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MASTER THESIS

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**Bayesian Optimization of Hyperparameters
Using Gaussian Processes**

Institute of Formal and Applied Linguistics

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Dedication.

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1. Introduction

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A machine learning algorithm is an algorithm that can learn from data. A commonly used definition is: "A computer program is said to learn from experience E with respect to some class of tasks T and performance measure P , if its performance at tasks in T , as measured by P , improves with experience E [Mitchell, 1997]. We only provide this definition for completeness and our following definitions will assume an intuitive translation to this definition.

Machine learning models are traditionally split into two categories, parametric and non-parametric. Parametric models have a fixed number of learnable parameters which are trained on a subset of the data called the training set. On the other hand, non-parametric models typically have a variable number of parameters which depends on the size of the data. This could mean that there is a parameter associated with each data point. Non-parametric does not mean that there are no parameters.

Most machine learning algorithms also have hyperparameters, which are parameters that the learning algorithm can not learn itself, and they usually control the its behavior. A parameter could be chosen to be a hyperparameter because it would not be reasonable to infer its value from the training data. An example could be the type of optimizer being used to train a neural network (e.g. SGD or Adam [Kingma and Ba, 2014]). The machine learning practitioner would not consider the optimizer to be a property of the data distribution, and as a result treat it as a hyperparameter set externally, rather than trying to infer it.

It could also be set as a hyperparameter simply for practical reasons, where in theory the parameter could be learned from the data, but optimizing it directly would be too difficult. An example here could be the learning rate of a stochastic gradient descent optimizer. Even automatic differentiation [Maclaurin et al., 2015] allows us to compute the gradient flow through arbitrary code, in practice it is not being used to compute the gradients of hyperparameters like the parameters of an optimizer, e.g. the learning rate. Instead, the learning rate is treated as a hyperparameter and is set ahead of time, or according to a fixed schedule. Even when early stopping or other heuristic methods are employed, it would still be treated as a hyperparameter from the perspective of the learning algorithm.

Bayesian statistics allows us to take a principled approach to setting hyperparameters. We would simply set a prior distribution on each hyperparameter and marginalize over them, but unfortunately this has two problems. The prior distribution almost always has a parameter of its own, such as the rate of a poisson distribution. We could go one step further and specify a prior on these parameters, which are often called hyperpriors. But the real problem of bayesian methods is that the integral in the marginalization often ends up being intractable, and in the case of more complicated as neural networks, we are already computationally bottlenecked and can not use methods such as Markov-Chain Monte Carlo (MCMC) to approximate it.

There are however cases when the bayesian approach does work. Either the model is small and simple enough so that the integral can be actually computed, or its properties (such as conditional independence in LDA [Blei et al., 2003]) allow us to perform more efficient MCMC sampling, or the model could actually have an analytic solution to the marginalization. The last case is something we will make use of later on when we introduce Gaussian Processes.

Unfortunately, in the field of deep learning [Goodfellow et al., 2016] and neural networks, our models are almost always so large that just computing a point estimate of the parameters is close to our computational limits. For that reason we do not usually employ bayesian methods, but look for alternative – less computationally heavy – approaches.

A simple approach to hyperparameter tuning is either via random search, where each parameter is sampled randomly from a given prior distribution, or via grid search, where a fixed grid over the hyperparameter space is chosen, and then each point on the grid is evaluated, and the best parameter combination is chosen. The evaluation can be done using an arbitrary metric of performance, called the **objective function**. This could simply be the loss achieved by the model on the validation set.

It is not difficult to see that neither of these approaches are optimal. Both do not take into account the already computed values of the loss. If the model is evaluated on one set of hyperparameters and achieves a high loss, we would like the hyperparameter tuning mechanism to take this into account, and possibly try a different combination. This process is similar to that of an agent trying to balance the exploration-exploitation tradeoff [Russell and Norvig, 2016]. On one hand, we would like to explore different combinations of hyperparameters and explore as much of the search space as possible. But once we find a combination with a high value of the objective function we would want to explore the space around that combination to exploit the high value and possibly find a close combination that is even better.

Therefore, we'd like our hyperparameter optimization procedure, also called the **meta-optimizer**, to balance the exploration-exploitation tradeoff, and take previous evaluation into account when choosing which point to evaluate next. Since the training of machine learning models – and neural networks in particular – can be computationally costly, we need to pick an optimization procedure that is sample efficient. Many modern deep learning models take on the order of days, weeks, or even months to train on high end hardware. To give a few examples, the recent OpenAI Five [ope] has consumed 800 PETAFLOPs-days over the course of 10 months. In comparison, a consumer grade GPU GTX 1080 Ti achieves just over 11 TFLOPs. A smaller and more realistic example would be the NVIDIA StyleGAN [Karras et al., 2018] trained on 1024×1024 images takes almost 7 days on $8 \times$ Tesla V100 GPUs. In our experiments (see chapter 6) we train a tagger and lemmatizer on Czech and English treebanks, where each evaluation takes about four GPU hours. Evaluating the objective function would mean training one such model from scratch with a given set of hyperparameters to obtain an unbiased estimate of its performance.

Even though we have the ability to evaluate the objective function, we have no way of computing its gradients, or obtain its analytic form. As a result we have to treat it as a black box and use optimization techniques which don't require either.

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But even with the smaller models we have just shown, it is easy to see that we can not perform more than a few hundred of evaluations without spending unreasonable costs on computational resources. This immediately disqualifies many of the common black box optimization techniques, such as evolution strategies or simulated annealing, which require on the order of thousands evaluations to converge [Golovin et al., 2017].

Bayesian optimization [Shahriari et al., 2016] is a black box optimization technique which utilizes a probabilistic model to take a set of evaluations of the objective function and computes a posterior over all possible functions give the observed data. As the next step, it computes an **acquisition function**, which is a function of the posterior, and represents the potential usefulness of the next sample. A popular example is the **expected improvement** function (??), which is roughly defined as *the expected improvement over the maximum obtained so far*. By sampling at the maximum of the acquisition function we obtain the point that is most likely going to help us the most. A key insight here is that the model is probabilistic. It does not simply fit a regression line through the data points and find the maximum. Instead, we fit a **Gaussian Process** (GP) which allows us to capture the uncertainty in the predictions. This uncertainty is taken into account by the acquisition function, and as a result it ends up balancing the exploration-exploitation tradeoff by both taking into account the predicted value, and our uncertainty in that value.

1.1 Our Contributions

We implemented a tool for optimizing arbitrary programs' hyperparameters using bayesian optimization, including a scheduler which runs the evaluations on a cluster, and a web interface visualizing the results. We do not provide any theoretical extensions to bayesian optimization – the benefit is only in implementation. This work however also serves as a thorough introduction to the theoretical background, specifically on GP. Understanding the theoretical aspects of GPs allows the user to interpret the behavior of the optimizer, as well as better understand why some result visualizations might look the way they do.

Our implementation of bayesian optimization utilizes the GPy library [GPy, since 2012] which implements the basic GP regression model. We chose to use the library mainly for the reasons of numerical stability. In theory, as we will show later chapter 3, implementing GP regression is simple for a small toy example. But with realistic data it is easy to run into numerical issues, some of which we will go over in the following chapter 2. Apart from numerically stable code, the GPy allows for more control over the hyperparameters of the GP using constrained optimization.

Fitting a GP model and optimizing the acquisition function is just the beginning. A non-trivial amount of the work is devoted to evaluating the function in a flexible way. In our case, we expect the user to provide a script which encapsulates the function, accepts its parameters in the form of command line arguments, and prints the result of the function on its standard output. This approach allows us to run the evaluations in parallel, or even run them on a cluster. The implementation is flexible enough so that a user could provide their own way of running the evaluations, should they have specific needs. The experimental data

is also stored in an easy to access text format, with command line utilities that allow the user a fine grained control over the experiment.

Lastly, running real-life experiments can be a time consuming process, and having the ability to monitor the process and interfere if needed is an important feature. This is why we provide a web interface that can visualize the progress of the optimization. The user can look at the evaluated samples, as well as the regression model at any point in time during the optimization.

2. Bayesian Optimization

Consider the problem of optimizing an arbitrary continuous function $f : \mathcal{X} \rightarrow \mathbb{R}$ where $\mathcal{X} \subset \mathbb{R}^d, d \in \mathbb{N}$. We call f the *objective function* and treat it as a black box, making no other assumptions on its analytical form, or on our ability to compute its derivatives. Our goal is to find the global minimum \mathbf{x}_{opt} over the set \mathcal{X} , that is

$$\mathbf{x}_{\text{opt}} = \arg \min_{\mathbf{x} \in \mathcal{X}} f(\mathbf{x}).$$

We also assume that the evaluation of f is expensive, as the goal of bayesian optimization is to find the optimum in as few evaluations as possible. Consider the case when evaluating f means performing a computation that is not only time consuming, but for example also costs a lot of money. We might only have a fixed budget which puts a hard limit on the number of evaluations we can perform. If the function can be evaluated cheaply, other global optimization approaches such as simulated annealing or evolution strategies could potentially yield better results [Golovin et al., 2017].

Bayesian optimization techniques are some of the most efficient approaches in terms of the number of function evaluations required. Much of the efficiency stems from the ability to incorporate prior belief about the problem and to trade of exploration and exploitation of the search space [Brochu et al., 2010].

It is called bayesian because it combines the prior knowledge $p(f)$ about the function together with the data in the form of the likelihood $p(\mathbf{x}|f)$ to formulate a posterior distribution on the set of possible functions $p(f|\mathbf{x})$. We will use the posterior distribution to figure out which point should be evaluated next to give a likely improvement over the currently obtained maximum. This improvement is defined by an **acquisition function**, which represents our optimization objective. A simple example of an acquisition function is the **probability of improvement**, which simply represents the probability of improving our objective compared to the previously achieved maximum. We will show a few other examples of acquisition functions in a later section 4.1.

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The optimization procedure is sequential, using a bayesian posterior update at each step, refining its model as more data are available. At each step the we maximize the acquisition function in order to obtain the next sample point \mathbf{x}_{i+1} . We then evaluate $f(\mathbf{x}_{i+1})$ to obtain y_{i+1} , and incorporate it into the dataset. This process is repeated for as many evaluations as we can perform. See algorithm 1 for pseudocode.

```
Initialize  $\mathbf{x}_1$  randomly and evaluate  $y_1 = f(\mathbf{x}_1), \mathcal{D}_1 = (\mathbf{x}_1, y_1)$ .  
for  $i = 1, 2, \dots$  do  
    Find  $\mathbf{x}_{i+1}$  by maximizing the acquisition function.  
    Evaluate  $y_{i+1} = f(\mathbf{x}_{i+1})$ .  
    Add the sample to the dataset  $\mathcal{D}_{i+1} = \mathcal{D}_i \cup (\mathbf{x}_{i+1}, y_{i+1})$ .  
    Update the probabilistic model.  
end
```

Algorithm 1: Bayesian Optimization, Brochu et al. [2010]

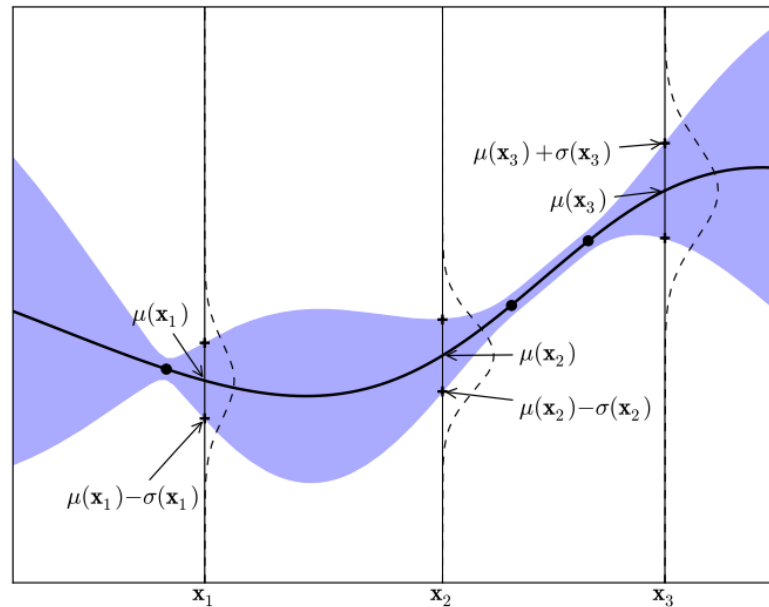
At its core, bayesian optimization only requires two things. A probabilistic regression model which combines prior beliefs $p(f)$ with the data. And an acquisition function which describes the optimality of the next sampling point.

2.1 Prior Distribution over Functions

Bayesian methods by definition require a prior distribution over the quantity of interest. Since we are building a probabilistic model over functions, we need to obtain a prior distribution over functions, which will capture our general beliefs about the properties of the objective function. For example, if we knew that our function was periodic, we would want a prior distribution over periodic functions. But in the case of hyperparameter optimization we will generally only consider continuous functions.

We will follow the general consensus of using a GP as a prior distribution over functions [Brochu et al., 2010], as it provides many nice theoretical properties, as well as tractable posterior inference. A GP is an extension of the multivariate Gaussian distribution to infinitely dimensional random variables. Just as a multivariate Gaussian can be thought of as a distribution over vectors, a GP can be thought of as a distribution over infinitely dimensional vectors, which when indexed by the real numbers are equivalent to functions. A GP assumes that any finite subset $\mathbf{x} = (\mathbf{x}_1, \dots, \mathbf{x}_n)$ is jointly Gaussian with some mean $\mathbf{m}(\mathbf{x})$ and covariance $\Sigma(\mathbf{x})$. A GP is defined by its mean function \mathbf{m} and covariance function k [Murphy and Bach, 2012]. We write

$$\mathcal{GP}(\mathbf{m}(\mathbf{x}), k(\mathbf{x}, \mathbf{x}')).$$



By convention, we assume that the prior mean is a constant zero function, that is $\mathbf{m}(\mathbf{x}) = 0$. Since the data is often normalized in practice, this does not reduce the flexibility of the model. The power of a GP comes from its covariance

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function, which for any two points x_i and x_j defines their covariance $k(x_i, x_j)$. If x_i and x_j have a high covariance, the values of the function at those points will be similar.

Intuitively, it is often useful to think of a GP as a function, which instead of returning a scalar $f(x)$ returns the mean and standard deviation of a Gaussian distribution over the possible values, centered at x . We leave a formal treatment of GPs until chapter 3.

2.2 Hyperparam vs. Architecture Search

Using our earlier definition, any parameter which the model does not learn on its own could be considered a hyperparameter. This definition is broad enough to allow a lot of flexibility, but some hyperparameters are better for the framework of bayesian optimization than others. Discrete and categorical hyperparameters require special consideration. Bayesian optimization itself is flexible in the sense that it allows for an arbitrary probabilistic model, but the specific choice does matter when we consider discrete values. In the case of GPs, the model itself does not have the ability to directly work with anything but continuous real valued vectors.

There has been some recent work [Garrido-Merchán and Hernández-Lobato, 2017] showing better approaches for handling integer valued variables. This is done by simply rounding the appropriate values before computing their covariance. As the kernel will see the values as equivalent, their covariance will be maximized, and the GP will be forced to predict a constant value over each integer region. While this approach does help a little bit with integer valued variables, it does not work for categorical (nominal) variables, which lack any form of ordering. If we simply treat them as integers, the GP prior will enforce relationships which do not exist.

An alternative approach to solving the problem with categorical variables is to use a different model than GPs, namely random forests [Shahriari et al., 2016]. Their main advantage is the ability to naturally handle various types of data. We however do not explore random forests in this work, as many of the hyperparameters of interest when tuning neural networks are either continuous or integer valued. Categorical variables, such as activation functions, are better suited to be tweaked as part of neural architecture search [Zoph et al., 2017].

Regardless of the probabilistic model, categorical variables cause many immediate problems. Consider the choice between SGD with momentum [Ruder, 2016] and Adam [Kingma and Ba, 2014]. While SGD with momentum has a *momentum* hyperparameter, Adam does not, but it has its own two extra hyperparameters, β_1 and β_2 . This gives us two different sets of mutually exclusive hyperparameters. Bayesian optimization however does not have any natural way of handling problems like this. Even if we did externally enforce two different modes based on which categorical values was chosen, it would essentially be the same as running two experiments in parallel, one with SGD, and one with Adam. Another issue arises in visualization, which is one of the goals of this work. Inspecting the samples from two or more different modes of the network at once is challenging at best, and with multiple categorical variables the problem grows exponentially.

For these reasons, we chose to not provide direct support for categorical variables, apart from converting them to integer variables with an ordering and treating them as such. Some categorical variables can be optimized by simply treating them as fixed within a particular experiment, and then running multiple instances of that experiment with a different value each. Other categorical variables, such as the types of layers, activation functions, or even the connections between modules, are better left for the framework of neural architecture search, which treats them in a principled way.

2.3 Related work

There are a few notable mentions of related work in the area of tuning hyperparameters of neural networks. The main motivation for this work, is Google Vizier [Golovin et al., 2017], which is a proprietary service at Google used for black box optimization. There also exist a few implementations of bayesian optimization. Spearmint [Group, 2014] is the most fully featured one, but comes with a very restrictive license, and does not perform any visualization of the results. GPy-Opt [authors, 2016] and scikit-optimize [Head et al., 2018] are the most notable libraries for bayesian optimization, but they only provide the basic optimization loop for bayesian optimization, and do not handle long running experiments in a possibly distributed environment.

3. Gaussian Processes

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This chapter goes into the technical details of the Gaussian distribution and its extension the Gaussian Process (GP). We think it is important to have at least a basic understanding of the underlying math to make intuitive claims about the behavior of the model, especially since GPs are a bit different from other parametric machine learning models.

Since our objective is bayesian optimization, we only derive the properties necessary for its implementation. Specifically, we are interested in the conditional and marginal distributions of a multivariate Gaussian. The conditional Gaussian distribution allows us to compute the posterior $p(f|x)$ at an arbitrary point, and the marginal allows us to fit a GP regression model to each hyperparameter separately for additional visualization.

Let us now continue with a more rigorous treatment of the Gaussian distribution. For a more thorough treatment see Bishop [2016] and Murphy and Bach [2012].

Definition 1. A random variable X has a **univariate Gaussian distribution**, written as $X \sim \mathcal{N}(\mu, \sigma^2)$, when its density is

$$p(x) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp \left\{ -\frac{1}{2\sigma^2}(x - \mu)^2 \right\}.$$

The parameters μ and σ are its mean and standard deviation.

Definition 2. We say X has a **degenerate Gaussian distribution** when $X \sim \mathcal{N}(\mu, 0)$.

Definition 3. A random variable $\mathbf{X} \in \mathbb{R}^n$ has a **multivariate Gaussian distribution** if any linear combination of its components is a univariate Gaussian, i.e. $\mathbf{a}^T \mathbf{X} = \sum_{i=1}^n \mathbf{a}_i \mathbf{X}_i$ is a Gaussian for all $\mathbf{a} \in \mathbb{R}^n$. We then write $\mathbf{X} \sim \mathcal{N}(\mu, \Sigma)$ where $\mathbb{E}[\mathbf{X}_i] = \mu_i$ and $\text{cov}(\mathbf{X}_i, \mathbf{X}_j) = \Sigma_{ij}$.

Remark. The parameters μ and Σ uniquely determine the distribution $\mathcal{N}(\mu, \Sigma)$.

Definition 4. A random variable $\mathbf{X} \sim \mathcal{N}(\mu, \Sigma)$ has a **degenerate multivariate Gaussian distribution** if $\det \Sigma = 0$.

Remark. Given a random variable $\mathbf{X} \sim \mathcal{N}(\mu, \Sigma)$, random variables $\mathbf{X}_1, \dots, \mathbf{X}_n$ are independent with distributions $\mathbf{X}_i \sim \mathcal{N}(\mu_i, \sigma_i^2)$ if and only if $\mu = (\mu_1, \dots, \mu_n)$ and $\Sigma = \text{diag}(\sigma_1^2, \dots, \sigma_n^2)$.

Theorem 1. If a random variable $\mathbf{X} \in \mathbb{R}^n$ is a multivariate Gaussian, then X_i, X_j are independent if and only if $\text{cov}(X_i, X_j) = 0$. Note that this is not true for any random variable, as it is a special property of the multivariate Gaussian.

Proof. TODO

□

Theorem 2. A Gaussian random variable $\mathbf{X} \sim \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Sigma})$ has a density iff it is non-degenerate (i.e. $\det \boldsymbol{\Sigma} \neq 0$, alternatively $\boldsymbol{\Sigma}$ is positive-definite). And in this case, the density is

$$p(\mathbf{x}) = \frac{1}{\sqrt{\det(2\pi\boldsymbol{\Sigma})}} \exp \left\{ -\frac{1}{2}(\mathbf{x} - \boldsymbol{\mu})^T \boldsymbol{\Sigma}^{-1}(\mathbf{x} - \boldsymbol{\mu}) \right\} \quad (3.1)$$

Remark. The normalizing constant in the denominator is also often in an alternate form as

$$\det(2\pi\boldsymbol{\Sigma}) = (2\pi)^n \det(\boldsymbol{\Sigma})$$

which follows from basic determinant properties. Alternatively we can also put the square root in the exponent $(2\pi)^{n/2}(\det \boldsymbol{\Sigma})^{1/2}$.

Remark. A special case of the multivariate gaussian is when $n = 1$, then Note that if $n = 1$, then $\boldsymbol{\Sigma} = \sigma^2$, meaning $\text{cov}(X, X) = \sigma^2$, $\boldsymbol{\Sigma}^{-1} = \frac{1}{\sigma^2}$, and hence the multivariate Gaussian formula becomes the univariate one

$$p(x) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp \left\{ -\frac{1}{2\sigma^2}(x - \mu)^2 \right\}. \quad (3.2)$$

3.1 Sampling

Even not of immediate interest for bayesian optimization, we will shortly show how to generate samples from a multivariate Gaussian, as this can be useful for visualization purposes with GPs.

Theorem 3. Given a random variable \mathbf{X} with $\text{cov}[\mathbf{X}] = \boldsymbol{\Sigma}$, it follows from the definition of covariance that $\text{cov}[\mathbf{A}\mathbf{X}] = \mathbf{A}\boldsymbol{\Sigma}\mathbf{A}^T$.

Proof.

$$\text{cov}[\mathbf{A}\mathbf{X}] = E[(\mathbf{A}\mathbf{X} - E[\mathbf{A}\mathbf{X}])(\mathbf{A}\mathbf{X} - E[\mathbf{A}\mathbf{X}])^T] \quad (3.3)$$

$$= E[(\mathbf{A}\mathbf{X} - \mathbf{A}E[\mathbf{X}])(\mathbf{A}\mathbf{X} - \mathbf{A}E[\mathbf{X}])^T] \quad (3.4)$$

$$= E[\mathbf{A}(\mathbf{X} - E[\mathbf{X}])(\mathbf{X} - E[\mathbf{X}])^T \mathbf{A}^T] \quad (3.5)$$

$$= \mathbf{A}E[(\mathbf{X} - E[\mathbf{X}])(\mathbf{X} - E[\mathbf{X}])^T] \mathbf{A}^T \quad (3.6)$$

$$= \mathbf{A}\text{cov}[\mathbf{X}]\mathbf{A}^T \quad (3.7)$$

$$= \mathbf{A}\boldsymbol{\Sigma}\mathbf{A}^T \quad (3.8)$$

□

Theorem 4. Given a random variable $\mathbf{X} \sim \mathcal{N}(\mathbf{0}, \mathbf{I})$ and a positive-definite matrix $\boldsymbol{\Sigma}$ with a cholesky decomposition $\boldsymbol{\Sigma} = \mathbf{L}\mathbf{L}^T$, then

$$\mathbf{L}\mathbf{X} \sim \mathcal{N}(\mathbf{0}, \boldsymbol{\Sigma}). \quad (3.9)$$

Proof. We can immediately use equation 3.8.

$$\mathbf{L}\mathbf{X} \sim \mathcal{N}(\mathbf{0}, \mathbf{L}\mathbf{I}\mathbf{L}^T) = \mathcal{N}(\mathbf{0}, \mathbf{L}\mathbf{L}^T) = \mathcal{N}(\mathbf{0}, \boldsymbol{\Sigma}) \quad (3.10)$$

□

Theorem 5. *Any affine transformation of a Gaussian is a Gaussian. In particular*

$$\mathbf{X} \sim \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Sigma}) \implies \mathbf{A}\mathbf{X} + \mathbf{b} \sim \mathcal{N}(\mathbf{A}\boldsymbol{\mu} + \mathbf{b}, \mathbf{A}\boldsymbol{\Sigma}\mathbf{A}^T)$$

for any $\boldsymbol{\mu} \in \mathbf{R}^n$, $\boldsymbol{\Sigma} \in \mathbf{R}^{n \times n}$ positive semi-definite, and any $\mathbf{A} \in \mathbf{R}^{m \times n}$, $\mathbf{b} \in \mathbf{R}^m$. We call this the **affine property** of a Gaussian.

Proof. Follows from the linearity of expectation together with Equation 3.9. \square

Since samples from $\mathcal{N}(\mathbf{0}, \mathbf{I})$ can be generated independently, using the affine property we can generate samples from an arbitrary multivariate Gaussian. All that is required is a procedure for cholesky decomposition, and a way of generating independent samples from a univariate gaussian, which can be achieved using the Box-Muller transform [Box, 1958].

3.2 Geometric Properties

If $\boldsymbol{\Sigma}$ is positive-definite, then $\mathbf{Y} \sim \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Sigma})$ implies $\mathbf{A}^{-1}(\mathbf{Y} - \boldsymbol{\mu}) \sim \mathcal{N}(\mathbf{0}, \mathbf{I})$ where $\boldsymbol{\Sigma} = \mathbf{A}\mathbf{A}^T$. The random variable $\mathbf{A}^{-1}(\mathbf{Y} - \boldsymbol{\mu})$ has a spherical shape in n -dimensional space.

Looking further at the density formula for a multivariate Gaussian (Equation 3.1) the term $(\mathbf{x} - \boldsymbol{\mu})^T \boldsymbol{\Sigma}^{-1} (\mathbf{x} - \boldsymbol{\mu})$ is called the Mahalanobis distance between \mathbf{x} and $\boldsymbol{\mu}$. If we consider $\boldsymbol{\mu}$ a constant, we can also view it as a quadratic form in \mathbf{x} . When $\boldsymbol{\Sigma}$ is an identity matrix, the Mahalanobis distance reduces to Euclidean distance. In general, it can be thought of as a distance on a hyper-ellipsoid. Let us now derive some intuition for this.

Since $\boldsymbol{\Sigma}$ is a covariance matrix, we know it is positive definite, and we can perform its eigendecomposition to get $\boldsymbol{\Sigma} = \mathbf{U}\boldsymbol{\Lambda}\mathbf{U}^T$, where \mathbf{U} is an orthogonal matrix of eigenvectors, and $\boldsymbol{\Lambda}$ is a diagonal matrix of eigenvalues. Basic matrix algebra gives us

$$\boldsymbol{\Sigma}^{-1} = (\mathbf{U}^T)^{-1} \boldsymbol{\Lambda}^{-1} \mathbf{U}^{-1} = \mathbf{U} \boldsymbol{\Lambda}^{-1} \mathbf{U}^T = \sum_{i=1}^D \frac{1}{\lambda_i} \mathbf{u}_i \mathbf{u}_i^T,$$

where the second to last equality comes from \mathbf{U} being orthogonal ($\mathbf{U}^{-1} = \mathbf{U}^T$). Substituting this in the Mahalanobis distance we get

$$(\mathbf{x} - \boldsymbol{\mu})^T \boldsymbol{\Sigma}^{-1} (\mathbf{x} - \boldsymbol{\mu}) = (\mathbf{x} - \boldsymbol{\mu})^T \left(\sum_{i=1}^D \frac{1}{\lambda_i} \mathbf{u}_i \mathbf{u}_i^T \right) (\mathbf{x} - \boldsymbol{\mu}) \quad (3.11)$$

$$= \sum_{i=1}^D (\mathbf{x} - \boldsymbol{\mu})^T \frac{1}{\lambda_i} \mathbf{u}_i \mathbf{u}_i^T (\mathbf{x} - \boldsymbol{\mu}) \quad (3.12)$$

$$= \sum_{i=1}^D \frac{y_i^2}{\lambda_i} \quad (3.13)$$

where $y_i = \mathbf{u}_i^T (\mathbf{x} - \boldsymbol{\mu})$ which has exactly the same form as a D dimensional ellipse. From this we conclude that the contour lines of a multivariate Gaussian will be elliptical, where the eigenvectors determine the orientation of the ellipse, and the eigenvalues determine the length of the principal axes [Bishop, 2016].

3.3 Conditional and Marginal Gaussian Distribution

In this section we derive the conditional $p(\mathbf{x}_1|\mathbf{x}_2)$ and marginal $p(\mathbf{x}_1)$ for a given joint distribution $p(\mathbf{x}_1, \mathbf{x}_2)$. One of the interesting properties of a multivariate Gaussian is that both the conditional and the marginal are also Gaussian, and we can easily compute their parameters in closed form based on the parameters of the joint distribution.

Before we derive the conditional and marginal distributions, let us state the partitioned inverse formula without proof.

Theorem 6 ([Murphy and Bach, 2012]). *Consider a partitioned matrix*

$$\mathbf{M} = \begin{bmatrix} \mathbf{E} & \mathbf{F} \\ \mathbf{G} & \mathbf{H} \end{bmatrix} \quad (3.14)$$

where we assume \mathbf{E} and \mathbf{H} are invertible. We have

$$\mathbf{M}^{-1} = \begin{bmatrix} (\mathbf{M}/\mathbf{H})^{-1} & -(\mathbf{M}/\mathbf{H})^{-1}\mathbf{F}\mathbf{H}^{-1} \\ -\mathbf{H}^{-1}\mathbf{G}(\mathbf{M}/\mathbf{H})^{-1} & \mathbf{H}^{-1} + \mathbf{H}^{-1}\mathbf{G}(\mathbf{M}/\mathbf{H})^{-1}\mathbf{F}\mathbf{H}^{-1} \end{bmatrix} \quad (3.15)$$

$$= \begin{bmatrix} \mathbf{E}^{-1} + \mathbf{E}^{-1}\mathbf{F}(\mathbf{M}/\mathbf{E})^{-1}\mathbf{G}\mathbf{E}^{-1} & -\mathbf{E}^{-1}\mathbf{F}(\mathbf{M}/\mathbf{E})^{-1} \\ -(\mathbf{M}/\mathbf{E})^{-1}\mathbf{G}\mathbf{E}^{-1} & (\mathbf{M}/\mathbf{E})^{-1} \end{bmatrix} \quad (3.16)$$

where

$$\mathbf{M}/\mathbf{H} = \mathbf{E} - \mathbf{F}\mathbf{H}^{-1}\mathbf{G} \quad (3.17)$$

$$\mathbf{M}/\mathbf{E} = \mathbf{H} - \mathbf{G}\mathbf{E}^{-1}\mathbf{F} \quad (3.18)$$

is called the **Schur complement**.

Proof. Since the proof is rather technical and only consists of applying the LDU decomposition and many algebraic manipulations, we leave it out and refer the reader to Murphy and Bach [2012] for details. \square

3.3.1 Conditional Distribution is a Gaussian

Suppose \mathbf{x} is a D -dimensional random vector with a multivariate Gaussian distribution $\mathcal{N}(\mathbf{x}|\boldsymbol{\mu}, \boldsymbol{\Sigma})$, and that \mathbf{x} is partitioned into two vectors \mathbf{x}_1 and \mathbf{x}_2 such that

$$\mathbf{x} = \begin{bmatrix} \mathbf{x}_1 \\ \mathbf{x}_2 \end{bmatrix} \quad (3.19)$$

We also partition the mean vector $\boldsymbol{\mu}$ and the covariance matrix $\boldsymbol{\Sigma}$ into a block matrix, and name the inverse of the covariance matrix $\boldsymbol{\Lambda} = \boldsymbol{\Sigma}^{-1}$, which will simplify a few of the equations that follow. We will derive the exact form of $\boldsymbol{\Lambda}$ and of its individual blocks later in this section. For now we simply use the fact that $\boldsymbol{\Sigma}$ is positive-definite, and thus it is invertible. The matrix $\boldsymbol{\Lambda}$ is also known as a **precision matrix**.

$$\boldsymbol{\mu} = \begin{bmatrix} \boldsymbol{\mu}_1 \\ \boldsymbol{\mu}_2 \end{bmatrix}, \boldsymbol{\Sigma} = \begin{bmatrix} \boldsymbol{\Sigma}_{11} & \boldsymbol{\Sigma}_{12} \\ \boldsymbol{\Sigma}_{21} & \boldsymbol{\Sigma}_{22} \end{bmatrix}, \boldsymbol{\Lambda} = \boldsymbol{\Sigma}^{-1} = \begin{bmatrix} \boldsymbol{\Lambda}_{11} & \boldsymbol{\Lambda}_{12} \\ \boldsymbol{\Lambda}_{21} & \boldsymbol{\Lambda}_{22} \end{bmatrix} \quad (3.20)$$

Note that since Σ is a symmetric matrix, $\Sigma_{12}^T = \Sigma_{21}$, and similarly $\Lambda_{12}^T = \Lambda_{21}$. Similarly, Σ_{11} , Σ_{22} , Λ_{11} , and Λ_{22} are all symmetrical.

Before we derive the parameters of the conditional, we show that the conditional distribution $p(x_1|x_2)$ is a Gaussian. To do this, we take the joint distribution $p(x_1, x_2)$ and fix the value of x_2 [Bishop, 2016]. Using the definition of conditional probability $p(x_1, x_2) = p(x_1|x_2)p(x_2)$ we can see that after fixing the value of x_2 , $p(x_2)$ is simply a normalization constant, and the remaining term $p(x_1|x_2)$ is a function of x_1 which together with the normalization constant gives us the conditional probability distribution on x_1 . We now use the partitioned form of the multivariate Gaussian defined by equation 3.20 to show that $p(x_1|x_2)$ is actually a Gaussian.

Let us begin by looking at the exponent in equation 3.1:

$$-\frac{1}{2}(\mathbf{x} - \boldsymbol{\mu})^T \boldsymbol{\Lambda}(\mathbf{x} - \boldsymbol{\mu}) = -\frac{1}{2} \left(\begin{bmatrix} \mathbf{x}_1 \\ \mathbf{x}_2 \end{bmatrix} - \begin{bmatrix} \boldsymbol{\mu}_1 \\ \boldsymbol{\mu}_2 \end{bmatrix} \right)^T \begin{bmatrix} \boldsymbol{\Lambda}_{11} & \boldsymbol{\Lambda}_{12} \\ \boldsymbol{\Lambda}_{21} & \boldsymbol{\Lambda}_{22} \end{bmatrix} \left(\begin{bmatrix} \mathbf{x}_1 \\ \mathbf{x}_2 \end{bmatrix} - \begin{bmatrix} \boldsymbol{\mu}_1 \\ \boldsymbol{\mu}_2 \end{bmatrix} \right) \quad (3.21)$$

$$= -\frac{1}{2} \begin{bmatrix} \mathbf{x}_1 - \boldsymbol{\mu}_1 \\ \mathbf{x}_2 - \boldsymbol{\mu}_2 \end{bmatrix}^T \begin{bmatrix} \boldsymbol{\Lambda}_{11} & \boldsymbol{\Lambda}_{12} \\ \boldsymbol{\Lambda}_{21} & \boldsymbol{\Lambda}_{22} \end{bmatrix} \begin{bmatrix} \mathbf{x}_1 - \boldsymbol{\mu}_1 \\ \mathbf{x}_2 - \boldsymbol{\mu}_2 \end{bmatrix} \quad (3.22)$$

To make the next few equations easier to follow we set $\mathbf{y}_1 = \mathbf{x}_1 - \boldsymbol{\mu}_1$ and $\mathbf{y}_2 = \mathbf{x}_2 - \boldsymbol{\mu}_2$.

$$-\frac{1}{2} \begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{bmatrix}^T \begin{bmatrix} \boldsymbol{\Lambda}_{11} & \boldsymbol{\Lambda}_{12} \\ \boldsymbol{\Lambda}_{21} & \boldsymbol{\Lambda}_{22} \end{bmatrix} \begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{bmatrix} = \quad (3.23)$$

$$= -\frac{1}{2} \begin{bmatrix} \mathbf{y}_1 \boldsymbol{\Lambda}_{11} + \mathbf{y}_2 \boldsymbol{\Lambda}_{21} \\ \mathbf{y}_1 \boldsymbol{\Lambda}_{12} + \mathbf{y}_2 \boldsymbol{\Lambda}_{22} \end{bmatrix}^T \begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{bmatrix} \quad (3.24)$$

$$= -\frac{1}{2} (\mathbf{y}_1^T \boldsymbol{\Lambda}_{11} \mathbf{y}_1 + \mathbf{y}_2^T \boldsymbol{\Lambda}_{21} \mathbf{y}_1 + \mathbf{y}_1^T \boldsymbol{\Lambda}_{12} \mathbf{y}_2 + \mathbf{y}_2^T \boldsymbol{\Lambda}_{22} \mathbf{y}_2) \quad (3.25)$$

$$\begin{aligned} &= -\frac{1}{2} (\mathbf{x}_1 - \boldsymbol{\mu}_1)^T \boldsymbol{\Lambda}_{11} (\mathbf{x}_1 - \boldsymbol{\mu}_1) + \\ &\quad -\frac{1}{2} (\mathbf{x}_2 - \boldsymbol{\mu}_2)^T \boldsymbol{\Lambda}_{21} (\mathbf{x}_1 - \boldsymbol{\mu}_1) + \\ &\quad -\frac{1}{2} (\mathbf{x}_1 - \boldsymbol{\mu}_1)^T \boldsymbol{\Lambda}_{12} (\mathbf{x}_2 - \boldsymbol{\mu}_2) + \\ &\quad -\frac{1}{2} (\mathbf{x}_2 - \boldsymbol{\mu}_2)^T \boldsymbol{\Lambda}_{22} (\mathbf{x}_2 - \boldsymbol{\mu}_2) \end{aligned} \quad (3.26)$$

We see that this is a quadratic form in \mathbf{x}_1 , and hence the corresponding conditional distribution $p(x_1|x_2)$ will be Gaussian. Because we know $p(x_1, x_2) = p(x_1|x_2)p(x_2)$ and that both $p(x_1, x_2)$ and $p(x_1|x_2)$ are multivariate Gaussians, fixing the value of x_1 means that $p(x_1|x_2)$ as a function of x_2 is just a normalization constant, and $p(x_2)$ must have the same form as $p(x_1, x_2)$ and therefore is also a multivariate Gaussian.

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Because the Gaussian distribution is completely defined by its mean and covariance, we do not need to figure out the value of the normalization constant. We simply have to derive the equations for $\boldsymbol{\mu}$ and Σ .

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We continue with the proof from Murphy and Bach [2012]. We will make use of the partitioned matrix inverse theorem Equation 3.16.

At this point we know that the joint distribution factors into two multivariate Gaussians, that is

$$p(\mathbf{x}_1, \mathbf{x}_2) = p(\mathbf{x}_1 | \mathbf{x}_2) p(\mathbf{x}_2) \quad (3.27)$$

$$= \mathcal{N}(\mathbf{x}_1 | \boldsymbol{\mu}_{1|2}, \boldsymbol{\Sigma}_{1|2}) \mathcal{N}(\mathbf{x}_2 | \boldsymbol{\mu}_2, \boldsymbol{\Sigma}_{22}) \quad (3.28)$$

and we only need to infer their parameters. To make the equations more readable, we again define

$$\mathbf{y}_1 = \mathbf{x}_1 - \boldsymbol{\mu}_1 \quad (3.29)$$

$$\mathbf{y}_2 = \mathbf{x}_2 - \boldsymbol{\mu}_2. \quad (3.30)$$

We then simply take the block definition of a multivariate Gaussian and multiply everything out

$$E = \exp \left\{ -\frac{1}{2} \begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{bmatrix}^T \begin{bmatrix} \boldsymbol{\Sigma}_{11} & \boldsymbol{\Sigma}_{12} \\ \boldsymbol{\Sigma}_{21} & \boldsymbol{\Sigma}_{22} \end{bmatrix} \begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{bmatrix} \right\} \quad (3.31)$$

$$= \exp \left\{ -\frac{1}{2} \begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{bmatrix}^T \begin{bmatrix} \mathbf{I} & \mathbf{0} \\ -\boldsymbol{\Sigma}_{22}^{-1} \boldsymbol{\Sigma}_{21} & \mathbf{I} \end{bmatrix} \begin{bmatrix} (\boldsymbol{\Sigma}/\boldsymbol{\Sigma}_{22})^{-1} & \mathbf{0} \\ \mathbf{0} & \boldsymbol{\Sigma}_{22}^{-1} \end{bmatrix} \begin{bmatrix} \mathbf{I} & -\boldsymbol{\Sigma}_{12} \boldsymbol{\Sigma}_{22}^{-1} \\ \mathbf{0} & \mathbf{I} \end{bmatrix} \begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{bmatrix} \right\} \quad (3.32)$$

$$= \exp \left\{ -\frac{1}{2} \begin{bmatrix} \mathbf{y}_1^T - \mathbf{y}_2^T (\boldsymbol{\Sigma}_{22}^{-1} \boldsymbol{\Sigma}_{21}) \\ \mathbf{y}_2 \end{bmatrix}^T \begin{bmatrix} (\boldsymbol{\Sigma}/\boldsymbol{\Sigma}_{22})^{-1} & \mathbf{0} \\ \mathbf{0} & \boldsymbol{\Sigma}_{22}^{-1} \end{bmatrix} \begin{bmatrix} \mathbf{y}_1 - \boldsymbol{\Sigma}_{12} \boldsymbol{\Sigma}_{22}^{-1} (\mathbf{y}_2) \\ \mathbf{y}_2 \end{bmatrix} \right\} \quad (3.33)$$

$$= \exp \left\{ -\frac{1}{2} \begin{bmatrix} (\mathbf{y}_1^T - \mathbf{y}_2^T \boldsymbol{\Sigma}_{22}^{-1} \boldsymbol{\Sigma}_{21}) (\boldsymbol{\Sigma}/\boldsymbol{\Sigma}_{22})^{-1} \\ \mathbf{y}_2^T \boldsymbol{\Sigma}_{22}^{-1} \end{bmatrix}^T \begin{bmatrix} \mathbf{y}_1 - \boldsymbol{\Sigma}_{12} \boldsymbol{\Sigma}_{22}^{-1} (\mathbf{y}_2) \\ \mathbf{y}_2 \end{bmatrix} \right\} \quad (3.34)$$

$$= \exp \left\{ -\frac{1}{2} (\mathbf{y}_1^T - \mathbf{y}_2^T \boldsymbol{\Sigma}_{22}^{-1} \boldsymbol{\Sigma}_{21}) (\boldsymbol{\Sigma}/\boldsymbol{\Sigma}_{22})^{-1} (\mathbf{y}_1 - \boldsymbol{\Sigma}_{12} \boldsymbol{\Sigma}_{22}^{-1} \mathbf{y}_2) \right\} \times \quad (3.35)$$

$$\times \exp \left\{ -\frac{1}{2} \mathbf{y}_2^T \boldsymbol{\Sigma}_{22}^{-1} \mathbf{y}_2 \right\}$$

We can immediately see that the second term is a quadratic form in \mathbf{x}_2 and corresponds to $\mathcal{N}(\mathbf{x}_2 | \boldsymbol{\mu}_2, \boldsymbol{\Sigma}_{22})$. Let us now consider the first term in isolation and move the terms around a little bit. We also make use of the fact that because $\boldsymbol{\Sigma}_{22}$ is a positive-definite matrix, its inverse is also symmetric, so $\boldsymbol{\Sigma}_{22}^{-1T} = \boldsymbol{\Sigma}_{22}^{-1}$. We also know that $\boldsymbol{\Sigma}_{12}^T = \boldsymbol{\Sigma}_{21}$.

$$E_{1|2} = \exp \left\{ -\frac{1}{2} (\mathbf{y}_1^T - \mathbf{y}_2^T \boldsymbol{\Sigma}_{22}^{-1} \boldsymbol{\Sigma}_{21}) (\boldsymbol{\Sigma}/\boldsymbol{\Sigma}_{22})^{-1} (\mathbf{y}_1 - \boldsymbol{\Sigma}_{12} \boldsymbol{\Sigma}_{22}^{-1} \mathbf{y}_2) \right\} \quad (3.36)$$

$$= \exp \left\{ -\frac{1}{2} (\mathbf{y}_1 - \boldsymbol{\Sigma}_{12} \boldsymbol{\Sigma}_{22}^{-1} \mathbf{y}_2)^T (\boldsymbol{\Sigma}/\boldsymbol{\Sigma}_{22})^{-1} (\mathbf{y}_1 - \boldsymbol{\Sigma}_{12} \boldsymbol{\Sigma}_{22}^{-1} \mathbf{y}_2) \right\} \quad (3.37)$$

$$= \exp \left\{ -\frac{1}{2} (\mathbf{x}_1 - \boldsymbol{\mu}_1 - \boldsymbol{\Sigma}_{12} \boldsymbol{\Sigma}_{22}^{-1} (\mathbf{x}_2 - \boldsymbol{\mu}_2))^T (\boldsymbol{\Sigma}/\boldsymbol{\Sigma}_{22})^{-1} \right. \quad (3.38)$$

$$\left. (\mathbf{x}_1 - \boldsymbol{\mu}_1 - \boldsymbol{\Sigma}_{12} \boldsymbol{\Sigma}_{22}^{-1} (\mathbf{x}_2 - \boldsymbol{\mu}_2)) \right\} \quad (3.39)$$

In equation 3.39 we again see a Gaussian density with parameters

$$\boldsymbol{\mu}_{1|2} = \boldsymbol{\mu}_1 + \boldsymbol{\Sigma}_{12}\boldsymbol{\Sigma}_{22}^{-1}(\mathbf{x}_2 - \boldsymbol{\mu}_2) \quad (3.40)$$

$$\boldsymbol{\Sigma}_{1|2} = (\boldsymbol{\Sigma}/\boldsymbol{\Sigma}_{22})^{-1} = \boldsymbol{\Sigma}_{11} - \boldsymbol{\Sigma}_{12}\boldsymbol{\Sigma}_{22}^{-1}\boldsymbol{\Sigma}_{21}. \quad (3.41)$$

This formula extremely important for the use of GPs as a probabilistic model in bayesian optimization. It will allow us to compute the exact parameters of the posterior $p(f|\mathbf{x})$ at any given point, and as a result compute the acquisition function.

3.4 Gaussian Processes

Gaussian Process is a stochastic process (a collection of random variables), such that every subset of those random variables has a multivariate Gaussian distribution. It is defined by a mean function $m(\mathbf{x})$ and a covariance function $\kappa(\mathbf{x}, \mathbf{x}')$. Formally, we write

$$p(\mathbf{x}) \sim \mathcal{GP}(m(\mathbf{x}), \kappa(\mathbf{x}, \mathbf{x}')). \quad (3.42)$$

Any finite subset $\mathbf{x} = (\mathbf{x}_1, \dots, \mathbf{x}_n)$ is jointly Gaussian with mean $m(\mathbf{x})$ and covariance $\boldsymbol{\Sigma}(\mathbf{x})$ where $\boldsymbol{\Sigma}(\mathbf{x})_{ij} = \kappa(\mathbf{x}_i, \mathbf{x}_j)$, where κ is any positive definite kernel function [Murphy and Bach, 2012].

The GP defines a prior distribution over functions f , which when combined with data \mathbf{x} can be converted into a posterior distribution over functions $p(f|\mathbf{x})$.

3.4.1 GP regression with noise-free observations

Consider the case when we are interested in predicting a function f based on a few observations $\mathcal{D} = \{(\mathbf{x}_1, y_1), \dots, (\mathbf{x}_n, y_n)\}$, and we are interested in predicting the value of y_* at a new point \mathbf{x}_* .

Using the definition of a GP, we know that \mathbf{y} and y_* are jointly Gaussian. We also know, that these are the only points we are interested in. Even though the GP is a distribution over functions, that is over infinitely dimensional vectors, we only need to look at finitely many points and can ignore the rest. This is a crucial property of the GP and essentially makes everything we are about to do possible.

By assuming a GP, we get all of the properties of a multivariate Gaussian for free, including a closed form solution to the conditional and marginal distribution parameters. Let us now write the joint distribution of \mathbf{y} and \mathbf{y}_* in a partitioned form

$$\begin{pmatrix} \mathbf{y} \\ \mathbf{y}_* \end{pmatrix} \sim \mathcal{N} \left(\begin{pmatrix} \boldsymbol{\mu} \\ \boldsymbol{\mu}_* \end{pmatrix}, \begin{pmatrix} \mathbf{K} & \mathbf{K}_* \\ \mathbf{K}_*^T & \mathbf{K}_{**} \end{pmatrix} \right)$$

where $\mathbf{K} = \kappa(\mathbf{X}, \mathbf{X})$, $\mathbf{K}_* = \kappa(\mathbf{X}, \mathbf{X}_*)$ and $\mathbf{K}_{**} = \kappa(\mathbf{X}_*, \mathbf{X}_*)$ [Williams and Rasmussen, 2006]. Note that \mathbf{y} and \mathbf{y}_* can be either single points, or they can be vectors, as we might be interested in computing the posterior over multiple points at once given an existing dataset. Because this is just a multivariate Gaussian, we can make use of the conditioning formula and compute the posterior

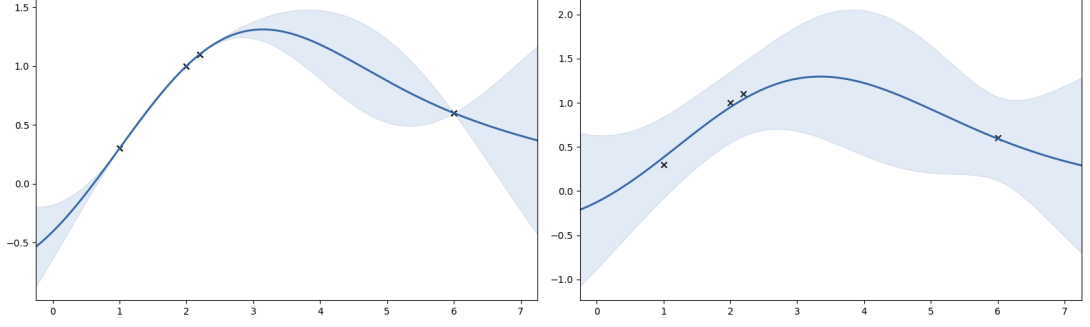


Figure 3.1: GP regression without noise on the left, and with a constant amount of noise added on the right.

$p(\mathbf{y}_\star | \mathbf{X}_\star, \mathbf{X}, \mathbf{y})$ exactly as

$$p(\mathbf{y}_\star | \mathbf{X}_\star, \mathbf{X}, \mathbf{y}) = \mathcal{N}(\mathbf{y}_\star | \boldsymbol{\mu}_\star, \boldsymbol{\Sigma}_\star) \quad (3.43)$$

$$\boldsymbol{\mu}_\star = \boldsymbol{\mu}(\mathbf{X}_\star) + \mathbf{K}_\star^T \mathbf{K}^{-1}(\mathbf{y} - \boldsymbol{\mu}(\mathbf{X})) \quad (3.44)$$

$$\boldsymbol{\Sigma}_\star = \mathbf{K}_{\star\star} - \mathbf{K}_\star^T \mathbf{K}^{-1} \mathbf{K}_\star. \quad (3.45)$$

where $\boldsymbol{\mu}_\star$ is the mean and $\boldsymbol{\Sigma}_\star$ the covariance of the multivariate Gaussian on \mathbf{y}_\star .

3.4.2 GP regression with noisy observations

Consider the case when f is not a deterministic function, but rather a stochastic function which returns a noisy output \mathbf{y} given some fixed input \mathbf{x} (meaning $f(\mathbf{x})$ is a random variable). GP regression is flexible enough to model Gaussian noise in the output directly. For now, let us consider the noise having a fixed variance σ^2 .

In practice, the noise becomes a baseline for the variance of each point of the posterior, as the variance can never be lower than the noise. Since the variance is represented on the diagonal of the covariance matrix computed by the kernel function κ , we can model the noise directly by simply adding a diagonal matrix to the output of the kernel, that is

$$\text{cov}(\mathbf{y}) = \kappa(\mathbf{X}, \mathbf{X}) + \sigma^2 \mathbf{I}.$$

See Figure 3.4.2 for a comparison of noise-less and noisy regression. It should also be noted that in principle nothing is preventing us from specifying a different noise value for each element of the diagonal. This could be useful if we had additional prior information about the function f . It could, for example, be an output of a measurement for which we know exactly the amount of noise for each \mathbf{x} .

3.4.3 Kernels

So far we have considered the covariance function κ to be an arbitrary positive-definite kernel. Even though in theory there are no restrictions on what kernel we can choose, there are a few more popular choices that are commonly used.

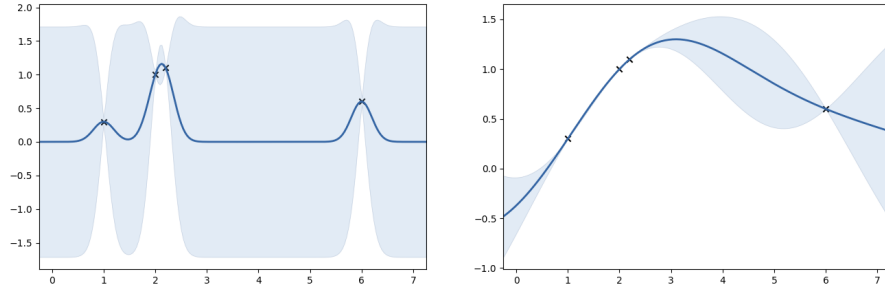


Figure 3.2: Lengthscale $l = 0.2$ on the left, and $l = 2$ on the right.

A prototypical example is the squared exponential (SE) kernel, also called the radial-basis function (RBF) kernel

$$\kappa(\mathbf{x}_1, \mathbf{x}_2) = \sigma_k^2 \exp \left\{ -\frac{1}{2l} (\mathbf{x}_1 - \mathbf{x}_2)^2 \right\}.$$

This kernel, among many others, falls under the category of stationary kernels. A **stationary kernel** is one which is shift-invariant, which means its value does not depend on the absolute values of \mathbf{x}_1 and \mathbf{x}_2 , but only on their distance $d = |\mathbf{x}_1 - \mathbf{x}_2|$. We can thus write it as

$$\kappa(\mathbf{x}_1, \mathbf{x}_2) = \sigma_k^2 \exp \left\{ -\frac{1}{2l} d^2 \right\}.$$

The values σ_k and l are called the variance and lengthscale, and control the behavior of the kernel, where σ_k changes the vertical scale of the function, and l changes the horizontal scale. Changing the lengthscale essentially allows the kernel to re-normalize the data. If \mathbf{x} is a vector we can define a lengthscale parameter l_i for each of the components. This becomes very useful in the context of hyperparameters where each hyperparameter can have a very different scale, and the individual lengthscale per component allows the kernel to capture it.

Figure Figure 3.4.3 show how the behavior of the kernel changes based on the changed value of the lengthscale l . When the lengthscale is set too low the values of \mathbf{y} become essentially uncorrelated, leading to a function with many spikes. On the other hand, a larger value for the lengthscale yields a much smoother function.

3.4.4 Optimizing GP hyperparameters

So far we have considered the noise, variance and lengthscale parameters to be fixed, but in this section we show how their value can be determined automatically from the data using maximum likelihood estimation.

Since the GP is a probabilistic model, we can ask it directly what is the likelihood of our data. Using the definition of a GP, we know that the likelihood of our data is a multivariate Gaussian, that is $p(\mathbf{y}|\mathbf{X}) = \mathcal{N}(\mathbf{y}|\mathbf{0}, \mathbf{K})$, giving us a log likelihood of

$$\log p(\mathbf{y}|\mathbf{X}) = -\frac{1}{2} \mathbf{y} \mathbf{K}^{-1} \mathbf{y} - \frac{1}{2} \log \det \mathbf{K} - \frac{N}{2} \log(2\pi).$$

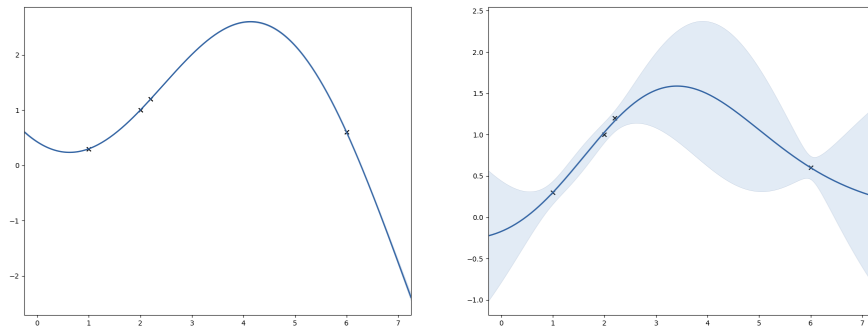


Figure 3.3: GP regression without optimizing kernel parameters on the left, and after optimizing using maximum likelihood on the right. Notice that the noise parameter is also optimized, as the regression model does not go directly through the data points, but instead considers the small variation as due to noise.

We leave out the technical details (see Williams and Rasmussen [2006] for more details) including the gradient of the marginal likelihood with respect to the kernel parameters, as they do not provide any useful insights.

One important detail we want to stress out is that computing K^{-1} takes $O(N^3)$, which puts a serious restriction on the size of the data we can fit with exact GP regression. This does not concern us in the context of hyperparameter optimization as we would always stay within low hundreds of evaluations anyway, but for other tasks it becomes a serious limitation. As a result many workarounds for approximate inference were developed [Williams and Rasmussen, 2006], which again, we omit from this text, because they are not relevant for hyperparameter optimization.

Implementing the kernel parameter optimization is easy in practice. One can simply implement the marginal likelihood formula shown in subsection 3.4.4 and use a package for automatic differentiation with an optimizer like SGD or L-BFGS to optimize the parameters. Since the objective is non-linear, a common practice [GPy, since 2012] is to optimize with multiple restarts. Figure 3.4.4 shows the effect of optimizing kernel parameters using maximum likelihood.

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4. Bayesian Optimization in depth

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4.1 Acquisition functions

An intuitive choice for an acquisition function is to maximize the probability of improving over our currently best achieved value, which is called the **probability of improvement**. This can be computed in closed form as

$$PI(\mathbf{x}) = \Phi\left(\frac{\mu(\mathbf{x}) - y_{\max}}{\sigma(\mathbf{x})}\right)$$

where y_{\max} is the maximum value achieved by sampling $f(\mathbf{x})$.

A natural extension is the **expected improvement** (EI) acquisition function which is simply the expected improvement over the currently achieved maximum. We define it as

$$EI(x) = \mathbb{E}[f(x) - y_{\max}].$$

At first it might seem that the expectation would be an intractable integral, but fortunately even this equation can be computed in closed form as

$$EI(x) = \Delta(x) + \sigma(x)\varphi\left(\frac{\Delta(x)}{\sigma(x)}\right) - |\Delta(x)|\Phi\left(\frac{\Delta(x)}{\sigma(x)}\right)$$

where $\Delta(x) = \mu(x) - y_{\max}$. In practice, improvement shows better results than probability of improvement. For more examples of acquisition functions see Frazier [2018].

In both of these cases, the next sampling point would be chosen by maximizing the acquisition function, that is

$$x_{\text{next}} = \arg \max_x EI(x)$$

for the case of expected improvement. This can again be done by any stochastic optimizer, such as the commonly chosen L-BFGS with restarts.

4.2 Parallel evaluations

In practice we might have the ability to evaluate $f(\mathbf{x})$ at multiple points in parallel, but the framework we have shown so far only allows for sequential optimization. In the previous section we've shown a few examples of the acquisition functions. A natural extension would be to not optimize with respect to a single x_{next} , but rather multiple points. In the context of EI this is called **parallel expected improvement**.

Unfortunately, there is no simple solution [Frazier, 2018]. A common solution is the so called **Constant Liar** approximation, which chooses \mathbf{x}_{i+1} assuming \mathbf{x}_i was already chosen, and has the corresponding value y_i equal to a constant, often chosen to be the expected value of $f(\mathbf{x}_i)$ under the GP posterior.

This allows us to trivially implement parallel evaluations by simply considering the μ prediction for unfinished evaluations as their y value and consider them part of the dataset \mathcal{D} .

4.3 Integer parameters

GP regression by itself does not have the ability to model integer values in X directly as some other models do (e.g. random forests chapter 2). A common solution, used by [Group, 2014] and which we also implement in this thesis, is to consider all parameters to be real valued and only round them at the end.

In recently published work by Garrido-Merchán and Hernández-Lobato [2017] they show a more principled approach. The effect of rounding causes the model to see variation and relationships even among constant-valued regions. A possible downside is that the model could predict values different enough so that the acquisition function would obtain a maximum within a constant region which already has an existing sample, and thus wasting an evaluation. A proposed solution to this problem, as mentioned in the paper, is to round the appropriate values right before they are input into the kernel function, such as

$$\kappa'(\mathbf{x}_1, \mathbf{x}_2) = \kappa(T(\mathbf{x}_1), T(\mathbf{x}_2))$$

where $T(\mathbf{x})$ is an identity for real valued elements and a rounding function for integers.

Our implementation however does not use this approach, as our GP regression is handled by the GPy [since 2012] library, which did not support it at the time, and implementing it would mean overriding many of the existing kernels. We did instead handle the problem explicitly by detecting the pathological cases, as described in chapter 5.

4.4 Logscale

When optimizing hyperparameters we might want to distinguish not only between real and integer valued ones, but also based on their scale. Optimizing the number of training epochs or layers are very well modelled by a linear scale, but a learning rate is better modelled with a logarithmic scale.

We provide a simple solution, which can work independently of Bayesian optimization, by simply transforming all of the appropriate value to logscale before inputting them into the model, and then transforming them back after we get a next sample x proposal.

4.5 Bayesian Optimization Algorithm in Detail

We will now show the algorithm for Bayesian optimization in greater detail as compared to 1. Let $\mathcal{D}_n = \{(\mathbf{x}_i, y_i), i \in 1 : n\}$ denote a set of n samples (eval-

uations) of the objective function f , that is $y_i = f(\mathbf{x}_i)$. Our goal is to pick the next \mathbf{x}_{n+1} to maximize our chance of finding the optimum quickly, assuming that already enough points were evaluated for us to fit the GP. 2 shows one iteration of Bayesian optimization as it picks \mathbf{x}_{n+1} .

Let \mathbf{X} be the matrix of all \mathbf{x}_i , and \mathbf{y} be a column vector of all y_i

Maximize the kernel log-likelihood

$p(\mathbf{X}) = -\frac{1}{2}\mathbf{y}\mathbf{K}^{-1}\mathbf{y} - \frac{1}{2}\log \det \mathbf{K} - \frac{N}{2}\log(2\pi)$, where $\mathbf{K} = \kappa(\mathbf{X}, \mathbf{X})$, by tuning the kernel hyperparameters

Maximize the acquisition function $A(\mathbf{X}, \mathbf{y}, \mathcal{GP})$ as a function of the GP using the kernel hyperparameters obtained in the previous step.

Sample $y_{n+1} = f(\mathbf{x})$ where $\mathbf{x} = \arg \max A(\mathbf{X}, \mathbf{y}, \mathcal{GP})$.

Add y_{n+1} to the dataset as $\mathcal{D}_{i+1} = \mathcal{D}_i \cup (\mathbf{x}_{i+1}, y_{i+1})$.

Algorithm 2: Bayesian Optimization with implementation details.

While the above shown algorithm is enough to explain how Bayesian optimization works, there are a few cases where numerical issues can arise, and we point them out next.

Firstly, the quadratic form $\mathbf{y}\mathbf{K}^{-1}\mathbf{y}$ does not need to be computed using a matrix inverse procedure, which can be numerically unstable and requires more intermediate computation (see Krishnamoorthy and Menon [2013] for details). In general, consider the equation $\mathbf{Ax} = \mathbf{b}$. We can instead write $\mathbf{x} = \mathbf{A}^{-1}\mathbf{b}$ for an invertible matrix \mathbf{A} . A naive solution would use a procedure for an inverse and then multiply to compute $\text{inv}(\mathbf{A})\mathbf{b}$, but because we do not actually need the inverse itself, but rather the multiplication, we can solve for $\mathbf{A}^{-1}\mathbf{b}$ directly using a `solve` procedure [van der Walt et al., 2011].

Because the \mathbf{K} matrix is a covariance matrix we also know it is positive definite. This allows us to take the computation one step further and compute its Cholesky factorization $\mathbf{L} = \text{chol}(\mathbf{K})$, and then use a procedure for `solve` directly on the factorized matrix \mathbf{L} (in TensorFlow available as `tf.linalg.cholesky_solve`).

Having just computed the Cholesky factorization we can re-use it in the second expression of the marginal log-likelihood, that is the $\log \det \mathbf{K}$, since

$$\log \det \mathbf{K} = \log \det(\mathbf{L}^T \mathbf{L}) = \log(\det(\mathbf{L}^T) \cdot \det(\mathbf{L})) = \quad (4.1)$$

$$= 2 \cdot \log \det \mathbf{L} = 2 \cdot \log \prod \text{diag } \mathbf{L} = 2 \cdot \sum \log \text{diag } \mathbf{L} \quad (4.2)$$

This allows us to compute the determinant, which is usually $O(n^3)$, in just linear time, because we're re-using the work already being done in the Cholesky factorization used in the previous step.

Another interesting note, discovered by our initial custom implementation, and confirmed in the implementation of the GPy [GPy, since 2012] library, is that when computing a Cholesky factorization of a covariance matrix computed on real world data, it will often fail for numerical reasons, and requires additional noise to be added to the diagonal to improve stability. What GPy does internally is to iteratively increase the amount of noise, up until some threshold, to make sure the factorization succeeds without any problems, while not adding excessive noise when not needed.

Lastly, the optimization procedures themselves used for maximizing the kernel log-likelihood and acquisition function can be sensitive. Our initial implementa-

tion in SciPy and TensorFlow showed very different restarts based on the type of optimizer (SGD, Adam, L-BFGS), and its meta-parameters, such as the number of restarts, stop tolerance criterion, learning rates, etc. These problems, along with the many numerical issues encountered along the way, contributed to the choice of using GPy for the final implementation. We outline a few more reasons in section 5.2.

5. Software

- co umime - vizualizace - jak se to pousti, runnery, serializace

This chapter describes the implementation part of this thesis. While we do not provide any theoretical extensions to Bayesian optimization, we instead provide a modular and fully working implementation which was tested on multiple experiments. The implementation is provided as a Python (van Rossum [1995]) package called **bopt** (short for Bayesian optimization).

The main features of the package are:

- Flexible experiment configuration with random search and GP backends.
- Parallel execution of evaluations, both on the local machine and on a cluster.
- Robust error handling with duplicate/similar sample detection.
- Command line interface for controlling the experiment evaluations, including running a manual evaluation with user specified hyperparameters.
- Simple filesystem based storage with user-readable and editable serialization format based on YAML.
- Web based visualizations of the whole optimization process, including 1D and 2D slices and marginal plots at all points during the evaluation.

5.1 Architecture

In this section we will explore the high level architecture of **bopt**. Everything is structured around a central class **Experiment**, which represents a single objective function together with a configuration of its hyperparameters, and configuration for the Bayesian optimization itself. The **Experiment** can contain multiple **Samples**, where each sample represents a single evaluation of the objective function.

We assume the function being optimized can be evaluated by running a script file. The hyperparameters will be passed as command line arguments, and the output will be parsed from the standard output using a regular expression provided by the user. This provides the user with maximum flexibility with regards how the actual function is being executed, as **bopt** will simply spawn the process, pass the command line arguments, and then wait for it to terminate to collect the output and parse the result. If the result is not found in the output, or the process exists with an exit code greater than 0 it will mark the evaluation as failed. We do not put any restrictions on the type of script the user might want to provide. It is solely at the discretion of the **Runner** (see subsection 5.1.2) to figure out how to run the provided file.

Each **bopt** experiment is located in its own directory on the filesystem (called the **meta_dir**), where it stores all of the information in a single **meta.yml** file, along with output files for each job. This makes it easy for the user to manually inspect and edit if needed, or even backup when performing more complicated

operations, such as deleting specific samples, or manually adding samples from a different experiment. Since Bayesian optimization is memory-less, that is always starting from scratch, the user can easily combine evaluations from multiple different experiments by hand, or even delete samples which were created by accident, such as when using manual evaluations.

5.1.1 Samples, Result Collection and Locking

Each evaluation of the objective function is split into two parts. One being the **Sample**, which contains the specific hyperparameter values for \mathbf{x} , kernel parameters of the GP model which was used to compute the sample, a posterior prediction of its mean and variance, and then the second part, which is an optional **Job** instance, which represents the actual running evaluation. The **Job** simply wraps the running process

Each **Sample** can also have an optional **Job**, which only wraps the process ID with runner-specific information on how to get the status of the running job, kill it, etc. The **Sample** only represents a snapshot at one point in time. Every time a **bopt** command is executed, or whenever a new state is required, a *result collection procedure* will be called, which checks the status of all running jobs, and updates their respective samples with any results or failure information. This is done mainly to avoid race conditions, as the evaluations themselves are running asynchronously from the main program flow in **bopt**. Apart from the collection procedure and a few exceptions, such as starting a new job, the main data structure is considered read only.

It is also worth mentioning, that since multiple instances of **bopt** could be running at any given time, we have employed a file locking mechanism which creates a **.lockfile** file in the experiment directory, which any other **bopt** instance would detect and wait on release. This allows the user to use the command line utilities while an experiment is running without worrying about data corruption.

5.1.2 Runners

Training neural networks is a computationally intensive task, and tuning hyperparameters makes it an order of magnitude more expensive. As a result, running some experiment on a local computer might not be an option for the user. The package was designed with different evaluation environments in mind and provides a flexible concept of a **Runner** class, which abstracts away the process of starting a new evaluation, that is figuring out how and where to run the script file representing the objective function.

We provide two different runners out of the box:

Local runs the process on the same machine as **bopt**.

SGE submits a job to the Son of Grid Engine [sge].

All runners support job parallelism using the Constant Liar approximation (see section 4.2), which is part of the reason why each **Sample** stores a mean prediction. This value is being used as y whenever a new evaluation point needs to be chosen during parallel evaluations.

When a job is started, its stdout and stderr will be redirected to a file within an `output` directory in the `meta_dir`. The file will be named with a process ID (PID) in case of a *local* job, and with a job ID in case of an *SGE* job. In case of the local runner we have to employ a minor trick, because when `popen` is being called with stdout redirection it already requires a file handle, but at that time the process ID is unknown. We work around this by creating a temporary file, redirecting the output to that, and then after `popen` returns a PID we rename the opened temporary file to a new name with the PID. Since UNIX systems can handle renaming of open files this workaround causes no issues, but the behavior on Microsoft Windows is unclear. If the user needs to support Microsoft Windows they might have to provide their own runner which does not use PIDs, but rather generates the ID based on some other process which makes the ID available before the child process is spawned. The SGE runner does not run into this issue, because we only specify the filename as a parameter to `qsub`, which then handles the process scheduling, creation, redirection, and names the output file accordingly.

5.2 GPy

Our library of choice for GP regression is the GPy [since 2012] library, as it is the most stable and robust package available, and is still being actively developed. We're mainly interested in the `GPy.models.GPRegression` class which implements the regression model itself, and the `GPy.kern` module, which implements the kernel functions. We initially used our own custom implementation of GP regression (partly shown in section 4.5) in TensorFlow [Abadi et al., 2015] and SciPy [Jones et al., 2001–], but despite the seemingly short and simple numeric algorithm for computing the regression, getting all the details right proved to be an exceedingly difficult task. Even simple numerical methods like Cholesky decomposition are often wrapped with layers of numerical stability tricks that one does not get out of the box with libraries like NumPy [van der Walt et al., 2011].

For these reasons we ended up switching to the GPy library, which apart from a numerically stable implementation provides many additional benefits. Being built upon a general purpose parameter optimization library `par`, GPy allows the user to both put arbitrary constraints on each of the parameters, as well as specify a prior distribution which is then used when optimizing the kernel marginal likelihood.

5.3 Random Search

The core optimization loop has the ability to generate samples randomly, which is useful for two reasons. It allows us to create a comparative baseline where all samples are generated using random search, so that we can measure the benefits and improvement of Bayesian optimization. But it also serves as a way of bootstrapping the Bayesian optimization driven search. When choosing an initial first point of evaluation, we don't have any data to fit the model to. We could optimize the acquisition function on the prior, but since our prior has zero mean,

it would simply be a uniform distribution. What we do instead is sample each hyperparameter randomly, until we have enough points to fit the probabilistic model.

The number of random samples can increase if we are using parallel evaluations, simply because if we need to start N jobs at the same time, with no prior data, we have no way of even calculating a mean prediction. As a result, we always start the first N evaluations using random search.

5.4 Command Line Interface

Since larger experiments will most likely always be run on a compute cluster we opted for a command line interface which can be easily used over an SSH connection, and is very flexible. The available subcommands of `bopt` are:

- init** Creates a new experiment with a given script, configuration of hyperparameters and runner options.
- exp** Prints out the current status of a given experiment, showing metadata on all the evaluations.
- web** Starts the web interface for visualizing the evaluations.
- run** Starts a run loop which tracks how many jobs are currently running, starting new as needed to fulfill the parallelism requirements, and collects the results as needed.
- run-single** Runs a single evaluation, regardless of how many are currently running.
- manual-run** Runs a single evaluation with hyperparameters provided by the user. This does not use Bayesian optimization and simply serves as an interface to manually start tasks as needed.
- suggest** Prints a suggestion for the next evaluation without running it, as well as an already formatted command for `manual-run` so that the user can inspect the hyperparameter values and run the command immediately if they see fit.
- debug** Starts a Python debugger with the given experiment loaded in, which can be useful both for diagnosing issues as well as exploring the internal data structures.
- clean** Kills all running jobs and removes all evaluations from the experiment, while keeping the initialization metadata. This command is basically just a shortcut for re-starting an experiment from scratch.

All commands are executed as `bopt COMMAND` and support the conventional `--help` command line argument, which prints out all of the available options, as well as their descriptions.

5.4.1 Meta Directory, Data Corruption, -C and Locks

When an experiment is initialized all of its information will be stored in its own directory. This includes both the meta information about hyperparameters, run configurations and evaluations, as well as the job outputs themselves.

The `bopt` command was designed such that it will always try to acquire an exclusive lock on the directory using a `.lockfile`, which is to prevent any race conditions and possible data corruption from running multiple instances of `bopt` at the same time. Such scenario could easily occur when the user would run a long running `bopt run` command, while also exploring the results, and possibly starting a few more evaluations manually using `bopt run-single`, `bopt manual-run`, or even another `bopt run`. Because of the locking behavior, it is completely safe to run as many instances of `bopt` as are needed, and the user does not need to concern themselves with causing any data corruption via the command line interface. We also make sure to always serialize the data into a new file, and then atomically move over the existing one, in order to minimize possible data corruption when the `bopt` process is killed.

It is important to note that `bopt` was designed with manual user intervention in mind. As such, the `meta.yml` file, which contains all of the experiment information, was created to be easily human editable. But because `bopt` does not use the UNIX `flock` mechanism (as editors do not obey it), the user has to be wary of editing the file by hand while other instances of `bopt` are running. Because the `meta.yml` file is overwritten atomically, the user can even edit the file while `bopt` is running, but they have to make sure to save at the appropriate time, e.g. not to discard the changes that were just written after the file was loaded in the editor. This problem is unlikely to occur in editors like Vim, which will notify the user of the file being changed after it was read, but it still does not prevent the user to overwrite it. If there are no existing `bopt` processes running, it is completely safe to alter the `meta.yml` file.

All of the `bopt` commands will also accept a `-C` command line argument, which specifies a directory to `cd` into before any of the main code is executed (similarly as a `Makefile` would behave). This behavior allows `bopt` to always assume it is being executed from within the `meta_dir` and simplify many possible problems with storing paths in the config files. While this behavior is unlikely to affect the user in a negative way, it is still useful to know the semantics of the program.

We now explore two of the most important commands in more detail, `bopt init` and `bopt run`.

5.4.2 `bopt init`

Initializing experiments is an important feature and as such the command line interface has been streamlined to allow the user to input the arguments without complicated config files. An example of a common `bopt init` call could look something like the following:

```
bopt init \  
--param "batch_size:int:4:128" \  
--param "gamma:logscale_float:0.5:1.0" \  
--param "lr:logscale_float:1e-6:1e-1" \  

```

```

--param "dropout:float:0.1:0.6"
-C experiments/reinforce \
--runner sge \
--ard=1 --gamma-prior=1 \
--gamma-a=1.0 --gamma-b=0.001 \
$PWD/reinforce.sh

```

Let us now go over the arguments one by one. The first four arguments specify four different hyperparameters, namely `batch_size`, `gamma`, `lr` and `dropout`, each with a different type and range. The general format is `NAME:TYPE:MIN:MAX` where `NAME` can be an arbitrary name, `TYPE` can be one of `int`, `float`, `logscale_int`, `logscale_float`, and `discrete`, and `MIN:MAX` are simply the bounds of the hyperparameter. If the type of `discrete` is specified, instead of providing the bounds the user would provide a colon separated list of possible values, which would then be encoded as ordinal integers. An example of that could be `activation:discrete:tanh:relu`. However, as mentioned in section 2.2, we do not recommend using `bopt` for architecture search, which discourages from most uses of the `discrete` type.

The next argument `-C experiments/reinforce` simply defines the `meta_dir` where the experiment data will be stored. Next we define the runner type, which can be one of `local` and `sge`.

After the runner is defined, we configure the GP regression itself, in this case by specifying the `ard` flag on, which uses a separate lengthscale parameter for each component of x (more details can be found in the `?` documentation). Next we specify that we want to use a Gamma prior on the hyperparameters, and its shape and scale parameters. A complete list of all flags for configuring the GP regression, acquisition function, kernel and the optimizer can be found using the help flag as `bopt init --help`.

Lastly, we provide `bopt` with the script to run, in this case it is `reinforce.sh`, which encapsulates our objective function. We also specify it as an absolute path using the `PWD` environment variable, but this is shown mainly as an interesting trick that can be useful if the `PATH` is not configured in the environment where the runner will execute the job.

After the command exists, it will create a directory `experiments/reinforce` with a `meta.yml` file inside. The following listing shows the contents of the file

```

gp_config: !!python/object:bopt.gp_config.GPConfig
  acq_n_restarts: 25
  acq_xi: 0.001
  acquisition_fn: ei
  ard: true
  gamma_a: 1.0
  gamma_b: 0.001
  gamma_prior: true
  kernel: Mat52
  num_optimize_restarts: 10
  random_search_only: false
hyperparameters:
  batch_size:
    high: 128

```

```

    low: 4
    type: int
  gamma:
    high: 1.0
    low: 0.5
    type: logscale_float
  hidden_layer:
    high: 128
    low: 2
    type: int
  learning_rate:
    high: 0.1
    low: 1.0e-06
    type: logscale_float
  result_regex: RESULT=(.*)
  runner:
    arguments: []
    manual_arg_fnames: []
    qsub_arguments: []
    runner_type: sge_runner
    script_path: ./reinforce.sh
  samples: []

```

Apart from the command line arguments we have provided it should be noted that a few unspecified values were filled in with the defaults. For example, the kernel function was chosen to be the default Matérn 5/2 kernel, which was shown [Snoek et al., 2012] to perform the best on many hyperparameter tuning tasks. We have tried to make the optimization procedure as configurable as possible in case the user has any additional prior knowledge which might help them optimize better.

5.4.3 `bopt run`

After the experiment was initialized the user can start running evaluations. Since everything is already configured in the `meta.yml` file the user simply needs to run `bopt run -C experiments/reinforce`, or `cd` into the directory and just run `bopt run`. Both of these variants are equivalent.

By default, this would run 20 evaluations in total with no parallelism. The number of evaluations can be controlled with the `--n_iter` switch, while the number of jobs running in parallel is controlled by the `--n_parallel` switch.

The way `bopt run` tracks the number of running jobs is by checking the `meta.yml` file for the IDs, and then checking the job status and counting how many are running. This allows it to respect the number of jobs running prior to the execution of `bopt run`. If the user first was to start say 5 evaluations by hand (e.g. using `bopt run-single`) and only then run `bopt run --n_parallel=5` while the first 5 jobs were still running, the instance of `bopt run` would correctly identify the running jobs and wait for some of them to finish before launching new ones.

5.5 Visualizations

6. Experiments

- toy tasky - porovnani existujici fce na optimalizaci - srovnani acq/kernel, random search (ze to neco dela)
 - maly ulohy
 - velka uloha
 - interpretace vysledku
- experimenty
 - parser - tokenizer/segmentace - speech recognition - opennmt lemmatizace - *reinforce_with_baseline*

Conclusion

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List of Abbreviations

A. Attachments

A.1 First Attachment