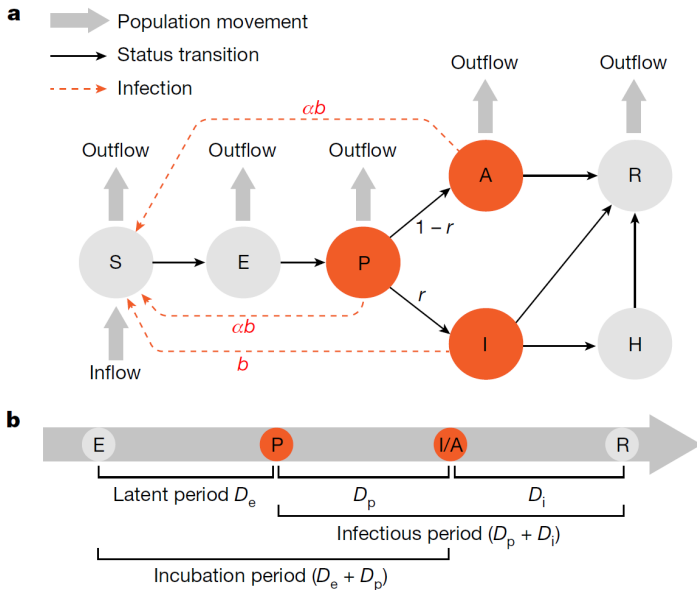


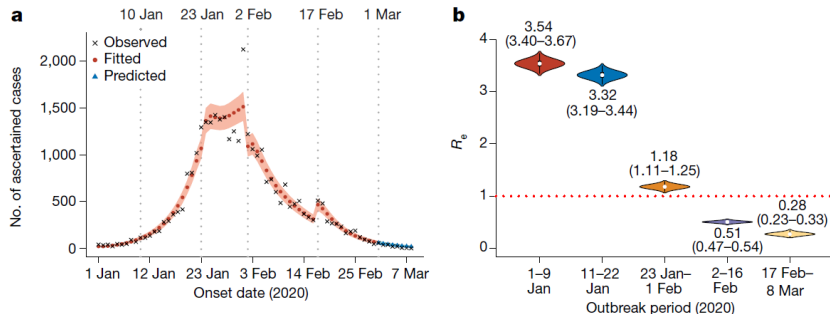
# Reconstruction of the full transmission dynamics of COVID-19 in Wuhan

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# Review of the SAPHIRE model [1]



# Modeling the COVID-19 pandemic in Wuhan



# DRAM algorithm

Expanding delayed rejection [2]:

$$\alpha_i(\vec{\lambda}, \vec{\beta}_1, \dots, \vec{\beta}_i) = 1 \wedge \left\{ \frac{\pi(\vec{\beta}_i) q_1(\vec{\beta}_i, \vec{\beta}_{i-1}) q_2(\vec{\beta}_i, \vec{\beta}_{i-1}, \vec{\beta}_{i-2}) \dots q_i(\vec{\beta}_i, \vec{\beta}_{i-1}, \dots, \vec{\lambda})}{\pi(\vec{\lambda}) q_1(\vec{\lambda}, \vec{\beta}_1) q_2(\vec{\lambda}, \vec{\beta}_1, \vec{\beta}_2), \dots q_i(\vec{\lambda}, \vec{\beta}_1, \dots, \vec{\beta}_i)} \right\} \\ \frac{[1 - \alpha_1(\vec{\beta}_1, \vec{\beta}_{i-1})][1 - \alpha_2(\vec{\beta}_i, \vec{\beta}_{i-1}, \vec{\beta}_{i-2})] \dots [1 - \alpha_{i-1}(\vec{\beta}_i, \dots, \vec{\beta}_1)]}{[1 - \alpha_1(\vec{\lambda}, \vec{\beta}_1)][1 - \alpha_2(\vec{\lambda}, \vec{\beta}_1, \vec{\beta}_2)] \dots [1 - \alpha_{i-1}(\vec{\lambda}, \dots, \vec{\beta}_{i-1})]}$$

Parameters:

- $\alpha_i$  is the probability of accepting the proposed step
- $q_i$  is the proposal distribution
- $\pi(x)$  is the target distribution
- $\lambda$  is the initial state ( $d = 1$ )
- $\beta_i$  are the delayed states ( $d > 1$ )

# Profiling

## Improving runtime

- 144 seconds overall to run 100,000 iterations
- 122 seconds to calculate the likelihood

## SAPHIRE differential equations

- Utilized in likelihood
- Attempted parallelization/re-ordering of terms

# DRAM parameters

Modified DR levels + adaptation intervals and measured performance

Table: Estimated parameters for each scenario

	Original	DR=3	DR=4	adaptl=1000	adaptl=2000
b12	1.31 (1.25 - 1.38)	1.31 (1.24 - 1.37)	1.31 (1.25 - 1.38)	1.31 (1.25 - 1.38)	1.31 (1.25 - 1.37)
b3	0.40 (0.38 - 0.43)	0.40 (0.38 - 0.43)	0.40 (0.37 - 0.43)	0.40 (0.38 - 0.42)	0.40 (0.38 - 0.43)
b4	0.18 (0.16 - 0.19)	0.17 (0.16 - 0.19)	0.17 (0.16 - 0.19)	0.17 (0.16 - 0.19)	0.17 (0.16 - 0.19)
b5	0.10 (0.08 - 0.12)	0.10 (0.08 - 0.11)	0.10 (0.08 - 0.12)	0.10 (0.08 - 0.11)	0.10 (0.08 - 0.11)
r12	0.15 (0.13 - 0.17)	0.15 (0.13 - 0.17)	0.15 (0.12 - 0.17)	0.15 (0.13 - 0.17)	0.15 (0.13 - 0.17)
delta3	-0.06 (-0.15 - 0.04)	-0.05 (-0.15 - 0.05)	-0.06 (-0.16 - 0.05)	-0.05 (-0.15 - 0.05)	-0.06 (-0.15 - 0.04)
delta4	-0.40 (-0.49 - -0.32)	-0.40 (-0.49 - -0.31)	-0.40 (-0.49 - -0.3)	-0.40 (-0.49 - -0.31)	-0.4 (-0.48 - -0.31)
delta5	0.57 (0.44 - 0.72)	0.58 (0.44 - 0.73)	0.58 (0.42 - 0.74)	0.57 (0.44 - 0.73)	0.58 (0.44 - 0.73)

# Simulation setup

- Stochastically simulated the dataset using multinomial random sampling.
- Two generative models:
  - ▶ SAPHIRE model
  - ▶ SEIRH model
- Input:
  - ▶ Initial values of each compartments:  $S^0, E^0, P^0, A^0, I^0, H^0, R^0$
  - ▶ True parameter values:  $b_{12}, b_3, b_4, b_5, r_{12}, r_3, r_4, r_5$
  - ▶ Fixed parameter values:  $\alpha, D_e, D_p, D_i, D_q, D_h, N, n$
- Daily ascertained cases in which individuals experienced symptom onset, for a period of 60 days

# Simulation procedure for the SAPHIRE model

- Sequentially update the compartments using the following sampling probabilities

$$\begin{aligned}(\Delta_{S^t \rightarrow E^t}, \Delta_{S^t \rightarrow O^t}, \Delta_{S^t \rightarrow S^{t+1}}) &\sim MN \left( S^{t-1}, \frac{b(\alpha P + I + \alpha A)}{N}, \frac{n}{N}, 1 - \frac{b(\alpha P + I + \alpha A)}{N} - \frac{n}{N} \right) \\(\Delta_{E^t \rightarrow P^t}, \Delta_{E^t \rightarrow O^t}, \Delta_{E^t \rightarrow E^{t+1}}) &\sim MN \left( E^{t-1}, \frac{1}{D_e}, \frac{n}{N}, 1 - \frac{1}{D_e} - \frac{n}{N} \right) \\(\Delta_{P^t \rightarrow I^t}, \Delta_{P^t \rightarrow A^t}, \Delta_{P^t \rightarrow O^t}, \Delta_{P^t \rightarrow P^{t+1}}) &\sim MN \left( P^{t-1}, \frac{r}{D_p}, \frac{1-r}{D_p}, \frac{n}{N}, 1 - \frac{r}{D_p} - \frac{1-r}{D_p} - \frac{n}{N} \right) \\(\Delta_{I^t \rightarrow H^t}, \Delta_{I^t \rightarrow R^t}, \Delta_{I^t \rightarrow I^{t+1}}) &\sim MN \left( I^{t-1}, \frac{1}{D_q}, \frac{1}{D_i}, 1 - \frac{1}{D_q} - \frac{1}{D_i} \right) \\(\Delta_{A^t \rightarrow R^t}, \Delta_{A^t \rightarrow R^t}, \Delta_{A^t \rightarrow A^{t+1}}) &\sim MN \left( A^{t-1}, \frac{1}{D_i}, \frac{n}{N}, 1 - \frac{1}{D_i} - \frac{n}{N} \right) \\(\Delta_{H^t \rightarrow R^t}, \Delta_{H^t \rightarrow H^{t+1}}) &\sim MN \left( H^{t-1}, \frac{1}{D_h}, 1 - \frac{1}{D_h} \right) \\(\Delta_{R^t \rightarrow O^t}, \Delta_{R^t \rightarrow R^{t+1}}) &\sim MN \left( R^{t-1}, \frac{n}{N}, 1 - \frac{n}{N} \right).\end{aligned}$$



# Simulation procedure for the SEIRH model

- Sequentially update the compartments using the following sampling probabilities

$$(\Delta_{S^t \rightarrow E^t}, \Delta_{S^t \rightarrow O^t}, \Delta_{S^t \rightarrow S^{t+1}}) \sim MN \left( S^{t-1}, \frac{bI}{N}, \frac{n}{N}, 1 - \frac{bI}{N} - \frac{n}{N} \right)$$

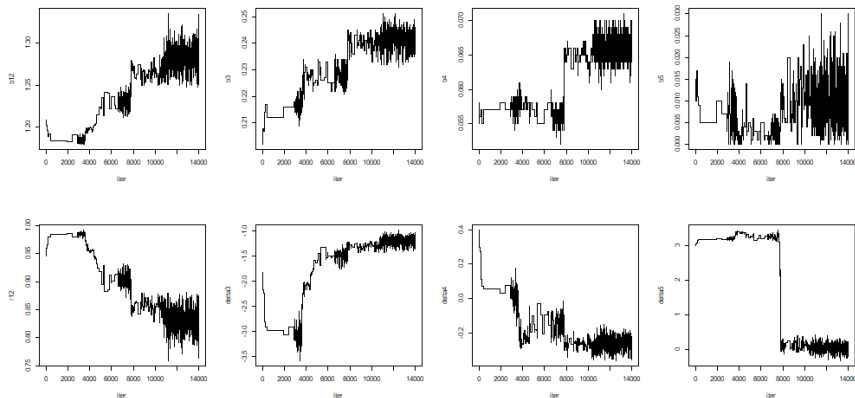
$$(\Delta_{E^t \rightarrow P^t}, \Delta_{E^t \rightarrow O^t}, \Delta_{E^t \rightarrow E^{t+1}}) \sim MN \left( E^{t-1}, \frac{1}{D_e}, \frac{n}{N}, 1 - \frac{1}{D_e} - \frac{n}{N} \right)$$

$$(\Delta_{I^t \rightarrow H^t}, \Delta_{I^t \rightarrow R^t}, \Delta_{I^t \rightarrow I^{t+1}}) \sim MN \left( I^{t-1}, \frac{1}{D_q}, \frac{1}{D_i}, 1 - \frac{1}{D_q} - \frac{1}{D_i} \right)$$

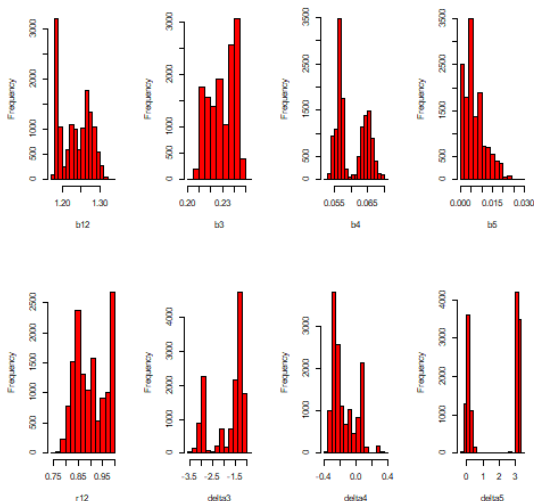
$$(\Delta_{H^t \rightarrow R^t}, \Delta_{H^t \rightarrow H^{t+1}}) \sim MN \left( H^{t-1}, \frac{1}{D_h}, 1 - \frac{1}{D_h} \right)$$

$$(\Delta_{R^t \rightarrow O^t}, \Delta_{R^t \rightarrow R^{t+1}}) \sim MN \left( R^{t-1}, \frac{n}{N}, 1 - \frac{n}{N} \right).$$

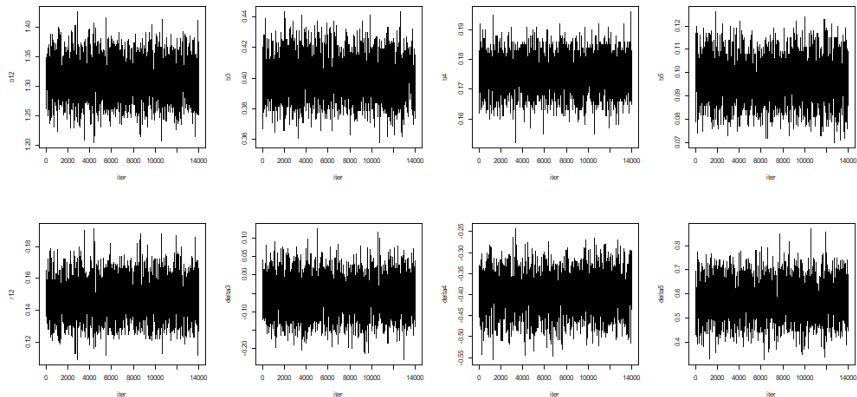
# MCMC chains do not converge under the SEIRH generative model



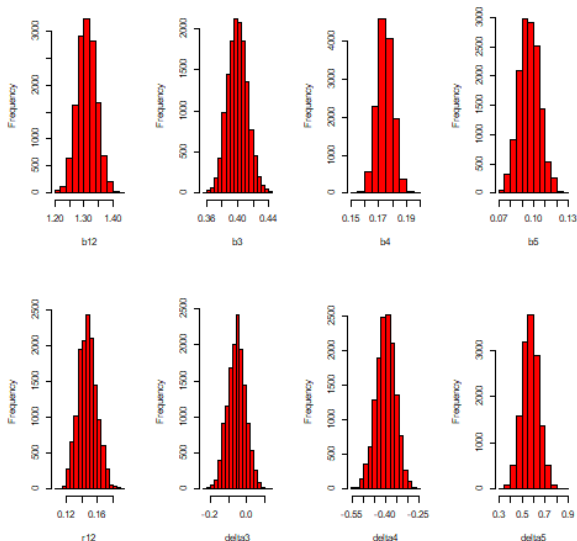
# MCMC chains do not converge under the SEIRH generative model



# Good mixing under the SAPHIRE generative model



# Good mixing under the SAPHIRE generative model



# Simulation results

Table: Absolute bias and RMSE for each approach among 100 replicates

	adaptl=1000	DR=3	DR=4	adaptl=500	adaptl=2000
Bias					
b12	0.01	0.01	0.01	0.00	0.01
b3	0.00	0.00	0.00	0.00	0.00
b4	0.00	0.00	0.00	0.00	0.00
b5	0.00	0.00	0.00	0.01	0.00
r12	0.00	0.01	0.00	0.00	0.01
delta3	0.01	0.02	0.01	0.00	0.01
delta4	0.00	0.00	0.00	0.01	0.01
delta5	0.01	0.01	0.01	0.02	0.01
RMSE					
b12	0.03	0.04	0.04	0.04	0.04
b3	0.02	0.01	0.01	0.04	0.02
b4	0.01	0.00	0.00	0.01	0.00
b5	0.01	0.01	0.01	0.06	0.01
r12	0.02	0.02	0.02	0.01	0.02
delta3	0.07	0.11	0.11	0.09	0.08
delta4	0.06	0.04	0.06	0.08	0.07
delta5	0.20	0.13	0.12	0.20	0.20

# Simulation results

Table: Coverage and length of the 95% CI for each approach among 100 replicates

	adaptl=1000	DR=3	DR=4	adaptl=500	adaptl=2000
Coverage					
b12	1.00	1.00	1.00	1.00	1.00
b3	1.00	1.00	1.00	0.99	1.00
b4	1.00	1.00	1.00	1.00	1.00
b5	1.00	1.00	1.00	0.99	1.00
r12	1.00	1.00	1.00	1.00	1.00
delta3	1.00	1.00	1.00	0.99	1.00
delta4	1.00	1.00	1.00	0.99	1.00
delta5	1.00	1.00	1.00	0.99	1.00
Length					
b12	0.16	0.15	0.15	0.16	0.15
b3	0.06	0.06	0.06	0.07	0.06
b4	0.03	0.03	0.03	0.03	0.03
b5	0.05	0.04	0.05	0.05	0.05
r12	0.06	0.06	0.06	0.06	0.06
delta3	0.26	0.28	0.27	0.25	0.26
delta4	0.24	0.25	0.24	0.22	0.23
delta5	0.51	0.46	0.36	0.37	0.41

# Simulation results

Table: Runtime (mean [Q1,Q3]) for each approach among 100 replicates

	adaptl=1000	DR=3	DR=4	adaptl=500	adaptl=2000
Runtime	593 [577,601]	862 [804,853]	1103 [1031,1072]	614 [587,637]	595 [577,615]



# Conclusion

- Extension of DRAM algorithm
  - ▶ To allow for more than two levels of delayed rejection and varying adaption intervals for model fitting.
- Simulation results
  - ▶ We considered different generative models for the observed case rates.
  - ▶ When the delayed rejection is set to 3 or 4 (baseline is 2), the RMSE is reduced for some parameters.
- Limitations of algorithm
  - ▶ Inflexibility
  - ▶ Prior information requirement

# Thank you for listening!

Question or comments?

# References



Xingjie Hao et al. “Reconstruction of the full transmission dynamics of COVID-19 in Wuhan”. In: *Nature* 584.7821 (2020), pp. 420–424.



Miquel Trias, Alberto Vecchio, and John Veitch. *Delayed rejection schemes for efficient Markov-Chain Monte-Carlo sampling of multimodal distributions*. 2009. arXiv: 0904.2207 [stat.ME].