



# Tools for real-time nowcasting and $R_t$ estimation

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# Thank you to our collaborators on the EpiNow2 and epinowcast teams



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Hugo Grunson  
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Felix Guenther  
Pratik Gupte  
Luis Rivas  
... and many community contributors

**EpiNow2** 1.3.5

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Joe Hickson  
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Sebastian Funk  
... and many community contributors

# Take-home messages

1. Epidemic data inevitably contain lags, reporting effects, and other imperfections. This makes real-time analysis challenging.
2. Methods and tools designed to deal with predictable problems in the data are developing rapidly. But expert judgement is needed to choose the right tools and interpret the outputs.
3. CDC is working to support real-time epidemic analysis through
  - Funding for collaborations and growth of the talent pipeline
  - Open-source tool development
  - Testing tools on historical outbreak data → continuous improvement
  - Full-time team to produce and publish analyses at the state and territory level

# Agenda

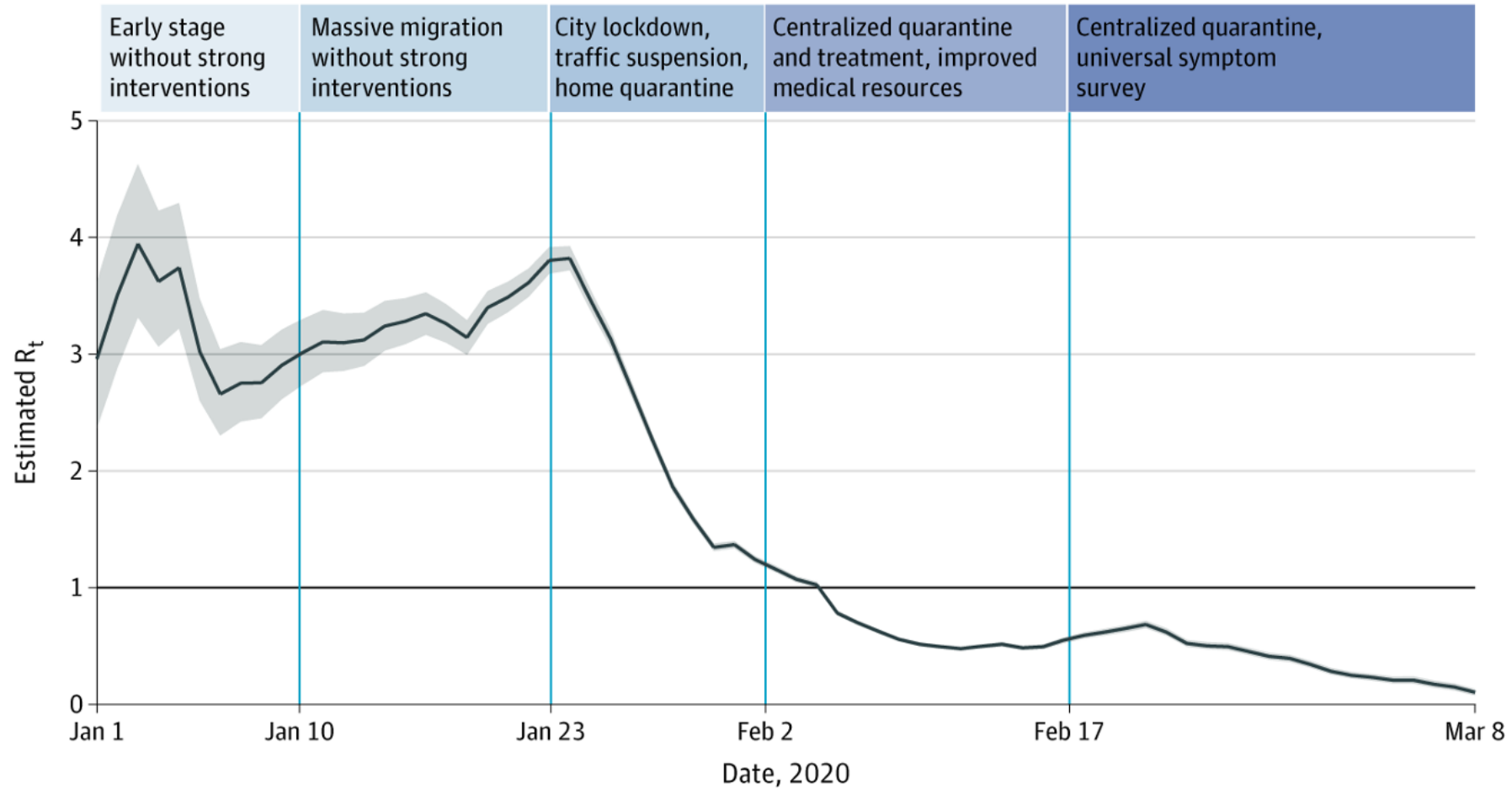
$R_t$  estimation with nowcasting

1. Case study:  $R_t$  estimation early in the COVID-19 pandemic
2.  $R_t$  definition and estimation
3. Pitfalls when estimating  $R_t$ 
  - Observation delays
  - Day-of-week effects and reporting artifacts
  - Partial observation at the end of the time series
4. Tools designed to avoid these pitfalls: EpiNow2, and epinowcast

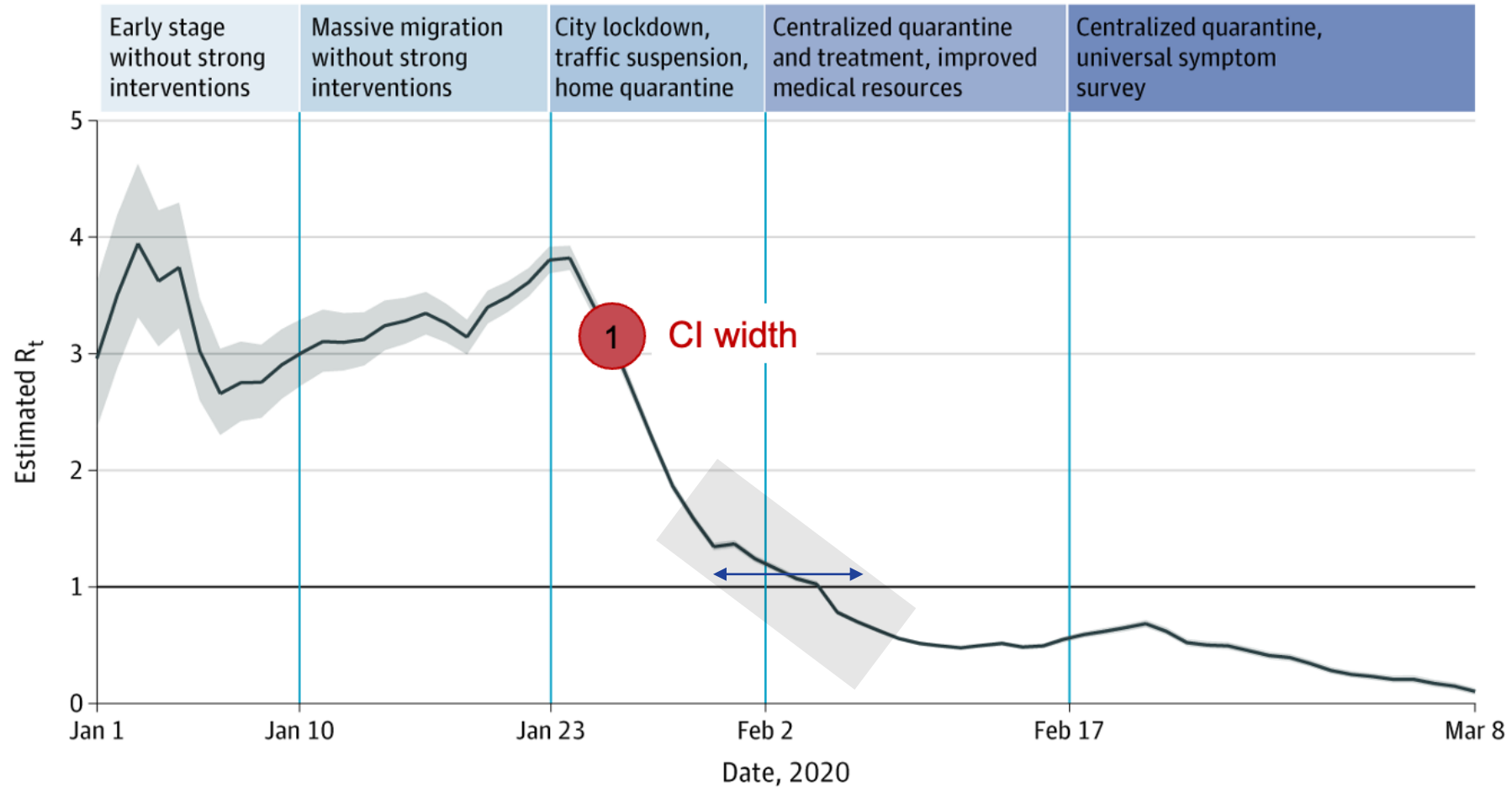


*1. Case study:  $R_t$  estimation early in the  
COVID-19 pandemic*

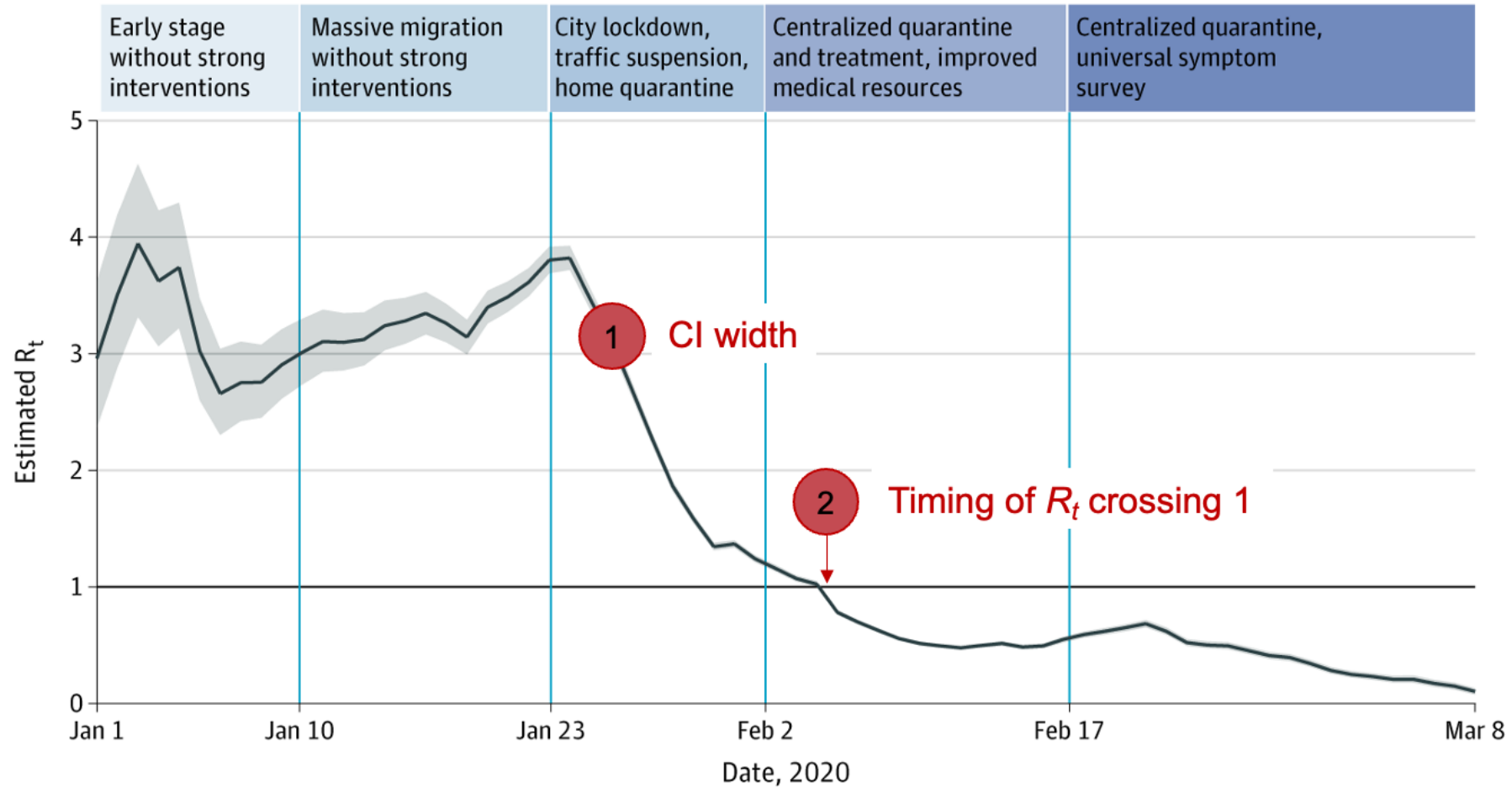
# Case study: $R_t$ estimation in practice



# Estimates must be accurate, timely, and account for uncertainty

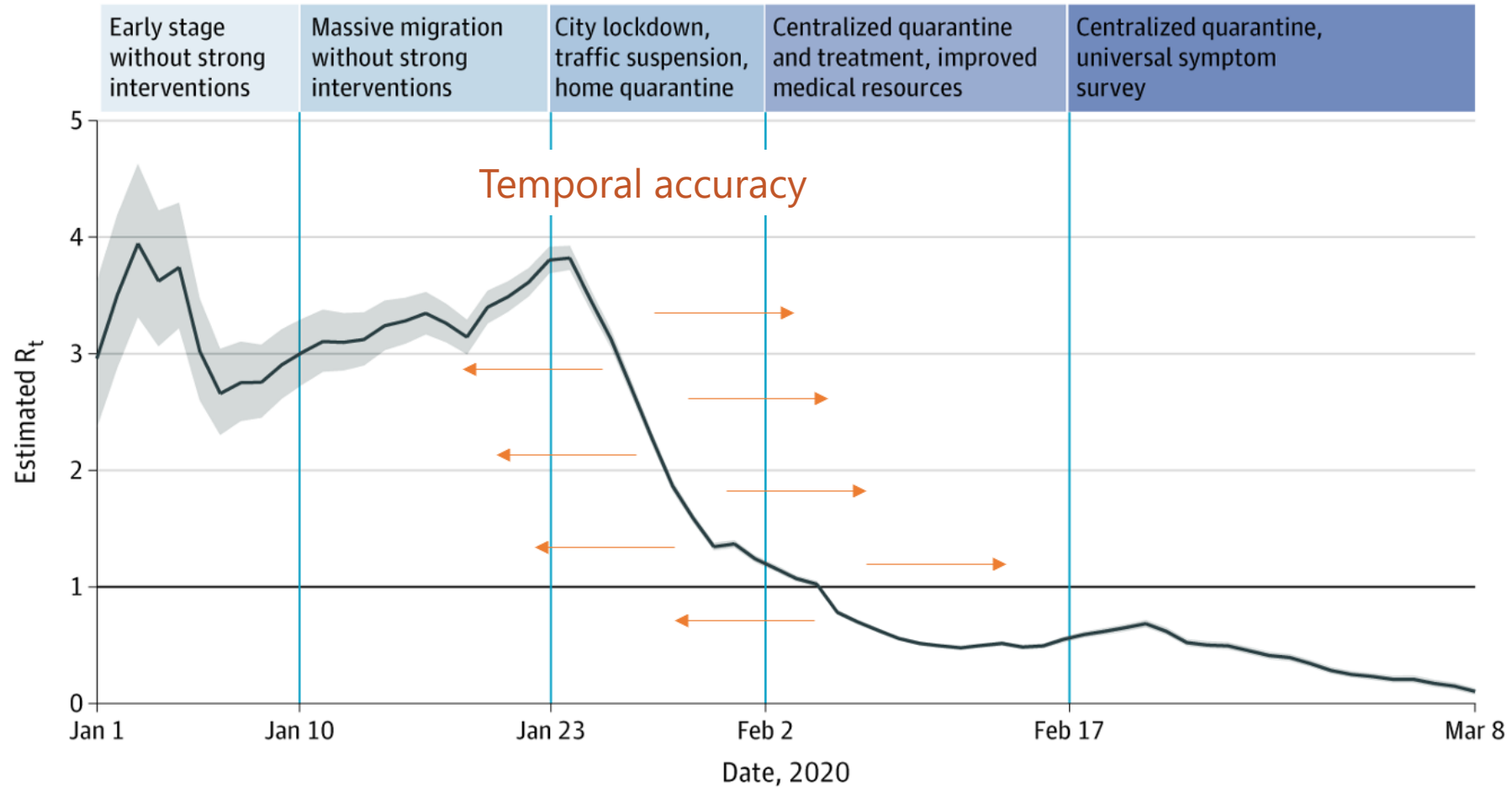


# Estimates must be correctly oriented to the calendar





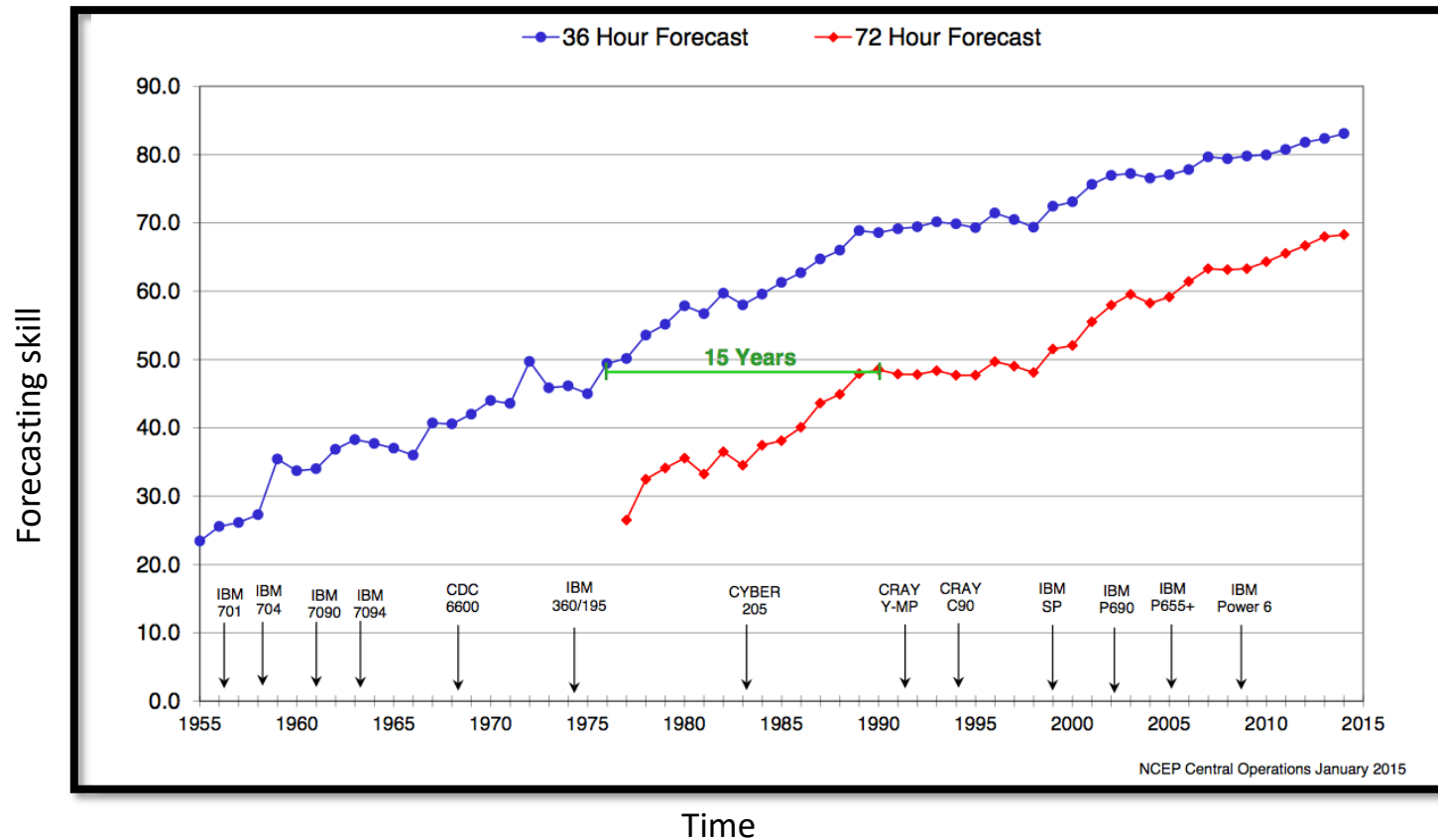
# Temporal inaccuracy can change our interpretation



# Developing Outbreak Analytics & Forecasting Takes Time and Resources

Advancing Weather Forecasting:  
took time, data, models, and resources to develop

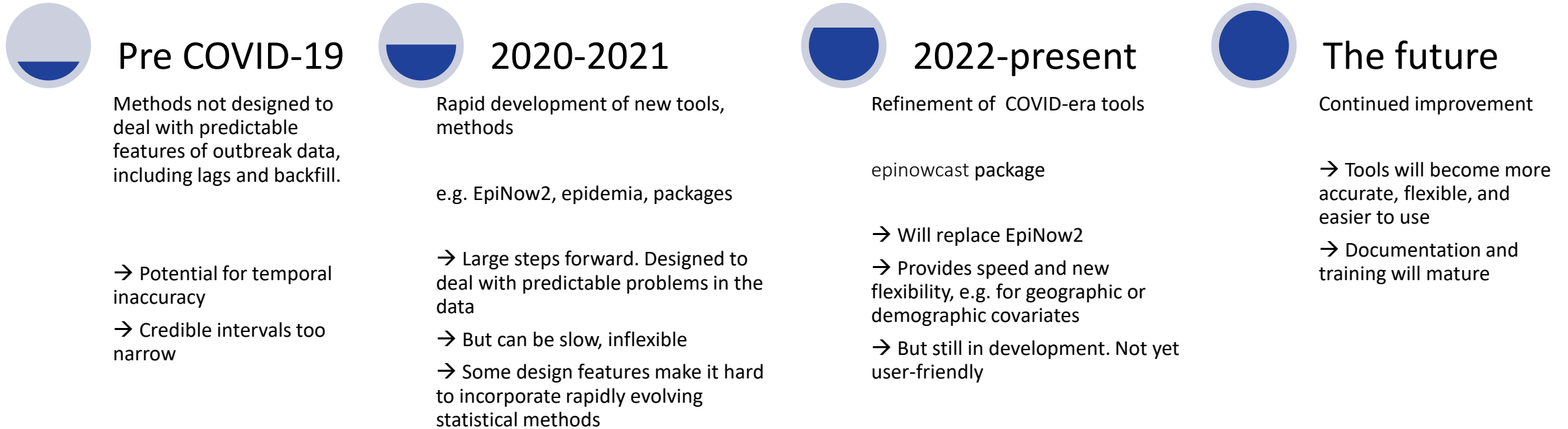
## Increases in Numerical Weather Forecasting Skill Through Time



- Advancing weather forecasting capabilities took decades
- Needed ingredients:
  - Data
  - Models
  - People
  - Computational Power
  - Specific Use Cases
  - Sustained Funding
- Disease forecasting and analytics are still in early stages

# $R_t$ estimation methods have improved rapidly since 2019

*But we still have a ways to go...*



- CDC is supporting this work through collaborations and open source tool development
- We are testing existing tools and identifying areas for improvement
- We are collaborating with the epinowcast team

## $2. R_t$

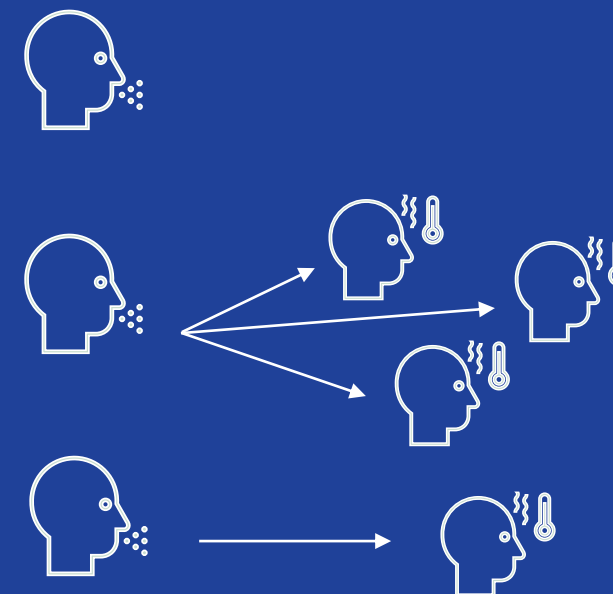
*Interpretation and estimation*



## $R_t$ : the time-varying effective reproductive number

- Defined as the average number of new infections caused by a single infectious individual at a specific time
- Accounts empirically for population susceptibility, interventions, and behavior
- Estimated from a time series of counts (e.g. cases, deaths, or hospitalizations per day)

*If  $R_t > 1$ , the epidemic is growing*



$$R_t = \frac{4 \text{ infectees}}{3 \text{ infectors}} = 1.33$$

$R_t$  is a data-driven quantity. If we could directly observe every transmission chain, we could identify all the individuals who are infectious at a particular time and count the number of new infections they caused.

# Estimating $R_t$ from a time series of counts

## Infectees

The number of infections observed on day  $t$

$$R_t = \frac{I_t}{\sum_{s=1}^t I_{t-s} \omega(s)}$$

*Note: In the original image, an orange arrow points from the text 'number of infections observed on day t' to the  $I_t$  in the numerator. A blue arrow points from the text 'number of individuals infected s days prior to time t' to the  $I_{t-s}$  in the denominator. A green arrow points from the text 'current infectiousness' to the  $\omega(s)$  in the denominator.*

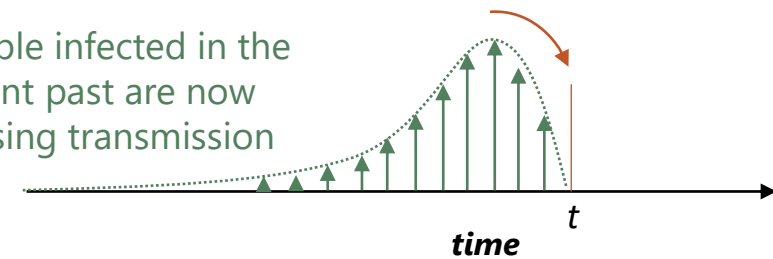
## Infectors

Sum up the number of individuals infected  $s$  days prior to time  $t$ , scaled by their current infectiousness

$$R_t = \frac{\text{total infectees}}{\text{total infectors}}$$

Arrows show times at which **infectors** and their **infectees** appear in the data.

People infected in the recent past are now causing transmission



The generation interval,  $\omega(s)$ , scales the infectiousness of individuals infected  $s$  days ago

## Inputs needed

1. A time series of incident events
2. An estimate of the generation interval distribution



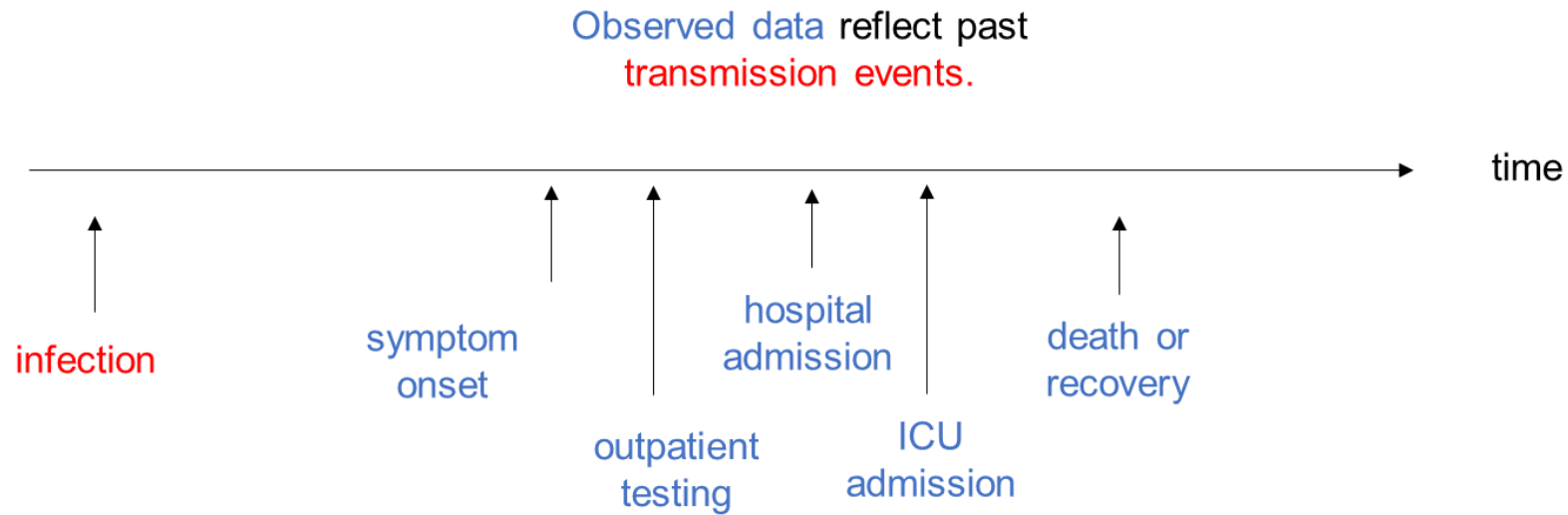
# *3. Pitfalls and how to avoid them*

*2.1 Observation delays*

*2.2 Day of week effects and other reporting anomalies*

*2.3 Partial observation at the end of the time series*

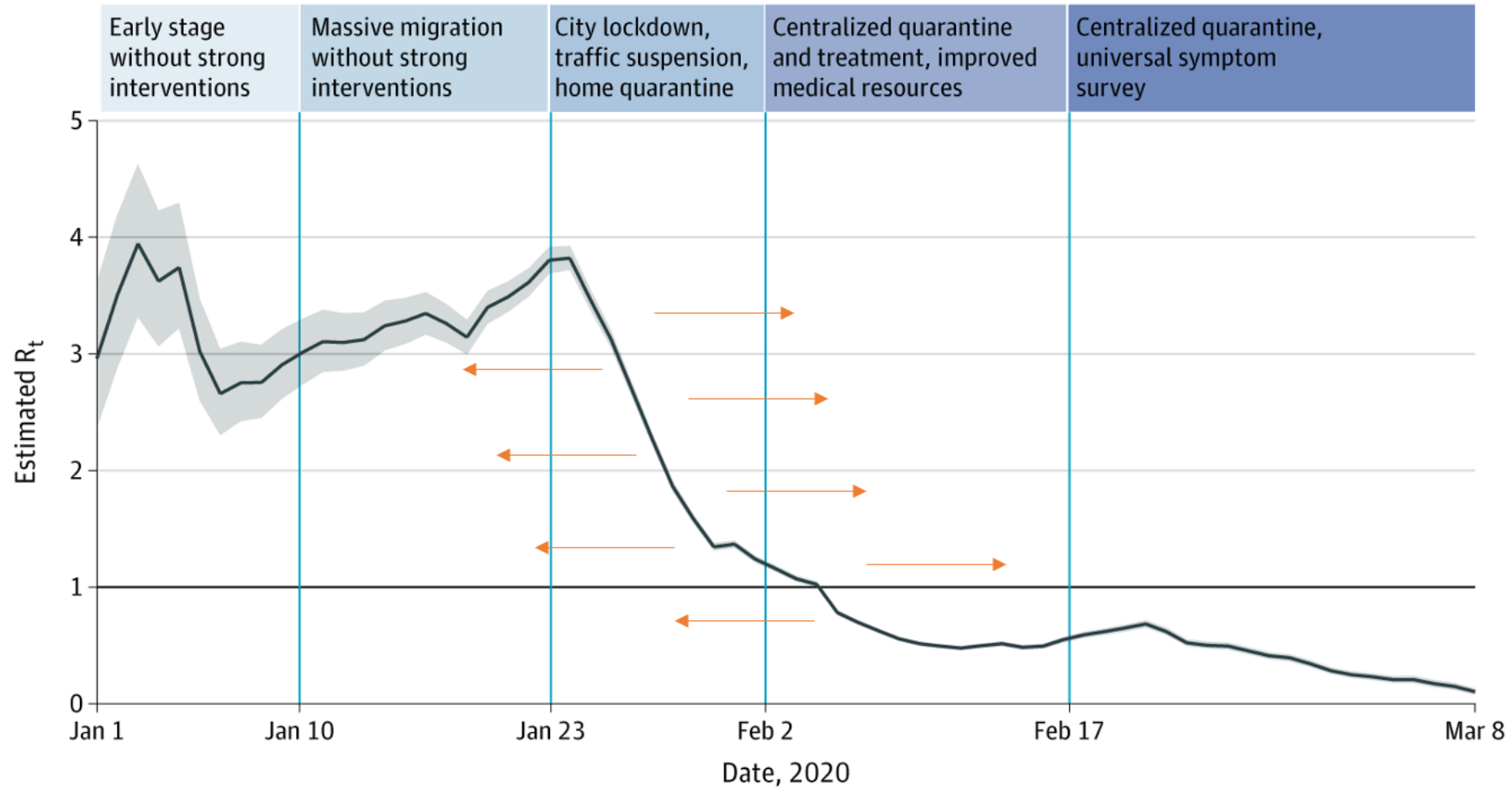
# Problem: Observation delays



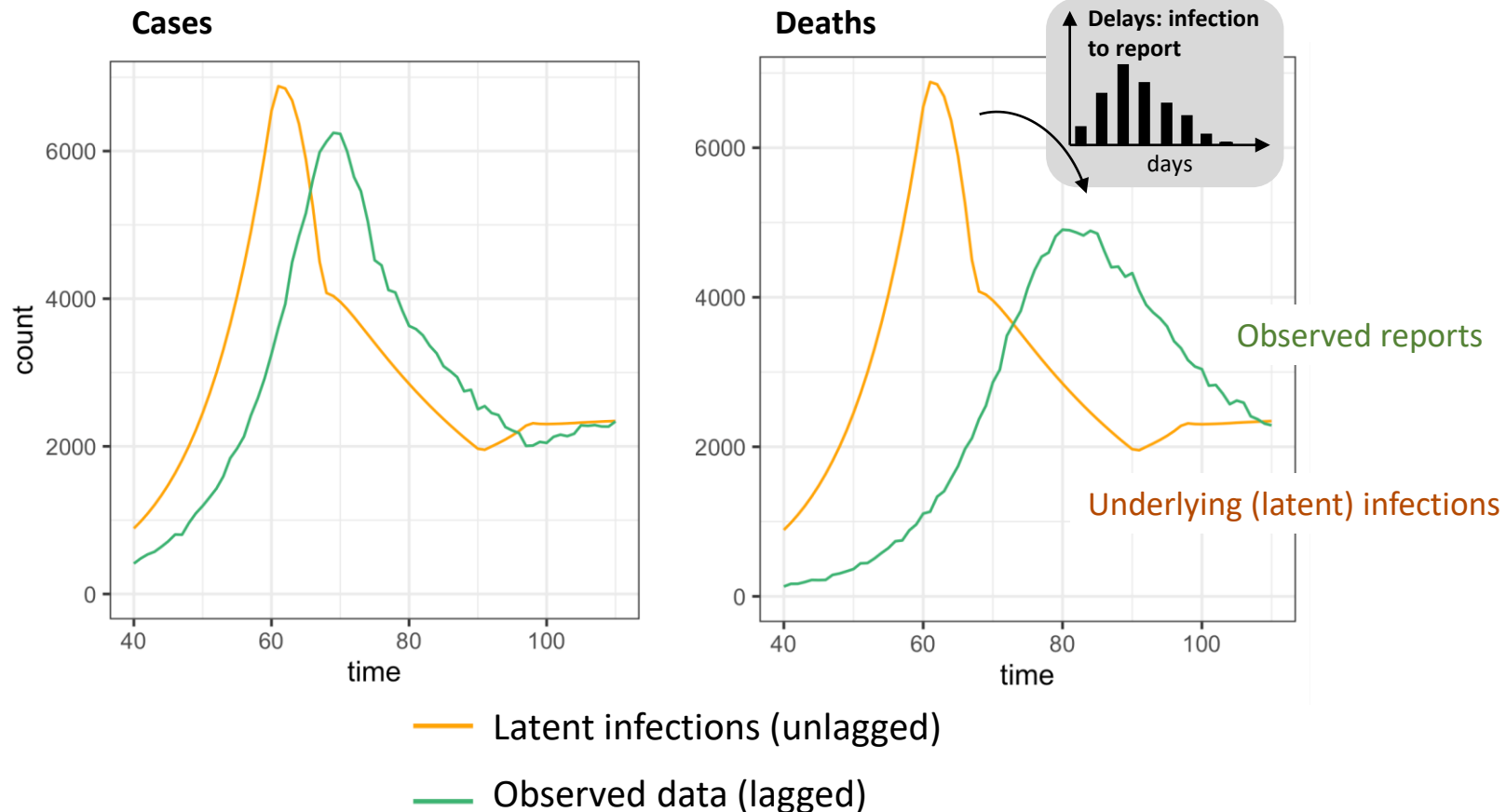
If we don't account for the delay between infection and observation, the  $R_t$  estimates that we obtain today actually reflect transmission levels days or weeks ago



# Temporal accuracy



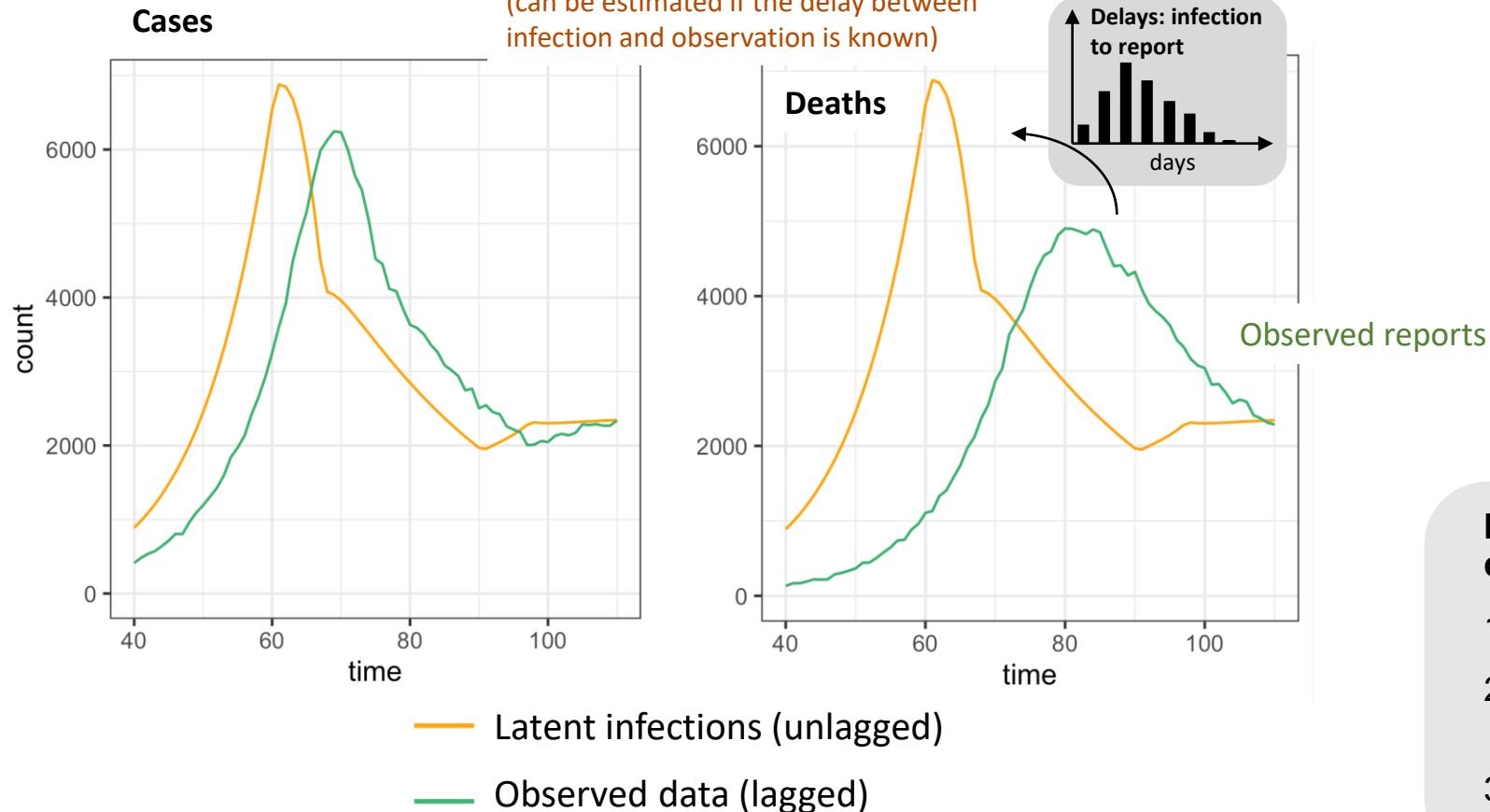
# Problem: delays change the shape and timing of the observed curve, relative to underlying infections



# Solution: Use a tool that estimates the unlagged infection curve along with $R_t$

e.g. *EpiNow2*, *epinowcast*, *epidemia* packages in R

**Underlying (latent) infections**  
(can be estimated if the delay between infection and observation is known)

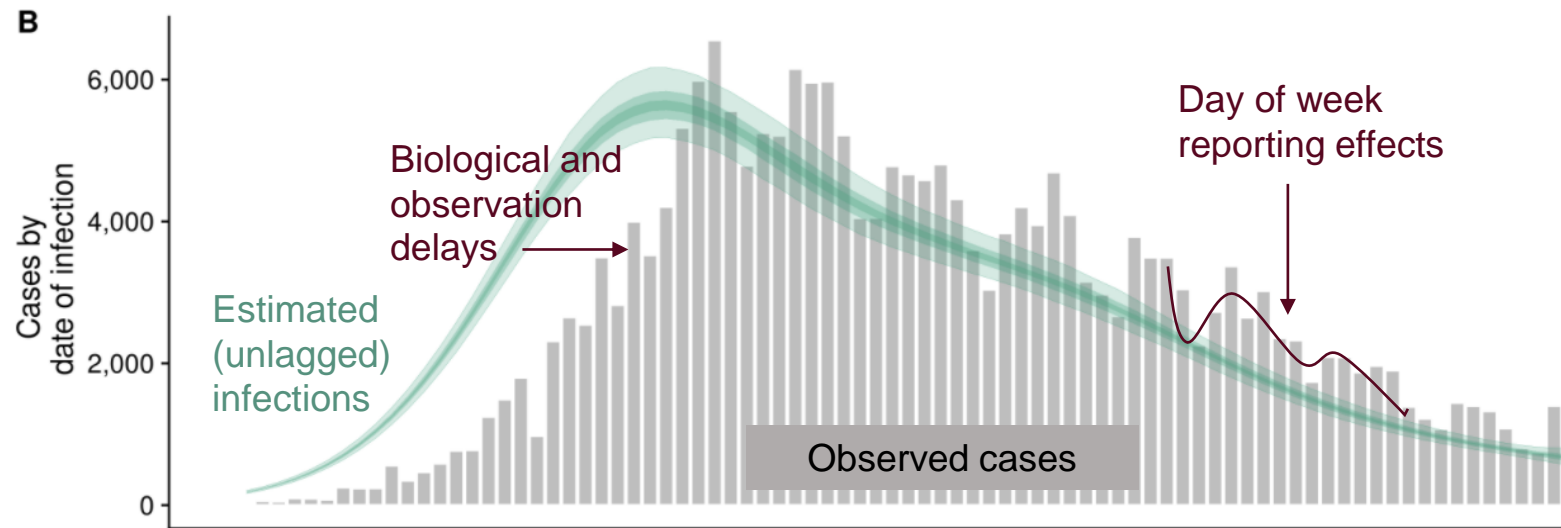


**Inputs needed to estimate  $R_t$ , accounting for delays**

1. A time series of observed reports
2. An estimate of the generation interval distribution
3. An estimate of infection-to-report delay distribution

# Problem: Day of week effects

Solution: Use a model in which the reporting hazard depends on the day of the week. Estimate a fixed effect for each day of the week.



Abbott, S. et al. (2020). EpiNow2. doi:10.5281/zenodo.3957489.

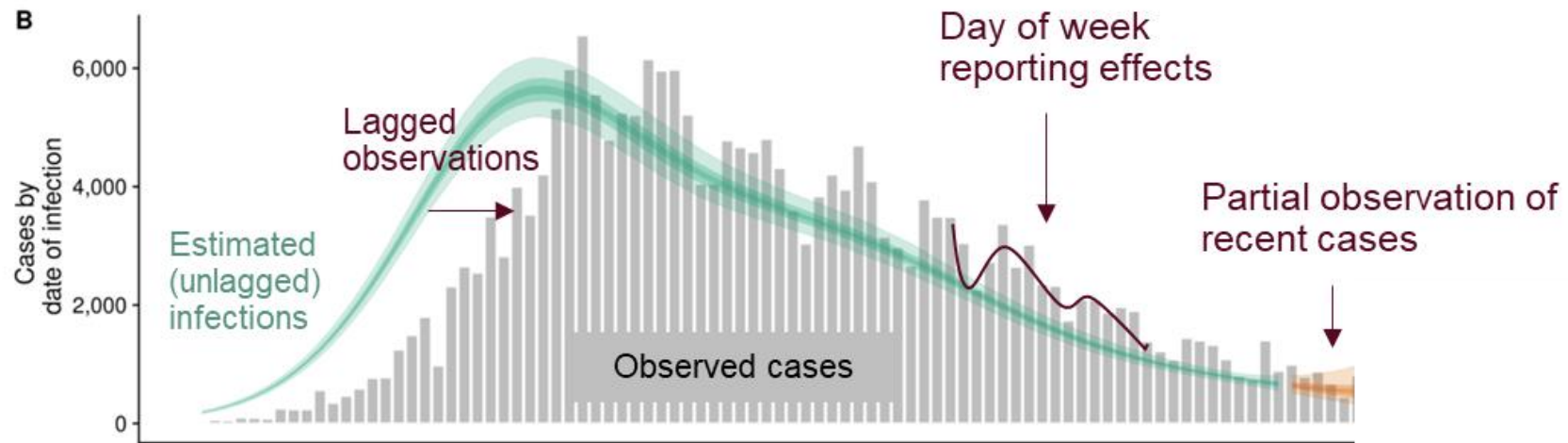
EpiNow2 and epinowcast are two packages that provide this option.

(Stay tuned for the coding demo!)

# Problem: Partial observation of recent counts

*Lags, backfill, revision, are inevitably present in epidemiological data*

Solution: Use a method that can **nowcast** the end of the time series and estimate  $R_t$  simultaneously

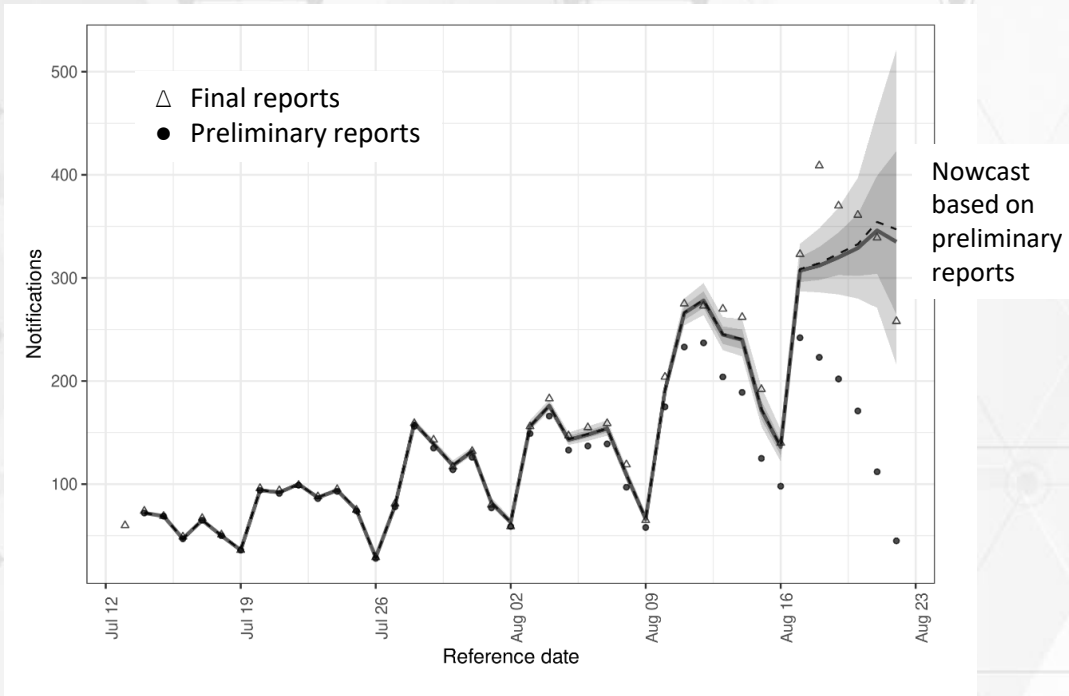


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# Nowcasting

*Estimate final reports from those observed so far*



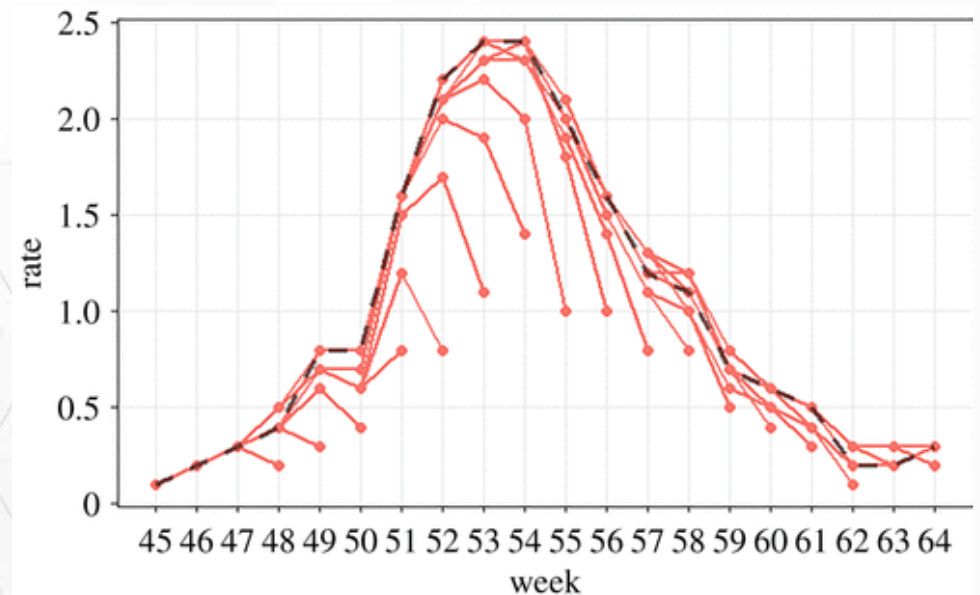
<https://package.epinowcast.org/>

- Basic nowcasting approach
  - Estimate the fraction of total reports we expect to have observed 1, 2, 3, ... n days after the fact
  - Scale up recent incomplete reports accordingly
- Several nowcasting packages available
  - [NobBS](#) ("Nowcasting by Bayesian Smoothing")
  - [epinowcast](#)
  - [nowcaster](#)
  - [surveillance](#)
  - [EpiNow2](#)
- Sophisticated tools can stratify by geographic, demographic factors, or allow reporting delays to evolve over time
  - [epinowcast](#)
  - [nowcaster](#)

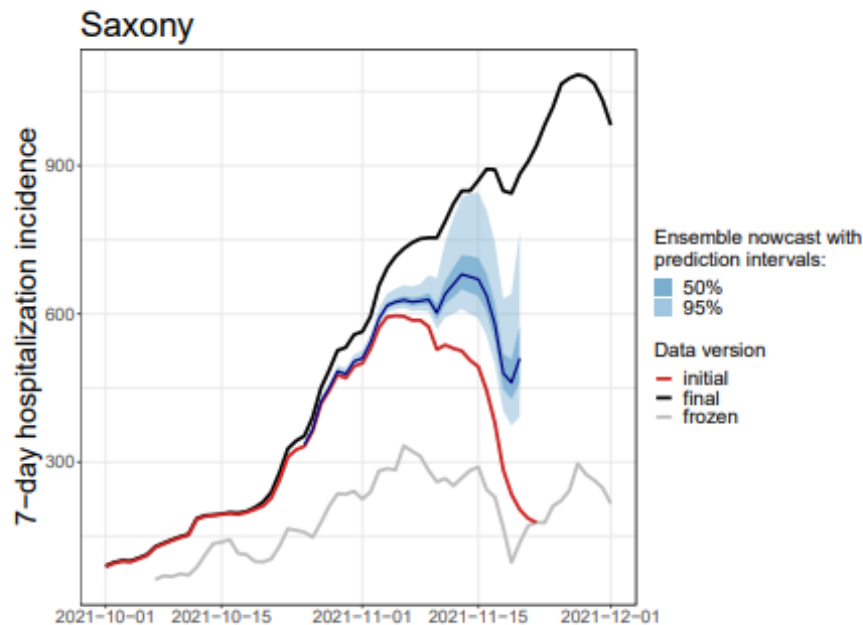
# Inputs needed for nowcasting

## *Estimate of the delays between initial and final reports*

- Need to characterize waiting times between event and report
- Data snapshots or line lists with event date and report date are sufficient
- Some public databases already store daily archives of key epidemic signals for this purpose
  - Covidcast
  - HealthData.gov
  - Stay tuned for the coding demo!
- Some existing R packages make it easy to
  - estimate delays (EpiNow2, epinowcast)
  - perform nowcasting (EpiNow2, epinowcast, NobBS)



Kandula et al. *Journ. Roy. Soc. Interface.* 2019.



(a) Saxony, nowcast made on 22 November 2022: overwhelmed hospitals lead to severe underreporting and thus too low nowcasts.

## Limitations

- Nowcast accuracy is greatest when the data observation process is stable and predictable
- Reporting anomalies and inaccurate nowcasts can occur at critical times for public health decision making
  - Early in an outbreak
  - When healthcare systems are over capacity
  - During periods of social upheaval
- Nowcasting is an active area of research
- CDC is using historical outbreak data to test and improve methods
- CDC's open funding opportunity will build on this research and support nowcast implementation at the state and local levels



## *4. Putting it all together*



# Two tools we recommend for $R_t$ estimation

*Designed to adjust for observation lags, day of week effects, and partial observation while estimating  $R_t$*

## EpiNow2

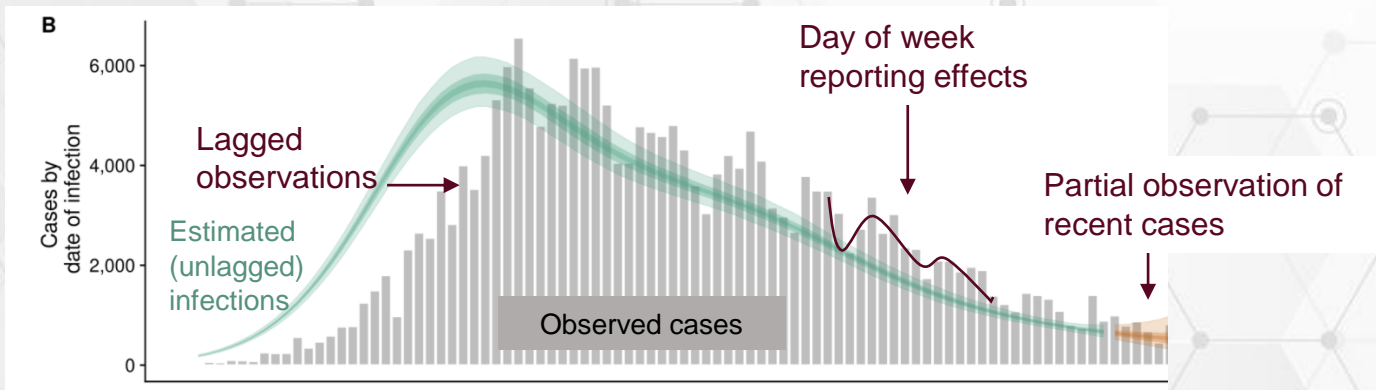
- Developed during the COVID-19 pandemic
- Used for CDC's mpox technical reports
- + Relatively easy to use and install
- Limited flexibility for nowcasting
  - Two-step process
  - When nowcasting, reporting delays can't vary over time or across demographic strata
- Model fitting is slower, less stable than it could be

Focus of coding demo

## epinowcast

- Developed by the same team and intended to replace EpiNow2
- + Faster, more stable, improved statistical methods
- + Nowcasting is a one-step plug-and-play process
- + More flexibility: model structure, covariates, changes over time in reporting
- Still in development
- Harder to install
- For now, requires expert knowledge to take advantage of flexibility, generate plots, etc.

# Real-time epidemic analysis requires models and tools designed for imperfect epidemic data



Abbott, S. et al. (2020). EpiNow2. doi:10.5281/zenodo.3957489.

*Imperfections in outbreak data are predictable and need to be dealt with before the analysis begins*

Pre-positioned, well-tested computational tools and data pipelines needed for accurate, timely decision support

Tools are rapidly improving, but there is still a long way to go

CDC is supporting these efforts

- Funding for collaborations, and growth of the talent pipeline
- Open-source tool development
- Testing tools on historical outbreak data → continuous improvement
- Full-time team to produce and publish analyses at the state and territory level



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# Thank you!

*Questions?*

For more information, contact CDC  
1-800-CDC-INFO (232-4636)  
TTY: 1-888-232-6348 [www.cdc.gov](http://www.cdc.gov)

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