Detecting Model Misspecification in Amortized Bayesian Inference

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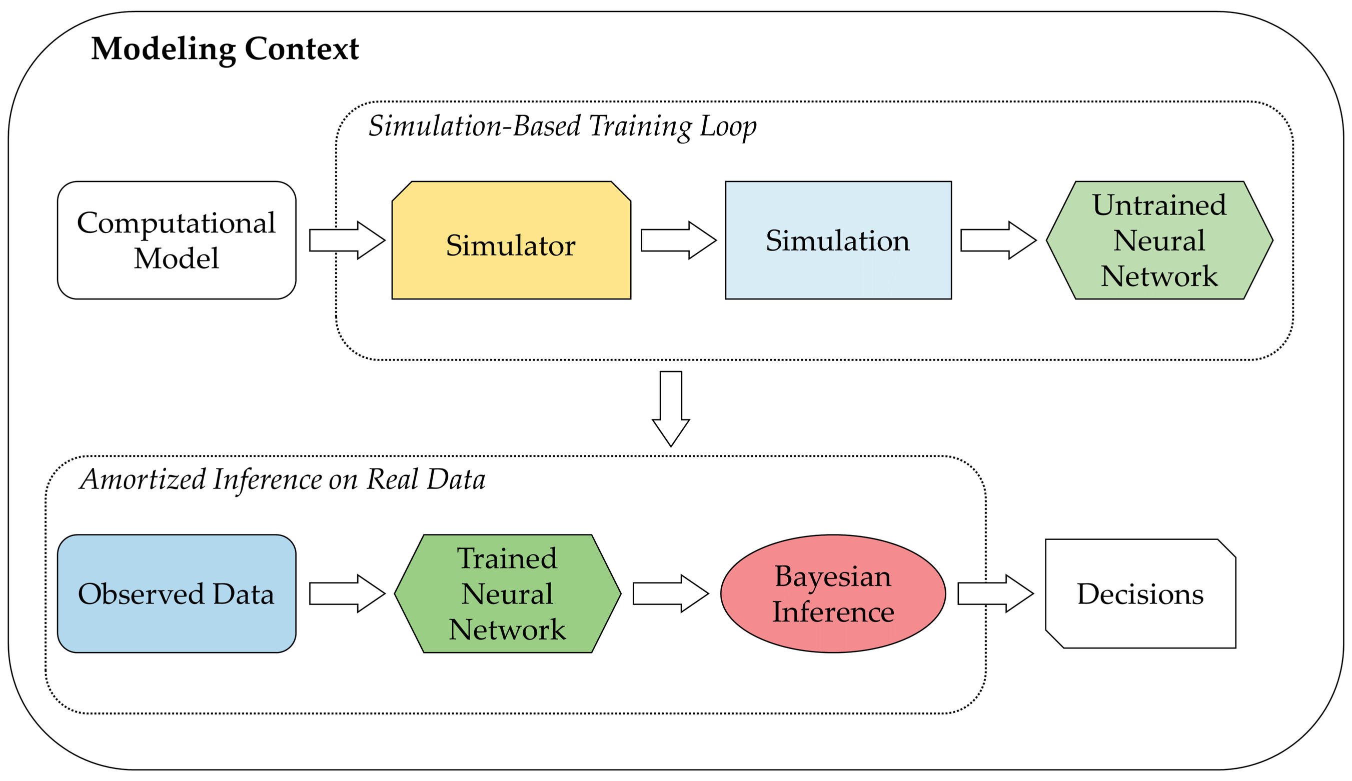
Amortized Bayesian Inference



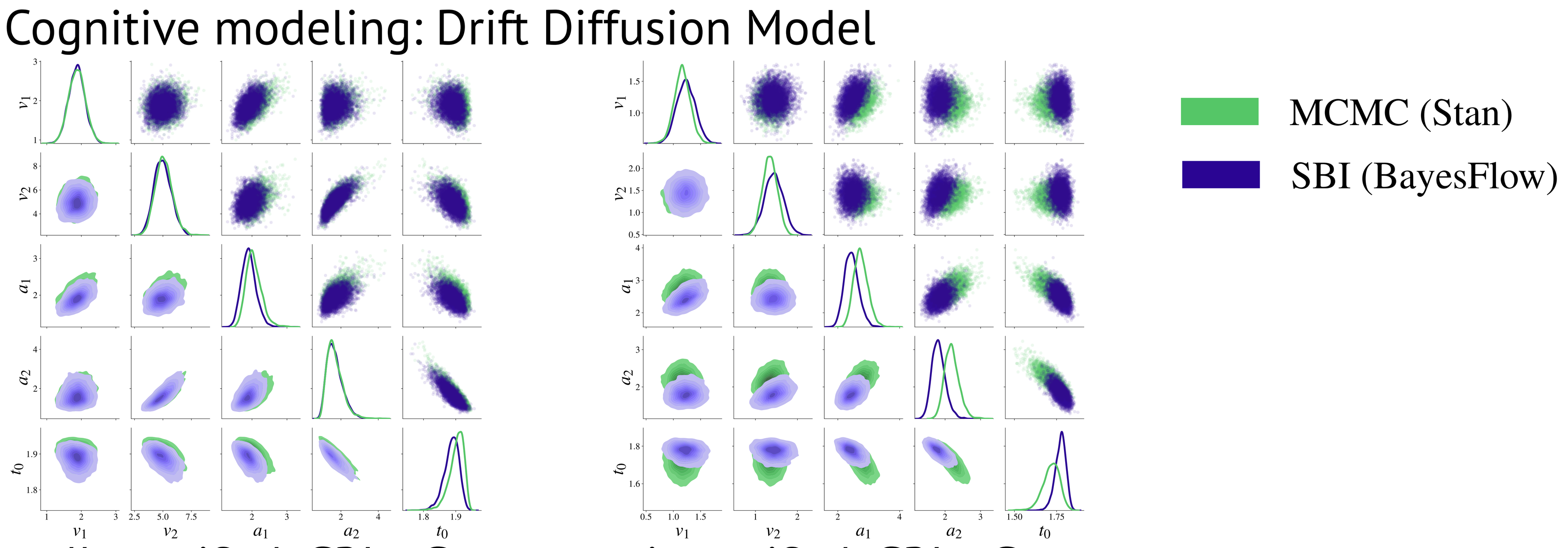
Simulation Paradigm

Generative model $\mathcal{G} = (g(\theta, \xi), p(\xi \mid \theta), p(\theta))$

simulator $x = g(\theta, \xi)$ contamination $\xi \sim p(\xi \mid \theta)$, prior $\theta \sim p(\theta)$

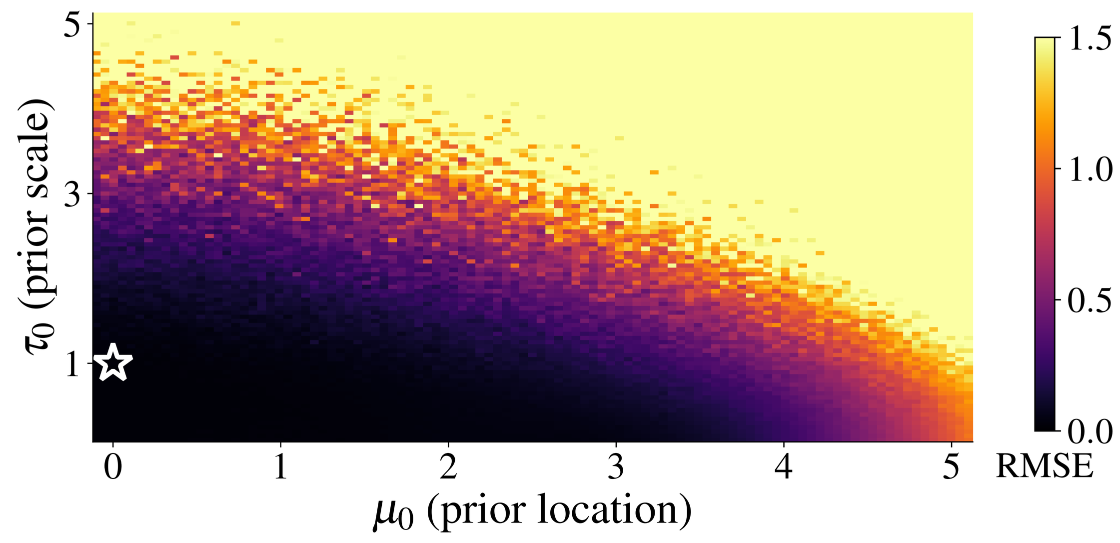
Model Misspecification → Posterior Errors

(1) Cognitive modeling: Drift Diffusion Model



well-specified: SBI ≈ Stan *misspecified: SBI ≠ Stan*

(2) Conjugate Model: 2D Gaussian Means

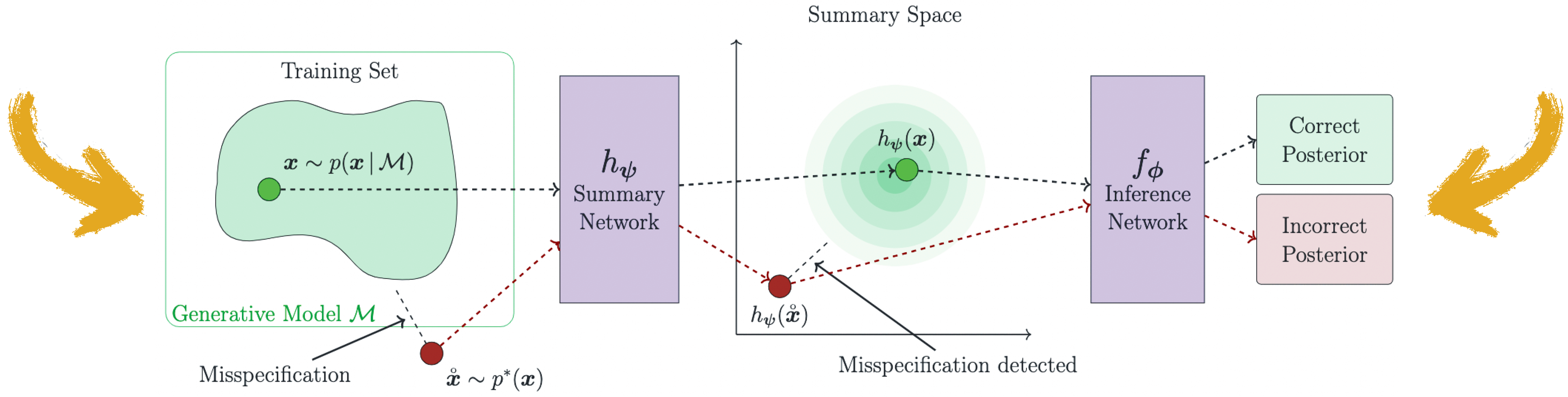


More severe model misspecification

↓

Larger deviation from analytic posterior

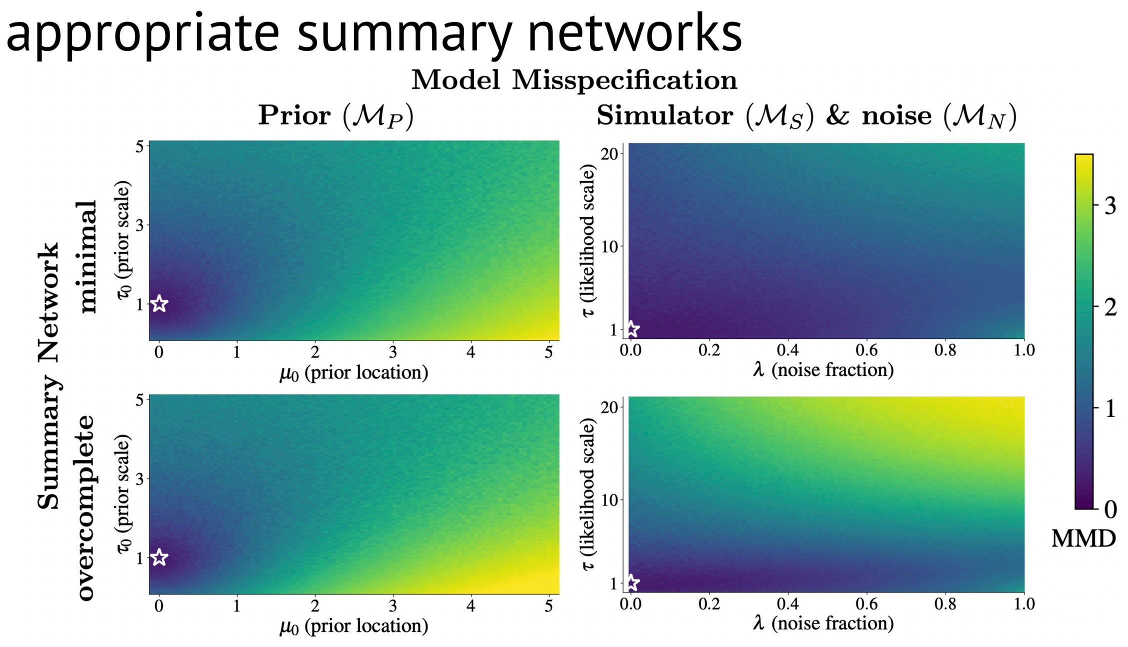
Our Framework to Detect Model Misspecification



Experiments

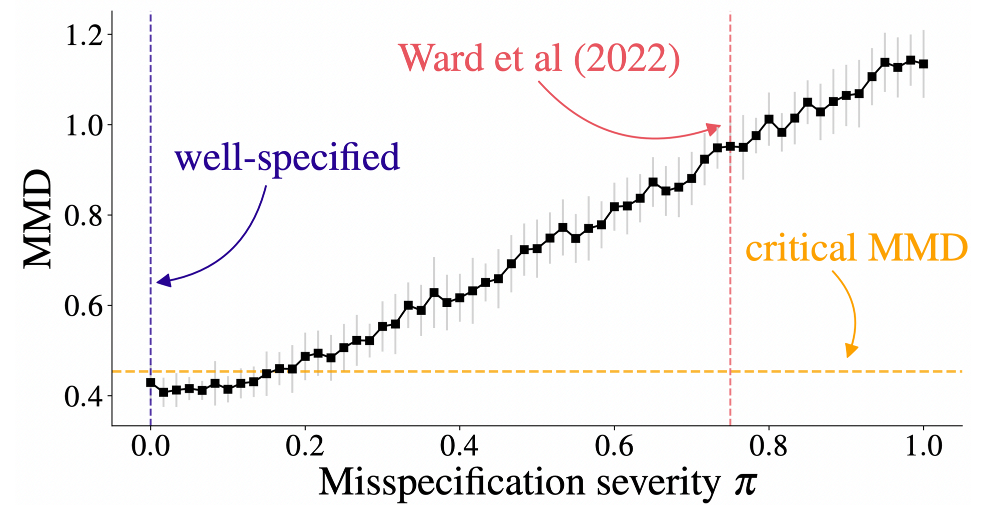
Toy 2D Gaussian

Model misspecification can be detected with appropriate summary networks

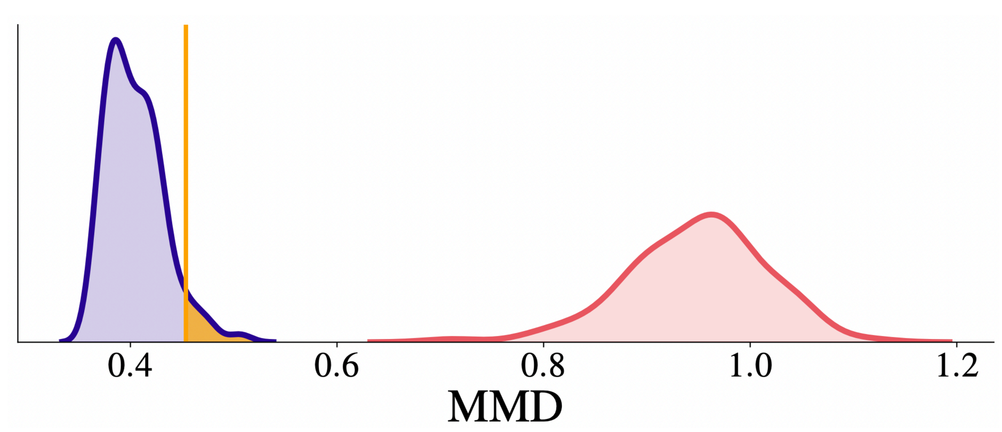


Cancer Cell Model

More severe misspecification → higher MMD (louder alarm)



Hypothesis test for misspecification



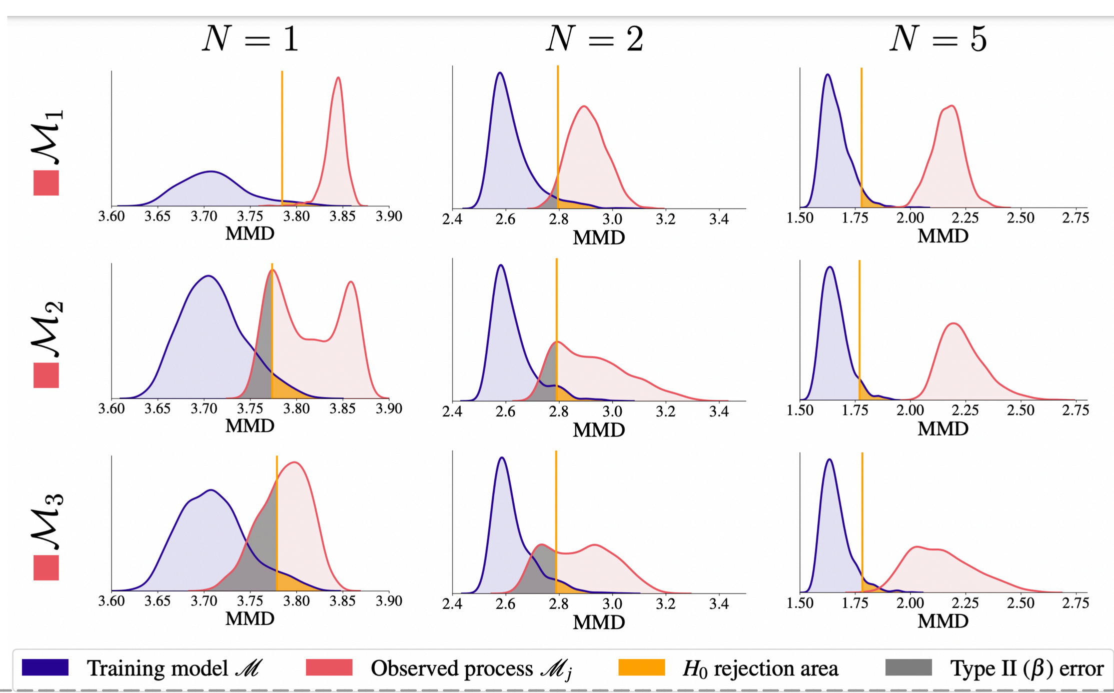
Drift Diffusion Model

Principal components (PCA) in the learned summary space align with true parameters

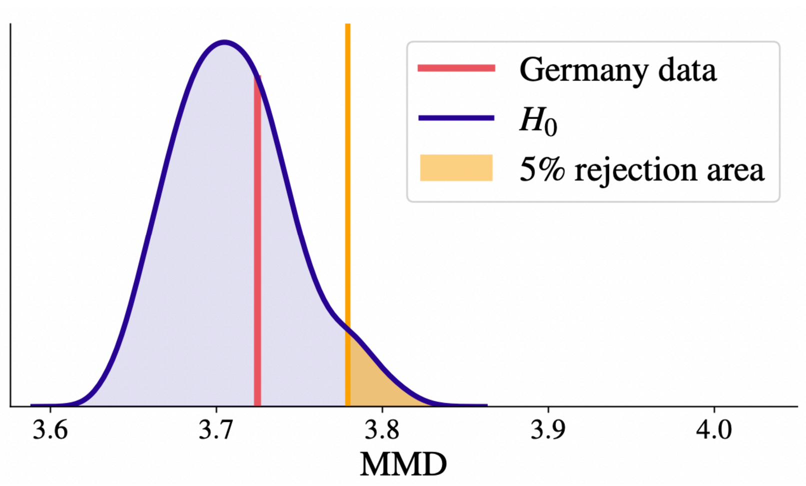
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
v_1	-0.03	-0.29	-0.48	-0.58	-0.23	-0.06	0.05	0.03	0.07	0.02
v_2	-0.00	-0.71	-0.06	0.44	-0.14	-0.04	0.09	0.00	0.08	0.04
a_1	0.10	-0.05	0.68	-0.21	-0.48	0.15	0.15	-0.10	0.02	0.13
a_2	0.04	0.49	-0.39	0.33	-0.50	0.06	0.19	0.01	0.04	0.02
t_0	0.99	-0.01	-0.07	-0.00	0.06	-0.03	-0.02	0.02	-0.02	0.00
$\sum R^2$	0.31	0.47	0.60	0.73	0.85	0.95	0.99	1.00	1.00	1.00

COVID-19 Time Series

Power ≈ 1 for as few as $N = 5$ data sets



Hypothesis test result:
"The model is well-specified for the observed data from Germany."



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