

Latent Force Models with Gaussian Processes

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Outline

Motivation

Gaussian Process Review

Motivation Continued

Covariance Functions

Motion Capture Example

PDE Example

Discussion and Future Work

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Dimensionality Reduction I

- ▶ Linear relationship between the data, $\mathbf{X} \in \mathbb{R}^{N \times d}$, and a reduced dimensional representation, $\mathbf{F} \in \mathbb{R}^{N \times q}$, where $q \ll d$.

$$\mathbf{X} = \mathbf{F}\mathbf{W} + \epsilon,$$

$$\epsilon \sim \mathcal{N}(\mathbf{0}, \Sigma)$$

- ▶ Integrate out \mathbf{F} , optimize with respect to \mathbf{W} .
- ▶ For temporal data and a particular Gaussian prior in the latent space: Kalman filter/smoother.
- ▶ More generally consider a Gaussian process (GP) prior,

$$p(\mathbf{F}|\mathbf{t}) = \prod_{i=1}^q \mathcal{N}(\mathbf{f}_{:,i} | \mathbf{0}, \mathbf{K}_{\mathbf{f}_{:,i}, \mathbf{f}_{:,i}}).$$

Dimensionality Reduction II

- ▶ Given the covariance functions for $\{f_i(t)\}$ the implied covariance functions for $\{x_i(t)\}$ — semi-parametric latent factor model (Teh et al., 2005).
- ▶ Kalman filter/smoothing approach has been preferred
 - ▶ linear computational complexity in N .
 - ▶ Advances in sparse approximations have made the general GP framework practical. (Titsias, 2009; Snelson and Ghahramani, 2006; Quiñero Candela and Rasmussen, 2005).

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Zero mean Gaussian distribution

- ▶ A multi-variate Gaussian distribution is defined by a mean and a covariance matrix.

$$N(\mathbf{f}|\mu, \mathbf{K}) = \frac{1}{(2\pi)^{\frac{N}{2}} |\mathbf{K}|^{\frac{1}{2}}} \exp\left(-\frac{(\mathbf{f} - \mu)^T \mathbf{K}^{-1} (\mathbf{f} - \mu)}{2}\right).$$

- ▶ We will consider the special case where the mean is zero,

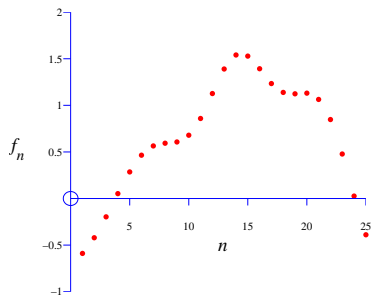
$$N(\mathbf{f}|\mathbf{0}, \mathbf{K}) = \frac{1}{(2\pi)^{\frac{N}{2}} |\mathbf{K}|^{\frac{1}{2}}} \exp\left(-\frac{\mathbf{f}^T \mathbf{K}^{-1} \mathbf{f}}{2}\right).$$

Multi-variate Gaussians

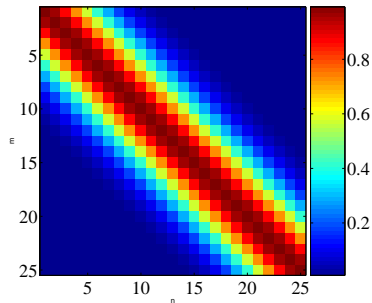
- ▶ We will consider a Gaussian with a particular structure of covariance matrix.
- ▶ Generate a single sample from this 25 dimensional Gaussian distribution, $\mathbf{f} = [f_1, f_2 \dots f_{25}]$.
- ▶ We will plot these points against their index.

Gaussian Distribution Sample

demGPsample



(a)



(b)

Figure: (a) 25 instantiations of a function, f_n , (b) colormap of covariance matrix.

The covariance matrix

- ▶ Covariance matrix shows correlation between points f_m and f_n if n is near to m .
- ▶ Less correlation if n is distant from m .
- ▶ Our ordering of points means that the *function appears smooth*.
- ▶ Let's focus on the joint distribution of two points from the 25.

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Prediction of f_2 from f_1

demGpCov2D([1 2])

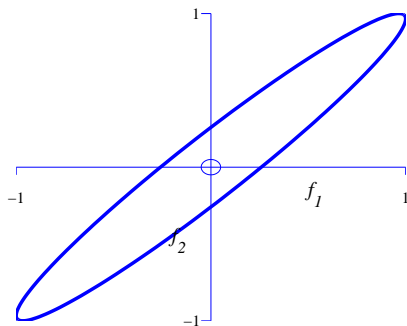


Figure: Covariance for $\begin{bmatrix} f_1 \\ f_2 \end{bmatrix}$ is $\mathbf{K}_{12} = \begin{bmatrix} 1 & 0.966 \\ 0.966 & 1 \end{bmatrix}$.

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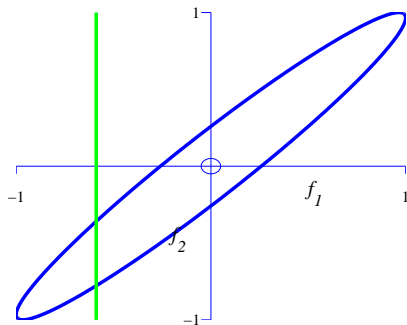


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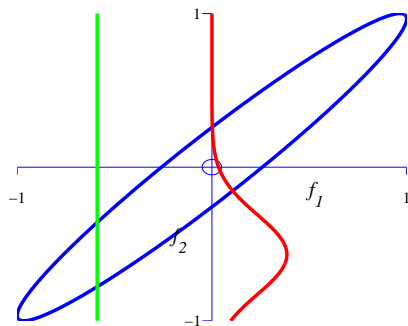


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Prediction of f_5 from f_1

demGpCov2D([1 5])

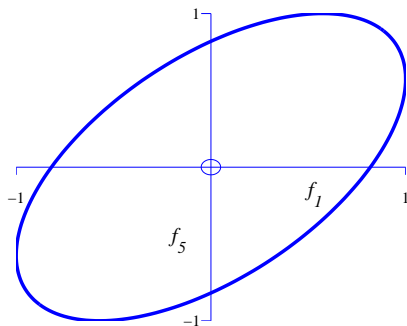


Figure: Covariance for $\begin{bmatrix} f_1 \\ f_5 \end{bmatrix}$ is $\mathbf{K}_{15} = \begin{bmatrix} 1 & 0.574 \\ 0.574 & 1 \end{bmatrix}$.

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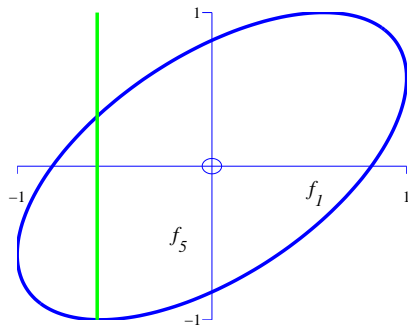


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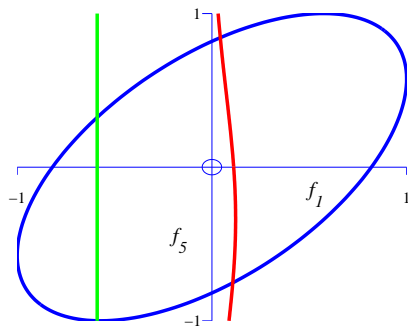


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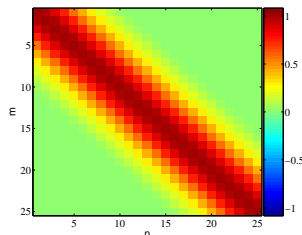
Covariance Functions

Where did this covariance matrix come from?

RBF Kernel Function

$$k(t, t') = \alpha \exp \left(-\frac{\|t - t'\|^2}{2l^2} \right)$$

- Covariance matrix is built using the *inputs* to the function t .
- For the example above it was based on Euclidean distance.
- The covariance function is also known as a kernel.



Covariance Samples

demCovFuncSample

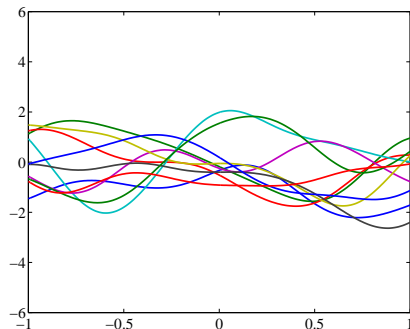


Figure: RBF kernel with $l = 10^{-\frac{1}{2}}$, $\alpha = 1$

Covariance Samples

demCovFuncSample

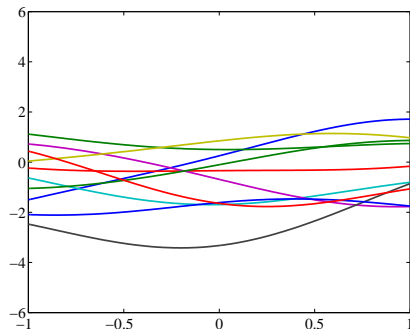


Figure: RBF kernel with $l = 1$, $\alpha = 1$

Covariance Samples

demCovFuncSample

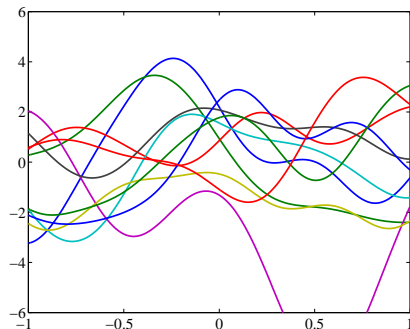


Figure: RBF kernel with $l = 0.3$, $\alpha = 4$

Gaussian Process Regression

demRegression

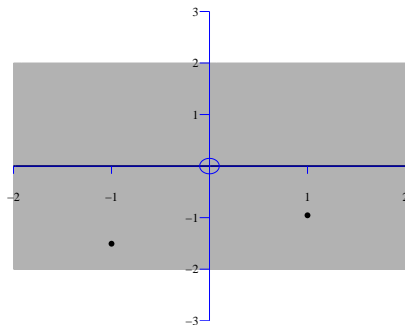


Figure: Examples include WiFi localization, C14 calibration curve.

Gaussian Process Regression

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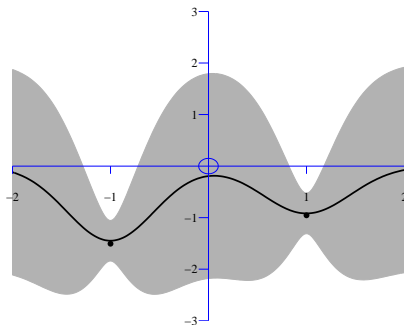


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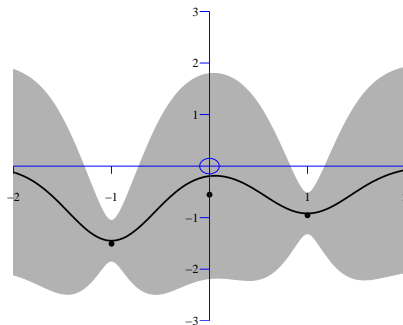


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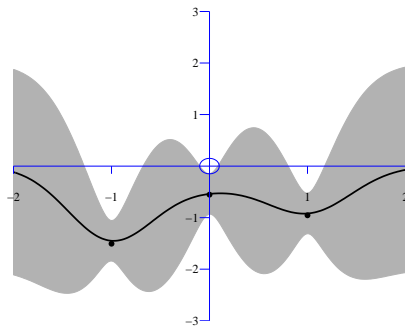


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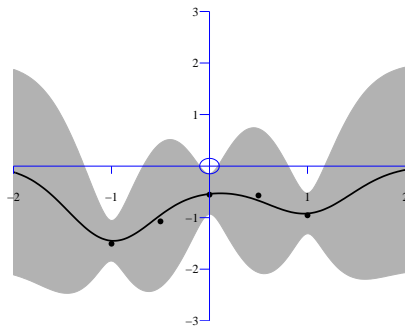


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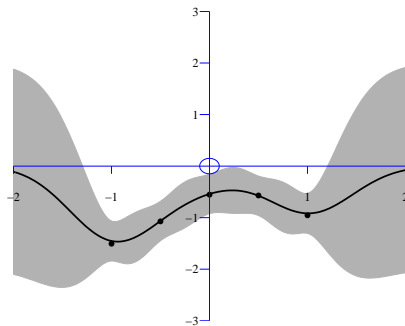


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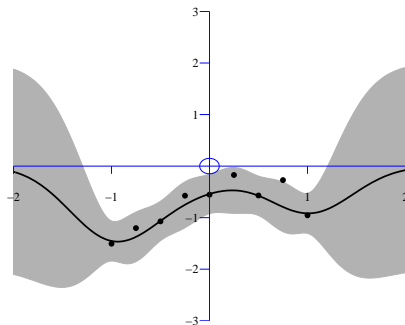


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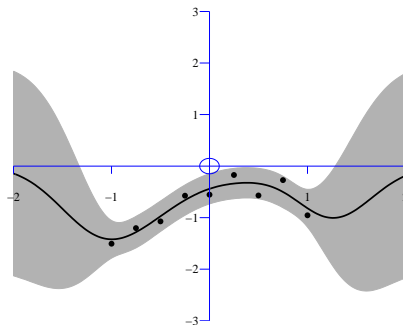
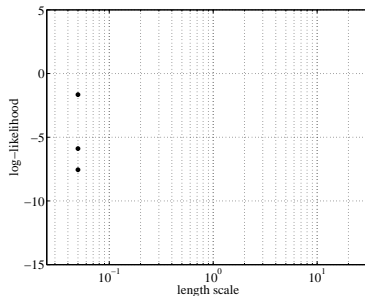
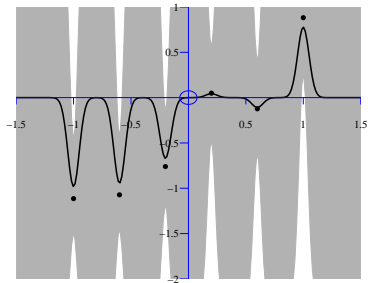


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Learning Kernel Parameters

Can we determine length scales and noise levels from the data?

demOptimiseGp

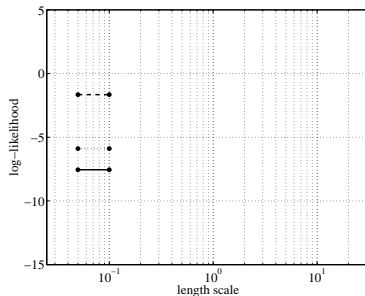
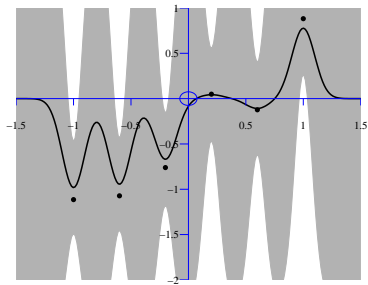


$$\log N(\mathbf{f}|\mathbf{0}, \mathbf{K}) = -\frac{N}{2} \log 2\pi - \frac{1}{2} \log |\mathbf{K}| - \frac{\mathbf{f}^T \mathbf{K}^{-1} \mathbf{f}}{2}$$

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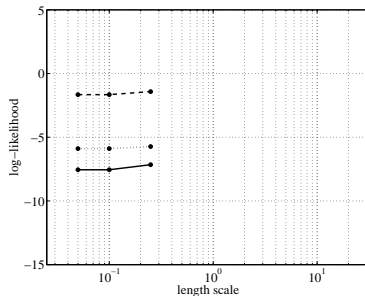
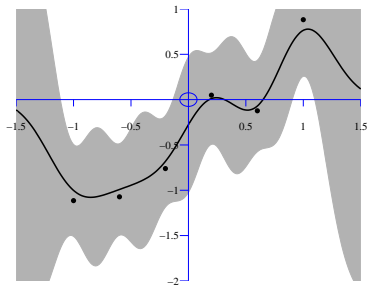


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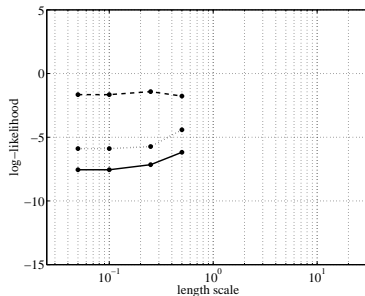
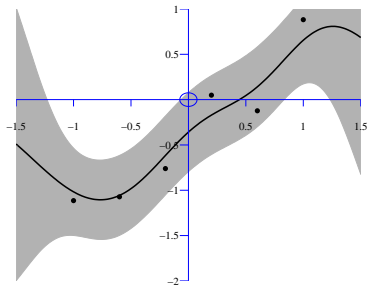


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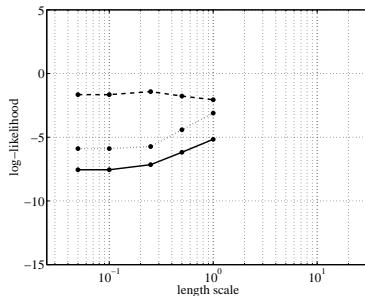
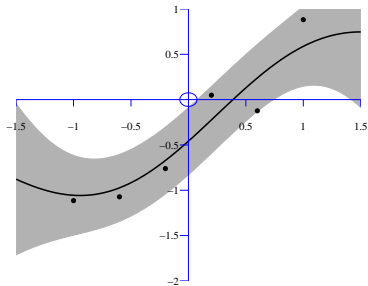


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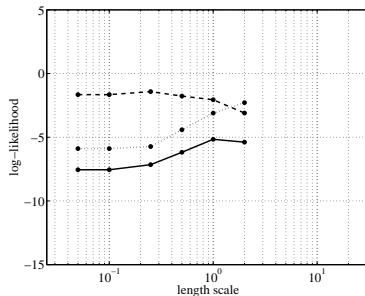
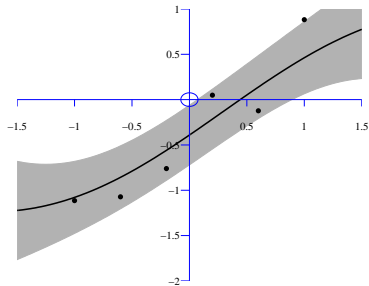


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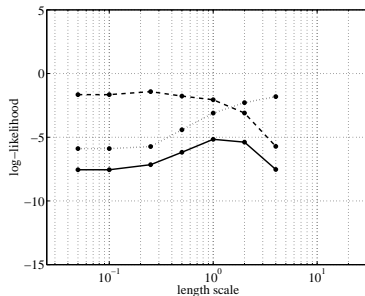
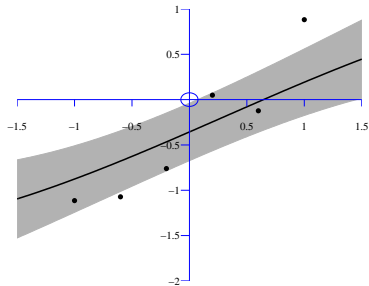


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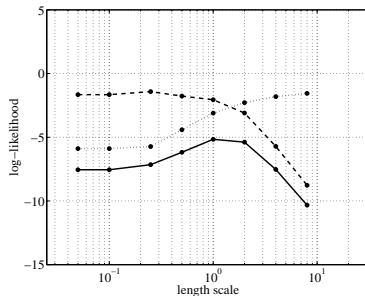
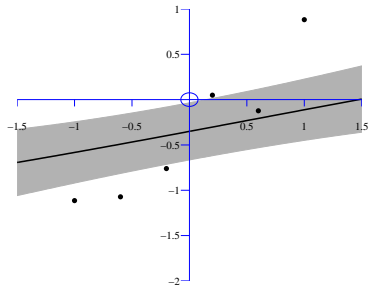


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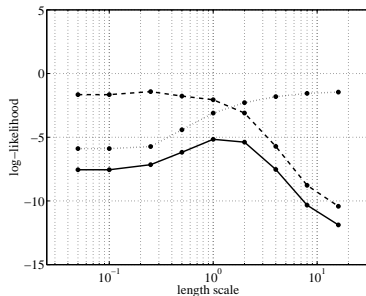
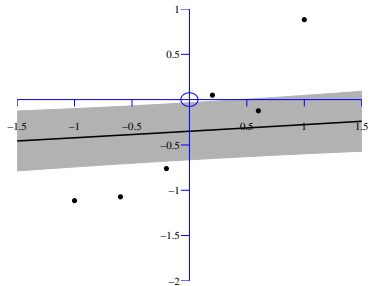


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Back to Latent Force Models!

- ▶ These models rely on the latent variables to provide the dynamic information.
- ▶ We now introduce a further dynamical system with a *mechanistic* inspiration.
- ▶ Physical Interpretation:
 - ▶ the latent functions, $f_i(t)$ are q forces.
 - ▶ We observe the displacement of d springs to the forces.,
 - ▶ Interpret system as the force balance equation, $\mathbf{X}\mathbf{D} = \mathbf{F}\mathbf{S} + \epsilon$.
 - ▶ Forces act, e.g. through levers — a matrix of sensitivities, $\mathbf{S} \in \mathbb{R}^{q \times d}$.
 - ▶ Diagonal matrix of spring constants, $\mathbf{D} \in \mathbb{R}^{d \times d}$.
 - ▶ Original System: $\mathbf{W} = \mathbf{S}\mathbf{D}^{-1}$.

- Add a damper and give the system mass.

$$\mathbf{F}\mathbf{S} = \ddot{\mathbf{X}}\mathbf{M} + \dot{\mathbf{X}}\mathbf{C} + \mathbf{X}\mathbf{D} + \epsilon.$$

- Now have a second order mechanical system.
- It will exhibit inertia and resonance.
- There are many systems that can also be represented by differential equations.
 - When being forced by latent function(s), $\{f_i(t)\}_{i=1}^q$, we call this a *latent force model*.

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Gaussian Process priors and Latent Force Models

Driven Harmonic Oscillator

- ▶ For Gaussian process we can compute the covariance matrices for the output displacements.
- ▶ For one displace the model is

$$m_k \ddot{x}_k(t) + c_k \dot{x}_k(t) + d_k x_k(t) = b_k + \sum_{i=0}^M s_{ik} f_i(t), \quad (1)$$

where, m_k is the k th diagonal element from \mathbf{M} and similarly for c_k and d_k . s_{ik} is the i , k th element of \mathbf{S} .

- ▶ Model the latent forces as q independent, GPs with RBF covariances

$$k_{f_i f_l}(t, t') = \exp \left(-\frac{(t - t')^2}{\sigma_i^2} \right) \delta_{il}.$$

Covariance for ODE Model

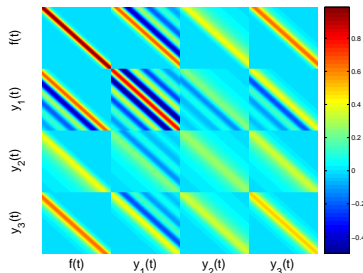
- RBF Kernel function for $f(t)$

$$x_j(t) = \frac{1}{m_j \omega_j} \sum_{i=1}^q S_{ji} \exp(-\alpha_j t) \int_0^t f_i(u) \exp(\alpha_j u) \sin(\omega_j(t-u)) du$$

- Joint distribution for $x_1(t)$, $x_2(t)$, $x_3(t)$ and $f(t)$.

Damping ratios:

ζ_1	ζ_2	ζ_3
0.125	2	1



Joint Sampling of $x(t)$ and $f(t)$

► demLfmSample

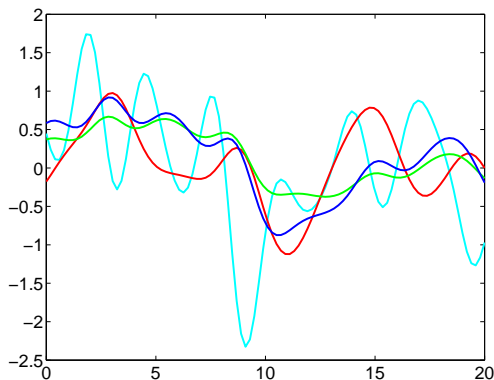


Figure: Joint samples from the ODE covariance, *cyan*: $f(t)$, *red*: $x_1(t)$ (underdamped) and *green*: $x_2(t)$ (overdamped) and *blue*: $x_3(t)$ (critically damped).

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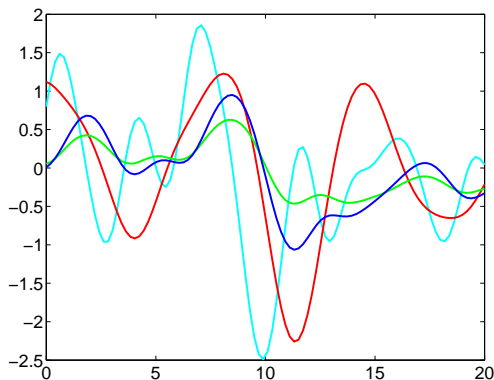


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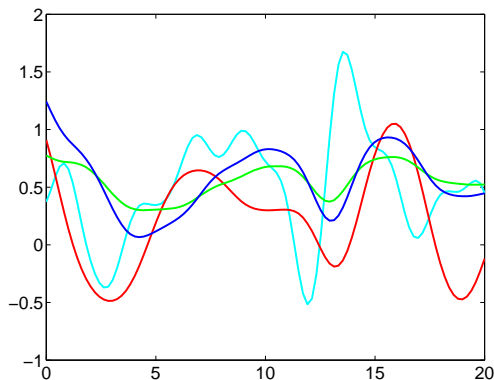


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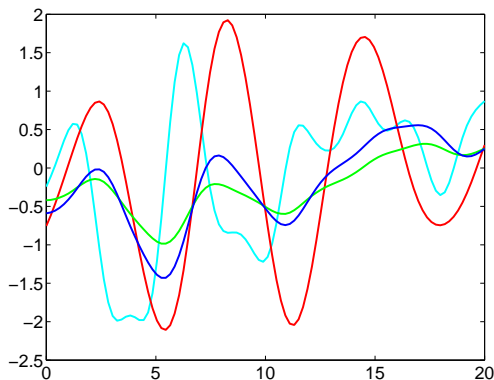


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Covariance for ODE

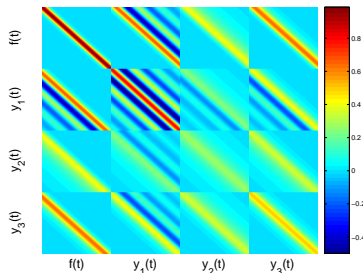
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Example: Motion Capture

Mauricio Alvarez and David Luengo (Álvarez et al., 2009)

- ▶ Motion capture data: used for animating human motion.
- ▶ Multivariate time series of angles representing joint positions.
- ▶ Objective: generalize from training data to realistic motions.
- ▶ Use 2nd Order Latent Force Model with mass/spring/damper (resistor inductor capacitor) at each joint.

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- ▶ Objective: generalize from training data to realistic motions.
- ▶ Use 2nd Order Latent Force Model with mass/spring/damper (resistor inductor capacitor) at each joint.

Mauricio Alvarez and David Luengo (Álvarez et al., 2009)

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Prediction of Test Motion

- ▶ Model left arm only.
- ▶ 3 balancing motions (18, 19, 20) from subject 49.
- ▶ 18 and 19 are similar, 20 contains more dramatic movements.
- ▶ Train on 18 and 19 and testing on 20
- ▶ Data was down-sampled by 32 (from 120 fps).
- ▶ Reconstruct motion of left arm for 20 given other movements.
- ▶ Compare with GP that predicts left arm angles given other body angles.

Mocap Results

Table: Root mean squared (RMS) angle error for prediction of the left arm's configuration in the motion capture data. Prediction with the latent force model outperforms the prediction with regression for all apart from the radius's angle.

Angle	Latent Force Error	Regression Error
Radius	4.11	4.02
Wrist	6.55	6.65
Hand X rotation	1.82	3.21
Hand Z rotation	2.76	6.14
Thumb X rotation	1.77	3.10
Thumb Z rotation	2.73	6.09

Mocap Results II

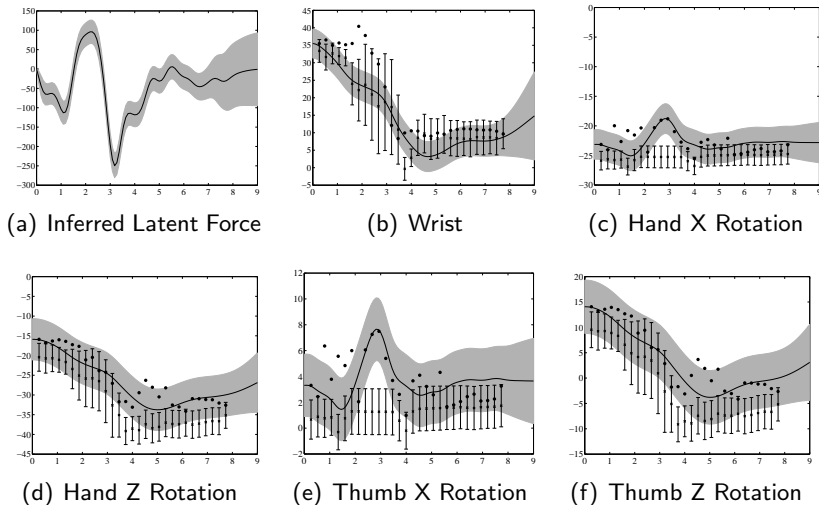


Figure: Predictions from LFM (solid line, grey error bars) and direct regression (crosses with stick error bars).

Outline

Motivation

Gaussian Process Review

Motivation Continued

Covariance Functions

Motion Capture Example

PDE Example

Discussion and Future Work

Partial Differential Equations and Latent Forces

- ▶ Can extend the concept to latent functions in PDEs.
- ▶ Jura data: concentrations of heavy metal pollutants from the Swiss Jura.
- ▶ Consider a latent function that represents how the pollutants were originally laid down (initial condition).
- ▶ Assume pollutants diffuse at different rates resulting in the concentrations observed in the data set.

$$\frac{\partial x_q(\mathbf{x}, t)}{\partial t} = \sum_{j=1}^d \kappa_q \frac{\partial^2 x_q(\mathbf{x}, t)}{\partial x_j^2},$$

- ▶ Latent function $f_r(\mathbf{x})$ represents the concentration of pollutants at time zero (i.e. the system's initial condition).

Solution to the PDE

- The solution to the system (Polyanin, 2002) is then given by

$$x_q(\mathbf{x}, t) = \sum_{r=1}^R S_{rq} \int_{\mathbb{R}^d} f_r(\mathbf{x}') G_q(\mathbf{x}, \mathbf{x}', t) d\mathbf{x}'$$

where $G_q(\mathbf{x}, \mathbf{x}', t)$ is the Green's function given as

$$G_q(\mathbf{x}, \mathbf{x}', t) = \frac{1}{2^d \pi^{d/2} T_q^{d/2}} \exp \left[- \sum_{j=1}^d \frac{(x_j - x'_j)^2}{4 T_q} \right],$$

with $T_q = \kappa_q t$.

Covariance Function

- For latent function given by a GP with the RBF covariance function this is tractable.

$$k_{\mathbf{x}_p \mathbf{x}_q}(\mathbf{x}, \mathbf{x}', t) = \sum_{r=1}^R \frac{S_{rp} S_{rq} |\mathbf{L}_r|^{1/2}}{|\mathbf{L}_{rp} + \mathbf{L}_{rq} + \mathbf{L}_r|^{1/2}} \\ \times \exp \left[-\frac{1}{2} (\mathbf{x} - \mathbf{x}')^\top (\mathbf{L}_{rp} + \mathbf{L}_{rq} + \mathbf{L}_r)^{-1} (\mathbf{x} - \mathbf{x}') \right],$$

where \mathbf{L}_{rp} , \mathbf{L}_{rq} and \mathbf{L}_r are diagonal isotropic matrices with entries $2\kappa_p t$, $2\kappa_q t$ and $1/\ell_r^2$ respectively. The covariance function between the output and latent functions is given by

$$k_{\mathbf{x}_q f_r}(\mathbf{x}, \mathbf{x}', t) = \frac{S_{rq} |\mathbf{L}_r|^{1/2}}{|\mathbf{L}_{rq} + \mathbf{L}_r|^{1/2}} \\ \times \exp \left[-\frac{1}{2} (\mathbf{x} - \mathbf{x}')^\top (\mathbf{L}_{rq} + \mathbf{L}_r)^{-1} (\mathbf{x} - \mathbf{x}') \right].$$

Prediction of Metal Concentrations

- ▶ Replicate experiments in (Goovaerts, 1997, pp. 248,249):
 - ▶ *Primary variable* (Cd, Cu, Pb, Co) predicted in conjunction with *secondary variables* (Ni and Zn for Cd; Pb, Ni, and Zn for Cu; Cu, Ni, and Zn for Pb; Ni and Zn for Co).¹
- ▶ Condition on the secondary variables to improve prediction for primary variables.
- ▶ Compare results for the diffusion kernel with independent GPs and “ordinary co-kriging” (Goovaerts, 1997, pp. 248,249).

¹Data available at <http://www.ai-geostats.org/>.

Table: Mean absolute error and standard deviation for ten repetitions of the experiment for the Jura dataset. IGPs stands for independent GPs, GPDK stands for GP diffusion kernel, OCK for ordinary co-kriging. For the Gaussian process with diffusion kernel, we learn the diffusion coefficients and the length-scale of the covariance of the latent function.

Metals	IGPs	GPDK	OCK
Cd	0.5823 ± 0.0133	0.4505 ± 0.0126	0.5
Cu	15.9357 ± 0.0907	7.1677 ± 0.2266	7.8
Pb	22.9141 ± 0.6076	10.1097 ± 0.2842	10.7
Co	2.0735 ± 0.1070	1.7546 ± 0.0895	1.5

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Discussion and Future Work

- ▶ Integration of probabilistic inference with mechanistic models.
- ▶ Ongoing/other work:
 - ▶ Biological systems.
 - ▶ Non linear response and non linear differential equations.
 - ▶ Scaling up to larger systems
 - ▶ Applications to other types of system, e.g. computational biology, spatial systems.
 - ▶ Stochastic differential equations

Acknowledgements

David Luengo's visit to Manchester was financed by the Comunidad de Madrid (project PRO-MULTIDIS-CM, S-0505/TIC/0233), and by the Spanish government (CICYT project TEC2006-13514-C02-01 and research grant JC2008- 00219). The project is financed by a Google Research Award, a Manchester School of Computer Science PhD Studentship, and EPSRC Grant No EP/F005687/1 "Gaussian Processes for Systems Identification with Applications in Systems Biology".

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ODE Model of Transcriptional Regulation

Efficient Approximations

Non-linear Response

Cascade Differential Equations

Example: Transcriptional Regulation

- First Order Differential Equation

$$\frac{dx_j(t)}{dt} = B_j + S_j f(t) - D_j x_j(t)$$

- Can be used as a model of gene transcription: Barenco et al., 2006; Gao et al., 2008.
- $x_j(t)$ – concentration of gene j 's mRNA
- $f(t)$ – concentration of active transcription factor
- Model parameters: baseline B_j , sensitivity S_j and decay D_j
- Application: identifying co-regulated genes (targets)
- Problem: how do we fit the model when $f(t)$ is not observed?

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[labels=skipGPProperties]Covariance for Transcription Model

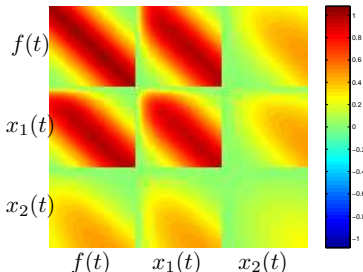
RBF covariance function for $f(t)$

$$x_i(t) = \frac{B_i}{D_i} + S_i \exp(-D_i t) \int_0^t f(u) \exp(D_i u) du.$$

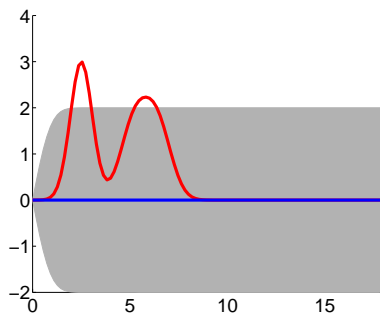
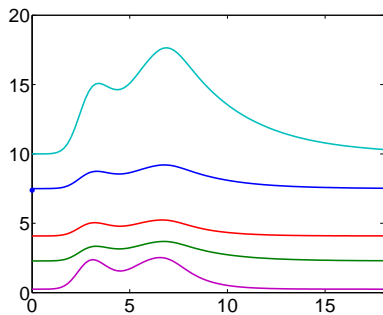
- Joint distribution for $x_1(t)$, $x_2(t)$ and $f(t)$.

- Here:

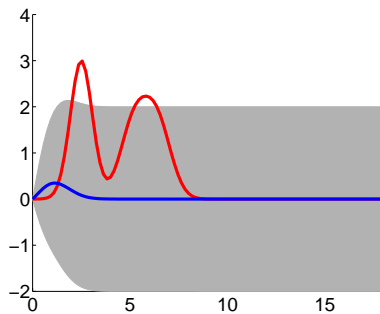
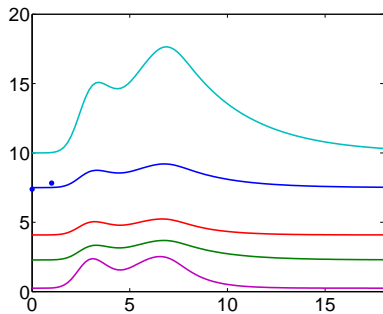
D_1	S_1	D_2	S_2
5	5	0.5	0.5



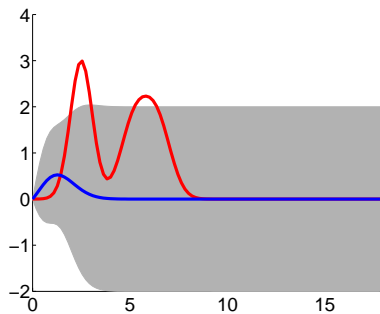
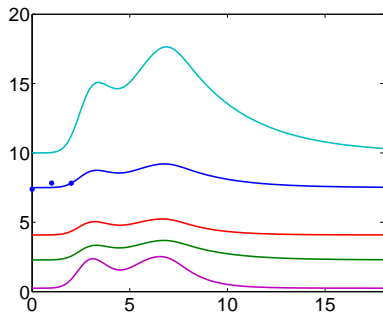
Artificial Example: Inferring $f(t)$



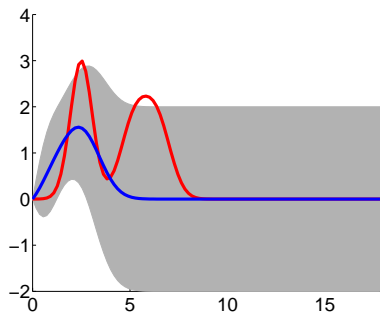
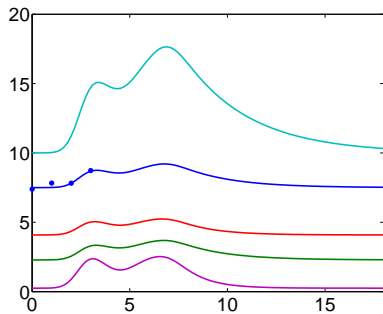
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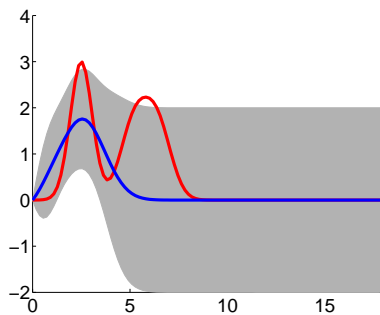
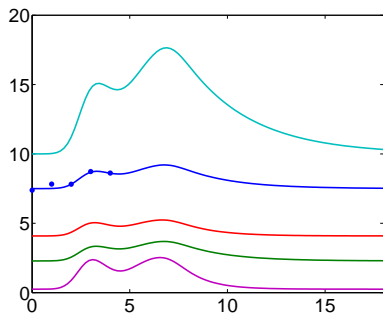
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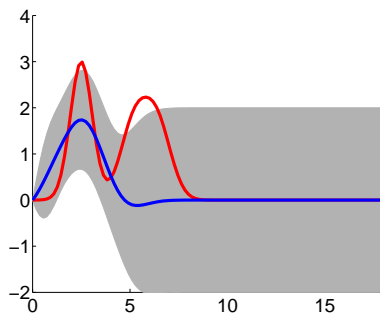
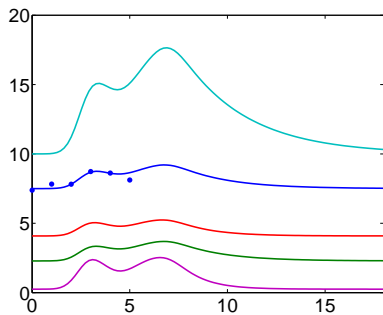
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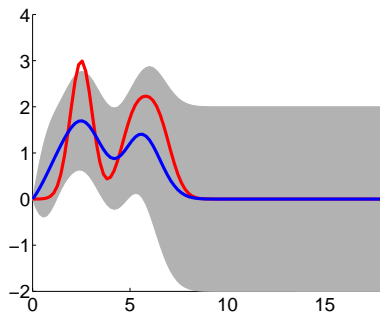
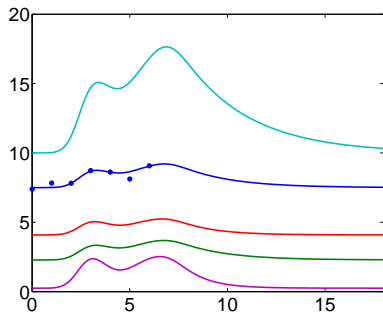
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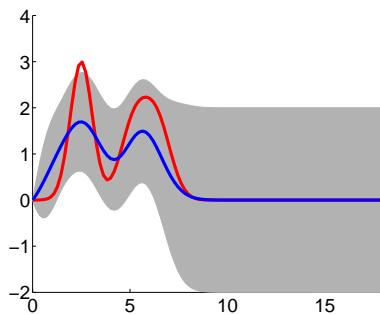
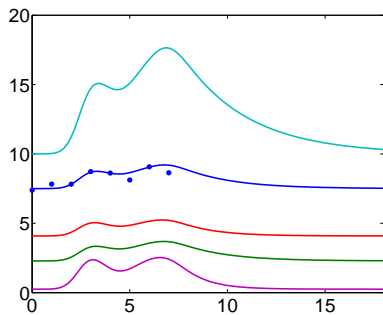
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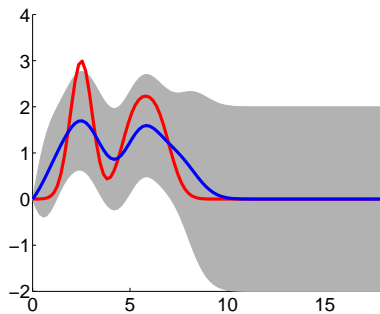
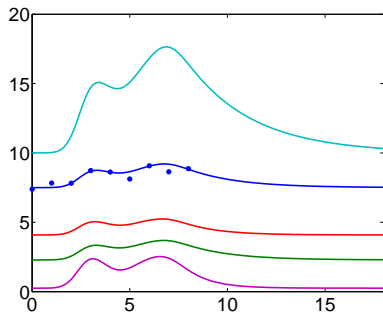
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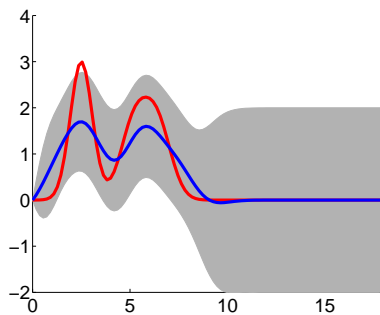
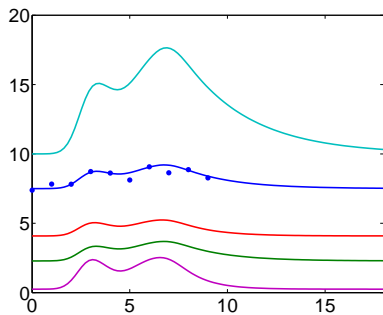
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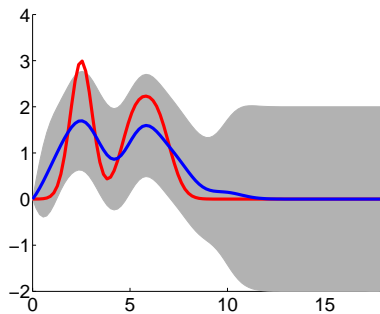
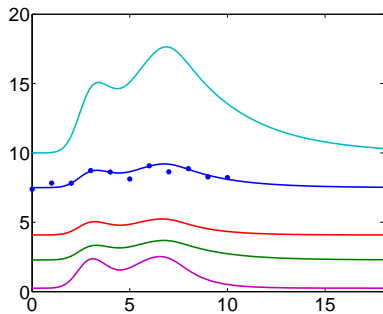
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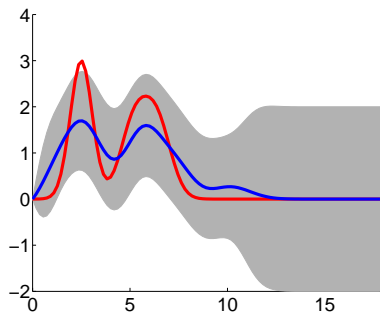
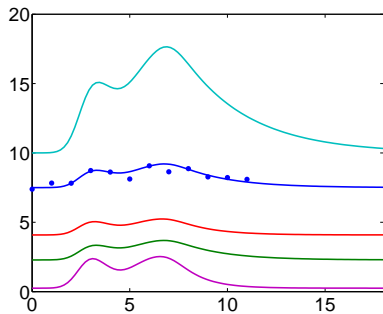
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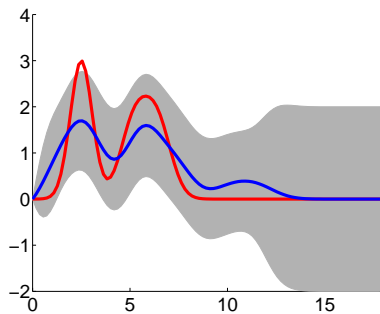
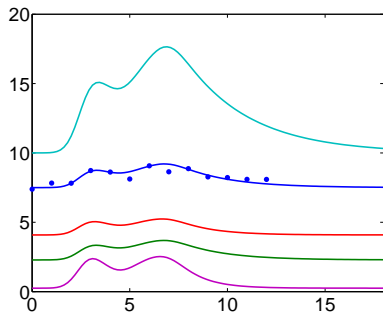
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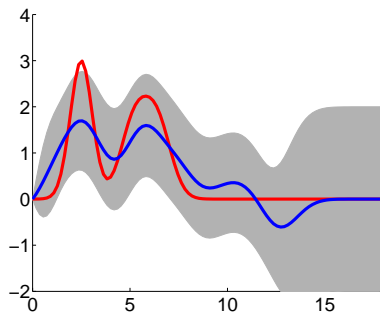
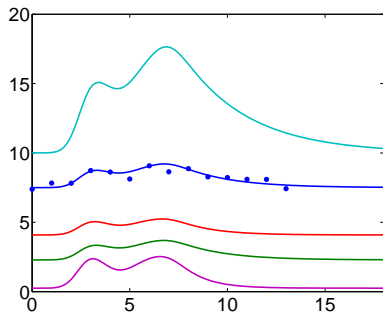
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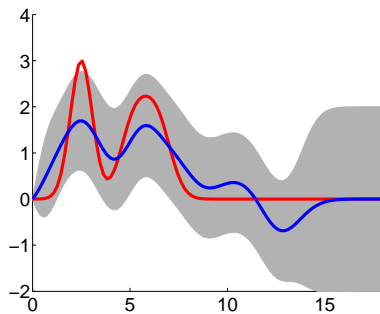
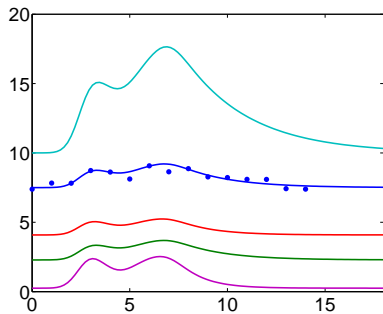
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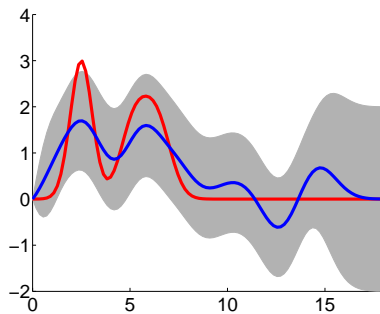
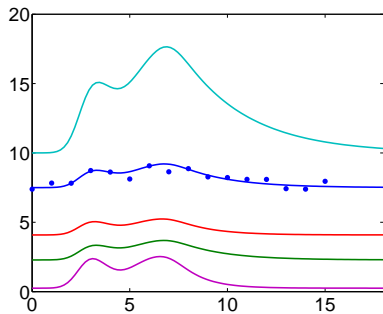
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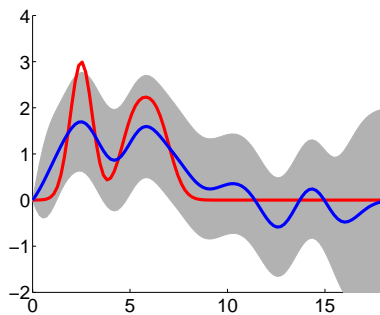
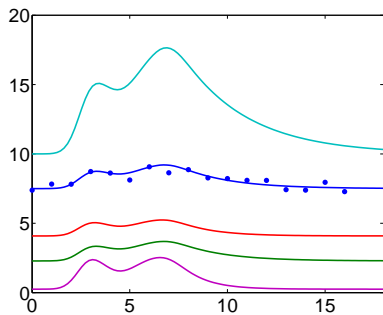
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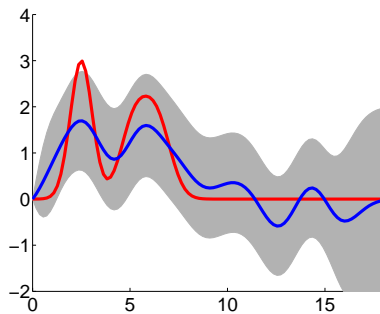
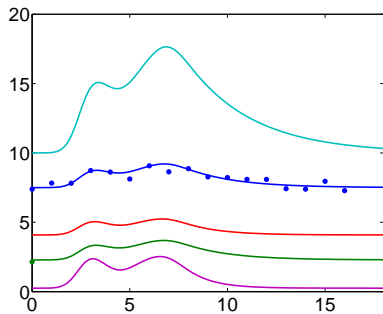
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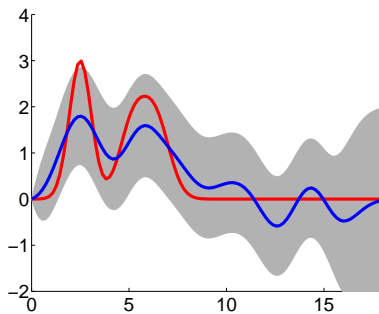
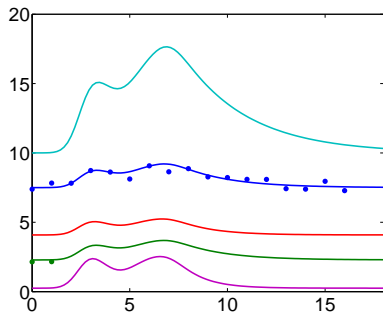
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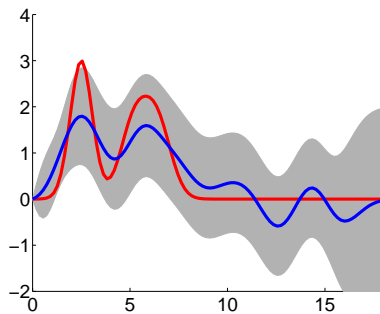
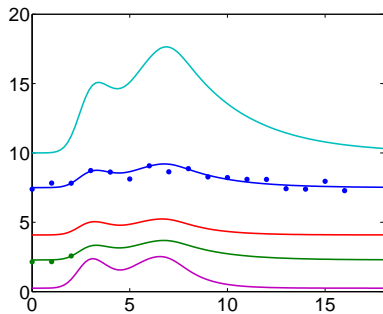
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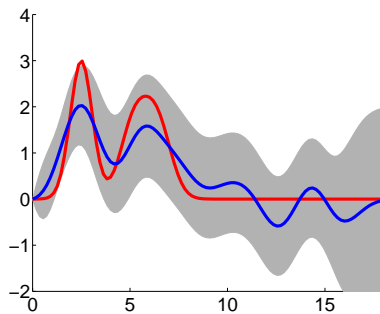
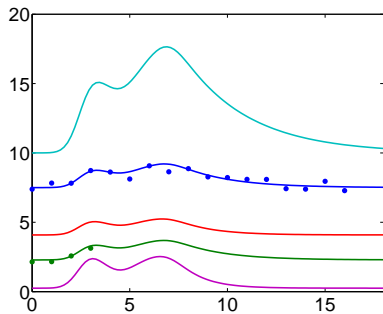
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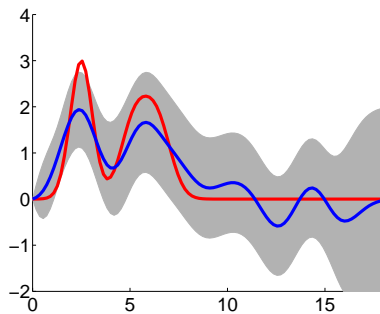
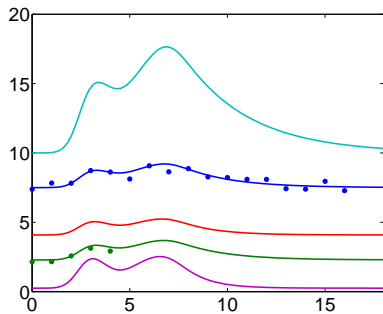
Artificial Example: Inferring $f(t)$



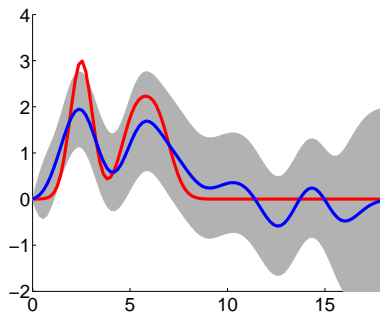
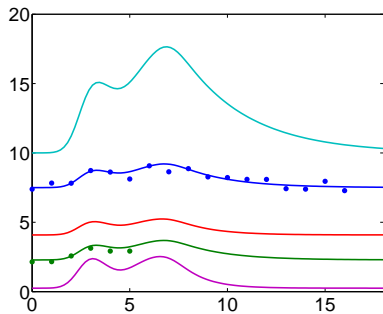
Artificial Example: Inferring $f(t)$



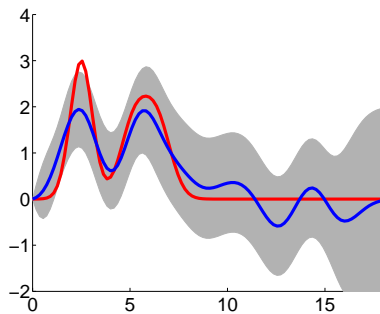
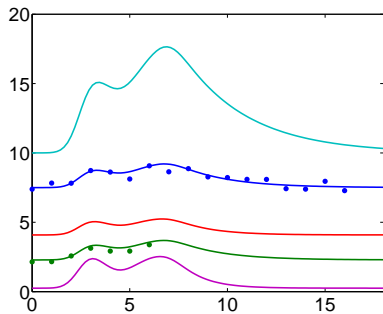
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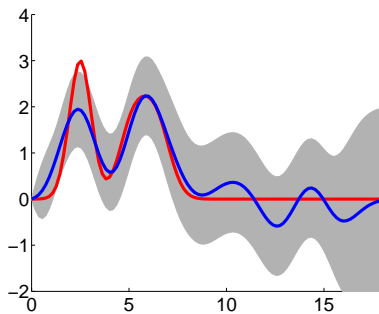
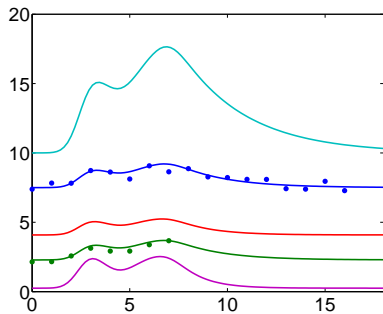
Artificial Example: Inferring $f(t)$



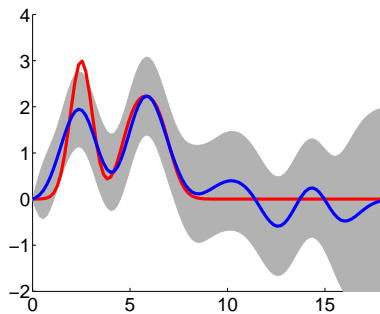
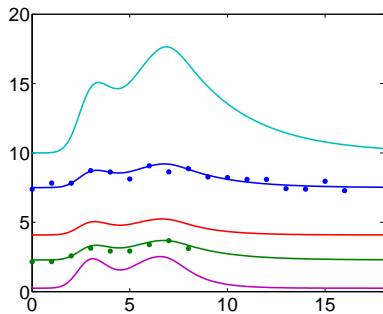
Artificial Example: Inferring $f(t)$



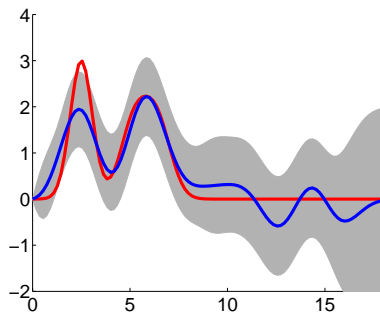
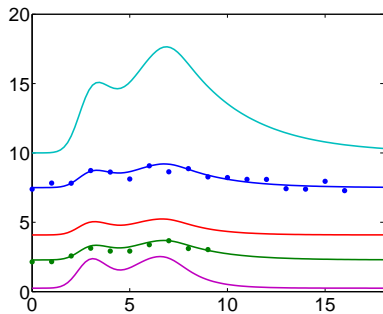
Artificial Example: Inferring $f(t)$



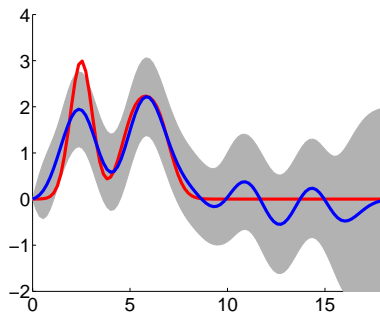
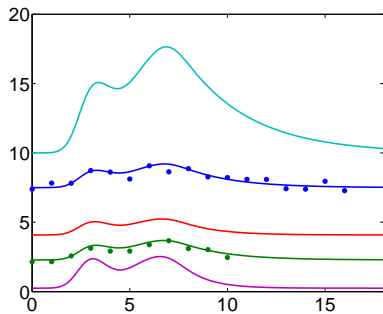
Artificial Example: Inferring $f(t)$



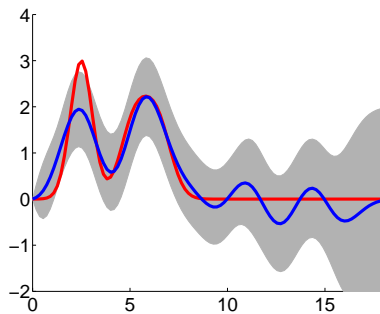
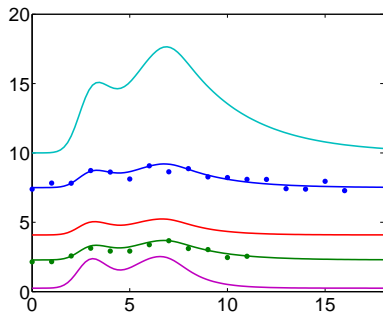
Artificial Example: Inferring $f(t)$



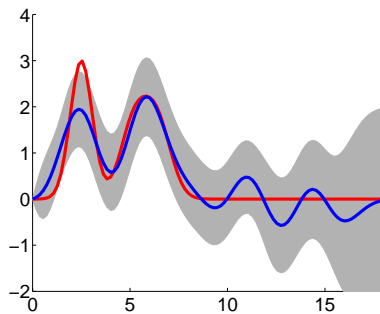
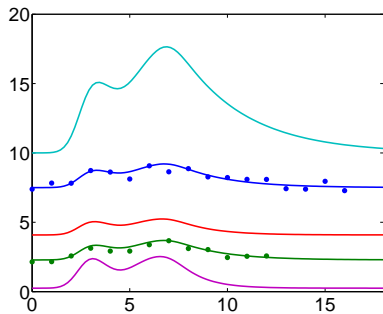
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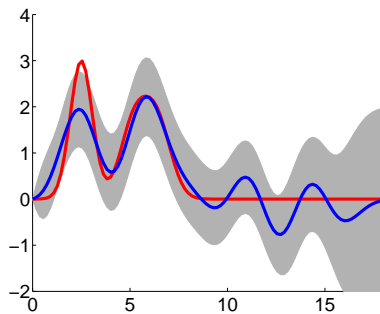
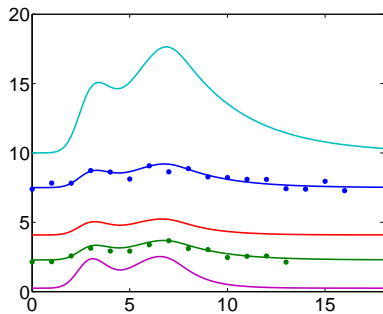
Artificial Example: Inferring $f(t)$



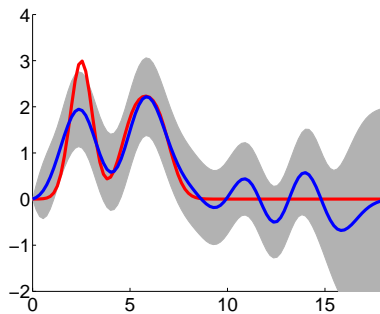
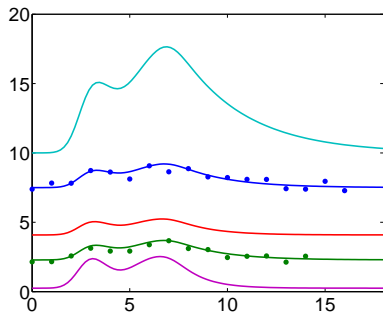
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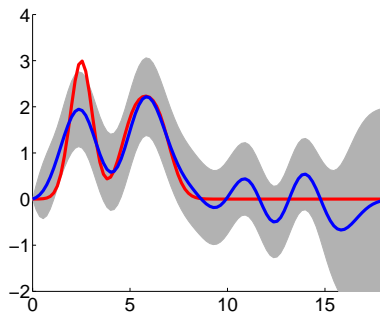
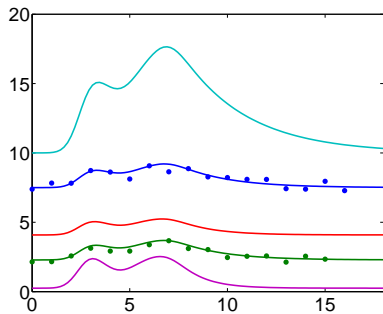
Artificial Example: Inferring $f(t)$



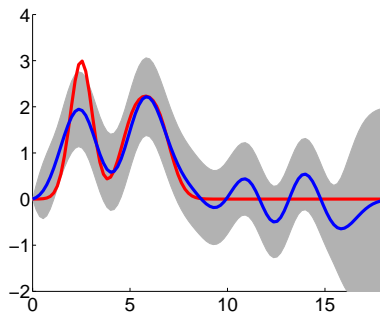
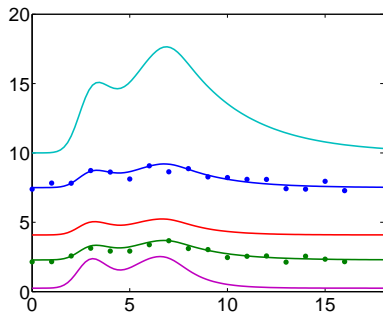
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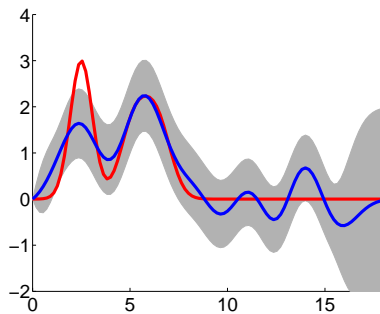
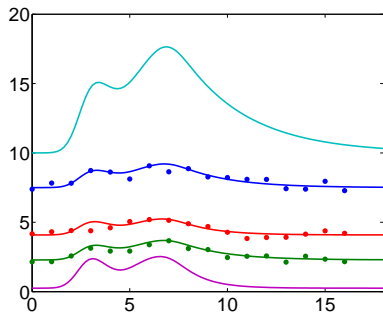
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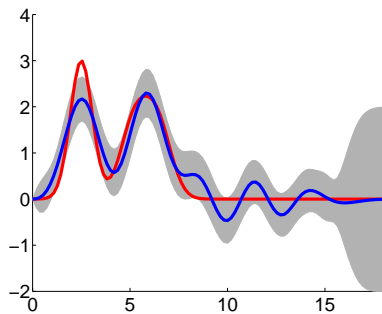
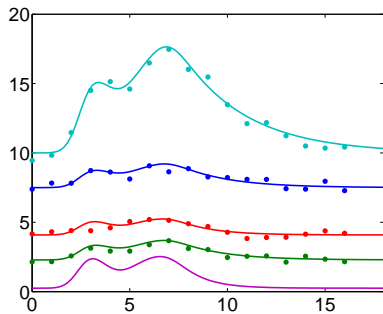
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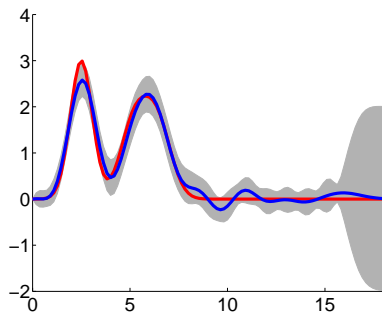
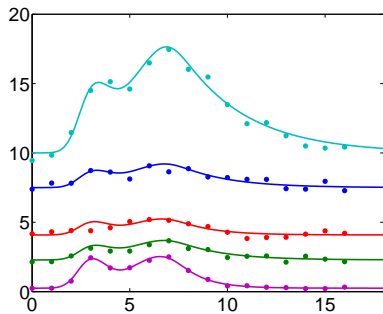
Artificial Example: Inferring $f(t)$



Artificial Example: Inferring $f(t)$



Artificial Example: Inferring $f(t)$



p53 “Guardian of the Cell”

- ▶ Responsible for Repairing DNA damage
- ▶ Activates DNA Repair proteins
- ▶ Pauses the Cell Cycle (prevents replication of damage DNA)
- ▶ Initiates *apoptosis* (cell death) in the case where damage can't be repaired.
- ▶ Large scale feedback loop with NF- κ B.

p53 DNA Damage Repair

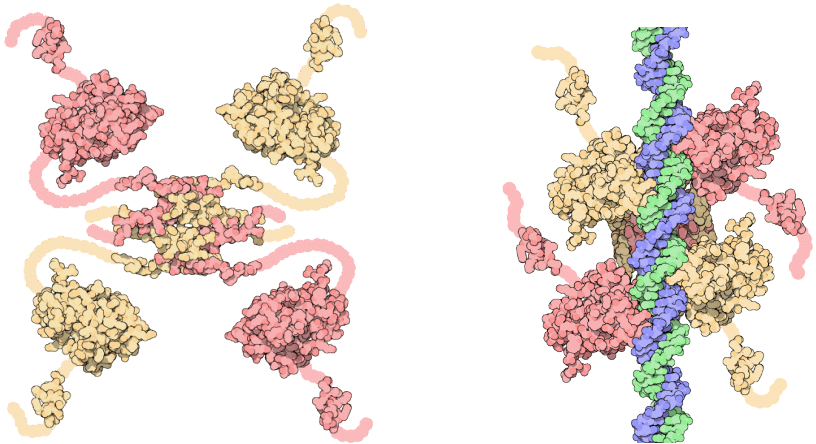


Figure: p53. *Left* unbound, *Right* bound to DNA. Images by David S. Goodsell from <http://www.rcsb.org/> (see the “Molecule of the Month” feature).

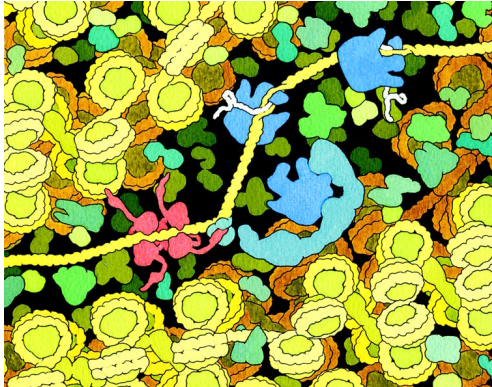


Figure: Repair of DNA damage by p53. Image from Goodsell (1999).

Modelling Assumption

- Assume p53 affects targets as a single input module network motif (SIM).

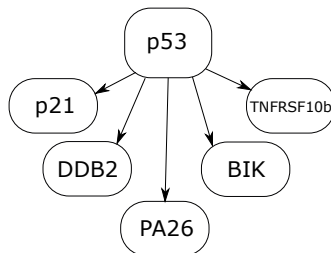
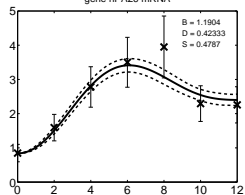
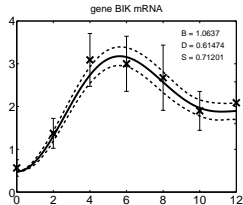
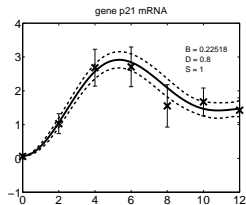
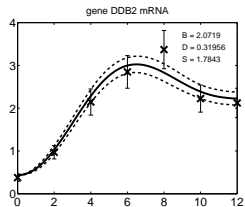
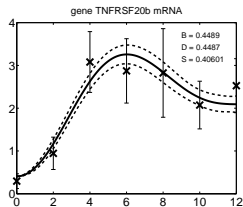
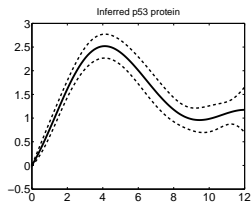


Figure: p53 SIM network motif as modelled by Barenco et al. 2006.

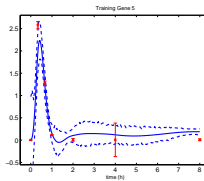
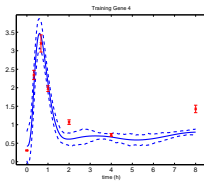
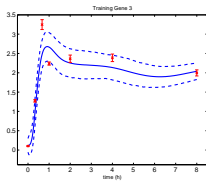
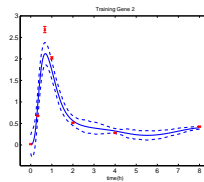
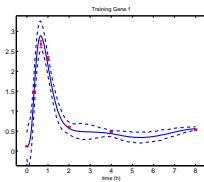
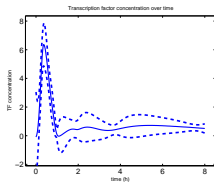


Ranking with ERK Signalling

- ▶ Target Ranking for Elk-1.
- ▶ Elk-1 is phosphorylated by ERK from the EGF signalling pathway.
- ▶ Predict concentration of Elk-1 from known targets.
- ▶ Rank other targets of Elk-1.

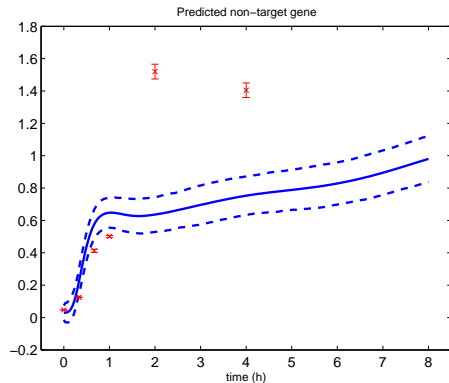
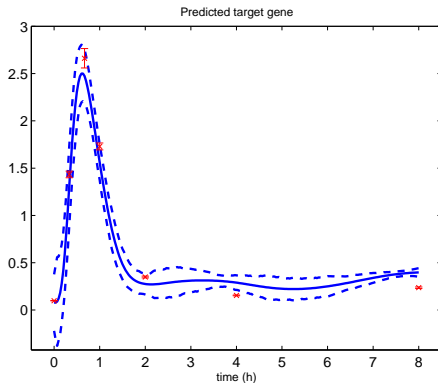
Elk-1 (MLP covariance)

Jennifer Withers



Elk-1 target selection

Fitted model used to rank potential targets of Elk-1



Outline

ODE Model of Transcriptional Regulation

Efficient Approximations

Non-linear Response

Cascade Differential Equations

Mauricio Alvarez

- Solutions to these differential equations is normally as a convolution.

$$x_i(t) = \int f(u) k_i(u - t) du + h_i(t)$$

$$x_i(t) = \int_0^t f(u) g_i(u) du + h_i(t)$$

- Convolution Processes (Higdon, 2002; Boyle and Freaan, 2005).
- Convolutions lead to $N \times d$ size covariance matrices $O(N^3 d^3)$ complexity, $O(N^2 d^2)$ storage.
- Model is conditionally independent over $\{x_i(t)\}_{i=1}^d$ given $f(t)$.

Mauricio Alvarez

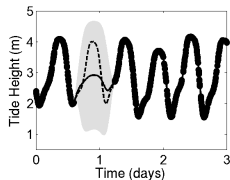
- ▶ Can assume conditional independence given $\{f(t_i)\}_{i=1}^k$.
(Álvarez and Lawrence, 2009)
 - ▶ Result is very similar to PITC approximation (Quiñonero Candela and Rasmussen, 2005).
 - ▶ Reduces to $O(N^3 dk^2)$ complexity, $O(N^2 dk)$ storage.
 - ▶ Can also do a FITC style approximation (Snelson and Ghahramani, 2006).
 - ▶ Reduces to $O(Ndk^2)$ complexity, $O(Ndk)$ storage.

Mauricio Alvarez

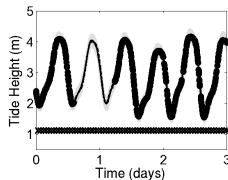
- ▶ Network of tide height sensors in the solent — tide heights are correlated.
- ▶ Data kindly provided by Alex Rogers (see Osborne et al., 2008).
- ▶ $d = 3$ and $N = 1000$ of the 4320 for the training set.
- ▶ Simulate sensor failure by knocking out one sensor for a given time.
- ▶ For the other two sensors we used all 1000 training observations.
- ▶ Take $k = 100$.

Tide Height Results

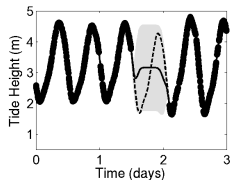
Mauricio Alvarez



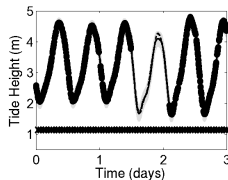
(a) Bramblemet Independent



(b) Bramblemet PITC



(c) Cambermet Independent

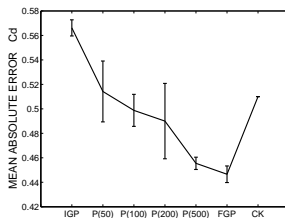


(d) Cambermet PITC

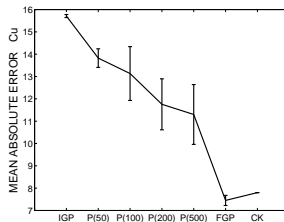
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- ▶ Jura dataset — concentrations of several heavy metals.
- ▶ Prediction 259 data, validation 100 data points.
- ▶ Predict *primary variables* (cadmium and copper) at prediction locations in conjunction with some *secondary variables* (nickel and zinc for cadmium; lead, nickel and zinc for copper) (Goovaerts, 1997, p. 248,249).

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(a) Cadmium



(b) Copper

Figure: Mean absolute error. IGP stands for independent GP, $P(M)$ stands for PITC with M inducing values, FGP stands for full GP and CK stands for ordinary co-kriging.

Outline

ODE Model of Transcriptional Regulation

Efficient Approximations

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Models of non-linear regulation

- Non-linear Activation: Michaelis-Menten Kinetics

$$\frac{dx_i(t)}{dt} = B_i + \frac{S_i f(t)}{\gamma_i + f(t)} - D_i x_i(t)$$

used by Rogers and Girolami (2006)

- Non-linear Repression

$$\frac{dx_i(t)}{dt} = B_i + \frac{S_i}{\gamma_i + f(t)} - D_i x_i(t)$$

used by Khanin et al., 2006, PNAS 103

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MAP Laplace Approximation

Consider the following modification to the model,

$$\frac{dx_j(t)}{dt} = B_j + S_j g(f(t)) - D_j x_j(t),$$

where $g(\cdot)$ is a non-linear function. The differential equation can still be solved,

$$x_j(t) = \frac{B_j}{D_j} + S_j \int_0^t e^{-D_j(t-u)} g_j(f(u)) du$$

Use Laplace's method (Laplace, 1774),

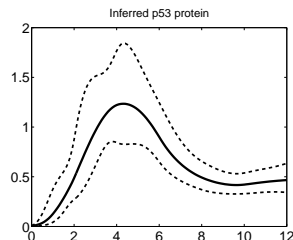
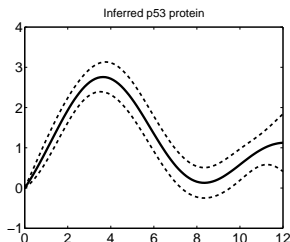
$$p(\mathbf{f} | \mathbf{x}) = N(\hat{\mathbf{f}}, \mathbf{A}^{-1}) \propto \exp\left(-\frac{1}{2} (\mathbf{f} - \hat{\mathbf{f}})^T \mathbf{A} (\mathbf{f} - \hat{\mathbf{f}})\right)$$

where $\hat{\mathbf{f}} = \operatorname{argmax}_{\mathbf{f}} p(\mathbf{f} | \mathbf{x})$ and $\mathbf{A} = -\nabla \nabla \log p(\mathbf{f} | \mathbf{y})|_{\mathbf{f}=\hat{\mathbf{f}}}$ is the Hessian of the negative posterior at that point.

- ▶ The Michaelis-Menten activation model uses the following non-linearity

$$g_j(f(t)) = \frac{e^{f(t)}}{\gamma_j + e^{f(t)}},$$

where we are using a GP $f(t)$ to model the log of the TF activity.



(a)

Validation of Laplace Approximation

Michalis Titsias

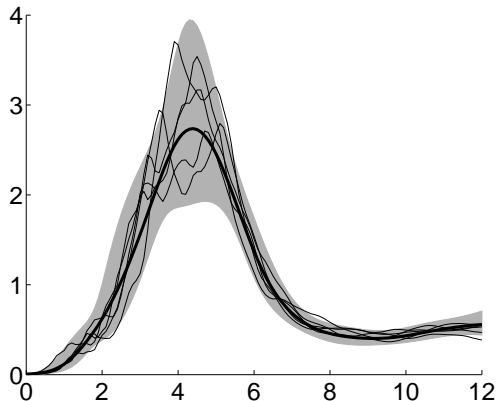


Figure: Laplace approximation error bars along with samples from the true posterior distribution.

Michalis Titsias

- ▶ Sample in Gaussian processes

$$p(\mathbf{f}|\mathbf{x}) \propto p(\mathbf{x}|\mathbf{f}) p(\mathbf{f})$$

- ▶ Likelihood relates GP to data through

$$x_j(t) = \alpha_j e^{-D_j t} + \frac{B_j}{D_j} + S_j \int_0^t e^{-D_j(t-u)} g_j(f(u)) du$$

- ▶ We use *control points* for fast sampling. (Titsias et al., 2009)

Sampling using control points

- ▶ Separate the points in \mathbf{f} into two groups:
 - ▶ few control points \mathbf{f}_c
 - ▶ and the large majority of the remaining points $\mathbf{f}_\rho = \mathbf{f} \setminus \mathbf{f}_c$
- ▶ Sample the control points \mathbf{f}_c using a proposal $q\left(\mathbf{f}_c^{(t+1)}|\mathbf{f}_c^{(t)}\right)$
- ▶ Sample the remaining points \mathbf{f}_ρ using the conditional GP prior $p\left(\mathbf{f}_\rho^{(t+1)}|\mathbf{f}_c^{(t+1)}\right)$
- ▶ The whole proposal is

$$Q\left(\mathbf{f}^{(t+1)}|\mathbf{f}^{(t)}\right) = p\left(\mathbf{f}_\rho^{(t+1)}|\mathbf{f}_c^{(t+1)}\right) q\left(\mathbf{f}_c^{(t+1)}|\mathbf{f}_c^{(t)}\right)$$

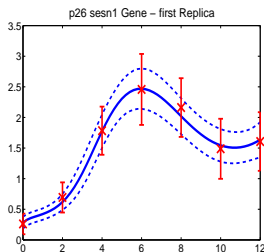
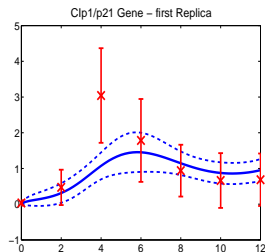
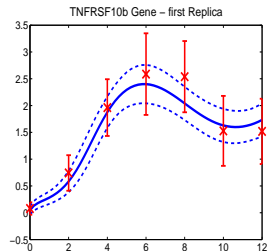
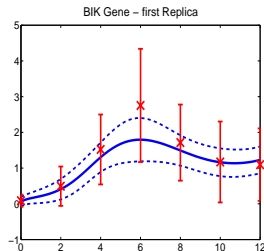
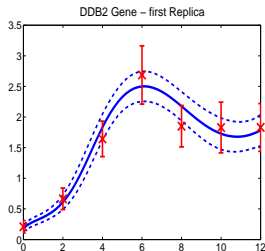
- ▶ Its like sampling from the prior $p(\mathbf{f})$ but imposing random walk behaviour through the control points.

- ▶ One transcription factor (p53) that acts as an activator. We consider the Michaelis-Menten kinetic equation

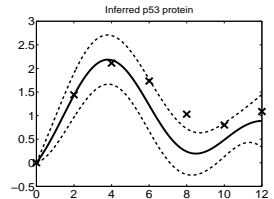
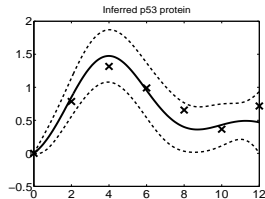
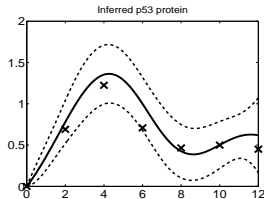
$$\frac{dx_j(t)}{dt} = B_j + S_j \frac{\exp(f(t))}{\exp(f(t)) + \gamma_j} - D_j x_j(t)$$

- ▶ MCMC details:
 - ▶ 7 control points are used (placed in a equally spaced grid)
 - ▶ Running time 4/5 hours for 2 million sampling iterations plus burn in
 - ▶ Acceptance rate for \mathbf{f} after burn in was between 15% – 25%

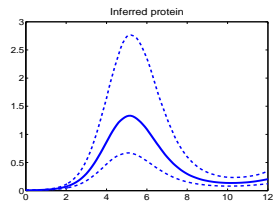
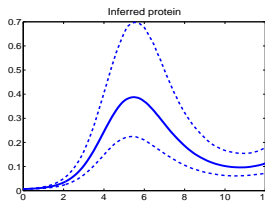
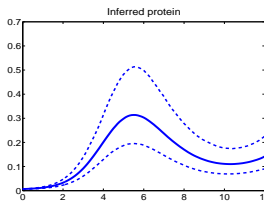
Data used by Barenco et al. (2006): Predicted gene expressions for the 1st replica



Data used by Barenco et al. (2006): Protein concentrations

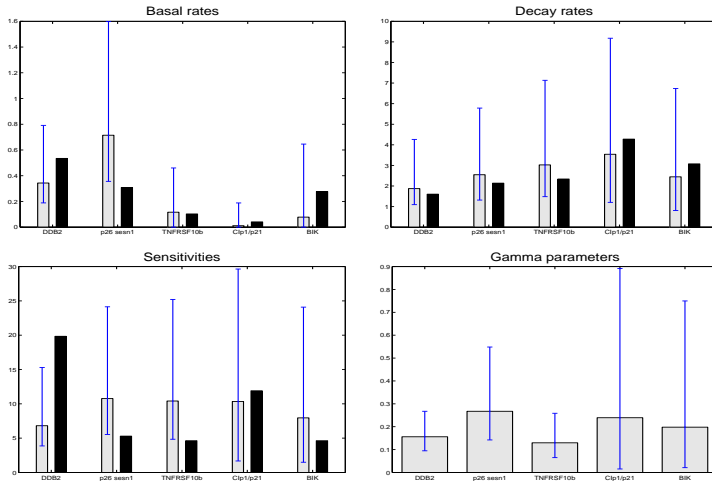


Linear model (Barenco et al. predictions are shown as crosses)



Nonlinear (Michaelis-Menten kinetic equation)

p53 Data Kinetic parameters



Our results (grey) compared with Barenco et al. (2006) (black).
Note that Barenco et al. use a linear model

Outline

ODE Model of Transcriptional Regulation

Efficient Approximations

Non-linear Response

Cascade Differential Equations

Antti Honkela

- ▶ Transcription factor protein also has governing mRNA.
- ▶ This mRNA can be measured.
- ▶ In signalling systems this measurement can be misleading because it is activated (phosphorylated) transcription factor that counts.
- ▶ In development phosphorylation plays less of a role.

Data from Furlong Lab in EMBL Heidelberg.

- ▶ Describe mesoderm development.

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We take the production rate of active transcription factor to be given by

$$\begin{aligned}\frac{df(t)}{dt} &= \sigma y(t) - \delta f(t) \\ \frac{dx_j(t)}{dt} &= B_j + S_j f(t) - D_j x_j(t)\end{aligned}$$

The solution for $f(t)$, setting transient terms to zero, is

$$f(t) = \sigma \exp(-\delta t) \int_0^t y(u) \exp(\delta u) du .$$

Covariance for Translation/Transcription Model

RBF covariance function for $y(t)$

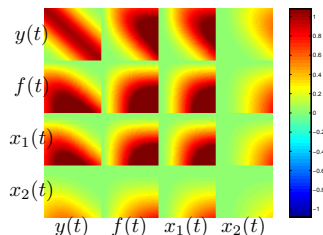
$$f(t) = \sigma \exp(-\delta t) \int_0^t y(u) \exp(\delta u) du$$

$$x_i(t) = \frac{B_i}{D_i} + S_i \exp(-D_i t) \int_0^t f(u) \exp(D_i u) du.$$

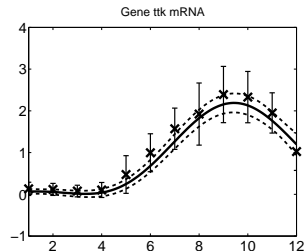
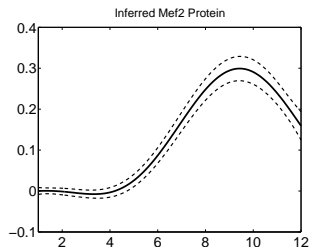
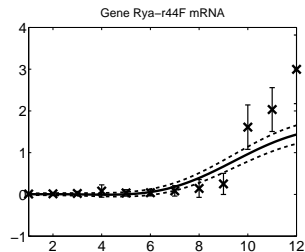
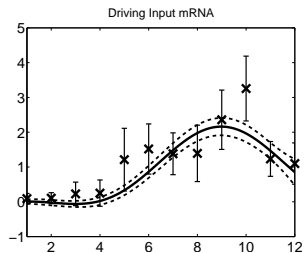
- Joint distribution for $x_1(t)$, $x_2(t)$, $f(t)$ and $y(t)$.

- Here:

δ	D_1	S_1	D_2	S_2
0.1	5	5	0.5	0.5



Results for Mef2 using the Cascade model



[c]