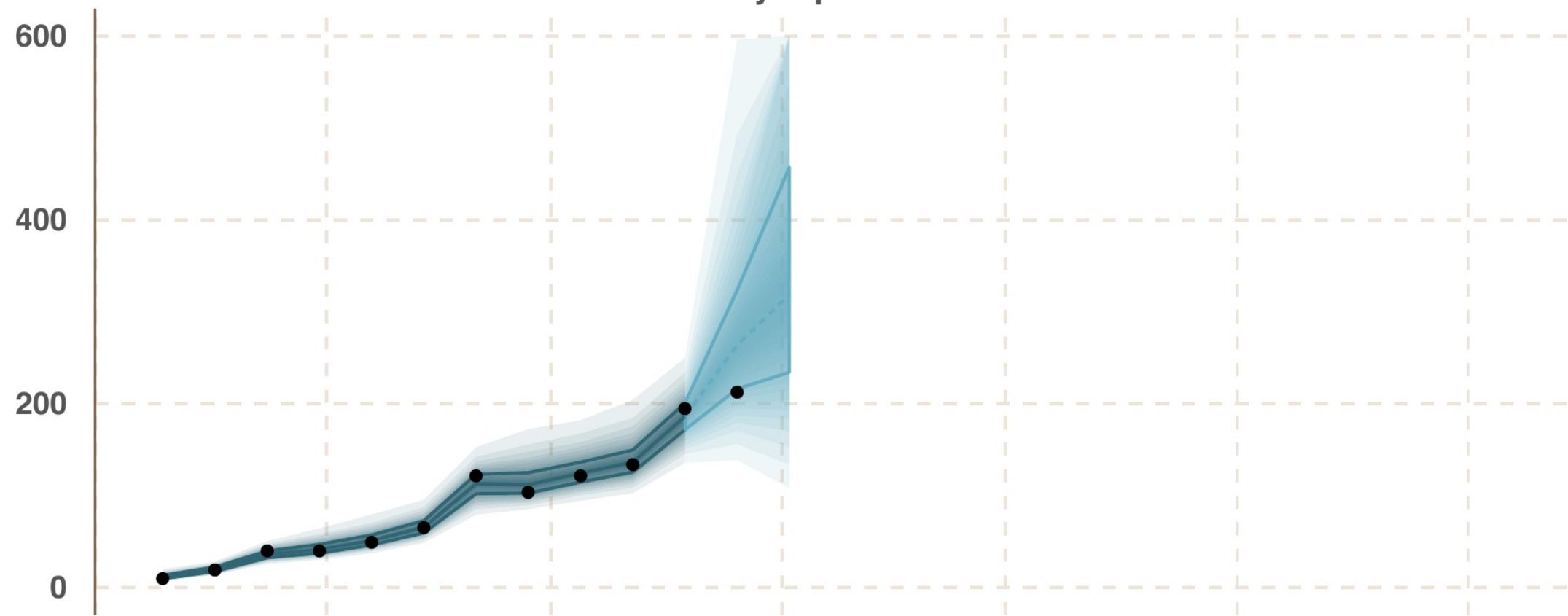
Weekly reported cases



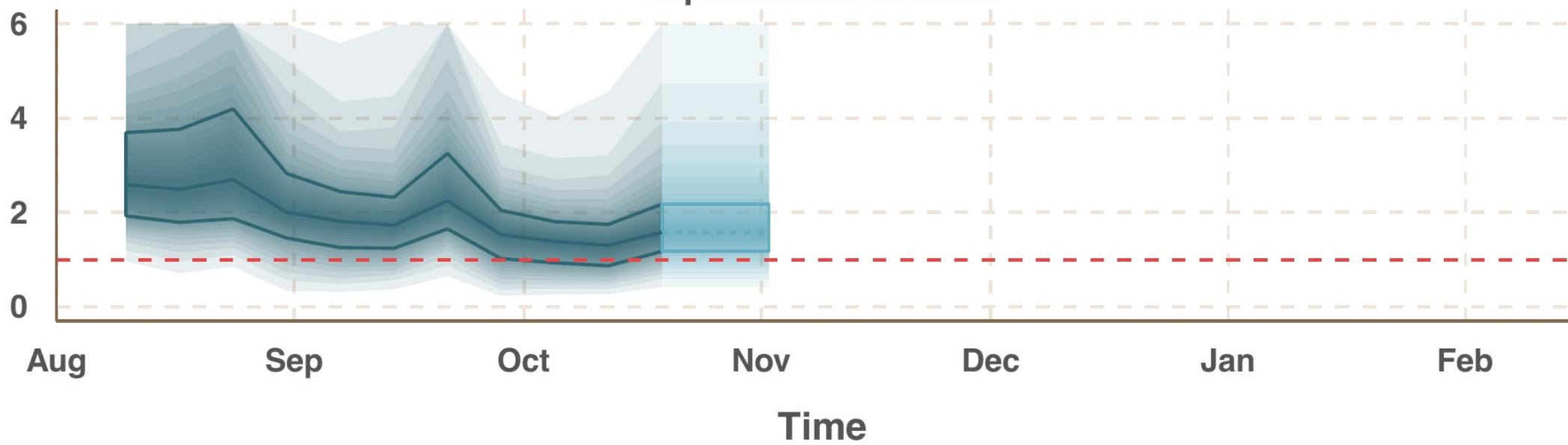
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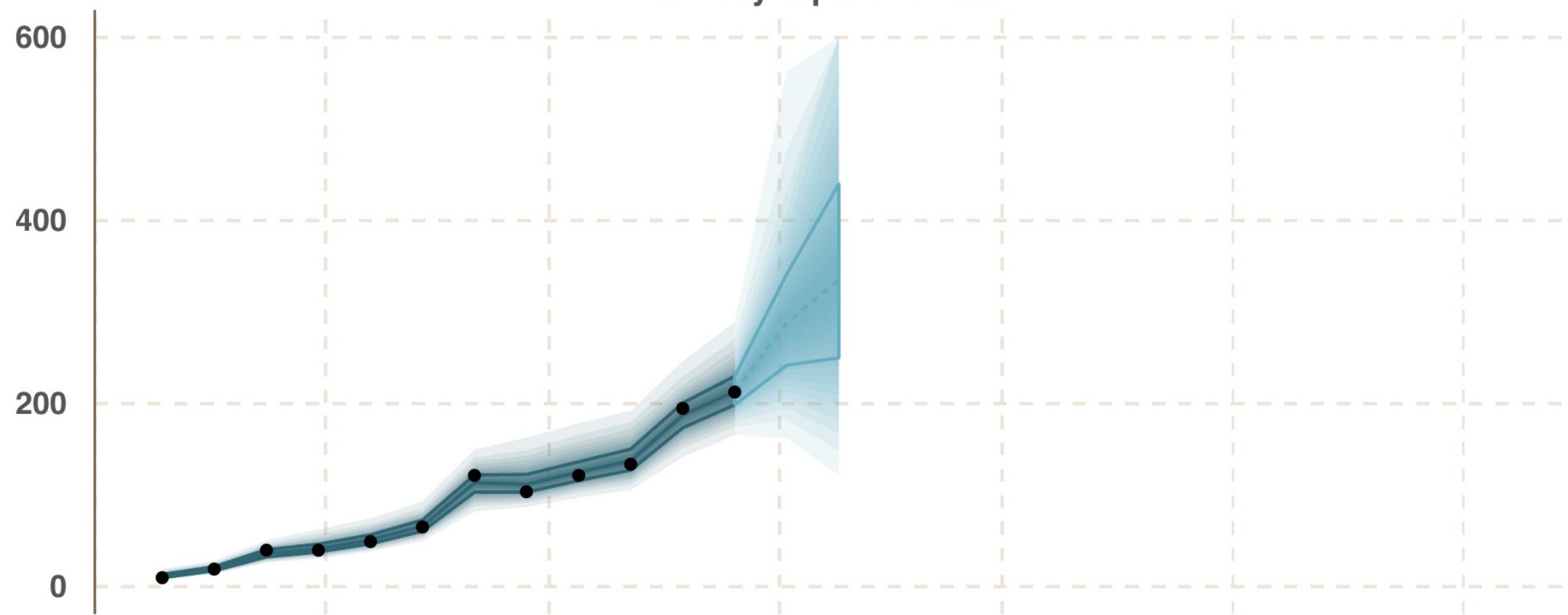
Weekly reported cases



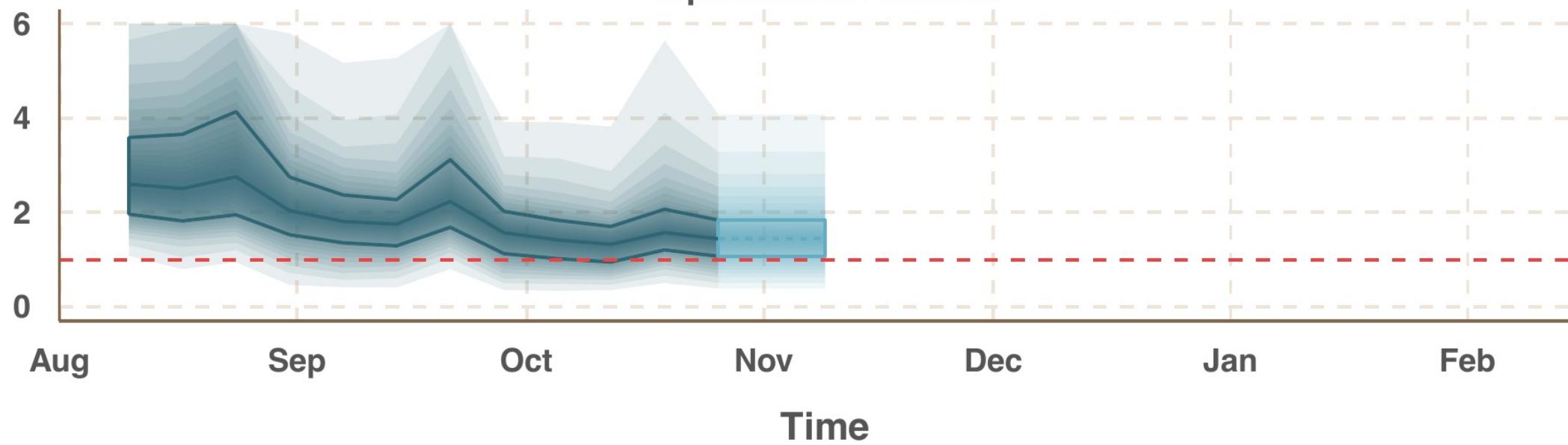
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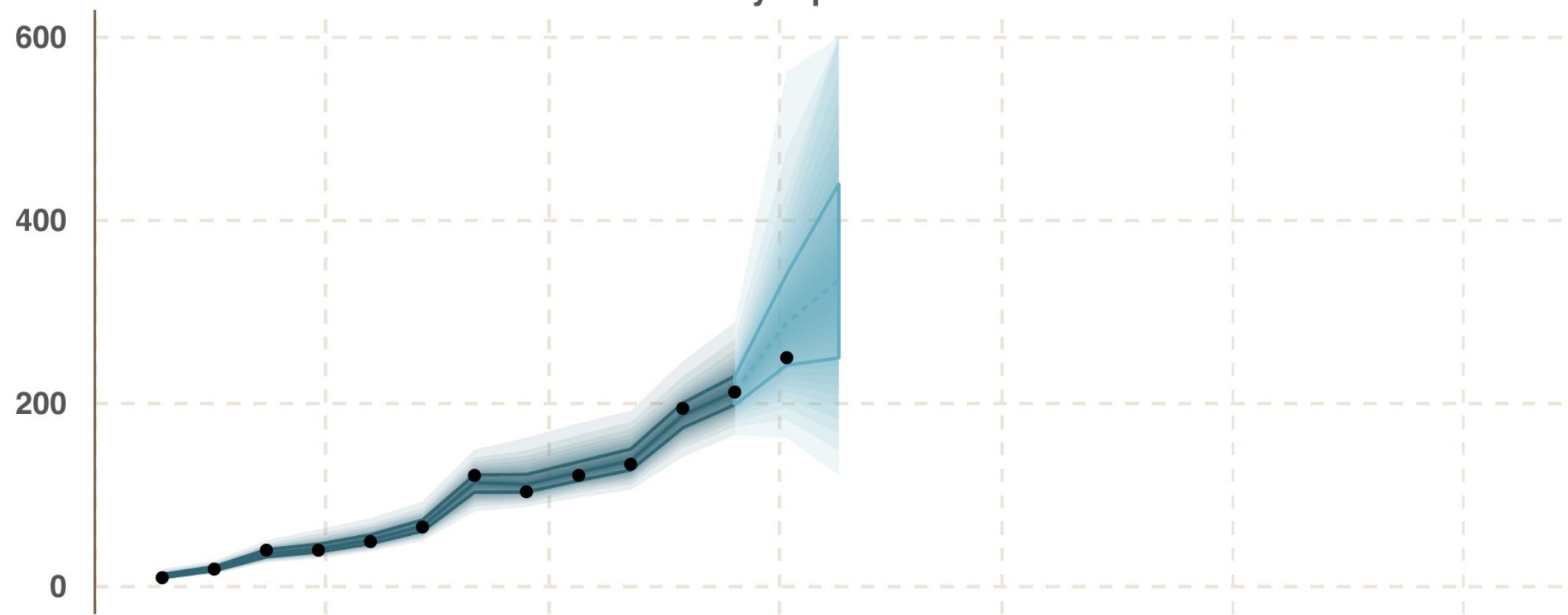
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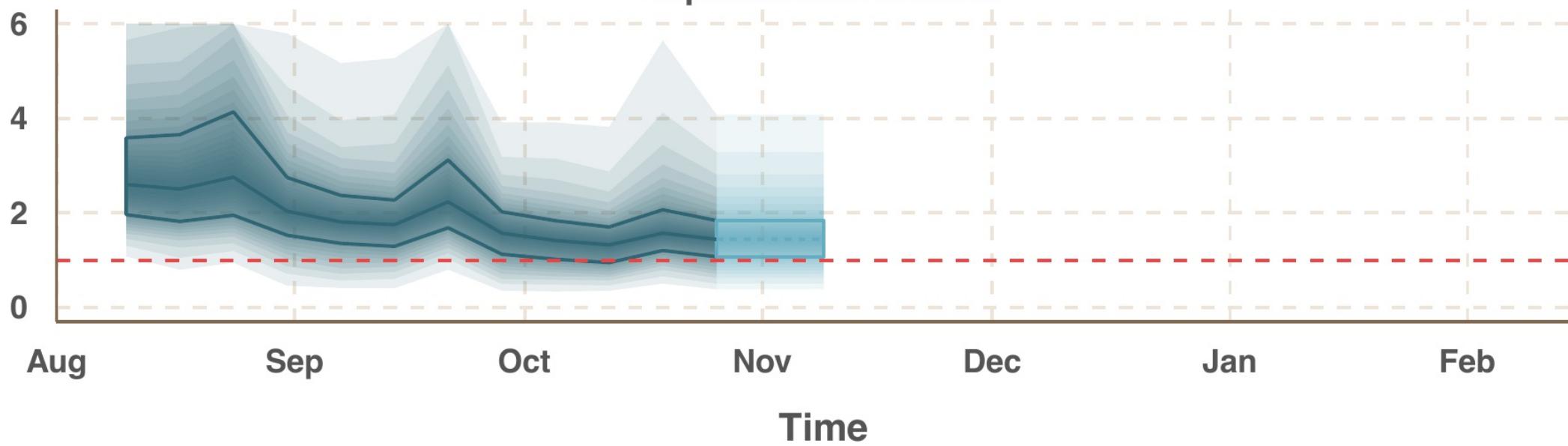
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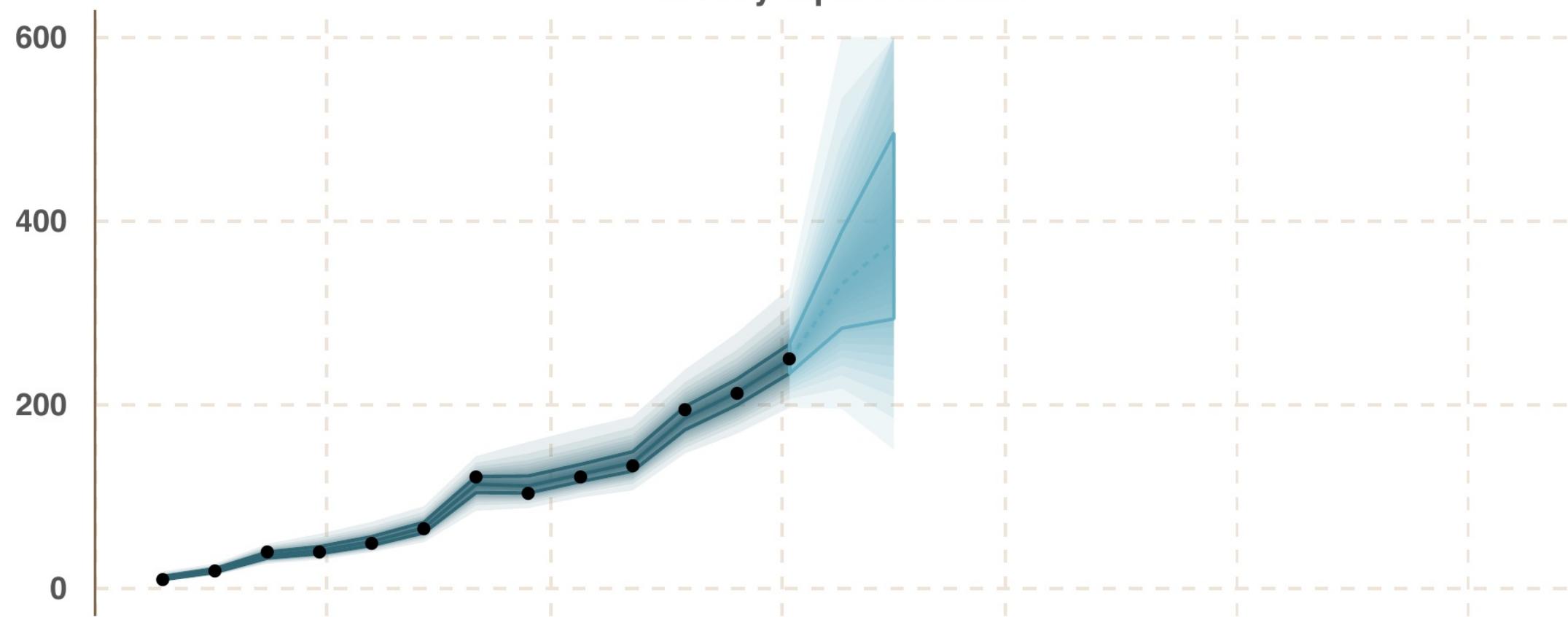
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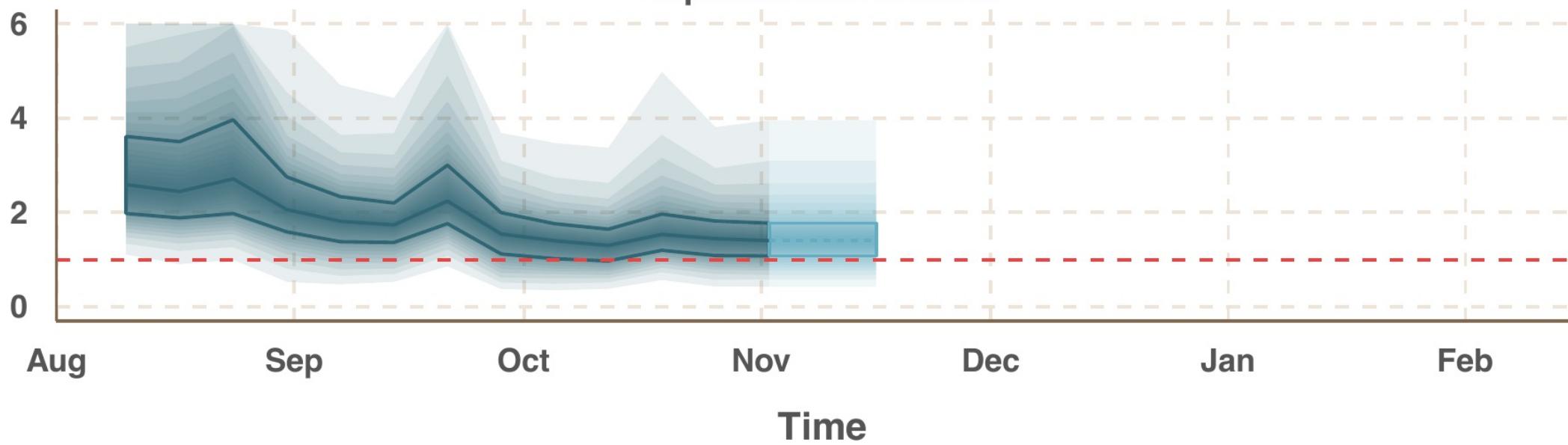
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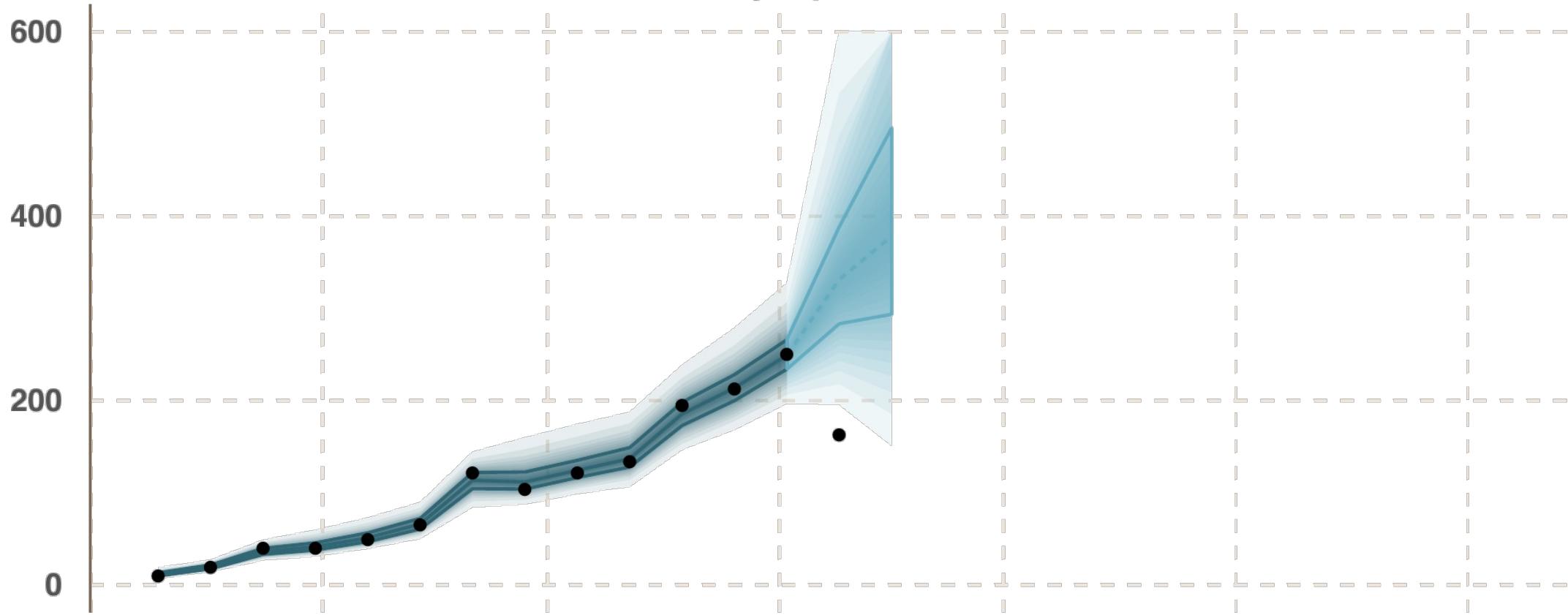
Weekly reported cases



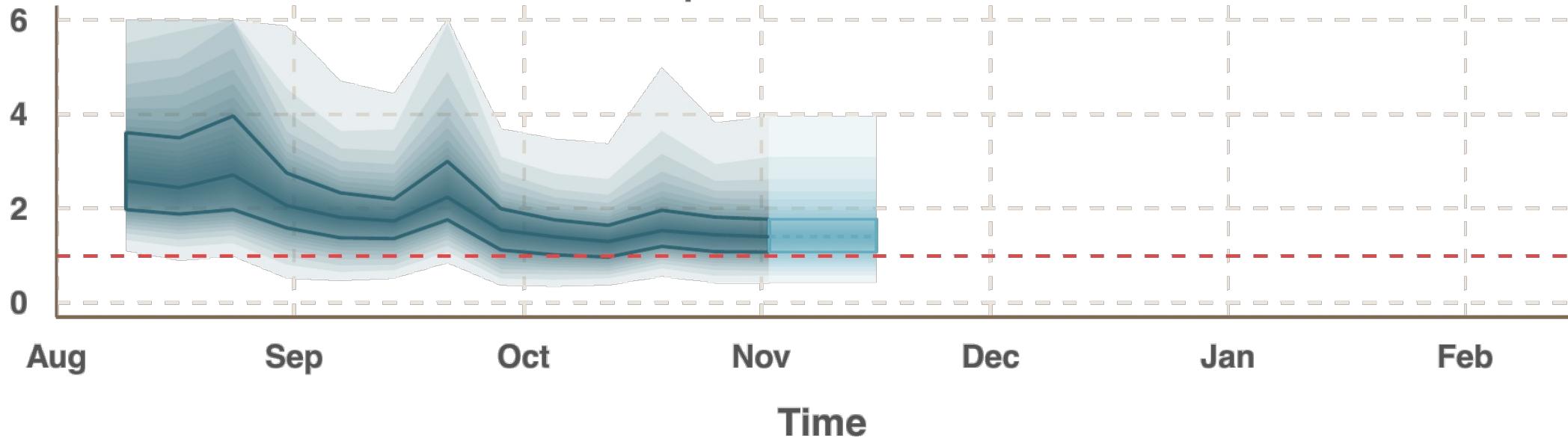
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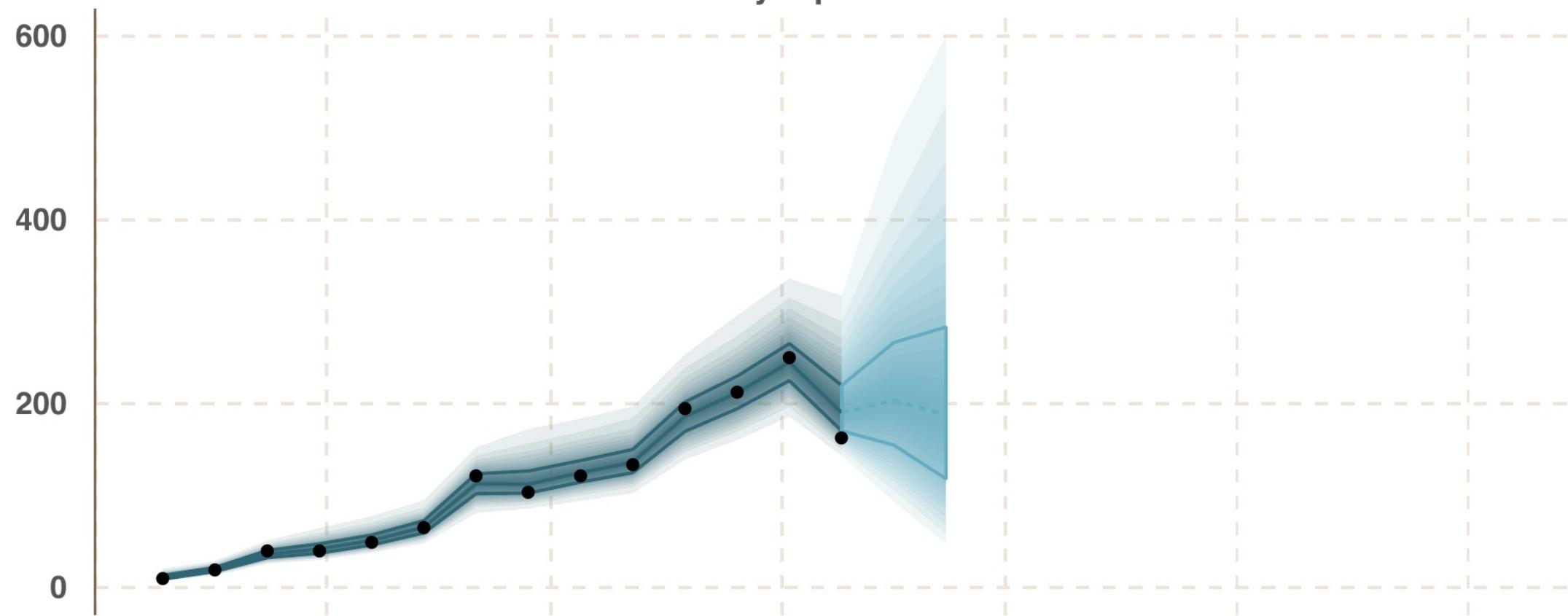
Weekly reported cases



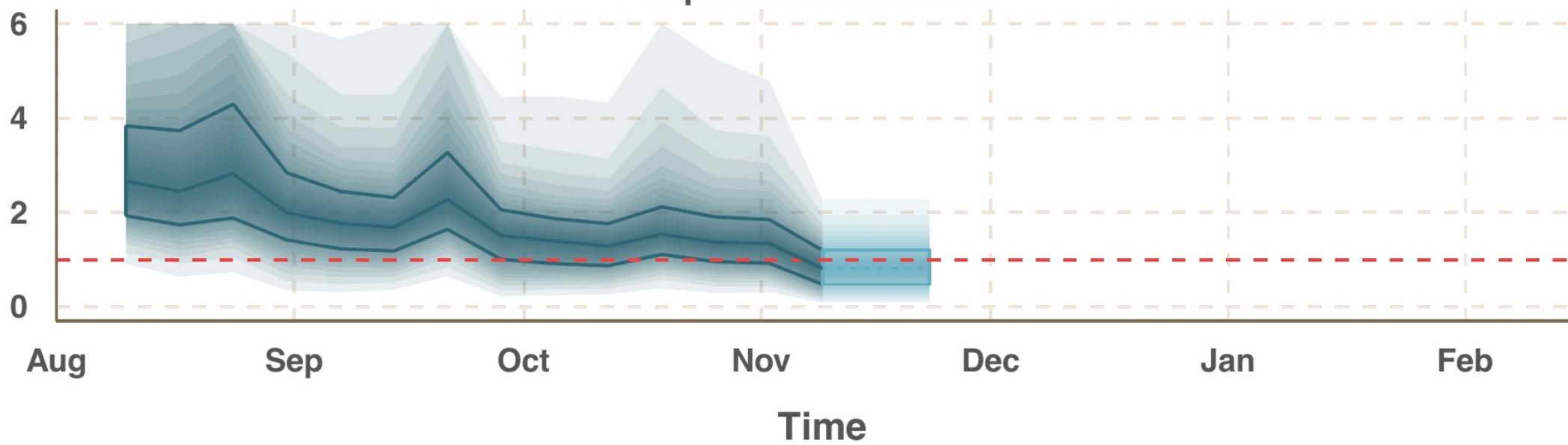
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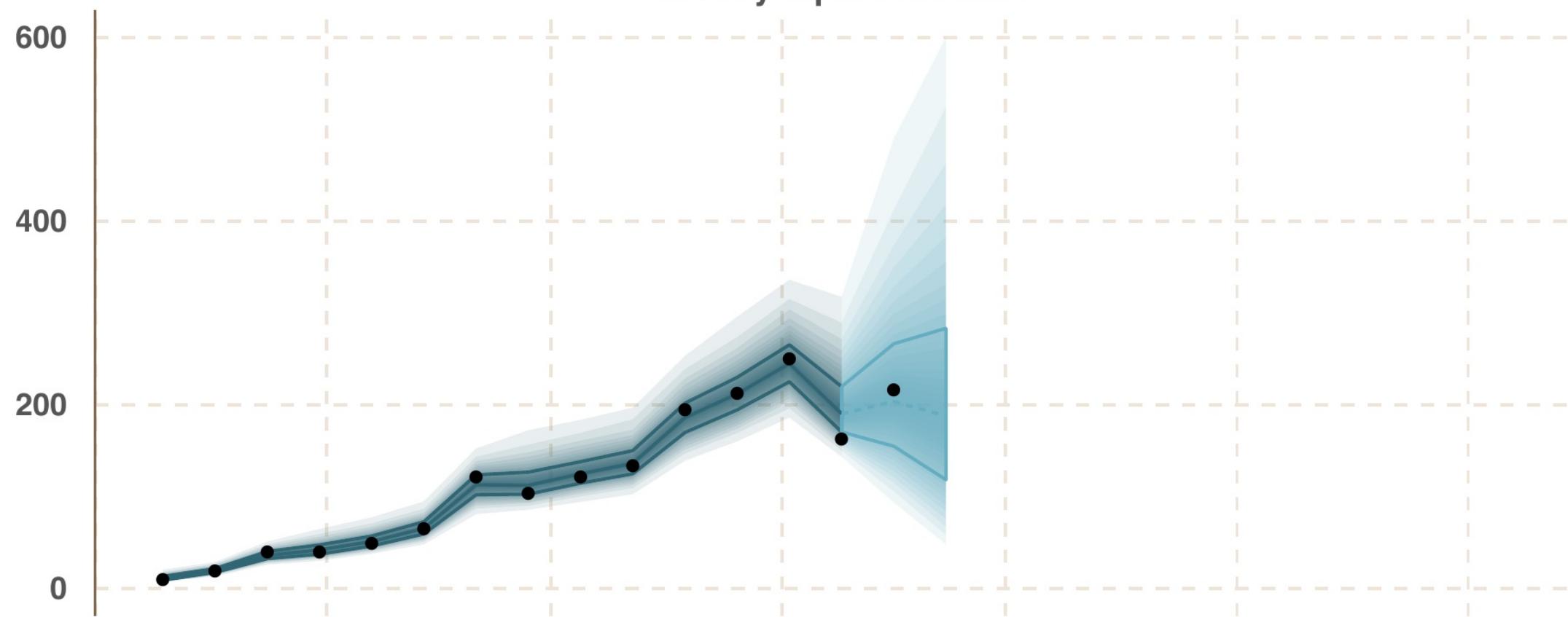
Weekly reported cases



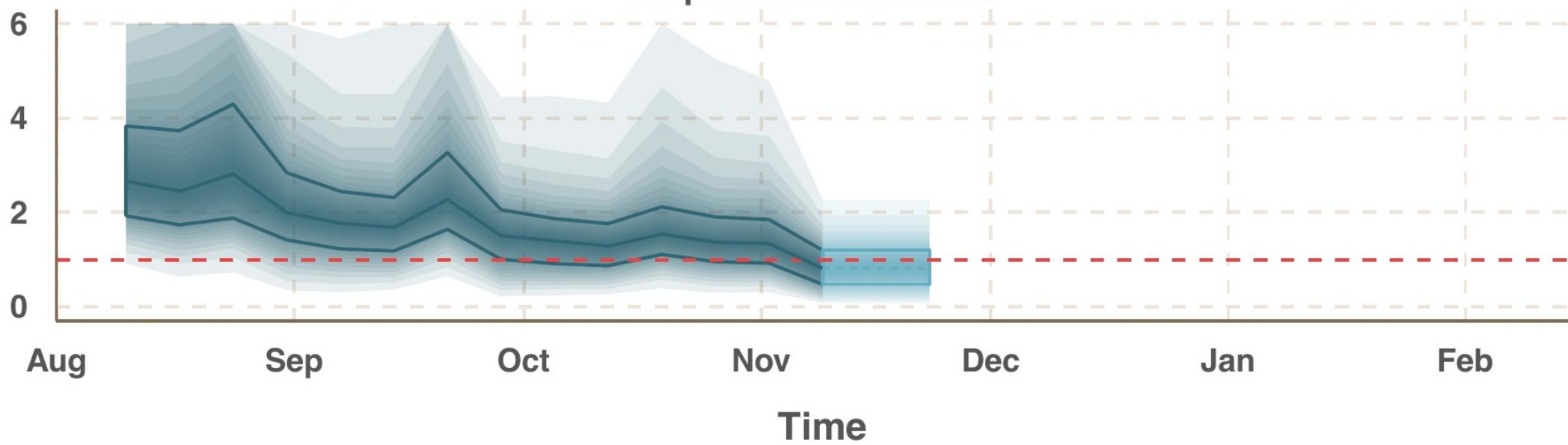
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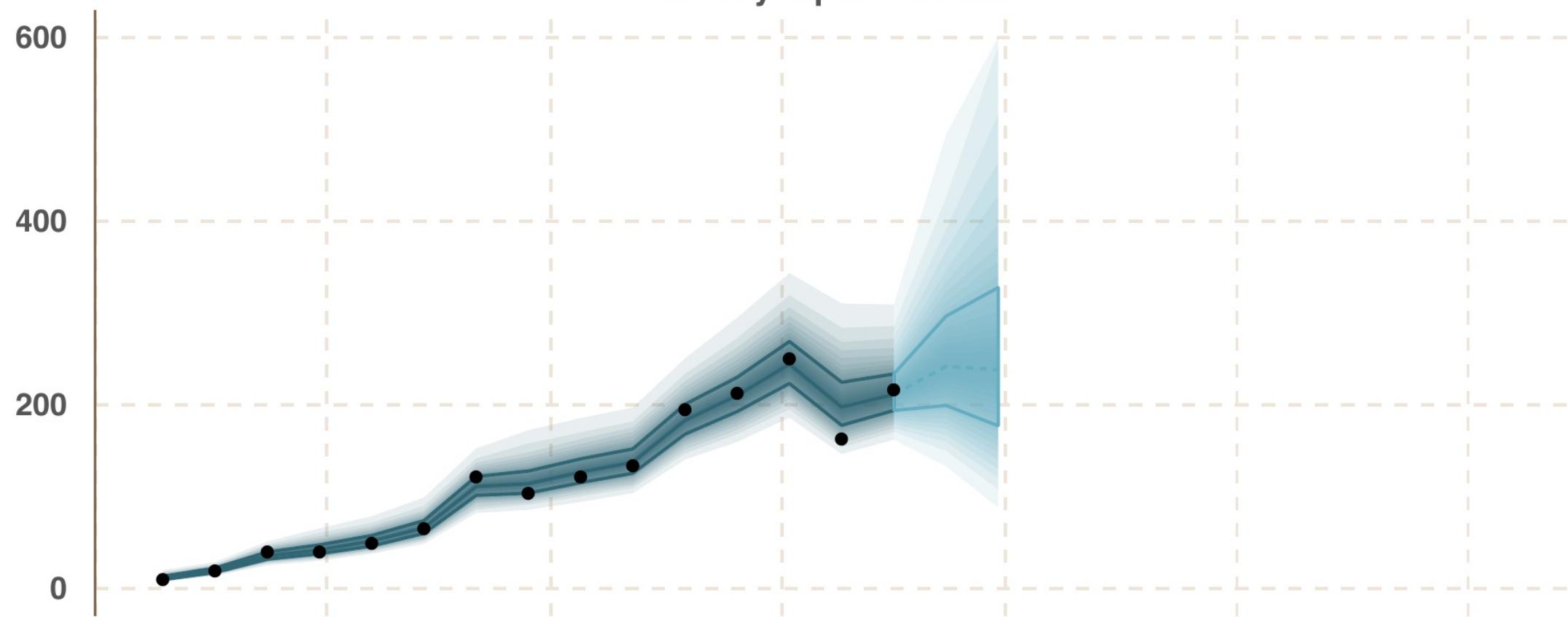
Weekly reported cases



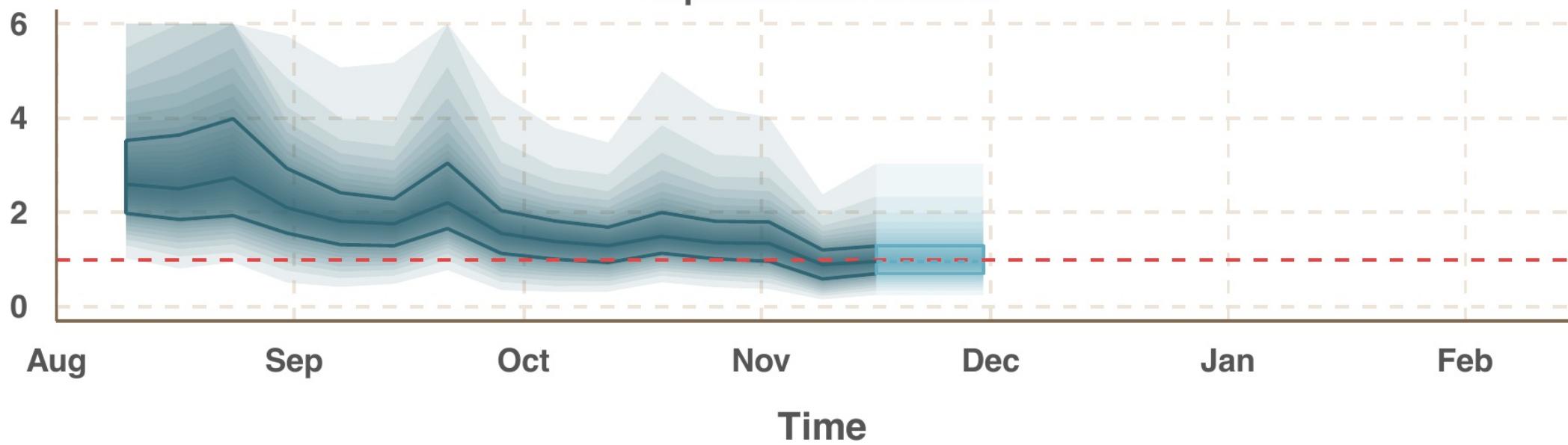
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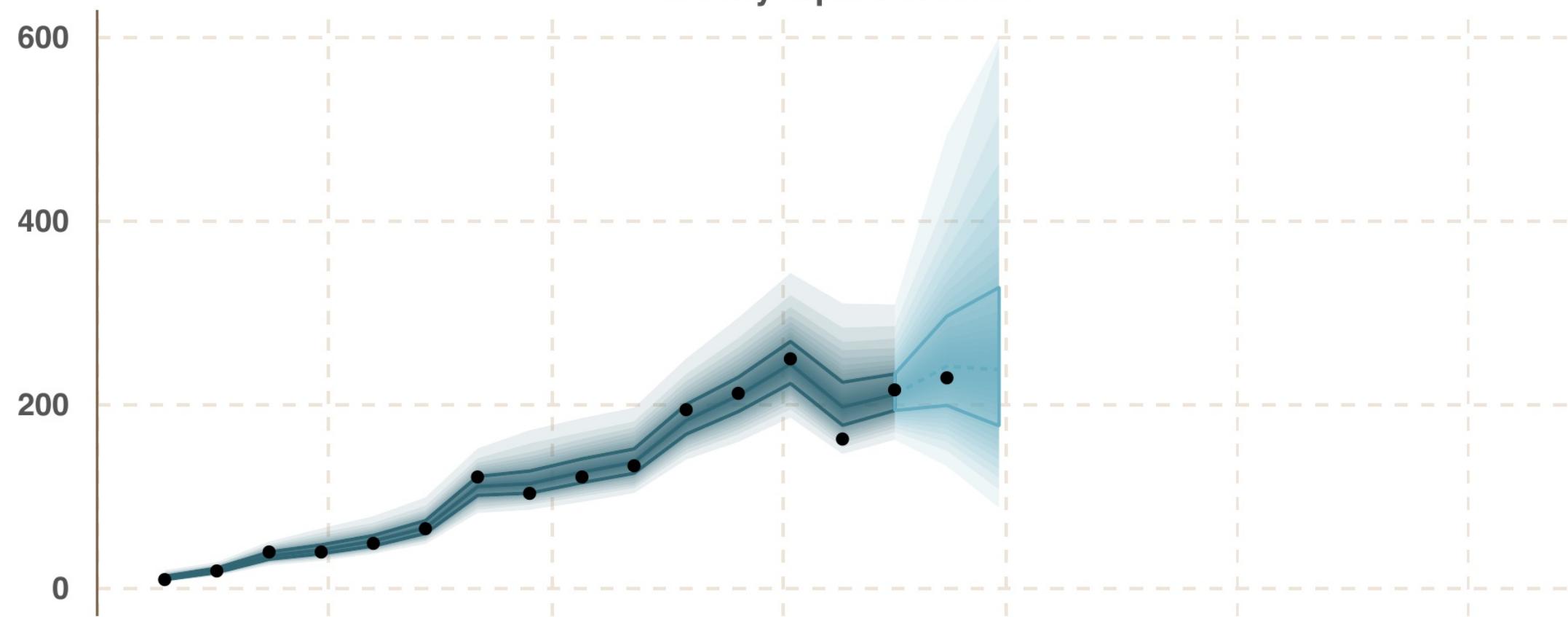
Weekly reported cases



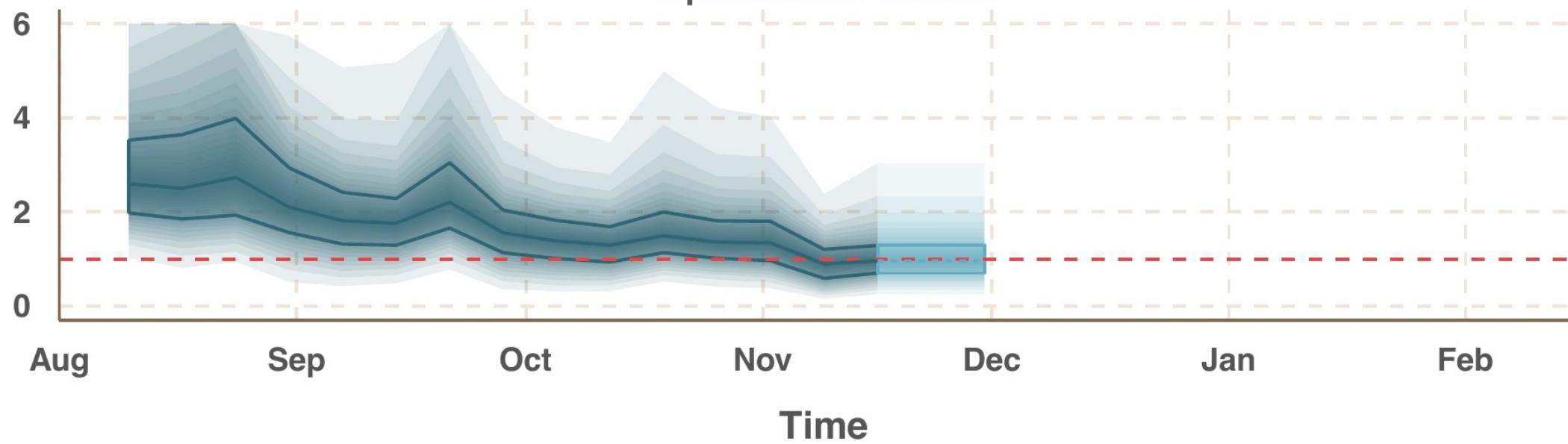
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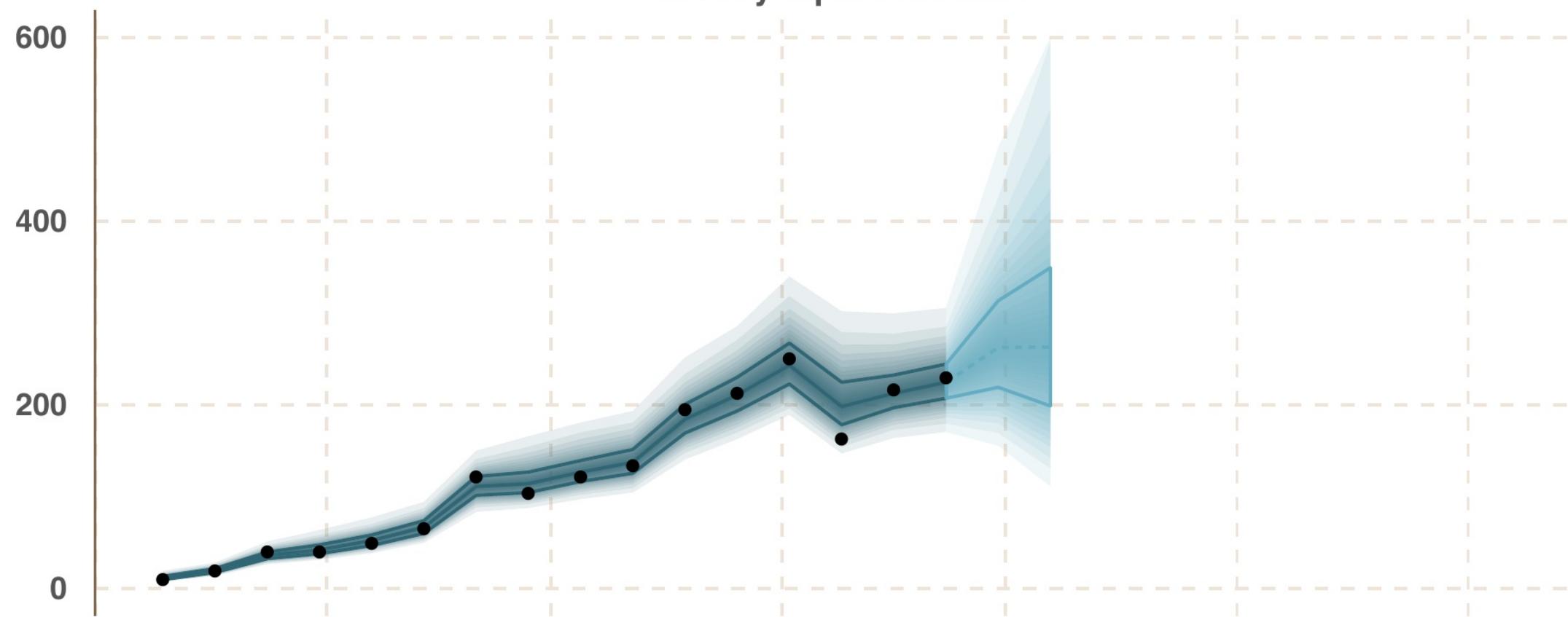
Weekly reported cases



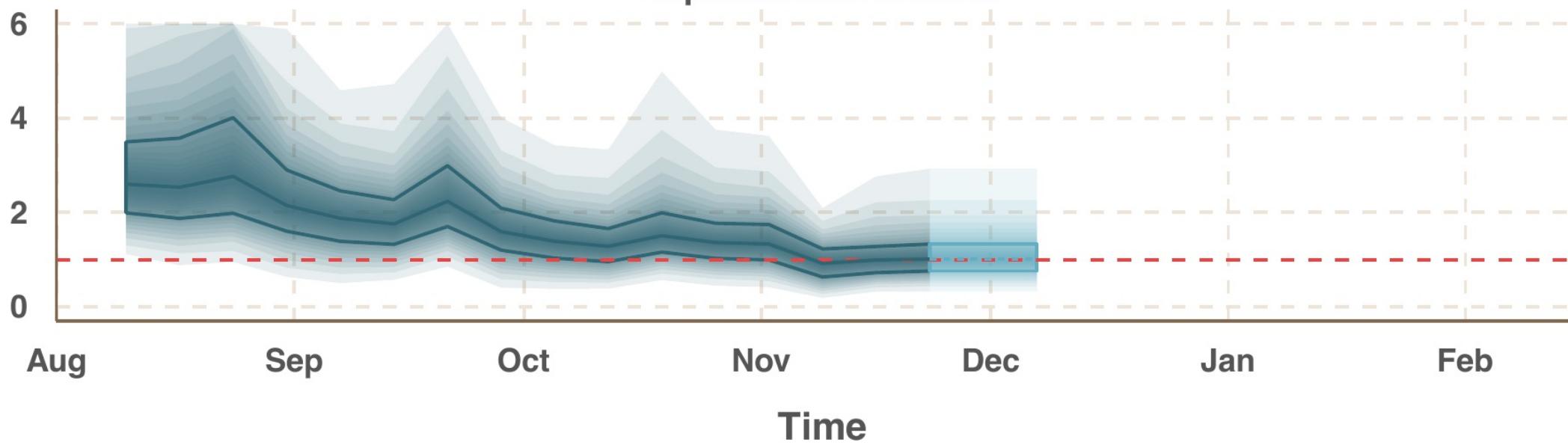
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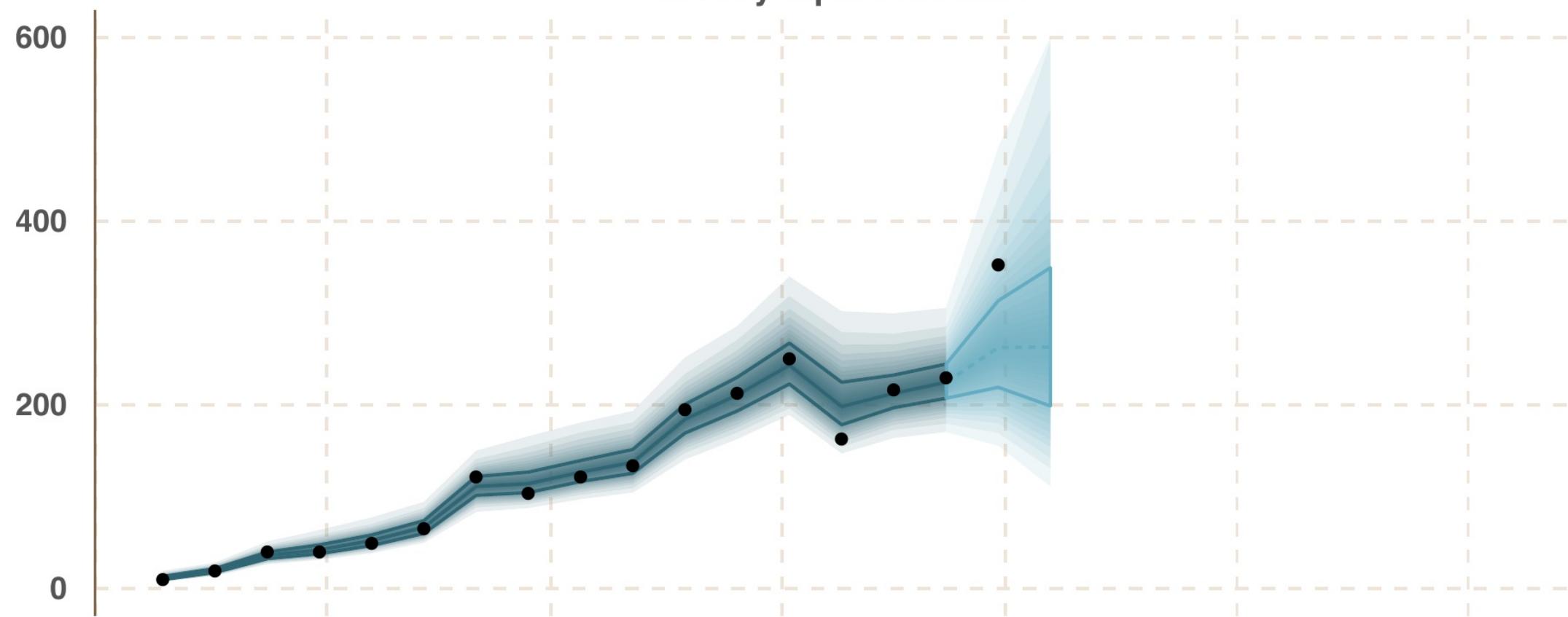
Weekly reported cases



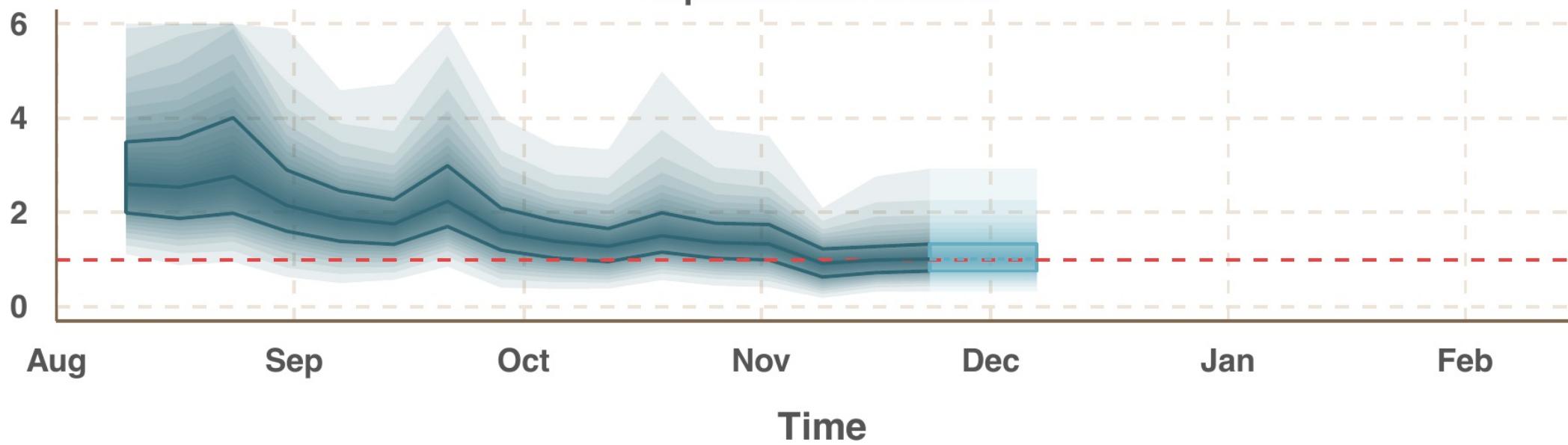
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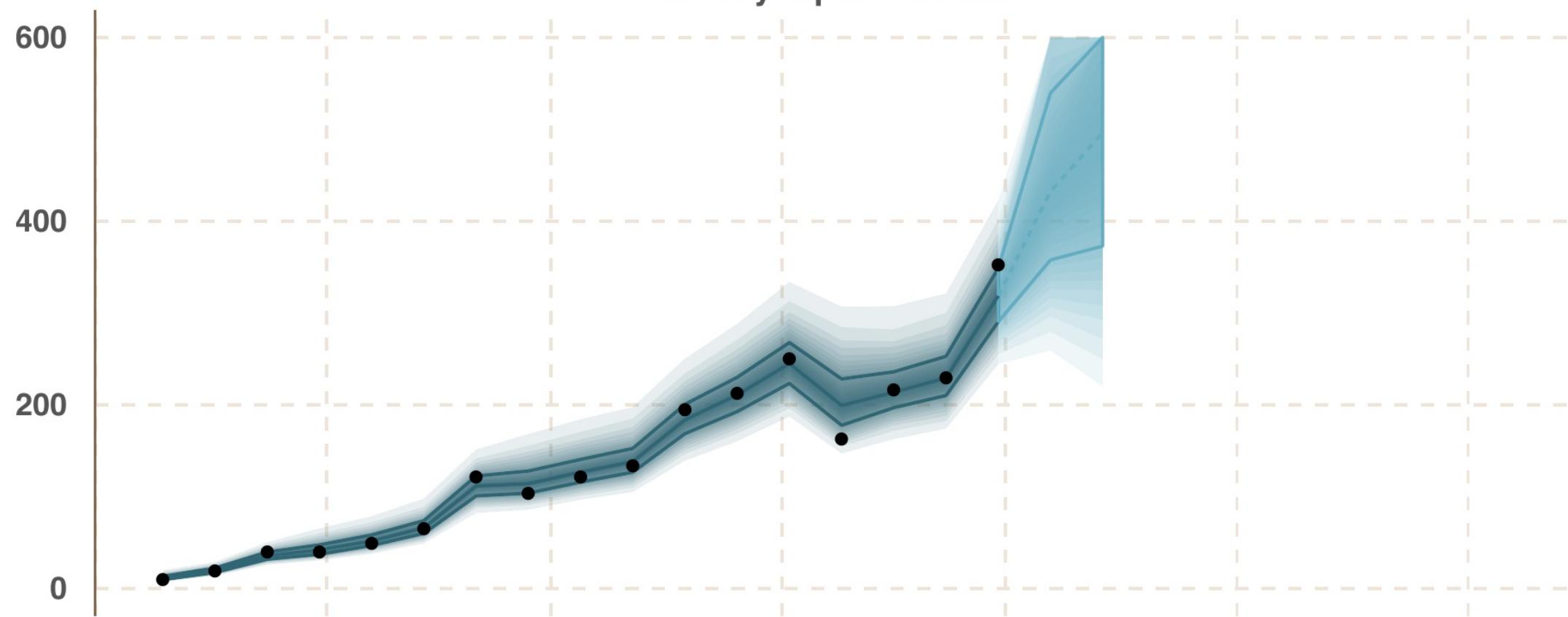
Weekly reported cases



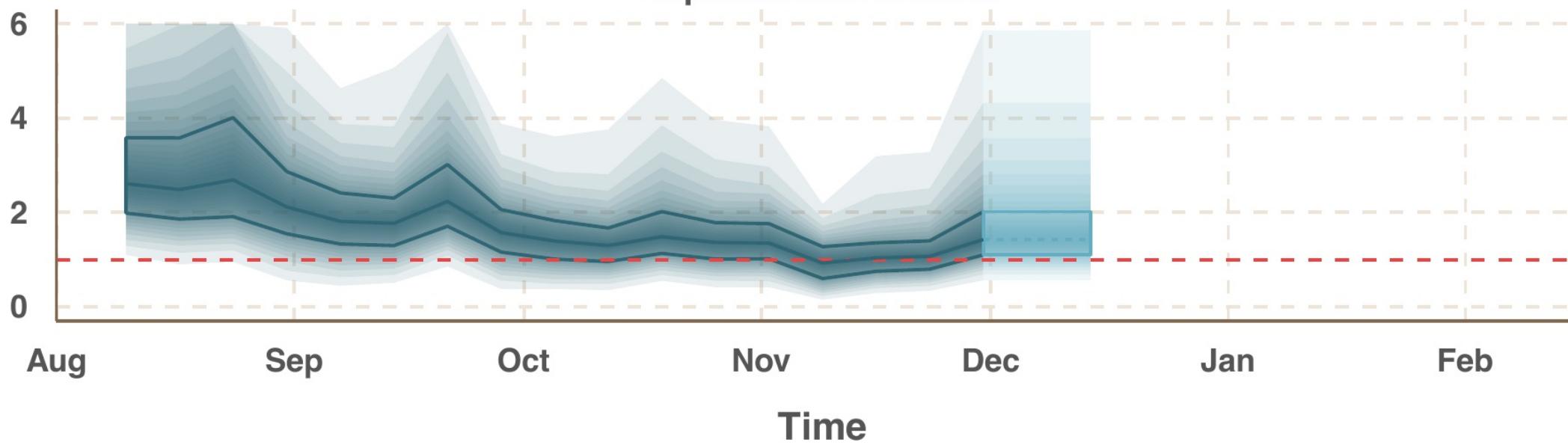
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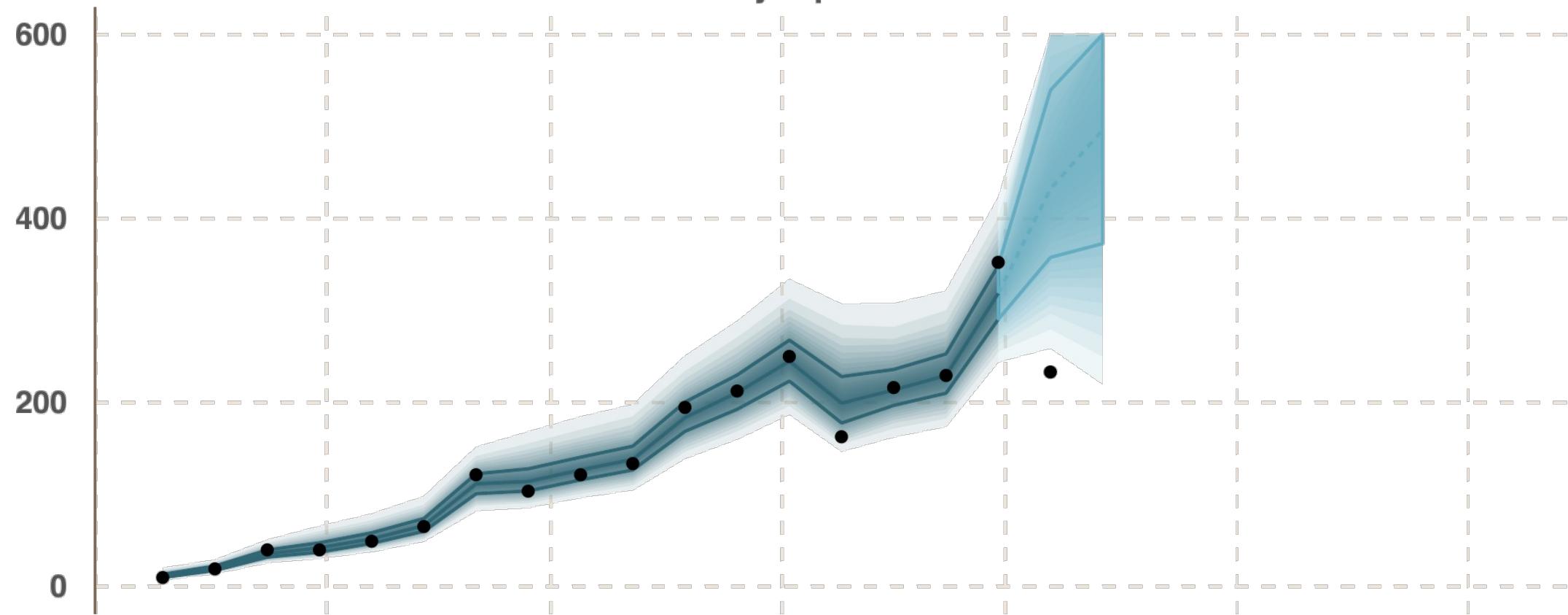
Weekly reported cases



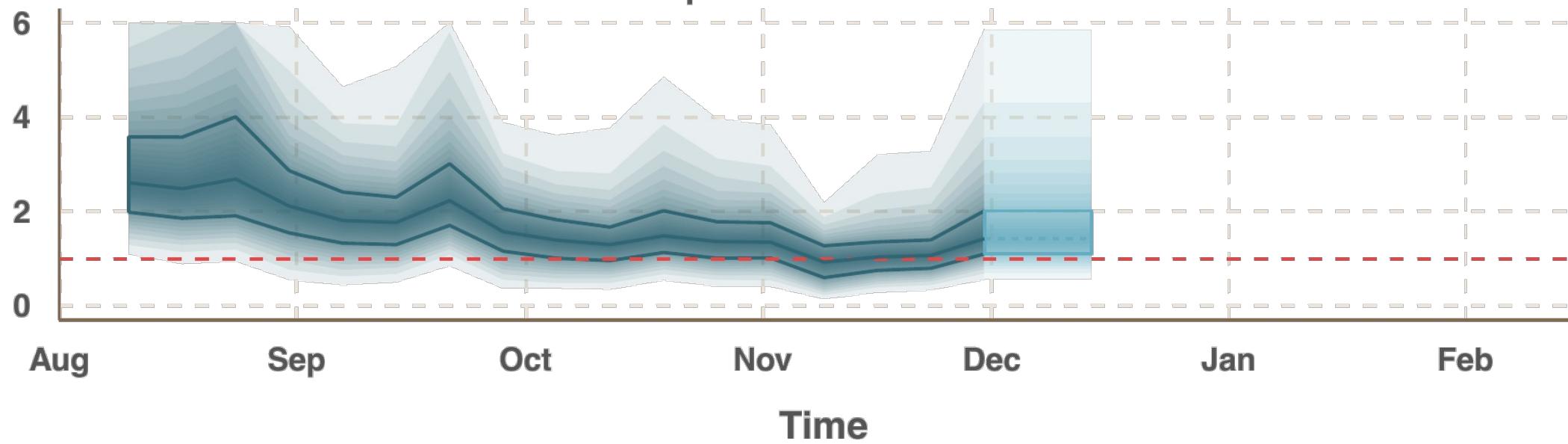
Reproduction number



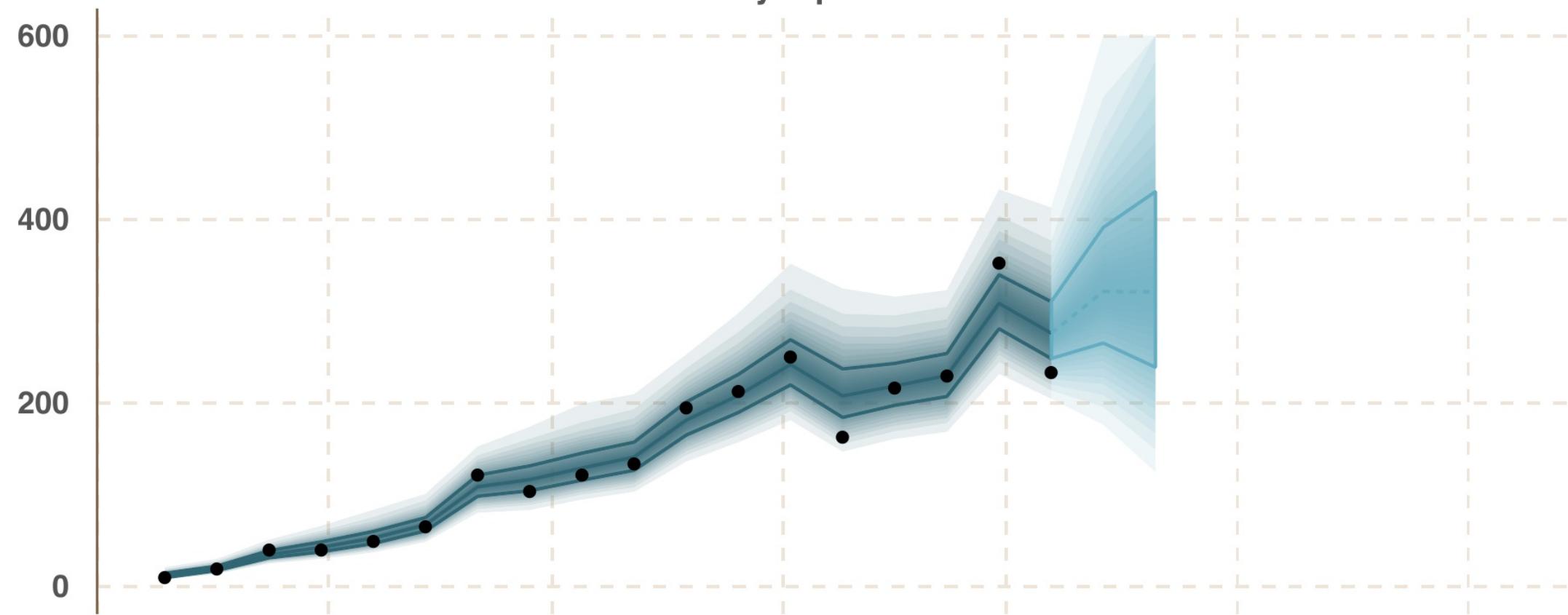
Weekly reported cases



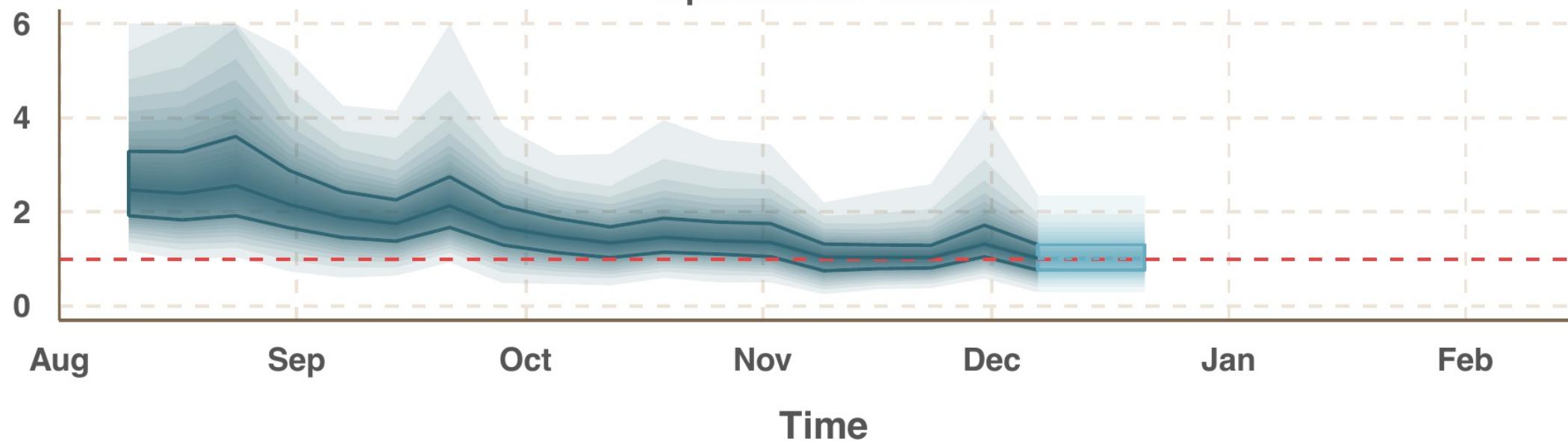
Reproduction number



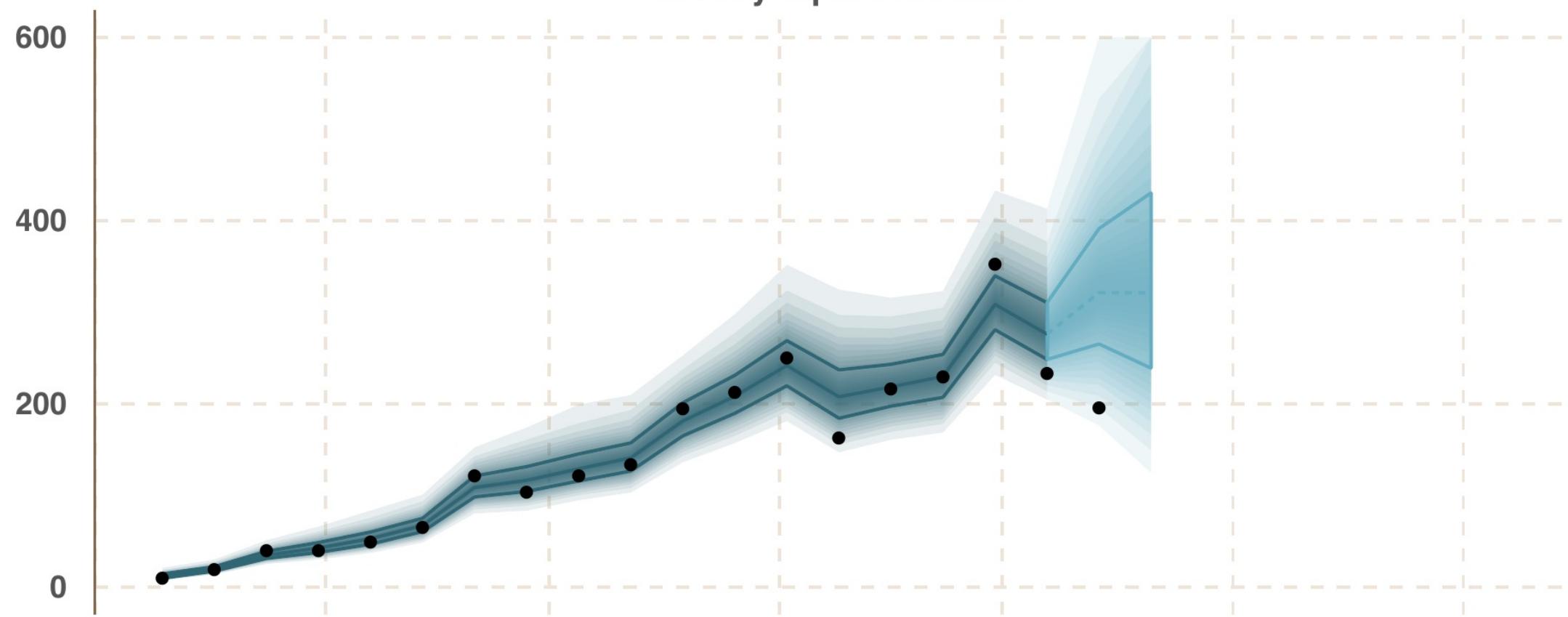
Weekly reported cases



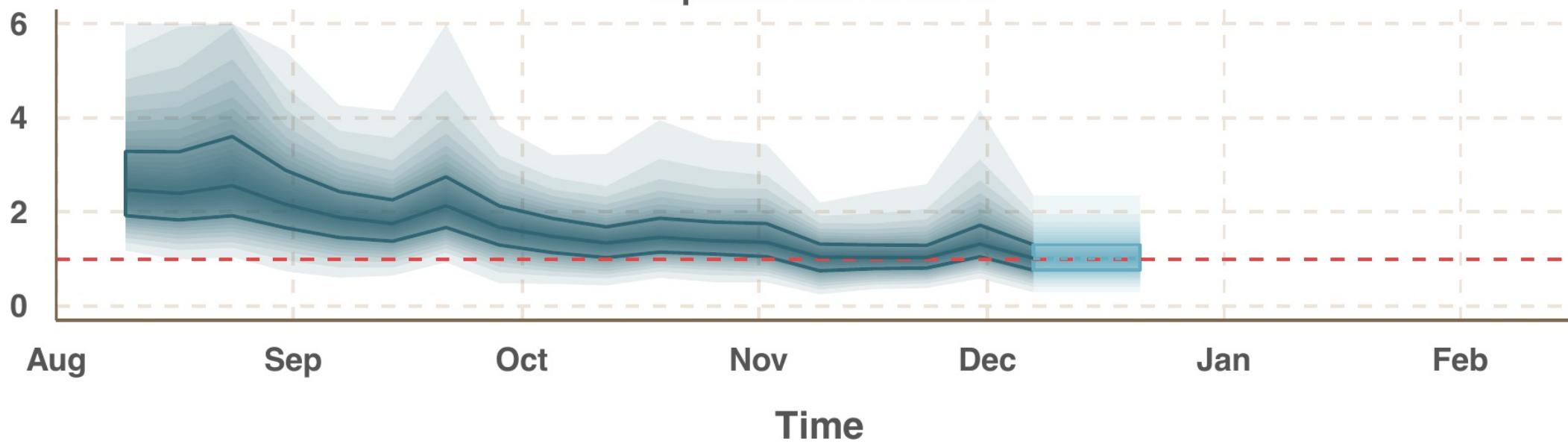
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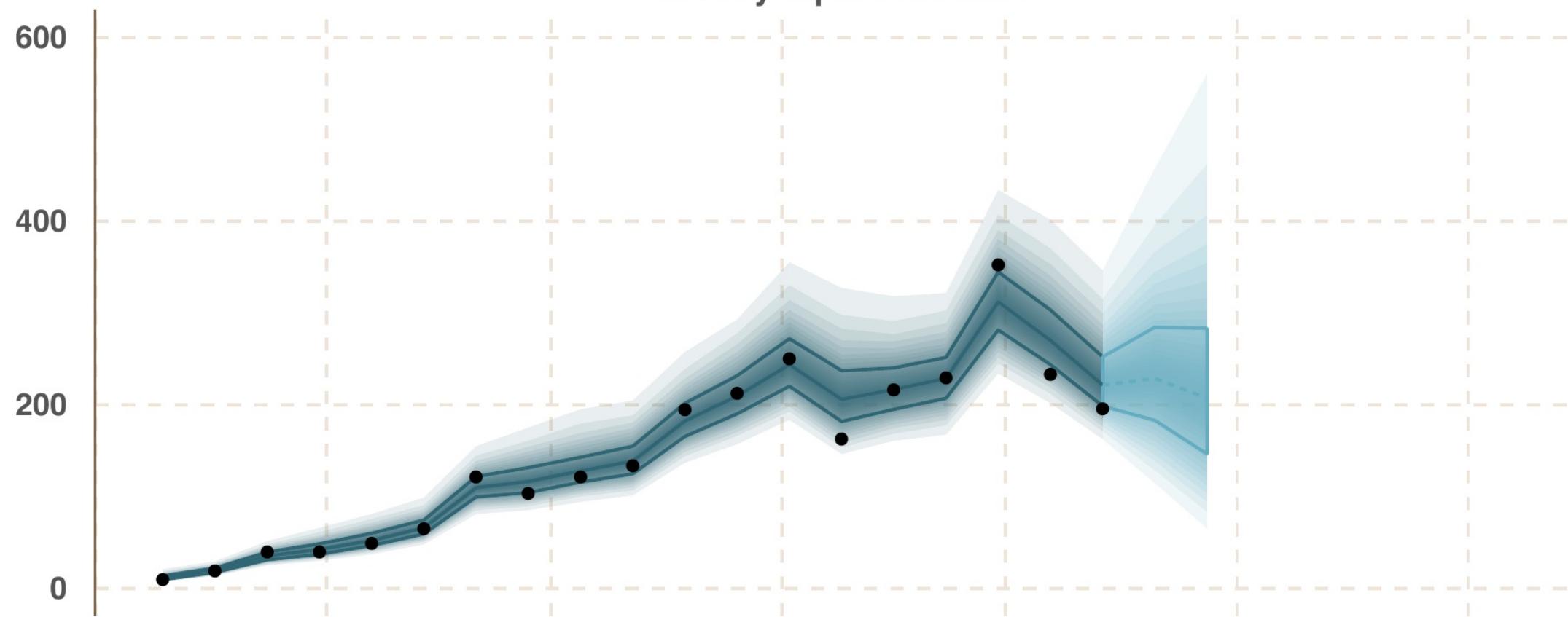
Weekly reported cases



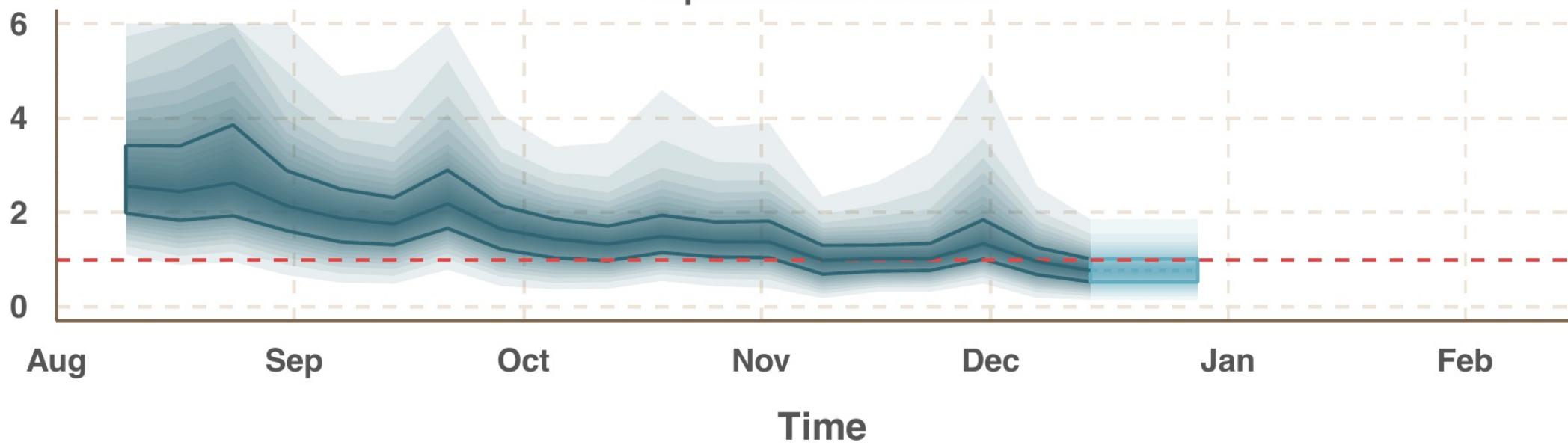
Reproduction number



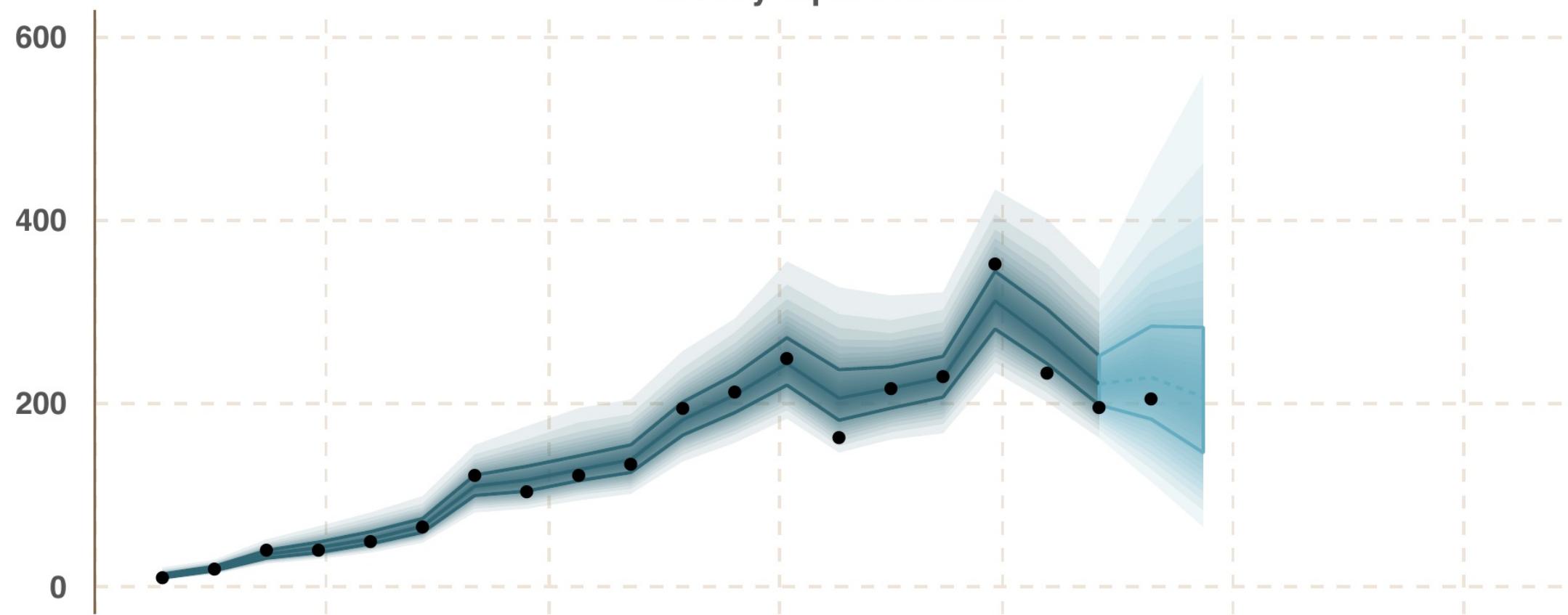
Weekly reported cases



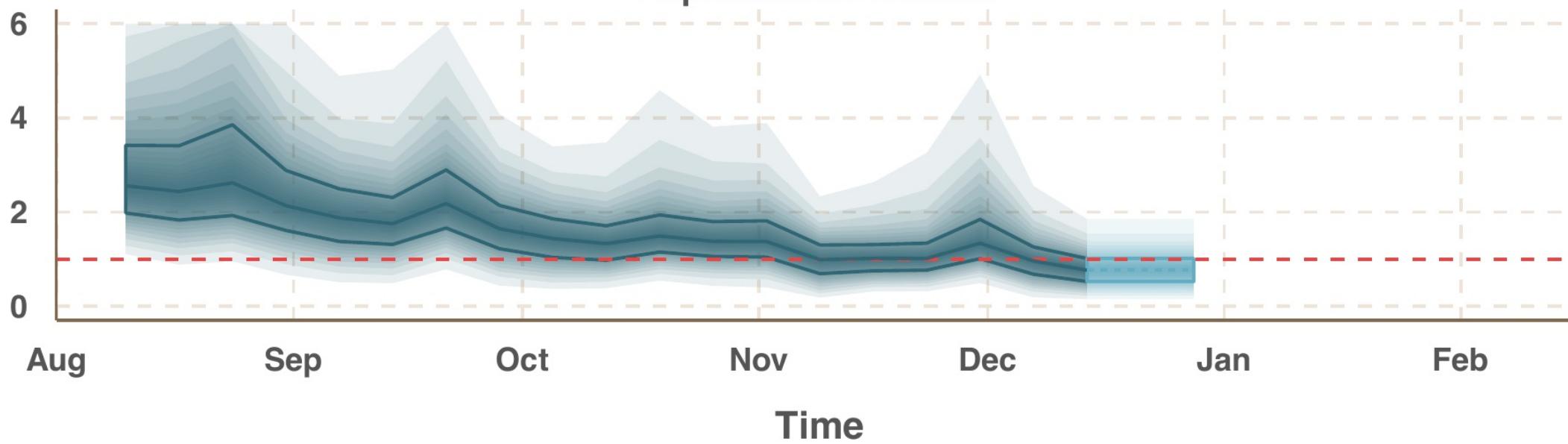
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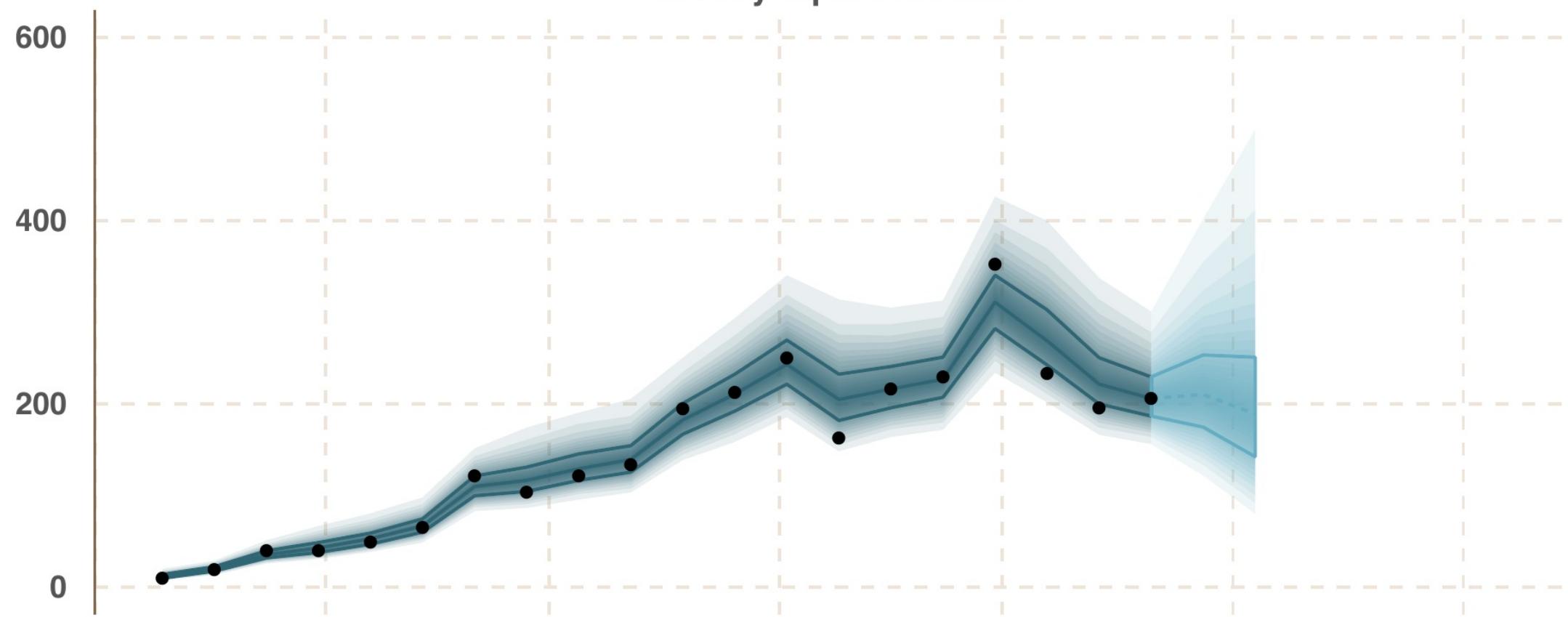
Weekly reported cases



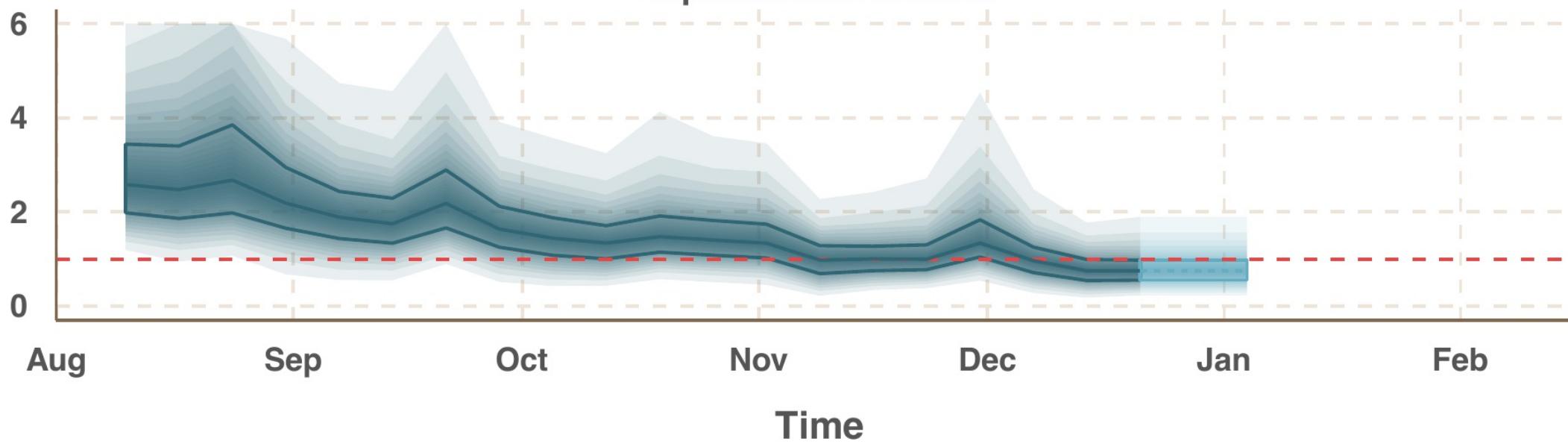
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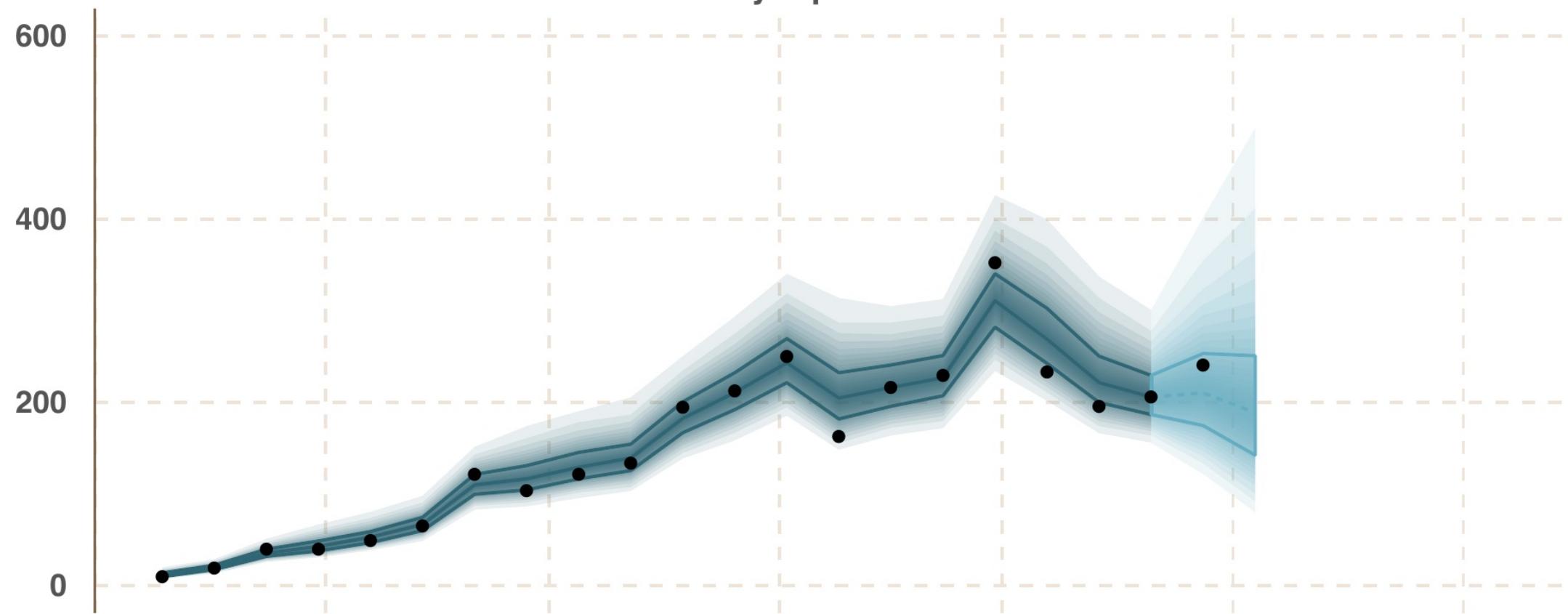
Weekly reported cases



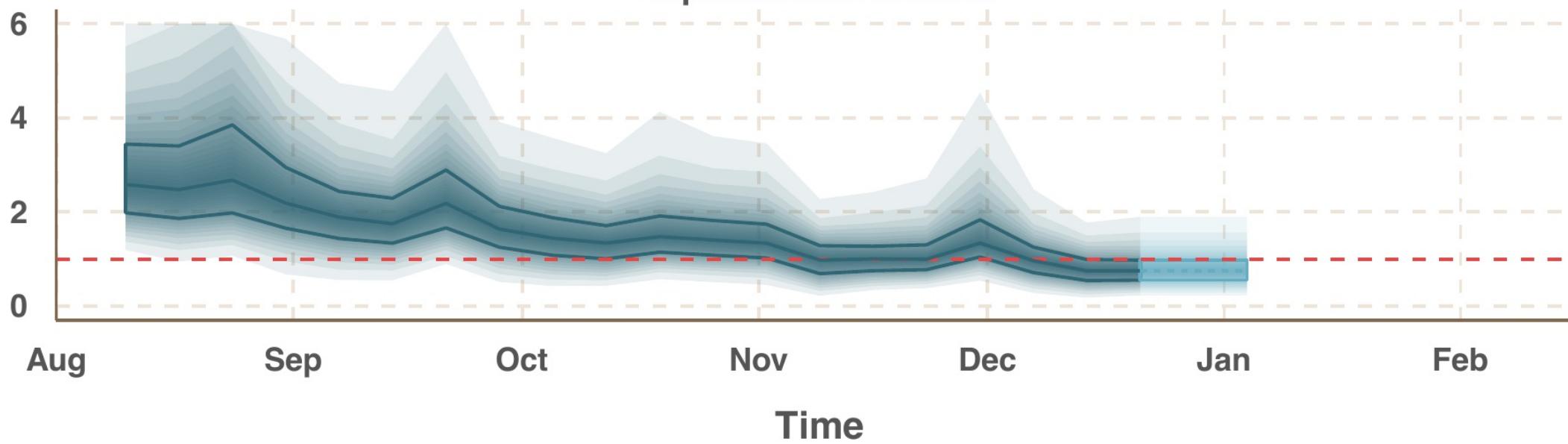
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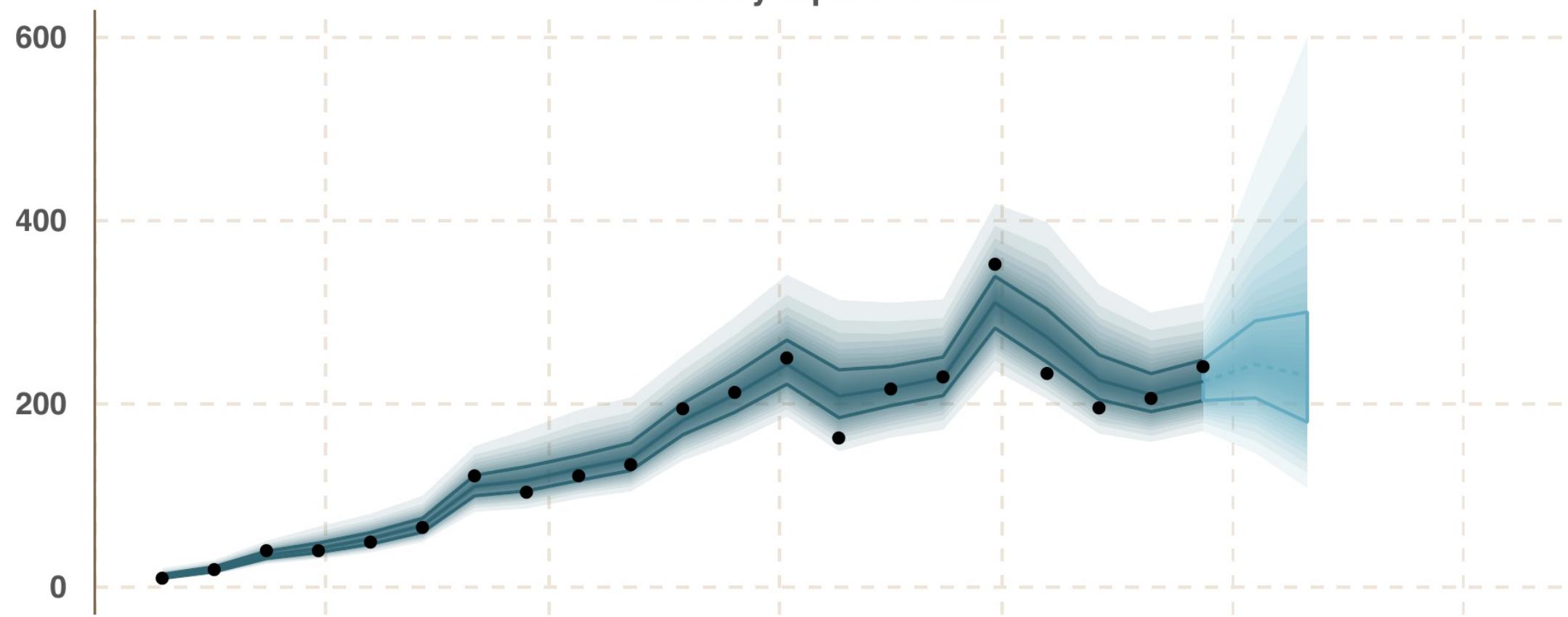
Weekly reported cases



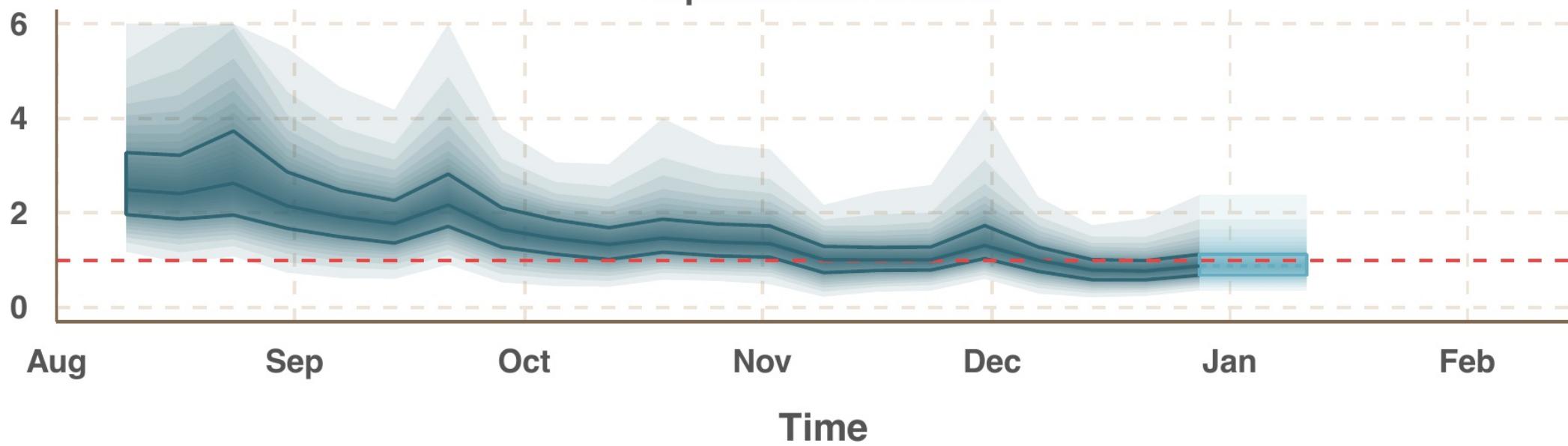
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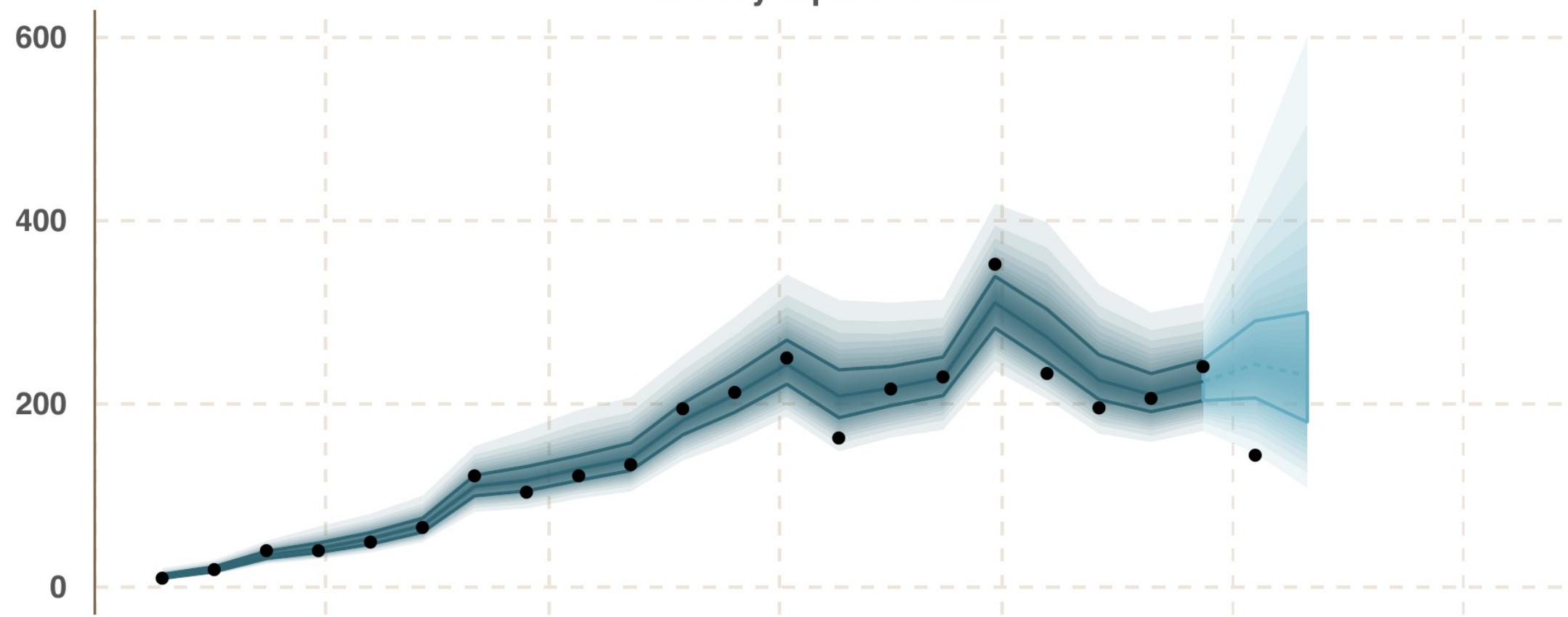
Weekly reported cases



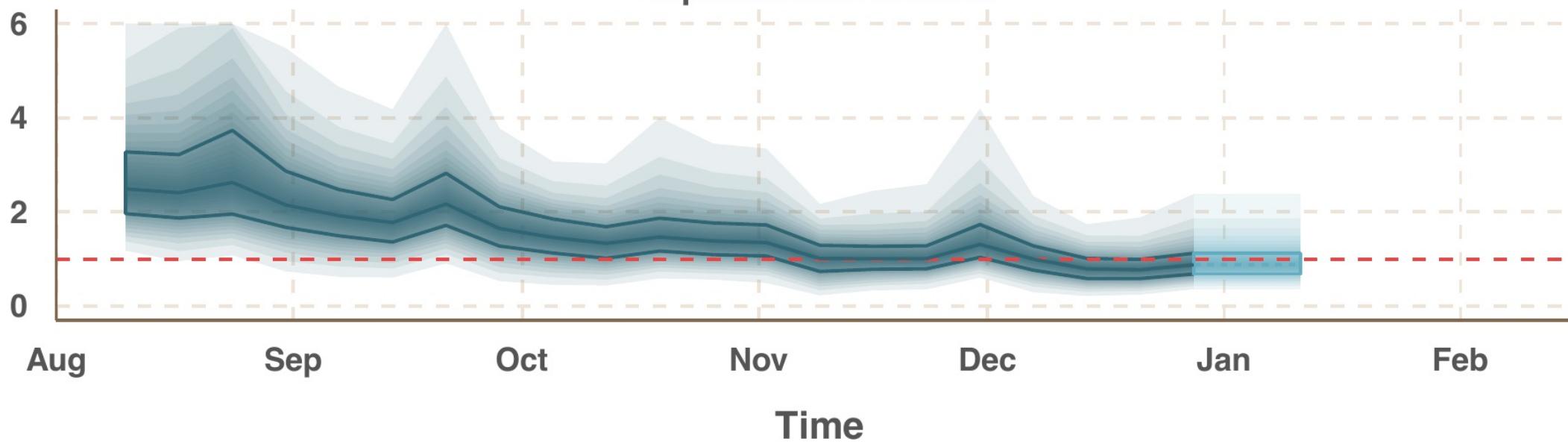
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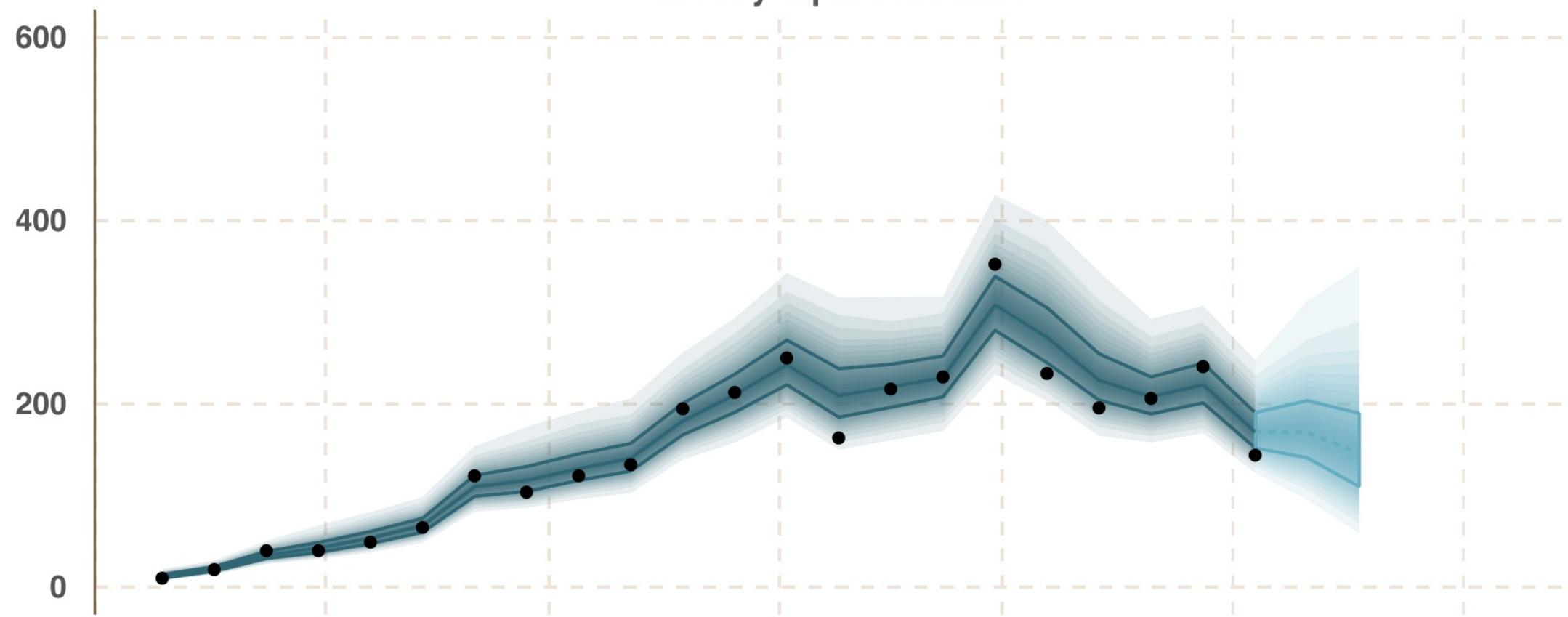
Weekly reported cases



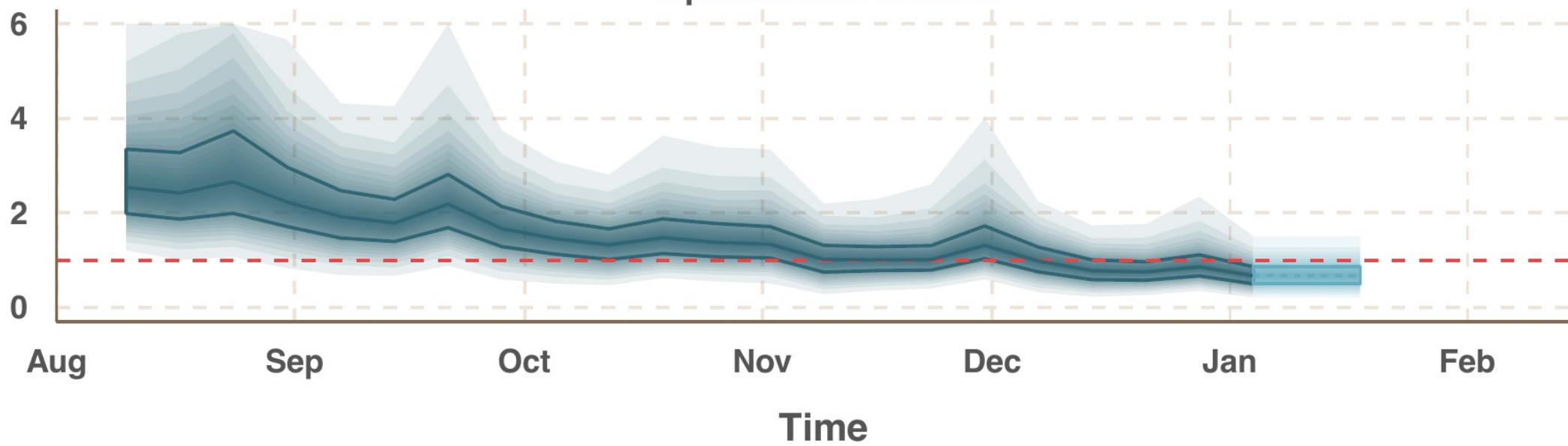
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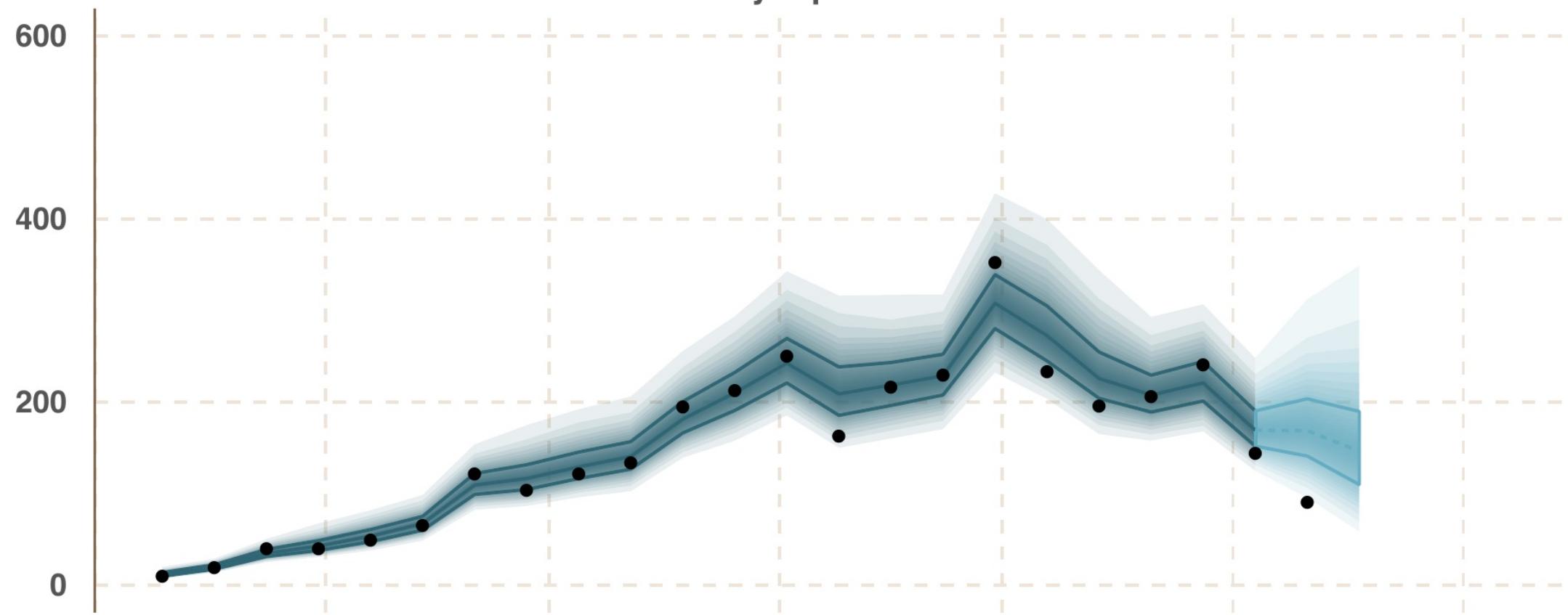
Weekly reported cases



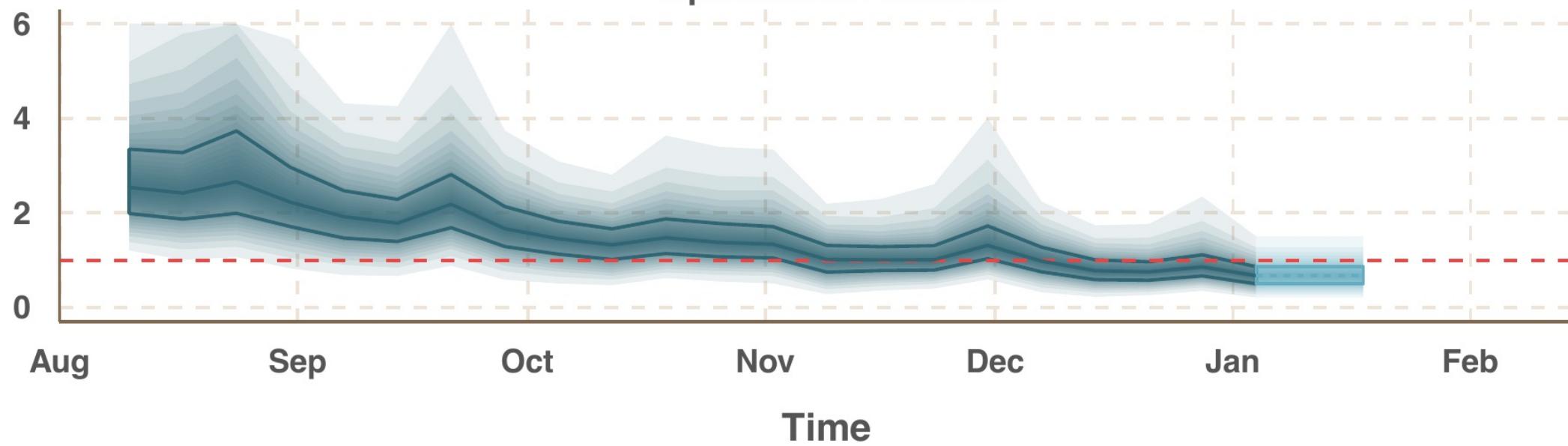
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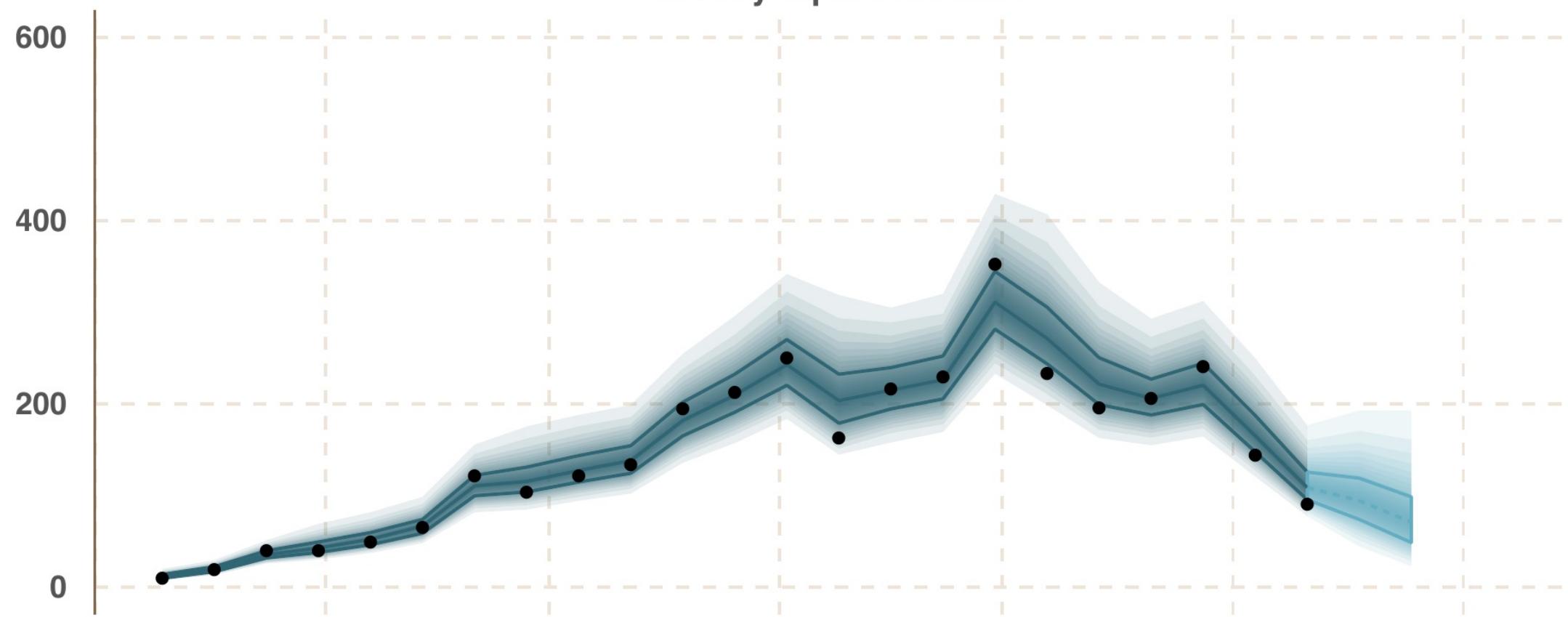
Weekly reported cases



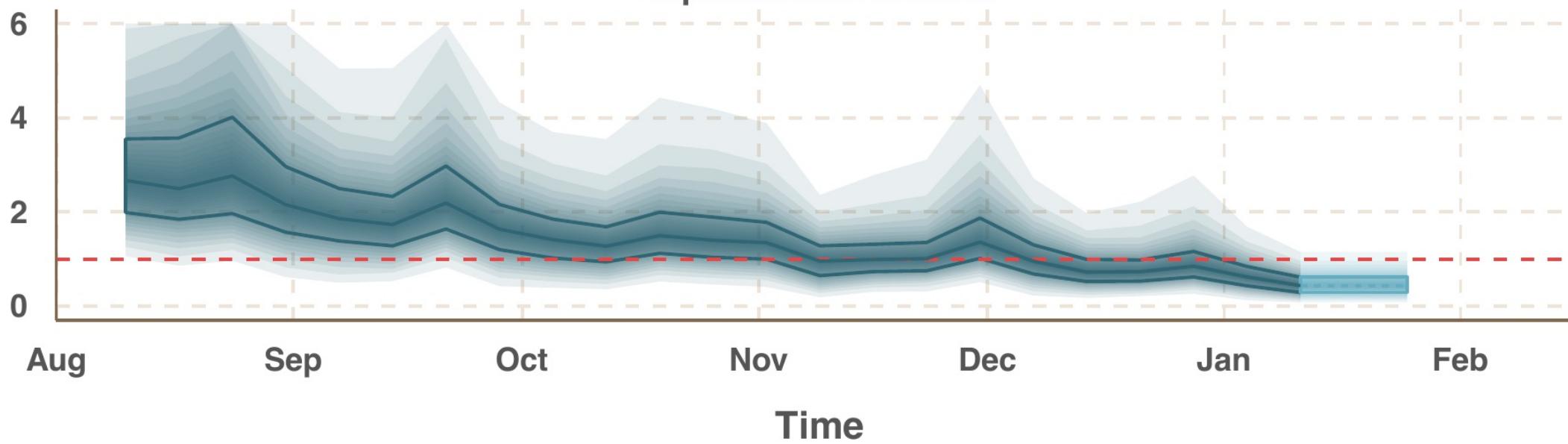
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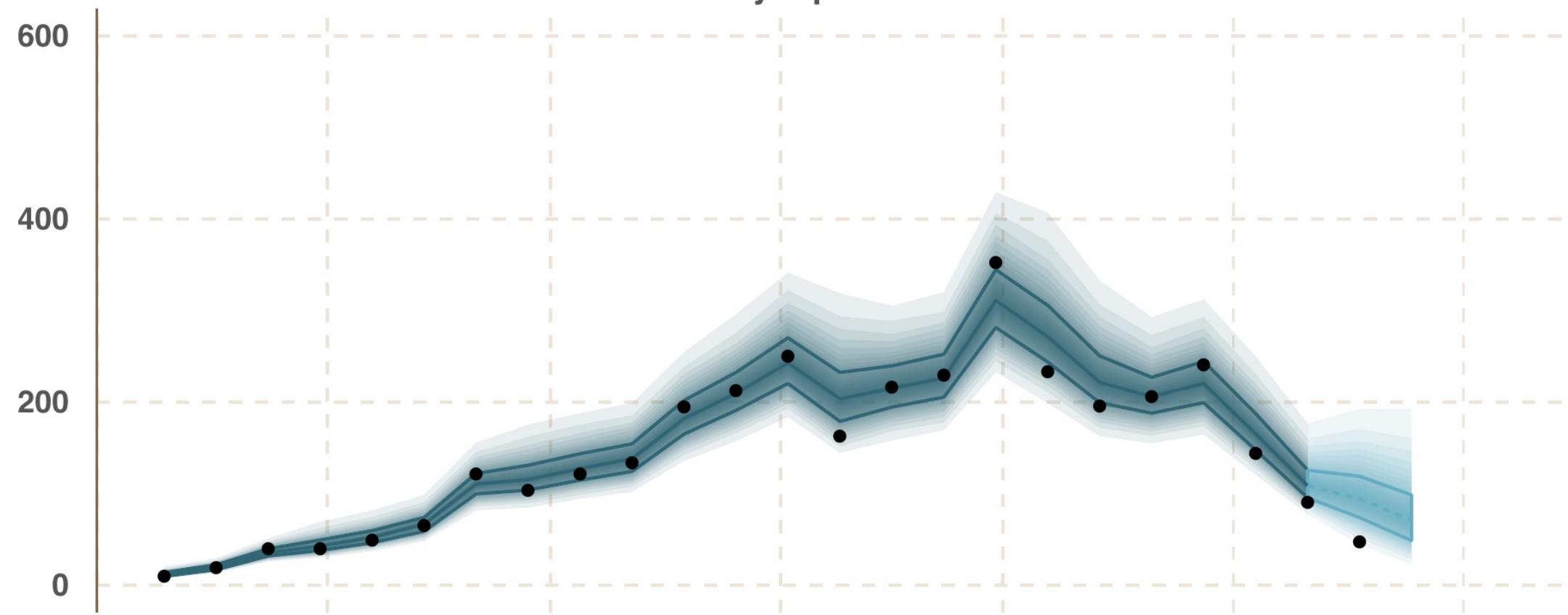
Weekly reported cases



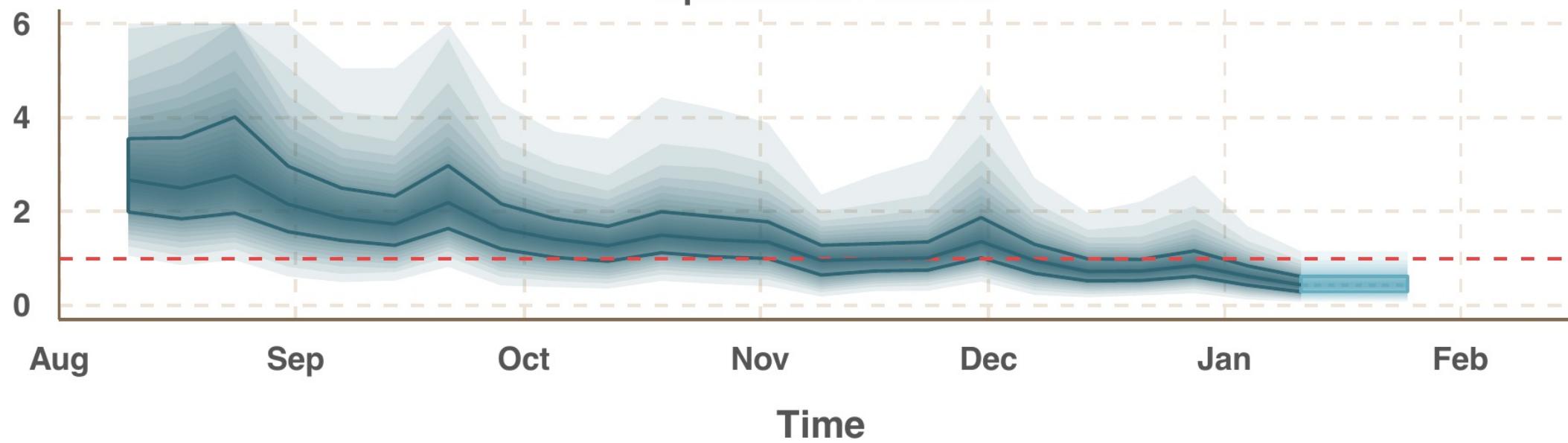
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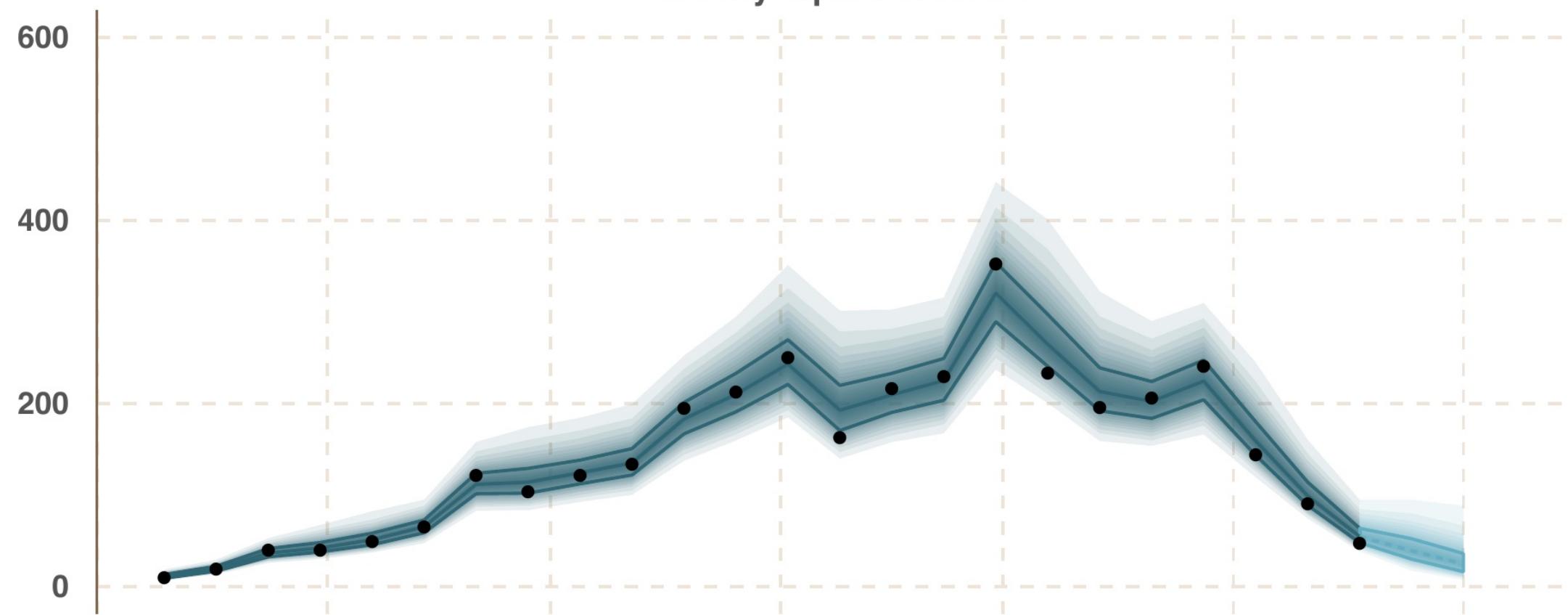
Weekly reported cases



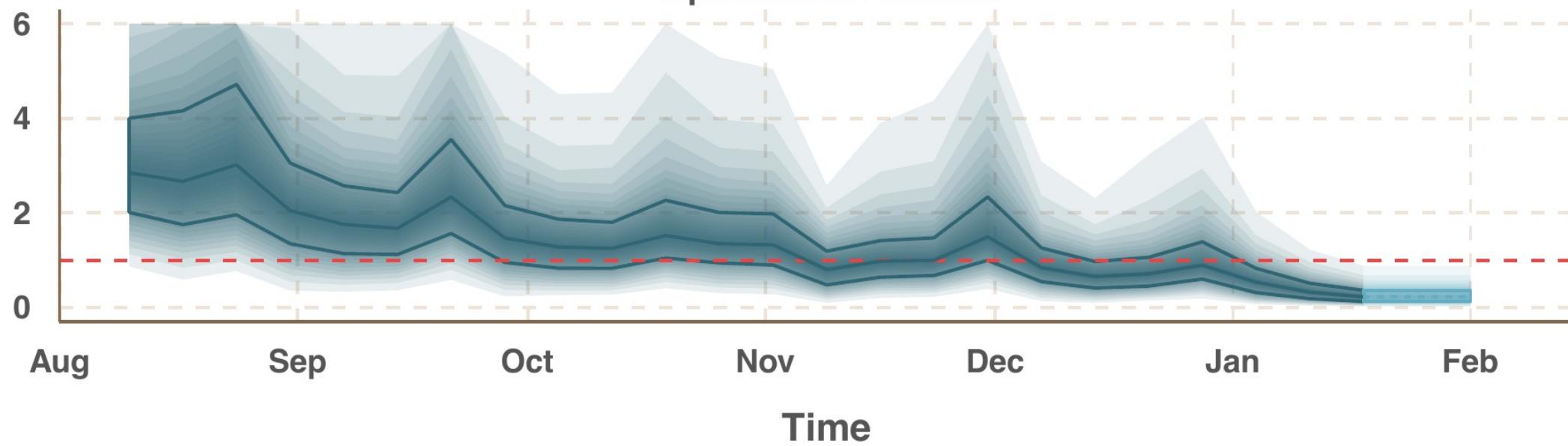
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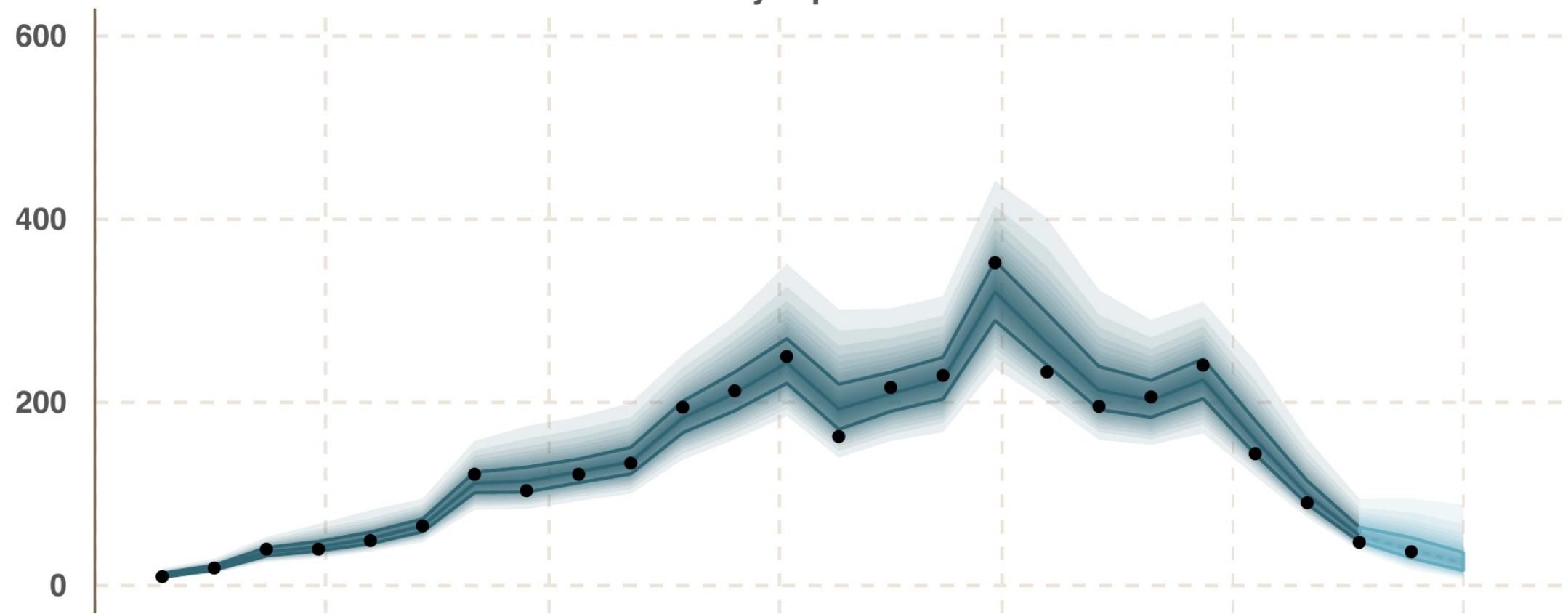
Weekly reported cases



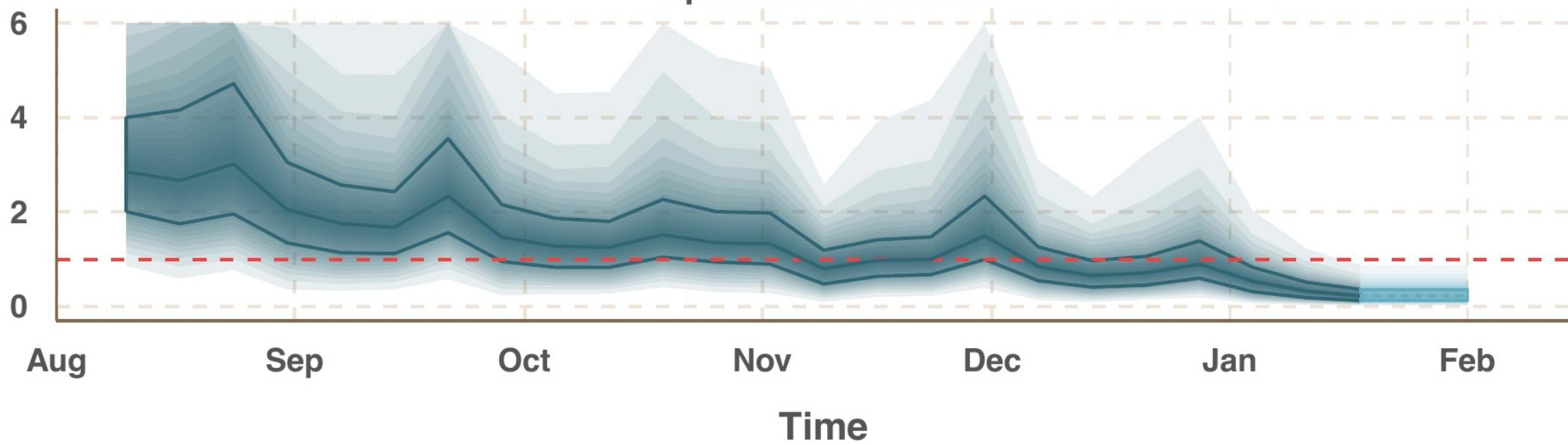
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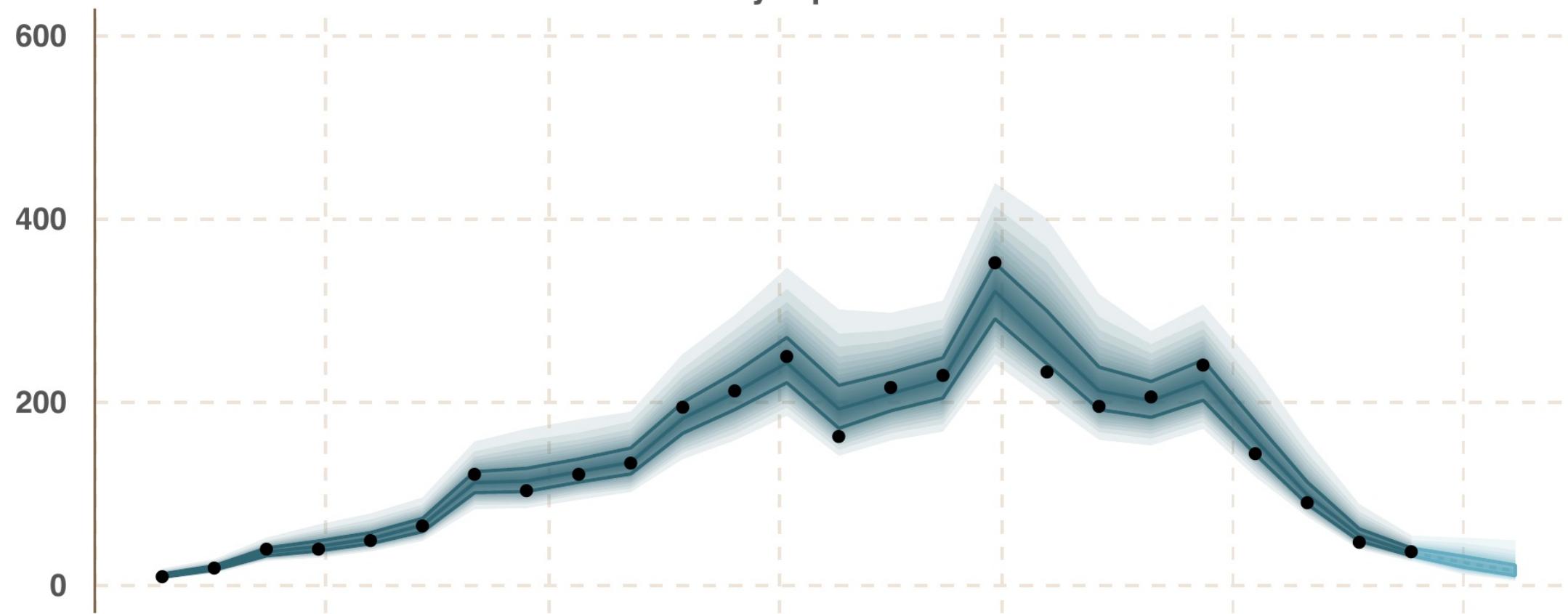
Weekly reported cases



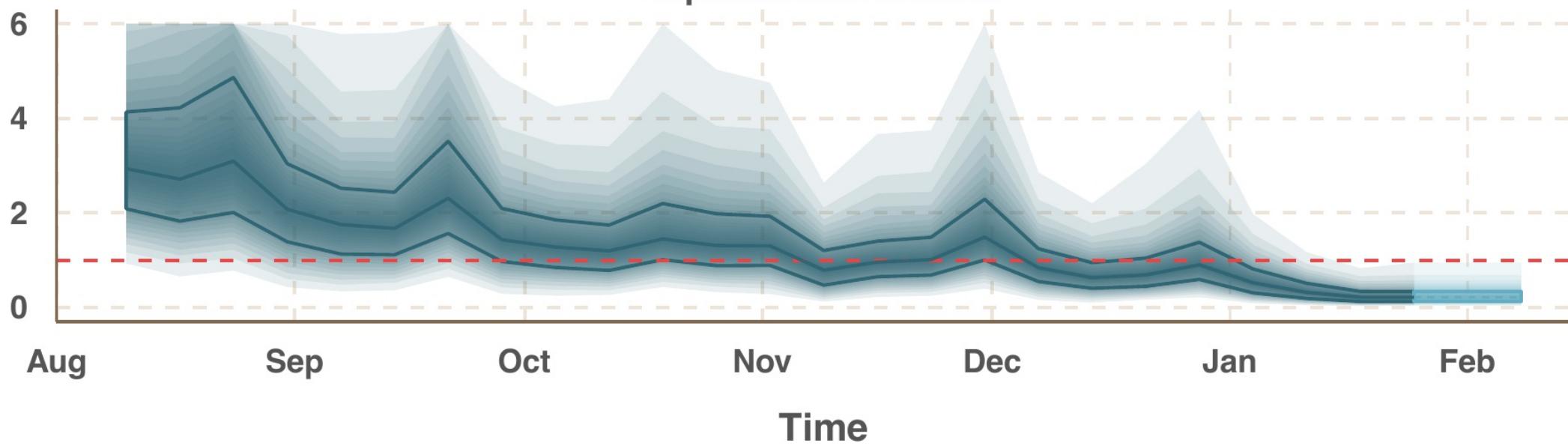
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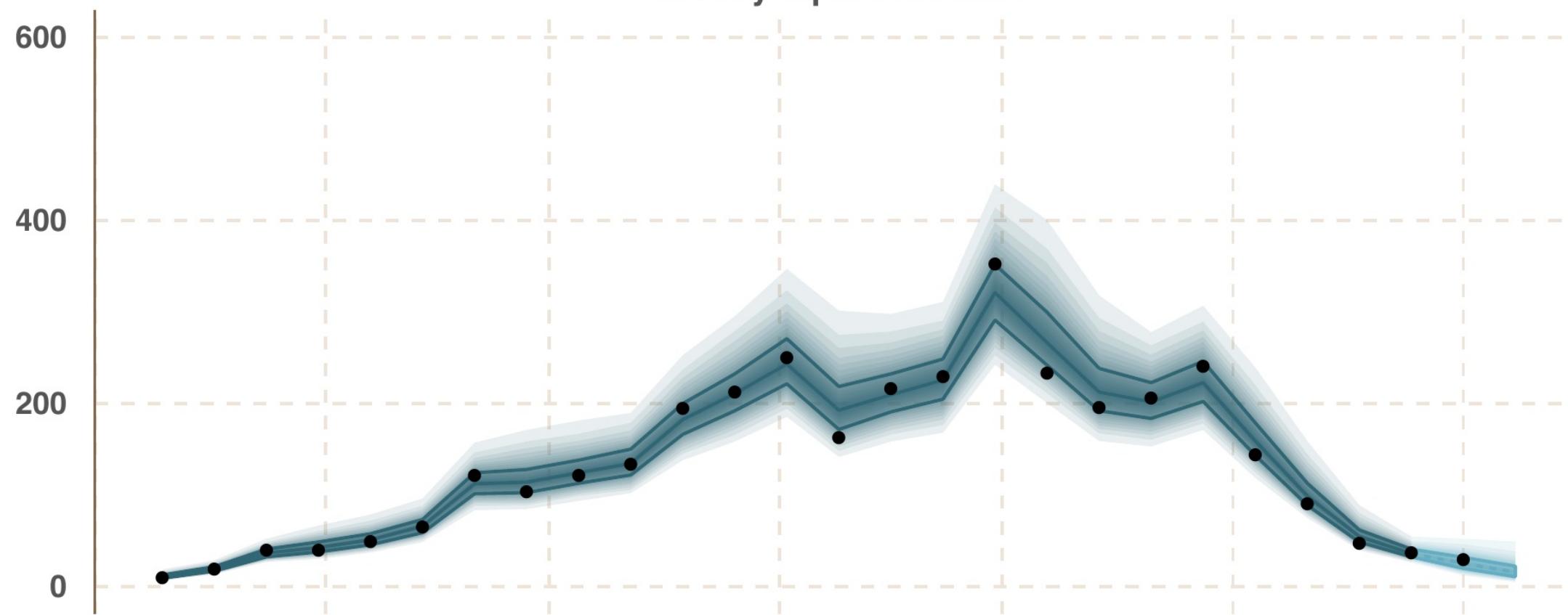
Weekly reported cases



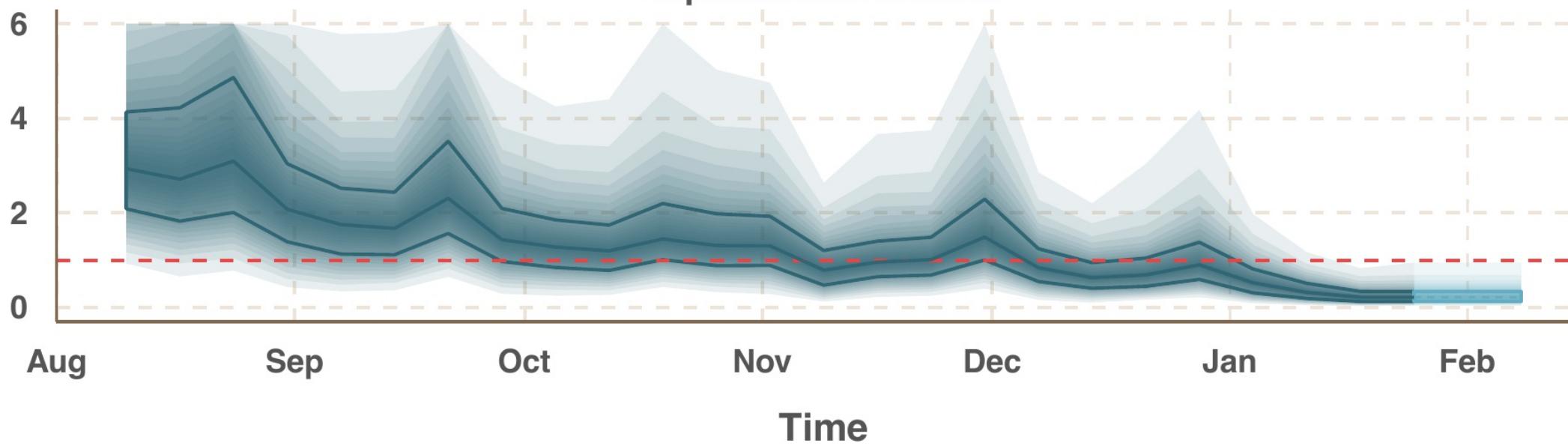
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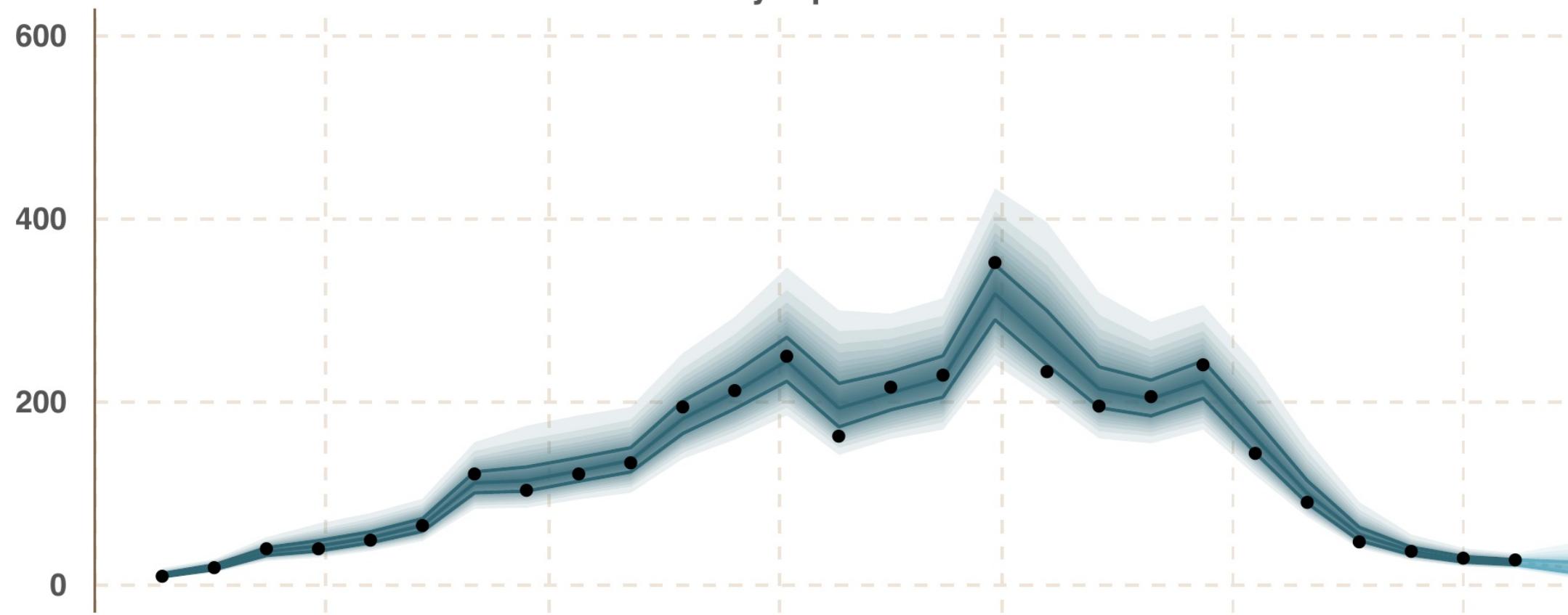
Weekly reported cases



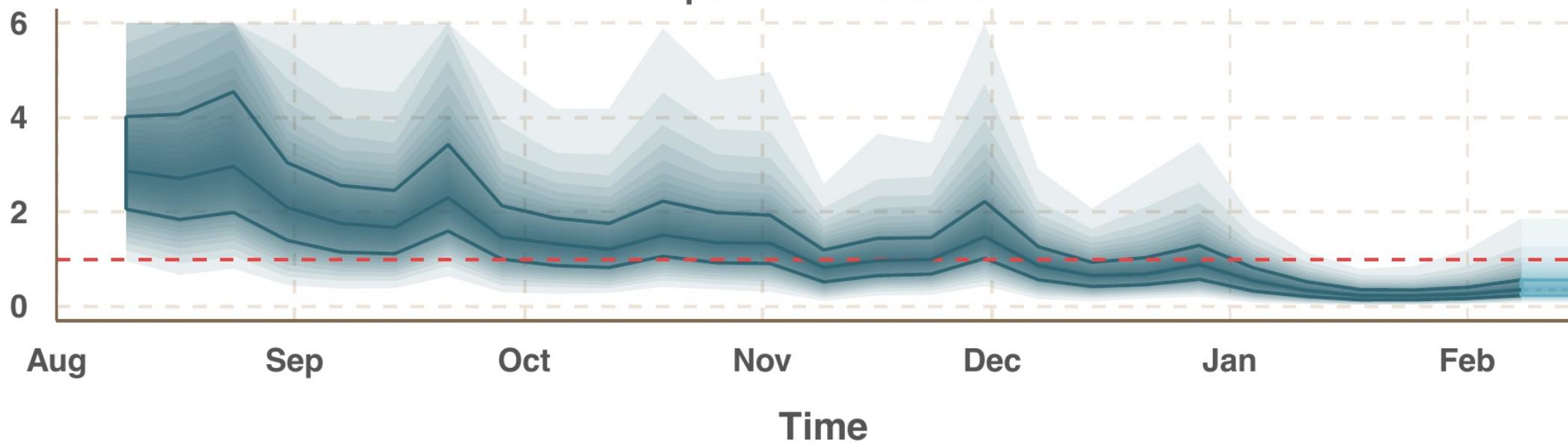
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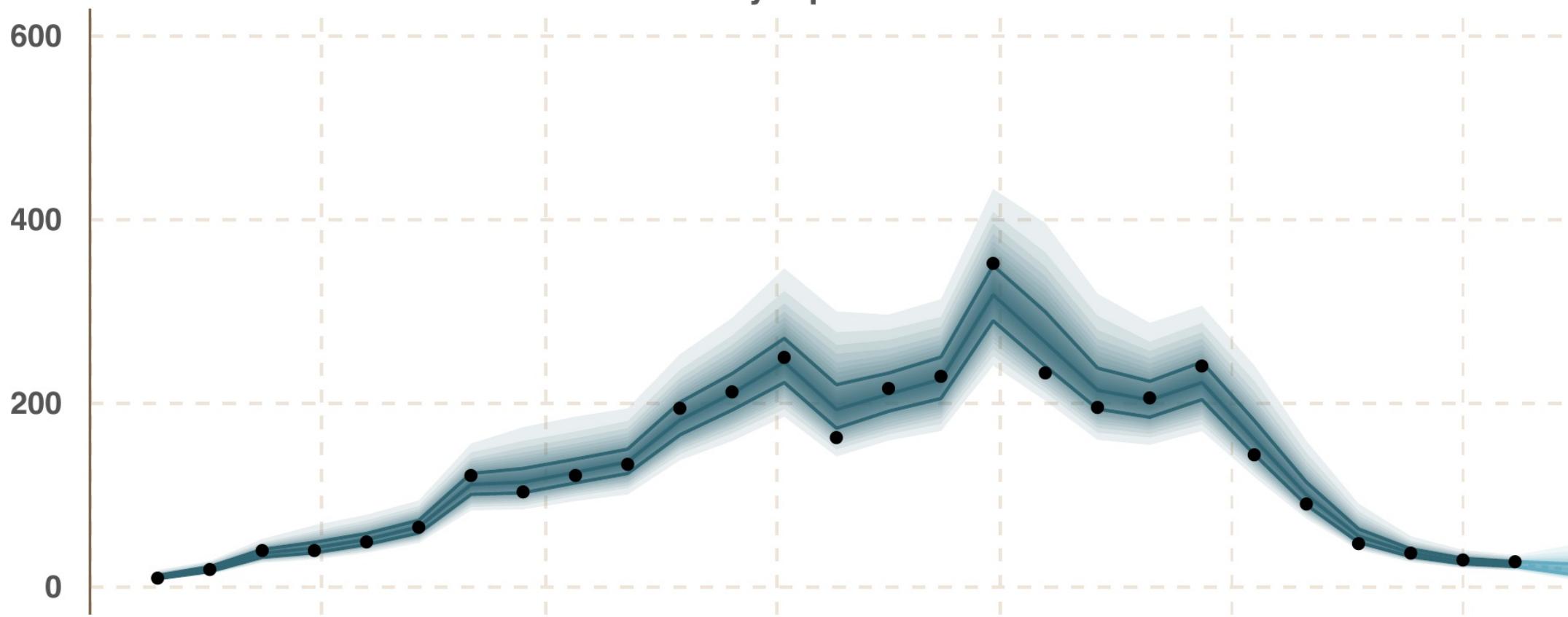
Weekly reported cases



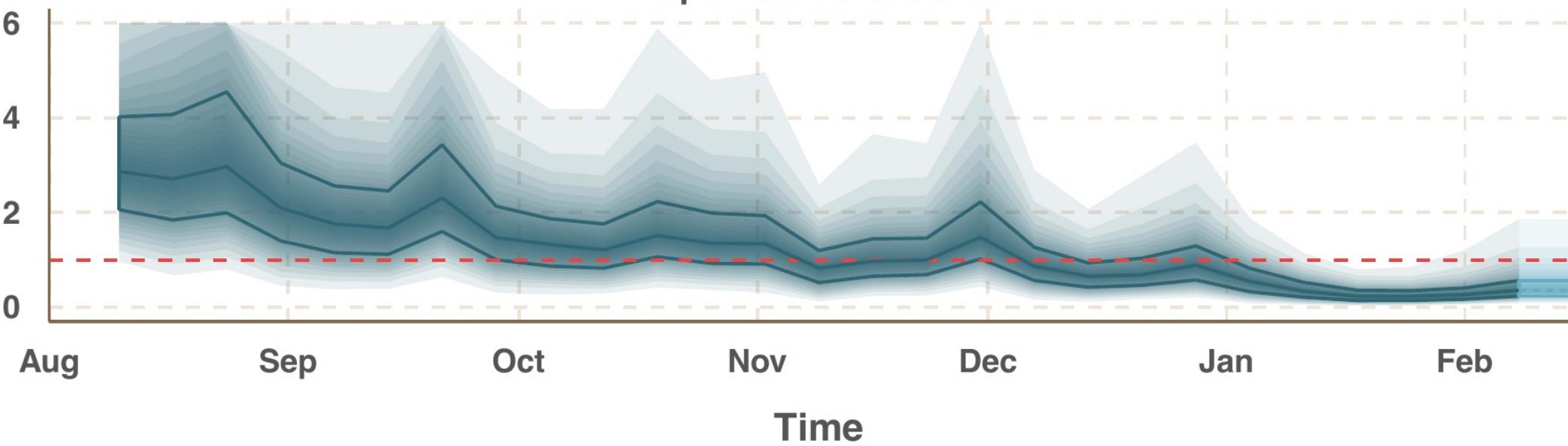
Reproduction number



Weekly reported cases



Reproduction number



The screenshot shows a web browser window with the URL `ntncmch.github.io` in the address bar. The main content is a dark-themed page with white text. The title is "Visualisation and projections of the Ebola outbreak in West Africa" by the Centre for the Mathematical Modelling of Infectious Diseases at the London School of Hygiene & Tropical Medicine. Below the title is a bulleted list of links: "Latest weekly reports", "Modelling and projections", "Interactive maps", "Motivation", and "Funding". Under "Latest weekly reports", there are three items: Liberia (up to 15 March 2015), Sierra Leone (up to 15 March 2015), and Guinea (up to 15 March 2015). Under "Modelling and projections", there are three items: Liberia currently does not have any confirmed cases of Ebola, Our modelling analysis is provided in a separate report, and We provide a summary of our projections. Under "Interactive maps", there is one item: Display a menu.

Visualisation and projections of the Ebola outbreak in West Africa

by the Centre for the Mathematical Modelling of Infectious Diseases
London School of Hygiene & Tropical Medicine

- [Latest weekly reports](#)
- [Modelling and projections](#)
- [Interactive maps](#)
- [Motivation](#)
- [Funding](#)

Latest weekly reports

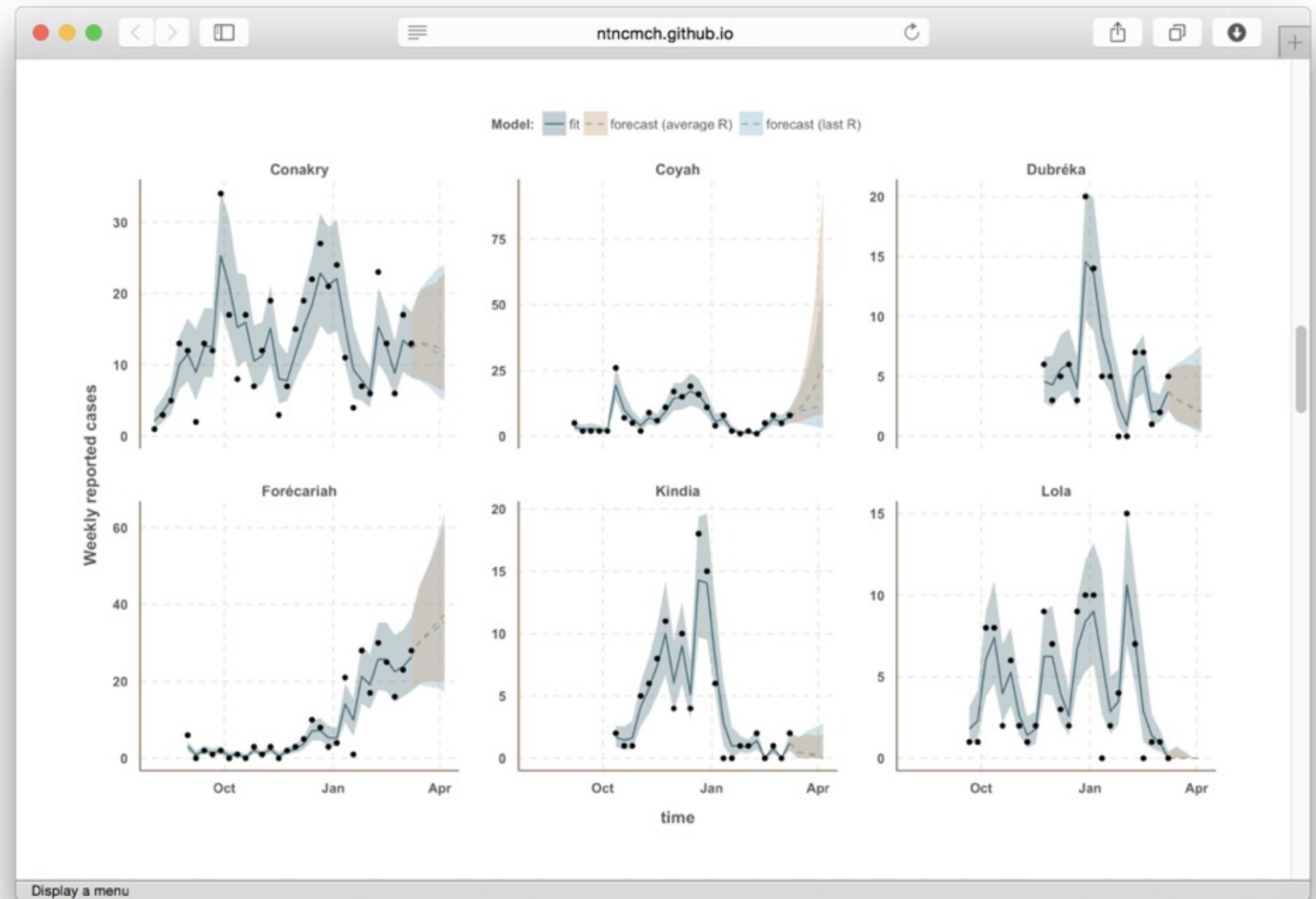
- Liberia (up to 15 March 2015): view [online version](#) or download [pdf slides](#)
- Sierra Leone (up to 15 March 2015): view [online version](#) or download [pdf slides](#)
- Guinea (up to 15 March 2015): view [online version \(French version\)](#) or download [pdf slides \(French version\)](#)

Modelling and projections

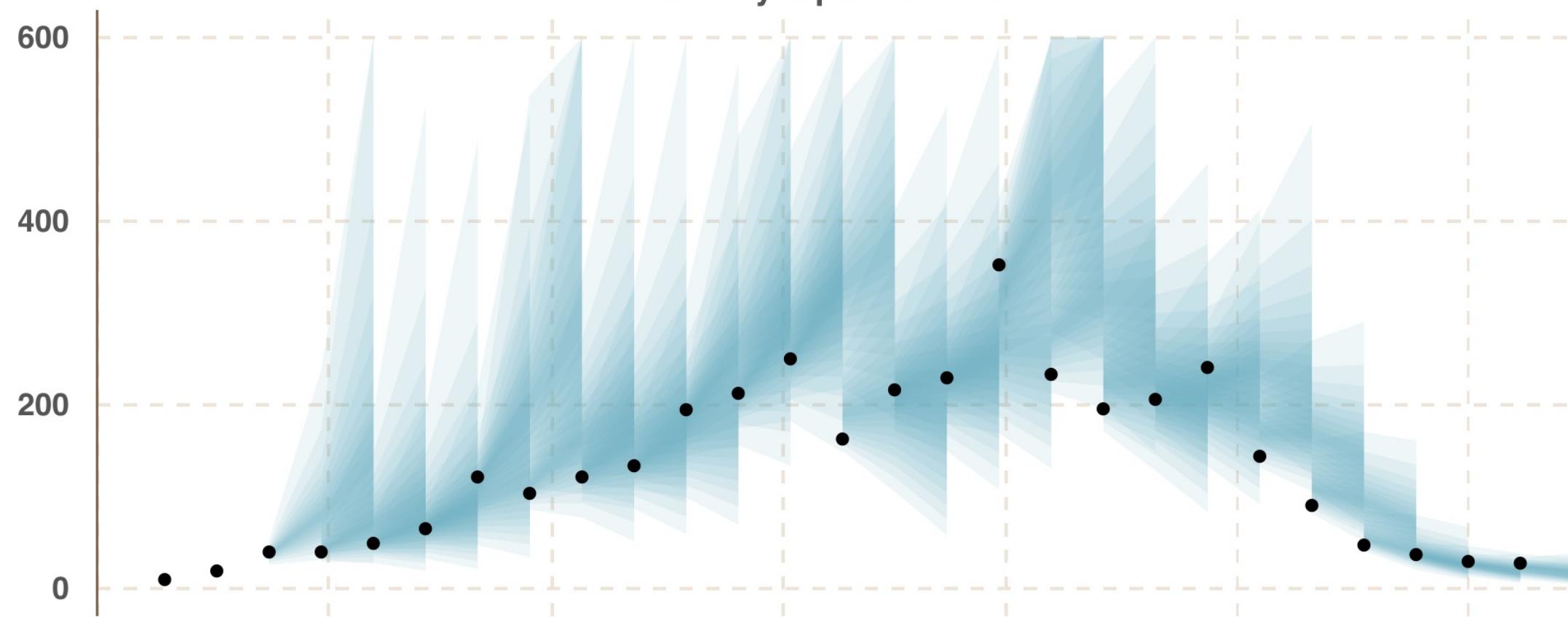
- Liberia currently does not have any confirmed cases of Ebola, and is therefore no longer included in the modelling and projections.
- Our modelling analysis is provided in a separate report, which also includes a comparison between the SitReps and the WHO linelist data:
[view online version](#) or download [pdf slides](#)
- We provide a summary of our projections: view [online version](#) or download [pdf slides](#)

Interactive maps

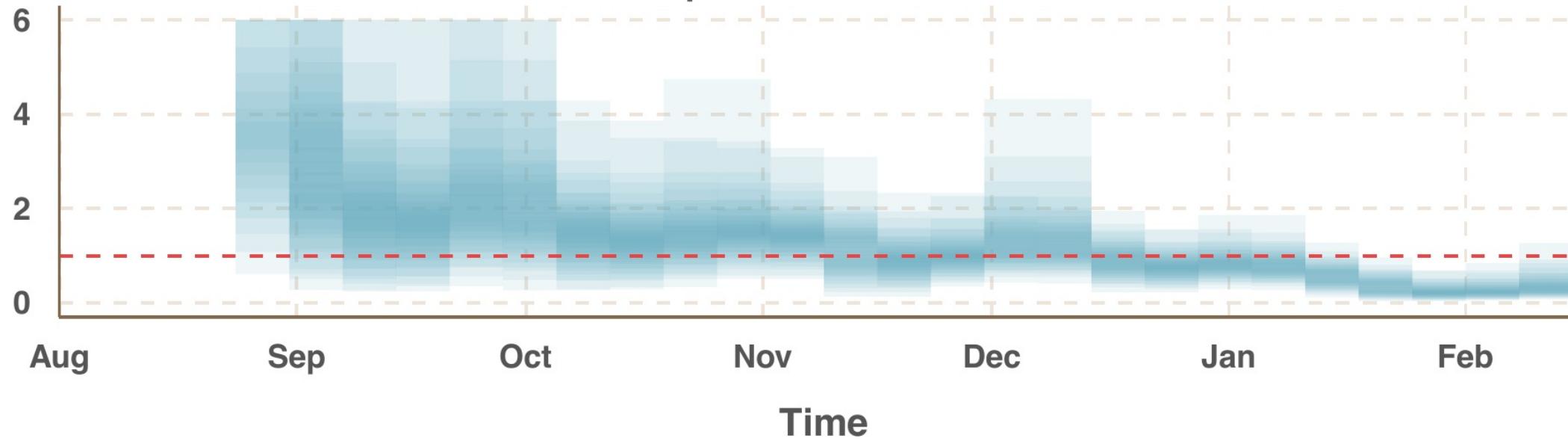
Display a menu



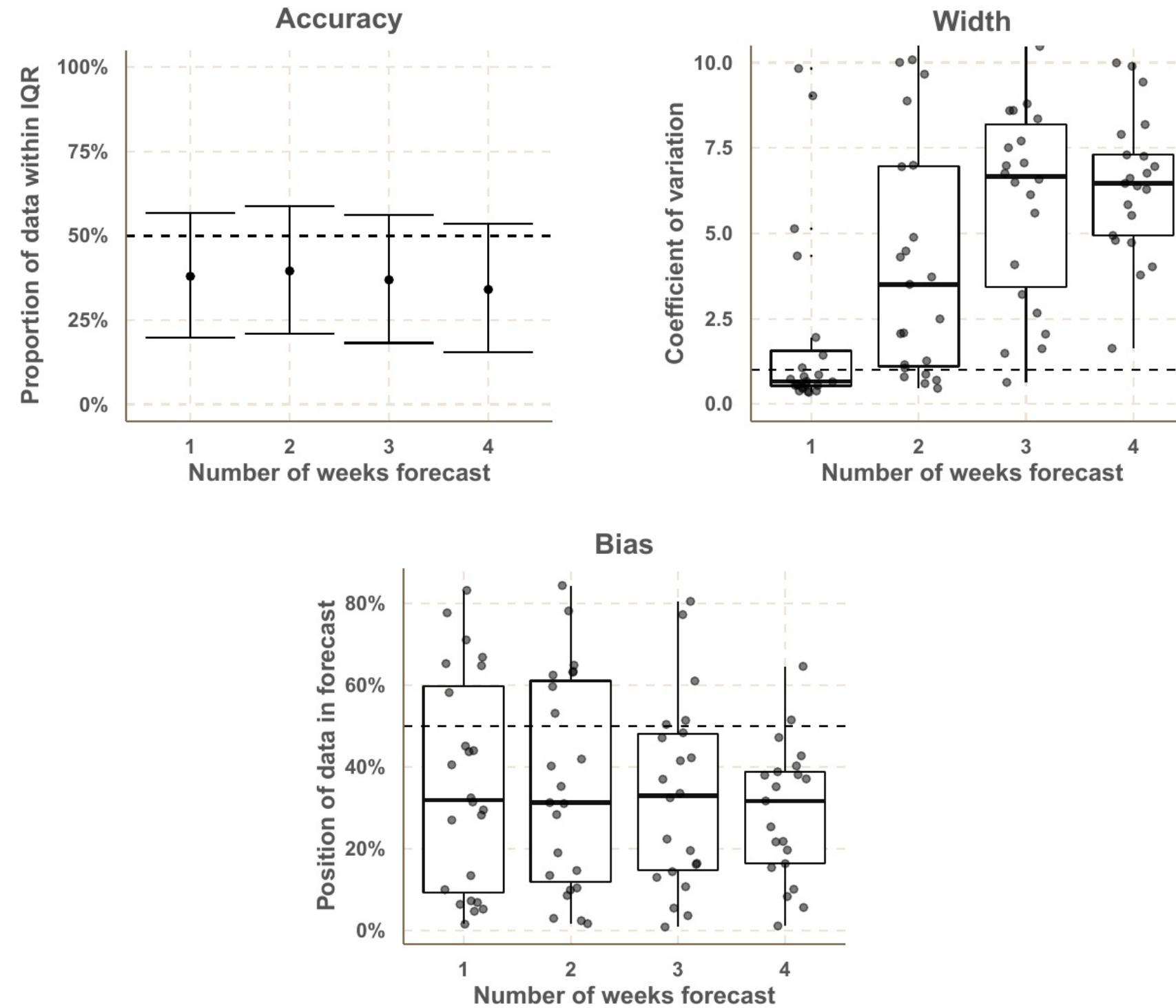
Weekly reported cases



Reproduction number

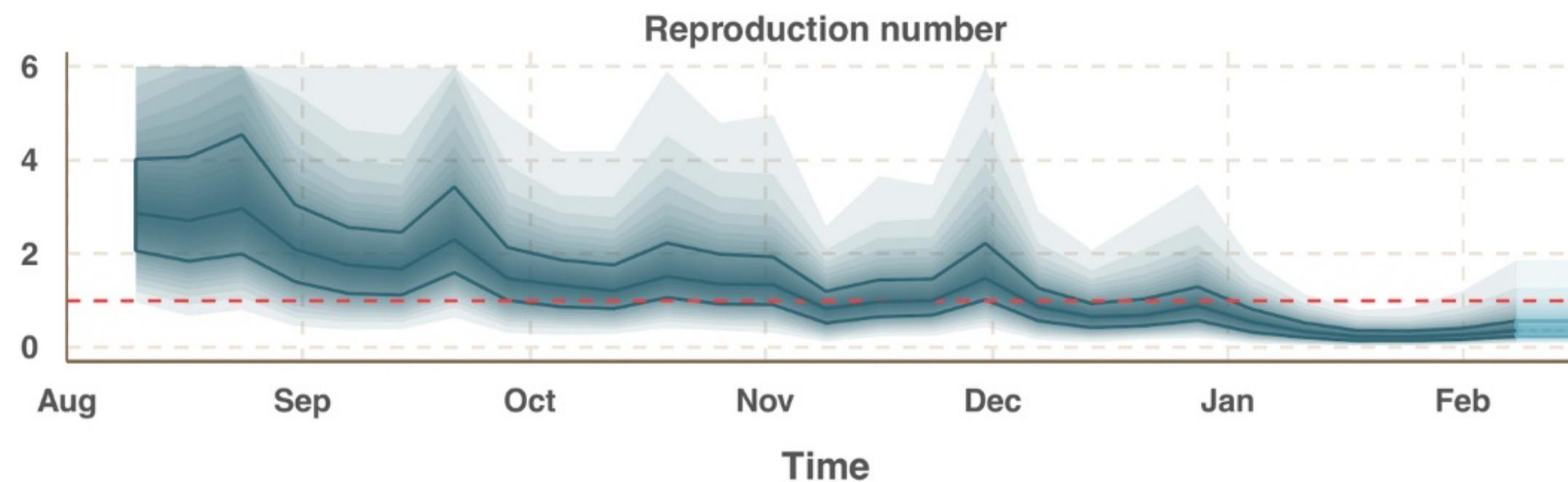


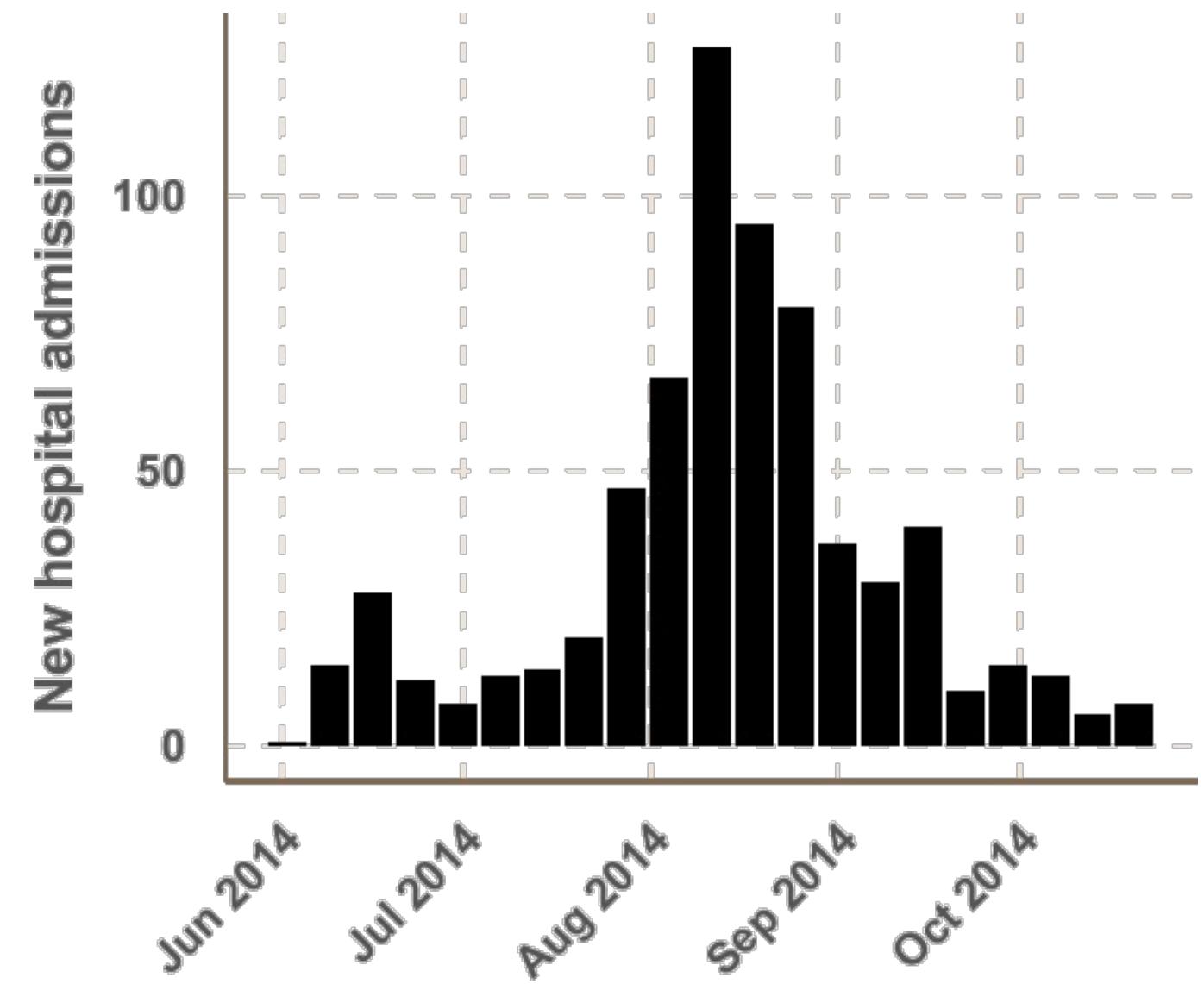
Assessing forecasts



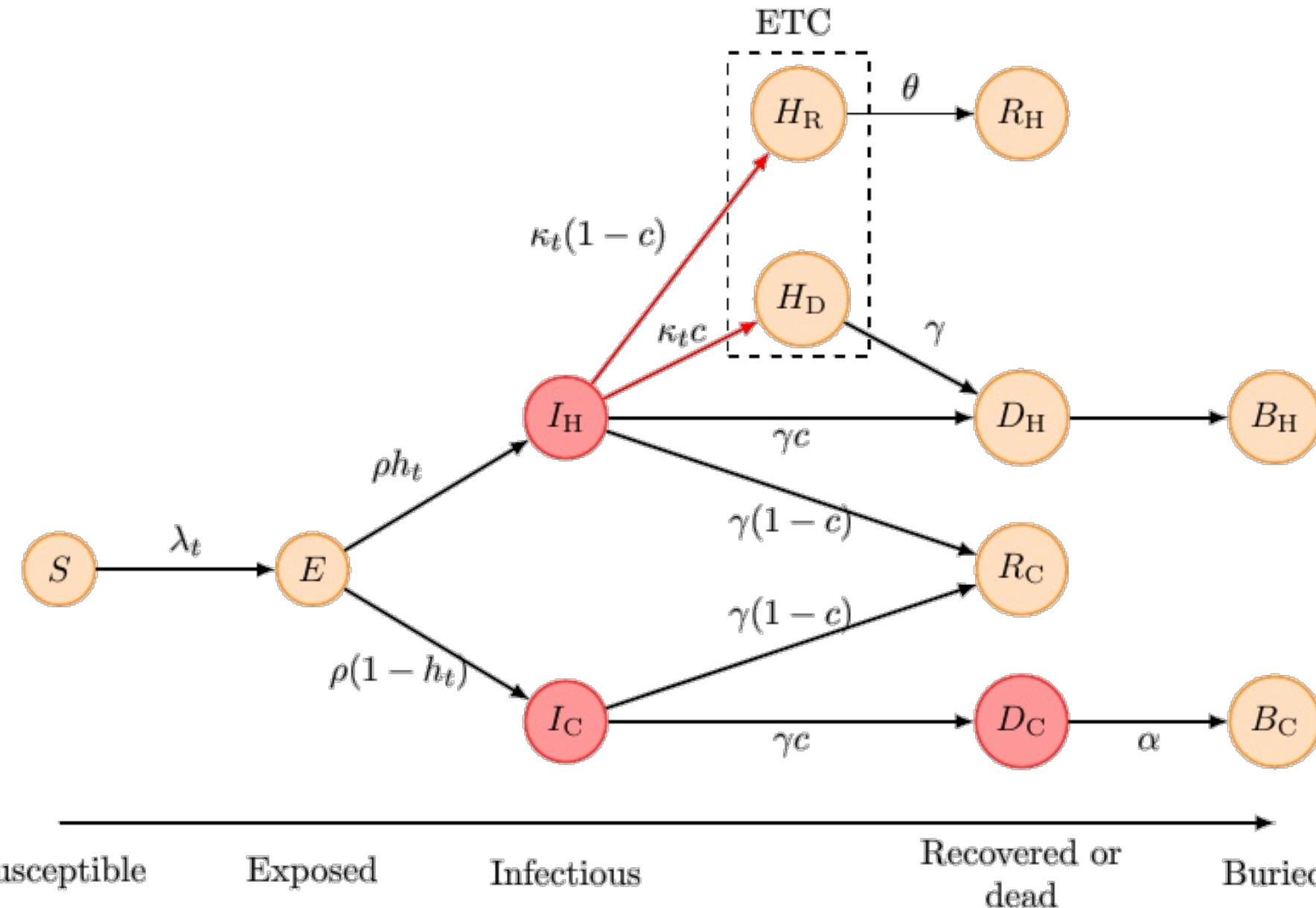
Learning from the uncertain

Filtered trajectories tell us something about dynamics

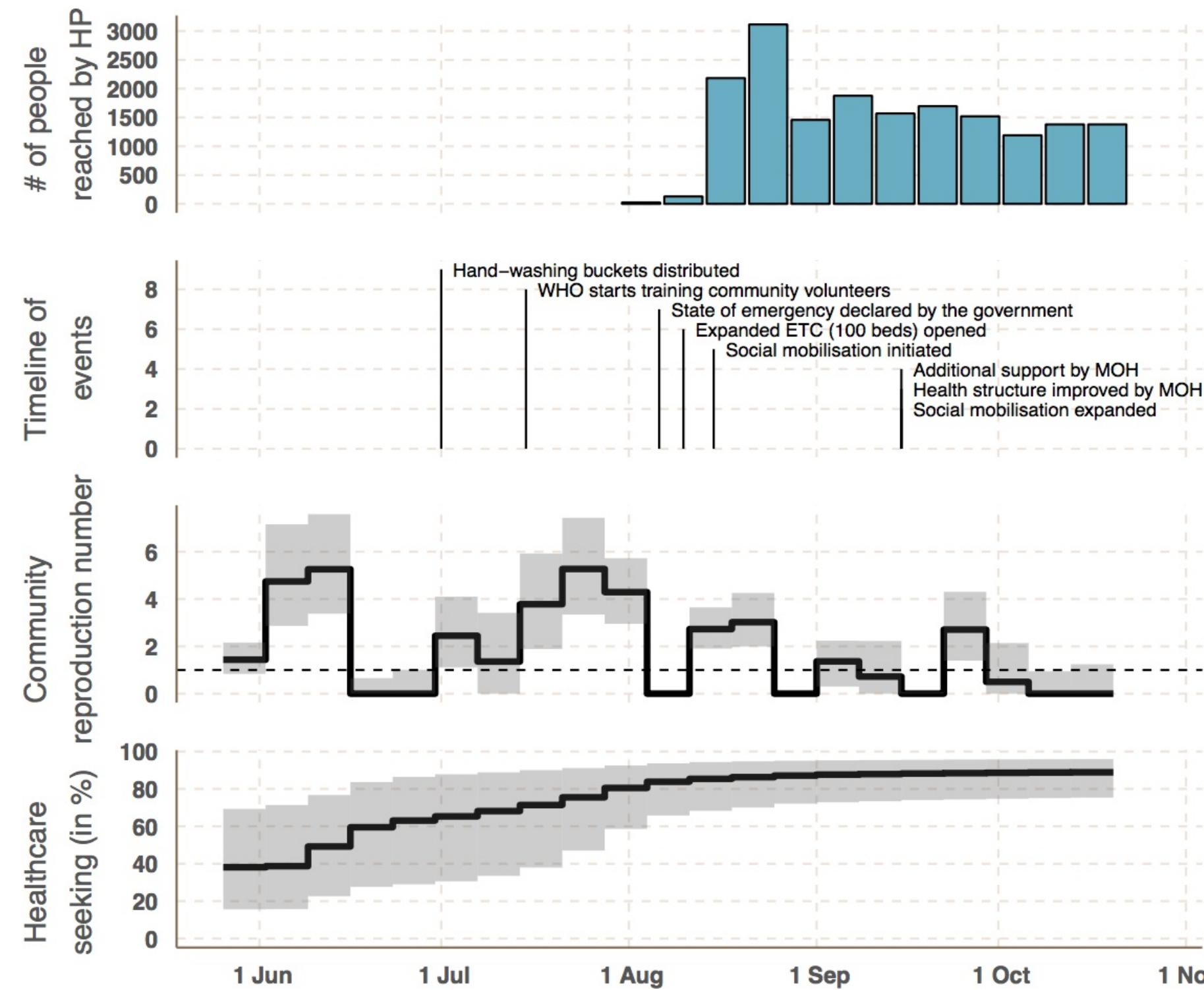




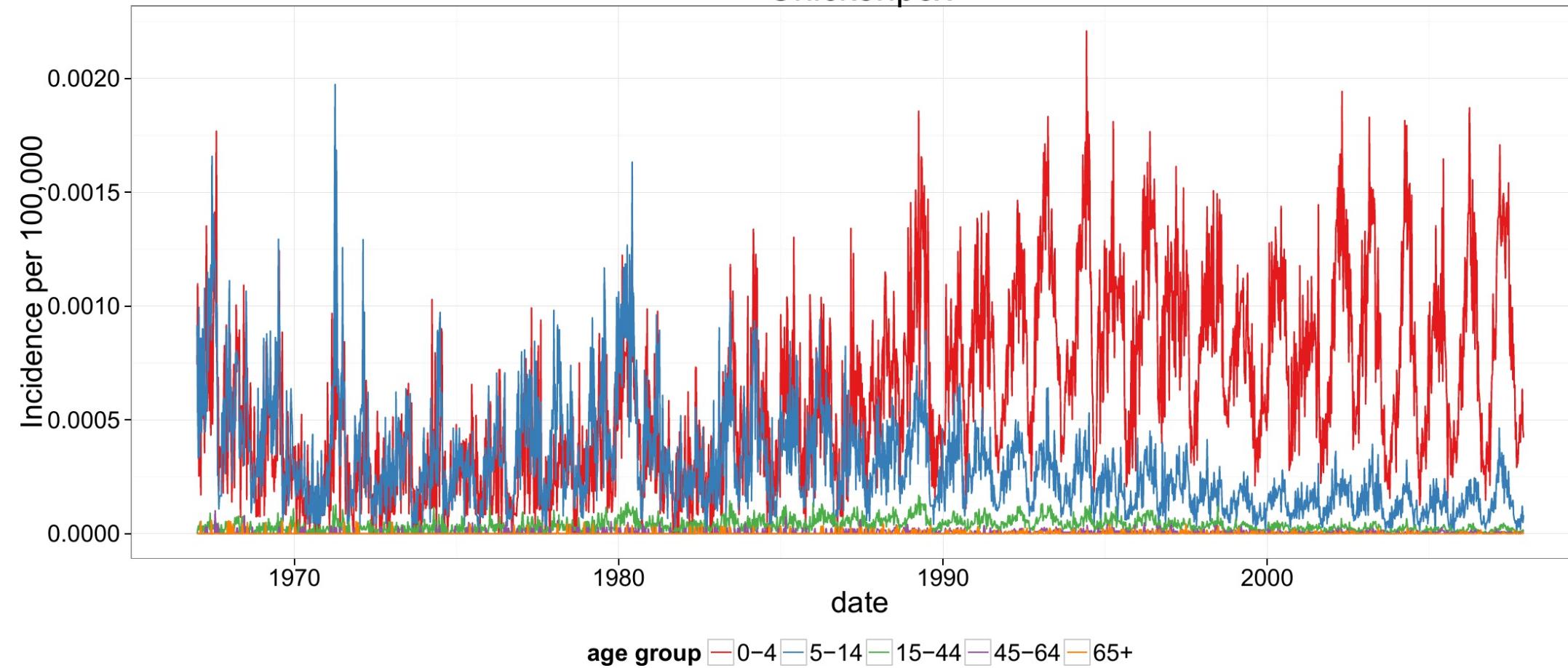
An attempt to tease out factors that controlled Ebola

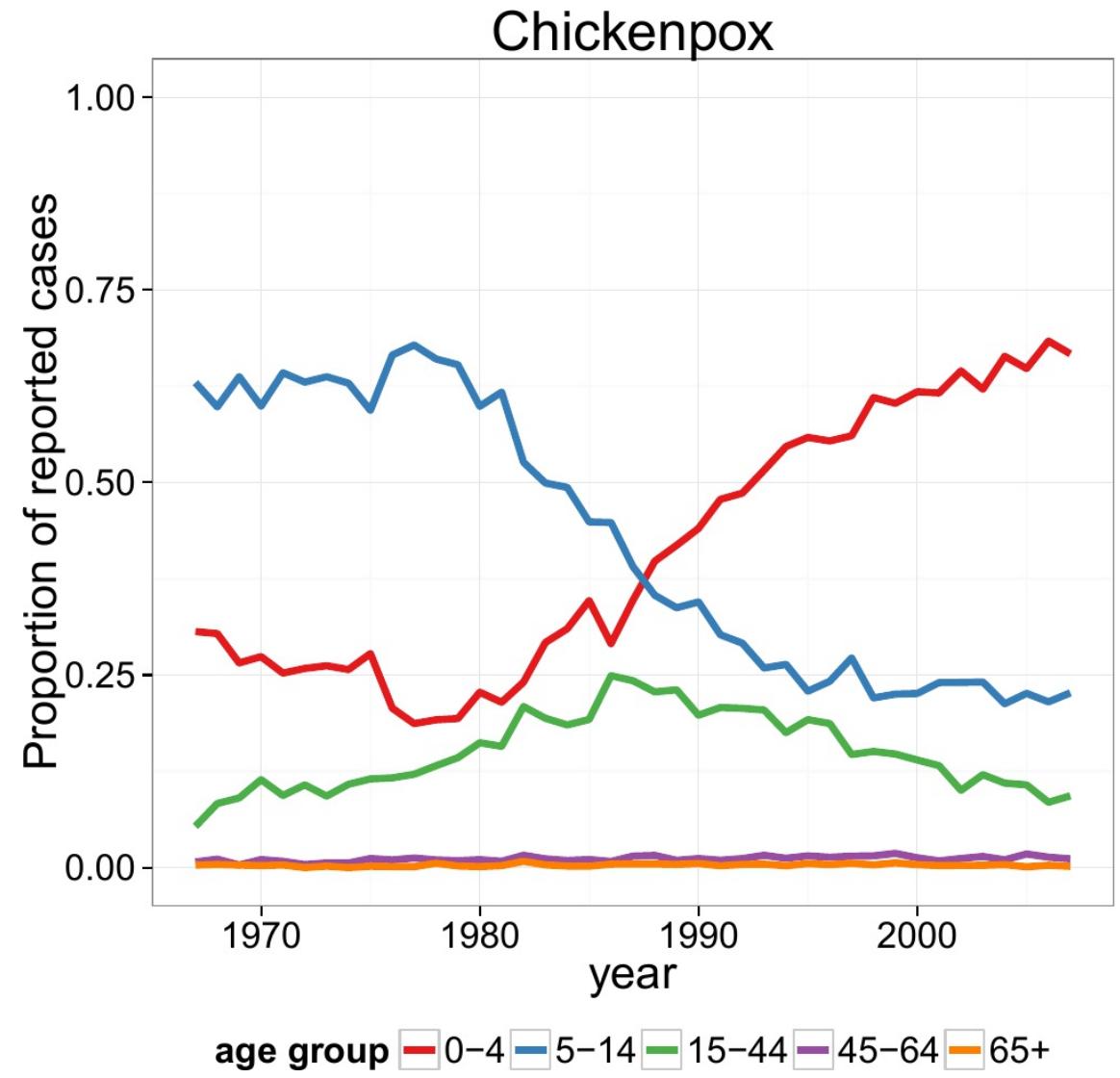


An attempt to tease out factors that controlled Ebola



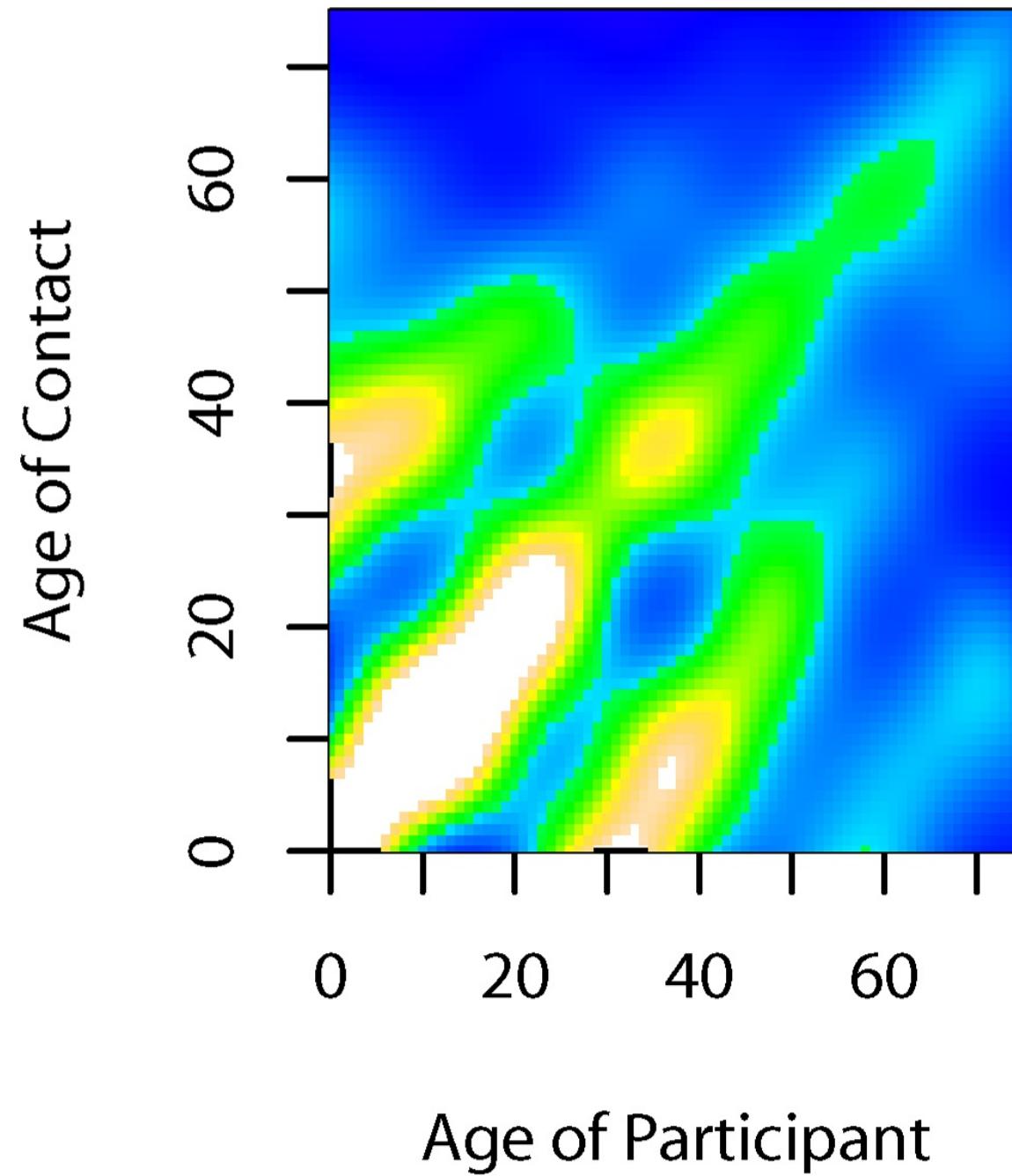
Chickenpox

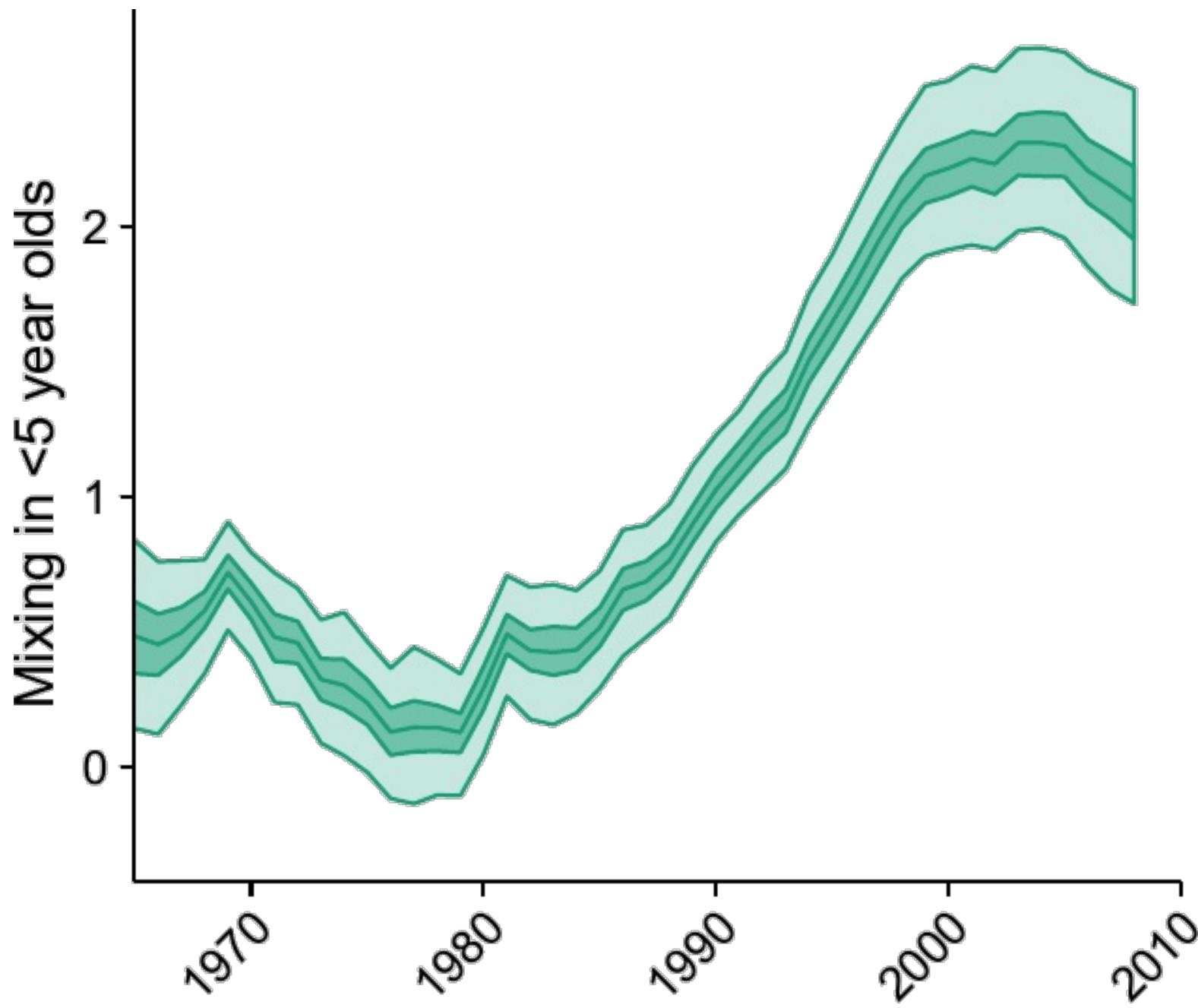




of varicella. Furthermore, an important shift in the age-specific incidence of infection has been observed in the United Kingdom. Interestingly, the shift in the age distribution of consultations in the United Kingdom coincides with a significant increase in children attending preschool [1, 42, 43]. Between 1970 and 1992 the number of children attending preschool has increased from 10 to 50% [1]. In contrast, the

GB





Outlook

Forecasts are becoming part of outbreak response

TOWARDS EPIDEMIC PREDICTION: FEDERAL EFFORTS AND OPPORTUNITIES IN OUTBREAK MODELING

PRODUCT OF THE
Pandemic Prediction and Forecasting
Science and Technology Working Group
OF THE NATIONAL SCIENCE AND TECHNOLOGY COUNCIL



December 2016

Forecasting challenges



The screenshot shows the FluSight 2016-17 website. At the top left is the 'Epidemic Prediction Initiative' logo with a 'BETA' button. To the right are 'LOGIN' and 'CREATE AN AC' buttons. The main title 'FluSight 2016-17' is prominently displayed. Below it, there are two navigation links: 'Home' (with a house icon) and 'National Forecasts' (with a circular icon). A sidebar on the right contains the text: 'FluSight: Seasonal Influenza Forecasting' and 'Influenza (flu) is a respiratory virus that can result in illness ranging from mild to severe. Each year, millions of people get sick with influenza, thousands are hospitalized and thousands of people die from flu-related complications.'

The screenshot shows the Dengue Forecasting project website, operated by the National Oceanic and Atmospheric Administration (NOAA). At the top left is the NOAA logo. The main title is 'DENGUE FORECASTING' in large, bold, black letters, with 'NATIONAL OCEANIC AND ATMOSPHERIC ADMINISTRATION' in smaller letters below it. Below the title are four navigation links: 'HOME', 'NEWS', 'ABOUT', and 'SEARCH'. A welcome message at the bottom states: 'Welcome to the Dengue Forecasting project website. This site is designed specifically for the data, rules and background about the effort.'

Forecasting methodology is underdeveloped

Need methods to **select the best model** and
combine all available **data streams**
(individual/spatial/genetic/media)

New tools



LibBi

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Stable

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Dev

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LibBi has been developed under a [CSIRO](#) project that forms part of the [Computational and Simulation Sciences](#) platform.

Website theme adapted from work by [orderedlist](#).

LibBi is used for state-space modelling and Bayesian inference on high-performance computer hardware, including multi-core CPUs, many-core GPUs (graphics processing units) and distributed-memory clusters.

The staple methods of LibBi are based on sequential Monte Carlo (SMC), also known as particle filtering. These methods include particle Markov chain Monte Carlo (PMCMC) and SMC². Other methods include the extended Kalman filter and some parameter optimisation routines.

LibBi consists of a C++ template library, as well as a parser and compiler, written in Perl, for its own modelling language.

News

- [LibBi 1.3.0 released, new anytime features](#)

14 Dec 2016

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19 Oct 2016

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14 Nov 2016
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19 Oct 2016

Bayesian inference with state-space models in R



rbi: R Interface to LibBi

Provides a complete R interface to LibBi, a library for Bayesian inference (see <<http://libbi.org>> for more information). This includes functions for manipulating LibBi models, for reading and writing LibBi input/output files, for converting LibBi output to provide traces for use with the coda package, and for running LibBi from R.

Version:	0.6.0
Depends:	methods, data.table
Imports:	reshape2 , ncdf4
Suggests:	coda , R.rsp
Published:	2016-12-23
Author:	Pierre E. Jacob [aut], Anthony Lee [ctb], Lawrence M. Murray [ctb], Sebastian Funk [aut, cre]
Maintainer:	Sebastian Funk < sebastian.funk@lshtm.ac.uk >
BugReports:	https://github.com/libbi/RBi/issues
License:	GPL-3
URL:	https://github.com/libbi/RBi
NeedsCompilation:	no
SystemRequirements:	LibBi (>= 1.2.0)
Materials:	README NEWS
CRAN checks:	rbi results

Acknowledgements

Anton Camacho, Adam Kucharski, Roz Eggo, John Edmunds (LSHTM)
Bruce Reeder, Etienne Gignoux, Iza Ciglenecki, Amanda Tiffany
(MSF)
James Hensman (Lancaster), Lawrence Murray (Uppsala)



Thank you!

<http://sbfnk.github.io>
@sbfnk