Bayesian Optimisation for Likelihood Free Inference

Make model parameterisation go brrr

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Notation

- Model is considered a (random) function $f(\boldsymbol{\theta})$ that maps $\boldsymbol{\theta}$ (a vector of parameters) to a model output, that can be transformed into $\mathbf{X}$, that has the same shape as:
- $\mathbf{X}_{\text{obs}}$, a vector of outputs given to us usually in the forms of summary statistics (incidence, prevalence, hospitalisations etc).

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- $\hat{\boldsymbol{\theta}} = \arg\max_{\boldsymbol{\theta}} \mathcal{L}(\boldsymbol{\theta}|S(\mathbf{X}_{\text{obs}}))$
- $\Pr(\boldsymbol{\theta}|S(\mathbf{X}_{\text{obs}})) \propto \Pr(S(\mathbf{X}_{\text{obs}})|\boldsymbol{\theta}) \Pr(\boldsymbol{\theta})$

The Sad Truth

- As models become more complicated, explicit likelihoods don't exist (think agent based models).

A Standard Bayesian Solution

- Approximate Bayesian Computation (ABC)
  1. Sample from prior
  2. Run model
  3. Accept or reject parameters run based on how well $\mathbf{X}$ 'matches' $\mathbf{X}_{\text{obs}}$.

What is 'matches'

- Discrepency function $D : \mathcal{X} \times \mathcal{X} \to \mathbb{R}$
  - Can be a norm such as $||S(\mathbf{X}) - S(\mathbf{X}_{\text{obs}})||_p := (\sum_{i=1}^{d} |S(\mathbf{X}) - S(\mathbf{X}_{\text{obs}})|^p)^{1/p}$

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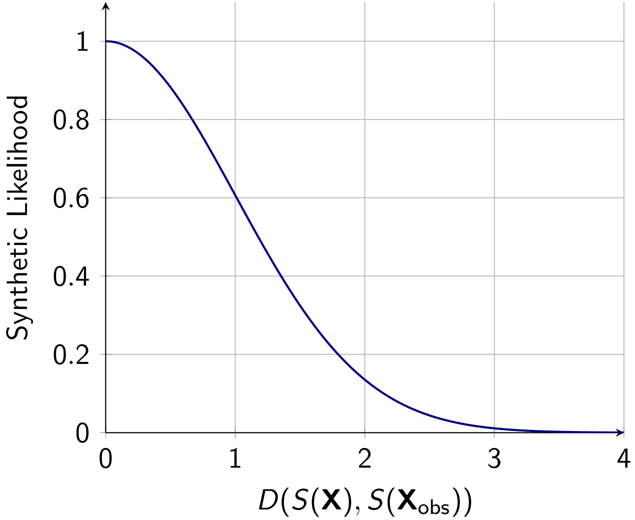
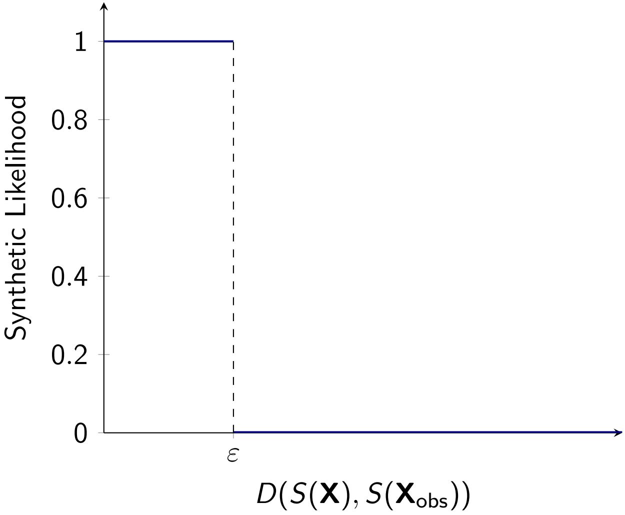
  - Care should be taken to rescale $S(\mathbf{X}_{\text{obs}})$ and $S(\mathbf{X})$ appropriately (ie via a covariance matrix).
- $D(S(\mathbf{X}), S(\mathbf{X}_{\text{obs}}))$, gives acceptance probability of $\boldsymbol{\theta}$.

Acceptance Probability



Uniform Acceptance Probability



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- For parameters 'close' to parameters we've already tried it should be easy.

Gaussian Processes

- Random functions
- Common examples - Brownian motion, Ornstein Uhlenbeck process

Gaussian Processes on $\mathbb{R}^d$

Definition (Gaussian Process)

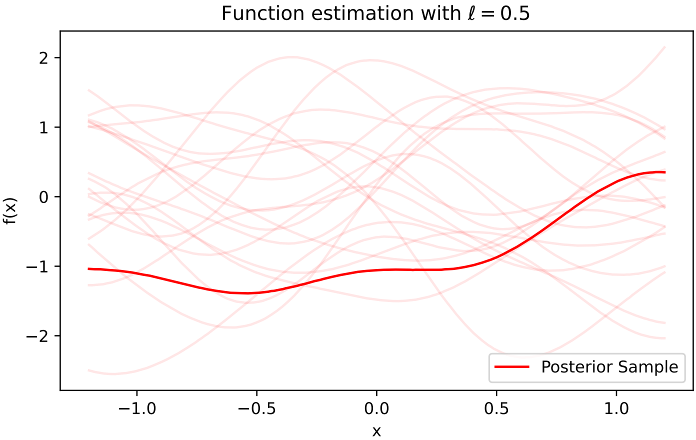
A collection of random variables $\{f(\mathbf{x})\}_{\mathbf{x}\in\mathbb{R}^d}$ *is a Gaussian process if all finite dimensional distributions are multivariate normal distributed. That is, there is a function* $m : \mathbf{x} \to \mathbb{R}$ *and kernel* $k : \mathcal{X} \times \mathcal{X} \to \mathbb{R}$ *such that for all finite sets* $\{\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_n\}$,

$$\begin{bmatrix} f(\mathbf{x}_1) \\ f(\mathbf{x}_2) \\ \vdots \\ f(\mathbf{x}_n) \end{bmatrix} \sim \text{MVN}\left(\begin{bmatrix} m(\mathbf{x}_1) \\ m(\mathbf{x}_2) \\ \vdots \\ m(\mathbf{x}_n) \end{bmatrix}, \mathbf{K} \right)$$

where

$$\mathbf{K} = \begin{bmatrix} k(\mathbf{x}_1, \mathbf{x}_1) & k(\mathbf{x}_1, \mathbf{x}_2) & \dots & k(\mathbf{x}_1, \mathbf{x}_n) \\ k(\mathbf{x}_2, \mathbf{x}_1) & \ddots & & \vdots \\ \vdots & & \ddots & \vdots \\ k(\mathbf{x}_n, \mathbf{x}_1) & \cdots & \cdots & k(\mathbf{x}_n, \mathbf{x}_n) \end{bmatrix}$$

Gaussian Process Example Realisations



Covariance Kernel Motivation

- Kernel determines the amount of covariance between sets of indices.
- When the distance between indices is small, covariance needs to be large

Common Covariance Kernels

- Matern Kernel

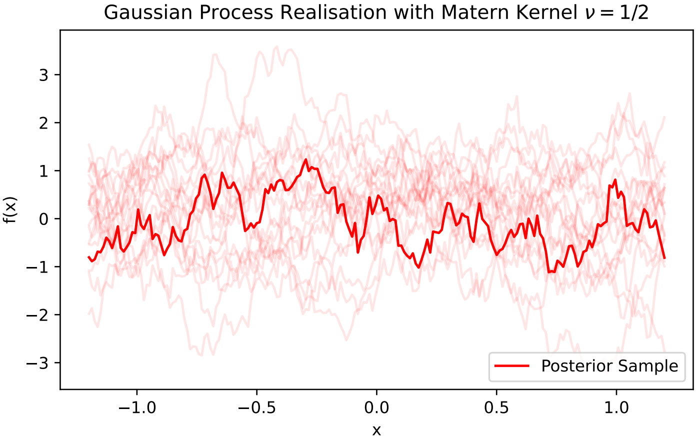
$$k_\nu(x, x') = \sigma^2 \frac{2^{1-\nu}}{\Gamma(\nu)} \left(\frac{\sqrt{2\nu}||x - x'||}{\ell} \right)^\nu K_\nu \left(-\frac{\sqrt{2\nu}||x - x'||}{\ell} \right)$$

  where K_ν is a modified Bessel function ($|| \cdot ||$ is the euclidean distance)

- $\lfloor \nu \rfloor$ times mean square differentiable.
- As $\nu \to \infty$ you get squared exponential covariance function, which results in realisations that are infinitely mean square differentiable:

$$k(x, x') = \sigma^2 \exp(-\frac{||x - x'||^2}{\ell})$$

Kernel Choices - Kernel Type



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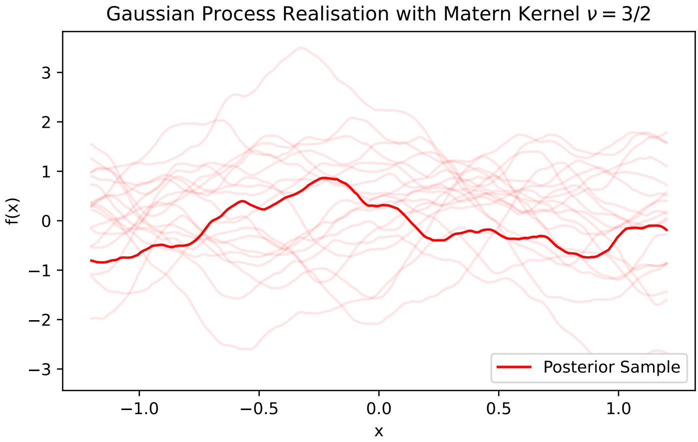

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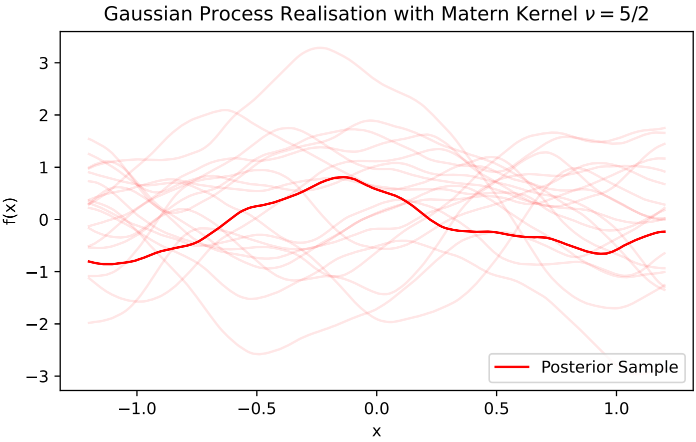

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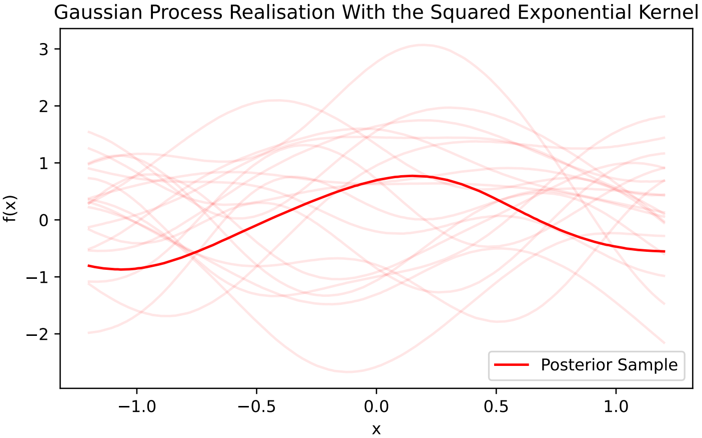

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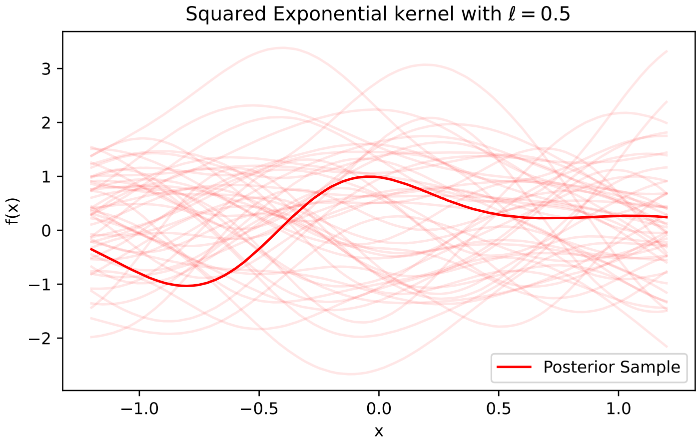

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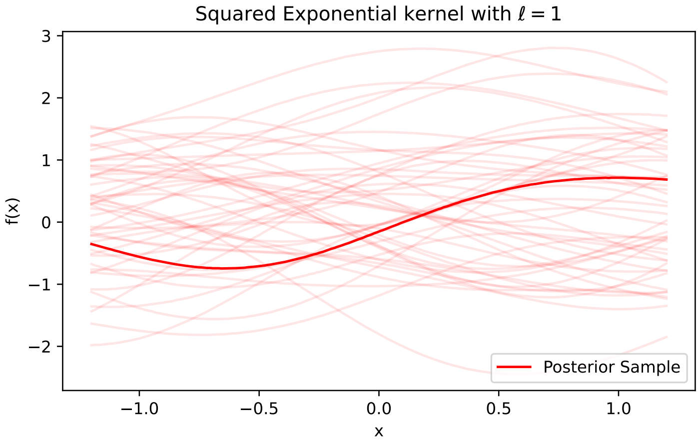

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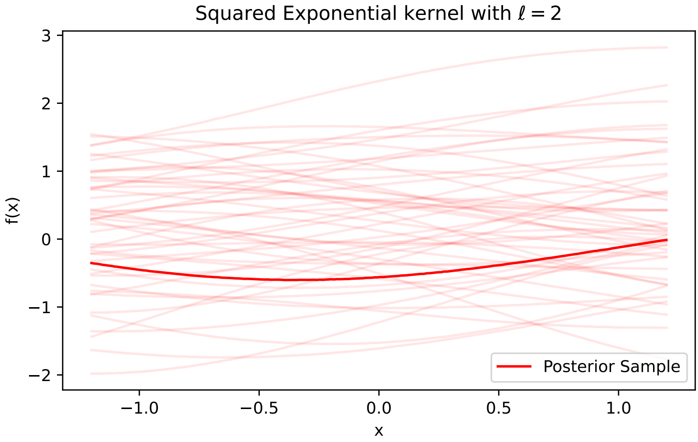

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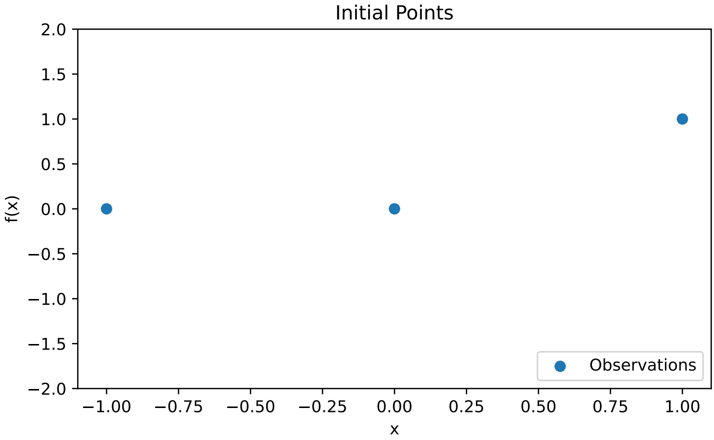

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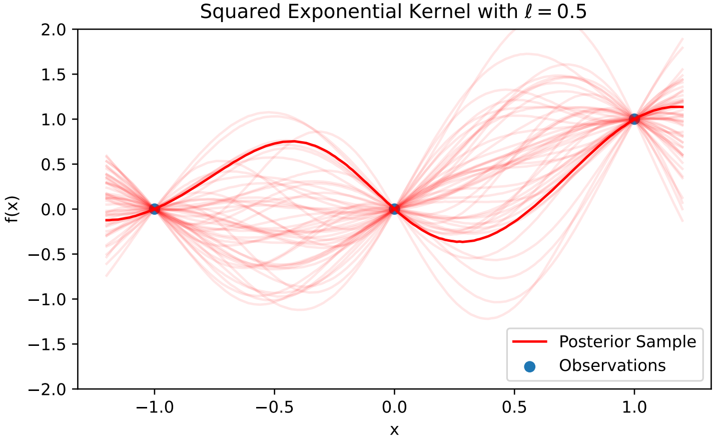

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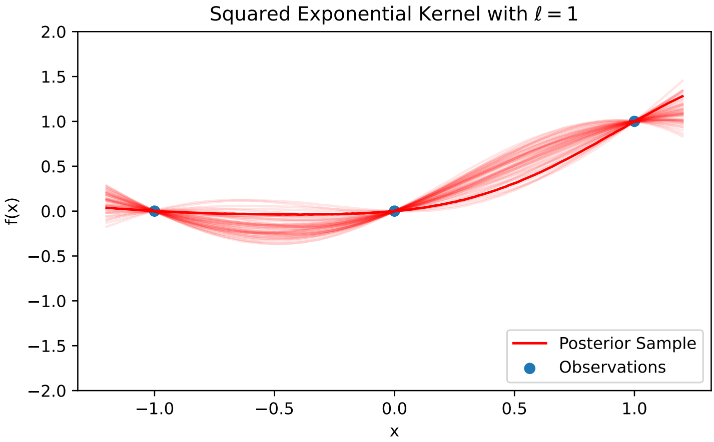

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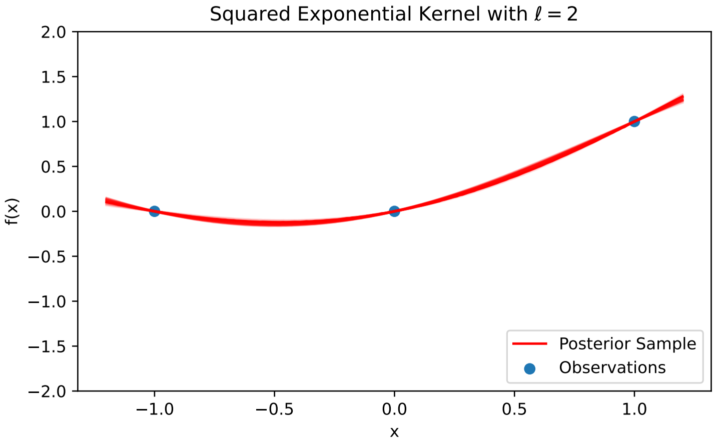

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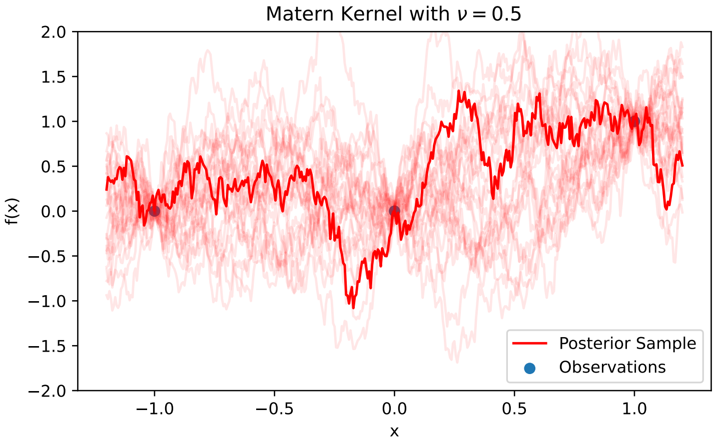

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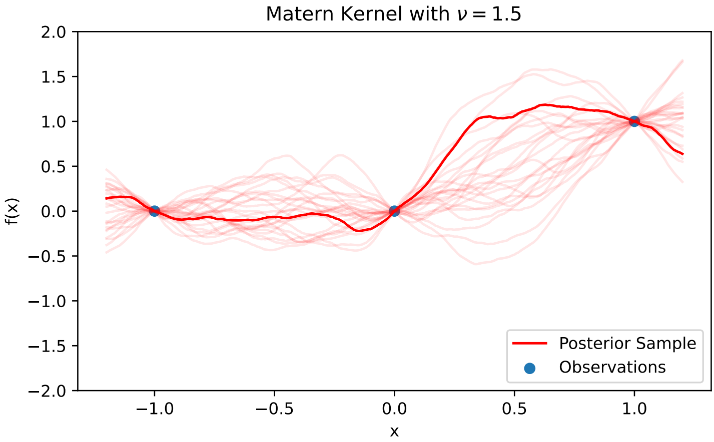

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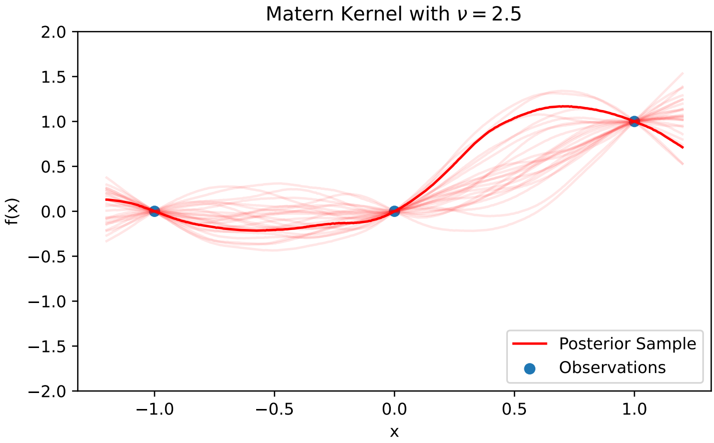

GP regression on $x(x-1)(x+1)$

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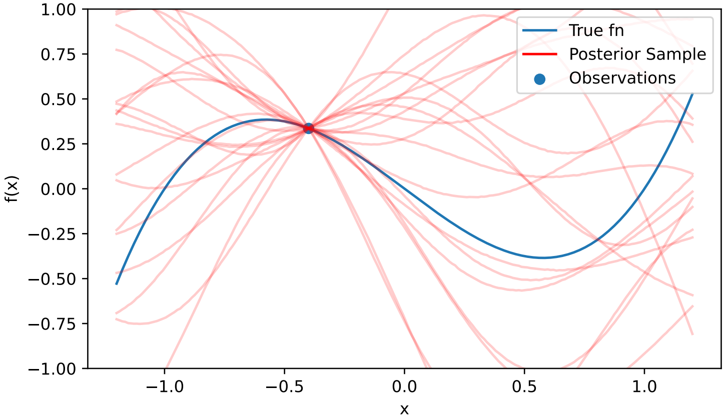

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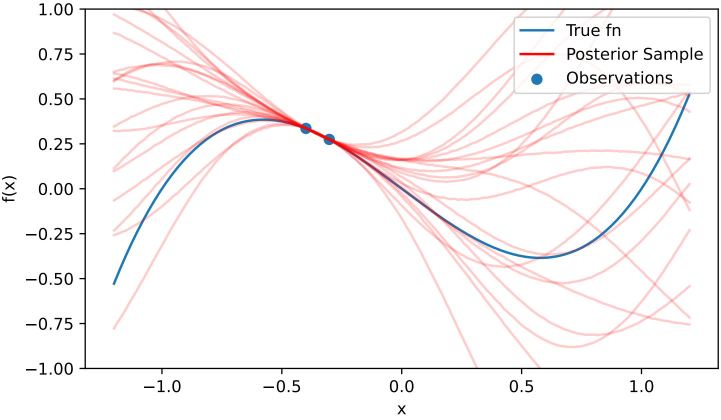

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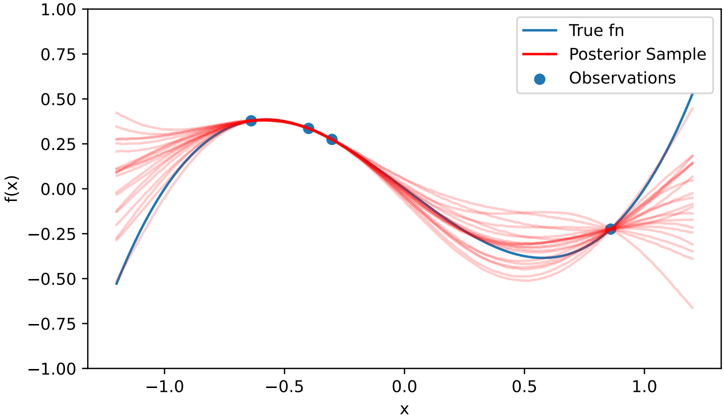

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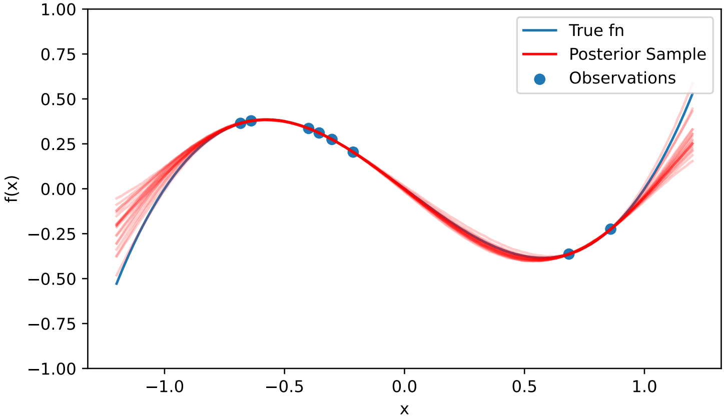

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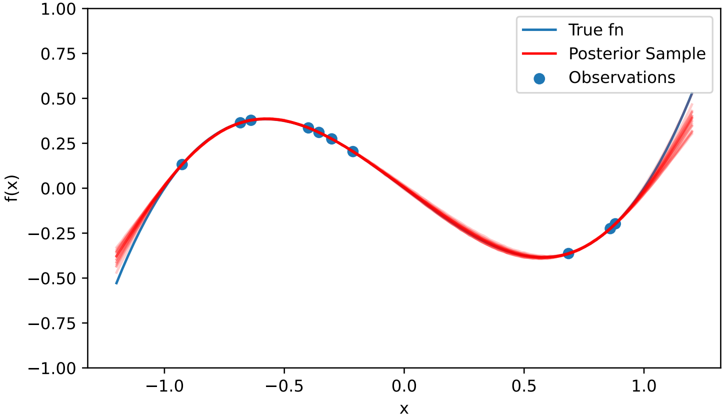

What if we have noise?

Add in observation variance, so that

$$\begin{bmatrix} f(\mathbf{x}_1) \\ f(\mathbf{x}_2) \\ \vdots \\ f(\mathbf{x}_n) \end{bmatrix} \sim \text{MVN}\left(\begin{bmatrix} m(\mathbf{x}_1) \\ m(\mathbf{x}_2) \\ \vdots \\ m(\mathbf{x}_n) \end{bmatrix}, \mathbf{K} + \sigma^2 \mathbf{I}_n \right)$$

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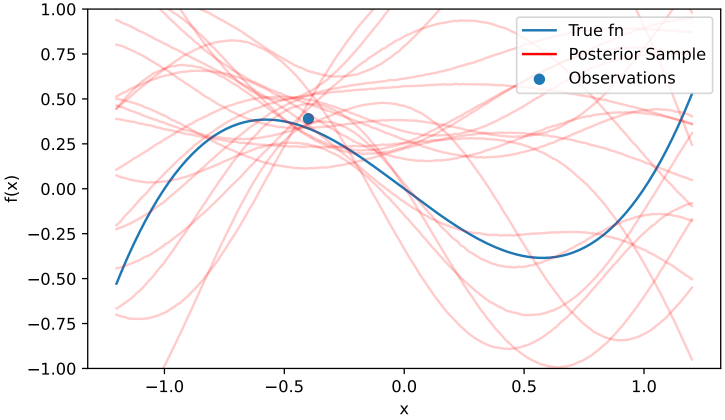

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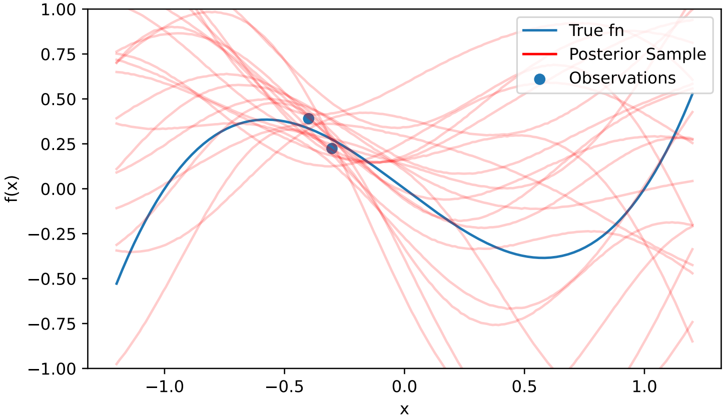

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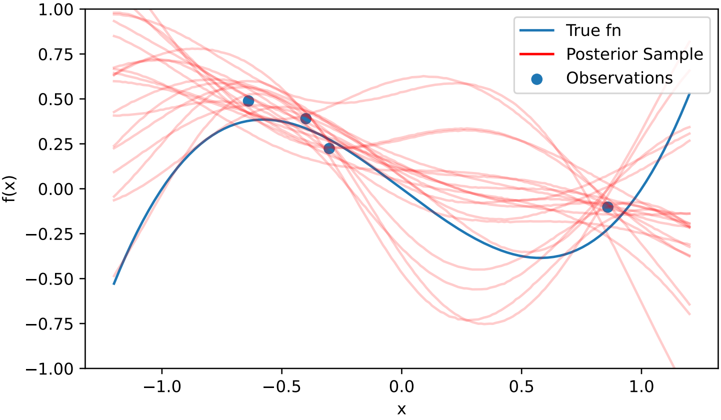

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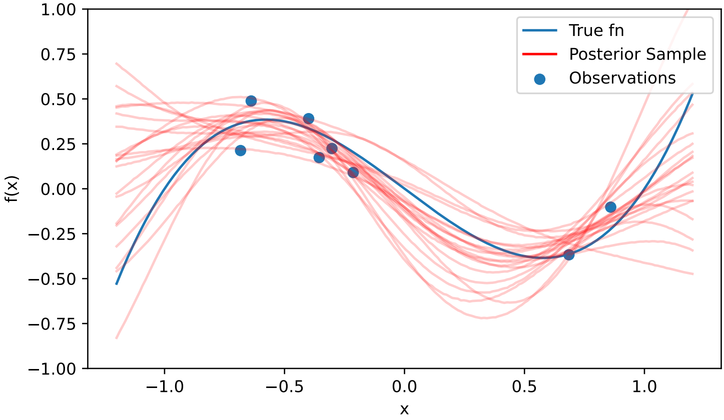

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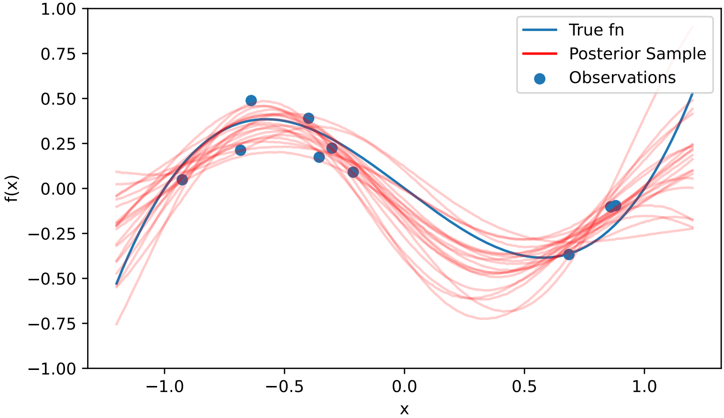

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Overall Idea again

- What if we could 'predict' discrepency values we hadn't seen before?
- Use Gaussian process to predict discrepency function

About Vivax Malaria

- Has dormant liver stage on top of blood stage infection

Champagne Model Parameters

- α : proportion of those infected but cleared of blood stage infections (through treatment)
- β : a further proportion that are also cleared of liver stage parasites, given that they were also cleared of blood stage infection (radical cure)
- λ : the rate of infection
- γ_L : rate of clearance of liver stage disease
- f : rate of relapse
- r : rate of blood stage clearance
- δ : importation rate (which we assume is 0)

Champagne ODEs

$$
\begin{aligned}
\frac{\mathrm{d}I_{\mathrm{L}}}{\mathrm{d}t} =& (1-\alpha)(\lambda I_{\mathrm{total}}+\delta)(S_0+S_{\mathrm{L}})+(\lambda I_{\mathrm{total}}+\delta)I_0 \\
& + (1-\alpha)fS_{\mathrm{L}} - \gamma_{\mathrm{L}} I_{\mathrm{L}} - rI_{\mathrm{L}} \\
\frac{\mathrm{d}I_0}{\mathrm{d}t} =& -(\lambda I_{\mathrm{total}}+\delta)I_0 + \gamma_{\mathrm{L}} I_{\mathrm{L}} - rI_0 \\
\frac{\mathrm{d}S_{\mathrm{L}}}{\mathrm{d}t} =& -(1-\alpha(1-\beta))(\lambda I_{\mathrm{total}}+\delta+f)S_{\mathrm{L}} + \alpha(1-\beta)(\lambda I_{\mathrm{total}} \\
& + \delta)S_0 - \gamma_{\mathrm{L}} S_{\mathrm{L}} + rI_{\mathrm{L}} \\
\frac{\mathrm{d}S_0}{\mathrm{d}t} =& -(1-\alpha\beta)(\lambda I_{\mathrm{total}}+\delta)S_0 + (\lambda I_{\mathrm{total}}+\delta)\alpha\beta S_{\mathrm{L}} + \alpha\beta fS_{\mathrm{L}} \\
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\end{aligned}
$$

Champagne Model Diagram

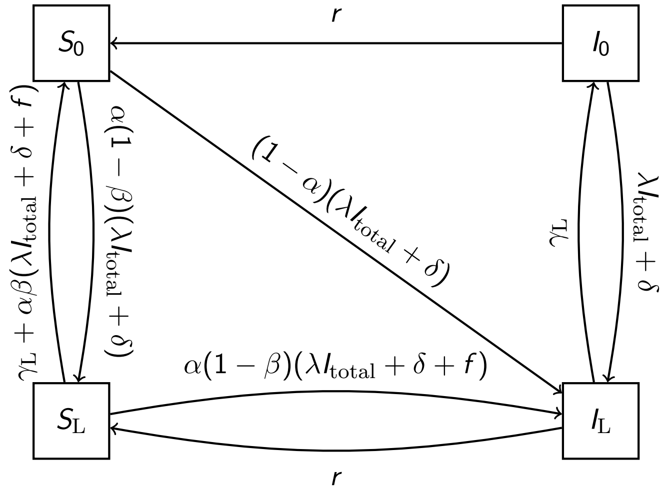

Figure: *P. vivax* model described by Champagne et al. 2022

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  - w_{obs} : weekly incidence around (stochastic) equilibrium
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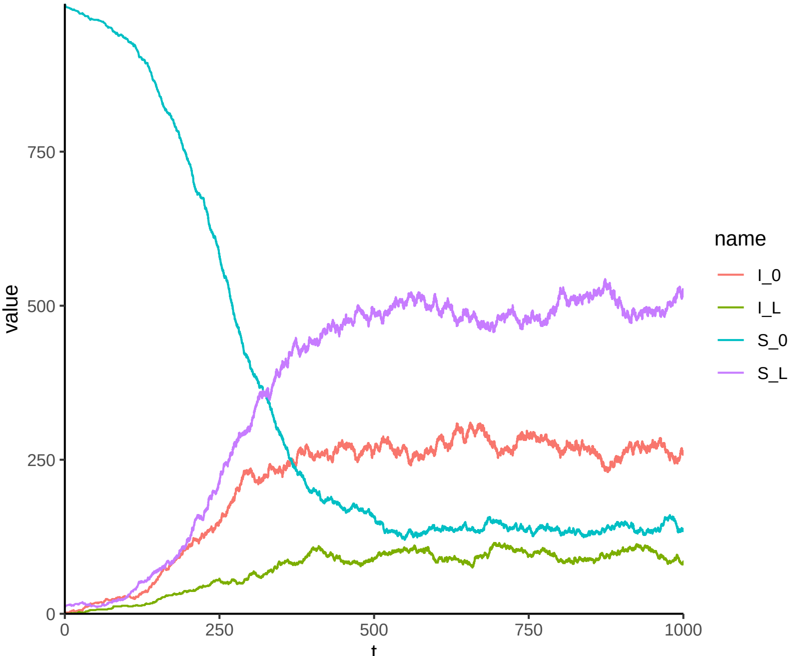
  - p_{obs} : prevalence around (stochastic) equilibrium
  - m_{obs} : incidence in the first month of the epidemic
- $D(S(\mathbf{X}), S(\mathbf{X}_{\text{obs}})) := \left|\frac{w_{\text{obs}}-w}{w_{\text{obs}}}\right| + \left|\frac{p_{\text{obs}}-p}{p_{\text{obs}}}\right| + \left|\frac{m_{\text{obs}}-m}{m_{\text{obs}}}\right|$
  - L_1 norm on the relative differences

Example Simulation



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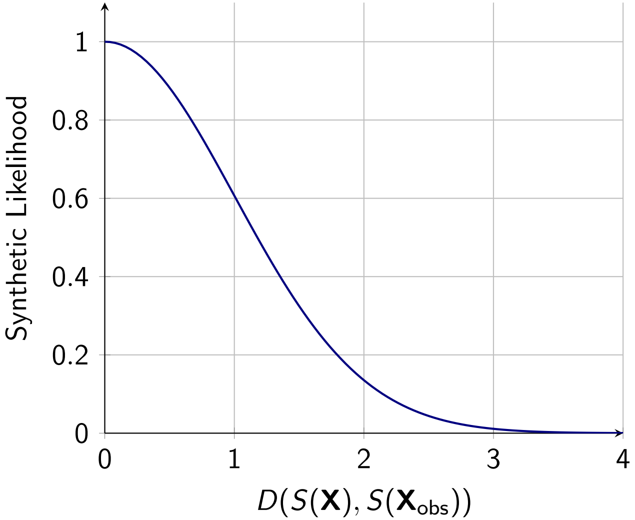
  - $\mu(\boldsymbol{\theta})$ and $\mathrm{v}(\boldsymbol{\theta})$ are the posterior mean and variance
- Could use expected information

$$(\mu_{\min} - \mu(\boldsymbol{\theta}))\Phi\left(\frac{\mu_{\min} - \mu(\boldsymbol{\theta})}{\sqrt{\mathrm{v}(\boldsymbol{\theta})}}\right) + \sqrt{\mathrm{v}(\boldsymbol{\theta})}\phi\left(\frac{\mu_{\min} - \mu(\boldsymbol{\theta})}{\sqrt{\mathrm{v}(\boldsymbol{\theta})}}\right)$$

  - $\mu_{\min} := \min_{\boldsymbol{\theta}} \mu(\boldsymbol{\theta})$
  - Φ, ϕ CDF and PDF of standard normal

Synthetic Likelihood

- $L(\boldsymbol{\theta}|\mathbf{X}_{\text{obs}}) \approx P(D_{\mathcal{GP}}(\theta) = 0)$ where $D_{\mathcal{GP}}$ is the discrepency modelled the Gaussian process
- This is equivalent to using the half normal acceptance criteria



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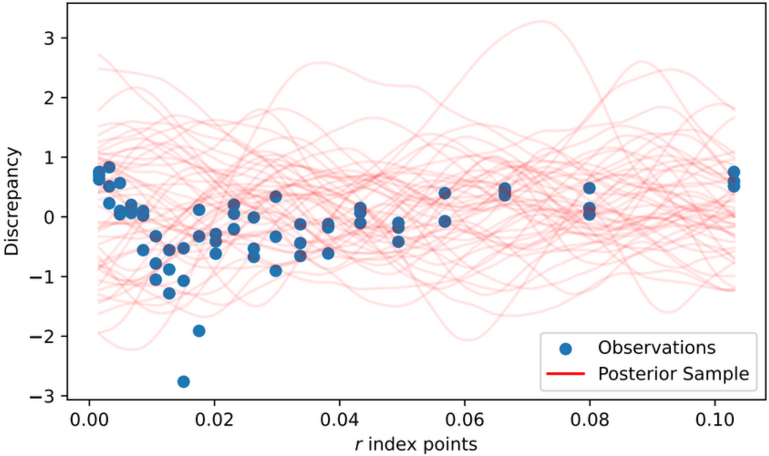

3
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Discrepancy
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r index points
Observations
Posterior Sample

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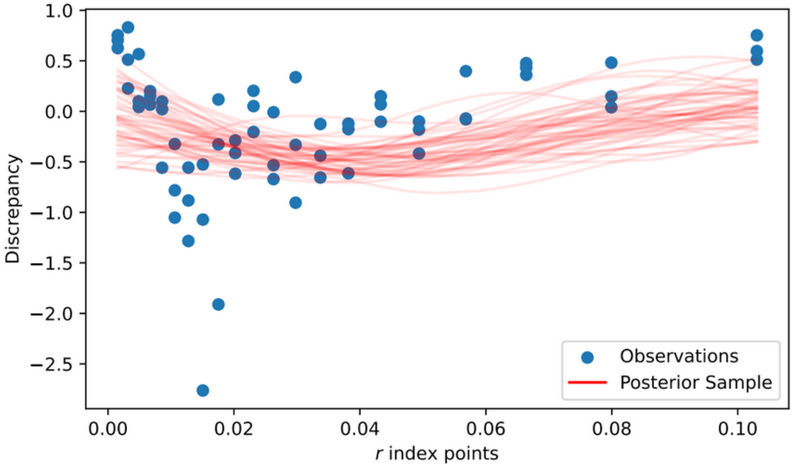
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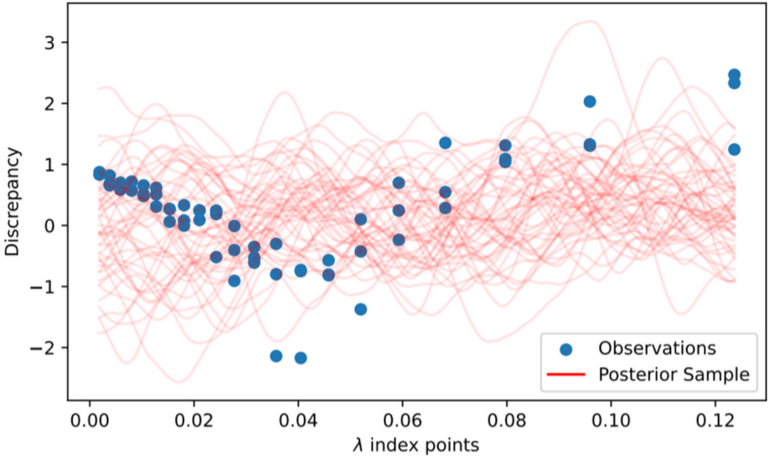

Discrepancy
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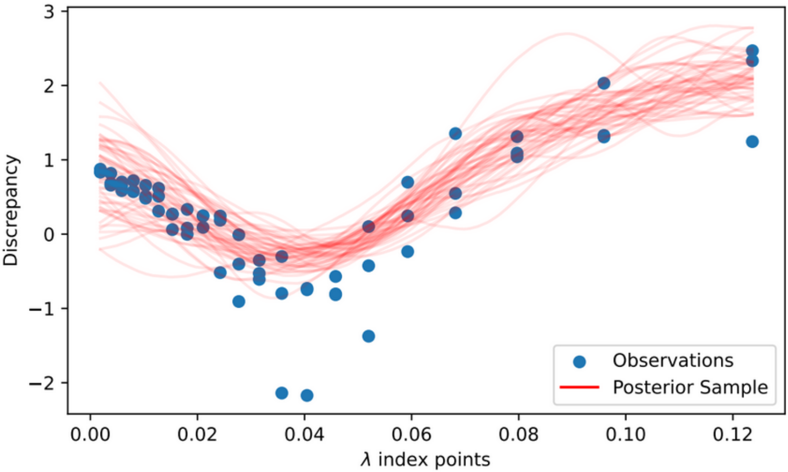

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Big Problem (Big Solutions?)

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  - Fix by modelling observation variance as another GP

Thanks to

- Eamon Conway and the Mueller lab at WEHI
- Jennifer Flegg at Unimelb
- Damon for explaining disease modelling so I don't have to