Gaussian Process Regression Bootstrapping

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... and find an estimate of the model parameters, $\hat{\theta}$.



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1.5 But what if we'd observed slightly 1 ۲ different data? 0.5 ç 20 10 30 40 50 60 1.4 1.2 0 0 $_{2}^{\mathsf{V}}$ 0.8 0.6 00 0.4L 10 20 30 40 50 60 t

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1.5 Would we have obtained a similar $\hat{\theta}$? ۲ 0.5 20 ň 10 30 40 50 60 1.4 1.2 $_{2}^{\mathsf{V}}$ 0.8 0.6 90 0.4L 10 20 30 40 50 60 t

The Bootstrap: A statistical resampling technique used to assess properties of quantities or statistics inferred from a data set.

Overview

Main requirement: An approximating distribution from which samples may be drawn.

- Ideally, we would repeat the experiment.
- Nonparametric bootstrap: Draw samples with replacement from original data set.
 - Time course data typically have few replicates, so hard to apply.
- Parametric bootstrap: Fit a parametric probability model to the original data.
 - How can we fit such a probability model to our time course data?

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Gaussian process regression (GPR)

Regression model:

$$y(t) = f(t) + \epsilon, \qquad \epsilon \sim \mathcal{N}(0, \sigma_{\epsilon}^2).$$

How do we choose f?

GPR: place a Gaussian process prior over f:

Gaussian process prior

• For any finite collection of times, s_1, \ldots, s_n , the function outputs $f(s_1), \ldots, f(s_n)$ are jointly distributed according to a multivariate Gaussian:

$$\forall n \in \mathbb{N} \text{ and } s_i \in \mathbb{R}_{\geq 0}, \quad [f(s_1), \dots, f(s_n)]^\top \sim \mathcal{N}(\mathbf{m}, S).$$

- $\mathbf{m}_i = m(s_i) \text{mean function}$.
- $S_{ij} = k(s_i, s_j)$ covariance function.
- Prior beliefs regarding properties of f expressed through m and k.

We write
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Gaussian process regression (GPR)... continued

We have the following:

We may update our GP prior in light of the observed data

Gaussian process posterior

- According to our GP prior, [f(s₁),..., f(s_n), f(t₁),...f(t_p)][⊤] are jointly distributed according to a multivariate Gaussian.
- 2 Also, $y(t) = f(t) + \epsilon$, where $\epsilon \sim \mathcal{N}(0, \sigma_{\epsilon}^2)$.
- It follows that [f(s₁),..., f(s_n)][⊤]|y₁,..., y_p are jointly distributed according to a multivariate Gaussian.
- We hence have a Gaussian process posterior, $f(t) \sim \mathcal{GP}(m_{post}, k_{post})$.

- From previously, $f(t) \sim \mathcal{GP}(m_{post}, k_{post})$.
- So, the posterior distribution of

$$[f(t_1),\ldots,f(t_p)]^{\top}$$
 is $\sim \mathcal{N}(\mu,\Sigma)$.

3 As $y(t) = f(t) + \epsilon$, the posterior distribution of

$$[y(t_1),\ldots,y(t_p)]^{\top}$$
 is $\mathcal{N}(\mu,\Sigma+\sigma_{\epsilon}^2 I)$.

We hence have a parametric probability model for our time course data. We may use this to obtain bootstrap samples.

(see Kirk and Stumpf, 2009, GPR bootstrapping, Bioinformatics.)

- First fit a GP regressor to the data to obtain a GP posterior.
- Draw bootstrap samples from resulting multivariate Gaussian.
- Infer quantity of interest for all data sets & assess variability.



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Example: JAK2-STAT5 Signalling Pathway



Figure: Adapted from Znamenkiy, 2006.

Example: A signalling pathway

JAK-STAT signalling pathway — The Model (Swameye et al, 2003)

• Parametric ODE model:

$$\begin{aligned} \frac{dv_1}{dt} &= -r_1 v_1 D + 2r_4 v_4 & \frac{dv_2}{dt} &= r_1 v_1 D - v_2^2 \\ \frac{dv_3}{dt} &= -r_3 v_3 + 0.5 v_2^2 & \frac{dv_4}{dt} &= r_3 v_3 - r_4 v_4. \\ y_1 &= r_5 (v_2 + 2v_3) & y_2 &= r_6 (v_1 + v_2 + 2v_3). \end{aligned}$$

- v_1 conc. unphosphorylated STAT5 in cytoplasm.
- v₂ conc. phosphorylated monomeric STAT5 in cytoplasm.
- v_3 conc. phosphorylated dimeric STAT5 in cytoplasm.
- v₄ conc. STAT5 in nucleus.
- D time-varying, experimentally determined quantity.
- r_i's unknown parameters.

Original Data

Parameter estimates from original ("DATA1_Hall") data set: $v_1(0) = 0.996$, $r_1 = 2.43$, $r_3 = 0.256$, $r_4 = 0.303$, $r_5 = 1.27$, $r_6 = 0.944$



Example: A signalling pathway

Results of estimating parameters from GPR bootstrapped data:



Second Parameter Set





Conclusions

- GPR can be used to bootstrap time-course data.
- JAK2-STAT5 model: identified 2nd set of plausible parameter estimates.
- Otherwise, parameter estimates relatively stable.
- Also considered gene networks: very sensitive!
 - ... due to very high levels of noise in the data.



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