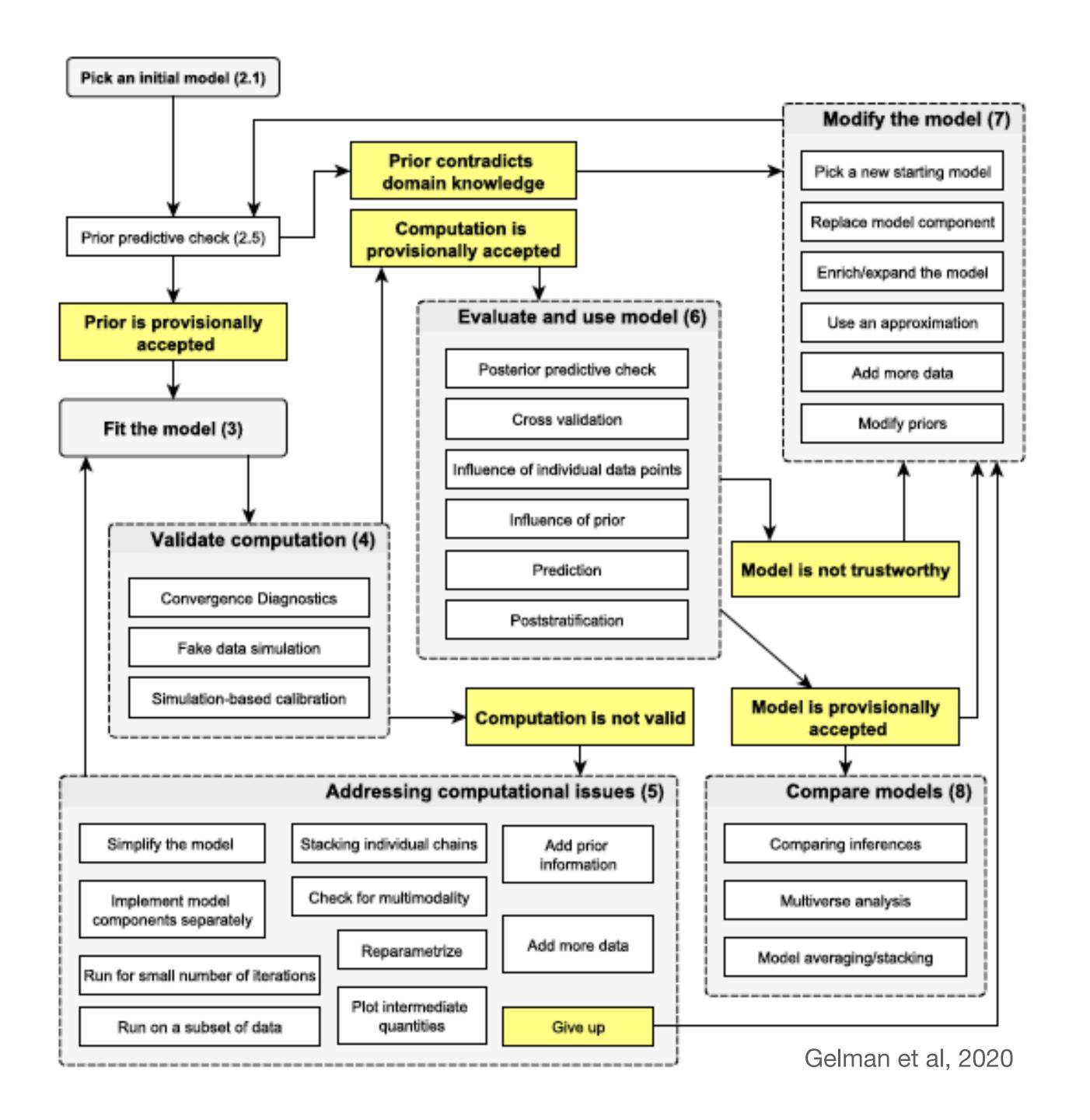
# Applied Bayesian Modeling module 12: **Bayesian workflow**

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# Background

- Setting:
  - You have a research question and a data set
    - Example: forecast COVID19 in Switzerland
  - Goal: Let's develop a Bayesian model to answer the question!
- How to go about model development?
  - Consider an iterative process...
  - Contrast this with eg clinical trial research: Sample size calculation & analysis plan -> data collection -> analysis as per plan

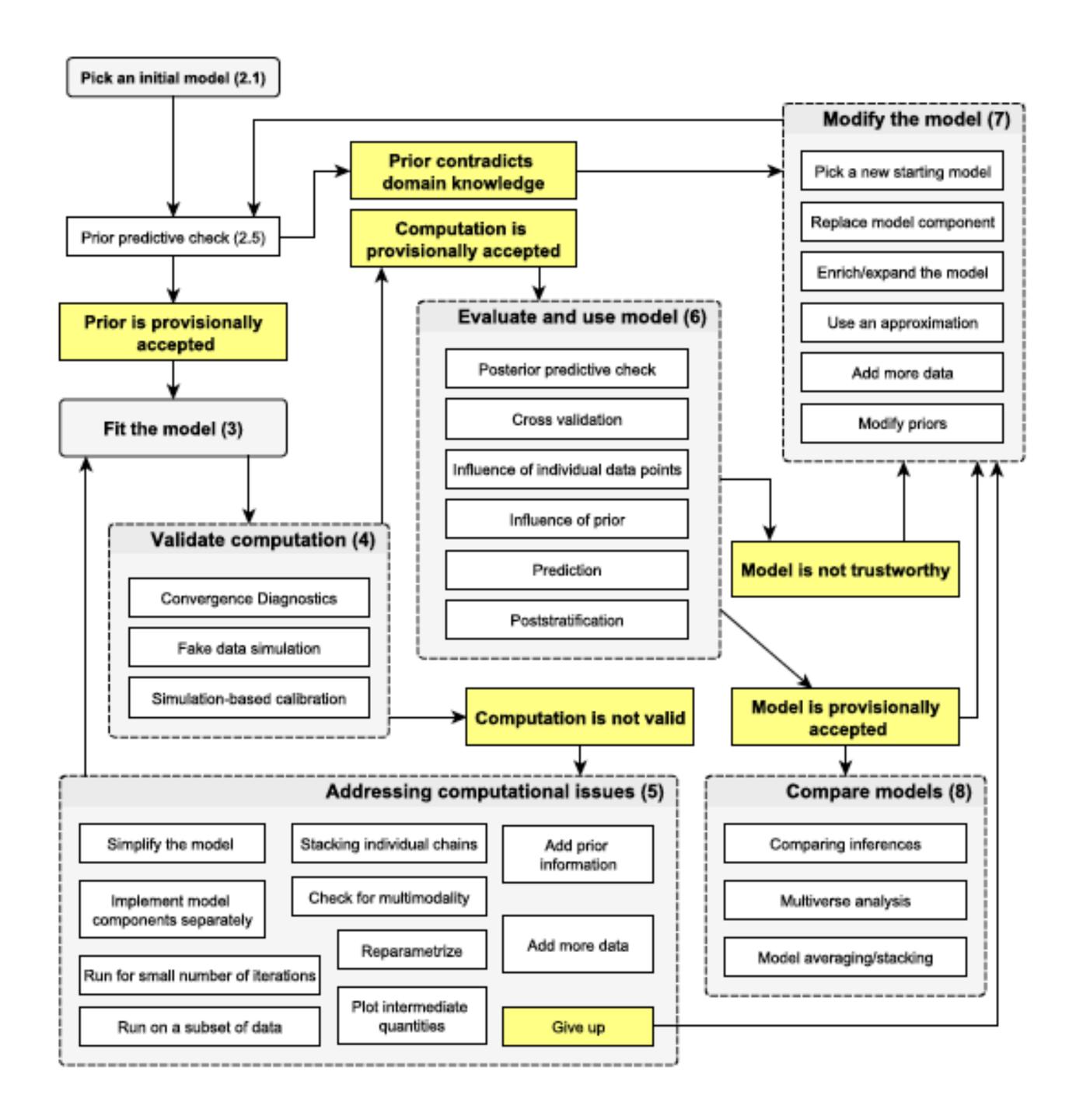


# Bayesian workflow

- Bayesian workflow refers to the steps/iterative process used to develop a model
  - Build, debug, improve, expand
- References
  - Gelman et al (2020). "Bayesian Workflow." <a href="http://arxiv.org/abs/2011.01808">http://arxiv.org/abs/2011.01808</a>
  - Gabry et al (2019). "Visualization in Bayesian Workflow." JRSS Series A 182, no. 2 (2019): 389–402. https://doi.org/10.1111/rssa.12378
  - Grinsztajn et al (2021). "Bayesian Workflow for Disease Transmission Modeling in Stan." Statistics in Medicine 40, no. 27 (2021): 6209–34. https://doi.org/10.1002/sim.9164
- By writing about Bayesian workflows, the authors (Gelman et al in particular)
  - Share guidance to help with model development
  - Help work towards formalize/systematize Bayesian model development
- Opinionated?

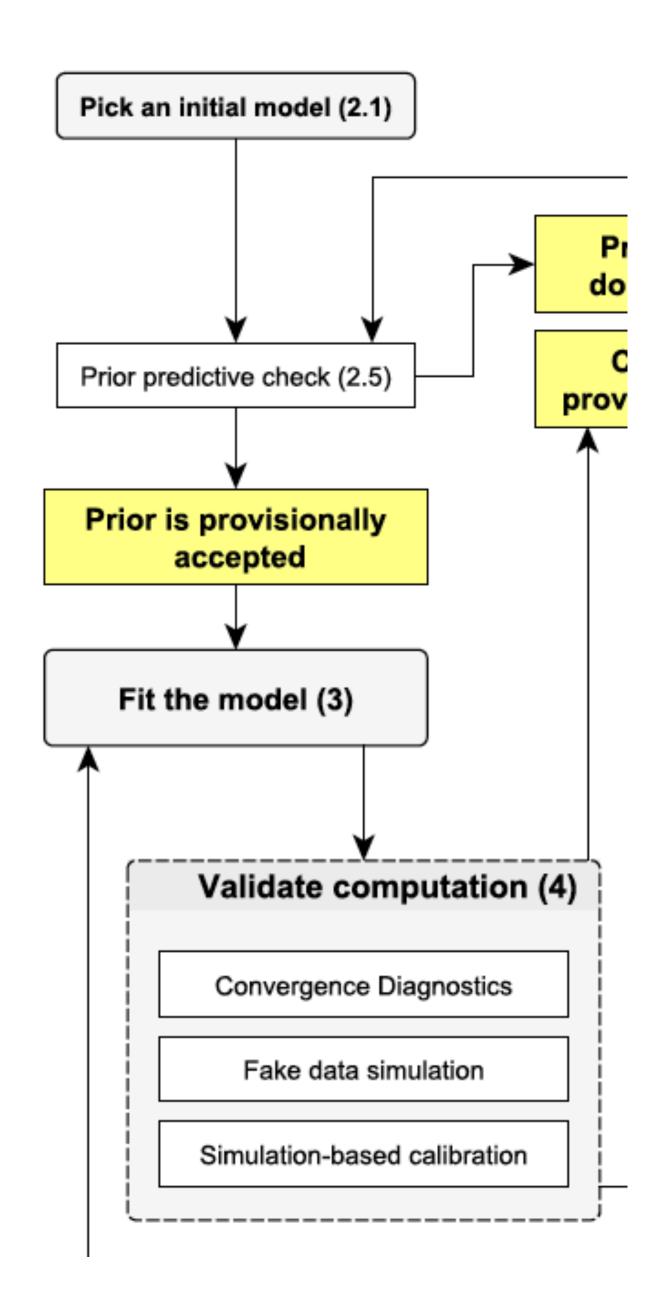
#### Elements

- (+) Exploratory data analysis
- Choose initial model(s)
- Troubleshoot before fitting
  - Prior predictive check
- Validate computation
  - Address computational issues
- Evaluate and use model
- Modify the model
- Model comparison



# Getting started

- Choose initial model(s)
  - Adopt a model from a previous analysis
  - Consider starting simple, to then expand
- Troubleshoot before fitting to actual data
  - Prior predictive check
- Fit the model and validate computation
  - Consider first running the model with a smaller number of iterations (fit fast, fail fast)
  - Then consider MCMC diagnostics
    - So far, we discussed general MCMC diagnostics to check mixing of chains (Rhat and effective sample size)
    - When using default computation in Stan, some additional warnings may come up that are helpful to detect issues

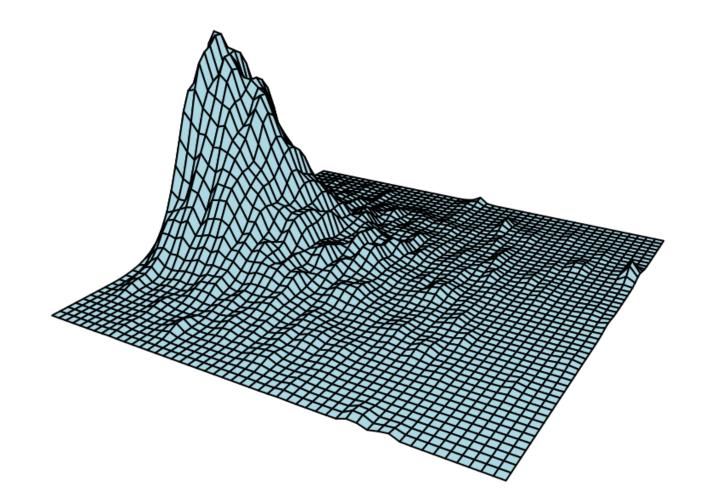


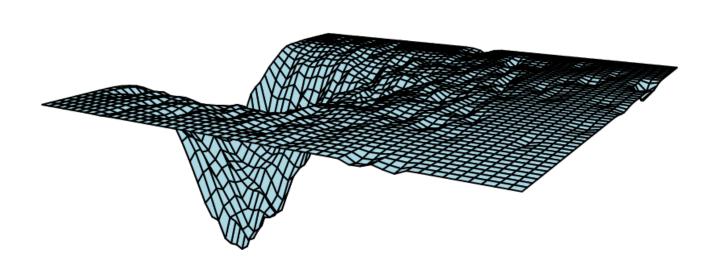
# Computation

- More details on Stan's default MCMC algorithm (HMC/NUTS)
  - Focus on main ideas, to understand the warnings and tuning parameters
- References
  - Nice intro to HMC: <a href="https://bookdown.org/marklhc/notes\_bookdown/markov-chain-monte-carlo.html#hamiltonian-monte-carlo">https://bookdown.org/marklhc/notes\_bookdown
  - Warnings: <a href="https://mc-stan.org/misc/warnings.html">https://mc-stan.org/misc/warnings.html</a>

#### Under the hood

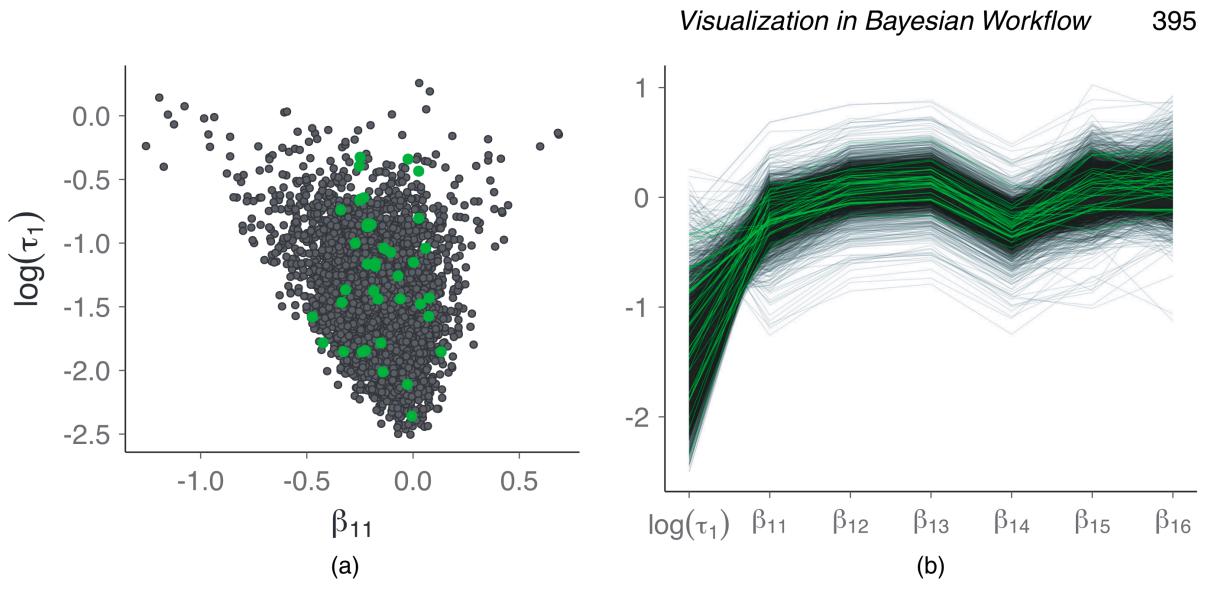
- Stan implements gradient-based Markov chain Monte Carlo (MCMC) algorithms for Bayesian inference, with the default algorithm being the No-U-Turn sampler (NUTS), a variant of Hamilton Monte Carlo (HMC)
- HMC: sampling from posterior == "considering the inverted posterior as a park for ice skating" (Lai, 2019)
  - You are randomly given a direction and an energy level
  - Where you end up (taking account of gravitational force [derivatives])
     == a sample from the posterior
- In practice: use numerical integration (leapfrog integrator)
  - Break path into discrete segments, referred to as leapfrog steps
    - Need to choose a step size and number of steps
  - NUTS version of HMC automates the algorithm
  - Once you stop somewhere, do a Metropolis step (accept or reject the proposed value), to make up for issues with numerical integration





# Stan warnings: divergences

- A divergence arises when the simulated Hamiltonian trajectory departs from the true trajectory as measured by departure of the Hamiltonian value from its initial value.
  - E.g. when log posterior doesn't have a continuous derivative
- This is a problem because it may mean that posterior distribution isn't thoroughly explored
- Check where divergences they occur to see if there is a problematic area (combination of parameter values)
- ShinyStan or Bayesplot visualization



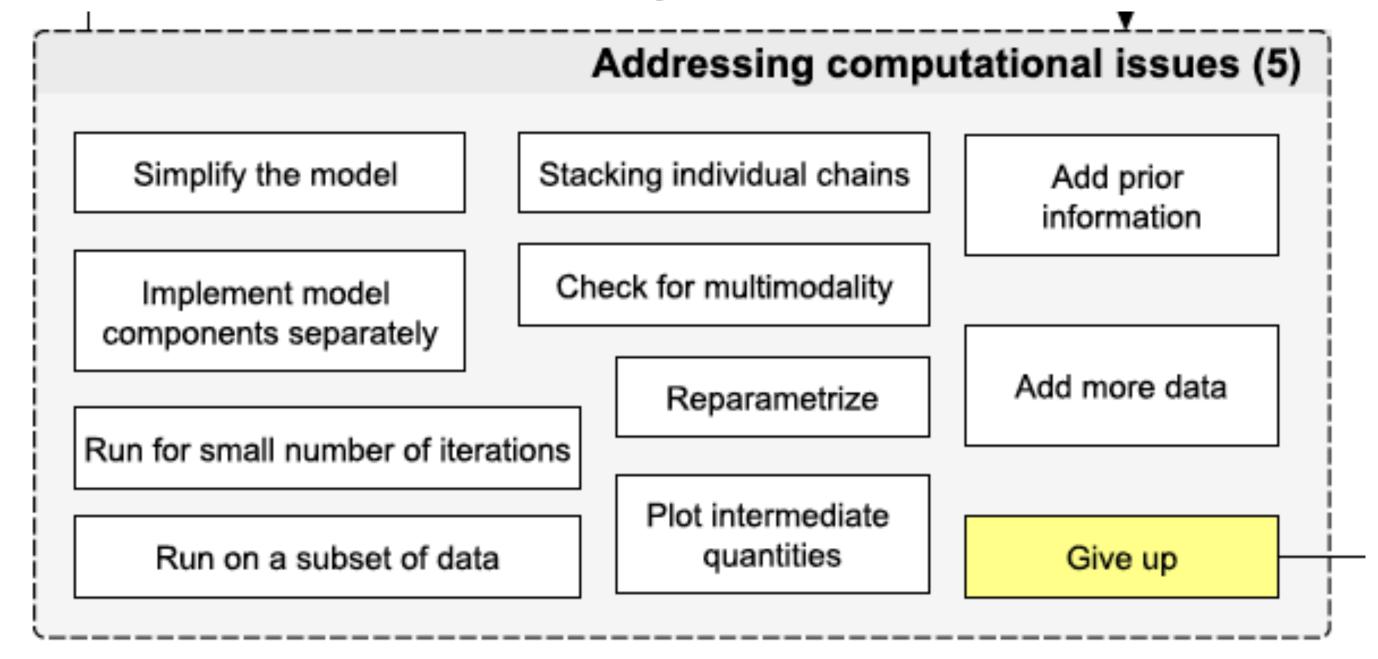
# Stan warnings: divergences (ctd)

- Only a few divergences in different places and good other diagnostics (Rhat and ESS), often a ok
  - Could be falsely labeled as a divergence
- If there is a systematic issue:
  - Reparametrize
  - Consider the "folk theorem of statistical computing":
    - When you have computational problems, often there's a problem with your model (Yao et al, 2020). Not always—sometimes you will have a model that is legitimately difficult to fit—but many cases of poor convergence correspond to regions of parameter space that are not of substantive interest or even to a nonsensical model (Gelman et al, 2020).
    - Reconsider your model
- If you do want to throw more computational power at it: consider Stan tuning parameter
  - Adapt\_delta = target acceptance rate in metropolis step
  - Defaults at 0.8
  - Increase to reduce the stepsize so algorithm won't go too far away in each jump (and is more likely to accept proposed value)

# Treedepth

- You may get a warning on max treedepth
  - An efficiency concern as compared to a validity concern
  - But reaching max treedepths may (again) suggest a model specification issue
- Tuning parameter "max\_treedepth" controls maximum number of leapfrog steps
  - Not typically recommended to increase as per stan warning reference

# Addressing computational issues



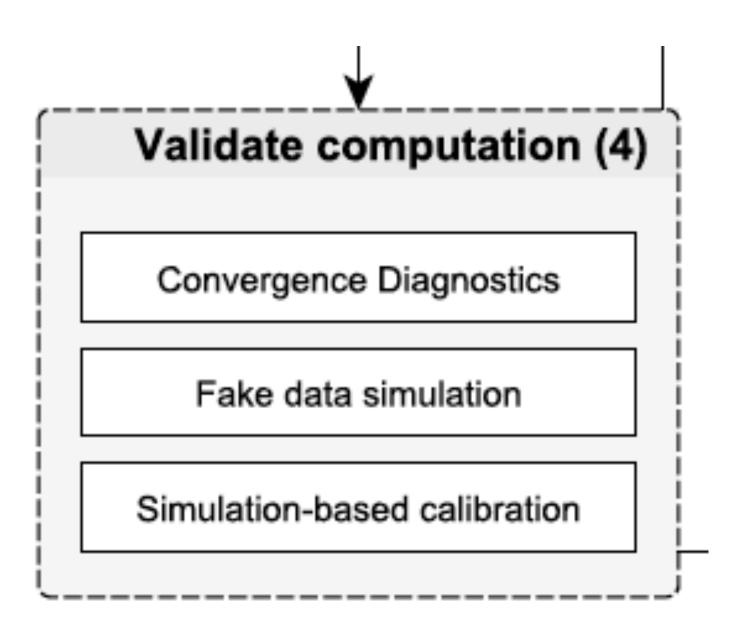
Simple models that can be fit successfully

Complex models that cannot be fit, or that give nonsensical results

- Reparametrize
- Consider simpler models/model components
- For debugging, fit to
  - Data that's simulated from the model
  - Subset of data

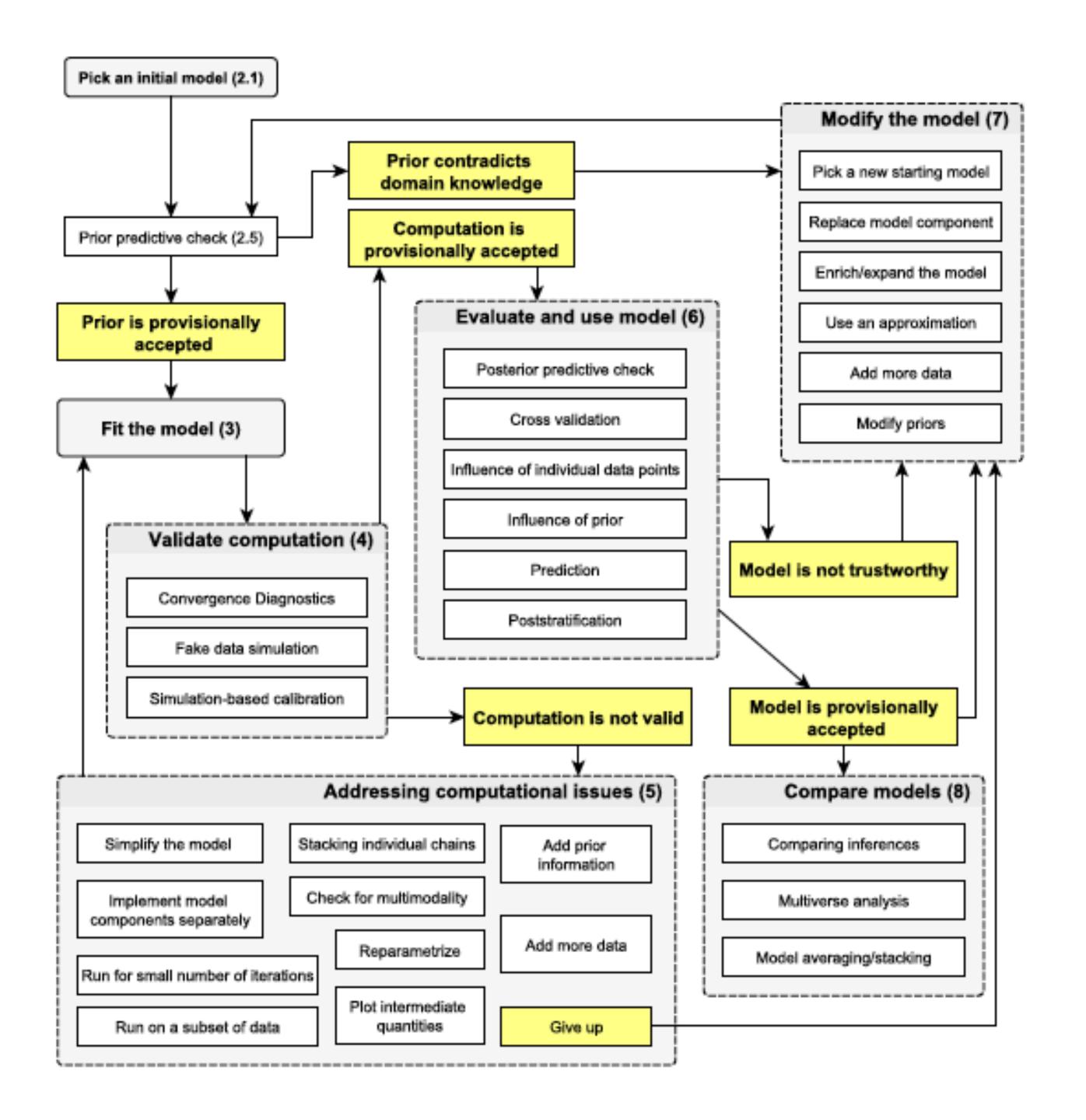
#### Weehaa "it works"!

- ... right?
- MCMC diagnostics only tell you whether computation for the probabilistic model is valid, not if the computation reflects the model you intended to specify
- Consider "fake data simulation" or simulation-based calibration
  - When fixing the truth (e.g., a draw from prior)
  - Can we reproduce that truth?



### Weehaa "it works"!

- But how useful is it for our context?
  - -> Evaluate and use model
- Use strategies from Module 11: model checking
  - Posterior predictive checks
  - Cross-validation
- Good enough?
  - No -> Modify the model
    - Informed by issues that were identified
  - Yes -> Model comparison
    - Compare (and consider reporting on) inferences from different models, combine models



#### Bayesian workflow for disease transmission modeling in Stan

#### Léo Grinsztajn<sup>1</sup> | Elizaveta Semenova<sup>2</sup> | Charles C. Margossian<sup>3</sup> | Julien Riou<sup>4</sup>

## Example: disease transmission

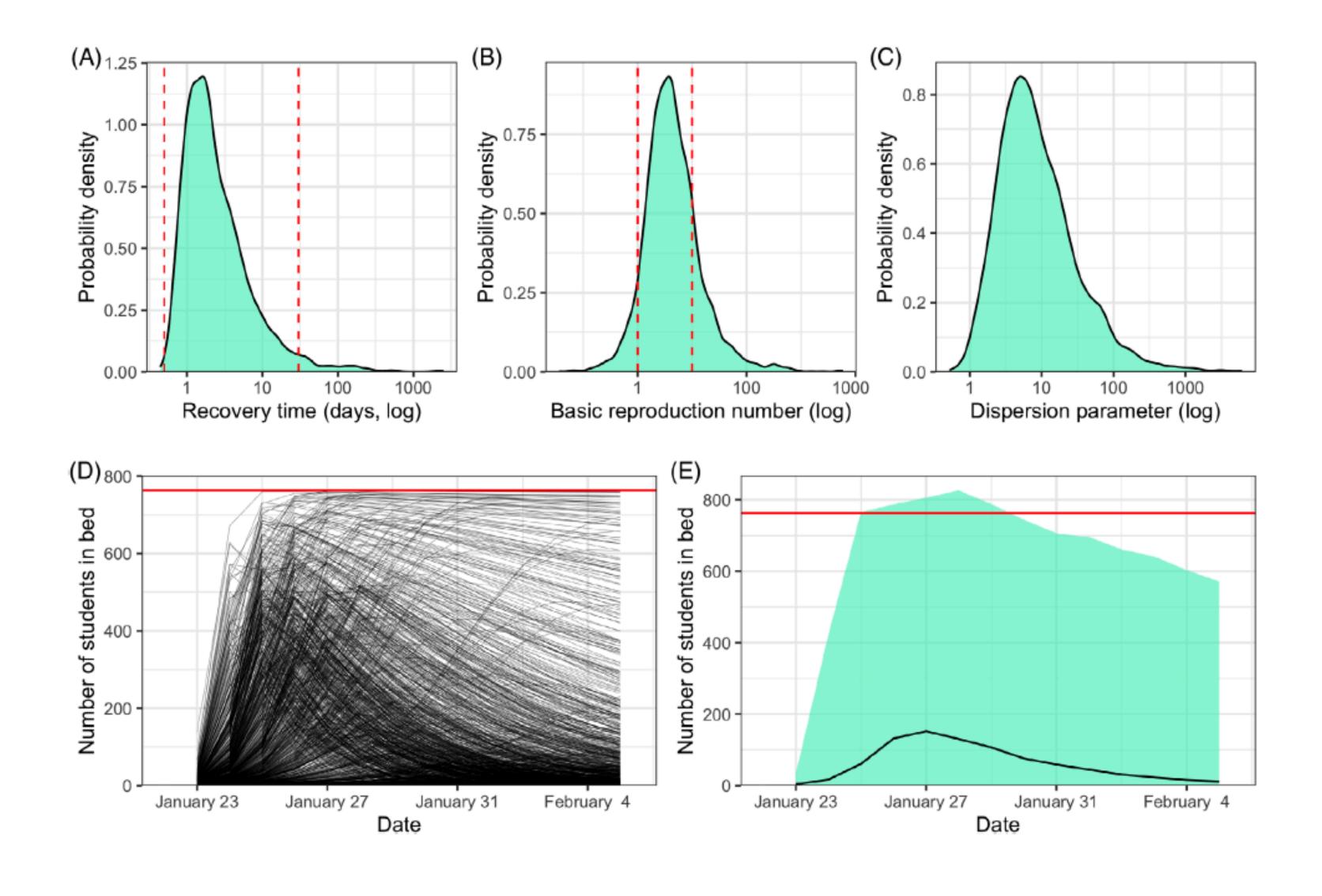
 Start with a simple SIR model: from a set of differential equations to Stan implementation



FIGURE 4 Diagram of the classic susceptible-infectious-recovered compartmental model

```
\begin{cases} \frac{dS}{dt} = -\beta S \frac{I}{N} \\ \frac{dI}{dt} = \beta S \frac{I}{N} - \gamma I \\ \frac{dR}{dt} = \gamma I \end{cases}
```

# Prior predictive check



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## Computational and model checks

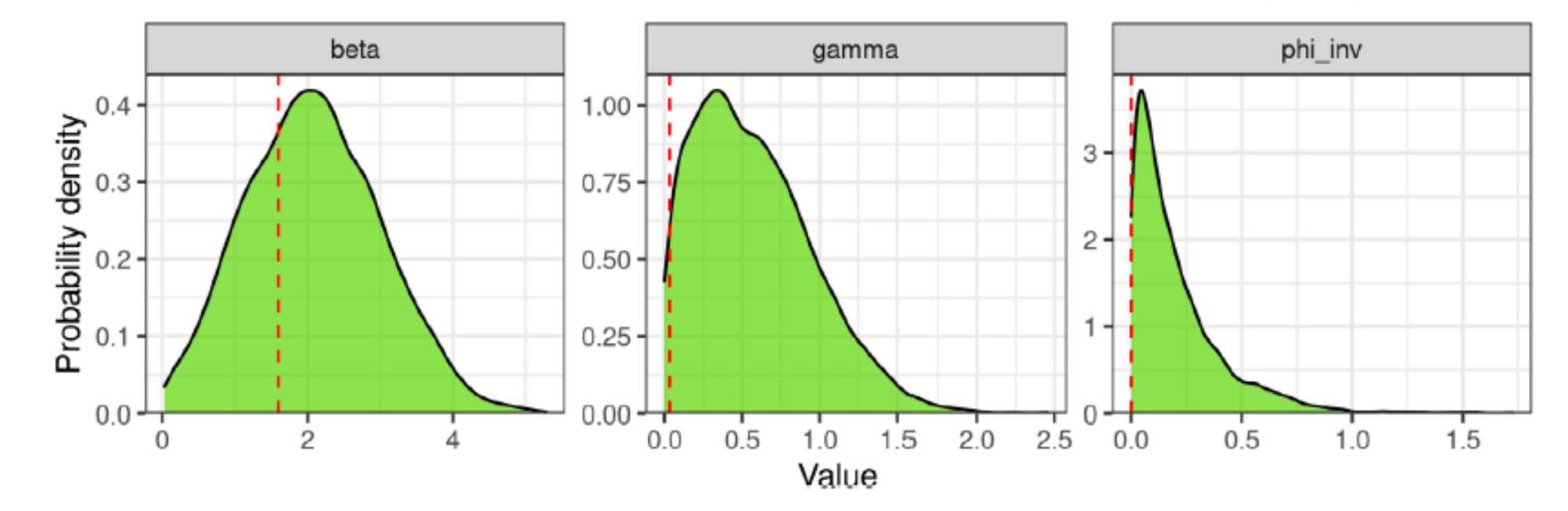


FIGURE 7 Marginal posterior densities for the transmission rate (beta or  $\beta$ ), the recovery rate (gamma or  $\gamma$ ) and the inverse dispersion parameter (phi\_inv or  $1/\phi$ ) obtained when fitting the model to simulated data. The red dashed lines show the fixed parameter values used for simulating the data [Colour figure can be viewed at wileyonlinelibrary.com]

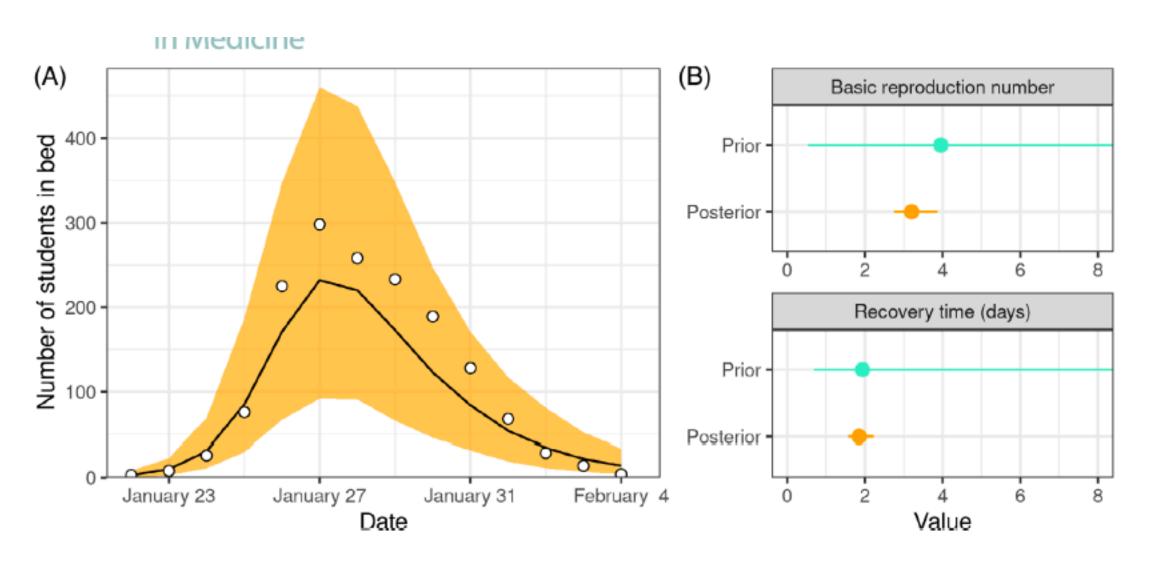
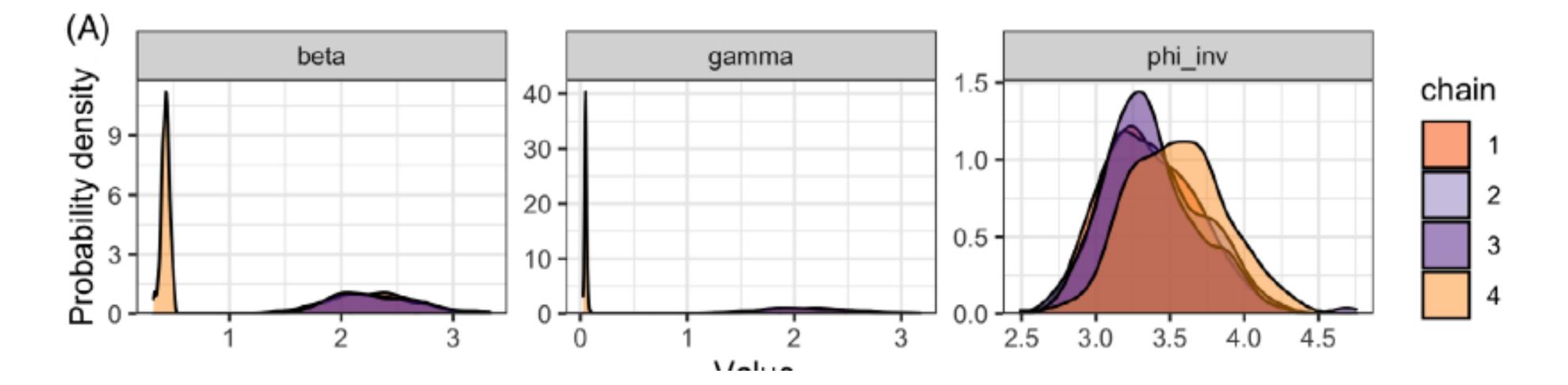
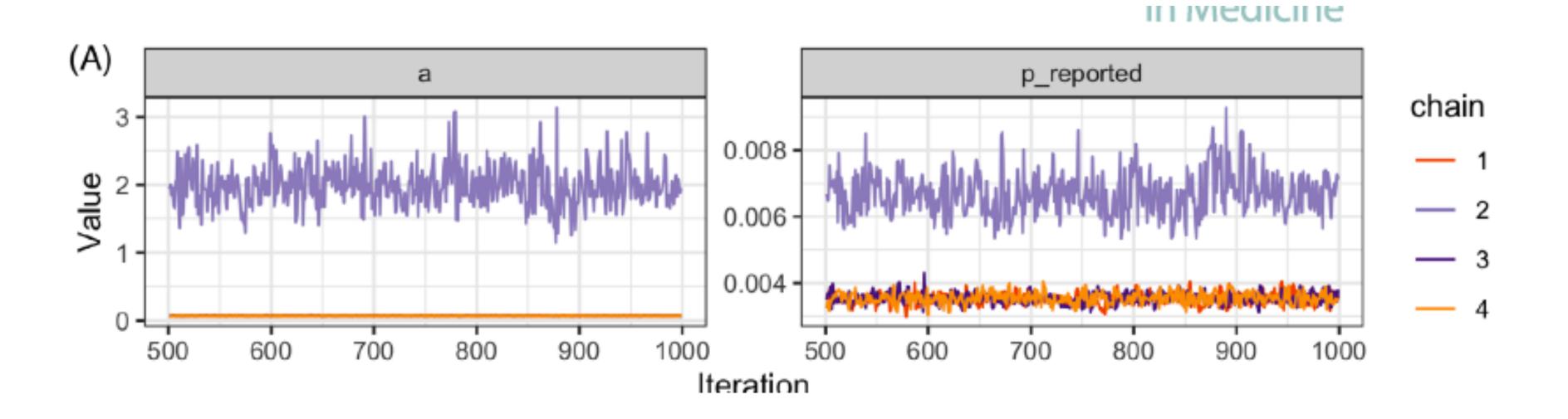


FIGURE 8 A, Posterior predictive check of the number of students in bed each day during an influenza A (H1N1) outbreak at a British boarding school. The line shows the median and the orange area the 90% prediction interval. B, Prior and posterior predictive checks of the basic reproduction number  $\mathcal{R}_0$  and of the recovery time (both truncated at 8). The dot shows the median posterior and the line shows the 95% credible interval [Colour figure can be viewed at wileyonlinelibrary.com]

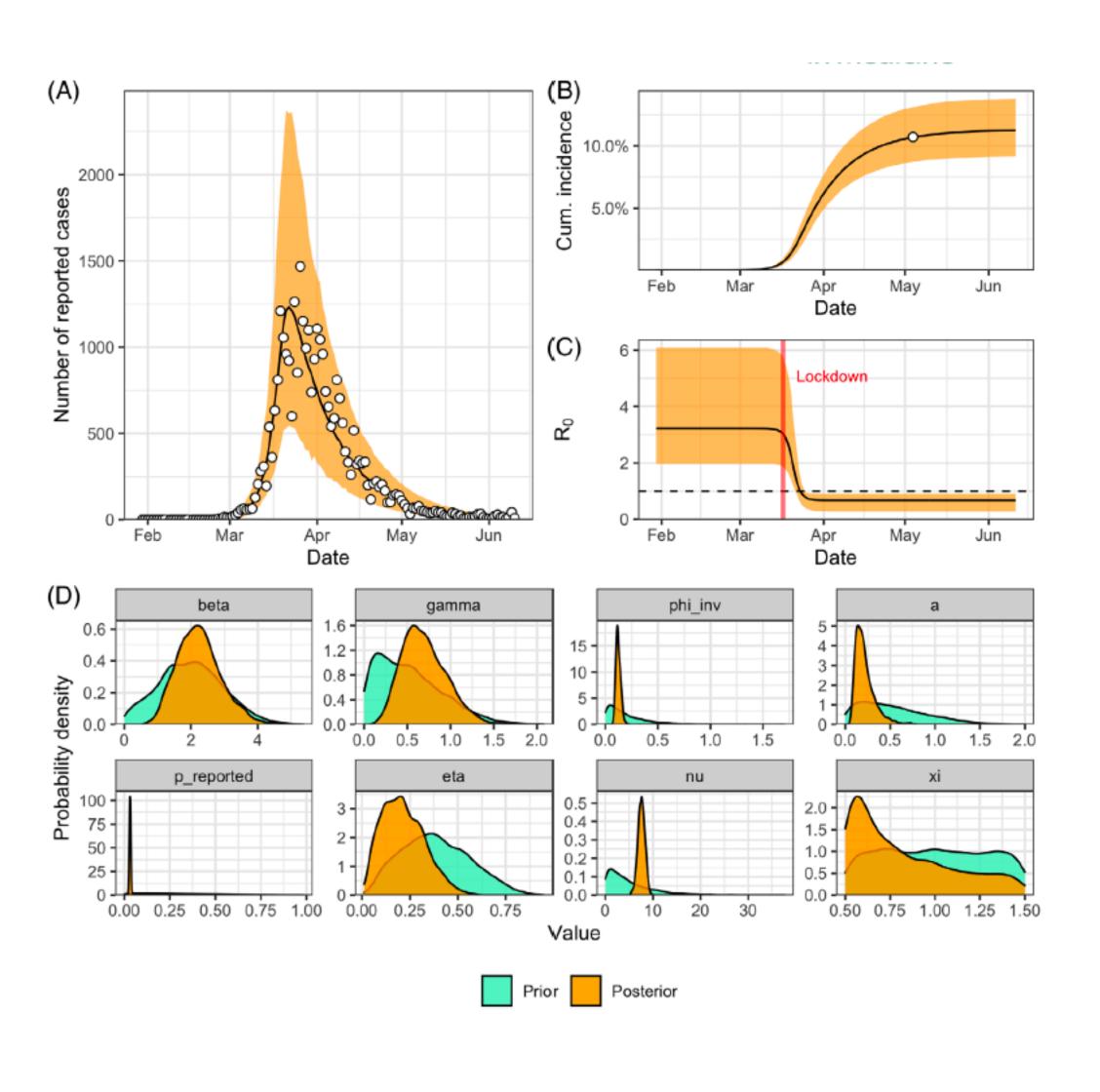
# COVID 19 application

Oops!





# After extending the model and adding data...



## Discussion of Bayesian workflow (Gelman et al. 2020)

- Potential issues with the Bayesian workflow:
  - Using the data multiple times, overfitting
    - Gelman et al advocate for reporting based on several models, models that encompasses as much information as possible,
       NOT to search for an optimally fitting model
  - Subjectivity, more of an art than a science?
- On the upside:
  - Iterative model building = gradual learning
  - The workflow allows for severe testing of model assumptions (contrast with pre-registered model)
  - This is only the start...
- Transformative steps in data science (Gelman et al):
  - Data summaries
  - Modeling
  - Computation (ongoing)
  - Towards formalizing the process of model navigation (exploring model space)