FROM FORECASTING THE FLU TO PREDICTING THE “NEXT” DISEASE

UP-STAT 2016 - Buffalo, NY

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We want to better predict of the spread of infectious diseases

INFECTIOUS DISEASES ARE DESTRUCTIVE

Infectious diseases are often …

- old
- deadly
- costly
- stochastic

WE WANT TO MITIGATE THE EFFECTS OF DISEASE THROUGH PREDICTION

With accurate predictions, the infectious diseases are

- old
- ~~deadly~~ → manageable
  - Resource allocation
  - Alert health officials
  - Issue warnings
- ~~costly~~ → feasible
  - Fewer sick days
  - More awareness
- ~~stochastic~~ → forecasted

PREDICTING THE FLU

WE FOCUS ON 10 CDC REGIONS

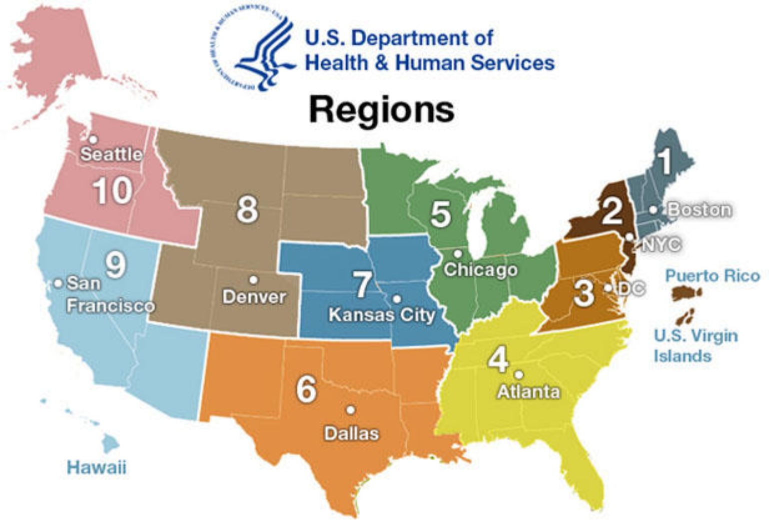


Figure: From cdc.gov

THE CDC COLLECTS DATA FROM PHYSICIANS VOLUNTARILY

Region	Year	Week	wILI
1	2015	25	0.55
2	2015	25	1.45
⋮	⋮	⋮	⋮
10	2015	25	0.44
⋮	⋮	⋮	⋮
1	2015	45	0.76
2	2015	45	1.57
⋮	⋮	⋮	⋮
10	2015	45	0.89

Table: Cross Section of Available data.
wILI - Weighted Influenza Like Illness

WE WANT TO PREDICT THE WILI FOR THE REMAINING WEEKS OF A SEASON

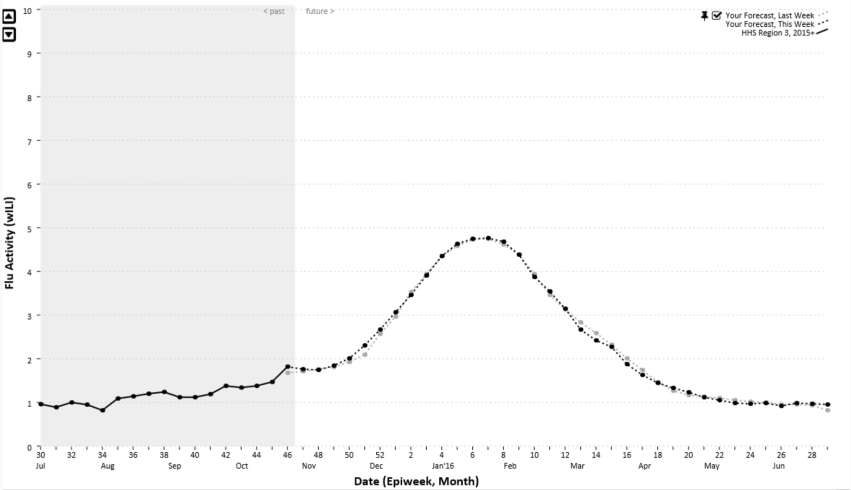


Figure: Examples of wILI curves. From David Farrow's FluV.

`epicast.org`

THE MODEL RELIES ON SEASONAL VARIABLES

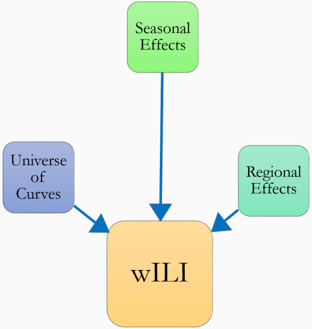
$$Y_t^{(r,s)} \sim N(\mu_t^{(r,s)}, \sigma^2)$$

where

$$\mu_t^{(r,s)} = [a_s \cdot \alpha_r] \cdot f(t - b_s - \beta_r)$$

for week t, region r, season s and priors:

$a_s \sim \text{Unif}(2, 10)$	-seasonal scaling
$b_s \sim \text{Unif}\{-6, -5, \ldots, 6\}$	-seasonal shifting
$\alpha_r \sim \text{Unif}(0.25, 1.25)$	-regional scaling
$\beta_r \sim \text{Unif}\{-3, -2, \ldots, 3\}$	-regional shifting
$f \sim \text{Unif}\{\hat{F}\}$	-smoothed observed curves
$\sigma^2 \sim \text{Unif}(0.5, 2.5)$	-variance



ESTIMATING A POINT IS SIMPLER THAN ESTIMATING A CURVE

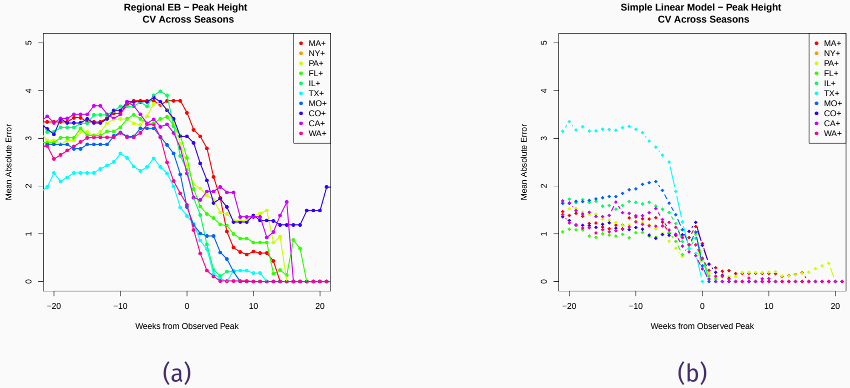


Figure: Leave-one-season-out cross validation for EB with regional effects (a) and a targetted regression (b). The x-axis is the weeks from the observed peak and the y-axis is the mean absolute error.

ULTIMATELY, WE WANT TO BIAS ESTIMATES/SHRINK POSTERIOR

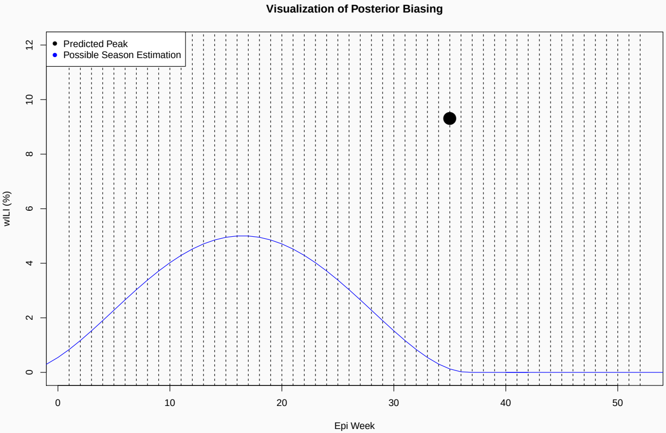


Figure: Image depicting of weighting curves whose peak values are closer to our estimated values. A thicker line represents a larger weight. The black dot is our estimated value of the peak height and week.

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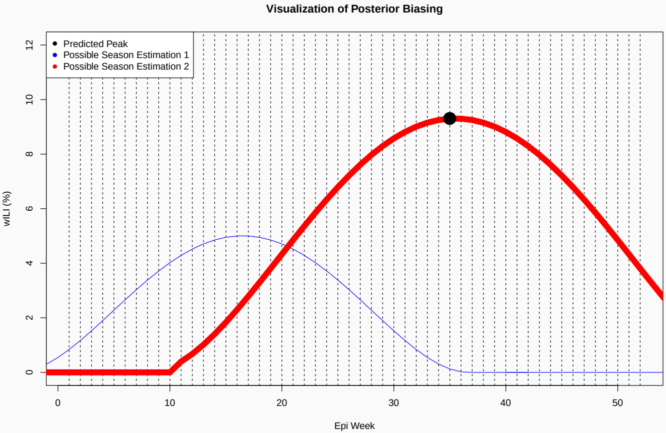

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POSTERIOR BIASING YIELDS IMPROVED RESULTS

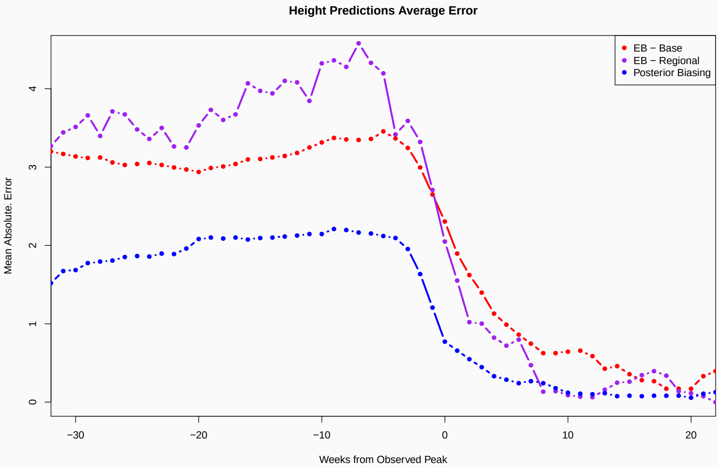

Figure: Cross Validation error averaged over the different seasons for the different model types.

THE “NEXT” DISEASE

THE TOOLS WE HAVE FOR NEW DISEASES ARE LIMITED

For past diseases like the flu, we have

- Years of data
- Knowledge of the disease
- Public awareness
- Specific models

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For past diseases like the flu, we have

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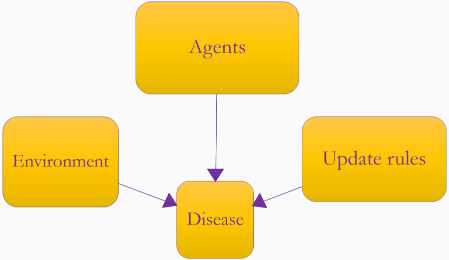
But for new diseases we have

- Little data
- Less knowledge
- Frenzied awareness
- Few, if any, models

AGENT-BASED MODELS (ABMS) USE AGENTS, AN ENVIRONMENT, AND UPDATE RULES

```
for (time in time steps)
   agents = update(agents, env)
end
```



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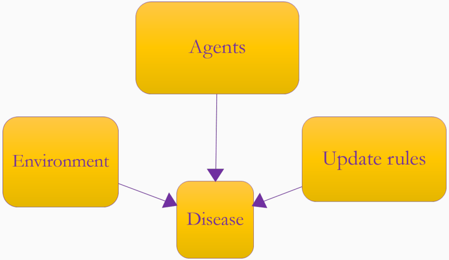

ABMs are flexible and modular!

POSSIBLE SOLUTION: SIMULATION VIA AGENT-BASED MODELING

An ABM can incorporate:

- Transmission Type
- Reproduction Rate
- Cultural factors
- Prevention strategies

ABMS REQUIRE HIGH QUALITY AGENTS - SPEW

Figure: Synthetic Populations and Ecosystems of the World

- $\sim$ 4 billion agents
- 80+ countries
- Automatic diagnostic reports
- 2 custom populations from users
  - Canada (Data from CDs)
  - California (Hispanic Population)
- 2 location sampling modules
  - Uniform and Road-Based
- 4 sampling schemes
  - Uniform, Moment Matching, IPF, Density Estimation
- Open Source
  - `https://github.com/leerichardson/spew`

IN SUMMARY

WE USE THE TOOLS AVAILABLE TO US

- When we have data, we can build rich models (Flu)

- Agent-Based Modeling can be used to simulate diseases previously unseen

THANK YOU

Questions?