Survival-Convolution Models for Predicting COVID-19 Pandemic and Assessing Effects of Mitigation Strategies

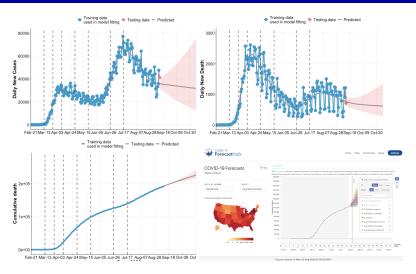
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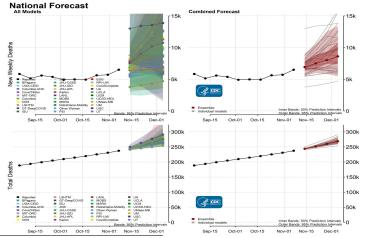
Daily Forecasts of COVID-19 Pandemic



We submit our forecasts to <u>COVID Forecast Hub</u>, which is used by the US Centers for Disease Control and Prevention (CDC)

CDC Forecasts

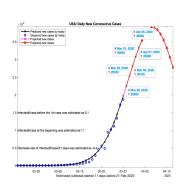
The ensemble forecast predicts that 260,000 to 282,000 total COVID-19 deaths will be reported by December 5^2 .

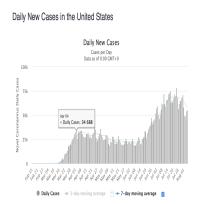


²CDC Forecasts: https://www.cdc.gov/coronavirus/2019-ncov/covid-data/forecasting-us.html

Starting Points

First patient reported in NYC on March 1. Stay-at-home-order issued on March 22. Unprecedented response measures: lockdown, travel restrictions, social distancing, closure of schools, businesses.

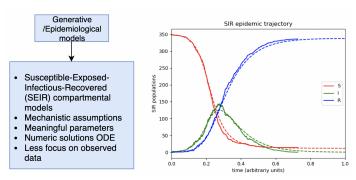




Methods

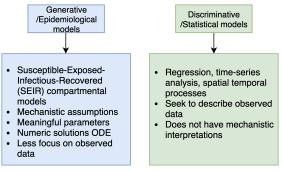
Infectious Disease Models

Figure. Epidemiological Compartmental Models (e.g., Susceptible-Infectious-Recovered; SIR)



Infectious Disease Models

Figure. Epidemiological Models and Statistical Models



Goal 1: Combine nonparametric curve fitting with mechanistic-based SEIR model (provide important parameters, i.e., effective reproduction number R_t).

Goal 2: Natural experiment to evaluate mitigation strategies. SEIR models rely on a large number of unknown parameters.

Modeling Considerations

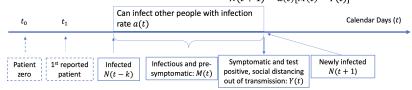
- ► What is the forecast target? Peak week, size, duration, cumulative/incident cases.

 Predict daily incident cases and incident deaths at the national-level and state-level.
- ► Important factors for modeling:
 - ► SARS-CoV-2 virus has a long incubation period (up to 14 days, extreme case 21 days)
 - ► Highly infectious in the pre-symptomatic phase: 50% transmission occurred during this phase (US CDC)
 - Time-varying transmission rate as public health interventions are implemented and societal behavior changes
 - ► Intervention effect may be time-dependent
- ► Transparency, robustness are important for policy decision making.

Survival-Convolution Model

•
$$M(t) = \sum_{k=0}^{\infty} N(t-k)S(k)$$

• $Y(t) = \sum_{k=0}^{\infty} N(t-k)[S(k) - S(k+1)]$
• $N(t+1) = a(t)[M(t) - Y(t)]$



- ightharpoonup N(t) number of new infections on date t.
- ▶ At time *t*, number of the patients who have been infected for *k* days and remain in the transmission chain (e.g., pre-symptomatic):

$$N(t-k)S(k)$$
,

S(k) proportion of infected persons remaining infectious and in the transmission chain after k days of exposure (discrete survival function of time to out of transmission).

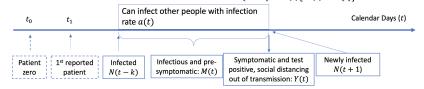
► Total number of infectious persons right before *t* (including pre-symptomatics):

$$M(t) = \sum_{k=1}^{C} N(t-k)S(k).$$

Survival-Convolution Model

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$$M(t) = \sum_{k=0}^{\infty} N(t-k)S(k)$$

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• $N(t+1) = a(t)[M(t) - Y(t)]$



► Total number of cases out of transmission on date t:

$$Y(t) = \sum_{k=1}^{C} N(t-k)[S(k) - S(k+1)].$$

ightharpoonup Denote the effective transmission rate by a(t),

$$N(t) = a(t)(M(t) - Y(t))$$

$$N(t) = a(t) \sum_{k=1}^{C} N(t - k)S(k + 1).$$
(1)

Equation (1) gives a convolution update for the number of new infections given the past infections $N(t-1), N(t-2), \dots, N(t_0)$.

Modeling Transmission Rate

Model a(t) as non-negative, piece-wise linear functions with knots placed at meaningful event times:

- ▶ Before report of first case t_1 , transmission rate is a constant a_0 .
- Once the first positive case was reported, the society starts to respond, so model the transmission rate with a linear function.
- ► When a massive public health intervention (e.g., nation-wide lockdown) is implemented, introduce an additional linear function with a new slope parameter.
- ▶ The simplest model has only 2 parameters (a_0, a_1) !

Time-varying Effective Reproduction Number

Effective reproduction number (R_t): the average number of secondary cases infected by primary cases who are infectious at time t^3

$$R_t = \frac{N(t)}{\sum_{k=1}^{C} N(t-k)w(k)}$$

w(k) probability mass function of the serial interval distribution between primary and secondary cases (Gamma distribution with shape and scale parameters $(4.36, 1.10)^4$).

 R_t captures the temporal changes in the disease spread.

³Cori, A., Ferguson, N. M., Fraser, C., Cauchemez, S. (2013). A new framework and software to estimate time-varying reproduction numbers during epidemics. American Journal of Epidemiology, 178(9), 1505-1512.

⁴Nishiura, H., Linton, N. M., Akhmetzhanov, A. R. (2020). Serial interval of novel coronavirus (COVID-19) infections. International Journal of Infectious Diseases.

Evaluation of Public Health Intervention Effect

Quasi-experiments longitudinal pre-post intervention design. Often used to study health policies when randomized trials are not feasible.

Assumptions:

- Local randomization: subjects infected before or after intervention are similar within a short period of time
- ► Continuity: the trend before implementation continues had the intervention not been implemented

Intervention effects estimated as the difference in the slope of a(t) before and after an intervention takes place. Corrects for the natural decline of the transmission rate over time.

Estimation Using Confirmed Daily Cases

Let θ denote all parameters in the infection rate a(t) and t_0 .

Let $Y_o(t_1)$, $Y_o(t_1 + 1)$, $Y_o(t_1 + 2)$,, $Y_o(t_n)$, denote the daily new COVID-19 cases reported from t_1 to the last date t_n in the training set.

Model observed cases accounting for measurement errors:

$$Y_o(t_i) = Y(t_i; \theta) + \sqrt{Y(t_i; \theta)} \epsilon(t_i),$$

 $\epsilon_i(t)$ is a normalized residual error (e.g., reporting error), with variability proportional to $Y(t; \theta)$.

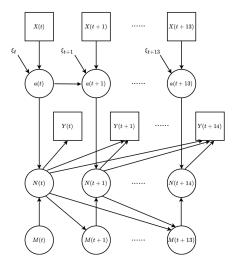


Figure A1: Illustration diagram of the spatial-temporal model for one consecutive 14 days (the maximum incubation period of COVID-19). M(t): number of infected subjects who remain in the transmission chain and can transmit virus to others (including those who are pre-symptomatic or asymptomatic) on day t. N(t): number of newly infected subjects on day t. Y(t): number of diagnosed subjects out of transmission chain on day t. Y(t): infection rate on day t, which depends on area characteristics Y(t) and spatial-temporal transmission model parameters t.

Optimization and Inference

Optimization:

► Objective function: squared error on the predicted number of cases and the observed after a square-root transformation:

$$\sum_{t_1 \leq t \leq t_n} \left[\sqrt{Y_o(t)} - \sqrt{Y(t; heta)}
ight]^2$$

► Stochastic gradient descent implemented in Tensorflow.

Inference:

► Assume that the standardized residuals are exchangeable.

$$[Y_o(t) - Y(t;\theta)] / \sqrt{Y(t;\theta)}$$

- ▶ Permutation of predicted standardized residuals over time $\tilde{\epsilon}(t) = \left[Y_o(t) Y(t; \widehat{\theta})\right] / \sqrt{Y(t; \widehat{\theta})}$.
- Generate new copies of daily cases, $\tilde{Y}(t) = Y(t; \hat{\theta}) + \sqrt{Y(t; \hat{\theta})} * \tilde{\epsilon}(t)$ and repeat permutation N times.

Forecast Daily Incident Deaths

Let Z(t) denote number of incidence deaths at day t, convolution

$$Z(t) = b(t) \sum_{k=0}^{C_2} N(t-k)P(T_1 + T_2 = k),$$

b(t) case fatality rate, T_1 time from initially infected to symptomatic, T_2 time from symptomatic to death.

Optimization: combine loss function of cases and deaths.

Inference: jointly permute residuals from the incident case and incident death model.

For forecasts, extrapolate current estimated parameters on a(t).

Analysis Details

Data

Numbers of daily confirmed new cases and new deaths can be obtained from many public sources.

- ► National level: a publicly available database that curates and validates multiple sources on COVID-19 statistics www.worldometers.info/coronavirus
- ► State level: JHU Center for System Science and Engineering (CSSE)

https://github.com/CSSEGISandData/COVID-19

Model Setups

Countries to analyze: China, South Korea, Italy, US

China and South Korea: a single piece for a(t). About two weeks data for training and the rest of data up to May 10 as testing data. Infection rate:

$$a(t) = \begin{cases} a_0^+ & t < t_1 \\ (a_0 + a_1(t - t_1))^+ & t \ge t_1 \end{cases}$$

3 parameters: t_0 , a_0 , a_1 .

Goal: examine prediction performance.

Model Setups

Italy: 4 pieces. A knot at nation-wide lockdown (March 11, t_2), two knots with two weeks apart afterwards (March 25, t_3 ; April 8, t_4). Capture the immediate, short-term and mid-term intervention effect (March 25, t_3 ; April 8, t_4).

$$a(t) = \begin{cases} a_0^+ & t < t_1, \\ (a_0 + a_1(t - t_1))^+ & t_1 \le t < t_2, \\ (a_0 + a_1(t_2 - t_1) + a_2(t - t_2))^+ & t_2 \le t < t_3, \\ (a_0 + a_1(t_2 - t_1) + a_2(t_3 - t_2) + a_3(t - t_3))^+ & t_3 \le t < t_4, \\ (a_0 + a_1(t_2 - t_1) + a_2(t_3 - t_2) + a_3(t - t_3) + a_4(t - t_4))^+ & t \ge t_4. \end{cases}$$

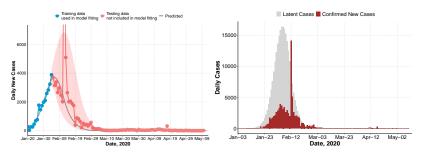
Goal: estimate lockdown effect, i.e., immediate effect (a_2 vs a_1), short-term (a_3 vs a_1), midterm (a_4 vs a_1).

US (10-20 days behind Italy): 5 pieces. A knot at the declaration of national emergency (March 13, t_2) and 3 knots (2-week apart) afterwards (March 27, April 10, April 24).

National-level Analysis Results

China

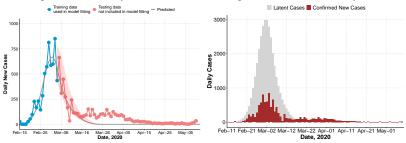
Training data: January 20 to February 4; testing data: February 5 to May 10.



- $ightharpoonup t_0$: Jan 3 (17 days before first report)
- ► Predicted total: 58,415; 95% CI: (42,516, 133,083)
- ▶ Observed total: 82,901. Two outliers on Feb 12, 13. Excluding outliers: 62,356.

South Korea

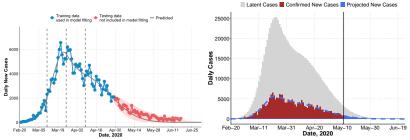
Training data: February 15 to March 4; testing data: March 4 to May 10.



- $ightharpoonup t_0$: Feb 11 (4 days before first report)
- Small outbreak after March 15 not captured
- ► Predicted total by March 15: 7,816
- ▶ Observed total: 8,162.

Italy

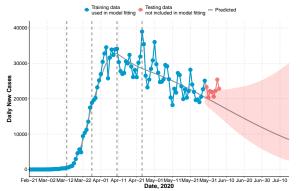
Training data: February 20 to April 29 (7 weeks after lockdown); testing data: April 30 to June 15.



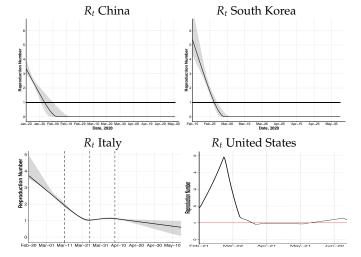
- $ightharpoonup t_0$: Feb 10 (10 days before first report)
- ► Predicted total by May 31: 223,079 (CI: 202,940, 263,152)
- ► Observed total: 232,997
- ► Rate of decrease after the peak is slower than rising (asymmetric)

US

Training data: February 21 to May 29. One knot on March 13 and 3 knots two-weeks apart (3/27, 4/10, 4/24).



Had the late spring trend continue, total cases: 2.7 million, total deaths: 157K. Date with < 100 cases: Nov 9. But already observed an uptick late May.



▶ R_t reduced to < 1.0 in 2 weeks in China and South Korea. R_t reduced to 1.0 in 6 weeks in Italy (remained around 1.0 for 3 weeks). Nation-wide lockdown in Italy did not significantly further reduce the rate of decrease (p > 0.05). US R_t reduced to < 1 in 7 weeks, flat for 6 weeks before increasing again.

Comparing Infection Rates a(t)

Country	Parameter	Estimate	95% CI
China	a_0	0.793	(0.68, 1.02)
	a_1	-0.693	(-1.13, -0.42)
	Duration	44	(39, 55)
South Korea	a_0	1.363	(1.03, 1.98)
	a_1	-1.496	(-2.39, -0.96)
	Duration	39	(37, 43)
Italy	a_0	0.789	(0.73, 1.10)
	a_1	-0.358	(-0.68, -0.26)
	a_2	-0.372	(-0.46, -0.31)
	a_3	0.061	(0.02, 0.12)
	a_4	-0.057	(-0.12, -0.01)
	Duration	123	(103, 179)
United States	a_0	0.774	(0.73, 0.78)
	a_1	-0.029	(-0.03, 0.03)
	a_2	-0.665	(-0.69, -0.54)
	a_3	-0.173	(-0.23, -0.13)
	a_4	0.018	(-0.01, 0.05)
	a_5	-0.005	(-0.02, 0.01)
Continue current [†]	Duration	262	$(187, \infty)$

National-level Forecasts

First time the model predicted a third surge: August 21, 2020. (Left: incident cases; Right: incident deaths).

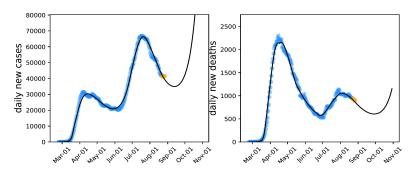
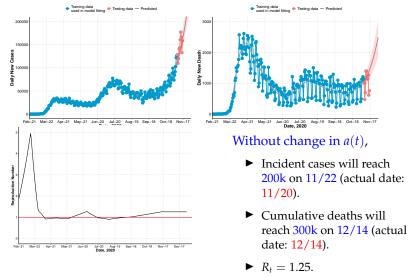


Figure. Current forecasts of incident cases, incident deaths and R_t . Training data up to November 7 (week 46).



Model using training data up to 12/24/2020 predicts cumulative deaths reaching 400k by 1/18/2021. New variant a huge concern.

Performance of Models During Summer Surge: July, 2020

Figure. Independent Evaluation by CovidComplete

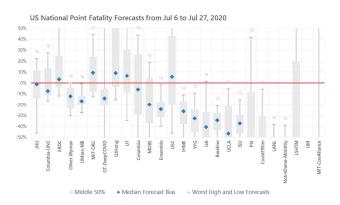


Figure. Example of Performance on Week 33 (7/12/2020)

Time Chart

The ensemble forecast combines models unconditional on particular interventions being in place with those cond distancing measures continuing. To ensure consistency, only models with 4 week-ahead forecasts ahead are included in the conditional of the conditional on the condition

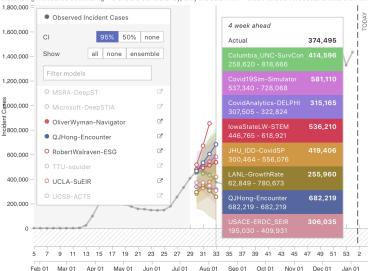
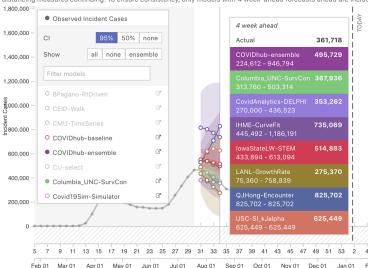


Figure. Example of Performance on Week 34 (7/19/2020)

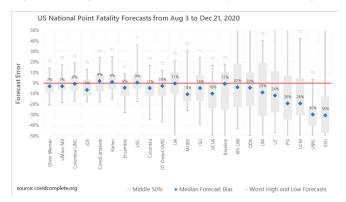
Time Chart

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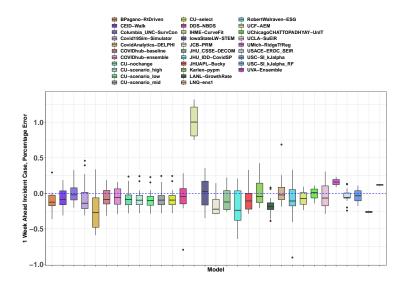


Performance of Models Post July: 8/3/2020 –12/21/2020

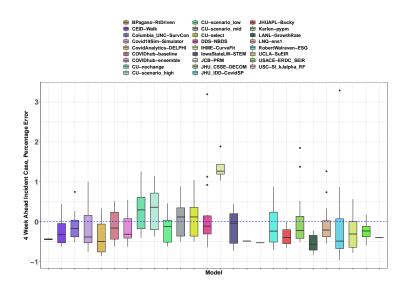
Figure. Independent Evaluation by CovidComplete



Performance of Cases Model 7/5/2020-1/2/2021



Performance of Cases Model 7/5/2020-1/2/2021



Coverage Probability

Table. Coverage Probability of 95% Prediction Intervals of Forecasts (since July 5, 2020)

Model	1 Week	2 Week	3 Week	4 Week
COVIDhub-ensemble	0.813	0.933	1.000	1.000
Columbia-UNC-SurvCon	0.938	0.933	1.000	0.923
GT-DeepCOVID	0.938	0.933	0.857	0.846
IowaStateLW-STEM	0.533	0.357	0.538	0.500
NotreDame mobility	0.250	0.267	0.286	0.308
CovidAnalytics DELPHI	0.750	0.600	0.500	0.462
IHME CurveFit	0.455	0.600	0.700	0.800

Discussion

Summary

Propose a survival convolution model for forecast daily incident cases, deaths, estimate R_t , and comparison of mitigation strategies.

Simpler hybrid statistical/epidemiological models can be useful and robust for population science (full SEIR models require careful calibration; may work better with individual level data).

Challenges: difficult to make long term forecast

- ► Incomplete knowledge on the drivers of the epidemic
- ► Lack of data on behavioral change and policy enforcement; difficult to predict societal behavioral change
- ► Lack of accurate data on cases and deaths (reporting delay, limited testing capacity)

References and Acknowledgements

- ► Wang Q et al. (2020). Survival-convolution models for predicting COVID-19 cases and assessing effects of mitigation strategies. Frontiers in public health 8: 325. Github: https://github.com/COVID19BIOSTAT/covid19_prediction
- ► Chen Y et al. (2021). Dynamic COVID risk assessment accounting for community virus exposure from a spatial-temporal transmission model. *NeurIPS*, 34.
- ➤ Xie S et al. (2022). Evaluating Public Health Intervention Strategies for Mitigating COVID-19 Pandemic. *Statistics in Medicine*. In press. https://doi.org/10.1002/sim.9482
- ► COVID-19 Forecast Hub Consortium (2022). *PNAS* 119 (15), e2113561119.
- ► Funding agency: GM124104A1-S1.

Thank You!