Early Detection of COVID-19 Hotspot Counties Using Data Science

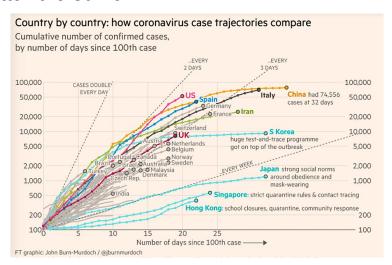
Zhaowei She ¹ Zilong Wang ¹ Jagpreet Chhatwal ² Turgay Ayer ¹

¹Georgia Institute of Technology

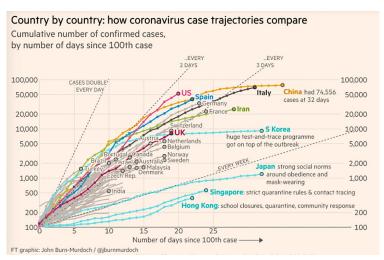
²Harvard Medical School and MGH

June 19th, 2020

Flatten the Curve!

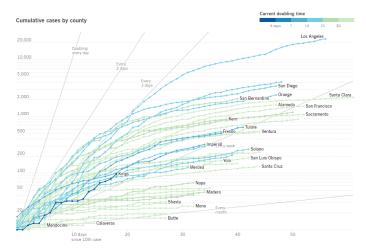


Separate the Flattened Ones from the Others!

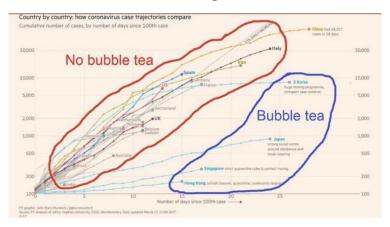




How Do We Know Which Curves are Flattened?



We Need a Classification Algorithm!





A Classification Algorithm A Statistical Model of the "Curves"

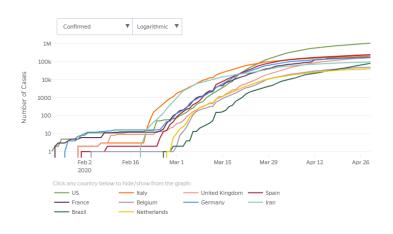
A Two-Parameter Exponential Growth Model (Heroy, 2020):

$$I_{t,c} = e^{r_c(t - t_{0,c})} + \epsilon_{t,c}$$

- **Dependent Variable** $(I_{t,c})$: The cumulative number of infected individuals in location c at time $t-t_{0,c}$ days
- Independent Variable (t): The current time
- Parameters $(r_c, t_{0,c})$:
 - $ightharpoonup r_c$: Exponential growth rate
 - ► $t_{0,c}$: The outbreak time of location c



A Classification Algorithm A Statistical Model of the "Curves"

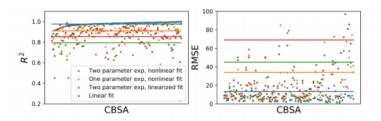


$$I_{t,c} = e^{r_c(t - t_{0,c})} + \epsilon_{t,c}$$



A Classification Algorithm A Statistical Model of the "Curves"

Shown to have good fit R^2 and RMSE

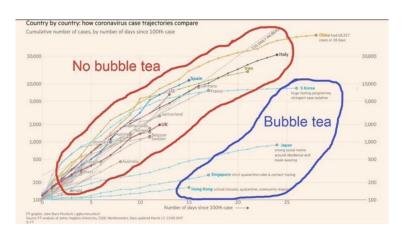


Goodness of Fit in terms of R^2 and Root Mean Square Error (RMSE)

$$I_{t,c} = e^{r_c(t - t_{0,c})} + \epsilon_{t,c}$$



A Classification Algorithm Classification Based On the "Curves"



"Curves": r_c and $t_{0,c}$ in

$$I_{t,c} = e^{r_c(t - t_{0,c})} + \epsilon_{t,c}$$



A Classification Algorithm Classification Based On the "Curves"

$$\begin{aligned} & \underset{(R_i, T_{0,i}) \in \mathbb{R}^2 \forall i \in I}{\min} \left\{ m_c(r_c, t_{0,c}) \right\}^T \left\{ m_c(r_c, t_{0,c}) \right\} \\ & x_i \in \{0,1\}^{|C|} \forall i \in I \\ & s.t. \sum_{i \in I} x_i = 1_{|C| \times 1} \\ & x_i(c) = 1 \Rightarrow \begin{bmatrix} r_c \\ t_{0,c} \end{bmatrix} = \begin{bmatrix} R_i \\ T_{0,i} \end{bmatrix} \ \forall i \in I \ \forall c \in C, \end{aligned}$$

where

$$m_c(r_c, t_{0,c}) := \partial_{\begin{bmatrix} r_c \\ t_{0,c} \end{bmatrix}} \mathbb{E}[(I_{t,c} - e^{r_c(t - t_{0,c})})^2].$$



A Classification Algorithm Statistical Justifications

Counterargument: Why not fit a curve to every county, then sort and cut off based off their rates?

- Autocorrelation: Time series violate exogeneity assumption for regression
- Sparse Data: County level data too sparse, potential overfitting
- No clear cutoffs: Debatable heuristics we want statistical guarantees



Two Staged Clustering and Regression Preprocessing

Feature Engineering: Convert forecasting into regression problem. For each county c's time series data:

 Lag Variables: Add rolling 7 day mean to smoothen data and capture autocorrelations

$$\bar{I}_{t,c} := \frac{1}{7} \sum_{i=1}^{7} I_{t-i,c}$$

Detrending: Apply diff log operation to consecutive lag variables

$$\hat{I}_{t,c} := \ln(\bar{I}_{t,c}) - \ln(\bar{I}_{t-1,c})$$

Time delayed embedding: Auto-regress on past variables + richer feature space (forecast next 7 days with past 14 days)

$$X_{t,c} = \begin{bmatrix} \hat{I}_{t,c} & \hat{I}_{t-1,c} & \dots & \hat{I}_{t-13,c} \\ \hat{I}_{t+1,c} & \hat{I}_{t,c} & \dots & \hat{I}_{t-12,c} \\ \vdots & \vdots & \ddots & \vdots \\ \hat{I}_{t+6,c} & \hat{I}_{t+5,c} & \dots & \hat{I}_{t-7,c} \end{bmatrix}$$



Two Staged Clustering and Regression Stage 1: Recursive Partitioning

Greedy Approximation to MICP Formulation

- Recursive Partitioning: Optimal Cluster Assignment is NP-hard (intractable), we split based on the sorted features of the time embedded matrix ala CART / C4.5 Decision Trees
- Split Criterion: The criterion we used is the conditional sum of Weighted Mean Absolute Percentage Errors (wMAPE) of the validation set using the XGBoost subroutine on each child
- Cross Validation and Backtesting: To determine the optimal depth (number of clusters) we cross validated against historical data in a sliding window approach



Two Staged Clustering and Regression Stage 2: Forecasting Each Cluster

Recovering the Results

Model Selection: The model with the lowest wMAPE from cross validation was selected

$$\mathsf{wMAPE}(\mathsf{Ground}\;\mathsf{Truth}=\vec{y},\mathsf{Predicted}=\hat{y}) := \frac{\sum_{i=1}^n |y_i - \hat{y}_i|}{\sum_{i=1}^n |y_i|}$$

Cluster Prediction: Ever county in the same cluster is then fitted with the same exponent growth model



A Case Study Based On Recent Georgia Data (5/14-6/16) Cross Validation Errors

Note: wMAPA:= 1-wMAPE

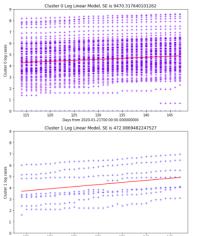
Cross Validation Results		
Fold	wMAPA (%)	Best Depth
1	99.69	2
2	99.51	2
3	99.65	2
4	99.70	2
5	99.69	2
6	99.74	2
7	99.67	3
8	99.83	2
9	99.77	2
10	99.80	2
11	99.49	2
12	99.67	2

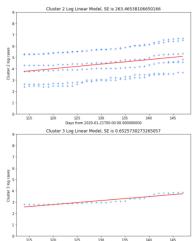
Runtime ≈ 10 minutes

Data Source: NYTimes-COVID-19 Data



A Case Study Based On Recent Georgia Data (5/14-6/16) Cluster Plots of County Cases







A Case Study Based On Recent Georgia Data (5/14-6/16) Choropleth of Forecasted Cases



```
0.04
      Highest Risk:
      Jenkins County
      Higher Risk:
0.035
      Harris County, Lanier County,
      Lowndes County, Tombs County,
      Troup County, Wayne County
      High Risk:
      Franklin County, Gordon County,
      Jasper County, Jeff Davis County,
       Montgomery County, Muscogee County,
0.025
      Tattnall County, Whitfiled County
      Low Risk:
      the rest
0.02
```

Algorithm Properties and Output

- Shape Matching: From the scatter plots, our method clusters time series together by general shape and trend, emulating Discrete Time Warping (DTW) methods
- Hierarchical Clustering: Unlike classical Agglomerative Clustering using DTW, which constructs clusters bottom up, ours construct it top down, making our model more interpretable
- Efficient Computationally: 13 folds of cross validated (with each split running 2 x 1000 boosted trees) models of large transformed data took less than 10 minutes on a notebook with a single Intel i7-9750H CPU @ 2.60GHz and 16 GB of RAM



Impact

- Highly Interpretable: Counties are clearly partitioned into stratified risk tiers
- Reasonable Advanced Warning: We are able to forecast which counties are potential hotspots 7 days in advance
- Surprising Results: Some high risk counties such as Montgomery have historically very low cases, which would have been missed out with simple prediction forecasting



Heroy, S. (2020). Metropolitan-scale covid-19 outbreaks: how similar are they? *arXiv preprint arXiv:2004.01248*.