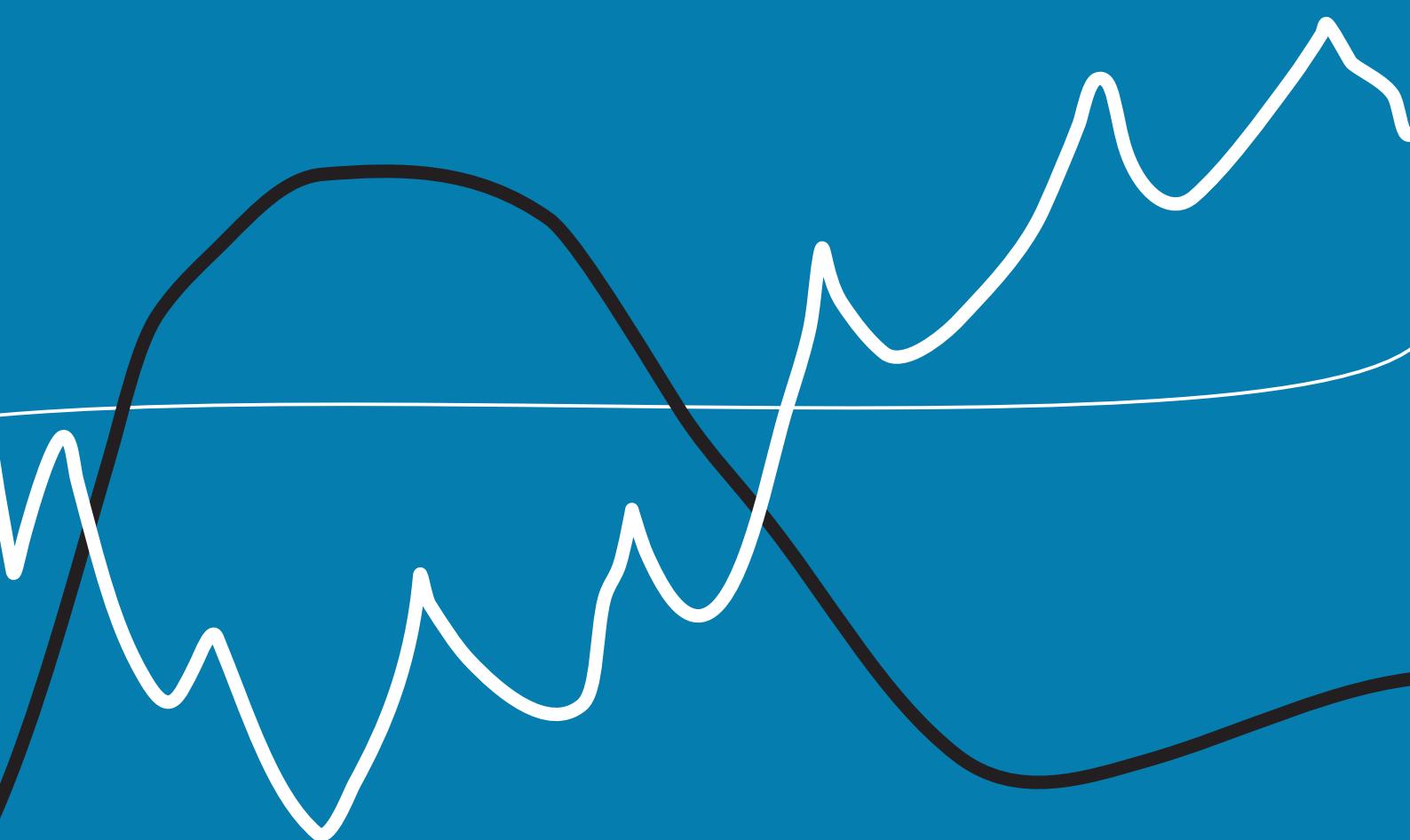


Investigation of Deep Probabilistic Surrogate-models in Bayesian Optimization

Master Thesis



Abstract

Bayesian optimization is the leading way in sample-efficient optimization and widely used in hyperparameter tuning in machine learning and deep learning.

However, from a decision theory standpoint, assuming the probabilistic surrogate model to be correct is crucial for the correct decision. We will investigate if other surrogate models could be better than a GP.

This thesis investigates surrogate models such as Mixture regression, SPNs and BNN and compare against GP.

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1 Introduction

Optimization plays an important part in our everyday life, science development, product design, and much more. Examples of optimization could be choosing the optimal way to commute from A to B, deciding what songs should land on your playlist, or constructing the strongest possible bridge using limited material. In general, optimization is the methodology of choosing the best decision among a set of possible decisions. Often we try to quantify how good a decision is: A specific bus takes 20 min to go from A to B, you rate a specific song 4 out of 5, and a particular bridge design costs 10 million DKK. Suppose it is possible to come up with a quantification of how good a decision is in terms of a real number. In that case, we can formulate the optimization problem as a *mathematical optimization problem* [1, p. 123]:

$$\min_{x \in \mathcal{X}} f(x)$$

where the functional $f : \mathcal{X} \rightarrow \mathbb{R}$ is called the *objective function* and \mathcal{X} is the set of possible decisions (or decisions you consider). Note that the optimization problem is formulated as a minimization problem. If one identifies the optimal decision as a maximum of f (instead of the minima), finding the minima in the negated objective function $-f(x)$ is equivalent. Throughout this thesis, we refer to optimization as minimizing the objective function. Solving the mathematical optimization problem is an active research field, and many algorithms have been developed to find the minimum of the function $f(\cdot)$ [1].

Evaluation of the objective function can be cheap (e.g., if it just requires summing/multiplying numbers) or highly expensive (e.g., if it involves human rating, large simulation, or physical experiments). In the latter case, we want to avoid evaluating the objective function as much as possible - we want to use *sample-efficient* optimization. The overall topic of this thesis, *Bayesian optimization* (BO), is one of the preferred frameworks for sample-efficient optimization [2].

Bayesian optimization is a probabilistic surrogate-based optimization methodology: Assuming some initial samples $\{(x_1, f(x_1)), \dots, (x_n, f(x_n))\}$ from a highly expensive objective, a cheap (surrogate) function is fitted to the samples. The next sample is found by minimizing the surrogate, and the process is repeated. Bayesian optimization seeks to enhance this procedure with probability theory, where the surrogate function becomes a probabilistic (Bayesian) regression model. The most common surrogate model is a Gaussian Process (GP), as it encapsulates the uncertainty very well, and its inference procedure (computing answers to probability queries like $p(y|x)$) is exact.

Even though GP has proven suitable for many cases, there will be problems where its assumptions do not hold. For example, the commonly seen GP with an isotropic kernel (covariance between two points is invariant to translation in input) yields a strong assumption about the continuity of the objective function and that the objective function behaves similarly throughout the domain \mathcal{X} . In Figure 1.1 we see an example of how the GP's uncertainty quantification is going wild due to a discontinuity in the underlying objective function. in some areas, it is prevalent to have these discontinuities, for instance, in material discovery, where it is well known that materials often change very suddenly [3]. To accommodate the strong assumptions of the GP the literature introduces more flexible kernel functions; however, this introduces additional hyperparameters. Since we often only deal with a small amount of data, tuning and computation of these more complex GPs can be significantly challenging [3].

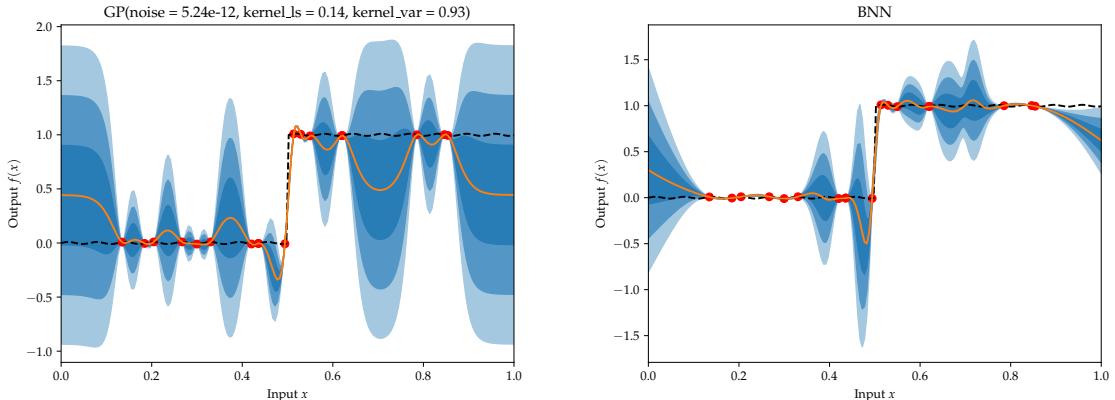


Figure 1.1: Gaussian process (GP) and Bayesian neural network (BNN) fitted to 18 data points. The objective function is the dashed black line. This exemplifies how a discontinuity makes the standard implemented GP (optimized with empirical Bayes) overreact to all other areas in the domain $[0, 1]$, while the Bayesian NN only express uncertainty where the discontinuity happens at $x = 0.5$

GPs are attractive models since they allow for exact inference, a closed-form expected improvement (see Section 2.3.1) and, in general, give a good uncertainty quantification. However, as we saw in the figure 1.1 we can maybe do better - especially if we have some insights into the behavior of the objective function (i.e. yielding a more transparent black-box optimization problem). A better surrogate model ultimately implies fewer samples to reach an optimal solution, and can, thereby, potentially save work hours, lots of money, or energy (depending on what makes the objective function expensive). Therefore, the investigation of the performance of other surrogate models is highly relevant. In this thesis, we aim to create surrogate models alternative to GPs, which can perform better on certain classes of (complex) problems, and just as well on most classes of problems.

1.1 Project limitation

Even though, it would be interesting to also look at different types of GPs such as deep kernel learning, we limit the scope of the project to deal with the following surrogate models:

- GP with Matérn kernel
- Bayesian neural network
- Mixture regression (Gaussian mixture, kernel density estimator, sum-product networks)

and we choose only to test the Bayesian optimization with the widely used acquisition function: *expected improvement*. Furthermore, we only deal with problems in continuous domains $\mathcal{X} \in \mathbb{R}^m$.

1.2 Contribution

This thesis investigates surrogate models alternative to the isotropic GP - more concretely Bayesian NN and mixture regression. The proposed hypotheses are,

1. There exists classes of BO problems where GP is not a preferred model.
2. Mixture regression models like SPN can be an effective surrogate model performing better than GPs and Neural Networks in some complex BO problems.

Note what is meant by performance is *sample efficiency*, i.e., how few evaluations/samples of the objective function are necessary to find the minima. So here it is assumed that the objective

function is so expensive (whatever that means to the stakeholder) that its cost outweigh the power and time spend on the surrogate modeling and optimization.

1.3 Related work

Here we give a short overview of research in different surrogates for Bayesian optimization and the very related field of active learning. The different surrogate models, which are in the research we found,

- Gaussian process
- Bayesian neural network
- Random forest regression
- Kernel density estimator
- Bayesian multivariate adaptive regression splines (BMARS)
- Bayesian additive regression trees (BART)

Since inference time of the GP scales cubic with the number of samples, often research in alternative surrogate models have its primary focus on lowering the computational complexity of inference while showing the sample efficiency is (or almost is) as good as the GPs. A popular model in the current time is a (deep) neural network and using a neural network as a probabilistic surrogate model (i.e. Bayesian Neural Network [4] or as basisfunctions in linear regression [5]) yields only linear complexity. However, as mentioned above, this thesis assumes that the objective function is always more costly than the inference cost. And cubic complexity for a GP does not matter for the small number of samples, which is often the case for highly expensive Bayesian optimization problems.

Inference complexity is also the main focus of the Ph.D. thesis "Sample-efficient Optimization Using Neural Networks" from 2020 [6], but his chapter 3 showcases empirically that using Bayesian neural networks as surrogate models performed better, or at least comparable to GPs on a wide number of problems. The performance difference was more evident for high-dimensional problems.

The 2021 nature paper "Bayesian optimization with adaptive surrogate models for automated experimental design" [3], focus on the sample efficiency of the BO applied to autonomous materials discovery, which yields a relatively high-dimensional design space and non-smooth patterns of objective functions. The paper shows that using Bayesian multivariate adaptive regression splines and Bayesian additive regression trees as alternative surrogate models outperform GP significantly, for complex BO problems.

Active learning is closely related to Bayesian Optimization, but here the focus is on learning the underlying function using as few samples as possible instead of just finding its minima. In active learning, a Gaussian process is also very common, but the paper "Active Learning with Statistical Models" [7] investigates using Gaussian mixtures and kernel estimator in active learning, i.e. as a surrogate model for selecting the next samples. These are regression models not seen much in the literature, which is modeling the joint distribution of x and y , and using the conditional distribution $p(y|x)$ as the regression model. The results were ... ??

1.4 Structure of the thesis

The structure of the thesis is first to build up the foundation around Bayesian optimization, then present different surrogate/Bayesian regression models, and then results on different types of problems are shown first on Bayesian regression and next on Bayesian optimization. Finally, a discussion and conclusion.

1. **Introduction to Bayesian optimization**, first by establishing its relevance as a sample-efficient solver, next by understanding its components: An acquisition function and a surrogate/Bayesian regression model.
2. **Discriminative models as surrogates**: Gaussian processes and Bayesian neural networks are presented and discussed in terms of inference procedures and regression performance.
3. **Generative(/mixture) models as surrogates**: Since the mixture models are not inherently Bayesian, we present the conditional distribution in a Bayesian setting. Next, the three different mixture regression models are presented: Kernel density regression, Gaussian mixture regression, and the novel (in a regression setting) Sum-product networks.
4. **Results** on regression performance and on Bayesian Optimization performance (sample-efficiency)
5. **Discussion and conclusion**

1.5 Notation

Following is the general notation used in the thesis, but some chapters (e.g. about GPs) will alter the notation a bit.

- y : Observation or sample at a given x .
- $x \in \mathcal{X}$: Location or point in the sample space.
- \mathbf{x} : Set of location or points in the sample space.
- \mathbf{y} : Set of observations or samples for corresponding \mathbf{x} .
- \mathcal{D} : Collection of samples in the optimization landscape.
- $\mathcal{N}(x|\mu, \Sigma)$: The density of a normal distribution evaluated in x .
- *optimization landscape*: joint set of points in the domain and the objective function evaluated in the points, i.e. $\{(x, f(x)) \in \mathcal{X} \times \mathbb{R} | x \in \mathcal{X}\}$.

1.5.1 Bayesian notation

Throughout this thesis we will be using Bayesian notation, i.e. $p(x) := P(X = x)$ is the probability density function of the random variable X evaluated in x . and $p(y|x) := P(Y = y|X = x)$ or $p(y|x) := P(Y|X = x)$. And writing $p(y^2|x)$ means $P(Y^2 = y^2|X = x)$ and **not** $P(Y = y^2|X = x)$

We will refer to y as an observation or sample at a given location or point x . This terminology will fit into the intuitive way of understanding an optimization problem as a (high dimensional) *landscape*, where the objective function is the altitude in the landscape. We refer to *optimization landscape* as the joint set of points in the domain and the objective function evaluated in the points, i.e. $\{(x, f(x)) \in \mathcal{X} \times \mathbb{R} | x \in \mathcal{X}\}$. Since the evaluation of $f(\cdot)$ might be noisy or imprecise, we just observe $y = \text{observe}(x)$. The typical connection between $f(x)$ and y are $y = f(x)$ or $y = f(x) + \epsilon$, where ϵ is additive white noise, but different connections might be present as well.

2 Bayesian Optimization

This chapter will introduce Bayesian optimization. We start with a general introduction to the concept of optimization (mainly based on [8]), which culminates with the introduction of the idea of Bayesian optimization (BO). Next, we dive into the first BO component: The Bayesian regression methodology. Finally, the concept of an acquisition function is introduced, with a focus on expected improvement and a brief description of the other types.

2.1 Optimization methodology

Given an objective function $f : \mathcal{X} \rightarrow \mathbb{R}$, where the domain \mathcal{X} could be a subset of \mathbb{R}^{n^1} , optimization is a methodology which seeks to find an optimal point, x^* , and value $f^* = f(x)$, given as

$$x^* \in \arg \min_{x \in \mathcal{X}} f(x), \quad f^* = \min_{x \in \mathcal{X}} f(x) = f(x^*). \quad (2.1)$$

Solving this problem (close to) exact is often intractable except for rare cases e.g. if f is convex and analytically directly solvable or the domain of f is very limited. The following example with linear least squares is an example of such a problem.

Example: Direct solution method

The unconstrained linear least squares,

$$\min_{x \in \mathbb{R}^n} f(x) := \|Ax - b\|_2^2$$

where $A \in \mathbb{R}^{m \times n}$ and $b \in \mathbb{R}^m$, is a convex problem, i.e. finding x^* such that $\nabla f(x^*) = 0$ is equivalent to finding the solution to the problem. Assuming $A^T A$ is invertable, linear least squares can be solved directly by the normal equations,

$$\nabla f(x) = 2A^T Ax + 2b^T A = 0 \quad \Leftrightarrow \quad x^* = (A^T A)^{-1} A^T b$$

Even if the gradient is given analytically, the problem can be non-convex, implying that the solution is found among a potentially infinitely large set of stationary points ($\nabla f(x) = 0$) or (for constraint problems) KKT points [1] - this might be tedious or impossible. Therefore, when the problem is not directly solvable, mathematical optimization takes an indirect approach: Design a sequence of experiments that reveal information about the objective function. This information can hopefully lead us to the solution of (2.1). This general way of sequentially solving is presented in the book "Bayesian Optimization" [8] and presented here as Algorithm 1.

Algorithm 1 Sequencial Optimization [8]

```

Input: Initial dataset  $\mathcal{D}$  ▷ can be empty
while Termination is not reached do
     $x \leftarrow \text{policy}(\mathcal{D})$  ▷ select next observation location
     $y \leftarrow \text{observe}(x)$  ▷ observe objective function at chosen location
     $\mathcal{D} \leftarrow \mathcal{D} \cup \{(x, y)\}$  ▷ update dataset
return:  $\mathcal{D}$ 

```

¹The thesis only work with this subset $\mathcal{X} \subset \mathbb{R}^n$

Given data points in the *optimization landscape* a policy selects a location $x \in \mathcal{X}$ where we make our next observation. Policies can be deterministic or probabilistic; examples of each type could be grid search and random search. The next observation provides us a $y = f(x)$ value², which combined with x is included in the available data \mathcal{D} . Finally, a stopping criterion decides whether to repeat or terminate the procedure. We will now present how different examples of well-known optimization routines fits into Algorithm 1.

Grid search

In grid search values along each dimension in \mathcal{X} is selected and combined with each other, which thereby defines a parallel grid in the optimization domain \mathcal{X} . All grid points are ordered and systematically selected. In the context of algorithm 1 we define the grid search policy as

$$\text{policy}_{GS}(\mathcal{D}) = x_{|\mathcal{D}|+1},$$

assuming $x_1, x_2, \dots, x_m \in \mathcal{X}$ are the ordered grid points and the size of the obtained data is $|\mathcal{D}|$. Termination will happen when $|\mathcal{D}| = m$.

Random search

In random search a point is randomly drawn from a uniform distribution supported over the domain space \mathcal{X} ,

$$\text{policy}_{RS}(\mathcal{D}) = x, \quad x \sim \text{Unif}(\mathcal{X}).$$

Gradient descent

Gradient descent (GD) is the most simple gradient-based optimization approach. The gradient of a continuous function points in the most ascending direction at the location it is evaluated. GD iteratively minimize the objective function by taking steps using opposite gradient direction, i.e. the most descending direction, weighted with a stepsize η . This yields the policy:

$$\text{policy}_{GD}(\mathcal{D}) = x_n - \eta \nabla f(x_n)$$

where we, for a brief moment, in Algorithm (1) modify y to be a vector since the observation is given as:

$$\text{observe}_{GD}(x) = [f(x), \nabla f(x)]$$

2.1.1 Sample-efficient optimization

Note that grid search, random search, and gradient descent are policies that entirely ignore the available data. Ignoring potentially valuable information is a shame if the objective function is expensive to evaluate. And indeed, improvements of the gradient descent algorithm, such as momentum and quasi-newton methods, indirectly remember and exploit obtained data, \mathcal{D} . They are examples of so-called *sample-efficient* solvers since they need fewer y -samples to minimize $f(\cdot)$. Choosing a more sample-efficient solver ultimately costs extra time/energy, due to the extra work of storing and exploiting the collected information for every iteration. In the end, solving the optimization problem can be divided into the following components,

- N_{iter} : The number of iterations to reach an acceptable solution. This number depends on the solver. If N_{iter} is relatively small, the solver is called sample-efficient.

²Since the evaluation of $f(\cdot)$ might be noisy or imprecise, we more generally write $y = \text{observe}(x)$. The typical connection between $f(x)$ and y are $y = f(x)$ or $y = f(x) + \epsilon$, where ϵ is additive white noise, but different connections might be present as well.

- C_{policy} : The solvers cost per iteration, i.e. what is the cost of calculating policy(\mathcal{D}), where cost is typically in terms of time and power usage.
- C_{observe} : Cost per evaluation of the objective function, i.e. the cost of observe(x), which can be in terms of power consumption, human resources, simulation time etc.

Assuming same cost pr iterations and for all evaluations, the total optimization cost, C_{total} , is given as

$$C_{\text{total}} = N_{\text{iter}} \cdot [C_{\text{policy}} + C_{\text{observe}}]$$

A sample efficient solver has a large C_{policy} and a small N_{iter} , which is completely opposite for a simple optimization scheme like random search. Choosing the right optimization solver depends highly on C_{observe} . For small C_{observe} it is favorable to find a good trade-off between N_{iter} and C_{policy} : In deep learning the solver Adam is very popular, due to its cheap but advanced policy [9]. This project deals with a dominating observation cost, i.e. the cost of the policy is assumed neglectable $C_{\text{observe}} \gg C_{\text{policy}}$. So focus is not on finding a cheap policy, but rather on improving the number of iterations to reach the minima N_{iter} .

Surrogate-based optimization

In surrogate-based optimization all available data is fitted by a cheap-to-evaluate approximation to the objective function - this approximation is called a *surrogate model*, $f_{\text{sur}}(x)$. Examples of surrogate models could be a radial basis function or a support vector regressor [10]. The next point is chosen as the point where the surrogate model is minimized.

$$\text{policy}_{\text{sur}}(\mathcal{D}) = \min_x f_{\text{sur}}(x)$$

where $f_{\text{sur}}(x) \approx f(x)$ for x close to the data \mathcal{D} . And we hope the approximation holds for x far away from the the data.

Figure 2.1 illustrates the idea of a sample-efficient solver; the solver adapts the obtained data into its decision and, thereby, faster discovers the minimum.

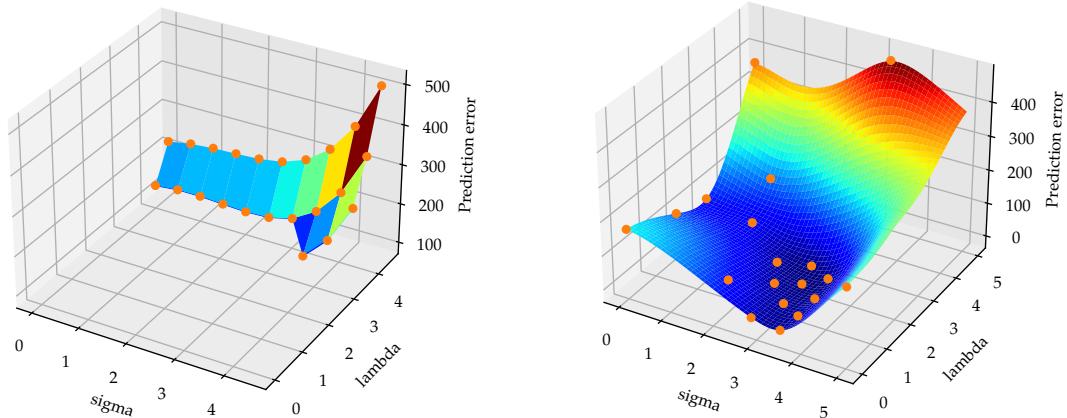


Figure 2.1: Example of an optimization task tuning a parameterised regression model with parameters λ and σ , on a test set, i.e. minimization of prediction error. We see the first 23 evaluations out of 100 in grid search vs 23 evaluations using a sample-efficient solver (Bayesian optimization).

2.1.2 Exploitation and exploration

The balance between an optimization procedure's local/exploitation and global/exploration elements is key to its performance (statement in thesis [6] ok?). Explained here:

1. Local element: Exploiting the obtained information \mathcal{D} to find the best point
2. Global element: Obtaining new information about the characteristics of the objective function.

Essentially, the only explorative phase of the deterministic surrogate optimization is the first initial samples from the objective, i.e. when creating the initial \mathcal{D} . If done poorly, the optimization might get stuck in a local minimum. This is a consequence of their nonexisting ability to express uncertainty about the objective function. Deterministic surrogate models do not pay attention to less-explored regions, which is the essential characteristic of a global optimization method [11].

Bayesian formalism is a powerful and sound tool for incorporating uncertainty into the surrogate model. Prior to any observed data, we can easily integrate our beliefs about the distribution of the objective function. When observing data, the likelihood and prior collaborate to create a predictive (posterior) distribution, $p(y|x, \mathcal{D})$. The next location x to explore is now determined with a theoretically motivated policy (acquisition function) which might balance the exploitation and exploration tradeoff.

Moreover, Bayesian optimization (or *probabilistic* surrogate-based optimization) is motivated by its ability to deal with noisy objective functions.

2.1.3 Noisy objective functions

Many optimization algorithms (e.g. gradient descent and grid search) assume *exact* evaluations of the objective function. However, this assumption is often wrong, especially for objective functions with real-life experiments, imperfect simulations, and human interaction where measurement noise is well known. A potentially noisy objective function is the main reason why we in Algorithm (1) use the terminology *observe*(x) and not just *evaluate*($f(x)$). The observation model is typically noisy and described as

$$y = f(x) + \epsilon,$$

where ϵ is the measurement error, this is typically assumed to be Gaussian with zero mean and a variance σ^2 (which could depend on x in a heteroskedastic setting) and implies a Gaussian observation model,

$$p(y|f(x), \sigma_x^2) = \mathcal{N}(y|f(x), \sigma_x^2)$$

where $f(x)$ is the mean value and σ_x^2 is the variance (with the subscript indicating the potentially dependency on x).

Note: "Sampling" from objective function

The terminology *to sample* is referring to a probabilistic observation model. Formally, we can extend this model to deal with noiseless observations as well, simply by setting $\sigma = 0$ and letting the model collapse into a Direct delta distribution, $p(y|f(x)) = \delta(y - f(x))$, i.e. all probability mass for y is on the value $f(x)$ giving the observation sample $y = f(x)$.

Bayesian optimization or probabilistic surrogate-based optimization deals with both noiseless and noisy objective functions, as it defines a Bayesian regression model over the observations.

Bayesian Optimization

Bayesian optimization is a *probabilistic* surrogate-based optimization methodology. Here a cheap probabilistic regression model $p(y|x)$ is fitted to the observations \mathcal{D} and in contrast to (deterministic) surrogate-based optimization, it is not possible right away to find the minima in the cheap surrogate model; first, we need to interpret the meaning of minima in a probabilistic regression model. This interpretation is done through a so-called acquisition function (AQ) - more about this later. The policy is as following,

$$\text{policy}_{BO}(\mathcal{D}) = \max_x AQ(p(y|x, \mathcal{D}))$$

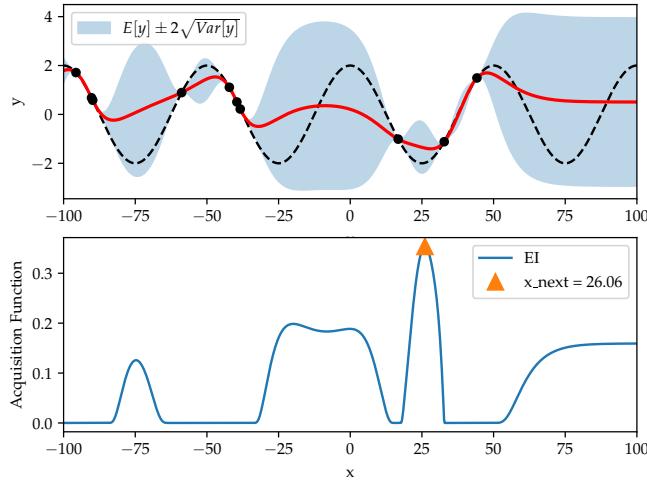


Figure 2.2: Top: Bayesian regression model (Gaussian Process) is fitted to the observed data, which are sampled from the underlying objective (black sin-function). Bottom: The expected improvement *acquisition function* is maximized at the orange arrow, i.e. the location of the next sample.
 $\text{policy}_{BO}(\mathcal{D}) = 26.06$

2.2 Bayesian regression

Whereas traditional regression workflow is the following: Given data, choose the best fitting model parameters, make predictions using those parameters. The Bayesian framework allows us to skip the dependency of a single set of parameters and instead use *all possible* parameters by treating the set of parameters as a random quantity, $\theta \sim p(\theta|\mathcal{D})$, where some values/realizations of θ are more probable than others given data. In Bayesian regression we are interested is the predictive posterior distribution,

$$p(y|x, \mathcal{D}) = \int p(y, \theta|x, \mathcal{D}) d\theta \quad (2.2)$$

$$= \int p(y|x, \theta)p(\theta|\mathcal{D})d\theta, \quad (2.3)$$

where the posterior $p(\theta|\mathcal{D})$ gives weighting to the proposed regression model $p(y|x, \theta)$. Note that the second equation is true because of the probability chain rule and that y is fully described by the parametric model $p(y|x, \theta)$ and the parameters θ are fully described by the posterior distribution $p(\theta|\mathcal{D})$.

2.2.1 Surrogate model

A surrogate model in a Bayesian optimization setting is a Bayesian regression model. The most used surrogate model is a Gaussian Process. But there have been investigations on other surrogates, such as Bayesian neural networks and Bayesian regression trees. These are all discriminative models, and another approach we focus on in this project is to model y and x jointly in a so-called

generative model, $p(x, y)$. A generative model can be used implicitly as a surrogate from the conditional distribution of y given x , $p(y|x)$.

In this thesis, the Bayesian regression models investigated as Bayesian optimization surrogates are the following:

- Gaussian process (GP)
- Bayesian neural network (BNN)
- Kernel density regression (KDE)
- Gaussian mixture regression (GMR)
- Sum-product networks (SPN)

We now introduce the concept of inference, which is necessary for using the probabilistic surrogate models in Bayesian Optimization.

2.2.2 Inference of surrogate models

Inference is the process of computing answers to queries about a probabilistic model after observing data. In Bayesian regression, the query is the predictive distribution, $p(y|x, \mathcal{D})$, as we are interested in the distribution of y given x and already observed data, \mathcal{D} . This often indirectly create the posterior query, $p(\theta|\mathcal{D})$, the probability of model parameters θ given data \mathcal{D} . Lastly, it is also inference when we train a Gaussian mixture model or SPN using the expectation-maximization algorithm (EM) since we are iteratively answering the query $E_{p(z|\theta^{(k)})}[z|\theta]$.

We distinguish between two different ways of inference: Exact and approximate inference. It is *exact inference* when a probabilistic query is calculated exact. It is possible to calculate exact inference on the predictive distribution for the Gaussian mixture model, Sum product network, and Gaussian processes. Models which allow for exact inference have a powerful advantage over the models with approximate inference since we can guarantee the answers to the queries are correct; however, they are usually also less expressive (unable to explain complicated models).

When it is not possible to answer a probabilistic query exact, we can approximate the answer using *approximate inference*. When dealing with complicated and expressive statistical models, exact inference is often intractable, and we need to use approximate inference. Approximate inference is a broad category of methods, which includes variational inference and Markov chain Monte Carlo (MCMC). The two Bayesian Neural networks, we deal with in this project, Bohamiann and Numpyro BNN are similar regression models but are inferred using two different MCMC methods, Hamiltonian Monte Carlo - giving different results. As revealed later (see in section 3.2) approximate inference might be flawed and inexact.

Model	Predictive inference	Learning
GP	Exact $O(n^3)$	Emperical Bayes
Numpyro BNN	No U-Turn Sampler	
Bohamiann BNN	Adaptive stochastic HMC	
Kernel density regression	Exact $O(n)$	
Gaussian mixture regression	Exact $O(K)$	EM
SPN	Exact $O(E)$	EM $O(E)$

Table 2.1: Overview of inference methods applied on the statistical models used in this project. E is the number of edges in the SPN. n is the number of data points. $K \leq n$ is the number of mixture components. We will soon learn that for an SPN the number of mixture components is exponentially larger than the number of edges i.e. $E \ll K$. In theory MCMC methods samples from true the posterior distribution, and do not need any fitting/learning.

2.3 Acquisition function

Given a correct predictive distribution $p(y|x\mathcal{D})$ the next step in Bayesian optimization is to select the next location $x \in \mathcal{X}$ to sample from. The next location is chosen according to a so-called acquisition function (AQ function), which balances out the well-known concept of exploitation and exploration. It is exploitation if the next chosen location according to its average improvement. It is exploration if the next point is chosen in a region of high uncertainty and thereby helps lower the overall uncertainty. First, we will look at the acquisition function used in the thesis: Expected improvement. Secondly, we shortly present other different types of acquisition functions. In Figure 2.3 we see three different acquisition functions. The expected improvement (EI) is known for being biased towards exploitation. In contrast, the negative lower confidence bound (LCB) has a parameter β , which can be tuned to make it focus more on exploration.

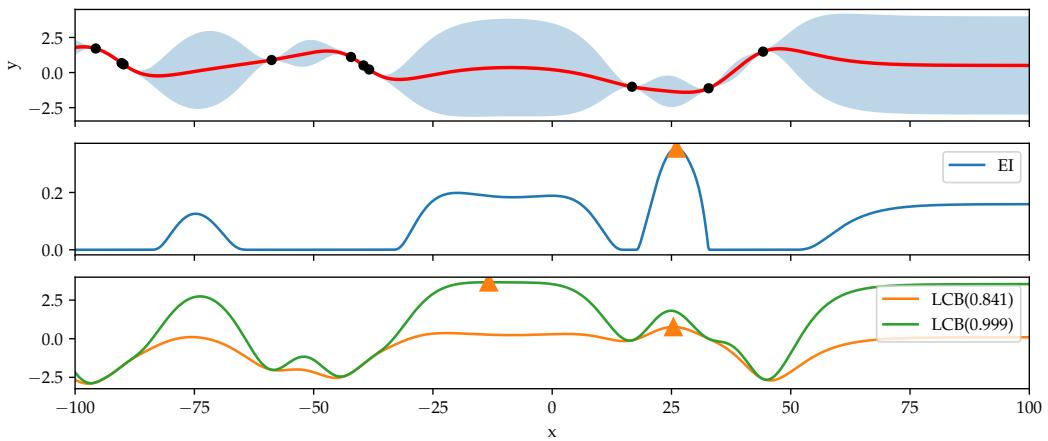


Figure 2.3: The same regression model and points as Figure 2.2, but with three different acquisition functions: Expected improvement and negative lower confidence bound for two different lower quantiles 0.841 and 0.999. The latter yields more exploration.

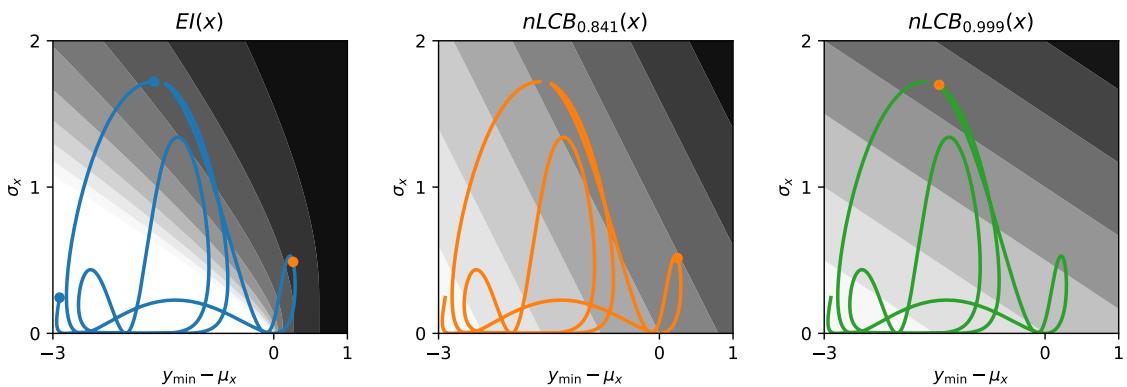


Figure 2.4: Contourplot of expected improvement and lower confidence bound (for two different quantiles) for different (Gaussian) predictive uncertainties $\sigma_x = \sqrt{\text{Var}_{p(y|x,\mathcal{D})}y}$ versus the average improvement $y_{\min} - \mu_x$, where $\mu_x = E_{p(y|x,\mathcal{D})}[y]$ (high values are dark). The colored lines are the mapping $x \mapsto (\sigma_x, y_{\min} - \mu_x)$ for $x = [-100, 100]$ for the Bayesian regression function in Figure 2.3 - and thereby explains how the acquisition functions balances exploitation and exploration. The orange dot represent the point maximizing the acquisition function

2.3.1 Expected improvement

A popular choice of acquisition function is expected improvement,

$$EI(x) = \mathbb{E}_{p(y|x, \mathcal{D})}[\max(0, y_{\min} - y)]$$

where we only consider the values y , which improves the current best value in the expectation of the predictive distribution, $p(y|x, \mathcal{D})$. Therefore, a x which yield a bad predictive mean value $\mathbb{E}_{p(y|x, \mathcal{D})}[y] > y_{\min}$ might still be maximizing the expected improvement, if the predictive uncertainty is very large at x . Figure 2.4 illustrates that a large uncertainty in the predictive distribution (represented as the predictive variance) can lead to relative large values even for non-improving mean predictions.

Note: Why defining expected improvement with max

Note that $\max(0, \cdot)$ is important since the Bayesian optimization otherwise reduces to a simple non-probabilistic surrogate-based optimization method,

$$\mathbb{E}_{p(y|x, \mathcal{D})}[y_{\min} - y] = y_{\min} - \mathbb{E}_{p(y|x, \mathcal{D})}[y]$$

i.e. maximizing the above is equivalent to maximizing the predictive mean, and thereby we loose all the valuable information about the predictive uncertainties from the Bayesian regression model.

Exact expected improvement

In the following derivation we assume the predictive distribution can be approxiamted by a normal distribution dependent on the point of interest x and the data \mathcal{D} (note for the GP it is in fact not an approximation),

$$p(y|x, \mathcal{D}) \approx \mathcal{N}(y|\mu(x, \mathcal{D}), \sigma^2(x, \mathcal{D}))$$

where we will change to a less clumsy notation $\mathcal{N}(y|\mu_x, \sigma_x^2) := \mathcal{N}(y|\mu(x, \mathcal{D}), \sigma^2(x, \mathcal{D}))$. This is completely fine since we x is fixed (and \mathcal{D} is fixed) when evaluating the expected improvement in a point x . Furthermore, the density of a standard normal distribution is denoted $\phi(\cdot) := \mathcal{N}(\cdot|0, 1)$, and the cumulative density function (CDF) of a standard normal distribution is denoted, $\Phi(\cdot) := \int_{-\infty}^{\cdot} \phi(\epsilon)d\epsilon$. We will now see that the normal approximation of the predictive distribution yields closed form solution to the expected improvement function,

$$\begin{aligned} E_{\mathcal{N}(y|\mu_x, \sigma_x^2)}[\max(0, y_{\min} - y)] &= \int \max(0, y_{\min} - y) \mathcal{N}(y|\mu_x, \sigma_x^2) dy \\ &= \int_{-\infty}^{y_{\min}} (y_{\min} - y) \frac{1}{\sigma_x} \phi\left(\frac{y - \mu_x}{\sigma_x}\right) dy \\ &= \int_{-\infty}^{\frac{y_{\min} - \mu_x}{\sigma_x}} (y_{\min} - \mu_x - \sigma_x \epsilon) \frac{1}{\sigma_x} \phi(\epsilon) \sigma_x d\epsilon \\ &= \int_{-\infty}^u \sigma_x \cdot (u - \epsilon) \phi(\epsilon) d\epsilon \\ &= \sigma_x \cdot \left(u \cdot \int_{-\infty}^u \phi(\epsilon) d\epsilon + \int_{-\infty}^u (-\epsilon) \phi(\epsilon) d\epsilon \right) \\ &= \sigma_x [u\Phi(u) + \phi(u)] \end{aligned}$$

where $u := \frac{y_{\min} - \mu_x}{\sigma_x}$.

Note: Derivation details

To understand the identity $\phi(u) = \int_{-\infty}^u (-\epsilon)\phi(\epsilon)d\epsilon$ used in the last equality, we first see that the antiderivative is $\phi(\epsilon) = \frac{1}{\sqrt{2\pi}} \exp\left(\frac{-\epsilon^2}{2}\right)$,

$$\frac{d}{d\epsilon}\phi(\epsilon) = \frac{1}{\sqrt{2\pi}} \frac{d}{d\epsilon} \exp\left(\frac{-\epsilon^2}{2}\right) = \frac{1}{\sqrt{2\pi}} \exp\left(\frac{-\epsilon^2}{2}\right) (-\epsilon) = -\epsilon\phi(\epsilon)$$

and evaluating the rieman integral is equivalent to evaluate the antiderivative in its boundaries, giving the solution,

$$\int_{-\infty}^u (-\epsilon)\phi(\epsilon)d\epsilon = [\phi(\epsilon)]_{-\infty}^u = \phi(u) - 0 = \phi(u)$$

We can also explicitly write the expected improvement as,

$$EI(x) = (y_{\min} - \mu_x)\Phi\left(\frac{y_{\min} - \mu_x}{\sigma_x}\right) + \sigma_x\phi\left(\frac{y_{\min} - \mu_x}{\sigma_x}\right)$$

where the first part can be interpreted as exploitation (favouring points with a large average improvement $I(x) := (y_{\min} - \mu_x)$) and the second part can be seen a exploitation (favouring points with high uncertainty.). This can also be seen in Figure (2.4), where it is clear that the expected improvement is growing for growing average improvement $I(x)$ and also for growing prediction uncertainty σ_x .

Approximate expected improvement

If the predictive distribution is non-Gaussian, it is either possible to approximate it as a Gaussian (By using the mean and variance of the predictive distribution to define the Gaussian approximation) or calculate the expected improvement approximately as follows,

$$\begin{aligned} E_{p(y|x, \mathcal{D})}[\max(0, y_{\min} - y)] &= \int \max(0, y_{\min} - y)p(y|x, \mathcal{D})dy \\ &\approx \frac{1}{K} \sum_{k=1}^K \max(0, y_{\min} - y^{(k)}) \end{aligned}$$

where $y^{(k)}$ are samples from the predictive distribution.

2.3.2 Lower confidense bound

Lower confidence bound is defined by a confidence paramter $\pi \in [0, 1]$ and then the lower quantile $\int_{\infty}^x p(y|x, \mathcal{D})dy = (1 - \pi)$ is chosen as the acquisition. For a Gaussian predictive distribution this is simply <more..>

$$nLCB(x) = -(\mu_x - \beta\sigma_x)$$

where $\beta = \Phi^{-1}(1 - \pi)$.

2.3.3 Entropy search

<copy> An information theoretic approach which accounts for the overall information gain on the optimizer ob- tained from a new evaluation has also been presented. This is known as informational approach to global optimization (IAGO), and uses en- tropy as a measure for information (Villemonteix, Vazquez, and Walter, 2009).

2.3.4 probability of improvement

3 Discriminative surrogate models

When talking about a probabilistic surrogate model we are always implicitly talking about a discriminative model: A statistical model of the conditional distribution of the observation, y , conditional on x often parameterized by parameters θ , i.e. $p(y|x, \theta)$ which, in a Bayesian context, is utilized in the *predictive posterior distribution*:

$$p(y|x, \mathcal{D}) = \int p(y|x, \theta)p(\theta|\mathcal{D})d\theta, \quad (3.1)$$

where we take all possible models $\theta \in \text{Dom}(\theta)$ into account weighted accordingly to how probable the model is $p(\theta|\mathcal{D})$ (the posterior distribution). Gaussian processes and Bayesian neural networks are both discriminative models and they both assume that the observation is noisy in the following way,

$$y = f_{\mathbf{w}}(x) + \epsilon, \quad \epsilon \sim \mathcal{N}(0, \sigma^2).$$

They are, however, using two very different approaches to define a discriminative model. A BNN define $f_{\mathbf{w}}(x)$ as the the neural network output for a specific realization of the network weights and biases \mathbf{w} . Given a realization of $\theta = (\mathbf{w}, \sigma^2)$, the BNN likelihood is defined as

$$p_{\text{BNN}}(y|x, \theta) = \mathcal{N}(y|f_{\mathbf{w}}(x), \sigma^2).$$

A GP takes a different approach and directly model the noisefree prediction $f_* := f(x)$ as a random variable. Given a realization of $\theta = (f_*, \sigma^2)$, the likelihood for a GP is given as

$$p_{\text{GP}}(y|x, \theta) = \mathcal{N}(y|f_*, \sigma^2). \quad (3.2)$$

In the following chapter, we will provide more details on both models, how they are defined, can be trained and used for predictions and discuss their properties. First, we dive into GPs.

3.1 Gaussian process surrogate

The most popular surrogate model is the Gaussian process, which we soon will understand in more detail. Typically, a probabilistic regression model is on the form

$$y = f_{\mathbf{w}}(x) + \epsilon$$

where weights are trained. f could describe a linear model, $f(x) = \mathbf{w}^T x$ or a polynomial $f(x) = \sum_i \mathbf{w}_i \cdot x_i^2$ etc. The Gaussian process takes a completely different approach; its noisefree prediction¹, $f(x)$, does not depend any parameters \mathbf{w} , instead it depends on the vector $\mathbf{f} := [f(x_1), \dots, f(x_n)]$ defined on the input/location data $\mathbf{x} = [x_1, \dots, x_n]$. We assign \mathbf{f} a multivariate normal distribution,

$$\mathbf{f}|\mathbf{x} \sim \mathcal{N}(\boldsymbol{\mu}, \Sigma),$$

where $\boldsymbol{\mu}$ typically is 0 and the covariance matrix, is dependent on the input, \mathbf{x} ,

$$\Sigma = c(\mathbf{x}, \mathbf{x}) = \begin{bmatrix} c(x_1, x_1) & \dots & c(x_1, x_n) \\ \vdots & \ddots & \\ c(x_n, x_1) & \dots & c(x_n, x_n) \end{bmatrix}, \quad c(x, y) := \text{Matern}(x, y) \dots$$

¹More correctly we here mean *predictive distribution*

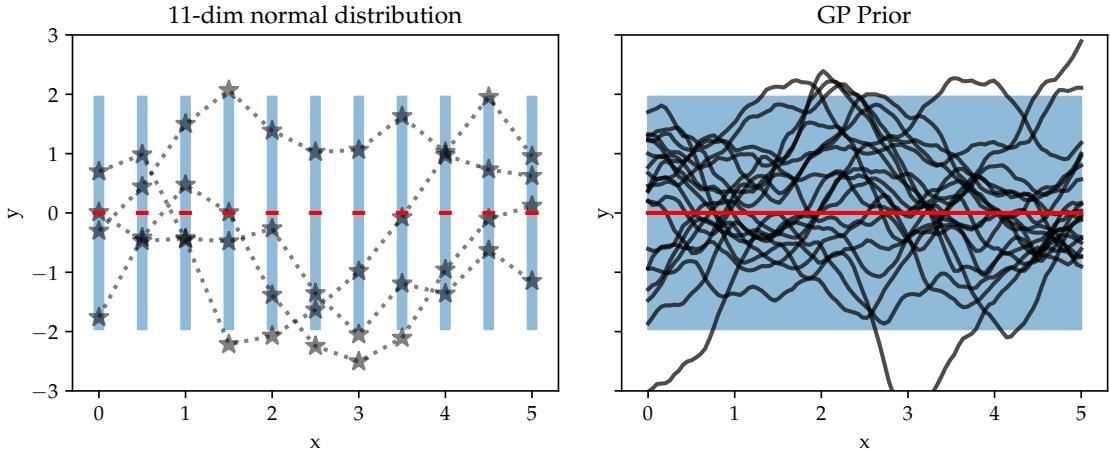


Figure 3.1: Left: Samples from $\mathcal{N}(\mathbf{f}|0, \kappa(x_1, \dots, x_{11}))$ where $x_i = 0.5(i - 1)$. Illustration that a samples from a Gaussian process is just samples from the multivariate normal distribution. We could potentially choose \mathbf{x} to be all of the real line, which will give us the GP - an infinitely large multivariate normal distribution (right).

this means that a realization of the vector \mathbf{f} is often close to 0 with a variance of the diagonal Σ , but also with a correlation between the elements in \mathbf{f} given by the off-diagonals in Σ . This is a very important ingredience of a GP, if $c(x_1, x_2) \approx 1$ (assuming that the variances of \mathbf{f} are 1, then Σ is a *correlation matrix*) then realizations of \mathbf{f} always lead to similar values of $f(x_1)$ and $f(x_2)$ (this can be seen in Figure 3.1). This encapsulates the idea of a GP: similarities (could be distance or other measures) in x should lead to similarities in $f(x)$. Now, in the case of extending it to a regression model, we need to introduce the observation y_* for an arbitrary location x_* ². Prior to observing any data, we assume that the corresponding $f_* = f(x_*)$ is just a new element in the multivariate normal distribution,

$$p(f_*, \mathbf{f}|x_*, \mathbf{x}) = \mathcal{N}\left(\begin{bmatrix} f_* \\ \mathbf{f} \end{bmatrix} \middle| \begin{bmatrix} 0 \\ \mathbf{0} \end{bmatrix}, \begin{bmatrix} c(x_*, x_*) & c(x_*, \mathbf{x}) \\ c(\mathbf{x}, x_*) & c(\mathbf{x}, \mathbf{x}) \end{bmatrix}\right), \quad (3.3)$$

which yields many possible outcomes for f_* with an average $E[f_*] = 0$ and variance of $V[f_*] = 1$. Note that given a realization of \mathbf{f} , then the distribution of f_* is changed due to the correlation $c(x_*, \mathbf{x})$. Fortunately, any conditional distribution from a multivariate normal distribution is easy to deal with. Using appendix... the conditional distribution of f_* given \mathbf{f} is,

$$p(f_*|\mathbf{x}, \mathbf{f}) = \mathcal{N}(f_*|c(x_*, x_*)^{-1}c(x_*, \mathbf{x})\mathbf{f}, c(x_*, x_*)^{-1}). \quad (3.4)$$

3.1.1 Exact predictive distribution

What we want is the predictive posterior distribution, $p(y_*|x_*, \mathcal{D})$, i.e. by marginalizing out the random variable $f_* := f(x_*)$ (as seen in (3.1)),

$$p(y_*|x_*, \mathcal{D}) = \int \mathcal{N}(y_*|f_*, \sigma^2)p(f_*|\mathcal{D})df_*. \quad (3.5)$$

We will soon see that the posterior $p(f_*|\mathcal{D})$ is also a normal distribution with mean μ_* and variance σ_*^2 so using <trick in appendix> we end up with the closed form Normal distribution,

$$p(y_*|x_*, \mathcal{D}) = \mathcal{N}(y_*|\mu_*, \sigma_*^2 + \sigma^2)$$

²The star subscript is included to help the reader easily relate f_* , y_* and x_* .

So now, we want to calculate $p(f_*|\mathcal{D})$, this can be done using the neat properties of Gaussian distributions.

Posterior function distribution

From observing the data $\mathcal{D} = \{x_1, y_1, \dots, x_n, y_n\} = (\mathbf{x}, \mathbf{y})$, we can marginalize over the noisefree predictions $\mathbf{f} = [f(x_1), \dots, f(x_n)]$,

$$p(f_*|\mathcal{D}) = \int p(f_*|\mathbf{x}, \mathbf{f})p(\mathbf{f}|\mathcal{D})d\mathbf{f}. \quad (3.6)$$

From (3.4) we already have $p(f_*|\mathbf{x}, \mathbf{f})$ as a Gaussian distribution, so we just need to calculate the posterior $p(\mathbf{f}|\mathcal{D})$, this is done through the prior and likelihood,

$$p(\mathbf{f}|\mathcal{D}) \propto p(\mathbf{f}|\mathbf{x})p(\mathbf{y}|\mathbf{f}). \quad (3.7)$$

As mentioned $f(\cdot)$ is the noisefree prediction, i.e. $y = f(x) + \epsilon$. So assuming iid data, and that ϵ is additive Gaussian noise with variance σ^2 , we get the likelihood,

$$p(\mathbf{y}|\mathbf{x}, \mathbf{f}) = \prod_{i=1}^n p(y_i|x_i, \mathbf{f}_i) = \prod_{i=1}^n \mathcal{N}(y_i|\mathbf{f}_i, \sigma^2) = \mathcal{N}(\mathbf{y}|\mathbf{f}, \sigma^2 I)$$

from (3.3) the prior of \mathbf{f} is defined using similarities between its corresponding \mathbf{x} , giving a multivariate normal distribution, $p(\mathbf{f}|\mathbf{x}) = \mathcal{N}(\mathbf{f}|\mathbf{0}, c(\mathbf{x}, \mathbf{x}))$ so we can specify the unnormalized posterior (3.7),

$$p(\mathbf{f}|\mathcal{D}) \propto \mathcal{N}(\mathbf{f}|\mathbf{0}, c(\mathbf{x}, \mathbf{x}))\mathcal{N}(\mathbf{y}|\mathbf{f}, \sigma^2 I).$$

Now we see that, this is a product between two Gaussians using appendix ... we have that the posterior is the following Gaussian:

$$p(\mathbf{f}|\mathcal{D}) = \mathcal{N}(\mathbf{f}|M^{-1}\sigma^{-2}\mathbf{y}, M^{-1}) \quad M := c(\mathbf{x}, \mathbf{x})^{-1} + \sigma^{-2}I_n$$

Finally, we see that both terms in the integral (3.6), are related such that it is possible to use (3.8) for arriving at (we define $A := c(x_*, x_*)^{-1}c(x_*, \mathbf{x})$),

$$\begin{aligned} p(f_*|\mathcal{D}) &= \mathcal{N}(f_*|\mu_*, \sigma_*^2) \\ \mu_* &= AM^{-1}\sigma^{-2}\mathbf{y} \\ \sigma_*^2 &= c(x_*, x_*)^{-1} + AM^{-1}A^T \end{aligned}$$

We now have a fully specified Gaussian process posterior function, which we sample from in Figure 3.2.

Background: Trick with normal distributions [from Bishops book?]

Given a marginal Gaussian distribution of x and a conditional Gaussian distribution of y given x of the form,

$$\begin{aligned} p(x) &= \mathcal{N}(x|\mu, \Lambda^{-1}) \\ p(y|x) &= \mathcal{N}(y|Ax + b, L^{-1}) \end{aligned}$$

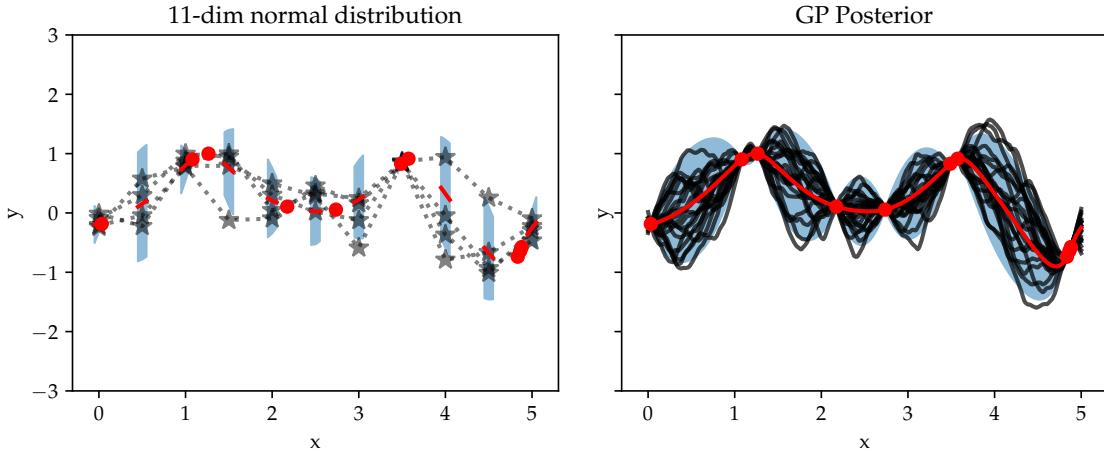


Figure 3.2: Left: Samples from posterior function distribution for $\mathcal{N}(\mathbf{f}_*|m(\mathbf{x}), V(\mathbf{x}))$ where $\mathbf{x} = \{x_1, \dots, x_{11}\}$ and $x_i = 0.5(i - 1)$. Illustration that a samples from a Gaussian process is just samples from the multivariate normal distribution. We could potentially choose \mathbf{x} to be all of the real line, which will give us the GP - an infinitely large multivariate normal distribution.

then the marginal distribution of y and the conditional distribution of x given y have the form,

$$p(y) = \mathcal{N}(y|A\mu + b, L^{-1} + A\Lambda^{-1}A^T) \quad (3.8)$$

$$p(x|y) = \mathcal{N}(x|\Gamma\mu + \Gamma[A^T L(y - b)], \Gamma) \quad (3.9)$$

$$\Gamma := (\Lambda + A^T L A)^{-1} \quad (3.10)$$

3.1.2 Learning - Empirical Bayes inference

The above deviation of prediction with the Gaussian process only acknowledged f_* as the unknown variable, however, in (3.2) we included the observation variance σ^2 as the unknown parameter set θ . Additionally, the similarity measurement, which is done in the kernel, $c(\cdot, \cdot)$, is also parameterized. We did assume those additional parameters were known because of the nice closed form predictive posterior. Instead we now call the variance σ^2 and kernel parameters hyperparameters. Very often GP hyperparameters are chosen using Empirical bayes, which is simply to choose the hyperparameters, which maximize the marginalized likelihood,

$$\nu = \arg \min_{\nu} p(\mathbf{y}|\mathbf{x}, \nu)$$

where for a Gaussian process the marginal is given as

$$\begin{aligned} p(\mathbf{y}|\mathbf{x}, \nu) &= \int p(\mathbf{y}, \mathbf{f}|\mathbf{x}, \nu) d\mathbf{f} \\ &= p(\mathbf{y}|\mathbf{f}, \nu)p(\mathbf{f}|\mathbf{x}, \nu) d\mathbf{f} \end{aligned}$$

where $p(\mathbf{y}|\mathbf{f}, \nu) = \mathcal{N}(\mathbf{y}|\mathbf{f}, \sigma^2)$ and the prior is just the Gaussian $p(\mathbf{f}|\mathbf{x}, \nu) = \mathcal{N}(\mathbf{f}|0, c_\nu(\mathbf{x}, \mathbf{x}))$ And now we can easily perform the integration using $\langle \dots \rangle$,

$$p(\mathbf{y}|\mathbf{x}, \nu) = -\frac{1}{2}[(y - \mu)^T (\Sigma + N)^{-1} (y - \mu) + \log |\Sigma + N| + n \log 2\pi]$$

we can define the predictive prior distribution, in the same way as (3.5), we have that $p(\mathbf{f}|\mathbf{x}) = \mathcal{N}(\mathbf{f}|0, c(\mathbf{x}, \mathbf{x}))$, thereby,

$$p(\mathbf{y}|\mathbf{x}) = \int \mathcal{N}(\mathbf{x}|\mathbf{f}, I\sigma^2)p(\mathbf{f}|\mathbf{x}) d\mathbf{f} \quad (3.11)$$

Using ... we arrive at just observe that $p(\mathbf{y}|\mathbf{x}) = \mathcal{N}(\mathbf{y}|0, c(\mathbf{x}, \mathbf{x}) + \sigma^2)$

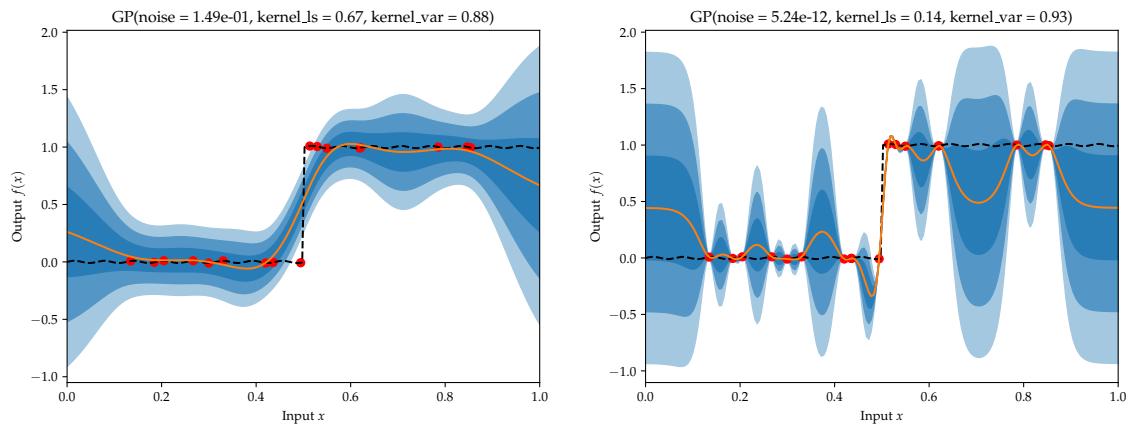


Figure 3.3: There is large difference between the two GPs the different length scales in the kernel matters a lot. Left is chosen 9 out of 10 times, when minimizing the

3.2 Bayesian Neural Networks

Neural networks have become increasingly popular in recent years, due to their ability to approximate any function arbitrary well (showed via the universal approximation theorem) and with the amount of data in the world today, neural networks are very powerful regression models for finding complex patterns. Bayesian neural networks are essentially neural networks, but instead of point estimates, each weight is assigned a distribution, which provides a probabilistic regression model (see Figure 3.5). Prior to any observed data, the weights are assigned a distribution (typically a standard Gaussian). After observing data a joint (posterior) distribution of the weights are inferred, such that the regression model is fitting the data and provides good uncertainty estimation (note that the weights might be complicated and correlated). In Figure 3.4 we see how the regression model can do predictions even when no data is observed, i.e. prior samples (left), when observing data the posterior combines the likelihood and the prior and we get the predictive posterior distribution (right).

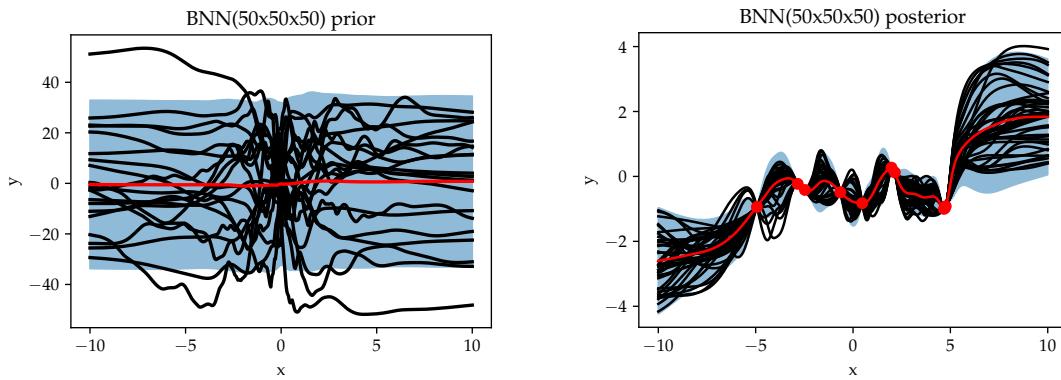


Figure 3.4: Left: 20 black predictive *prior* samples from a 3 layers BNN with 50 tanh nodes, with standard Gaussian prior distributions. Right: 20 predictive *posterior* samples. The blue areas are ± 2 predictive standard deviations from the red predictive mean.

The likelihood of a Bayesian Neural network is typically defined as a normal distribution with mean equal the neural network output and a observation variance σ^2 (both are random variables) which in the thesis is assumed constant throughout the domain.

$$p_{\text{BNN}}(y|x, \theta) = \mathcal{N}(y|f_{\mathbf{w}}(x), \sigma^2)$$

The prior distribution of the weights (including the biases) are typically assumed uncorrelated standard normal distributed and the observation variance σ^2 can be assigned a lognormal or half-Cauchy, with support on the positive real domain, since a variance parameter can only be non-negative. We can write the priors of the BNN model as

$$p(\theta = (w, \sigma)) = \mathcal{N}(w; \mathbf{0}, I) \log \mathcal{N}(\sigma; \dots)$$

Now we can define the posterior distribution, i.e. the probability of the unknown quantaties given the observations. We define it using Bayes rule,

$$\begin{aligned} p(\theta|x, y) &= \frac{p(\theta, y|x)}{p(y|x)} \\ &= \frac{p_{\text{BNN}}(y|x, \theta)p(\theta|x)}{p(y|x)}. \end{aligned}$$

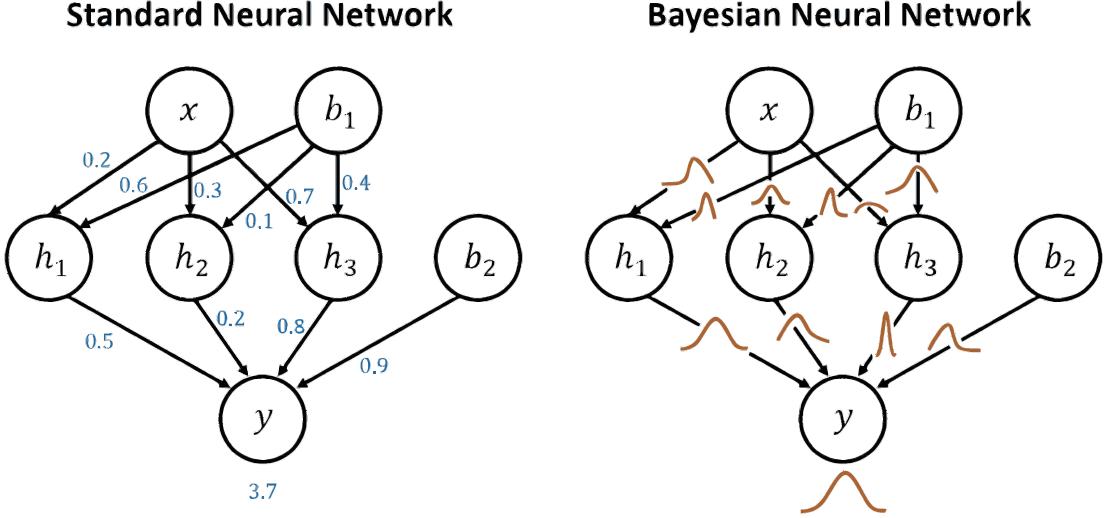


Figure 3.5: Graphical representation of a Bayesian neural network compared to a neural network. The weights are assigned a probability density. Note that we often prior assume no correlation and a standard normal distribution, but the posterior (after observing data) might contain correlations between the weights (from CYDA)

Note that the prior distribution $p(\theta|x)$ just like the likelihood can depend on x - we could for example extend σ to depend on the location of the sample x and define it as $\sigma(x)$. Note that the posterior distribution of the weights and σ^2 is complex and correlated due to the multiplication of the complicated likelihood and the prior. Therefore, exact inference of BNNs is intractable and we approximate the predictive posterior distribution with Monte Carlo samples from posterior,

$$\begin{aligned} p(y_*|x_*, \mathcal{D}) &= \int p_{\text{BNN}}(y_*|x_*, \theta)p(\theta|\mathcal{D})d\theta \\ &\approx \frac{1}{K} \sum_{k=1}^K p_{\text{BNN}}(y_*|x_*, \theta^{(k)}) \end{aligned}$$

where the integral is intractable. As indicated in the second line, we can approximate the integral with Monte Carlo sampling: $\theta^{(k)}$ are iid samples from the posterior distribution, $\theta^{(k)} \sim p(\theta|\mathcal{D})$.

Background: Monte Carlo approximation

Assuming we have a number of iid samples, $\theta^{(1)}, \dots, \theta^{(K)}$ drawn from the distribution $p(x)$, then the following approximation

$$E[f(x)] \approx \frac{1}{K} \sum_{k=1}^K f(x^{(k)}) =: \Theta_K(f)$$

holds according to the law of large numbers. In fact,

$$E[f(x)] = \lim_{K \rightarrow \infty} \Theta_K(f)$$

and the central limit theorem ensures that the variance of the unbiased estimator of the expectation decreases with number of samples, K , i.e.

$$p(\hat{\Theta}) \approx \mathcal{N}(\hat{\Theta}|\mu_f, \frac{\sigma_f^2}{K}),$$

where $\mu_f := E[f(x)]$ and $\sigma_f^2 = \text{Var}(f(x))$. [??]

We try to get iid samples from the posterior distribution using MCMC.

Posterior samples

For BNN the joint distribution $p(\mathcal{D}, \theta)$ is available, but calculating the posterior distribution requires the marginalized likelihood, $p(\mathcal{D}) = \int_{\theta} p(\mathcal{D}, \theta)$. This integral is often intractable since the space of θ typically is abnomous - so not even numerical approximations of the intergral is tractable. From Bayes rule, we have the equality,

$$p(\theta|\mathcal{D}) = \frac{p(\mathcal{D}, \theta)}{p(\mathcal{D})} \propto p(\mathcal{D}, \theta),$$

where the propotional sign is true, since $p(\theta|\mathcal{D})$ is a function of θ . Knowing the joint distribution, $p(\mathcal{D}, \theta)$, allow for using Markov chain Monte Carlo (MCMC) to obtain samples from the posterior distribution.

Background: Markov chain Monte Carlo (MCMC)

We can use MCMC for sampling from a probability density $p(x)$, with only the knowledge of a proportional/unnormalised density $\hat{p}(x) \geq 0$ i.e

$$\hat{p}(x) = c \cdot p(x) \propto p(x), \quad c = \int \hat{p}(x) dx,$$

where $\int \hat{p}(x) dx$ may be intractable. The MCMC procedure constructs an ergodic Markov chain/process, such that its stationary distribution is exactly $p(x)$, but only with the knowledge of $\hat{p}(x)$. <short more details on MCMC>

- **Ergodic:** A Markov process which spans/visits all the space.
- **Stationary distribution:** A Markov process has reached stationary distribution if we stay there at the next sample.
- **Detailed balance relation:** A way to check if a Markov chain is stationary is by the detailed ballance equation:

$$p(x)p(x \rightarrow y) = p(y)p(y \rightarrow x)$$

note we introduce the notation $p(x \rightarrow y)$ for the transition probablity from x to y , this can also be interpreted as a conditional distribution of state y given state x

So since the known joint distribution is proportional to the posterior distribution, we can use MCMC to get samples from the posterior distribution, even when it is intractable. To better introduce what MCMC is, we here present a simple MCMC procedure, the Metropolis-Hasting algorithm (HM), and give proof of why its produced Markov chain stays in its stationary distribution.

MCMC example: Metropolis-Hasting (MH)

At iteration n we already have a sample x_n ,

1. Propose \hat{x} from a proposal density $q(\cdot|x_n)$
2. Compute acceptance probability

$$\alpha(x_n, \hat{x}) = \min \left(1, \frac{p(\hat{x})}{p(x_n)} \frac{q(x_n|\hat{x})}{q(\hat{x}|x_n)} \right)$$

3. Set the next sample

$$x_{n+1} = \begin{cases} \hat{x} & \text{with probability } \alpha(x_n, \hat{x}) \\ x_n & \text{with probability } 1 - \alpha(x_n, \hat{x}) \end{cases}$$

note that $\alpha(x_n, \hat{x})$ uses $p(x)$ in the fraction $\frac{p(\hat{x})}{p(x_n)} = \frac{p(\hat{x}) \cdot c}{p(x_n) \cdot c} = \frac{\hat{p}(\hat{x})}{\hat{p}(x_n)}$, so we only need $\hat{p}(x)$.

Proof: Assuming discrete states, the transition probability between the states are given as,

$$p(x \rightarrow y) = \begin{cases} q(y|x)\alpha(x, y) & \text{if } x \neq y \\ q(x|x) + \sum_{z \neq x} q(z|x)(1 - \alpha(x, z)) & \text{if } x = y \end{cases}$$

Now, let us look at the detailed balance relation. Assume $x \neq y$,

$$\begin{aligned} p(x)p(x \rightarrow y) &= p(x)q(y|x)\alpha(x, y) \\ &= p(x)q(x, y) \min\left(1, \frac{p(\hat{x})}{p(x_n)} \frac{q(\hat{x}, x_n)}{q(x_n, \hat{x})}\right) \\ &= \min(p(x)q(x, y), p(y)q(y, x)) \end{aligned}$$

Observing that the right hand side yields symmetric result in x and y , therefore we obtain,

$$p(x)p(x \rightarrow y) = p(y)p(y \rightarrow x)$$

and summing over x on both sides yields,

$$\sum_x p(x)p(x \rightarrow y) = p(y) \sum_x p(y \rightarrow x) \quad (3.12)$$

$$\implies p(y) = \sum_x p(x)p(x \rightarrow y). \quad (3.13)$$

The detailed balance is trivially obtained for $x = y$, all in all, this reveals that $p(x)$ is in fact invariant for the chain $\{x_1, \dots, x_n\}$ and thereby that MH is a MCMC algorithm.

HM with its random walk transition is very simple and it comes with some serious disadvantages: Slow convergence speed, it might stay in the same region for a long time and produce highly correlated samples(i.e. not the iid samples we need for the Monte Carlo approximation to be correct) [??]. The gold standard in MCMC, Hamiltonian Monte Carlo (HMC), replaces HMs random walk with gradient-guided movements and interpret the probability landscape as a physical system.

Hamiltonian Monte Carlo (HMC)

HMC exploits arguments from classical mechanics around the Hamiltonian equations. This method leads to more efficient sampling as the Hamiltonian interpretation allows the system to consider regions with high probability more - this is obtained using a gradient of the probability landscape, $\frac{-\partial E(x)}{\partial x}$.

We introduce the potential energy $E(x)$ by defining the joint probability as,

$$p(x) = \frac{1}{Z_E} \exp(-E(x))$$

Now, a latent vector q is introduced in order to represent the momentum of the system, which

gives us the kinetic energy of the system.

$$K(q) = \frac{1}{2} \sum_{i=1}^l q_i^2$$

Combining the kinetic and potential energy yields, the the Hamilton function and its corresponding distribution

$$H(x, q) = E(x) + K(q)$$

and

$$p(x, q) = \frac{1}{Z_H} \exp(-H(x, q)) \quad (3.14)$$

$$= \frac{1}{Z_E} \exp(-E(x)) \frac{1}{Z_K} \exp(-K(x)) \quad (3.15)$$

$$= p(x)p(q) \quad (3.16)$$

The desired distribution $p(x)$ is found as the marginal of $p(x, q)$. The sampling procedure is as follows,

1. At the (x_n, q_n) sample momentum q_n by gibbs sampling
2. Simulate the Hamiltonian dynamics with Leap-frog integration (i.e. walking the contour lines of $p(x, q)$). New position is (x_{n+1}, q_{n+1})
3. Accept new position with MH acceptance probability $\min(1, \frac{p(x_{n+1}, q_{n+1})}{p(x_n, q_n)})$

3.2.1 MCMC used in thesis

Since some intuition is now established around Hamiltonian Monte Carlo, we look a bit at the two versions used in the thesis. Our implementation in Numpyro and the one from the paper, BOHamANN,

NUTS

<LAV om> Often the physical simulation in HMC goes back and forth the same path (a u-turn), and we risk getting bad samples. No U-turn (NUTS) sampling avoids this, by forcing the HMC path to not take u-turns.

Adaptive stochastic HMC

<Læs BOHamANN paper igennem> BOHAMANN is using an adaptive stochastic Hamiltonian monte carlo method to train the BNN.

3.2.2 Design and properties of Bayesian neural network

The architecture of a BNN is a large topic to discuss. There are certain tradeoffs to be taken into consideration: How expressive should the network be (i.e. how deep and how many nodes per layer) versus how much time do we have for the sampler to converge to the true posterior distribution? A challenging part of MCMC is that it is difficult to know when the samples are true samples from the posterior. A consideration when training deterministic neural networks are overfitting however this is not a big consideration when fitting Bayesian neural networks; Choosing a prior around 0 will regulate the parameters, and thereby postpone overfitting.

This thesis is inspired by the PhD thesis [6], which uses an architecture of a 2 layers with 50 sigmoid nodes in each layer, and the BOHAMANN paper [4], default uses an architecture of 3 layers with 50 tanh-nodes in each layer. As we want to make sure always to do the inference correctly, we want to be able to take a proper amount of samples, while also having an explicit model. Figure (3.6) shows prior samples of BNN with a different number of tanh-nodes on each of the 3 layers,

this provides an intuition that choosing a larger BNN leads to a more expressive regression model. When doing Bayesian optimization the model as a small amount of training data, i.e. complicated patterns in data is not possible to discover, and hence highly expressive models are not important.

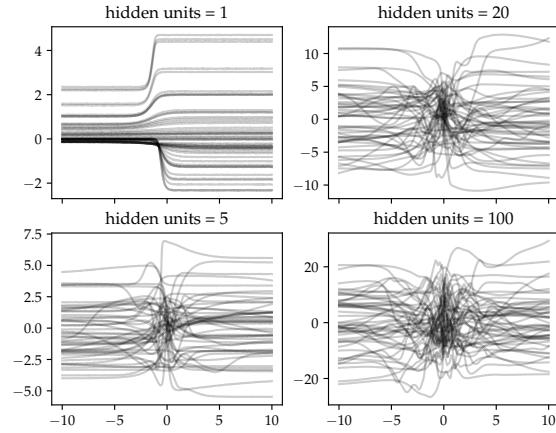


Figure 3.6: Number of units in each of the 3 layers have a large influence of the BNNs ability to be expressive <lav om>

$\mathcal{N}(\mathbf{w}|\mathbf{0}, I)$, and the prior distribution of the observation variance is following a inverse gamma distribution $\text{InvGa}(\sigma^2|1000, 1)$ yielding a quite informative prior of $\sigma^2 \approx 0$, i.e. believing that there is no observation noise.

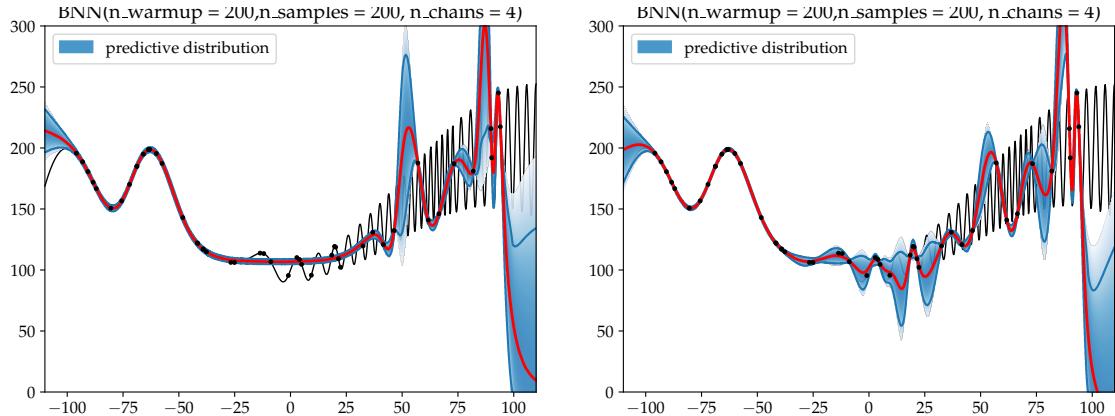


Figure 3.7: Example where 100 nodes on each of three layers, lead to a much more expressive model. σ^2 follows a informative prior $\text{InvGamma}(1000, 1)$, i.e. prior mean $E[\sigma^2] \approx \frac{1}{1000}$, and variance $\approx \frac{1}{1000^3}$, however since the data is distributed in such a complex way the limited expressiveness of the model, forces the model to infer make σ^2 large, i.e. including the data in the noise

4 Generative models as surrogate

Generative models are statistical models of the joint distribution $p(x, y)$. We need, however, a discriminative model for regression, i.e. a model of the conditional distribution of y given x , i.e. $p(y|x)$. All generative models we deal with in this thesis allow for exact inference of the conditional distribution. So given a well-fitted generative model, one could immediately think they would be feasible to use as surrogate models. However, in this project, we only look at Gaussian mixture models as generative models - and they have a problem for x -values where the probability of the observed input data, the marginal $p(x)$, is low. Recall the conditional distribution is

$$p(y|x) = \frac{p(x, y)}{p(x)}$$

and can be interpreted as a slice of the joint distribution $p(x, y)$ for a fixed value of x , but normalized with $p(x) = \int p(x, y) dy$. So even if there is a very small probability of the data, the conditional probability $p(y|x)$ gets artificially certain in the case of Gaussian mixtures. We, therefore, need to introduce a prior distribution for y , which will take over in areas for no data, i.e. small $p(x)$. This is discussed in section 4.1.

Using generative models as regression models is not used much in the literature. Using the conditional of a Gaussian mixture model (or kernel estimator) for regression has been discussed briefly in [12] and using kernel estimator [7] and [13] for active learning. According to these sources, the good reasons for using the mixtures for regression are that they can be used to represent any relations between the variables, e.g., $p(y|x)$ or $p(x|y)$. They are both applicable in supervised and unsupervised machine learning. And they are good at dealing with incomplete data, i.e. missing values in the data set <change this>. We hypothesize that it will allow for an expressive surrogate model, which competently can deal with complex BO tasks, as they do not assume continuity. In this thesis we will first look at the most simple approach to a generative model, i.e. putting an equally weighted Gaussian mixture component on each data point. This is also referred to as a kernel estimator (some might know this from kde-plots/estimating a distribution from data), but with a twist of including a prior distribution to it. Next, we look at the more intelligent models, Gaussian mixture models, which hopefully can capture some correlations between the variables. And finally, we look at the more complicated sum-product networks, which introduce a generalization element and have a flavor of a neural network. To summarize, the mixture regression models are:

- Kernel density estimator regression,
- Gaussian mixture regression,
- Sum-product networks.

4.1 Conditional distribution in a Bayesian setting

As mentioned above the conditional itself is not enough as a probabilistic regression model used as a surrogate model. This is showcased in the middle right illustration in Figure 4.1, where the conditional distribution would have the same distance between its confidence bounds even for those x far away. To our knowledge, this problem has not been dealt with in the literature before. We want to manipulate the conditional distribution to transform into a very uncertain prior probability for y in areas where there is small evidence of the data $p(x)$. Two of the ideas for manipulating the conditional distributions (denoted $\hat{p}(y|x)$),

- Include a new Gaussian mixture component with zero mean and large variance, $p_{prior}(y)$, and choose an x -depended weighting, $\alpha_x \in [0, 1]$, such that

$$\hat{p}(y|x) = \alpha_x p(y|x) + (1 - \alpha_x) p_{prior}(y)$$

- Assuming both the conditional and prior distribution to be a Gaussian, we could choose an x depended weighting, $\alpha_x \in [0, 1]$ such that the manipulate conditional is a Gaussian with mean $\hat{\mu}$ and variance $\hat{\sigma}^2$ such that,

$$\begin{aligned}\hat{\mu} &:= \alpha \cdot \mu_{y|x} + (1 - \alpha) \cdot \mu_{prior} \\ \hat{\sigma}^2 &:= \alpha \cdot \sigma_{y|x}^2 + (1 - \alpha) \cdot \sigma_{prior}^2\end{aligned}$$

We define x -depending weighting to be a function of the evidence $p(x)$ and how much data is observed N , and we additionally introduce a parameter $\Delta > 0$,

$$\alpha_x = \frac{N \cdot p(x) \cdot \Delta}{N \cdot p(x) \cdot \Delta + 1}$$

note that $\alpha_x = 0$ for $p(x) = 0$ and $\alpha_x \rightarrow 1$ for $N \cdot p(x) \cdot \Delta \rightarrow \infty$. Illustration of idea 1 can be seen in left illustration in Figure 4.1 where we call $S(x) := N \cdot p(x) \cdot \Delta$ the scaling.

Idea 1 would work on any kind of conditional distribution, while idea 2 would be an intuitive transformation but only if the conditional is Gaussian, alternative, as we are working with mixtures of Gaussians, these could be manipulated in the same way.

Note: Idea 1 defines a valid distribution

The manipulated conditional in idea 1, is a convex combination of valid distributions, and it is always positive and integrates to 1, as easily seen here,

$$\begin{aligned}\int_y \hat{p}(y|x) dy &= \int_y [\alpha_x p(y|x) + (1 - \alpha_x) p_{prior}(y)] dy \\ &= \alpha_x \int_y p(y|x) dy + (1 - \alpha_x) \int_y p_{prior}(y) dy \\ &= \alpha_x + (1 - \alpha_x) = 1.\end{aligned}$$

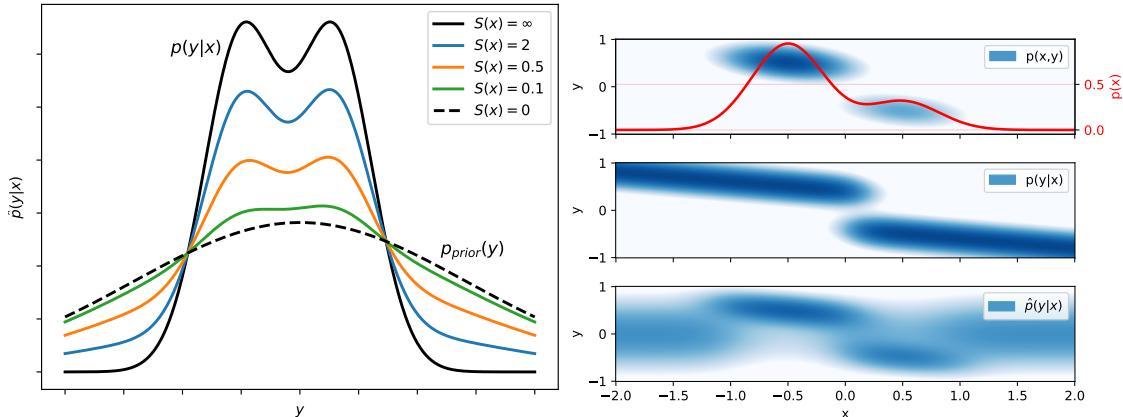


Figure 4.1: Left: Illustration of how the predictive distribution is manipulated according the the scaling function $S(x) := p(x) \cdot N \cdot \Delta$. Right: Illustration of why it makes sense to manipulate the predictive distribution $p(y|x)$, if there is a small amount of input data at a region, then the predictive distribution should transform into the uncertain prior

4.1.1 Mean and variance of predictive distribution v1

If we just are interested in a Gaussian approximation of the predictive distribution, this can be easily done assuming we know the mean, variance and the second moment of the conditional distribution, first the predictive mean is calculate,

$$\begin{aligned} E_{\hat{p}(y|x)}[y] &= \int y \cdot (\alpha_x \cdot p(y|x) + (1 - \alpha_x)p_{prior}(y)) dy \\ &= \alpha_x \cdot E_{p(y|x)}[y] + (1 - \alpha_x) \cdot E_{p_{prior}(y)}[y] \end{aligned}$$

And the predictive variance is calcualted, using the definition of variance, $V_{\hat{p}(y|x)}[y] = E_{\hat{p}(y|x)}[y^2] - E_{\hat{p}(y|x)}[y]^2$. So we only need to calculate the second moment,

$$\begin{aligned} E_{\hat{p}(y|x)}[y^2] &= \int y^2 \cdot \alpha_x \cdot p(y|x) + (1 - \alpha_x)p_{prior}(y) dy \\ &= \alpha_x \cdot E_{p(y|x)}[y^2] + (1 - \alpha_x) \cdot E_{p_{prior}(y)}[y^2] \\ &= \alpha_x \cdot (Var_{p(y|x)}[y] + E_{p(y|x)}[y]^2) + (1 - \alpha_x)Var_{p_{prior}(y)}[y] \end{aligned}$$

Assuming $E_{p_{prior}(y)}[y] = 0$.

Note: Implementation

If we use $\alpha_x \propto p(x)$, then it is not necessary to calculate the conditional distribution at all. Assuming c is a constant in y .

$$\hat{p}(y|x) = \frac{c \cdot p(x) \cdot p(y|x) + p_{prior}(y)}{c \cdot p(x) + 1} = \frac{c \cdot p(x, y) + p_{prior}(y)}{c \cdot p(x)}$$

4.2 Conditional of mixture model

To exploit a generative model as a surrogate model in Bayesian optimization, we need to calculate the conditional distribution. Fortunately, all generative models used in this thesis are mixture models, which simplifies the upcomming deveriations. We define a general mixture model with Z mixture components as,

$$p(x, y) = \sum_{z=1}^Z \lambda_z p_z(x, y)$$

where $p_z(x, y)$ are mixture components, i.e. simpler generative models with same support, $(x, y) \in \mathcal{X} \times \mathbb{R}$. The goal is to define the conditional distribution exact for all the mixture models. As we will soon see, this is again a mixture model,

$$p(y|x) = \sum_z \gamma_z(x) p_z(y|x).$$

with $\sum_z \gamma_z(x) = 1$ and $\gamma_z(x) \in [0, 1]$. First, we calcalculate the marginal distribution $p(x)$ of the mixture,

$$p(x) = \int p(x, y) dy = \sum_z \lambda_z \int p_z(x, y) dy = \sum_z \lambda_z p_z(x).$$

Next, we can calculate the conditional in terms of the conditional of the individual mixture components,

$$\begin{aligned}
p(y|x) &= \frac{p(y,x)}{p(x)} \\
&= \sum_z \frac{\lambda_z}{p(x)} p_z(x,y) \\
&= \sum_z \frac{\lambda_z p_z(x)}{p(x)} p_z(y|x) \\
&= \sum_z \underbrace{\frac{\lambda_z p_z(x)}{\sum_{z^*} \lambda_{z^*} p_{z^*}(x)}}_{\gamma_z(x)} p_z(y|x).
\end{aligned}$$

So we see that the conditional of a mixture model is again a mixture model. We also see that $\sum_z \gamma_z(x) = 1$ and hence we can interpret the above as the following,

$$p(y|x) = p_z(y|x), \quad z \sim \text{Cat}(\gamma_1(x), \dots, \gamma_Z(x)).$$

And we name $p(z|x) = \gamma_z(x) \in [0, 1]$ the *responsibility* of mixture component z at a given location $x \in \mathcal{X}$, (The probability that y to belong to component z at a given location x). For implementation we notice that the denominator in $\gamma_z(x)$ can be reused for all components.

Gaussian approximation of mixture conditional

As discussed in Section 4.1.1, in order to obtain the closed-form solution in the expected improvement, we can approximate the mixture with a gaussian distribution, i.e. calculation of the conditional mean and variance.

The mean of the conditional is just

$$\begin{aligned}
E_{p(y|x)}[y] &= \sum_z \gamma_z(x) \int y \cdot p_z(y|x) dy \\
&= \sum_z \gamma_z(x) E_{p_z(y|x)}[y].
\end{aligned}$$

The variance is found using the variance definition $V[y] = E[y^2] - E[y]^2$,

$$\begin{aligned}
E_{p(y|x)}[y^2] &= \sum_z \gamma_z(x) \int y^2 p_z(y|x) dy \\
&= \sum_z \gamma_z(x) (Var_{p_z(y|x)}[y] + E_{p_z(y|x)}[y]^2).
\end{aligned}$$

We will now present all the models and show how their conditional distributions are calculated concretely.

4.3 Kernel estimator regression

Maybe the most simple mixture model one could think about is to put a small variance Gaussian mixture component around all data points and weight all the components equally. So for n data-points, $\{(x_i, y_i)\}_{i=1}^n$, the generative model is given as,

$$p(x, y) = \frac{1}{N} \sum_{i=1}^n \mathcal{N} \left(\begin{bmatrix} x \\ y \end{bmatrix} \middle| \begin{bmatrix} x_i \\ y_i \end{bmatrix}, \sigma^2 I \right) = \frac{1}{N} \sum_{i=1}^n \mathcal{N}(x|x_i, \sigma^2 I) \mathcal{N}(y|y_i, \sigma^2),$$

where σ^2 is referred as the bandwidth, when the literature refers to the above as a kernel estimator. Small σ^2 yields a complex model and large σ^2 yields a simple model. Therefore choosing σ^2 just right is crucial for a good model.

4.3.1 Conditional of Kernel density estimator

Since the kernel density estimator is just a Gaussian mixture model, with no correlation between any of the variables, yielding i.e. $p_z(y|x) = p_z(y)$, therefore the conditional distribution is given as,

$$p(y|x) = \sum_{z=1}^n \gamma_z(x) \mathcal{N}(y|\mu_y^{(z)}, \Sigma_{yy}^{(z)}), \quad (4.1)$$

$$\gamma_z(x) = \frac{\lambda_z \mathcal{N}(x|\mu_x^{(z)}, \Sigma_{xx}^{(z)})}{\sum_{z^*} \lambda_{z^*} \mathcal{N}(x|\mu_x^{(z^*)}, \Sigma_{xx}^{(z^*)})}. \quad (4.2)$$

The computational complexity of calculating the conditional or the predictive distribution is $O(n)$, since we reused the denominator of $\gamma_z(x)$ for all components z .

4.4 Gaussian mixture regression

Extending the kernel estimator regression with covariance between the variables, only $K \leq N$ components and different weighting on each component, we arrive at a Gaussian mixture model. The conditional of GMM gives the Gaussian mixture regression model [14].

We can model our data, as a generative model $p(x, y)$,

$$p(x, y) = \sum_{z=1}^K \lambda_z \mathcal{N}(x, y|\mu^{(z)}, \Sigma^{(z)}), \quad \mu^{(z)} = \begin{bmatrix} \mu_x^{(z)} \\ \mu_y^{(z)} \end{bmatrix}, \quad \Sigma^{(z)} = \begin{bmatrix} \Sigma_{xx}^{(z)} & \Sigma_{xy}^{(z)} \\ \Sigma_{yx}^{(z)} & \Sigma_{yy}^{(z)} \end{bmatrix},$$

where $\sum_{z=1}^K \lambda_z = 1$. The parameters $(\lambda_z, \mu^{(z)}, \Sigma^{(z)})_{z=1}^K$ need to be trained, which is done using the EM algorithm. We will now show how the conditional is calculated exactly.

4.4.1 Conditional of Gaussian mixture model

Since the components are multivariate Gaussian distributions, we use <REF> and can define the conditional of a multivariate Gaussian as

$$p_z(y|x) = \mathcal{N}(y|\mu_{y|x}^{(z)}, \Sigma_{y|x}^{(z)}) \quad (4.3)$$

$$\mu_{y|x}^{(z)} := \mu_y^{(z)} + \Sigma_{yx}^{(z)} (\Sigma_{xx}^{(z)})^{-1} (x - \mu_x^{(z)}) \quad (4.4)$$

$$\Sigma_{y|x}^{(z)} := \Sigma_{yy}^{(z)} - \Sigma_{yx}^{(z)} (\Sigma_{xx}^{(z)})^{-1} \Sigma_{xy}^{(z)}. \quad (4.5)$$

Now, the conditional is defined straight forward from Section (4.2),

$$p(y|x) = \sum_{z=1}^K \gamma_z(x) \mathcal{N}(y|\mu_{y|x}^{(z)}, \Sigma_{y|x}^{(z)}) \quad (4.6)$$

$$\gamma_z(x) := \frac{\lambda_z \mathcal{N}(x|\mu_x^{(z)}, \Sigma_{xx}^{(z)})}{\sum_{z^*=1}^K \lambda_{z^*} \mathcal{N}(x|\mu_x^{(z^*)}, \Sigma_{xx}^{(z^*)})} \quad (4.7)$$

The computational complexity is $O(K \cdot d^3)$ (d is the dimension of x), since the matrix inversion of the covariance matrix $(\Sigma_{xx}^{(z)})^{-1}$ is the dominating cost and it happens for all the K components.

4.5 Sum product networks

A sum-product network (SPN) is a mixture model, which allows for exponentially many mixture components, but with only <linearly many parameters> and, thereby, tractable inference (i.e. conditionalization and marginalization queries). In short, the SPN consists of a computational graph, with tractable leaf distributions, which are combined using products and sums nodes, recursively. To keep the inference of the SPN tractable, we want to maintain certain properties when designing the SPN graph. First we need to define a scope.

Scope of nodes in SPN

A scope (sc) of a leaf node is the set of random variables among each dimension of $x = \{x_1, \dots, x_{\text{dim}(x)}\}$ and y of which the leaf distribution, $p_i(\cdot)$, defines a distribution function (in our implementation the leaf scopes are all singletons). The scope of a sum or product node, i , are defined recursively, $sc(i) = \cup_{j \in ch(i)} sc(j)$.

- A sum nodes children must have the same scope (completeness).
- A product nodes children must have distinct scopes (decomposability).
- Leaf nodes must have tractable inference.

The density of the mixture models is calculated in the following way,

Calculation of $p(x, y)$

Input: Fully trained SPN, with leaf distributions $p_i(\cdot)$ for $i \in \text{Leaf}(S)$ and weights $w_{i,j}$ for $(i, j) \in \{(i, j) | i \in \text{Sum}(S), j \in ch(i)\}$

```

function Eval(node i)
    if  $i \in \text{Leaf}(S)$  then
        return:  $p_i(x, y)$                                  $\triangleright$  evaluate leaf distributions at point  $(x, y)$ 
    if  $i \in \text{Sum}(S)$  then
        return:  $\sum_{j \in ch(i)} w_{i,j} \text{Eval}(j)$ 
    if  $i \in \text{Prod}(S)$  then
        return:  $\prod_{j \in ch(i)} \text{Eval}(j)$ 
     $p(x, y) = \text{Eval}(\text{root node})$ 

```

In this thesis, we implement the SPN similar to the RAT-SPN presented in [15], which ensures that we have a Complete and decomposable SPN. The following is the structure of the RAT-SPN,

1. Define C leaf distributions per random variable¹ (C is called "channels").
2. Pair up the elements in the set of random variables in a random way. If uneven set, then one element pairs with the empty set.
3. For each pair: Define C^2 product nodes by combining each combination of leaf nodes.
4. For each pair: Give the C^2 product nodes the same C sum node parents.
5. Now, pair up the pairs and repeat step 3 (with sum-nodes instead of leaf nodes) and 4.
6. At the final iterations: Give the C^2 product nodes 1 sum node parent.

This is a scalable and easy way to construct the SPN. For high-dimensional problems, we can limit the number of pairs defined in step 2 and instead, combine more of the randomly defined SPNs in several tracks T . This allows the model to be lucky in the case e.g. dimension x_3 and x_5 was a

¹Note that we define the random variables as the dimensions in the joints distribution, i.e. $\{x_1, \dots, x_{\text{Dim}(x)}, y\}$.

powerful combination. Figure 4.2 illustrates the concept of RAT-SPN for only one track $T = 1$ (more tracks would shuffle the pairs).

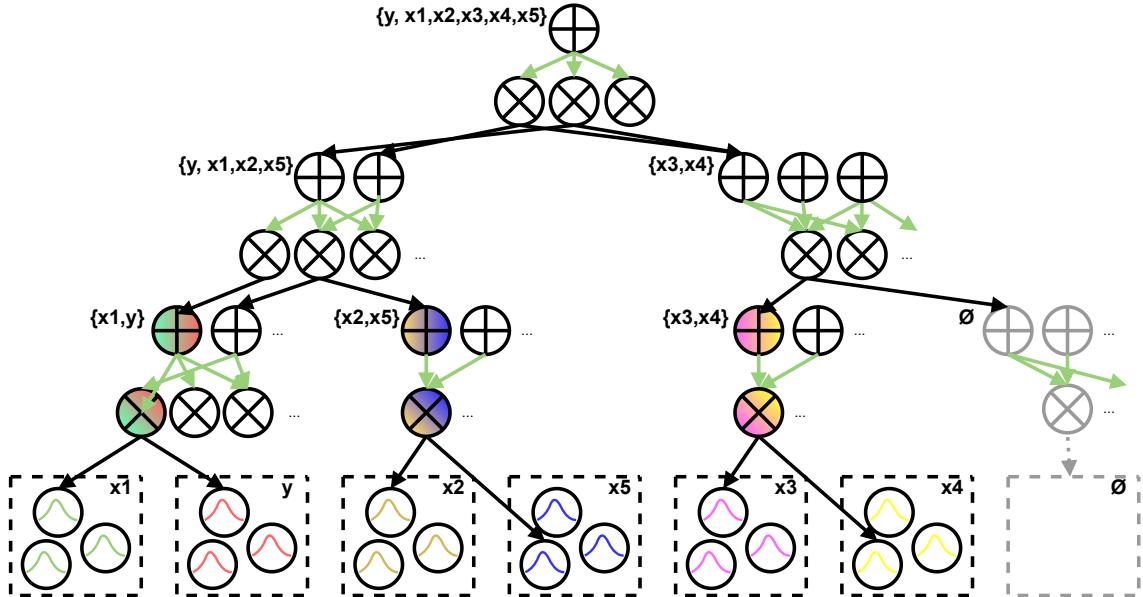


Figure 4.2: Illustration of random constructed sum-product network (RAT-SPN) for the joint distribution $p(x_1, \dots, x_5, y)$. The product nodes, \otimes , always combine 2 nodes from different scopes, while sum nodes, \oplus , sum all of the product nodes for similar scopes. Note the drawing is not complete; This illustrates a RAT-SPN with 3 channels, so every cluster of product nodes has size 9 and every cluster of sum nodes (except the root) has size 3.

Figure 4.4 illustrates how 3 simple Gaussian distributions from two different scopes x and y can be multiplied together and defined as many mixtures as the product of the numbers of distributions in each scope (i.e. 9). So by only training parameters for 6 distributions we obtain 9 distributions. In the middle figure, we see a data distribution with no need for all 9 mixture components and the weighting ensures that the unnecessary components are turned off. Figure 4.3 illustrates the graphical representation of the SPN for 2 dimensions - and shows that the SPN for small dimensions is not deep or complicated. In fact, if we look at the right figure in Figure 4.4, the SPN is just adding less flexibility.

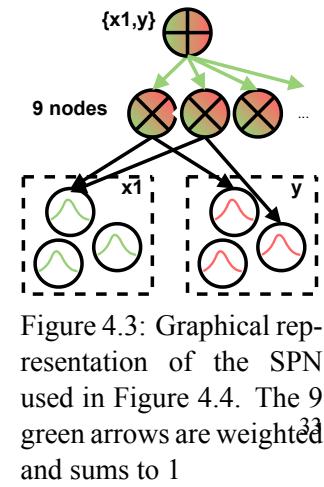


Figure 4.3: Graphical representation of the SPN used in Figure 4.4. The 9 green arrows are weighted and sums to 1

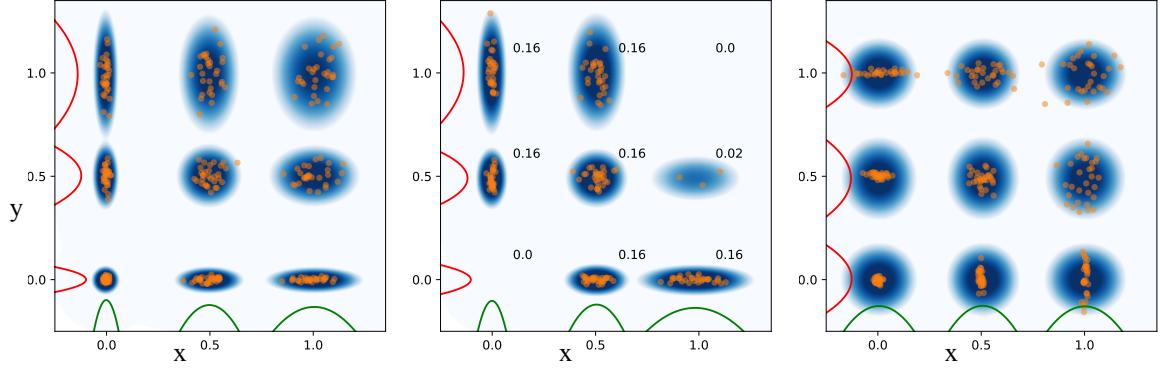


Figure 4.4: SPN on the joint probability $p(x, y)$ with 3 leaf distributions in each scope (shown on the axes), trained on 3 different data sets. Left: The data lies perfect for the SPN. Middle: Numbers in the graph represent how the weight of each mixture component is weighted. Right: The data is distributed badly for the SPN.

Note: SPN as neural network

<Lav om> The interpretation of an SPN as a neural network citevergari (what motivated us to look at them in the first place) Here, imagine the weights of the sum nodes are parameters, leaf distributions are input neurons, root node is output and all other nodes correspond to hidden neurons. Note: the depth is at most $\log_2(\#variables)$, yielding not much depth in Bayesian optimization tasks, where the number of dimensions typically is small.

4.5.1 SPN as a mixture model

Each sum-node can be interpreted as a categorical variable [??], i.e. a weighted dice. So each mixture component can be found by starting at the root sum-node and rolling the dice of which green arrow to continue the path through the SPN. If the path meets a product-node all children are included in the path. If the path meets a sum-node we roll a dice. Finally, if the path meets a leaf-node it terminates. The defined path is referred to as a sub-network, S_z , in the SPN and is equivalent to a mixture component. The total number mixture components equal the product of all sum-nodes children, i.e. $Z = \prod_{i \in \mathcal{S}_{\text{sum}}(S)} |\text{ch}(i)|$. i.e. an exponentially large amount.

Denote the set of edges in the sub-network $\mathcal{E}(S_z)$. Now we define a mixture coefficient, λ_z and component for each S_z as

$$\lambda_z := \prod_{(i,j) \in \mathcal{E}(S_z)} w_{i,j}, \quad p_z(x, y | \theta) := \prod_{i \in \mathcal{L}(S_z)} \phi_i(x, y),$$

where $\phi_i(x, y)$ is the leaf distribution at leaf node i parametrised with θ . It can now be proven that the SPN can be interpreted as the following mixture model,

$$p(x, y | w, \theta) = \sum_{z=1}^Z \lambda_z(w) p_z(x, y | \theta)$$

i.e. by the weighted sum of all Z sub-networks.

4.5.2 Conditional of SPN

Conviniently we can define the mixture model as

$$p_z(x, y) = \prod_{i \in x\text{Leaf}(z)} \phi_i(x) \prod_{i \in y\text{Leaf}(z)} \phi_i(y) \\ := p_{z_x}(x)p_{z_y}(y)$$

<obs connect til forgående sections> giving the conditional of the mixture and the responsibility

$$p(y|x) = \sum_{z=1}^n \gamma_z(x)p_{z_y}(y) \quad (4.8)$$

$$\gamma_z(x) = \frac{\lambda_z p_{z_x}(x)}{\sum_{z \in \Sigma(S)} \lambda_z p_{z_x}(x)} \quad (4.9)$$

calculation of responsibility

The responsibility of a datapoint to belong to one mixture component, is given by

$$\gamma_z(x) = \frac{\lambda_z p_z(x)}{\sum_{z^*} \lambda_{z^*} p_{z^*}(x)}$$

We can prove that the responsibility is equal to the gradient of the log likelihood,

$$L := \sum_n \log \sum_z \lambda_z \exp \psi_z(x_n)$$

where we define $\psi_z(x_n) = \log p_z(x_n)$. Take the gradient

$$\frac{\partial L}{\partial \psi_z(x_n)} = \frac{\lambda_z p_z(x_n)}{\sum_{z^*} \lambda_{z^*} p_{z^*}(x)}$$

Note that the gradient easily can be found using automatic differentiation.

4.6 Mixture model training

The following section presents the expectation-maximization algorithm, which is used to train the Gaussian mixture model and the SPN.

4.6.1 Expectation-maximization for mixture models

Mixture models can be seen as probabilistic graphical models, <fig> there one mixture component is picked according to the realization of a categorical variable \mathbf{Z} with parameters according the the mixture weights, i.e we can reformulate,

$$p(x) = \sum_{k=1}^K w_k p_k(x) \quad (4.10)$$

$$\iff p(x) = p_z(x), \quad z \sim \text{Cat}(w_1, \dots, w_K). \quad (4.11)$$

In fact $p_z(x)$ is a conditional distribution, $p(x|z)$, and combined with the distribution of Z we can define the joint

$$p(x, z) := p_z(x)p(z)$$

In the case of a statistical model, data \mathcal{D} is fitted by the mixture model by tuning the model parameters $\theta = \{w, \text{paramers for } p_i\}$. Then the joint distribution $p(\mathcal{D}, z|\theta)$ is referred as the *complete-data* likelihood in the EM algorithm.

$$p(\mathcal{D}, z|\theta) := p(\mathcal{D}|z, \theta)p(z|\theta)$$

When fitting model parameters we essentially want to find the parameters, that maximize the probability of the parameters given the data, $p(\theta|\mathcal{D})$. Assuming an uninformative/flat prior $p(\theta)$,

$$\begin{aligned} p(\theta|\mathcal{D}) &= \frac{p(\mathcal{D}|\theta)p(\theta)}{p(\mathcal{D})} \\ \Rightarrow \arg \max_{\theta} p(\theta|\mathcal{D}) &= \arg \max_{\theta} p(\mathcal{D}|\theta) \end{aligned}$$

we arrive at the maximum likelihood estimate (MLE). The task of finding the MLE is conveniently done using EM algorithm, since we can look at the likelihood as the marginalized *complete-data* likelihood,

$$p(\mathcal{D}|\theta) = \sum_z p(\mathcal{D}, z|\theta)$$

Background: Expectation-maximization EM <based on [16]

Expectation maximization is a convenient method for finding ML (or MAP) estimate of a latent variable model. We consider a probabilistic model parametrised with θ ,

$$p(\mathbf{X}, \mathbf{Z}|\theta)$$

where we denote all latent variables \mathbf{Z} , and observed variables \mathbf{X} . Our goal is to find the maximum of the likelihood,

$$p(\mathbf{X}|\theta) = \int p(\mathbf{X}, \mathbf{Z}|\theta)\mu(d\mathbf{Z})$$

maximizing the likelihood itself $p(\mathbf{X}|\theta)$ is assumed difficult but maximizing of the *complete-data* likelihood $p(\mathbf{X}, \mathbf{Z}|\theta)$ is much easier. The algorithm iterates over two steps: The expectation (E) step and the maximization (M) step, defined in the following way for iteration t ,

E-step

Define the functional $Q(\theta, \theta^{(t)})$, to be the expected value of the complete-data log likelihood (log likelihood function of θ), with respect to the only random quantity \mathbf{Z} , which is assumed to follow a distribution with the density $p(\mathbf{Z}|\mathbf{X}, \theta^{(t)})$, i.e. the conditional distribution of \mathbf{Z} given \mathbf{X} and the current parameter point estimate $\theta^{(t)}$:

$$Q(\theta, \theta^{(t)}) := E_{p(\mathbf{Z}|\mathbf{X}, \theta^{(t)})}[\log p(\mathbf{X}, \mathbf{Z}|\theta)]$$

M-step

After the E-step we find the point estimate $\theta^{(t+1)}$ which maximizes $Q(\cdot|\theta^{(t)})$, i.e.

$$\theta^{(t+1)} = \arg \max_{\theta} Q(\theta|\theta^{(t)})$$

(local) maximization of $p(\mathcal{D}|\theta)$

```
Input: dataset  $\mathcal{D}$ , joint model  $p(\mathcal{D}, \mathbf{Z}|\theta)$ 
while Not converged do
     $Q(\cdot, \theta^{(t)}) \leftarrow E_{p(\mathbf{Z}|\mathcal{D}, \theta^{(t)})}[\log p(\mathcal{D}, \mathbf{Z}|\cdot)]$   $\triangleright$  E-step
     $\theta^{(t+1)} \leftarrow \arg \max_{\theta} Q(\theta|\theta^{(t)})$   $\triangleright$  M-step
return:  $\theta^{(end)}$ 
```

Proof of correctness

We will now give a short proof that maximizing $Q(\cdot|\theta^{(t)})$ maximizes the likelihood $p(\mathbf{X}|\theta)$, where we assume that \mathbf{Z} is a random vector with a discrete distribution. This allow us to use Gibbs inequality:

$$\sum_z p_1(z) \log p_1(z) \geq \sum_z p_2(z) \log p_2(z)$$

where $p_1(\cdot)$ and $p_2(\cdot)$ are densities belonging to two discrete distributions of Z , equality if $p_1(\cdot) = p_2(\cdot)$. From now on we will alter the subscript on the expectations, just have in mind that

$$E_{\theta^{(t)}}[g(Z)] := E_{p(\mathbf{Z}|\mathbf{X}, \theta^{(t)})}[g(Z)] = \sum_z g(z)p(\mathbf{z}|\mathbf{X}, \theta^{(t)})$$

Now to the proof: From bayes rule $p(\mathbf{X}|\theta) = \frac{p(\mathbf{X}, \mathbf{Z})}{p(\mathbf{Z})}$ we can write

$$\log p(\mathbf{X}|\theta) = \log p(\mathbf{X}, \mathbf{Z}) - \log p(\mathbf{Z}|\mathbf{X}, \theta)$$

Now, taking the expectation of the above w.r.t. $p(\mathbf{Z}|\mathbf{X}, \theta^{(t)})$, yields,

$$\begin{aligned} \log p(\mathbf{X}|\theta) &= E_{\theta^{(t)}}[\log p(\mathbf{X}, \mathbf{Z}|\theta)] - E_{\theta^{(t)}}[\log p(\mathbf{Z}|\mathbf{X}, \theta)] \\ &= Q(\theta, \theta^{(t)}) + E_{\theta^{(t)}}[\log p(\mathbf{Z}|\mathbf{X}, \theta)] \end{aligned}$$

Since the above equation holds for any θ , it also holds for $\theta^{(t)}$ now we have,

$$\log p(\mathbf{X}|\theta^{(t)}) = Q(\theta^{(t)}, \theta^{(t)}) + E_{\theta^{(t)}}[\log p(\mathbf{Z}|\mathbf{X}, \theta^{(t)})]$$

Subtracting the two equations, we get,

$$\log p(\mathbf{X}|\theta) - \log p(\mathbf{X}|\theta^{(t)}) = Q(\theta, \theta^{(t)}) - Q(\theta^{(t)}, \theta^{(t)}) + E_{\theta^{(t)}}[\log p(\mathbf{Z}|\mathbf{X}, \theta)] - E_{\theta^{(t)}}[\log p(\mathbf{Z}|\mathbf{X}, \theta^{(t)})]$$

From Gibb's inequality we have that $E_{\theta^{(t)}}[\log p(\mathbf{Z}|\mathbf{X}, \theta^{(t)})] \leq E_{\theta^{(t)}}[\log p(\mathbf{Z}|\mathbf{X}, \theta)]$ where equality only holds for $\theta^{(t)} = \theta$, giving

$$\log p(\mathbf{X}|\theta) - \log p(\mathbf{X}|\theta^{(t)}) \geq Q(\theta, \theta^{(t)}) - Q(\theta^{(t)}, \theta^{(t)})$$

so optimizing $Q(\theta, \theta^{(t)})$ will optimize $\log p(\mathbf{X}|\theta)$ as least as much.

4.6.2 EM for Gaussian mixture

For a Gaussian mixture the p_k distributions in (4.10) is substituted by Gaussian pdfs, i.e. $p_k(x) = \mathcal{N}(x|\mu_k, \Sigma_k)$ and the density of a categorical distribution is $p(z) = \sum_{k=1}^K 1_{z=k} w_k = w_z$, combining the two we get the joint distribution,

$$p(x, z|w, \mu, \Sigma) = w_z \mathcal{N}(x|\mu_z, \Sigma_z)$$

Taking the log and defining $\theta = \{\mu_1, \Sigma_1, w_1, \dots, \mu_K, \Sigma_K, w_K\}$, and assuming iid data

$$\log p(X, Z|\theta) = \sum_i^n (\log(w_{z_i}) + \log(\mathcal{N}(x_i|\mu_{z_i}, \sigma_{z_i})))$$

Now we are ready to calculate $Q(\theta, \theta^{(t)})$, by taking the expectation of the complete-data log likelihood with respect to the distribution, $p(Z|X, \theta)$,

$$\begin{aligned} E_{p(Z|X, \theta^{(t)})}[\log p(X, Z|\theta)] &= \sum_i^n E_{p(Z|X, \theta^{(t)})}[p(X_i, Z_i|\theta)] \\ &= \sum_i^n E_{p(z_i|x_i, \theta^{(t)})}[p(x_i, z_i|\theta)] \end{aligned}$$

Expectation with respect to unnecessary variables

the last equation holds since taking expectation over a function of a random variable x with respect to a that random variable and more random variables, x, y , is equivalent to the expectation with respect to just x , i.e.

$$\begin{aligned} E_{x,y}[g(x)] &= \int \int g(x)p(x, y)dydx \\ &= \int g(x) \int p(x, y)dydx \\ &= \int g(x)p(x)dy = E_x[g(x)] \end{aligned}$$

the posterior distribution is calculated the following way,

$$\begin{aligned} p(z|x, \theta^{(t)}) &= \frac{p(x, z|\theta^{(t)})}{p(x|\theta^{(t)})} \\ &= \frac{p(x, z|\theta^{(t)})}{\sum_z p(x, z|\theta^{(t)})} \\ &= \frac{w_z^{(t)} \mathcal{N}(x|\mu_z^{(t)}, \Sigma_z^{(t)})}{\sum_{k=1}^K w_k^{(t)} \mathcal{N}(x|\mu_k^{(t)}, \Sigma_k^{(t)})} \end{aligned}$$

For simplification we will denote, $\gamma^{(t)}(z_i) := p(z_i|x_i, \theta^{(t)})$, interpreted as the probability of datapoint x_i to belong to class z_i . Bishop [16] calls this probability function the *responsibility*. We can now conclude the **E-step**.

$$\begin{aligned}
Q(\cdot, \theta^{(t)}) &= \sum_{i=1}^n p(x_i, z_i | \cdot) \gamma^{(t)}(z_i) \\
&= \sum_{i=1}^n \left[\gamma^{(t)}(z_i) \log(\cdot_{z_i}) + \gamma^{(t)}(z_i) \log(\mathcal{N}(x_i | \cdot_{z_i}, \cdot_{z_i})) \right]
\end{aligned}$$

or more concretely $\theta = \{\mu_1, \Sigma_1, w_1, \dots, \mu_K, \Sigma_K, w_K\}$,

$$Q(\theta, \theta^{(t)}) = \sum_{i=1}^n \gamma^{(t)}(z_i) \log(w_{z_i}) + \gamma^{(t)}(z_i) \log(\mathcal{N}(x_i | \mu_{z_i}, \Sigma_{z_i})).$$

$Q(\cdot, \theta^{(t)})$ is a concave function - the Gaussian is log-concave and a sum of concave functions is also concave - so it is sufficient and necessary to find its maxima by the root of its derivative,

$$\frac{d}{d\theta} Q(\theta^*, \theta^{(t)}) = 0 \iff \theta^* = \arg \max_{\theta} Q(\theta, \theta^{(t)})$$

Giving the updates...

EM for SPN

5 Results

Lav systematiske resultater. Udvælg functionsklasser at kigge på

<reproducer resultater fra Arayns thesis> Egne forsøg med SPN og mixture regression

5.1 Implementation

The Gaussian process regression is implemented using the Scikit-learn Gaussian process implementation with the Matern kernel with $\nu = 1.5$ and the y-values are normalized for the prior distribution to be reasonable (mean 0 and variance 1). The lengthscale is optimized by maximizing the marginalized likelihood using the limited memory quasi-newton solver with bounds l-bfgs-b with 200 restarts.

The Bayesian neural network is implemented using Numpyro - which is a python library for probabilistic machine learning, developed by some of the people behind Pyro, but instead of using PyTorch as backend, Numpyro uses Jax. This allows for a significantly large speedup when doing MCMC, i.e. NUTS sampling. This was however still very slow and we, therefore, limited the network size to a small 3 layer with 10 nodes on each layer network. The prior distribution for weights is a standard normal distribution, and the bias normal priors are set a bit less restrictive with a standard deviation of 2 instead. This is reasonable since the data is always standardized.

5.1.1 standardized data

Before the data reach any of the models, it is standardized. Which is a scaling and translation such that the data's empirical mean and standard deviation are 0 and 1, respectively. In that way is much easier to control the parameters in the models, since the data it fits and predicts is always on the same scale. The transformation is as follows, the first time the models see the data, the empirical mean and standard deviation is recorded both for x and y , (note x can be a vector), giving μ_x, μ_y, σ_x and σ_y . Next, all data is transformed using the transformation,

$$T_x(\cdot) := \frac{\cdot - \mu_x}{\sigma_x}$$

When we predict the x is transformed, the model output a prediction and then the inverse transform is mapping the prediction from the standardised domain to the original domain, $T_y^{-1}(\hat{y}) := \hat{y} \cdot \sigma_x + \mu_x$

5.2 Model compartment on test problems

Bayesian optimization is typically performed on black-box functions, and thereby the Bayesian regression model is trained on data from all kinds of underlying problems. Now we want to test the performance of different regression models on different types of 1D problems, all in the interval $x \in [-100, 100]$:

- Test 1: A well-behaved sine-function,
- Test 2: A highly discontinuous function,
- Test 3: A multi-modal objective function,
- Test 4: An anisotropic objective function.

It is common to have many parameters to tune in Bayesian optimization (in 1D a human could potentially assist the surrogate model since the regression can be plotted and judged by eye). Nevertheless, we will keep the domain in 1D to establish a more informative evaluation of the model performance. This will establish some intuition about the models and

Model	Specification	Training
BNN	3 layers of 50 tanh nodes $p(\mathbf{w}, b) \sim \mathcal{N}(0, 1)$ $p(\sigma) \sim \text{InvGa}(1000, 1)$	NUTS(500 burn-in, 500 samples)
BOHamiANN	3 layers of 50 tanh nodes $p(\mathbf{w}, b) \sim \mathcal{N}(0, \sigma_w)$ $p(\sigma) \sim \text{LogNormal}(??)$ $p(\sigma_w) \sim \text{Gamma}(??)$	Adaptive stochastic HMC (1000 burn-in, every 5 of 2000 samples)
GP	Mantern kernel 52	Maximize marginalized likelihood 20 restarts of BFGS optimization
GMR	Training sklearn GMM, EM of MLE with 3 restarts. pluggin into GMR software [14].	BO Cross-validation 30 fold, tuning number of components and prior weight
SPN	Trained using 3 restarts of EM of MAP	BO Cross-validation 30 fold, tuning: hyperpriors and prior weight
KDE	Gaussian around all datapoints with a x-variance and y-variance	BO Cross-validation 30 fold, testing x-variance and y-variance and prior weight

Table 5.1: Overview of chosen models

Whereas a true Bayesian would not choose a specific type of model, but using all models , however, this would indeed be infeasible. We need to limit the scope, For the GP, we do 20 restarts in the emperical maximization. And the manteen kernel prior with $\nu = 2.5$. BNN, is a 50x50x50 tanh layers with standard Gaussain priors on. And a inverse gamma (1000, 1) prior on the noise. Trained with 100 burn in and 100 samples. BOHAMIANN is similar but uses a different noise prior, and trains using adaptive HMC method. The mixture models are trained using crossvalidation scored on the mean predictive log .. posterior (formally speaking this is not a likelihood, but we will keep it as it is almost the same) The tuning parameters We do 40 iterations SPN is trained using EM with maximum 1000 epochs (is terminated if the progress is stalling). it is trained 2 times. [Lav den historie](#) GMR is trained using EM but this is done by the sklearn software.

Test1: Well-behaved problem

The first problem will establish some benchmark since this is a simple function to fit. Its exact definition is,

$$f(x) = x \cdot \sin\left(\frac{x}{50}\pi\right) + 150 + \frac{x}{10} + \sin(x) \quad x \in [-100, 100]$$

giving a smooth wave function, with the optimum around -80 . Note that $\sin(x) \in [-1, 1]$ contribute with some small high frequency surface waves. This should be an easy task for the discriminative models, this is indeed also what we see in the learning curve left of Figure 5.1 where the beginning is dominated by them.

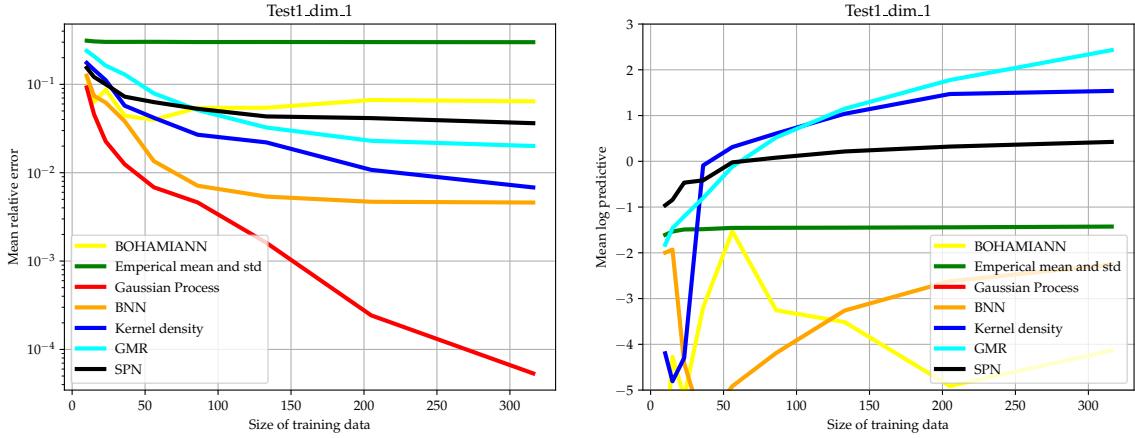


Figure 5.1: Mean predictive performance MAE (left) and mean predictiv probalility (right) as functions of number of data points. All curves represent the average across 10 runs for each model. The Gaussian process has the bedst predictive power, however it scores very low in the

To get a deeper understanding of Figure 5.1, we plot one of the 10 runs for 23 data points, in Figure 5.2, and for 56 data points in Figure 5.3.

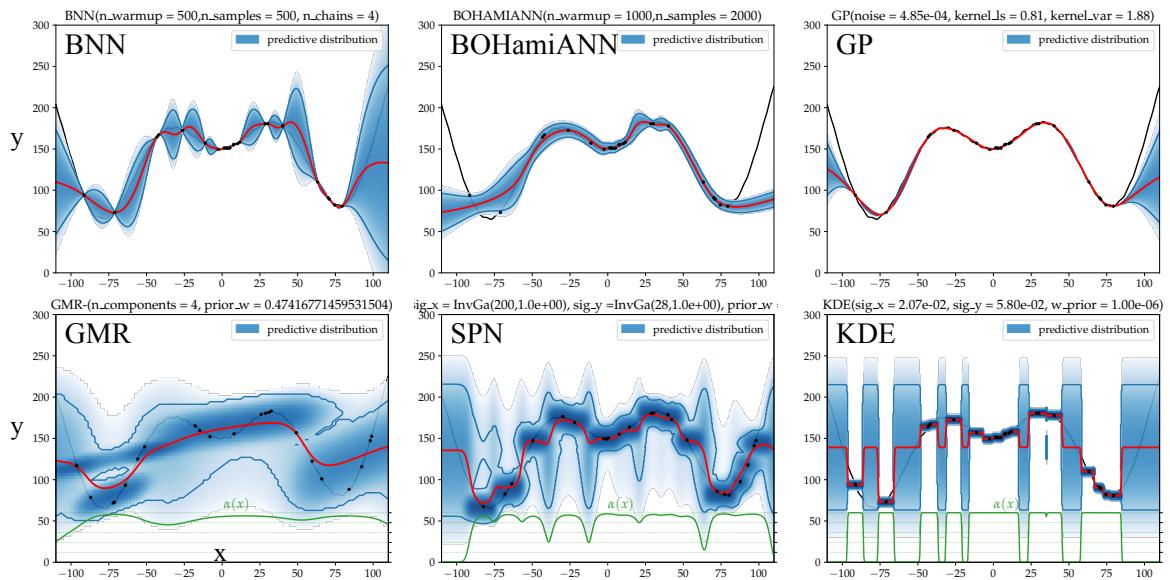


Figure 5.2: Plots visulising the results in figure at $n_{data} = 23$

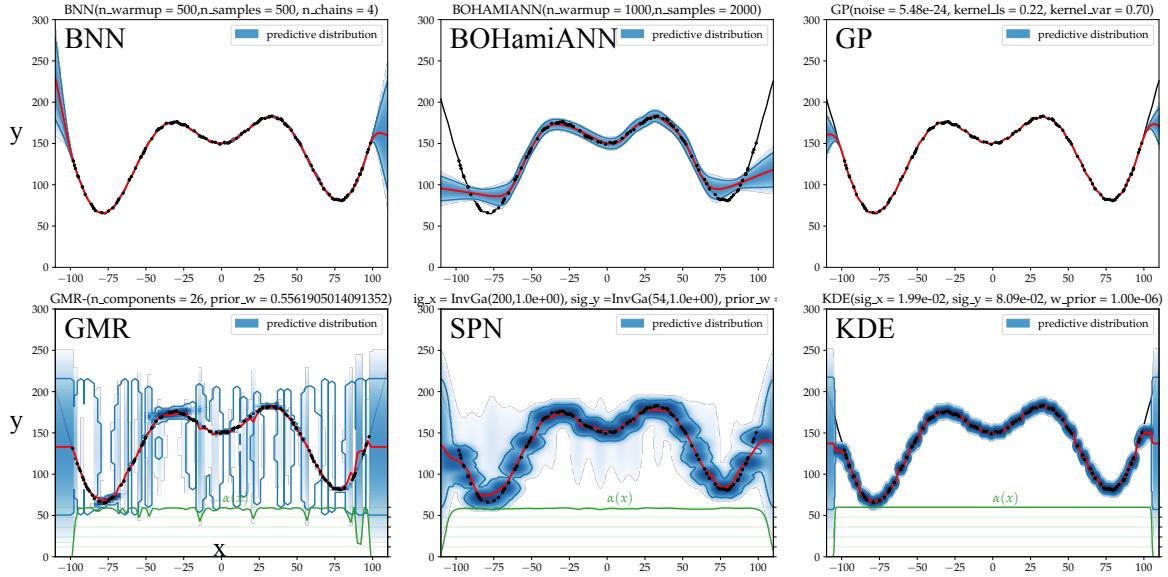


Figure 5.3: Plots visualising the results in figure at $n_{data} = 133$

The Gaussian process is however overconfident in its prediction and assigns almost 0 probability to some of the 10000 test points, yielding very low mean log predictive likelihood. The Bayesian neural networks learning curve stagnates around 100 data points, however, it provides a decent mean log predictive likelihood. BOHamIANN performs well in the beginning but seems not expressive enough for this task. The architecture of the neural network is besides they use a log-normal prior on the variance and a hyper prior on the variance parameter of the weights. But it seems like the algorithm does not converge?. The mixture models are crossvalidated to maximize the predive likelihood,

Test2: Discontinuous problem

As GP and BNN have a natural assumption of continuity we want to investigate their performance on a discontinuous problem. The problem is a step function, ...

This is a type of problem where we would expect the GP to not perform well, BNN should be the better

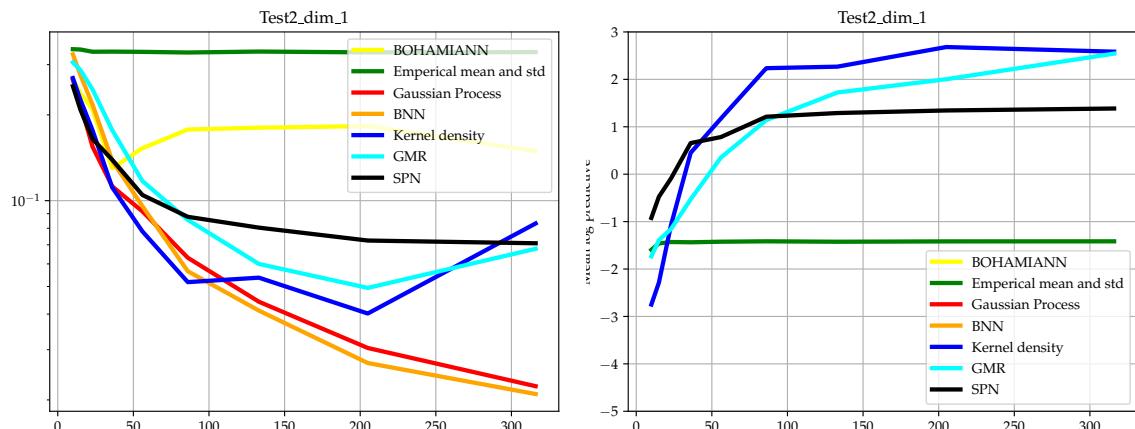


Figure 5.4: Plots visualising the results in above figure.

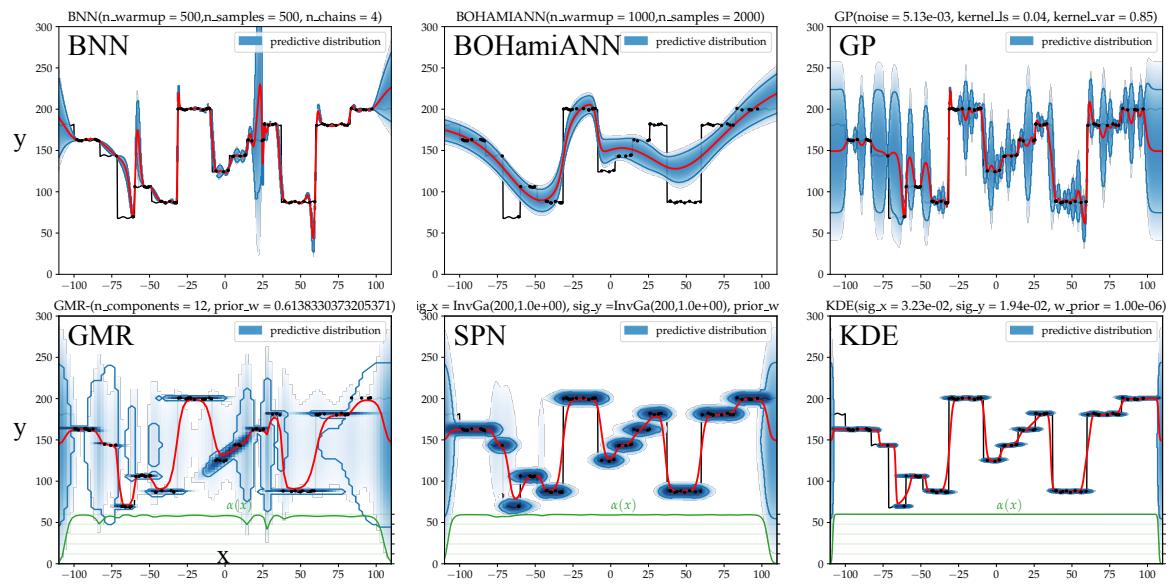


Figure 5.5: Plots visualising the results in figure at $n_{data} = ?$

5.2.1 Test3: multi-modal problem

Multimodal problems.

Here are the more interesting problems for the mixture regression methods.

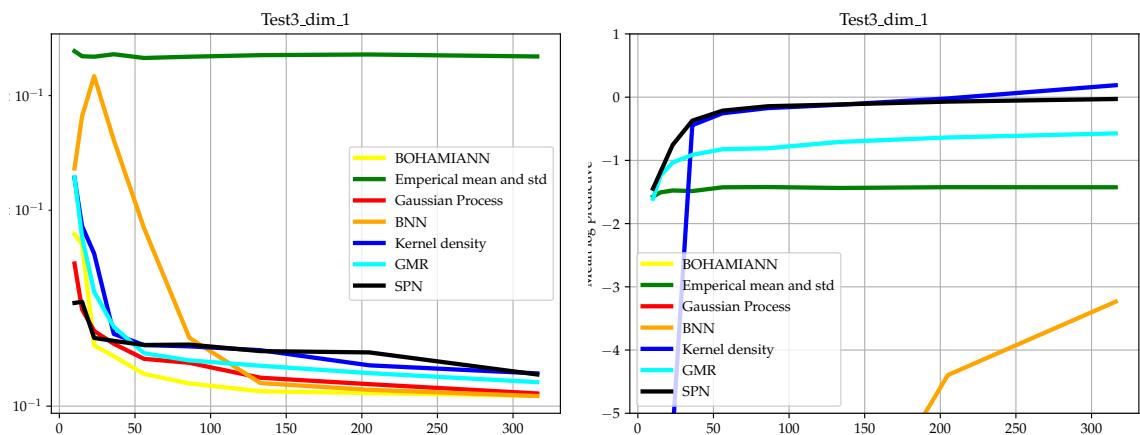


Figure 5.6: Plots visualising the results in above figure.

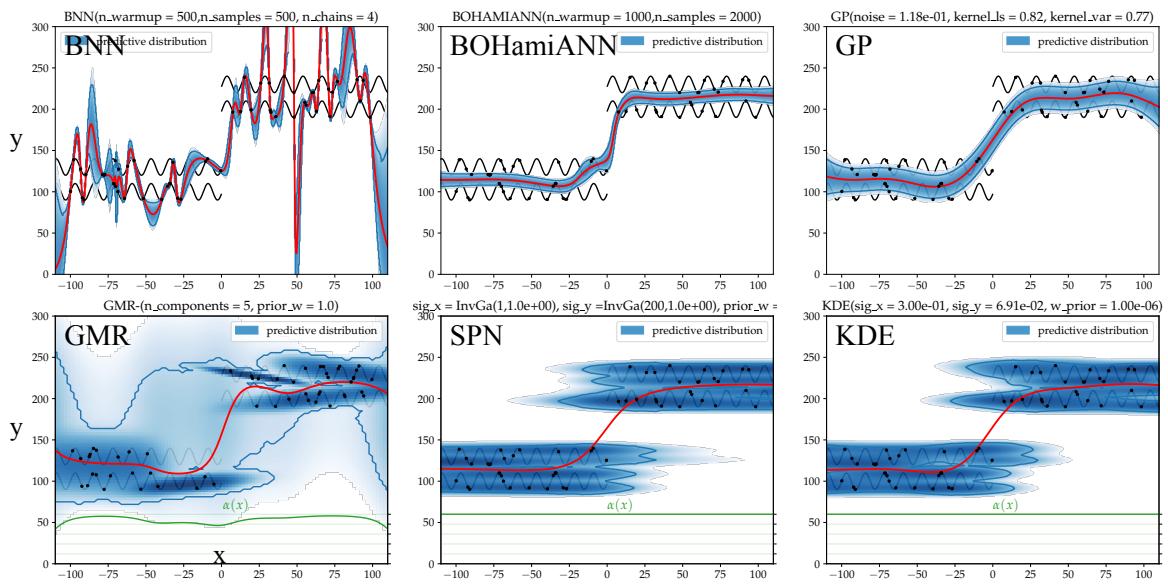


Figure 5.7: Plots visualising the results in figure at $n_{data} = ?$

5.2.2 Test4: anisotropic problem

Finally this problem has low frequency in the beginning but ends out with a very high frequency. This is a difficult problem for the GP as its

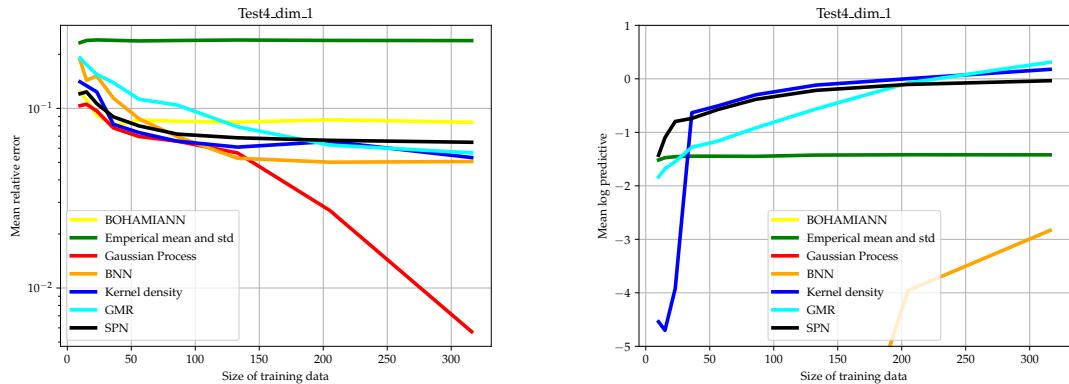


Figure 5.8: Plots visualising the results in above figure.

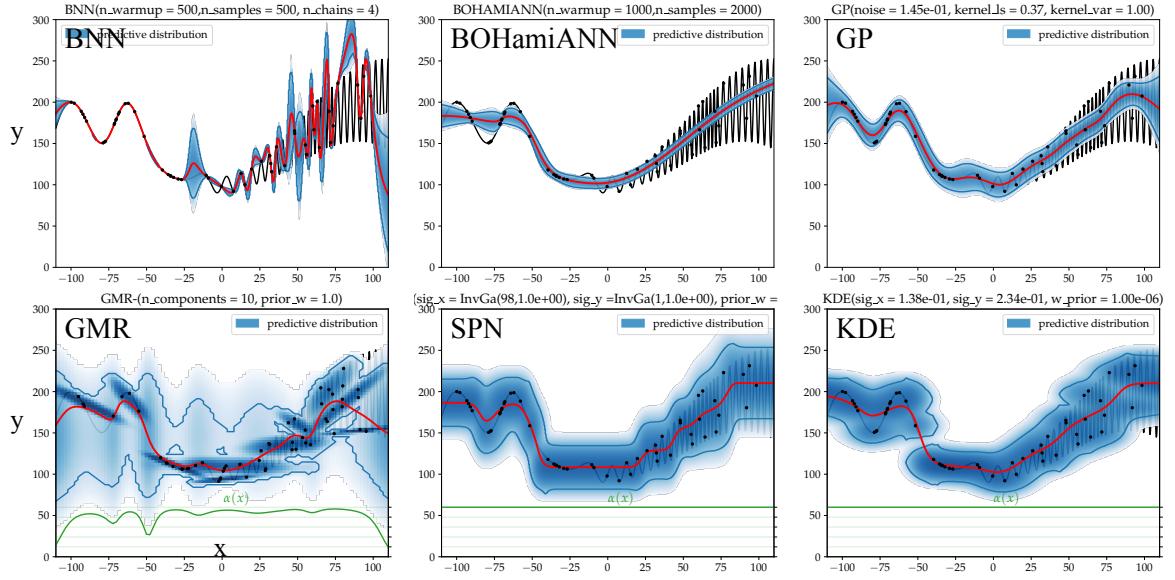


Figure 5.9: Plots visualising the results in figure at $n_{data} = ?$

5.3 Regression analysis

As described in the previous sections, an essential part of Bayesian optimization and the decision theory built around Bayesian optimization is that the regression model is correct. We will therefore look at how good the regression models are in terms of accurate prediction and correct uncertainty estimation.

5.3.1 uncertainty quantification

The probabilistic model is given as

$$p(y|x, \mathcal{D}) = \mathcal{N}(y|\mu_{\mathcal{D}}(x), \sigma_{\mathcal{D}}^2(x))$$

where the mean, and variance functions are different for all the models. Given a trained model, we quantify its ability to capture uncertainty with the average predictive likelihood/ probability of the observation, given a test input x_i the the density of predictive distribution is evaluated in the corresponding test output y_i ,

$$\overline{p(y_i|x_i, \mathcal{D})} := \frac{1}{n} \sum_{i=1}^n p(y_i|x_i, \mathcal{D})$$

note that the above might lead to that it is more important to classify one test point really well, so what we actually would rather test is the test point evaluated in the predictive posterior

$$p(\mathbf{y}|\mathbf{x}, \mathcal{D}) = \prod p(y_i|x_i, \mathcal{D})$$

where it is much more convenient to deal with it in the log space,

$$\log p(\mathbf{y}|\mathbf{x}, \mathcal{D}) = \sum \log p(y_i|x_i, \mathcal{D})$$

which makes it convenient to get the mean log prediction.

there the bigger the mean predictive likelihood is, the better. **it is not called predictive likelihood!!**

Figure 5.10: Regression of a probabilistic objective function, is not a smart choice using anything else than a mixture regression model. Top we see the performance of 5 different regression models fitted to an increasing amount of training data, the underlying function is tricky, as it jumps between multiple objective functions yielding a violation to most of the generative models, where most are capable of handling gaussian noise this is not gaussian noise and hence a very difficult problem. This kind of objective function could definitely be relevant in certain cases.

Figure 5.11: Plots visualising the results in above figure.

5.3.2 prediction quantification

Here we use the mean absolute error to quantify the prediction error. The i'th test point is (x_i, y_i) and the mean absolute error is given as, $MAE := \frac{1}{n} \sum_{i=1}^n |\mu_{\mathcal{D}}(x_i) - y_i|$

5.3.3 regression benchmark

We will benchmark our different regression models against a simple empirical mean and empirical std. normal distribution benchmark,

$$p(y|x\mathcal{D}) = \mathcal{N}(y|\bar{y}, \bar{\sigma}^2(\mathbf{y}))$$

where $\bar{y} = \frac{1}{n} \sum_{i=1}^n y_i$ and $\bar{\sigma}^2(\mathbf{y}) = \frac{1}{n-1} \sum_{i=1}^n (y_i - \bar{y})^2$ this is however not a good model for Bayesian optimization, as it will not provide a new candidate point, as all points are equally good.

5.4 Mixture regression

One could define a generative story, flip a coin, then the data will be fitted with this Gaussian.!

<data generating process> Model do well when they are the data generating process, but if they are not, then they do bad. If you collect all model,

What model to chose? the standard answer of a Bayesian should be: Why choose? If there is uncertainty about them, then we can just average them. Pic the maximum would be frquencialistic.

Could we combine GP and SPN?

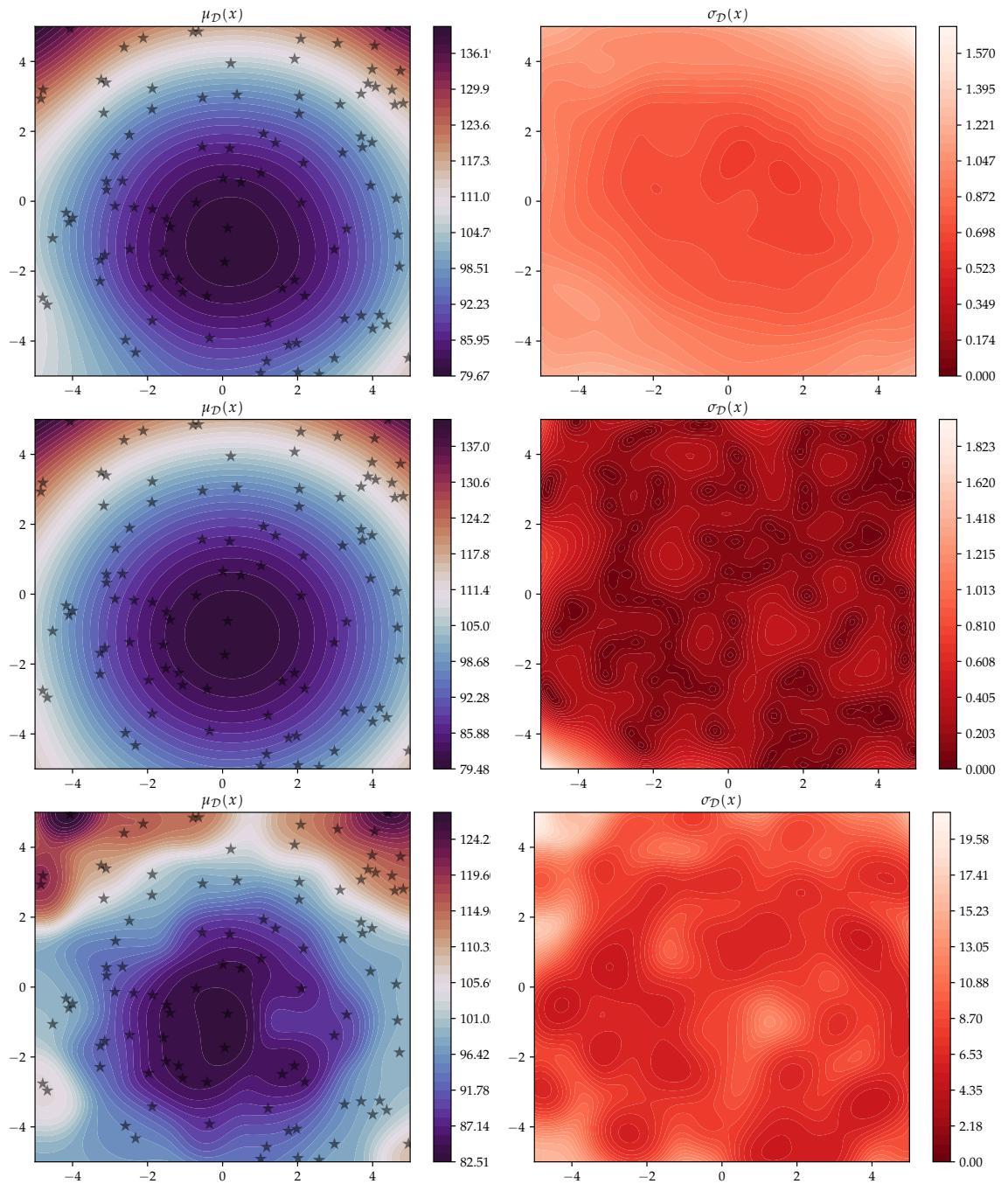
ensample of models .. Simulation studies.

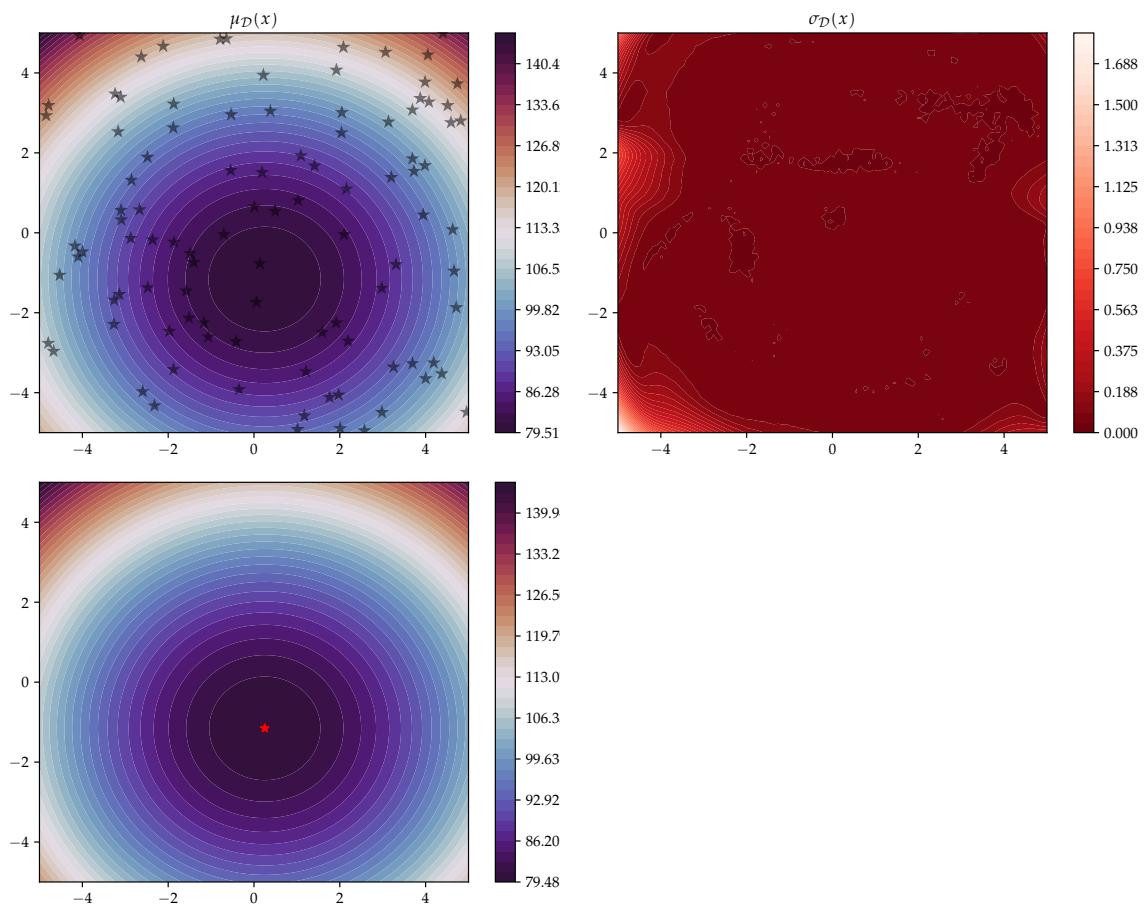
5.5 Regression analysis of GP, BOHAMIANN and NumpyNN 1D

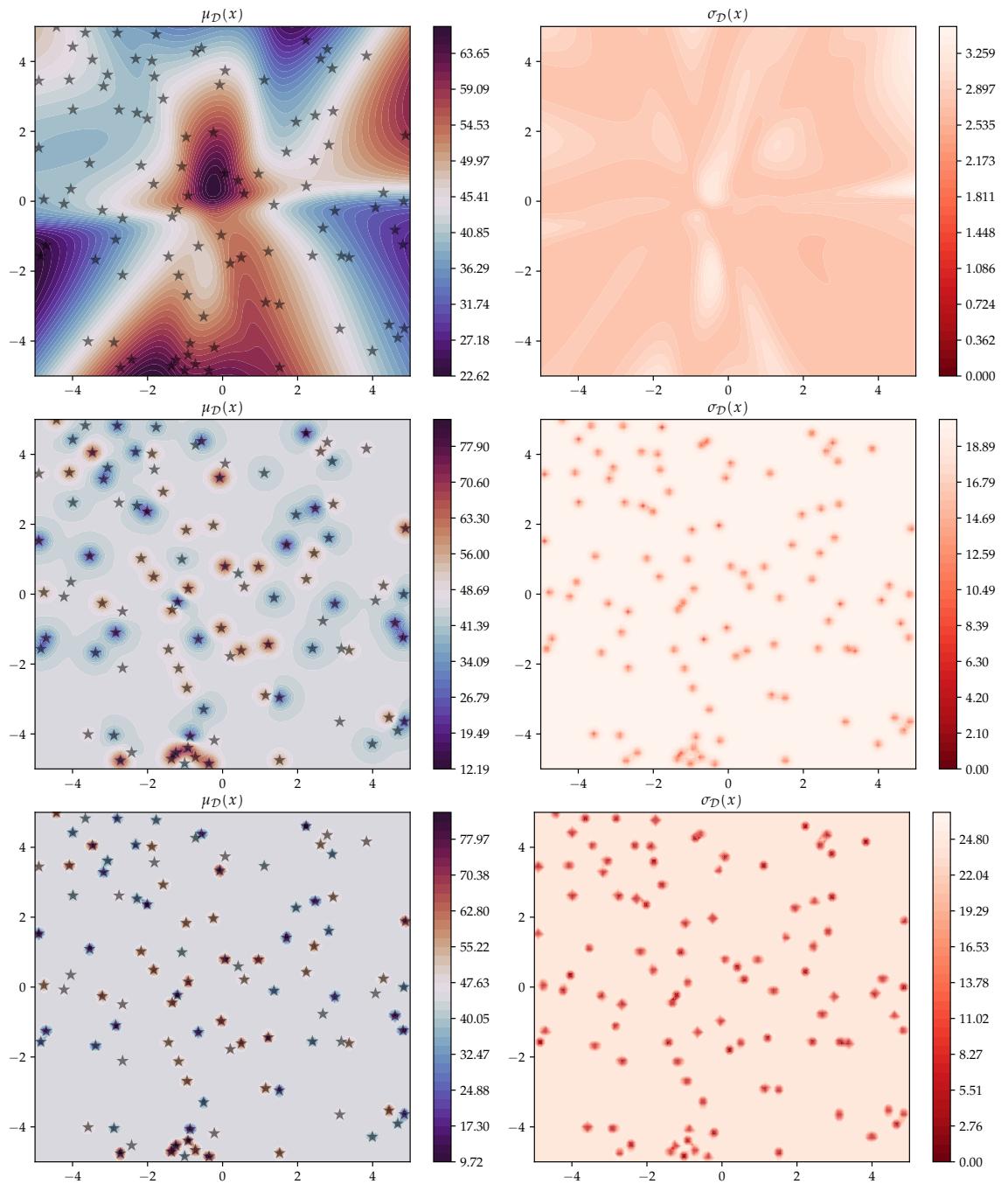
5.6 Regression analysis of GP, BOHAMIANN and NumpyNN 2D

5.7 Mixture regression on simple functions

Choosing a good set of design parameters is crucial, the manipulation...







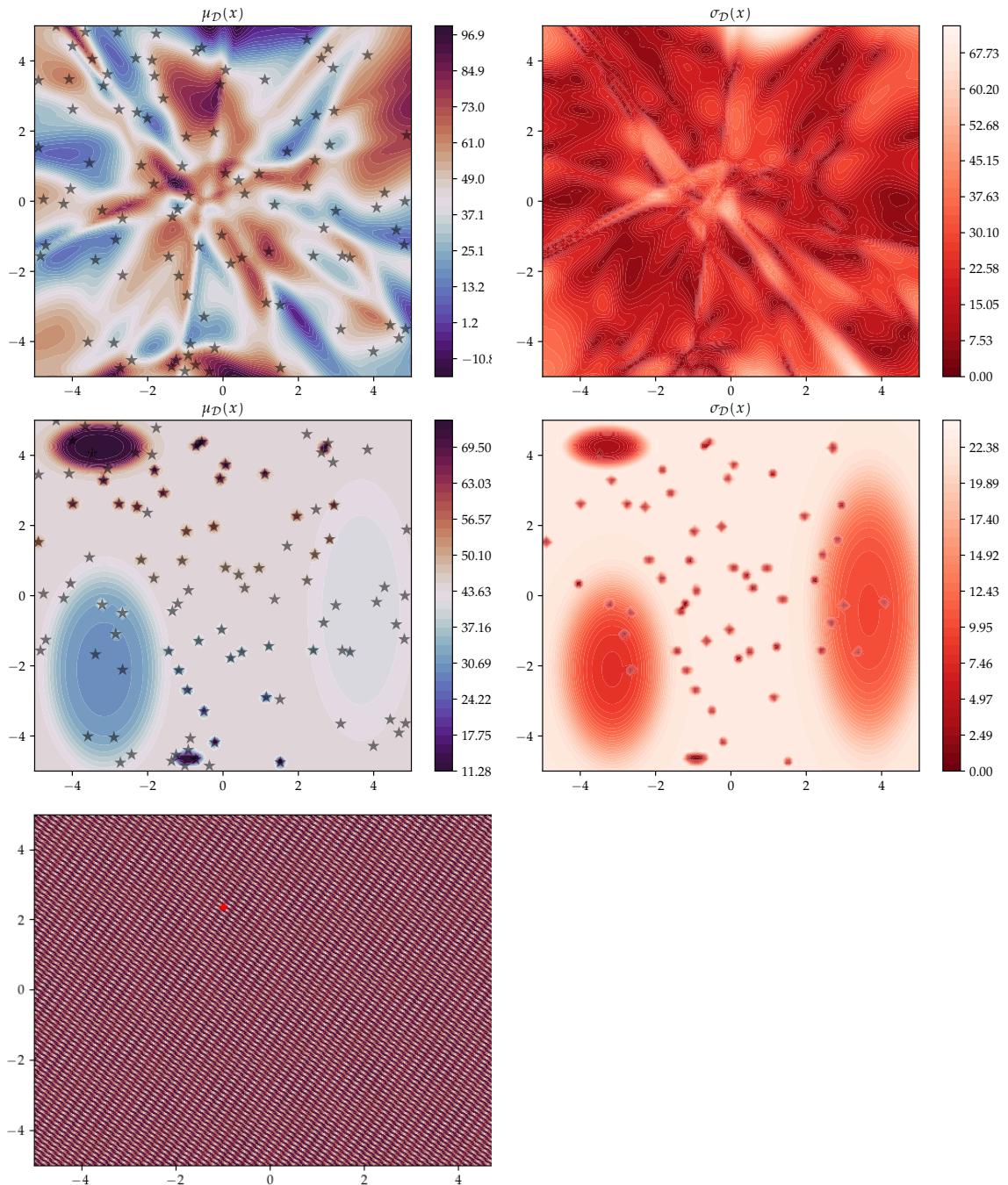


Figure 5.12: 2D Regression plot for a few of the problems, with the correct

Figure 5.13: Regression plot for one problem with all dims: Number of data points / dims, mean squared error, with bayesline mean prediction

Figure 5.14: Regression plot for another problem

	f1	f2	f3	f4	f5
BO_numpy	4.62(13.0)	897.13(39.0)	2.07(36.0)	10.14(39.0)	0.03(28.0)
BO_BOH	0.33(32.5)	552.83(27.0)	5.51(33.0)	10.33(37.0)	0.03(28.0)
BO_Gaus	0.89(8.0)	21.48(31.5)	21.86(21.0)	16.32(25.5)	0.03(22.5)
BO_Naiv	3.25(9.0)	72571.84(28.0)	19.41(15.0)	19.61(8.5)	4.35(21.0)
BO_em	1.23(24.5)	455.28(10.0)	6.74(8.5)	5.98(30.5)	6.00(22.5)

Figure 5.15: Distance to optima $f(x^{best}) - f^*$ using Bayesian optimization with different surrogates and using expected improvement with a budget of 40 samples for group 1: "5 separable functions"

	f6	f7	f8	f9
BO_numpy	1.31(28.0)	2.65(10.5)	nan(nan)	nan(nan)
BO_BOH	0.05(33.0)	1.68(17.0)	10.70(16.0)	2.31(39.0)
BO_Gaus	6.53(32.0)	0.60(12.0)	1.14(18.8)	0.27(25.0)
BO_Naiv	4.74(20.0)	4.71(25.5)	11.87(2.0)	20.09(15.5)
BO_em	5.43(20.5)	1.97(24.5)	5.11(24.0)	68.97(8.0)

Figure 5.16: Distance to optima $f(x^{best}) - f^*$ using Bayesian optimization with different surrogates and using expected improvement with a budget of 40 samples for group 2: "4 functions with low or moderate conditioning"

	f10	f11	f12	f13	f14
BO_numpy	nan(nan)	nan(nan)	nan(nan)	nan(nan)	nan(nan)
BO_BOH	286.57(30.0)	7.48(35.0)	2770.49(31.0)	4.98(16.0)	0.03(30.0)
BO_Gaus	16.52(33.2)	638.31(32.0)	3033.71(27.8)	8.84(23.8)	0.01(36.5)
BO_Naiv	49166.58(27.0)	2848.42(22.0)	23714.17(24.0)	52.21(2.0)	0.61(31.0)
BO_em	61391.71(14.0)	10317.74(20.5)	673.63(12.5)	10.04(19.0)	0.80(28.0)

Figure 5.17: Distance to optima $f(x^{best}) - f^*$ using Bayesian optimization with different surrogates and using expected improvement with a budget of 40 samples for group 3: "5 functions with high conditioning, unimodal"

	f15	f16	f17	f18	f19
BO_numpy	nan(nan)	nan(nan)	nan(nan)	nan(nan)	nan(nan)
BO_BOH	10.05(20.0)	9.02(33.0)	4.00(4.0)	3.55(38.0)	2.05(27.0)
BO_Gaus	17.12(28.0)	2.86(10.0)	3.15(18.5)	3.26(10.0)	13.31(27.0)
BO_Naiv	34.09(20.5)	3.20(20.5)	1.69(9.5)	11.72(24.0)	3.36(5.0)
BO_em	14.75(24.5)	10.70(19.0)	2.27(21.5)	9.63(13.5)	1.99(9.5)

Figure 5.18: Distance to optima $f(x^{best}) - f^*$ using Bayesian optimization with different surrogates and using expected improvement with a budget of 40 samples for group 4: "5 multi-modal functions with adequate global structure"

	f20	f21	f22	f23	f24
BO_numpy	nan(nan)	nan(nan)	nan(nan)	nan(nan)	nan(nan)
BO_BOH	2.44(34.0)	1.99(1.0)	1.98(25.0)	2.64(15.0)	8.98(14.0)
BO_Gaus	1.67(29.0)	1.23(22.5)	2.61(12.8)	5.24(17.2)	9.99(19.2)
BO_Naiv	2.43(15.5)	0.27(21.5)	2.04(4.0)	5.15(5.0)	7.15(26.5)
BO_em	3.16(17.0)	1.07(15.0)	0.90(22.0)	5.66(13.5)	3.82(6.5)

Figure 5.19: Distance to optima $f(x^{best}) - f^*$ using Bayesian optimization with different surrogates and using expected improvement with a budget of 40 samples for group 5: "5 multi-modal functions with weak global structure"

Figure 5.20: BayesOpt plot: Number of iterations, distance to optima using EI, with bayesline random search

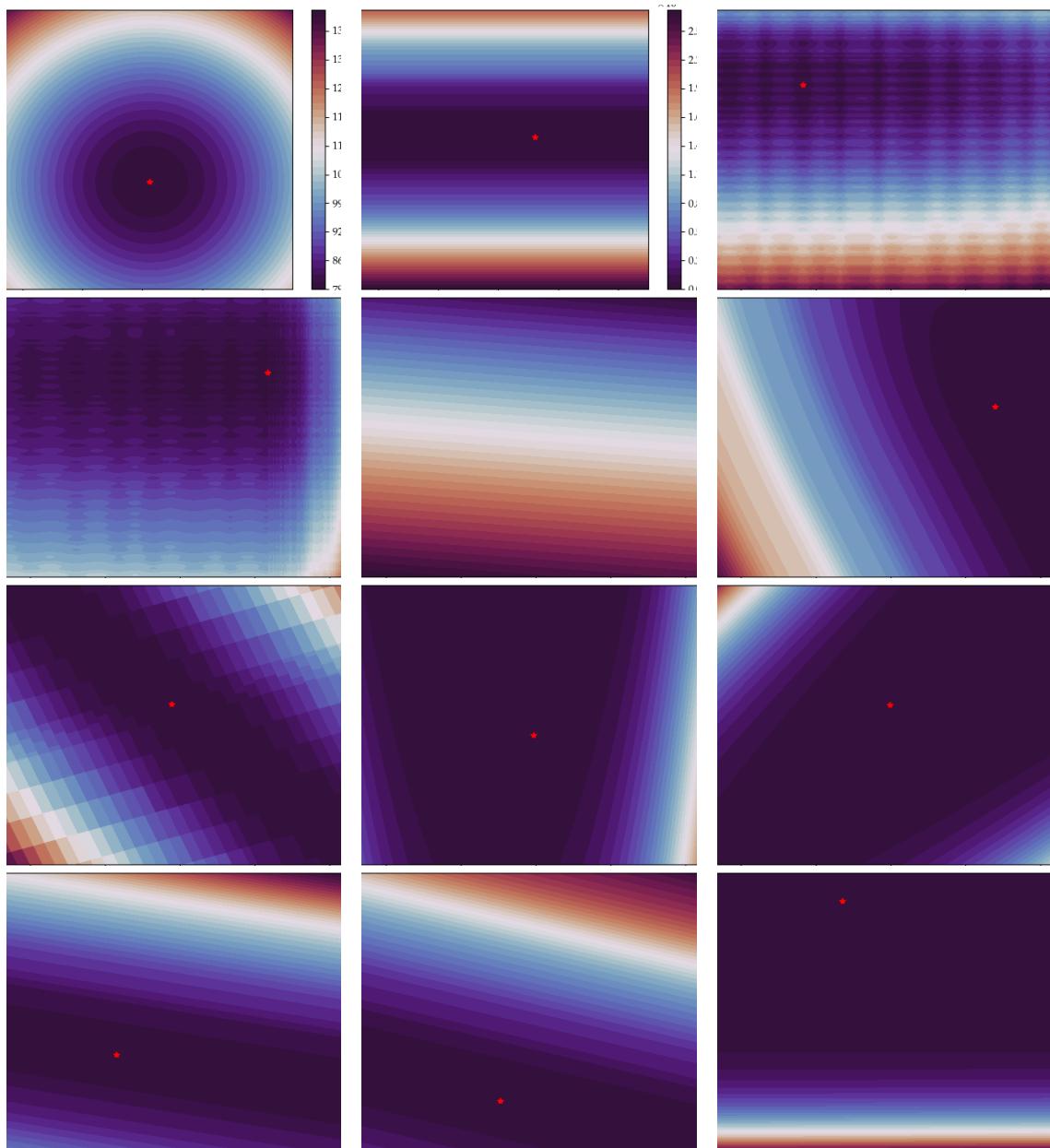


Figure 5.21: Test functions f1 to f12

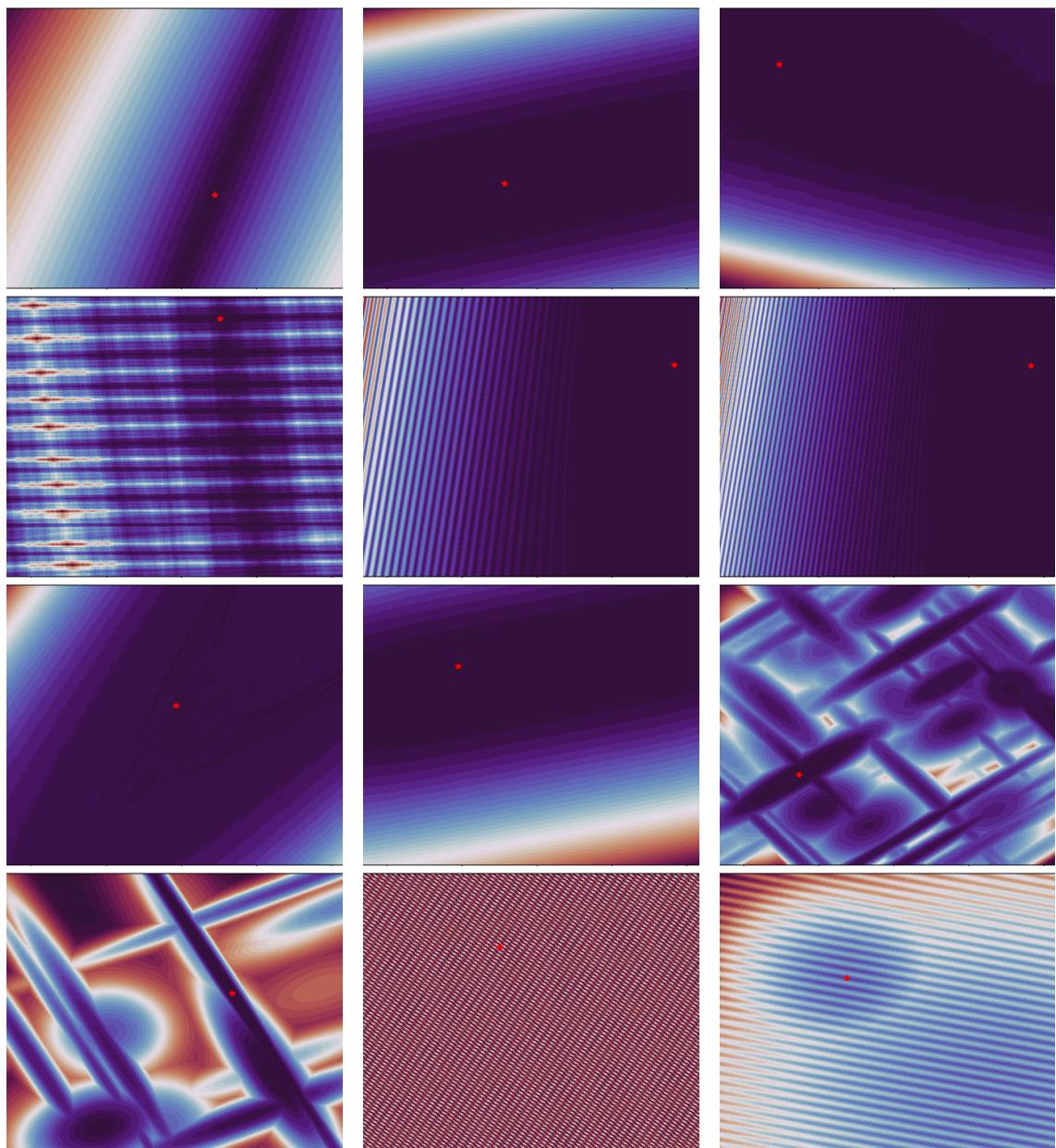


Figure 5.22: Test functions f13-24

6 Conclusion and further work

discussion: Using a generative model as a surrogates model is a novel idea - maybe it is not a good idea.. Discretized regression

Maybe manipulation of variance could be done, or same mean prediction?!? Or mean prediction using the means of the close by x-values.

6.1 further work

Many problems have dimensions of no relevance. Here This might be relevant to investigate

More dimensions of prior weighting?

<Using mixtures of more complicated components, i.e. hundebens distribution>

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Bayesian optimization is an effective framework for finding optimizers of a highly expensive (in terms of money, time, human attention or computational processing) or noisy objective function. First a prior is defined over possible functions and updated to a posterior according to already obtained observations/samples of the objective function. Next an acquisition function uses this posterior, also called an surrogate model, and is then utilized to find the next location in the optimization landscape to sample from. The far most common surrogate model is Gaussian Process (GP), partially due to its ability to represent its posterior in closed form. However, it also comes with short comings: Its inference, although it is exact, scales cubic with amount of samples and it impose strong assumptions of a well behaved objective function.

This thesis aims to investigate surrogate models different from GPs in order to improve on either the accuracy of the surrogate model or the inference cost of it. Meanwhile Bayesian Neural Networks (BNN) already have proven useful as surrogate models [6][17][18] (with cost of inference, which scales linearly and less strong assumptions) this thesis additionally wants to investigate Sum Product networks (SPN). An SPN is - similarly to a BNN - a deep probabilistic model and still expressive but with tractable inference, which potentially could lead to advantages over BNNs.

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