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1. Review: Main Literature

- Title: Estimation of COVID-19 spread curves integrating global data and borrowing information[[lee](#)]
- Authors: Se Yoon Lee , Bowen Lei, Bani Mallick
- Year: 2020
- Journal: PLOS ONE
- Issue: 15(7)

1. Review: Main Literature

- Bayesian Hierarchical Richards Model (BHRM)

$$f(t; \theta_1, \theta_2, \theta_3, \xi) = \theta_1 \cdot [1 + \xi \cdot \exp\{-\theta_2 \cdot (t - \theta_3)\}]^{-1/\xi}$$

$$y_{it} = f(t; \theta_{1i}, \theta_{2i}, \theta_{3i}, \xi_i) + \epsilon_{it}, \quad \epsilon_{it} \sim \mathcal{N}$$

$$\theta_{li} = \alpha_l + \mathbf{x}_i^\top \boldsymbol{\beta}_l + \varepsilon_{li}, \quad \varepsilon_{li} \sim \mathcal{N}$$

$$\xi_i \sim \log \mathcal{N}(0, 1), \quad (i = 1, \dots, N)$$

$$\beta_{lj} \mid \lambda_{lj}, \tau_{lj}, \sigma_I^2 \sim \mathcal{N}\left(0, \sigma_I^2 \tau_I^2 \lambda_{lj}^2\right),$$

$$\lambda_{lj}, \tau_{lj} \sim \mathcal{C}^+(0, 1), \quad (l = 1, 2, 3, j = 1, \dots, p)$$

$$\alpha_l \sim \pi(\alpha) \propto 1$$

$$\sigma_I^2 \sim \pi(\sigma^2) \propto 1/\sigma^2, \quad (l = 1, 2, 3)$$

1. Review: Literature Review

- Horseshoe Prior[**horseshoe**]
 - Given high dimensional data, detect the sparse signal
 - Since it is continuous, efficient to compute
 - Discover strong signal and noises
- Elliptical Slice Sampling[**elliptical**]
 - When difficult to generate samples from given distribution, Elliptical Slice Sampling is useful.
 - There is no rejection while sampling, so the algorithm is efficient
 - More fitted when gaussian distribution is assumed.

2. Scope and Purposes

Main Purpose

- Construct the Bayesian hierarchical Richards model in order to estimate the COVID-19 curves

Specific Purpose

- Update 2021 COVID-19 data and generate new design to reflect the changed information and consider new types of variables
- Compare the results of 2020 and 2021
- Generate BHRM using JAGS

3. Data

Time Series Dataset

country_region	1/22/20	1/23/20	1/24/20	1/25/20	1/26/20	1/27/20	1/28/20	1/29/20	1/30/20	1/31/20	2/1/20	2/2/20	2/3/20	2/4/20	2/5/20	2/6/20	2/7/20
Australia	0	0	0	0	4	5	5	6	9	9	12	12	12	13	13	14	15
Austria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Belgium	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Brazil	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Canada	0	0	0	0	1	1	2	2	2	4	4	4	4	5	5	5	7
Chile	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
China	548	643	920	1406	2075	2877	5509	6087	8141	9802	11891	16630	19716	23707	27440	30587	34110
Czechia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Denmark	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Egypt	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Finland	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1
France	0	0	2	3	3	3	4	5	5	5	6	6	6	6	6	6	6
Germany	0	0	0	0	0	1	4	4	4	5	8	10	12	12	12	12	13
India	0	0	0	0	0	0	0	0	1	1	1	2	3	3	3	3	3
Indonesia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

- Provided by COVUD-19 Data Repository of Center for Systems Science and Engineering (CSSE) at Johns Hopkins University¹
- Dimension: 40×704
- $N = 40$ countries proposed by (Lee, 2020)
- Cumulative confirmed cases of COVID-19 from 2020-01-22 to 2021-12-25

¹<https://github.com/CSSEGISandData>

3. Data

Design Matrix

I	Country	Total_over_65	Female_per	Physician	Underweight_total	Median_age	Birth_rate	Alcohol_cons_rec	Alcohol_cons_unrec
1	US	15.80765406	0.505200148	2.587433333	1.1	37.4	13.2	8.8	0.8
2	Russia	14.67470832	0.536617625	4.0434	1.4	38.3	11.8	8.1	3.6
3	Spain	19.37850752	0.508966414	3.9053	0.6	41.4	10.4	8.5	1.8
4	United Kingdom	18.39586567	0.506352743	2.78915	1	40.2	12.2	9.8	1.1
5	Italy	22.7516796	0.513766703	4.0004	0.8	44.3	9.2	7.1	1.9
6	Brazil	8.922837832	0.50829917	2.15005	2.7	30.3	14.9	6.5	1.2
7	France	20.03462475	0.515842404	3.223433333	1.6	40.6	12.3	11.8	2.4
8	Germany	21.461962	0.506603674	4.143233333	0.8	45.5	8.5	11.3	4.3
9	Iran	6.184573806	0.494391296	1.3131	3.7	28.5	18.8	0	1
10	China	10.92088354	0.48679374	1.7422	4.9	37.4	13.3	5.7	1.5
11	India	6.179955649	0.480235397	0.754133333	23.3	26.4	20.4	3	2.6
12	Peru	8.088392792	0.50337754	1.27	1.3	26.5	19.7	5.1	1.2
13	Canada	17.23200668	0.503915312	2.552975	1.1	40.1	11.3	8.1	0.9
14	Belgium	18.78874374	0.505933164	3.103366667	0.9	41.6	11.7	10.4	1.8
15	Saudi Arabia	3.314088023	0.424458472	2.4835	2	27.5	19.4	0.1	0
16	Netherlands	19.19619263	0.502209417	3.4714	0.9	41.8	10.7	7.5	0.6
17	Chile	11.52980166	0.507270321	1.08	0.7	33.1	13.9	7.9	1.4

- Downloaded from the World Bank Data² and World Health Organization Data³
- Dimension: 40×716

²<https://data.worldbank.org>

³<https://www.who.int/en/>

3. Data

Covariates of Design Matrix

Category	Covariates
General country and population distribution	Total_over_65, Female_per Life_expect_total_60, Dis_to_China
Health Care Resources	Physician, Doc_num_per, Hosp_bed Alcohol_cons_rec,
Tobacco and alcohol use	Alcohol_cons_unrec, Alochol_consumers_total, Heavy_drinking_alcohol
Disease and unhealthy prevalence	Underweight_total
Testing and immunization statistics	Dtt_dtp_immun Persons_Vaccinated
COVID-19 vaccination statistics	1plus_Dose_Per100, Persons_Fully_Vaccinated_Per100, First_Date_Int

4. Analysis: BHRM

Bayesian Hierarchical Richards Model (Review)

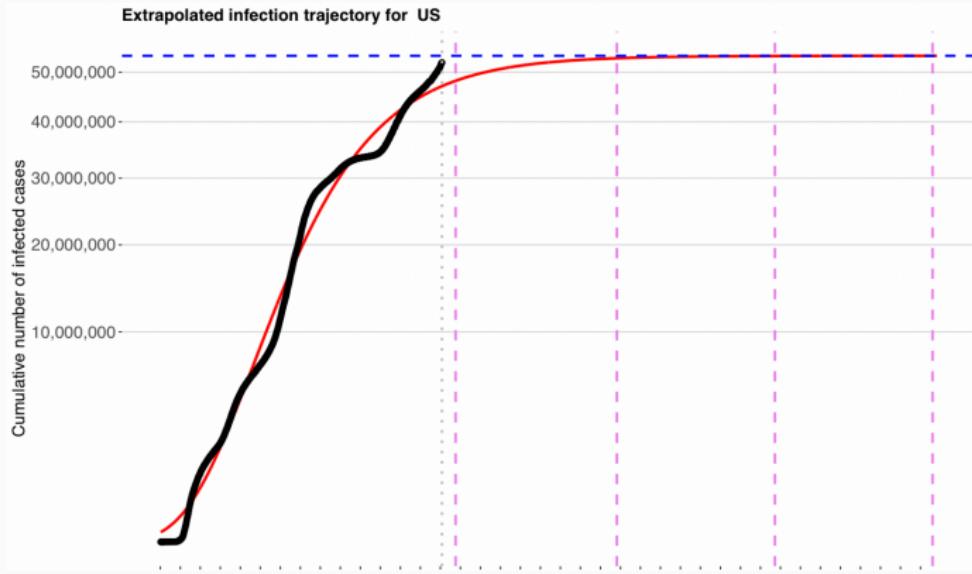
- $\theta_1, \theta_2, \theta_3$ represents the final epidemic size, infection rate and a lag phase, respectively.
- ξ_i indicates the shape parameter of the curve.
- α, β is the regression coefficients to explain the θ using covariates.

Model Simulation

- Use Gibbs sampling to approximate the model
- Derive the full conditional distributions for the parameter in the BHRM
- Implement Metropolis-Hastings algorithm, Slice sampling and Elliptical Slice sampling

4. Analysis: BHRM Results

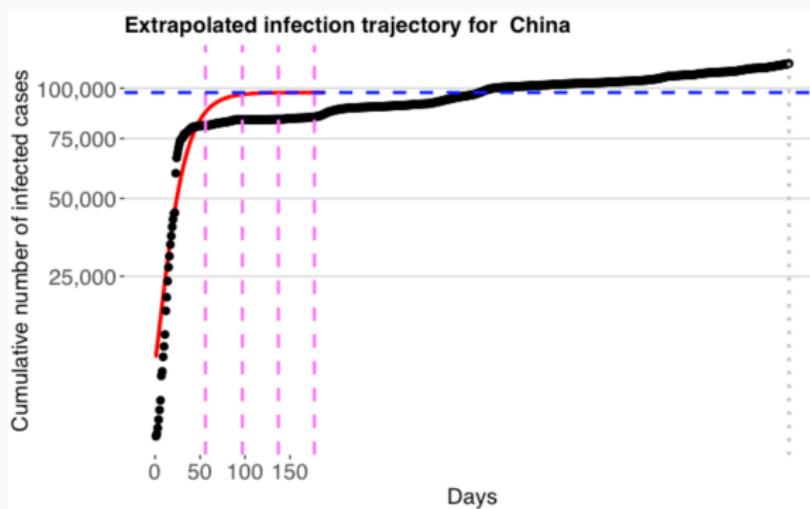
Extrapolated infection trajectory for the US



- Estimated Epidemic size is about 53 million people.
- $t_{\text{flat}, \gamma=0.9}$ is 2022 January 22nd and $t_{\text{flat}, \gamma=0.99}$ is 2023 March 8th.

4. Analysis: BHRM Results

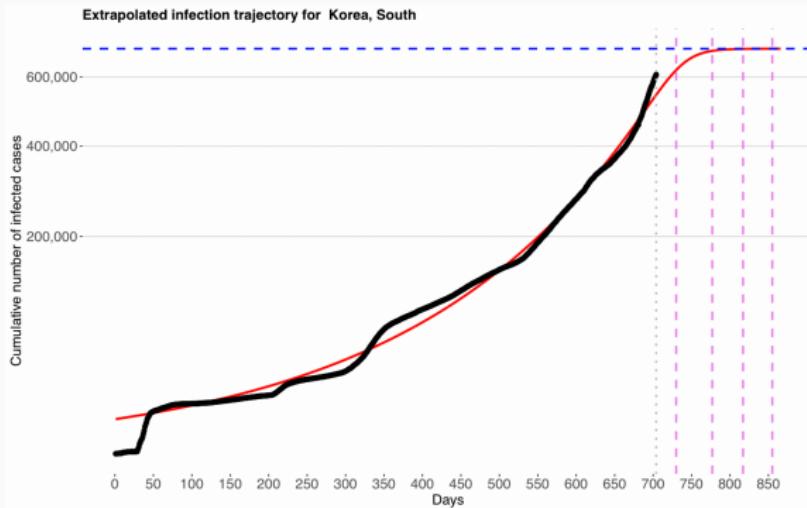
Extrapolated infection trajectory for China



- Estimated Epidemic size is about 97700 people.
- $t_{\text{flat}, \gamma=0.9}$ is 2020 March 18th and $t_{\text{flat}, \gamma=0.99}$ is 2020 April 28th which implies the fitted model conclude the COVID-19 in China is already over.

4. Analysis: BHRM Results

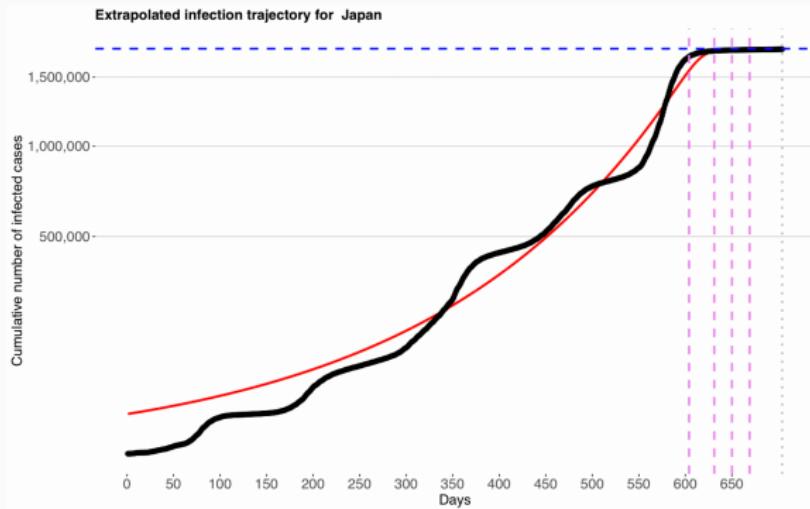
Extrapolated infection trajectory for South Korea



- Estimated Epidemic size is about 1,734,600 people.
- $t_{\text{flat},\gamma=0.9}$ is 2021 Jan 21th and $t_{\text{flat},\gamma=0.99}$ is 2022 March 9th.

4. Analysis: BHRM

Extrapolated infection trajectory for the Japan



- Estimated Epidemic size is about 693,000 people.
- $t_{\text{flat}, \gamma=0.9}$ is 2021 Sep 17th and $t_{\text{flat}, \gamma=0.99}$ is 2021 Oct 14th.

4. Analysis: BHRM

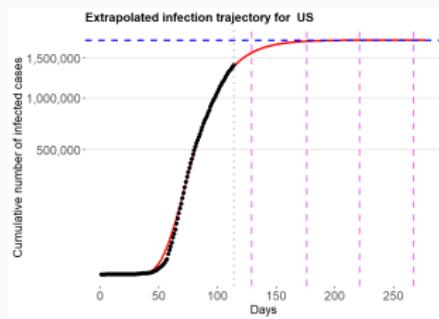
BHRM results

Country	Epidemic Size	$t_{\gamma=0.9}$	$t_{\gamma=0.99}$	$t_{\gamma=0.9}$	$t_{\gamma=0.9}$
U.S	5,356,556	2022 Jan	2023 Mar	2024 Apr	2025 May
Korea	693,058	2022 Jan	2022 Mar	2022 Apr	2022 May
Japan	1,734,466	2021 Sep	2021 Oct	2021 Nov	2021 Nov
China	97,712	2020 Mar	2020 Apr	2020 June	2020 July

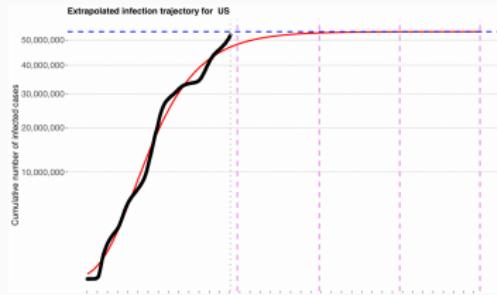
- The pandemic situation in the U.S and Korea will be continued at least in 2022.
- In Japan and China, still confirmed cases appear but the model conclude the pandemic situation was over.
- Based on the current data, it seems difficult to the endpoint of COVID-19 in the U.S.

4. Analysis: Comparison

Comparison between 2020 and 2021 for the U.S



(a)



(b)

- Left curve shows the extrapolated infection trajectory curve using 2020 data and the right curve represents the curve using 2020 and 2021 data.
- It seems difficult to predict the duration the COVID-19 rapid increase lasts.

4. Analysis: JAGS

JAGS

- Just Another Gibbs Sampler (JAGS) is a program for the statistical analysis of Bayesian hierarchical models by Markov Chain Monte Carlo.
- Implements JAGS as the full conditional for parameters in BHRM are already derived.
- Compare the efficiency of approximating BHRM

4. Analysis: JAGS

JAGS code

```
jags.model="
model{
  for(i in 1:N){
    for(j in 1:Tsi){
      Y[i,j] ~ dnorm(theta1[i]*((1+xi[i])*exp(-theta2[i]*(j-theta3[i])))^(-1/xi[i])), 1/global.sigma)
    }
    theta1[i] ~ dnorm(alpha1+X[i,]%%beta1, 1/sig1.sq)
    theta2[i] ~ dnorm(alpha2+X[i,]%%beta2, 1/sig2.sq)
    theta3[i] ~ dnorm(alpha3+X[i,]%%beta3, 1/sig3.sq)

    xi[i] ~ dlnorm(0,1)
  }
  for(k in 1:p){
    beta1[k] ~ dnorm(0, 1/(sig1.sq*tau1.sq[k]*lambda1[k]))
    beta2[k] ~ dnorm(0, 1/(sig2.sq*tau2.sq[k]*lambda2[k]))
    beta3[k] ~ dnorm(0, 1/(sig3.sq*tau3.sq[k]*lambda3[k]))

    lambda1[k] ~ dscaled.gamma(1,1)
    lambda1[k] = 1/sqrt(lambda1[k])
    lambda2[k] ~ dscaled.gamma(1,1)
    lambda2[k] = 1/sqrt(lambda2[k])
    lambda3[k] ~ dscaled.gamma(1,1)
    lambda3[k] = 1/sqrt(lambda3[k])

    gamma.tau1[k] ~ dscaled.gamma(1,1)
    tau1.sq[k] = 1/sqrt(gamma.tau1[k])
    gamma.tau2[k] ~ dscaled.gamma(1,1)
    tau2.sq[k] = 1/sqrt(gamma.tau2[k])
    gamma.tau3[k] ~ dscaled.gamma(1,1)
    tau3.sq[k] = 1/sqrt(gamma.tau3[k])
  }
}
```

- Helpful to fit the BHRM model easily
- Take more time to run the chain

5. Conclusion

- BHRM estimates the final epidemic size and the endpoint of COVID-19 integrating many countries data.
- Unlike other North East Asia countries, the COVID-19 in South Korea still continue.
- It seems difficult to predict or estimate the period of epidemic Level 2 which implies the rapidly increasing time of epidemic.
- Introduce new parameters in the model to improve or Consider other models (e.g. non-parametric models).

Reference