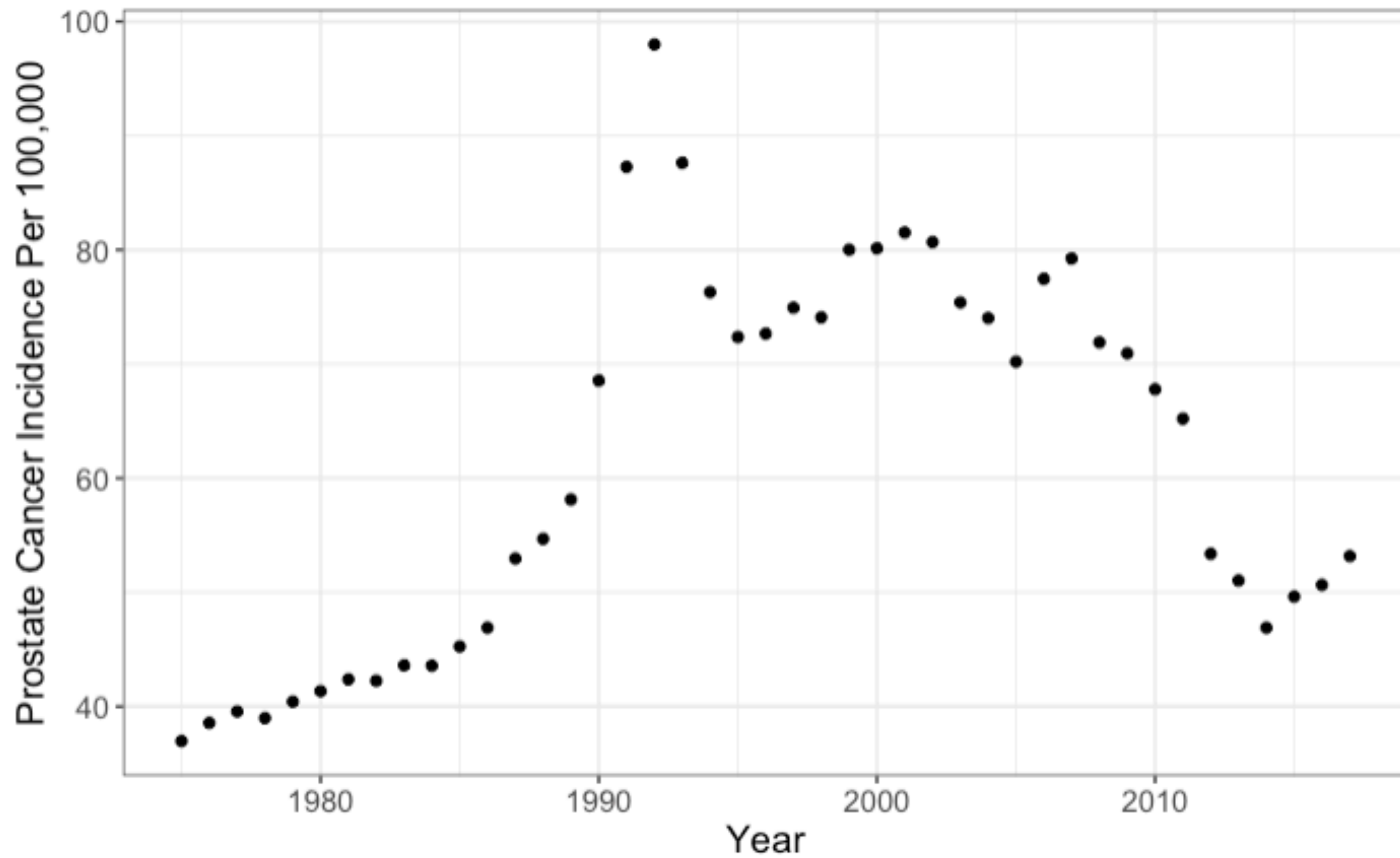


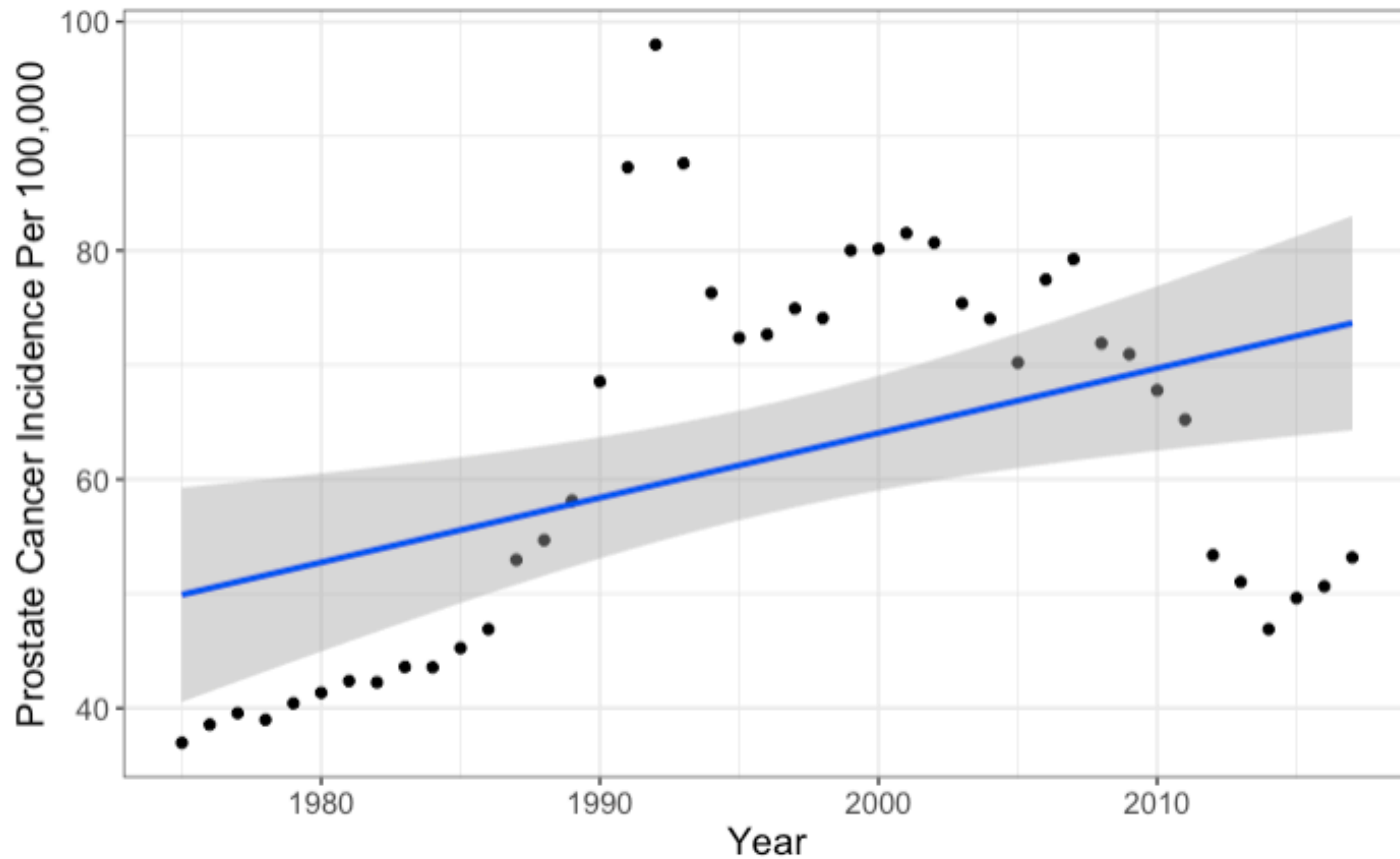
Modeling data using horseshoe processes

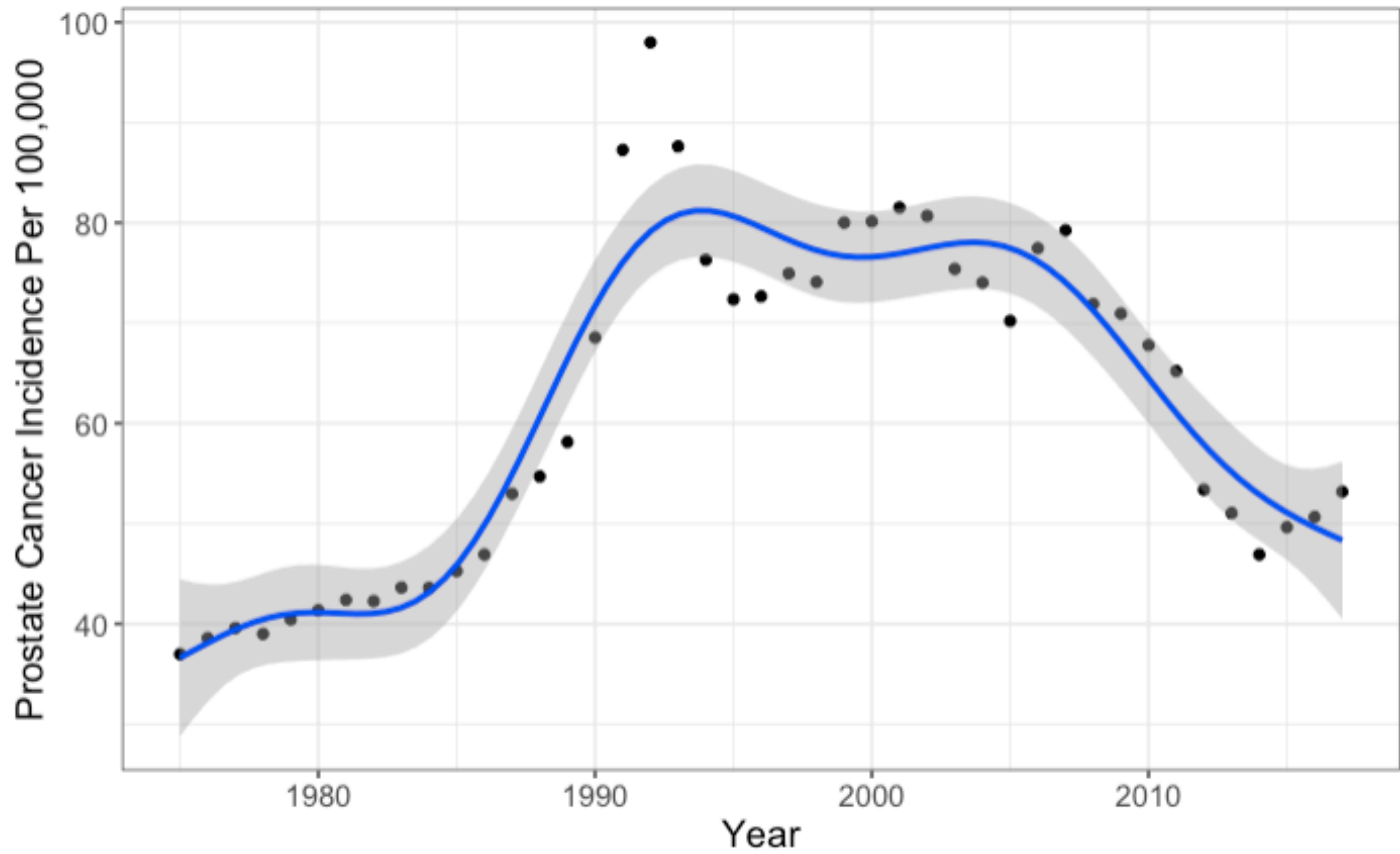
JSM 2021 Contributed Speed Talk: Advanced Bayesian Topics

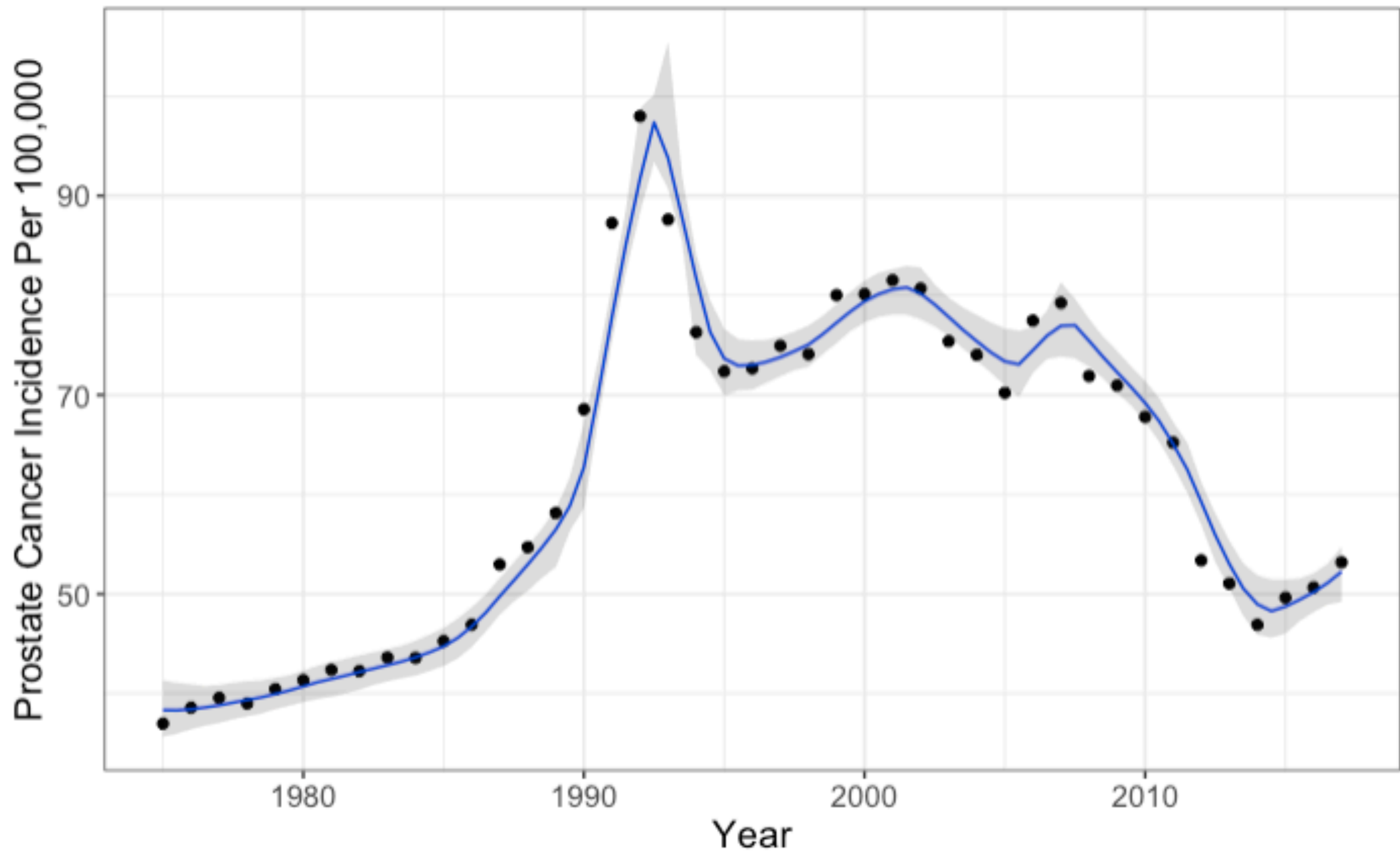
Elizabeth Chase, University of Michigan Biostatistics

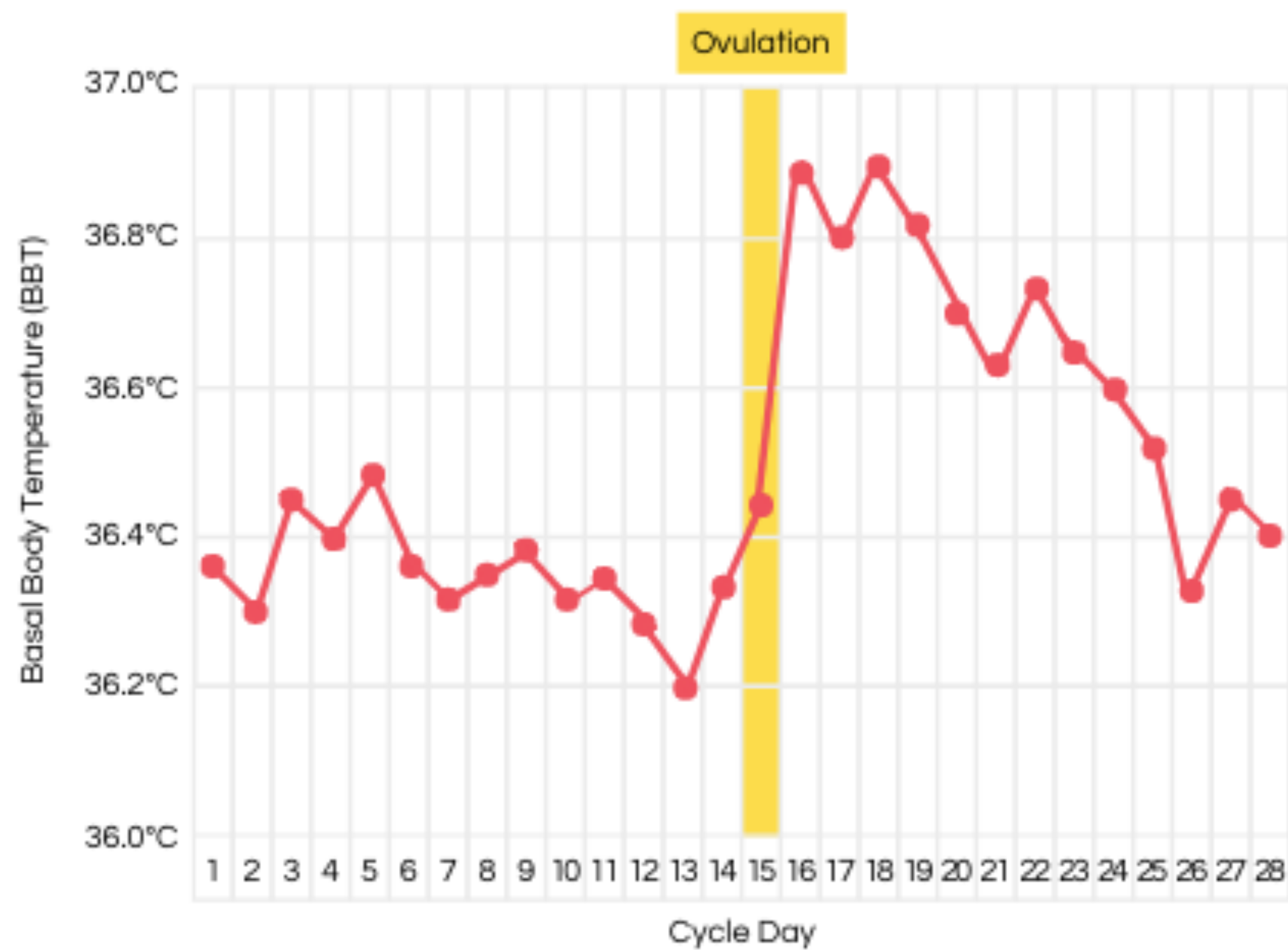
Aug. 8, 2021

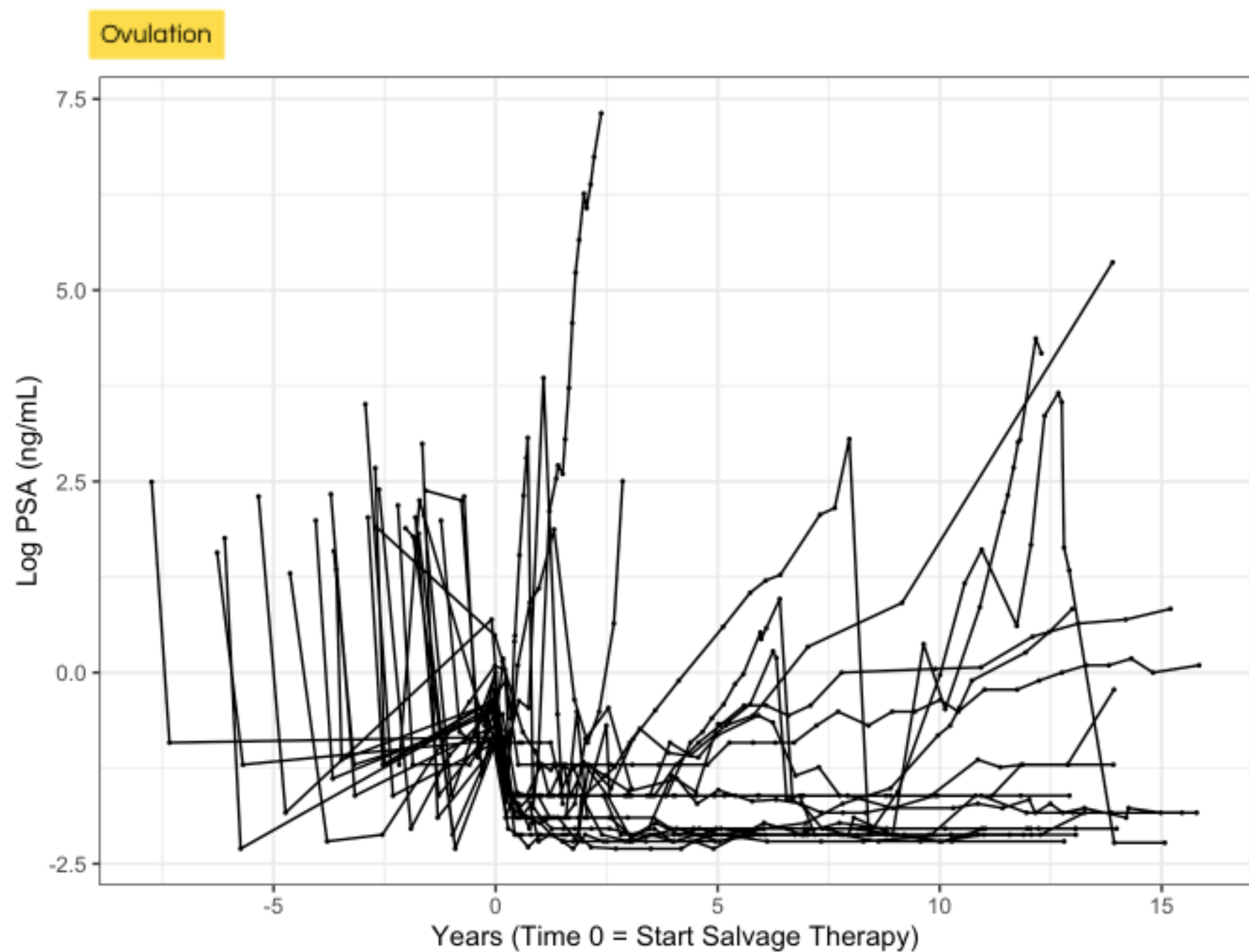
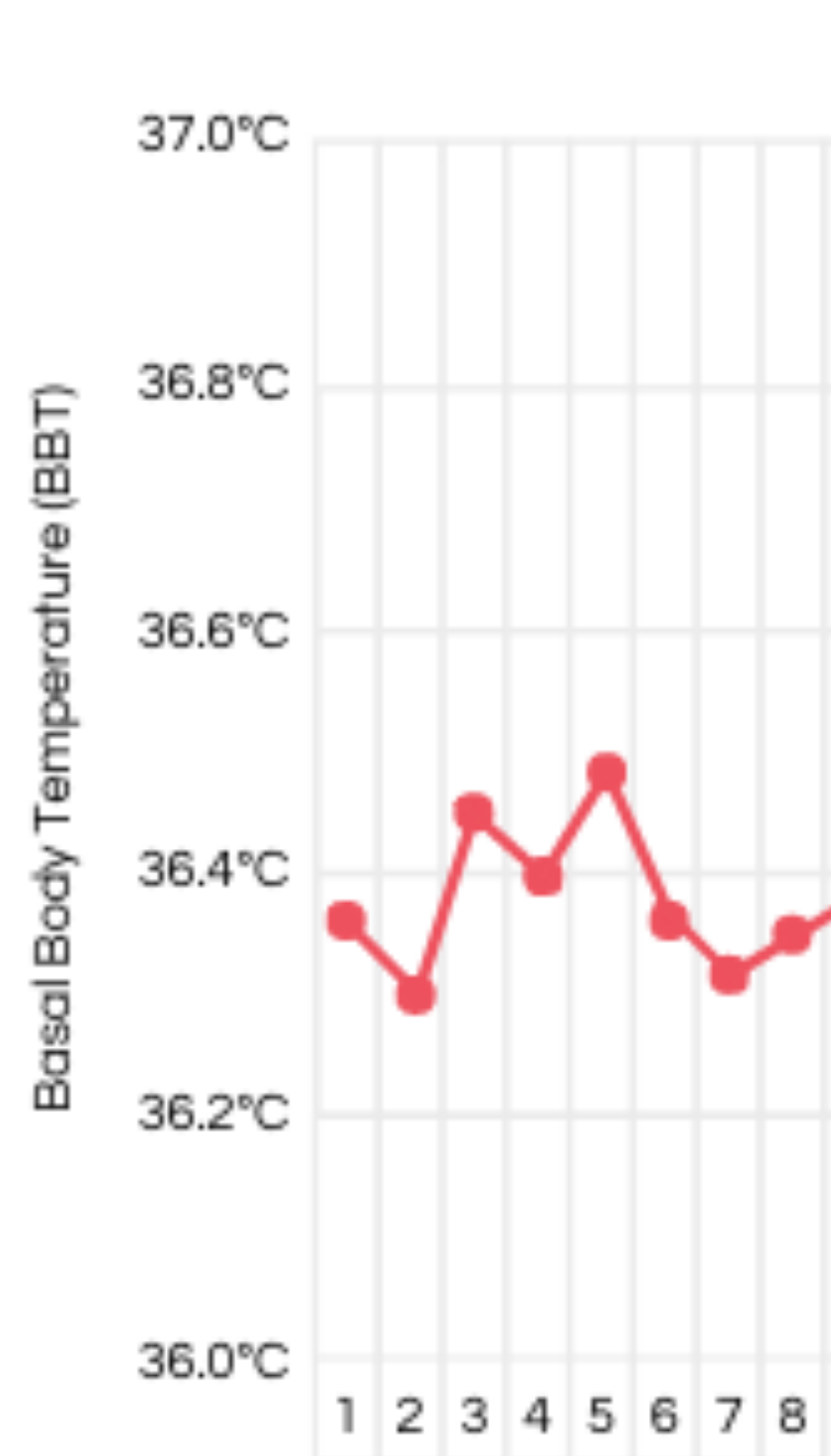












Motivation

- Desired end-product: a flexible curve-fitting approach of a (possibly non-Gaussian) outcome on a continuous predictor that allows for *local changes in variance*
- Additional desirable features:
 - Equipped to work with small and large numbers of observations
 - Both equally and unequally spaced grids of the predictor
 - Possibly multiple measurements at the same value of the predictor
 - Provides uncertainty quantification

The Horseshoe Prior

- The horseshoe prior was developed as a Bayesian approach for variable shrinkage.
- Suppose we are considering the model for subjects $i = 1, \dots, n$ and predictors $j = 1, \dots, p$:

$$y_i = \beta_1 x_{1i} + \beta_2 x_{2i} + \dots + \beta_p x_{pi} + \epsilon_i$$

$$\epsilon_i \sim N(0, \sigma^2)$$

- If p is large, we might expect that most of our coefficients are zero, and just a couple effects are very large.

The Horseshoe Prior

- In 2010, Carvalho et al. proposed a continuous mixture prior, which they called the horseshoe:

$$\beta_j \sim N(0, \tau^2 \omega_j^2)$$

$$\omega_j \sim C^+(0, 1), \tau \sim C^+(0, c)$$

- τ^2 is the global shrinkage parameter, and controls the overall level of shrinkage for all the effects.
- ω_j^2 is the local shrinkage parameter, and allows for a mixture of very large signals and zero signals.

A Horseshoe Process

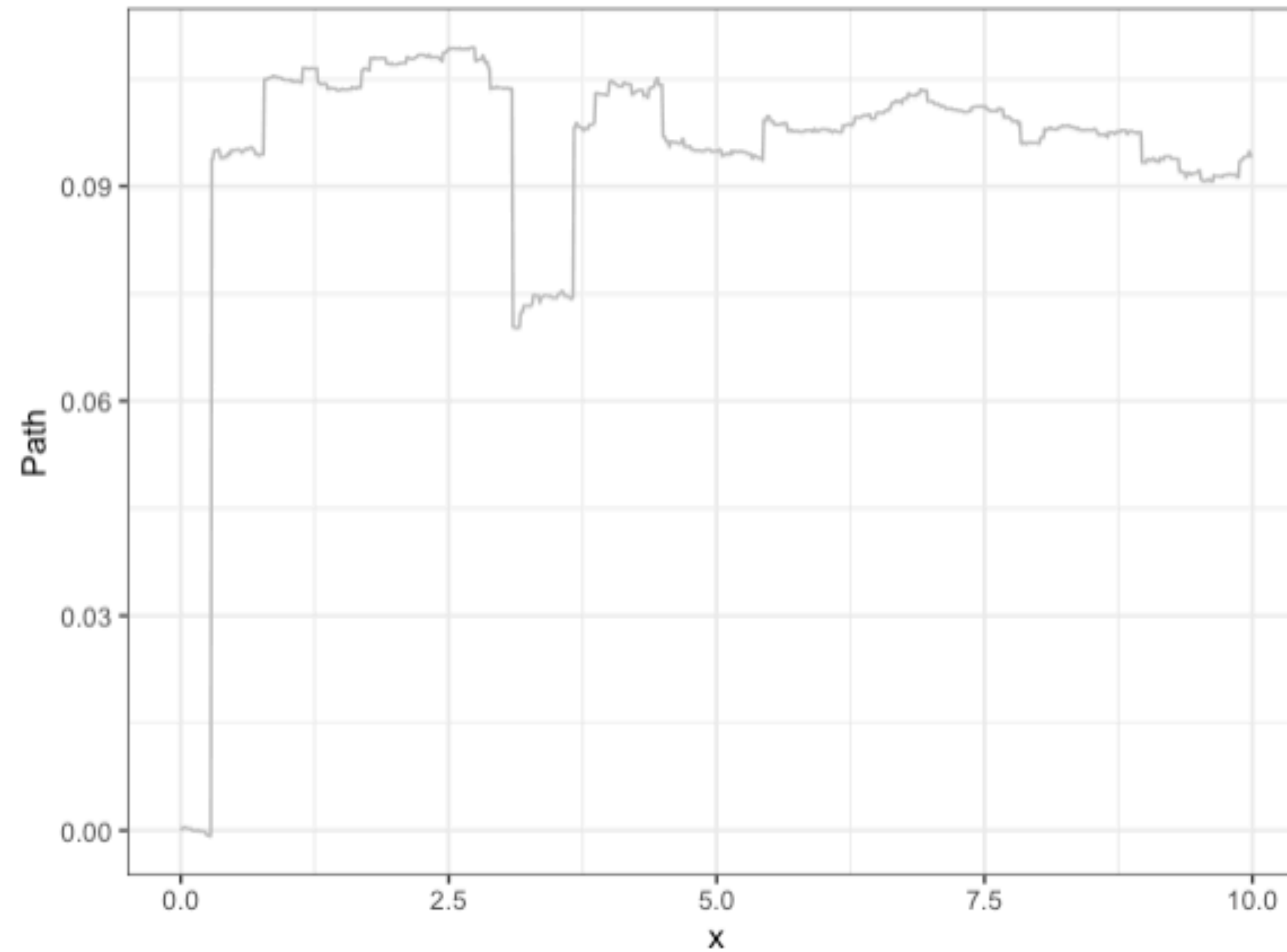
- We can extend the horseshoe distribution to the stochastic process setting, following Polson & Scott (2012).
- We define a horseshoe process $H(x)$ observed at discrete locations x_0, x_1, \dots, x_m as:

$$H(x_j) - H(x_{j-1}) \sim N(0, \tau^2 \omega_j^2 (x_j - x_{j-1}))$$

$$\omega_j \sim C^+(0, 1), j = 1, \dots, m$$

$$\tau \sim C^+(0, c), H(x_0) = 0$$

A Horseshoe Process



Second Derivative Shrinkage

Let y_{t_k} indicate some outcome (i.e. biomarker reading, disease incidence, etc.) at time $t_k, k = 0, \dots, m$ with $t_0 = 0$.

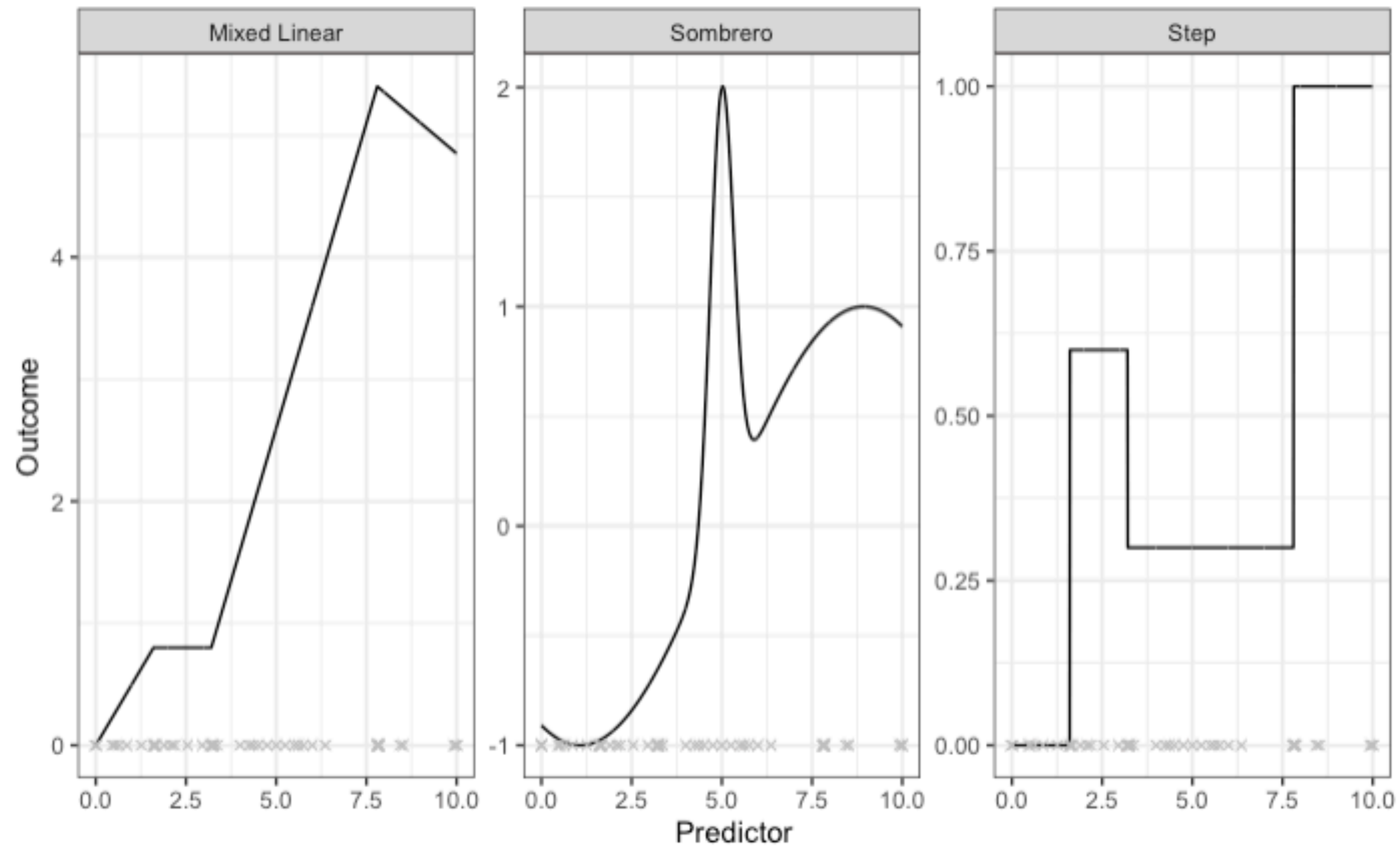
$$g(E(y_t)) = \alpha + \int_0^t H(u) du$$

- $\alpha \sim N(a, b^2)$
- $H(u) - H(u - s) \sim N(0, c^2 \tau^2 \omega(u)^2 s), \quad H(t_0) = 0$
- $\omega(u) \sim C^+(0, 1), \quad u = t_1, \dots, t_m, \quad \omega(t_0) = 0$
- $\tau \sim C^+(0, 1)$

Computation

- The model is currently implemented using Hamiltonian Monte Carlo in Stan (via cmdstanr in R) using decentered parameterizations.
- This yields faster computational performance than other Bayesian methods that seek to address this problem.
- However, computation time is still a constraint, and issues with divergences still appear occasionally for select datasets.

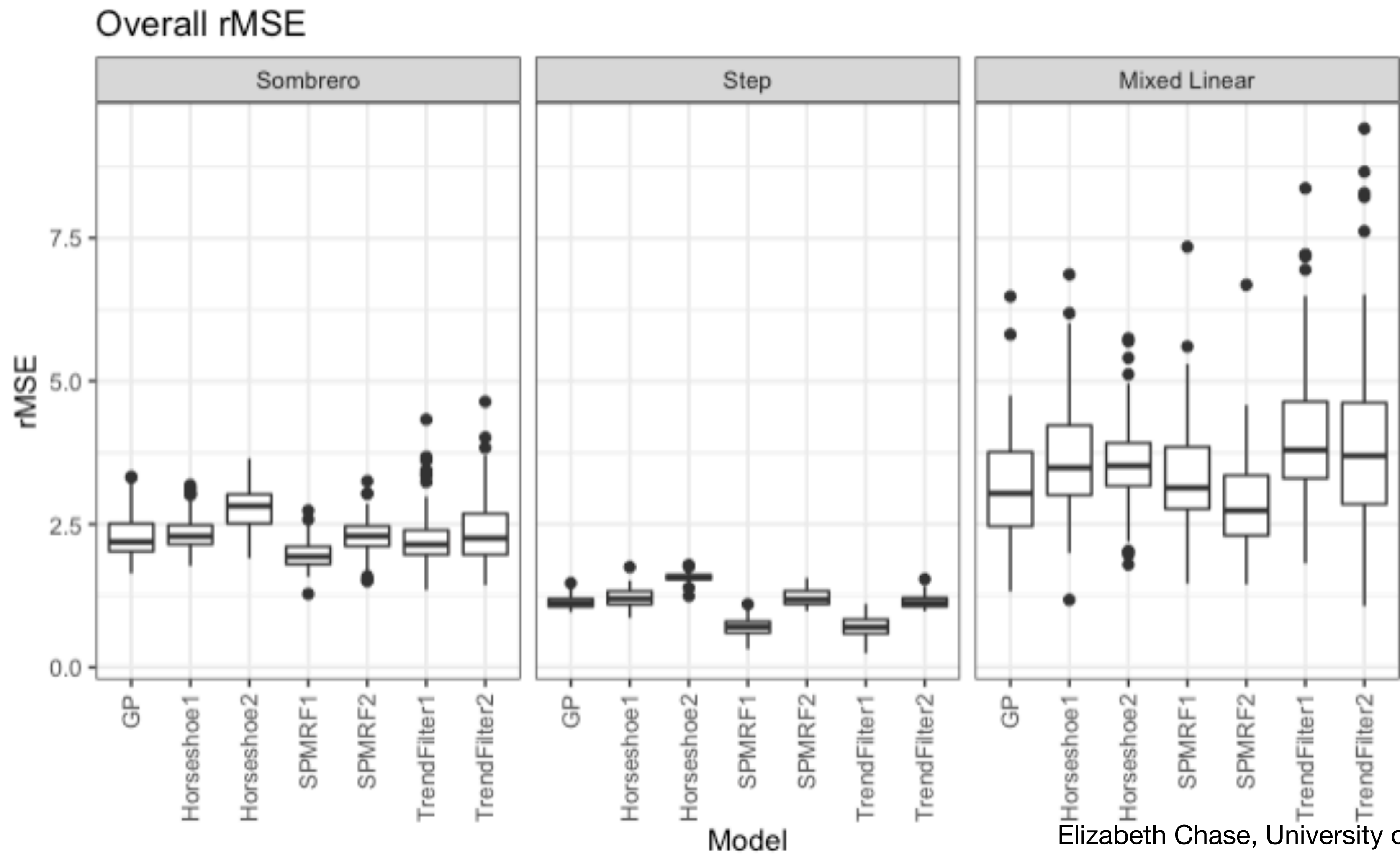
Simulation Study



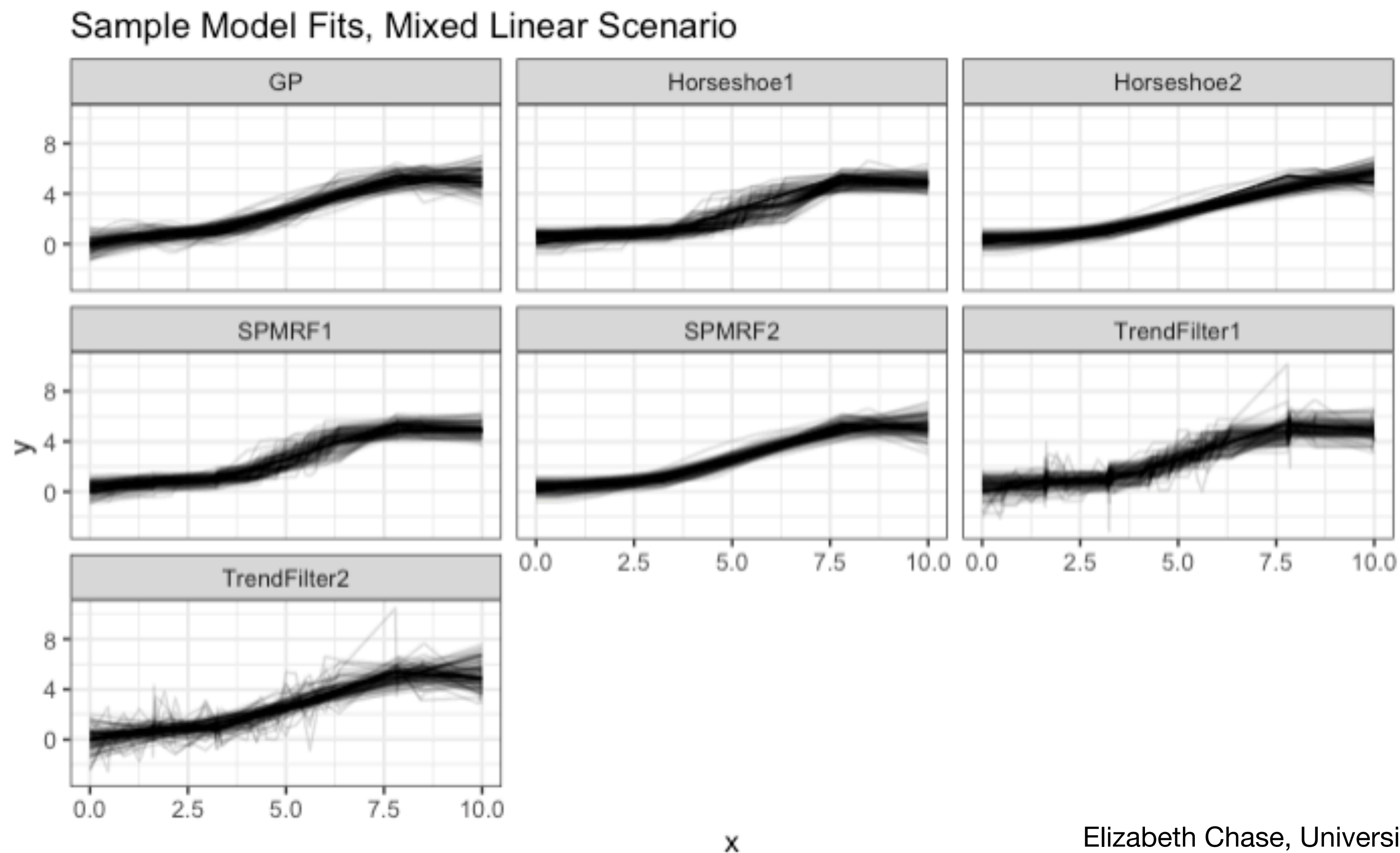
Simulation Study

- Considered 3 data-generating scenarios, 2 sample sizes ($n = 50$, $n = 100$), and 3 types of outcome data (Gaussian, Binomial, Poisson)
- Ran 100 replicates of each scenario
- Comparison methods: Gaussian process regression, trend filtering model (Tibshirani 2014), shrinkage process Markov random fields (Faulkner & Minin 2018)

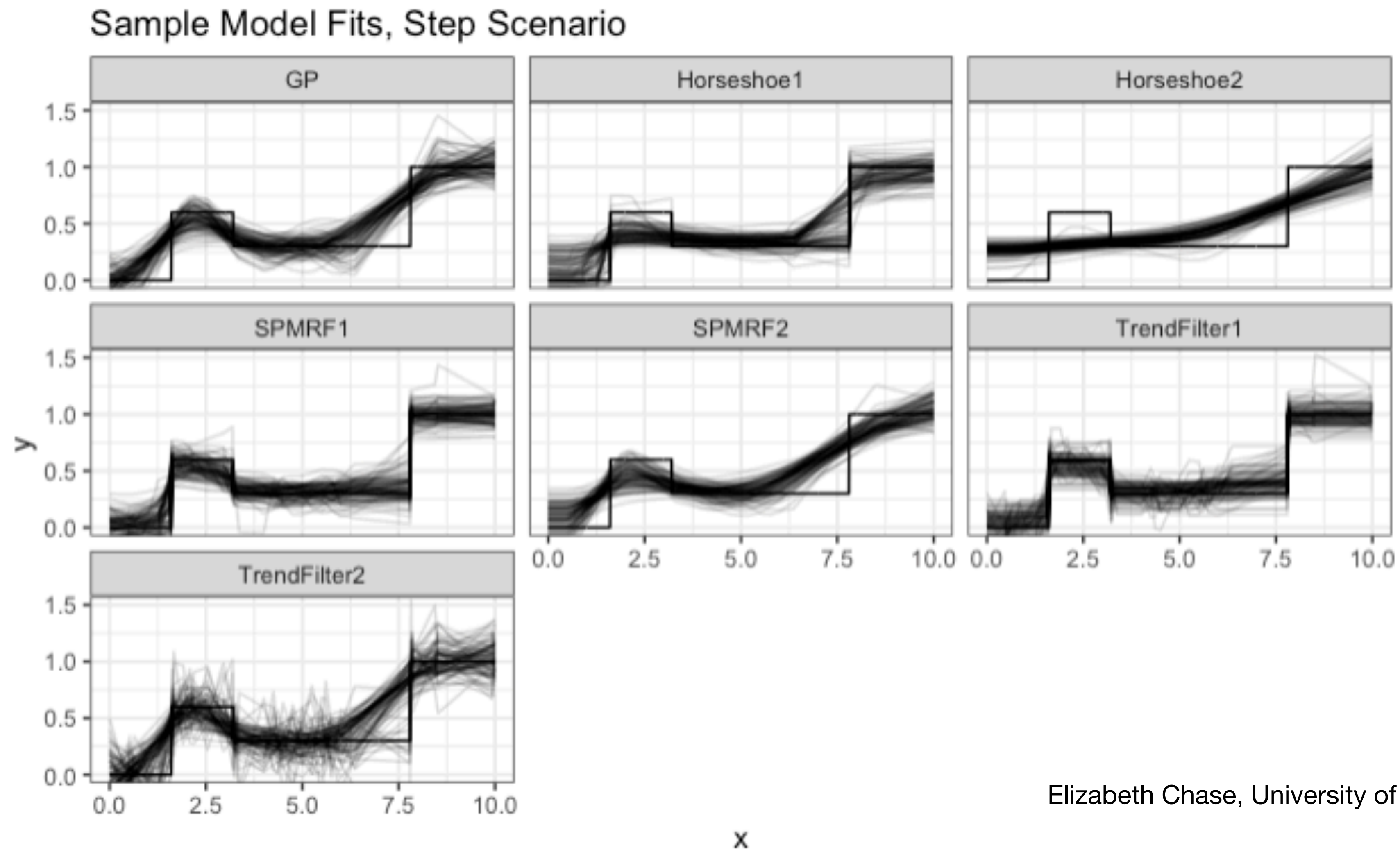
Simulation Study



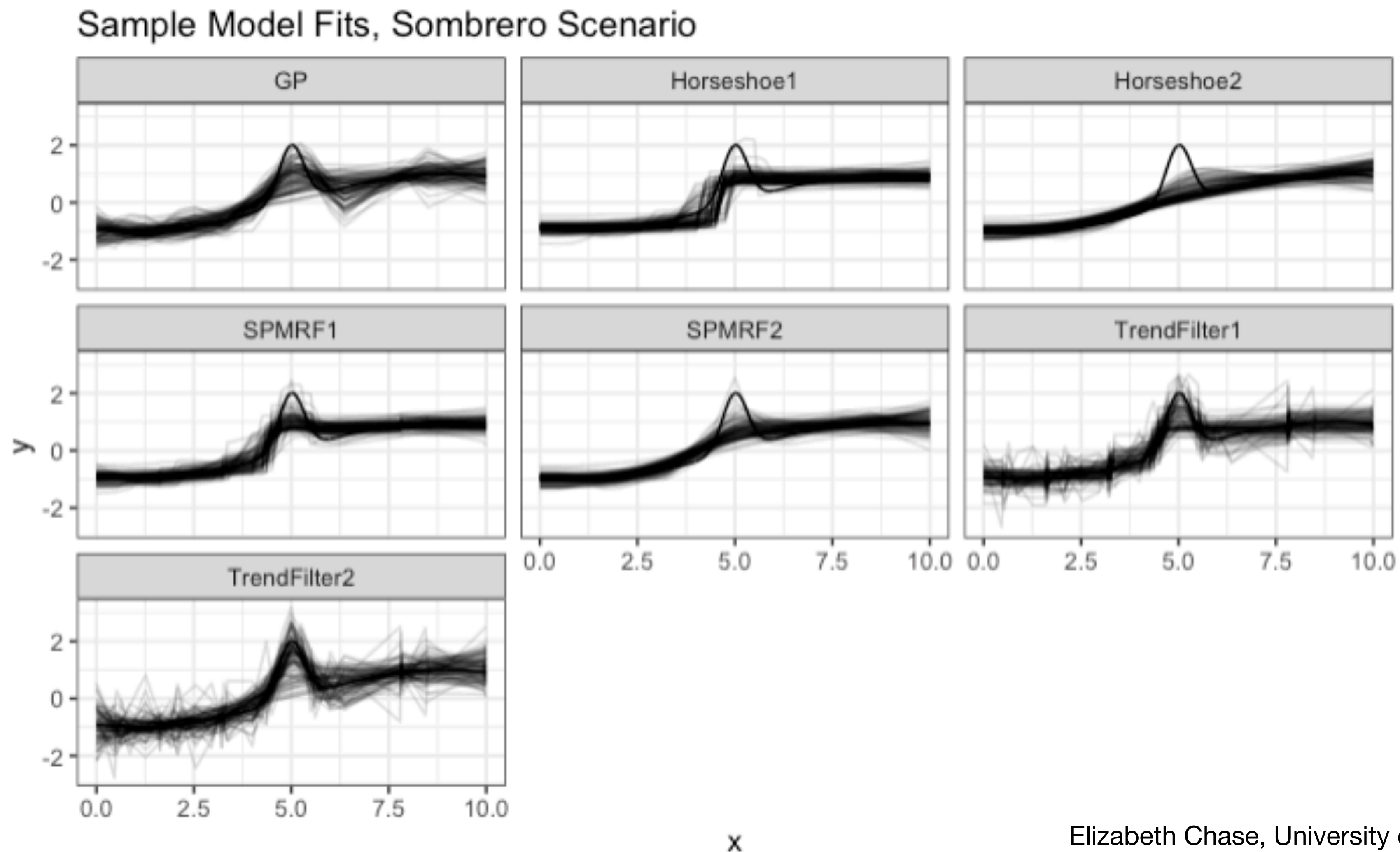
Simulation Study



Simulation Study



Simulation Study



Future Work

- Continue workshopping method—how to set initial values, recommendations for setting hyperpriors
- Perhaps a variational Bayes implementation to further accelerate computation
- Consider use of regularized horseshoe or horseshoe + priors

References

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