Scalable Thompson Sampling using Sparse Gaussian Process Models

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Overview

- ◇ Thompson Sampling (TS) is a classical statistical learning method (1933, Thompson)
- \diamond Sample from the current belief
- \diamond Efficient sample complexity
- \diamond Sampling from approximate distribution for computational reasons
- ◇ That may invalidate performance guarantees [Phan et al., 2019]
- ◇ Our contribution: complete analytical and empirical study of a scalable TS using sparse approximation of GP models

Problem Formulation

- \diamond Consider an objective function $f : \mathcal{X} \to \mathbb{R}$, $\mathcal{X} \subset \mathbb{R}^d$
- \diamond A sequential learning policy selects a batch $\{x_{t,b}\}_{b\in[B]}$ of observations at each time t = 1, 2, ...
- \diamond Recieves noisy evaluation of f: $y_{t,b} = f(x_{t,b}) + \epsilon_{t,b}$
- ♦ Objective: minimize *regret*

$$R(T, B; f) = \mathbb{E}\left[\sum_{t=1}^{T} \sum_{b=1}^{B} f(x^*) - f(x_{t,b})\right]$$

 \diamond Assumption 1: The function *f* is in the reproducing kernel Hilbert space (RKHS) of a positive definite kernle *k*

 $||f||_{H_k} \leq \mathcal{B}$

 \diamond Assumption 2: $\epsilon_{t,b}$ are independent *R*-sub-Gaussian random variables

$$\mathbb{E}[e^{h\epsilon_{t,b}}] \le \exp(\frac{h^2 R^2}{2}), \ \forall h \in \mathbb{R}, \forall t, b \in \mathbb{N}.$$

 \diamond We provide our regret bounds under these two assumptions.

Surrogate Gaussian Process Model

- \diamond Provided data $\mathcal{H}_t = \{\mathbf{X}_t, \mathbf{y}_t\}$
- ♦ A surrogate GP model provides us with a posterior mean and covariance

$$\mu_t(x) = k_{\mathbf{X}_t,x}^\top (K_{\mathbf{X}_t,\mathbf{X}_t} + \tau \mathbf{I})^{-1} \mathbf{y}_t$$

$$k_t(x, x') = k(x, x') - k_{\mathbf{X}_t, x}^\top (K_{\mathbf{X}_t, \mathbf{X}_t} + \tau \mathbf{I})^{-1} k_{\mathbf{X}_t, x'}$$

 \diamond we may use this posterior distribution to sample from

Computational Complexity and Approximations

- ♦ TS using GP models has two computational bottlenecks
- $\diamond O(tB)^3$ computational complexity of the posterior distribution (matrix inverse)
- $\diamond O(N^3)$ computational complexity of a joint sample on N points (Cholesky decomposition)
- These two can be resolved, respectively, by sparse variational GP (SVGP) [Titsias, 2009] and decoupled sampling [Wilson et al., 2020]
- Both methods introduce approximation errors which need careful treatment to guarantee performance

SVGP

- \diamond Inducing points $\mathbf{Z}_t = \{z_1, ..., z_{m_t}\}$
- \diamond Inducing variables $\mathbf{u}_t = \hat{f}(\mathbf{Z}_t)$
- $\diamond A$ prior Gaussian density $q_t(\mathbf{u}_t) = \mathcal{N}(\mathbf{m}_t, \mathbf{S}_t)$

$$\mu_t^{(s)}(x) = k_{\mathbf{Z}_t,x}^{\top} K_{\mathbf{Z}_t,\mathbf{Z}_t}^{-1} \mathbf{m}_t$$
$$k_t^{(s)}(x, x') = k(x, x') + k_{\mathbf{Z}_t,x}^{\top} K_{\mathbf{Z}_t,\mathbf{Z}_t}^{-1} (\mathbf{S}_t - K_{\mathbf{Z}_t,\mathbf{Z}_t}) K_{\mathbf{Z}_t,\mathbf{Z}_t}^{-1} k_{\mathbf{Z}_t,x'}$$

♦ Computational complexity:

$$\mathcal{O}((tB)^3) \rightarrow \mathcal{O}(tbm_t^2)$$

SVGP with inducing features

- \diamond Inducing variables can be also be given with respect to integral transforms of \hat{f} : $u_{t,i} = \int_{\mathcal{X}} \hat{f}(x)\psi_i(x)dx$
- \diamond We choose the inducing features as the Mercer eigenfunctions of k

 \diamond Approximate posterior

$$\mu_t^{(s)}(x) = \boldsymbol{\phi}_{m_t}^{\top}(x)\mathbf{m}_t$$

$$k_t^{(s)}(x, x') = k(x, x') + \boldsymbol{\phi}_{m_t}^{\top}(x)(\mathbf{S}_t - \Lambda_{m_t})\boldsymbol{\phi}_{m_t}(x')$$

• $\boldsymbol{\phi}_m(x) \triangleq [\phi_1(x), ..., \phi_m(x)]^{\top}$

Decoupled Sampling with Inducing Points

- ♦ Sample from prior plus the effect of data [Wilson et al., 2020]
- \diamond Sample from prior: using truncated feature representations

$$\hat{f}(x) = \sum_{j=1}^{\infty} \sqrt{\lambda_j} w_j \phi_j(x)$$
$$\hat{f}(x) = \sum_{j=1}^{M} \sqrt{\lambda_j} w_j \phi_j(x)$$

 \diamond The effect of data: using SVGP

Scalable Thompson Sampling

 \diamond In addition to the decoupled sampling of Wilson et al. [2020], we scale the posterior variance with α_t , to ensure sufficient exploration

$$\tilde{f}_t(x) = \sum_{j=1}^M \alpha_t \sqrt{\lambda_j} w_j \phi_j(x) + \sum_{j=1}^{m_t} v_{t,j} k(x, z_j)$$

$$\diamond v_{t,j} = [K_{\mathbf{Z}_t,\mathbf{Z}_t}^{-1}(\alpha_t(\mathbf{u}_t - \mathbf{m}_t) + \mathbf{m}_t - \alpha_t \mathbf{\Phi}_{m_t,M} \Lambda_M^{\frac{1}{2}} \mathbf{w}_M)]_j$$

$$\diamondsuit \mathbf{\Phi}_{m_t,M} = [\boldsymbol{\phi}_M(z_1), ..., \boldsymbol{\phi}_M(z_{m_t})]^{\mathsf{T}}$$

$$\diamond \mathbf{w}_M = [w_1, ..., w_M]^{\mathsf{T}}, \ w_i \sim \mathcal{N}(0, 1)$$

♦ Computational complexity:

$$\mathcal{O}(N^3) \rightarrow \mathcal{O}((m_t + M)BN)$$

Scalable Thompson Sampling (inducing features)

 \diamond In addition to the decoupled sampling of Wilson et al. [2020], we scale the posterior variance with α_t , to ensure sufficient exploration

$$\tilde{f}_t(x) = \sum_{j=1}^M \alpha_t \sqrt{\lambda_j} w_j \phi_j(x) + \sum_{j=1}^{m_t} v_{t,j} \lambda_j \phi_j(x)$$

$$\diamond v_{t,j} = [\Lambda_{m_t}^{-1}(\alpha_t(\mathbf{u}_t - \mathbf{m}_t) + \mathbf{m}_t - \alpha_t \Lambda_{m_t}^{\frac{1}{2}} \mathbf{w}_{m_t})]_j$$

 $\Diamond \Lambda_{m_t}$ is the diogonal matrix of eigenvalues

 \diamond For vanilla GP-TS Chowdhury and Gopalan [2017]: $R(T;F) = \tilde{\mathcal{O}}(\gamma_T \sqrt{T})$

$$\diamond \gamma_s = \max_{A \subset \mathcal{X}, |A|=s} \mathcal{I}([y(x)]_{x \in A}; [\hat{f}(x)]_{x \in A})$$

- \diamond Mutual information: $\mathcal{I}([y(x)]_{x \in A}; [\hat{f}(x)]_{x \in A})$
- Outual information is closely related to the effective dimension of the kernel
- $\Leftrightarrow \text{Matérn: } \gamma_T = \mathcal{O}\left(T^{\frac{d}{2\nu+d}}(\log(T))^{\frac{2\nu}{2\nu+d}}\right),$ Squared Exponential: $\gamma_T = \mathcal{O}\left((\log(T))^{d+1}\right)$ [Srinivas et al., 2010, Vakili et al., 2021]

Setting Up Our Theorem

♦ Assumption 3: quality of the approximate standard deviation

$$\frac{1}{\underline{a}}\sigma_t(x) - \epsilon \le \tilde{\sigma}_t(x) \le \bar{a}\sigma_t(x) + \epsilon$$

♦ Assumption 4: quality of the approximate prediction

$$|\tilde{\mu}_t(x) - \mu_t(x)| \le c\sigma_t(x)$$

- \diamond We show that this conditions are satisfied with proper parameters m_t and M
- \diamond The additive error in $\tilde{\sigma}_t(x)$ in particular makes the analysis challenging

Regret Bound for S-GP-TS

Theorem: S-GP-TS with $\alpha_t = 2\tilde{u}_t(1/(t^2))$, Under Assumptions 1,2,3 and 4, satisfies

$$R(T; f) = \mathcal{O}(\underline{a}\overline{a}BR\sqrt{d\gamma_T(\gamma_{TB} + \log(T))T\log(T)} - \underline{a}\epsilon TBR\sqrt{d(\gamma_{TB} + \log(T))\log(T)})$$

 $\diamond \tilde{u}_t(\delta)$, is a confidence interval width multiplier

$$\tilde{u}_t(\delta) = \underline{a}_t \left(\mathcal{B} + R\sqrt{2(\gamma_{tB} + 1 + \log(1/\delta))} + c_t \right)$$

 \diamond That is with probability at least $1 - \delta$,

$$|f(x) - \tilde{\mu}_t(x)| \le \tilde{u}_t(\tilde{\sigma}_t(x) + \epsilon_t)$$

Regret Bound for S-GP-TS

Theorem Under assumptions 1 and 2, with parameters given in the table, S-GP-TS offers

$$R(T, B; f) = O(B\sqrt{\gamma_T \gamma_T B}T \log(T))$$



 \diamond with B = 1, the same regret bound as exact GP-TS is recovered

Experiments

- ♦ Experiments on benchmark functions: Shekel and Hartmann
- ♦ Experiments on a high throughput molecular screening problem
- ♦ Our implementation is based on *gpflow* and *gpflux* for modeling and *trieste* for BO

Experiments on Benchmark Functions



♦ Shekel (4D, left) and Hartmann (6D, right)

Experiments on Molecular Screening



♦ S-GP-TS performs comparable to the established baseline of Bayesian NNs

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