gptools Documentation

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Source home: https://github.com/markchil/gptools Releases: https://pypi.python.org/pypi/gptools/

Installation is as simple as:
pip install gptools

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CHAPTER

ONE

OVERVIEW

gptools is a Python package that provides a convenient, powerful and extensible implementation of Gaussian process regression (GPR). Central to gptool's implementation is support for derivatives and their variances. Furthermore, the implementation supports the incorporation of arbitrary linearly transformed quantities into the GP.

There are two key classes:

- GaussianProcess is the main class to represent a GP.
- Kernel (and its many subclasses) represents a covariance kernel, and must be provided when constructing a GaussianProcess. Separate kernels to describe the underlying signal and the noise are supported.

A third class, JointPrior, allows you to construct a hyperprior of arbitrary complexity to dictate how the hyperparameters are handled.

Creating a Gaussian process is as simple as:

```
import gptools
k = gptools.SquaredExponentialKernel()
qp = qptools.GaussianProcess(k)
```

But, the default bounds on the hyperparameters are very wide and can cause the optimizer/MCMC sampler to fail. So, it is usually a better idea to define the covariance kernel as:

```
k = gptools.SquaredExponentialKernel(param_bounds=[(0, 1e3), (0, 100)])
```

You will have to pick appropriate numbers by inspecting the typical range of your data.

Furthermore, you can include an explicit mean function by passing the appropriate MeanFunction instance into the *mu* keyword:

```
gp = gptools.GaussianProcess(k, mu=gptools.LinearMeanFunction())
```

This will enable you to perform inference (both empirical and full Bayes) for the hyperparameters of the mean function. Essentially, <code>gptools</code> can perform nonlinear Bayesian regression with a Gaussian process fit to the residuals.

You then add the training data using the add_data() method:

```
gp.add_data(x, y, err_y=stddev_y)
```

Here, err_y is the 1σ uncertainty on the observations y. For exact values, simply omit this keyword. Adding a derivative observation is as simple as specifying the derivative order with the n keyword:

```
gp.add_data(0, 0, n=1)
```

This will force the slope at x=0 to be exactly zero. Quantities that represent an arbitrary linear transformation of the "basic" observations can be added by specifying the T keyword:

```
gp.add_data(x, y, T=T)
```

This will add the value(s) y = TY(x) to the training data, where here Y represents the "basic" (untransformed) observations and y represents the transformed observations. This also supports the err_y and n keywords. Here, err_y is the error on the transformed quantity y. n applies to the latent variables Y(x).

Once the GP has been populated with training data, there are two approaches supported to handle the hyperparameters.

The simplest approach is to use an empirical Bayes approach and compute the maximum a posteriori (MAP) estimate. This is accomplished using the <code>optimize_hyperparameters()</code> method of the <code>GaussianProcess</code> instance:

```
gp.optimize_hyperparameters()
```

This will randomly start the optimizer at points distributed according to the hyperprior several times in order to ensure that the global maximum is obtained. If you have a machine with multiple cores, these random starts will be performed in parallel. You can set the number of starts using the *random_starts* keyword, and you can set the number of processes used using the *num_proc* keyword.

For a more complete accounting of the uncertainties in the model, you can choose to use a fully Bayesian approach by using Markov chain Monte Carlo (MCMC) techniques to produce samples of the hyperposterior. The samples are produced directly with sample_hyperparameter_posterior(), though it will typically be more convenient to simply call predict() with the *use_MCMC* keyword set to True.

In order to make predictions, use the predict () method:

```
y_star, err_y_star = gp.predict(x_star)
```

By default, the mean and standard deviation of the GP posterior are returned. To compute only the mean and save some time, set the *return_std* keyword to False. To make predictions of derivatives, set the *n* keyword. To make a prediction of a linearly transformed quantity, set the *output_transform* keyword.

For a convenient wrapper for applying <code>gptools</code> to multivariate data, see <code>profiletools</code> at <code>https://github.com/markchil/profiletools</code>

CHAPTER

TWO

KERNELS

A number of kernels are provided to allow many types of data to be fit:

- DiagonalNoiseKernel implements homoscedastic noise. The noise is tied to a specific derivative order.
 This allows you to, for instance, have noise on your observations but have noiseless derivative constraints,
 or to have different noise levels for observations and derivatives. Note that you can also specify potentially
 heteroscedastic noise explicitly when adding data to the process.
- $\bullet \ \ {\tt SquaredExponentialKernel\ implements\ the\ SE\ kernel\ which\ is\ infinitely\ differentiable}.$
- MaternKernel implements the entire Matern class of covariance functions, which are characterized by a
 hyperparameter ν. A process having the Matern kernel is only mean-square differentiable for derivative order
 n < ν. Note that this class does not support arbitrary derivatives at this point. If you need this feature, try using
 MaternKernelArb, but note that this is very slow!
- Matern 52 Kernel implements a specialized Matern kernel with $\nu=\frac{5}{2}$ which efficiently supports 0th and 1st derivatives.
- RationalQuadraticKernel implements the rational quadratic kernel, which is a scale mixture over SE kernels.
- GibbsKernelld and its subclasses implements the Gibbs kernel, which is a nonstationary form of the SE kernel.
- MaskedKernel creates a kernel that only operates on a subset of dimensions. Use this along with the sum and product operations to create kernels that encode different properties in different dimensions.
- ArbitraryKernel creates a kernel with an arbitrary covariance function and computes the derivatives as needed using mpmath to perform numerical differentiation. Naturally, this is very slow but is useful to let you explore the properties of arbitrary kernels without having to write a complete implementation.

In most cases, these kernels have been constructed in a way to allow inputs of arbitrary dimension. Each dimension has a length scale hyperparameter that can be separately optimized over or held fixed. Arbitrary derivatives with respect to each dimension can be taken, including computation of the covariance for those observations.

Other kernels can be implemented by extending the Kernel class. Furthermore, kernels may be added or multiplied together to yield a new, valid kernel.

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CHAPTER

THREE

NOTES

 ${\tt gptools}$ has been developed and tested on Python 2.7 and scipy 0.14.0. It may work just as well on other versions, but has not been tested.

If you find this software useful, please be sure to cite it:

M.A. Chilenski (2014). gptools: Gaussian processes with arbitrary derivative constraints and predictions, GNU General Public License. github.com/markchil/gptools

A formal publication on this software and its applications is in preparation. Once this is published, this readme will be updated with the relevant citation.

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CHAPTER

FOUR

CONTENTS

4.1 gptools package

4.1.1 Subpackages

gptools.kernel package

Submodules

gptools.kernel.core module

Core kernel classes: contains the base Kernel class and helper subclasses.

Bases: object

Covariance kernel base class. Not meant to be explicitly instantiated!

Initialize the kernel with the given number of input dimensions.

Parameters num_dim: positive int

Number of dimensions of the input data. Must be consistent with the *X* and *Xstar* values passed to the GaussianProcess you wish to use the covariance kernel with. Default is 1.

num_params: Non-negative int

Number of parameters in the model.

initial_params: Array or other Array-like, (num_params,), optional

Initial values to set for the hyperparameters. Default is None, in which case 1 is used for the initial values.

fixed_params: Array or other Array-like of bool, (num_params,), optional

Sets which hyperparameters are considered fixed when optimizing the log likelihood. A True entry corresponds to that element being fixed (where the element ordering is as defined in the class). Default value is None (no hyperparameters are fixed).

param_bounds : list of 2-tuples (num_params,), optional

List of bounds for each of the hyperparameters. Each 2-tuple is of the form (lower', *upper*). If there is no bound in a given direction, it works best to set it to something big like 1e16. Default is (0.0, 1e16) for each hyperparameter. Note that this is overridden by the *hyperprior* keyword, if present.

param_names : list of str (num_params,), optional

List of labels for the hyperparameters. Default is all empty strings.

enforce bounds: bool, optional

If True, an attempt to set a hyperparameter outside of its bounds will result in the hyperparameter being set right at its bound. If False, bounds are not enforced inside the kernel. Default is False (do not enforce bounds).

hyperprior: JointPrior instance or list, optional

Joint prior distribution for all hyperparameters. Can either be given as a JointPrior instance or a list of *num_params* callables or py:class:*rv_frozen* instances from scipy.stats, in which case a IndependentJointPrior is constructed with these as the independent priors on each hyperparameter. Default is a uniform PDF on all hyperparameters.

Raises ValueError:

If *num_dim* is not a positive integer or the lengths of the input vectors are inconsistent.

GPArgumentError:

if *fixed_params* is passed but *initial_params* is not.

Attributes

num_params	int	Number of parameters
num_dim	int	Number of dimensions
params	Array of float,	Array of parameters.
	(num_params,)	
fixed_params	Array of bool,	Array of booleans indicated which parameters in params are
	(num_params,)	fixed.
param_names	list of str, (num_params,)	List of the labels for the hyperparameters.
hyperprior	JointPrior instance	Joint prior distribution for the hyperparameters.

param_bounds

```
__call__(Xi, Xj, ni, nj, hyper_deriv=None, symmetric=False)
```

Evaluate the covariance between points Xi and Xj with derivative order ni, nj.

Note that this method only returns the covariance – the hyperpriors and potentials stored in this kernel must be applied separately.

Parameters Xi: Matrix or other Array-like, (*M*, *D*)

M inputs with dimension *D*.

Xj: Matrix or other Array-like, (M, D)

M inputs with dimension *D*.

 \mathbf{ni} : Matrix or other Array-like, (M, D)

M derivative orders for set i.

nj: Matrix or other Array-like, (M, D)

M derivative orders for set j.

hyper_deriv : Non-negative int or None, optional

The index of the hyperparameter to compute the first derivative with respect to. If None, no derivatives are taken. Default is None (no hyperparameter derivatives).

symmetric: bool, optional

Whether or not the input *Xi*, *Xj* are from a symmetric matrix. Default is False.

Returns Kij: Array, (M,)

Covariances for each of the M Xi, Xj pairs.

Notes

THIS IS ONLY A METHOD STUB TO DEFINE THE NEEDED CALLING FINGERPRINT!

set_hyperparams (new_params)

Sets the free hyperparameters to the new parameter values in new params.

Parameters new_params: Array or other Array-like, (len(self.params),)

New parameter values, ordered as dictated by the docstring for the class.

num_free_params

Returns the number of free parameters.

free_param_idxs

Returns the indices of the free parameters in the main arrays of parameters, etc.

free_params

Returns the values of the free hyperparameters.

Returns free params: Array

Array of the free parameters, in order.

free_param_bounds

Returns the bounds of the free hyperparameters.

Returns free_param_bounds: Array

Array of the bounds of the free parameters, in order.

free_param_names

Returns the names of the free hyperparameters.

Returns free_param_names: Array

Array of the names of the free parameters, in order.

___add___(other)

Add two Kernels together.

Parameters other: Kernel

Kernel to be added to this one.

Returns sum: SumKernel

Instance representing the sum of the two kernels.

mul (other)

Multiply two Kernels together.

```
Parameters other: Kernel
                    Kernel to be multiplied by this one.
              Returns prod: ProductKernel
                    Instance representing the product of the two kernels.
class gptools.kernel.core.BinaryKernel(k1, k2)
     Bases: gptools.kernel.core.Kernel
     Abstract class for binary operations on kernels (addition, multiplication, etc.).
          Parameters k1, k2: Kernel instances to be combined
     Notes
     k1 and k2 must have the same number of dimensions.
     enforce bounds
          Boolean indicating whether or not the kernel will explicitly enforce the bounds defined by the hyperprior.
     fixed_params
     free_param_bounds
          Returns the bounds of the free hyperparameters.
              Returns free_param_bounds: Array
                    Array of the bounds of the free parameters, in order.
     free_param_names
          Returns the names of the free hyperparameters.
              Returns free_param_names: Array
                     Array of the names of the free parameters, in order.
     params
     set_hyperparams (new_params)
          Set the (free) hyperparameters.
              Parameters new_params: Array or other Array-like
                     New values of the free parameters.
              Raises ValueError:
                    If the length of new_params is not consistent with self.params.
class qptools.kernel.core.SumKernel(<math>k1, k2)
     Bases: gptools.kernel.core.BinaryKernel
     The sum of two kernels.
     ___call___(*args, **kwargs)
          Evaluate the covariance between points Xi and Xj with derivative order ni, nj.
              Parameters Xi: Matrix or other Array-like, (M, D)
                    M inputs with dimension D.
                  \mathbf{X}\mathbf{j}: Matrix or other Array-like, (M, D)
                    M inputs with dimension D.
```

```
ni: Matrix or other Array-like, (M, D)
                     M derivative orders for set i.
                   \mathbf{nj}: Matrix or other Array-like, (M, D)
                     M derivative orders for set j.
                   symmetric: bool, optional
                     Whether or not the input Xi, Xj are from a symmetric matrix. Default is False.
               Returns Kij: Array, (M,)
                     Covariances for each of the M Xi, Xj pairs.
               Raises NotImplementedError:
                     If the hyper_deriv keyword is given and is not None.
class gptools.kernel.core.ProductKernel(k1, k2)
     Bases: gptools.kernel.core.BinaryKernel
     The product of two kernels.
      \_call\_(Xi, Xj, ni, nj, **kwargs)
           Evaluate the covariance between points Xi and Xj with derivative order ni, nj.
               Parameters Xi: Matrix or other Array-like, (M, D)
                     M inputs with dimension D.
                   Xj: Matrix or other Array-like, (M, D)
                     M inputs with dimension D.
                   ni: Matrix or other Array-like, (M, D)
                     M derivative orders for set i.
                   \mathbf{nj}: Matrix or other Array-like, (M, D)
                     M derivative orders for set j.
                   symmetric: bool, optional
                     Whether or not the input Xi, Xj are from a symmetric matrix. Default is False.
               Returns Kij: Array, (M,)
                     Covariances for each of the M Xi, Xj pairs.
               Raises NotImplementedError:
                     If the hyper_deriv keyword is given and is not None.
class gptools.kernel.core.ChainRuleKernel(num_dim=1,
                                                                            num\_params=0,
                                                                                                     ini-
                                                       tial_params=None,
                                                                                    fixed_params=None,
                                                       param_bounds=None,
                                                                                   param_names=None,
                                                       enforce_bounds=False, hyperprior=None)
     Bases: gptools.kernel.core.Kernel
     Abstract class for the common methods in creating kernels that require application of Faa di Bruno's formula.
       _call__(Xi, Xj, ni, nj, hyper_deriv=None, symmetric=False)
           Evaluate the covariance between points Xi and Xj with derivative order ni, nj.
               Parameters Xi: Matrix or other Array-like, (M, D)
                     M inputs with dimension D.
```

```
Xj: Matrix or other Array-like, (M, D)
```

M inputs with dimension *D*.

ni: Matrix or other Array-like, (M, D)

M derivative orders for set i.

nj: Matrix or other Array-like, (M, D)

M derivative orders for set j.

hyper_deriv : Non-negative int or None, optional

The index of the hyperparameter to compute the first derivative with respect to. If None, no derivatives are taken. Hyperparameter derivatives are not supported at this point. Default is None.

symmetric: bool

Whether or not the input Xi, Xj are from a symmetric matrix. Default is False.

Returns Kij: Array, (M,)

Covariances for each of the M Xi, Xj pairs.

Raises NotImplementedError:

If the *hyper_deriv* keyword is not None.

Bases: gptools.kernel.core.Kernel

Covariance kernel from an arbitrary covariance function.

Computes derivatives using mpmath.diff() and is hence in general much slower than a hard-coded implementation of a given kernel.

Parameters num_dim: positive int

Number of dimensions of the input data. Must be consistent with the *X* and *Xstar* values passed to the GaussianProcess you wish to use the covariance kernel with.

```
cov_func: callable, takes >= 2 args
```

Covariance function. Must take arrays of *Xi* and *Xj* as the first two arguments. The subsequent (scalar) arguments are the hyperparameters. The number of parameters is found by inspection of *cov_func* itself, or with the num_params keyword.

num_proc : int or None, optional

Number of procs to use in evaluating covariance derivatives. 0 means to do it in serial, None means to use all available cores. Default is 0 (serial evaluation).

```
num_params : int or None, optional
```

Number of hyperparameters. If None, inspection will be used to infer the number of hyperparameters (but will fail if you used clever business with *args, etc.). Default is None (use inspection to find argument count).

**kwargs:

All other keyword parameters are passed to Kernel.

Attributes

cov_func	callable	The covariance function
num_proc	non-negative	Number of processors to use in evaluating covariance derivatives. 0 means
	int	serial.

__call__ (Xi, Xj, ni, nj, hyper_deriv=None, symmetric=False)

Evaluate the covariance between points *Xi* and *Xj* with derivative order *ni*, *nj*.

Parameters Xi: Matrix or other Array-like, (M, D)

M inputs with dimension D.

Xj: Matrix or other Array-like, (M, D)

M inputs with dimension *D*.

 \mathbf{ni} : Matrix or other Array-like, (M, D)

M derivative orders for set *i*.

nj: Matrix or other Array-like, (*M*, *D*)

M derivative orders for set *j*.

hyper_deriv : Non-negative int or None, optional

The index of the hyperparameter to compute the first derivative with respect to. If None, no derivatives are taken. Hyperparameter derivatives are not supported at this point. Default is None.

symmetric: bool, optional

Whether or not the input Xi, Xj are from a symmetric matrix. Default is False.

Returns Kij: Array, (M,)

Covariances for each of the M Xi, Xj pairs.

Raises NotImplementedError:

If the *hyper_deriv* keyword is not None.

```
class gptools.kernel.core.MaskedKernel (base, total_dim=2, mask=[0], scale=None)
    Bases: gptools.kernel.core.Kernel
```

Creates a kernel that is only masked to operate on certain dimensions, or has scaling/shifting.

This can be used, for instance, to put a squared exponential kernel in one direction and a Matern kernel in the other.

Overrides __getattribute__() and __setattr__() to make all setting/accessing go to the *base* kernel.

Parameters base: Kernel instance

The Kernel to apply in the dimensions specified in *mask*.

total_dim: int, optional

The total number of dimensions the masked kernel should have. Default is 2.

mask: list or other array-like, optional

1d list of indices of dimensions *X* to include when passing to the *base* kernel. Length must be *base.num_dim*. Default is [0] (i.e., just pass the first column of *X* to a univariate *base* kernel).

scale: list or other array-like, optional

1d list of scale factors to apply to the elements in Xi, Xj. Default is ones. Length must be equal to 2'base.num_dim'.

__getattribute__(name)

Gets all attributes from the base kernel.

The exceptions are 'base', 'mask', 'maskC', 'num_dim', 'scale' and any special method (i.e., a method/attribute having leading and trailing double underscores), which are taken from MaskedKernel.

__setattr__(name, value)

Sets all attributes in the base kernel.

The exceptions are 'base', 'mask', 'maskC', 'num_dim', 'scale' and any special method (i.e., a method/attribute having leading and trailing double underscores), which are set in MaskedKernel.

__call__(*Xi*, *Xj*, *ni*, *nj*, **kwargs)

Evaluate the covariance between points Xi and Xj with derivative order ni, nj.

Note that in the argument specifications, *D* is the *total_dim* specified in the constructor (i.e., num_dim for the MaskedKernel instance itself).

Parameters Xi: Matrix or other Array-like, (M, D)

M inputs with dimension D.

Xj: Matrix or other Array-like, (M, D)

M inputs with dimension D.

ni: Matrix or other Array-like, (*M*, *D*)

M derivative orders for set i.

nj: Matrix or other Array-like, (*M*, *D*)

M derivative orders for set *j*.

hyper_deriv: Non-negative int or None, optional

The index of the hyperparameter to compute the first derivative with respect to. If None, no derivatives are taken. Default is None (no hyperparameter derivatives).

symmetric: bool, optional

Whether or not the input *Xi*, *Xj* are from a symmetric matrix. Default is False.

Returns Kij: Array, (M,)

Covariances for each of the M Xi, Xj pairs.

gptools.kernel.gibbs module

Provides classes and functions for creating SE kernels with warped length scales.

gptools.kernel.gibbs.tanh_warp_arb(X, l1, l2, lw, x0)

Warps the *X* coordinate with the tanh model

$$l = \frac{l_1 + l_2}{2} - \frac{l_1 - l_2}{2} \tanh \frac{x - x_0}{l_w}$$

Parameters X: Array, (M,) or scalar float

M locations to evaluate length scale at.

11: positive float

Small-*X* saturation value of the length scale.

12: positive float

Large-*X* saturation value of the length scale.

lw: positive float

Length scale of the transition between the two length scales.

x0: float

Location of the center of the transition between the two length scales.

Returns 1: Array, (M,) or scalar float

The value of the length scale at the specified point.

 $gptools.kernel.gibbs.gauss_warp_arb(X, l1, l2, lw, x0)$

Warps the *X* coordinate with a Gaussian-shaped divot.

$$l = l_1 - (l_1 - l_2) \exp\left(-4 \ln 2 \frac{(X - x_0)^2}{l_w^2}\right)$$

Parameters $X : Array, (M_1)$ or scalar float

M locations to evaluate length scale at.

11: positive float

Global value of the length scale.

12: positive float

Pedestal value of the length scale.

lw: positive float

Width of the dip.

x0: float

Location of the center of the dip in length scale.

Returns 1: Array, (M,) or scalar float

The value of the length scale at the specified point.

class gptools.kernel.gibbs.GibbsFunction1dArb (warp_function)

Bases: object

Wrapper class for the Gibbs covariance function, permits the use of arbitrary warping.

The covariance function is given by

$$k = \left(\frac{2l(x)l(x')}{l^2(x) + l^2(x')}\right)^{1/2} \exp\left(-\frac{(x - x')^2}{l^2(x) + l^2(x')}\right)$$

Parameters warp_function : callable

The function that warps the length scale as a function of X. Must have the fingerprint (Xi, l1, l2, lw, x0).

 $_$ call $_$ (Xi, Xj, sigmaf, l1, l2, lw, x0)

Evaluate the covariance function between points Xi and Xj.

Parameters Xi, Xj: Array, mpf or scalar float

Points to evaluate covariance between. If they are Array, scipy functions are used, otherwise mpmath functions are used.

sigmaf: scalar float

Prefactor on covariance.

11, 12, lw, x0: scalar floats

Parameters of length scale warping function, passed to warp_function.

Returns k: Array or mpf

Covariance between the given points.

class gptools.kernel.gibbs.GibbsKernel1dTanhArb(**kwargs)

Bases: gptools.kernel.core.ArbitraryKernel

Gibbs warped squared exponential covariance function in 1d.

Computes derivatives using mpmath.diff() and is hence in general much slower than a hard-coded implementation of a given kernel.

The covariance function is given by

$$k = \left(\frac{2l(x)l(x')}{l^2(x) + l^2(x')}\right)^{1/2} \exp\left(-\frac{(x - x')^2}{l^2(x) + l^2(x')}\right)$$

Warps the length scale using a hyperbolic tangent:

$$l = \frac{l_1 + l_2}{2} - \frac{l_1 - l_2}{2} \tanh \frac{x - x_0}{l_w}$$

The order of the hyperparameters is:

0	sigmaf	Amplitude of the covariance function
1	11	Small-X saturation value of the length scale.
2	12	Large-X saturation value of the length scale.
3	lw	Length scale of the transition between the two length scales.
4	x0	Location of the center of the transition between the two length scales.

Parameters **kwargs:

All parameters are passed to Kernel.

class gptools.kernel.gibbs.GibbsKernel1dGaussArb(**kwargs)

Bases: gptools.kernel.core.ArbitraryKernel

Gibbs warped squared exponential covariance function in 1d.

Computes derivatives using mpmath.diff() and is hence in general much slower than a hard-coded implementation of a given kernel.

The covariance function is given by

$$k = \left(\frac{2l(x)l(x')}{l^2(x) + l^2(x')}\right)^{1/2} \exp\left(-\frac{(x - x')^2}{l^2(x) + l^2(x')}\right)$$

Warps the length scale using a gaussian:

$$l = l_1 - (l_1 - l_2) \exp\left(-4 \ln 2 \frac{(X - x_0)^2}{l_w^2}\right)$$

The order of the hyperparameters is:

0	sigmaf	Amplitude of the covariance function
1	11	Global value of the length scale.
2	12	Pedestal value of the length scale.
3	lw	Width of the dip.
4	x0	Location of the center of the dip in length scale.

Parameters **kwargs:

All parameters are passed to Kernel.

class gptools.kernel.gibbs.GibbsKernelld(l_func, num_params=None, **kwargs)
 Bases: gptools.kernel.core.Kernel

Univariate Gibbs kernel with arbitrary length scale warping for low derivatives.

The covariance function is given by

$$k = \left(\frac{2l(x)l(x')}{l^2(x) + l^2(x')}\right)^{1/2} \exp\left(-\frac{(x - x')^2}{l^2(x) + l^2(x')}\right)$$

The derivatives are hard-coded using expressions obtained from Mathematica.

Parameters l_func : callable

Function that dictates the length scale warping and its derivative. Must have fingerprint (x, n, p1, p2, ...) where p1 is element one of the kernel's parameters (i.e., element zero is skipped).

num_params: int, optional

The number of parameters of the length scale function. If not passed, introspection will be used to determine this. This will fail if you have used the *args syntax in your function definition. This count should include sigma_f, even though it is not passed to the length scale function.

**kwargs:

All remaining arguments are passed to Kernel.

 $__$ call $__(Xi, Xj, ni, nj, hyper_deriv=None, symmetric=False)$

Evaluate the covariance between points *Xi* and *Xj* with derivative order *ni*, *nj*.

Parameters Xi: Matrix or other Array-like, (M, D)

M inputs with dimension *D*.

Xj: Matrix or other Array-like, (M, D)

M inputs with dimension *D*.

ni: Matrix or other Array-like, (*M*, *D*)

M derivative orders for set i.

 \mathbf{nj} : Matrix or other Array-like, (M, D)

M derivative orders for set i.

hyper_deriv : Non-negative int or None, optional

The index of the hyperparameter to compute the first derivative with respect to. If None, no derivatives are taken. Hyperparameter derivatives are not supported at this point. Default is None.

symmetric: bool, optional

Whether or not the input *Xi*, *Xj* are from a symmetric matrix. Default is False.

Returns Kij: Array, (M,)

Covariances for each of the M Xi, Xj pairs.

Raises NotImplementedError:

If the *hyper_deriv* keyword is not None.

 ${\tt gptools.kernel.gibbs.tanh_warp}\,(x,n,l1,l2,lw,x0)$

Implements a tanh warping function and its derivative.

$$l = \frac{l_1 + l_2}{2} - \frac{l_1 - l_2}{2} \tanh \frac{x - x_0}{l_w}$$

Parameters x: float or array of float

Locations to evaluate the function at.

n: int

Derivative order to take. Used for ALL of the points.

11: positive float

Left saturation value.

12: positive float

Right saturation value.

lw: positive float

Transition width.

x0: float

Transition location.

Returns 1: float or array

Warped length scale at the given locations.

Raises NotImplementedError:

If n > 1.

class gptools.kernel.gibbs.GibbsKernel1dTanh(**kwargs)

Bases: gptools.kernel.gibbs.GibbsKernelld

Gibbs warped squared exponential covariance function in 1d.

Uses hard-coded implementation up to first derivatives.

The covariance function is given by

$$k = \left(\frac{2l(x)l(x')}{l^2(x) + l^2(x')}\right)^{1/2} \exp\left(-\frac{(x - x')^2}{l^2(x) + l^2(x')}\right)$$

Warps the length scale using a hyperbolic tangent:

$$l = \frac{l_1 + l_2}{2} - \frac{l_1 - l_2}{2} \tanh \frac{x - x_0}{l_w}$$

The order of the hyperparameters is:

0	sigmaf	Amplitude of the covariance function
1	11	Small-X saturation value of the length scale.
2	12	Large-X saturation value of the length scale.
3	lw	Length scale of the transition between the two length scales.
4	x0	Location of the center of the transition between the two length scales.

Parameters **kwargs:

All parameters are passed to Kernel.

gptools.kernel.gibbs.double_tanh_warp (x, n, lcore, lmid, ledge, la, lb, xa, xb) Implements a sum-of-tanh warping function and its derivative.

$$l = a \tanh \frac{x - x_a}{l_a} + b \tanh \frac{x - x_b}{l_b}$$

Parameters x: float or array of float

Locations to evaluate the function at.

n: int

Derivative order to take. Used for ALL of the points.

lcore: float

Core length scale.

lmid: float

Intermediate length scale.

ledge: float

Edge length scale.

la: positive float

Transition of first tanh.

lb: positive float

Transition of second tanh.

xa: float

Transition of first tanh.

xb: float

Transition of second tanh.

Returns 1: float or array

Warped length scale at the given locations.

${\bf Raises\ \ Not Implemented Error:}$

If n > 1.

class gptools.kernel.gibbs.GibbsKernel1dDoubleTanh(**kwargs)

Bases: gptools.kernel.gibbs.GibbsKernelld

Gibbs warped squared exponential covariance function in 1d.

Uses hard-coded implementation up to first derivatives.

The covariance function is given by

$$k = \left(\frac{2l(x)l(x')}{l^2(x) + l^2(x')}\right)^{1/2} \exp\left(-\frac{(x - x')^2}{l^2(x) + l^2(x')}\right)$$

Warps the length scale using two hyperbolic tangents:

$$l = a \tanh \frac{x - x_a}{l_a} + b \tanh \frac{x - x_b}{l_b}$$

The order of the hyperparameters is:

0	sigmaf	Amplitude of the covariance function
1	lcore	Core length scale
2	lmid	Intermediate length scale
3	ledge	Edge length scale
4	la	Width of first tanh
5	lb	Width of second tanh
6	xa	Center of first tanh
7	xb	Center of second tanh

Parameters **kwargs:

All parameters are passed to Kernel.

gptools.kernel.gibbs.cubic_bucket_warp (x, n, l1, l2, l3, x0, w1, w2, w3)

Warps the length scale with a piecewise cubic "bucket" shape.

Parameters x: float or array-like of float

Locations to evaluate length scale at.

n: non-negative int

Derivative order to evaluate. Only first derivatives are supported.

11 : positive float

Length scale to the left of the bucket.

12: positive float

Length scale in the bucket.

13: positive float

Length scale to the right of the bucket.

x0: float

Location of the center of the bucket.

w1: positive float

Width of the left side cubic section.

w2: positive float

Width of the bucket.

w3: positive float

Width of the right side cubic section.

class qptools.kernel.qibbs.GibbsKernel1dCubicBucket (**kwargs)

Bases: gptools.kernel.gibbs.GibbsKernelld

Gibbs warped squared exponential covariance function in 1d.

Uses hard-coded implementation up to first derivatives.

The covariance function is given by

$$k = \left(\frac{2l(x)l(x')}{l^2(x) + l^2(x')}\right)^{1/2} \exp\left(-\frac{(x - x')^2}{l^2(x) + l^2(x')}\right)$$

Warps the length scale using a "bucket" function with cubic joins.

The order of the hyperparameters is:

sigmaf	Amplitude of the covariance function
11	Length scale to the left of the bucket.
12	Length scale in the bucket.
13	Length scale to the right of the bucket.
x0	Location of the center of the bucket.
w1	Width of the left side cubic section.
w2	Width of the bucket.
w3	Width of the right side cubic section.
	11 12 13 x0 w1 w2

Parameters **kwargs:

All parameters are passed to Kernel.

qptools.kernel.qibbs.quintic_bucket_warp(x, n, l1, l2, l3, x0, w1, w2, w3)

Warps the length scale with a piecewise quintic "bucket" shape.

Parameters x: float or array-like of float

Locations to evaluate length scale at.

n: non-negative int

Derivative order to evaluate. Only first derivatives are supported.

11: positive float

Length scale to the left of the bucket.

12: positive float

Length scale in the bucket.

13: positive float

Length scale to the right of the bucket.

x0: float

Location of the center of the bucket.

w1: positive float

Width of the left side quintic section.

w2: positive float

Width of the bucket.

w3: positive float

Width of the right side quintic section.

class gptools.kernel.gibbs.GibbsKernel1dQuinticBucket(**kwargs)

Bases: gptools.kernel.gibbs.GibbsKernelld

Gibbs warped squared exponential covariance function in 1d.

Uses hard-coded implementation up to first derivatives.

The covariance function is given by

$$k = \left(\frac{2l(x)l(x')}{l^2(x) + l^2(x')}\right)^{1/2} \exp\left(-\frac{(x - x')^2}{l^2(x) + l^2(x')}\right)$$

Warps the length scale using a "bucket" function with quintic joins.

The order of the hyperparameters is:

0	sigmaf	Amplitude of the covariance function
1	11	Length scale to the left of the bucket.
2	12	Length scale in the bucket.
3	13	Length scale to the right of the bucket.
4	x0	Location of the center of the bucket.
5	w1	Width of the left side quintic section.
6	w2	Width of the bucket.
7	w3	Width of the right side quintic section.

Parameters **kwargs:

All parameters are passed to Kernel.

gptools.kernel.matern module

Provides the MaternKernel class which implements the anisotropic Matern kernel.

Matern covariance function of arbitrary dimension, for use with ArbitraryKernel.

The Matern kernel has the following hyperparameters, always referenced in the order listed:

0	sigma	prefactor
1	nu	order of kernel
2	11	length scale for the first dimension
3	12	and so on for all dimensions

The kernel is defined as:

$$k_M = \sigma^2 \frac{2^{1-\nu}}{\Gamma(\nu)} \left(\sqrt{2\nu \sum_i \left(\frac{\tau_i^2}{l_i^2}\right)} \right)^{\nu} K_{\nu} \left(\sqrt{2\nu \sum_i \left(\frac{\tau_i^2}{l_i^2}\right)} \right)$$

Parameters Xi, Xj: Array, mpf, tuple or scalar float

Points to evaluate the covariance between. If they are Array, scipy functions are used, otherwise mpmath functions are used.

*args:

Remaining arguments are the 2+num_dim hyperparameters as defined above.

class gptools.kernel.matern.MaternKernelArb (**kwargs)

Bases: gptools.kernel.core.ArbitraryKernel

Matern covariance kernel. Supports arbitrary derivatives. Treats order as a hyperparameter.

This version of the Matern kernel is painfully slow, but uses mpmath to ensure the derivatives are computed properly, since there may be issues with the regular MaternKernel.

The Matern kernel has the following hyperparameters, always referenced in the order listed:

0	sigma	prefactor
1	nu	order of kernel
2	11	length scale for the first dimension
3	12	and so on for all dimensions

The kernel is defined as:

$$k_M = \sigma^2 \frac{2^{1-\nu}}{\Gamma(\nu)} \left(\sqrt{2\nu \sum_i \left(\frac{\tau_i^2}{l_i^2}\right)} \right)^{\nu} K_{\nu} \left(\sqrt{2\nu \sum_i \left(\frac{\tau_i^2}{l_i^2}\right)} \right)$$

Parameters **kwargs:

All keyword parameters are passed to ArbitraryKernel.

nu

Returns the value of the order ν .

class gptools.kernel.matern.MaternKernelld(**kwargs)

Bases: gptools.kernel.core.Kernel

Matern covariance kernel. Only for univariate data. Only supports up to first derivatives. Treats order as a hyperparameter.

The Matern kernel has the following hyperparameters, always referenced in the order listed:

0	sigma	prefactor
1	nu	order of kernel
2	11	length scale

The kernel is defined as:

$$k_{M} = \sigma^{2} \frac{2^{1-\nu}}{\Gamma(\nu)} \left(\sqrt{2\nu \left(\frac{\tau^{2}}{l_{1}^{2}}\right)} \right)^{\nu} K_{\nu} \left(\sqrt{2\nu \left(\frac{\tau^{2}}{l_{1}^{2}}\right)} \right)$$

where $\tau = X_i - X_j$.

Note that the expressions for the derivatives break down for $\nu < 1$.

Parameters **kwargs:

All keyword parameters are passed to Kernel.

__call__(Xi, Xj, ni, nj, hyper_deriv=None, symmetric=False)

Evaluate the covariance between points Xi and Xj with derivative order ni, nj.

Parameters Xi: Matrix or other Array-like, (*M*, *D*)

M inputs with dimension *D*.

Xj: Matrix or other Array-like, (M, D)

M inputs with dimension *D*.

ni: Matrix or other Array-like, (*M*, *D*)

M derivative orders for set i.

nj: Matrix or other Array-like, (*M*, *D*)

M derivative orders for set *j*.

hyper_deriv : Non-negative int or None, optional

The index of the hyperparameter to compute the first derivative with respect to. If None, no derivatives are taken. Hyperparameter derivatives are not supported at this point. Default is None.

symmetric: bool, optional

Whether or not the input *Xi*, *Xj* are from a symmetric matrix. Default is False.

Returns Kij: Array, (M,)

Covariances for each of the M Xi, Xj pairs.

Raises NotImplementedError:

If the *hyper_deriv* keyword is not None.

class gptools.kernel.matern.MaternKernel(num_dim=1, **kwargs)

Bases: gptools.kernel.core.ChainRuleKernel

Matern covariance kernel. Supports arbitrary derivatives. Treats order as a hyperparameter.

EXPERIMENTAL IMPLEMENTATION! DO NOT TRUST FOR HIGHER DERIVATIVES!

The Matern kernel has the following hyperparameters, always referenced in the order listed:

0	sigma	prefactor
1	nu	order of kernel
2	11	length scale for the first dimension
3	12	and so on for all dimensions

The kernel is defined as:

$$k_M = \sigma^2 \frac{2^{1-\nu}}{\Gamma(\nu)} \left(\sqrt{2\nu \sum_i \left(\frac{\tau_i^2}{l_i^2}\right)} \right)^{\nu} K_{\nu} \left(\sqrt{2\nu \sum_i \left(\frac{\tau_i^2}{l_i^2}\right)} \right)$$

Parameters num_dim: int

Number of dimensions of the input data. Must be consistent with the *X* and *Xstar* values passed to the GaussianProcess you wish to use the covariance kernel with.

**kwargs:

All keyword parameters are passed to ChainRuleKernel.

Raises ValueError:

If *num_dim* is not a positive integer or the lengths of the input vectors are inconsistent.

GPArgumentError:

If *fixed_params* is passed but *initial_params* is not.

nu

26

Returns the value of the order ν .

class gptools.kernel.matern.Matern52Kernel(num_dim=1, **kwargs)

Bases: gptools.kernel.core.Kernel

Matern 5/2 covariance kernel. Supports only 0th and 1st derivatives and is fixed at nu=5/2. Because of these limitations, it is quite a bit faster than the more general Matern kernels.

The Matern52 kernel has the following hyperparameters, always referenced in the order listed:

0	sigma	prefactor
1	11	length scale for the first dimension
2	12	and so on for all dimensions

The kernel is defined as:

$$k_M(x, x') = \sigma^2 \left(1 + \sqrt{5r^2} + \frac{5}{3}r^2 \right) \exp(-\sqrt{5r^2})$$
$$r^2 = \sum_{d=1}^{D} \frac{(x_d - x'_d)^2}{l_d^2}$$

Parameters num dim: int

Number of dimensions of the input data. Must be consistent with the *X* and *Xstar* values passed to the GaussianProcess you wish to use the covariance kernel with.

**kwargs:

All keyword parameters are passed to Kernel.

Raises ValueError:

If *num_dim* is not a positive integer or the lengths of the input vectors are inconsistent.

GPArgumentError:

If *fixed_params* is passed but *initial_params* is not.

__call__(*Xi*, *Xj*, *ni*, *nj*, *hyper_deriv=None*, *symmetric=False*)

Evaluate the covariance between points Xi and Xj with derivative order ni, nj.

Parameters Xi: Matrix or other Array-like, (*M*, *D*)

M inputs with dimension D.

Xj: Matrix or other Array-like, (M, D)

M inputs with dimension *D*.

 \mathbf{ni} : Matrix or other Array-like, (M, D)

M derivative orders for set i.

 \mathbf{nj} : Matrix or other Array-like, (M, D)

M derivative orders for set *j*.

hyper deriv: Non-negative int or None, optional

The index of the hyperparameter to compute the first derivative with respect to. If None, no derivatives are taken. Hyperparameter derivatives are not supported at this point. Default is None.

symmetric: bool

Whether or not the input Xi, Xi are from a symmetric matrix. Default is False.

Returns Kij: Array, (M,)

Covariances for each of the M Xi, Xj pairs.

Raises NotImplementedError:

If the *hyper_deriv* keyword is not None.

gptools.kernel.noise module

Provides classes for implementing uncorrelated noise.

```
class gptools.kernel.noise.DiagonalNoiseKernel (num\_dim=1, initial\_noise=None, fixed\_noise=False, noise\_bound=None, n=0, hyperprior=None)
```

Bases: gptools.kernel.core.Kernel

Kernel that has constant, independent noise (i.e., a diagonal kernel).

Parameters num_dim : positive int

Number of dimensions of the input data.

initial_noise : float, optional

Initial value for the noise standard deviation. Default value is None (noise gets set to 1).

fixed_noise: bool, optional

Whether or not the noise is taken to be fixed when optimizing the log likelihood. Default is False (noise is not fixed).

noise_bound : 2-tuple, optional

The bounds for the noise when optimizing the log likelihood with scipy.optimize.minimize(). Must be of the form (*lower*, *upper*). Set a given entry to None to put no bound on that side. Default is None, which gets set to (0, None).

n: non-negative int or tuple of non-negative ints with length equal to num_dim, optional
 Indicates which derivative this noise is with respect to. Default is 0 (noise applies to value).

hyperprior: callable, optional

Function that returns the prior log-density for a possible value of noise when called. Must also have an attribute called bounds that is the bounds on the noise and a method called random_draw() that yields a random draw. Default behavior is to assign a uniform prior.

```
__call__ (Xi, Xj, ni, nj, hyper\_deriv=None, symmetric=False)

Evaluate the covariance between points Xi and Xj with derivative order ni, nj.
```

Parameters Xi: Matrix or other Array-like, (M, D)

M inputs with dimension D.

Xi: Matrix or other Array-like, (M, D)

M inputs with dimension *D*.

ni: Matrix or other Array-like, (*M*, *D*)

M derivative orders for set *i*.

nj: Matrix or other Array-like, (*M*, *D*)

M derivative orders for set j.

hyper_deriv : Non-negative int or None, optional

The index of the hyperparameter to compute the first derivative with respect to. Since this kernel only has one hyperparameter, 0 is the only valid value. If None, no derivatives are taken. Default is None (no hyperparameter derivatives).

symmetric: bool, optional

Whether or not the input Xi, Xj are from a symmetric matrix. Default is False.

Returns Kij: Array, (M,)

Covariances for each of the M Xi, Xj pairs.

class gptools.kernel.noise.ZeroKernel (num_dim=1)

Bases: gptools.kernel.noise.DiagonalNoiseKernel

Kernel that always evaluates to zero, used as the default noise kernel.

Parameters num_dim : positive int

The number of dimensions of the inputs.

__call__ (*Xi*, *Xj*, *ni*, *nj*, *hyper_deriv=None*, *symmetric=False*)

Return zeros the same length as the input Xi.

Ignores all other arguments.

Parameters Xi: Matrix or other Array-like, (*M*, *D*)

M inputs with dimension D.

 $\mathbf{X}\mathbf{j}$: Matrix or other Array-like, (M, D)

M inputs with dimension D.

ni: Matrix or other Array-like, (*M*, *D*)

M derivative orders for set *i*.

 \mathbf{nj} : Matrix or other Array-like, (M, D)

M derivative orders for set *j*.

hyper_deriv: Non-negative int or None, optional

The index of the hyperparameter to compute the first derivative with respect to. Since this kernel only has one hyperparameter, 0 is the only valid value. If None, no derivatives are taken. Default is None (no hyperparameter derivatives).

symmetric: bool, optional

Whether or not the input *Xi*, *Xj* are from a symmetric matrix. Default is False.

Returns Kij: Array, (M,)

Covariances for each of the M Xi, Xj pairs.

gptools.kernel.rational_quadratic module

Provides the Rational Quadratic Kernel class which implements the anisotropic rational quadratic (RQ) kernel.

Bases: gptools.kernel.core.ChainRuleKernel

Rational quadratic (RQ) covariance kernel. Supports arbitrary derivatives.

The RQ kernel has the following hyperparameters, always referenced in the order listed:

0	sigma	prefactor.
1	alpha	order of kernel.
2	11	length scale for the first dimension.
3	12	and so on for all dimensions.

The kernel is defined as:

$$k_{RQ} = \sigma^2 \left(1 + \frac{1}{2\alpha} \sum_{i} \frac{\tau_i^2}{l_i^2} \right)^{-\alpha}$$

Parameters num_dim: int

Number of dimensions of the input data. Must be consistent with the *X* and *Xstar* values passed to the GaussianProcess you wish to use the covariance kernel with.

**kwargs:

All keyword parameters are passed to ChainRuleKernel.

Raises ValueError:

If *num_dim* is not a positive integer or the lengths of the input vectors are inconsistent.

GPArgumentError:

If *fixed_params* is passed but *initial_params* is not.

gptools.kernel.squared exponential module

Provides the SquaredExponentialKernel class that implements the anisotropic SE kernel.

Bases: gptools.kernel.core.Kernel

Squared exponential covariance kernel. Supports arbitrary derivatives.

The squared exponential has the following hyperparameters, always referenced in the order listed:

0	sigma	prefactor on the SE
1	11	length scale for the first dimension
2	12	and so on for all dimensions

The kernel is defined as:

$$k_{SE} = \sigma^2 \exp\left(-\frac{1}{2} \sum_{i} \frac{\tau_i^2}{l_i^2}\right)$$

Parameters num_dim: int

Number of dimensions of the input data. Must be consistent with the *X* and *Xstar* values passed to the GaussianProcess you wish to use the covariance kernel with.

**kwargs:

All keyword parameters are passed to Kernel.

Raises ValueError:

If *num_dim* is not a positive integer or the lengths of the input vectors are inconsistent.

GPArgumentError:

```
If fixed_params is passed but initial_params is not.

_call__(Xi, Xj, ni, nj, hyper_deriv=None, symmetric=False)

Evaluate the covariance between points Xi and Xj with derivative order ni, nj.
```

Parameters Xi: Matrix or other Array-like, (M, D)

M inputs with dimension *D*.

Xj: Matrix or other Array-like, (M, D)

M inputs with dimension *D*.

ni: Matrix or other Array-like, (*M*, *D*)

M derivative orders for set i.

 \mathbf{nj} : Matrix or other Array-like, (M, D)

M derivative orders for set j.

hyper_deriv: Non-negative int or None, optional

The index of the hyperparameter to compute the first derivative with respect to. If None, no derivatives are taken. Default is None (no hyperparameter derivatives). Hyperparameter derivatives are not support for n > 0 at this time.

symmetric: bool, optional

Whether or not the input *Xi*, *Xj* are from a symmetric matrix. Default is False.

Returns Kij: Array, (M,)

Covariances for each of the M Xi, Xj pairs.

Raises NotImplementedError:

If hyper deriv is not None and n > 0.

gptools.kernel.warping module

Classes and functions to warp inputs to kernels to enable fitting of nonstationary data. Note that this accomplishes a similar goal as the Gibbs kernel (which is a nonstationary version of the squared exponential kernel), but with the difference that the warpings in this module can be applied to any existing kernel. Furthermore, whereas the Gibbs kernel implements nonstationarity by changing the length scale of the covariance function, the warpings in the module act by transforming the input values directly.

The module contains two core classes that work together. WarpingFunction gives you a way to wrap a given function in a way that allows you to optimize/integrate over the hyperparameters that describe the warping. WarpedKernel is an extension of the Kernel base class and is how you apply a WarpingFunction to whatever kernel you want to warp.

Two useful warpings have been implemented at this point: BetaWarpedKernel warps the inputs using the CDF of the beta distribution (i.e., the regularized incomplete beta function). This requires that the starting inputs be constrained to the unit hypercube [0, 1]. In order to get arbitrary data to this form, LinearWarpedKernel allows you to apply a linear transformation based on the known bounds of your data.

So, for example, to make a beta-warped squared exponential kernel, you simply type:

```
k_SE = gptools.SquaredExponentialKernel()
k_SE_beta = gptools.BetaWarpedKernel(k_SE)
```

Furthermore, if your inputs X are not confined to the unit hypercube [0, 1], you should use a linear transformation to map them to it:

```
k_SE_beta_unit = gptools.LinearWarpedKernel(k_SE_beta, X.min(axis=0), X.max(axis=0))
```

Bases: object

Wrapper to interface a function with WarpedKernel.

This lets you define a simple function fun(X, d, n, p1, p2, ...) that operates on one dimension of X at a time and has several hyperparameters.

Parameters fun: callable

Must have fingerprint fun(X, d, n, p1, p2, ...) where X is an array of length M, d is the index of the dimension X is from, n is a non-negative integer representing the order of derivative to take and p1, p2, ... are the parameters of the warping. Note that this form assumes that the warping is applied independently to each dimension.

num_dim : positive int, optional

Number of dimensions of the input data. Must be consistent with the *X* and *Xstar* values passed to the GaussianProcess you wish to use the warping function with. Default is 1.

num_params : Non-negative int, optional

Number of parameters in the model. Default is to determine the number of parameters by inspection of *fun* or the other arguments provided.

initial_params : Array, (num_params,), optional

Initial values to set for the hyperparameters. Default is None, in which case 1 is used for the initial values.

fixed_params: Array of bool, (num_params,), optional

Sets which hyperparameters are considered fixed when optimizing the log likelihood. A True entry corresponds to that element being fixed (where the element ordering is as defined in the class). Default value is None (no hyperparameters are fixed).

param_bounds: list of 2-tuples (num_params,), optional

List of bounds for each of the hyperparameters. Each 2-tuple is of the form (lower', *upper*). If there is no bound in a given direction, it works best to set it to something big like 1e16. Default is (0.0, 1e16) for each hyperparameter. Note that this is overridden by the *hyperprior* keyword, if present.

param names: list of str (num params,), optional

List of labels for the hyperparameters. Default is all empty strings.

enforce bounds: bool, optional

If True, an attempt to set a hyperparameter outside of its bounds will result in the hyperparameter being set right at its bound. If False, bounds are not enforced inside the kernel. Default is False (do not enforce bounds).

hyperprior: JointPrior instance or list, optional

Joint prior distribution for all hyperparameters. Can either be given as a JointPrior instance or a list of *num_params* callables or rv_frozen instances from scipy.stats, in which case a IndependentJointPrior is constructed with these as the independent priors on each hyperparameter. Default is a uniform PDF on all hyperparameters.

$_$ call $_$ (X, d, n)

Evaluate the warping function.

Parameters X: Array, (M,)

M inputs corresponding to dimension *d*.

d: non-negative int

Index of the dimension that *X* is from.

n: non-negative int

Derivative order to compute.

param_bounds

set_hyperparams (new_params)

Sets the free hyperparameters to the new parameter values in new_params.

Parameters new_params: Array or other Array-like, (len(self.params),)

New parameter values, ordered as dictated by the docstring for the class.

num_free_params

Returns the number of free parameters.

free_param_idxs

Returns the indices of the free parameters in the main arrays of parameters, etc.

free_params

Returns the values of the free hyperparameters.

Returns free_params: Array

Array of the free parameters, in order.

free_param_bounds

Returns the bounds of the free hyperparameters.

Returns free_param_bounds: Array

Array of the bounds of the free parameters, in order.

free param names

Returns the names of the free hyperparameters.

Returns free_param_names: Array

Array of the names of the free parameters, in order.

```
gptools.kernel.warping.beta\_cdf\_warp(X, d, n, *args)
```

Warp inputs that are confined to the unit hypercube using the regularized incomplete beta function.

Applies separately to each dimension, designed for use with WarpingFunction.

Assumes that your inputs X lie entirely within the unit hypercube [0, 1].

Note that you may experience some issues with constraining and computing derivatives at x=0 when $\alpha<1$ and at x=1 when $\beta<1$. As a workaround, try mapping your data to not touch the boundaries of the unit hypercube.

Parameters X: array, (M,)

M inputs from dimension *d*.

d: non-negative int

The index (starting from zero) of the dimension to apply the warping to.

n: non-negative int

The derivative order to compute.

*args: 2N scalars

The remaining parameters to describe the warping, given as scalars. These are given as *alpha_i*, *beta_i* for each of the *D* dimensions. Note that these must ALL be provided for each call.

References

[R1]

 $gptools.kernel.warping.linear_warp(X, d, n, *args)$

Warp inputs with a linear transformation.

Applies the warping

$$w(x) = \frac{x - a}{b - a}$$

to each dimension. If you set a=min(X) and b=max(X) then this is a convenient way to map your inputs to the unit hypercube.

Parameters X: array, (M,)

M inputs from dimension *d*.

d: non-negative int

The index (starting from zero) of the dimension to apply the warping to.

n: non-negative int

The derivative order to compute.

*args: 2N scalars

The remaining parameters to describe the warping, given as scalars. These are given as a_i , b_i for each of the D dimensions. Note that these must ALL be provided for each call

class gptools.kernel.warping.WarpedKernel (k, w)

Bases: gptools.kernel.core.Kernel

Kernel which has had its inputs warped through a basic, elementwise warping function.

In other words, takes $k(x_1, x_2, x'_1, x'_2)$ and turns it into $k(w_1(x_1), w_2(x_2), w_1(x'_1), w_2(x'_2))$.

__call__(Xi, Xj, ni, nj, hyper_deriv=None, symmetric=False)

enforce_bounds

Boolean indicating whether or not the kernel will explicitly enforce the bounds defined by the hyperprior.

fixed_params

params

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```
param_names
     free_params
     free_param_bounds
     free_param_names
     set_hyperparams (new_params)
          Set the (free) hyperparameters.
              Parameters new_params: Array or other Array-like
                    New values of the free parameters.
              Raises ValueError:
                    If the length of new_params is not consistent with self.params.
class gptools.kernel.warping.BetaWarpedKernel(k, **w_kwargs)
     Bases: gptools.kernel.warping.WarpedKernel
     Class to warp any existing Kernel with the beta CDF.
     Assumes that your inputs X lie entirely within the unit hypercube [0, 1].
     Note that you may experience some issues with constraining and computing derivatives at x=0 when \alpha<1
     and at x=1 when \beta<1. As a workaround, try mapping your data to not touch the boundaries of the unit
     hypercube.
          Parameters k: Kernel
                  The Kernel to warp.
              **w_kwargs: optional kwargs
                  All additional kwargs are passed to the constructor of WarpingFunction. If no
                  hyperprior or param_bounds are provided, takes each \alpha, \beta to follow the log-normal
                  distribution.
     References
     [R2]
class qptools.kernel.warpinq.LinearWarpedKernel(k, a, b)
     Bases: gptools.kernel.warping.WarpedKernel
     Class to warp any existing Kernel with the linear transformation given in linear_warp().
     If you set a to be the minimum of your X inputs in each dimension and b to be the maximum then you can
     use this to map data from an arbitrary domain to the unit hypercube [0, 1], as is required for application of the
     BetaWarpedKernel, for instance.
          Parameters k: Kernel
                  The Kernel to warp.
              a: list
                  The a parameter in the linear warping defined in linear_warp(). This list must
                  have length equal to k.num_dim.
```

b: list

The b parameter in the linear warping defined in linear_warp(). This list must have length equal to $k.num_dim$.

Module contents

Subpackage containing a variety of covariance kernels and associated helpers.

4.1.2 Submodules

4.1.3 gptools.error_handling module

Contains exceptions specific to the gptools package.

```
exception gptools.error_handling.GPArgumentError
Bases: exceptions.Exception
```

Exception class raised when an incorrect combination of keyword arguments is given.

4.1.4 gptools.gaussian_process module

Provides the base GaussianProcess class.

```
class gptools.gaussian_process.GaussianProcess(k, noise_k=None, X=None, y=None, err\_y=0, n=0, T=None, diag\_factor=100.0, mu=None)
```

Bases: object

Gaussian process.

If called with one argument, an untrained Gaussian process is constructed and data must be added with the add_data() method. If called with the optional keywords, the values given are used as the data. It is always possible to add additional data with add_data().

Note that the attributes have no write protection, but you should always add data with add_data() to ensure internal consistency.

```
Parameters k: Kernel instance
```

Kernel instance corresponding to the desired noise-free covariance kernel of the Gaussian process. The noise is handled separately either through specification of *err_y*, or in a separate kernel. This allows noise-free predictions when needed.

```
noise k : Kernel instance
```

Kernel instance corresponding to the noise portion of the desired covariance kernel of the Gaussian process. Note that you DO NOT need to specify this if the extent of the noise you want to represent is contained in *err_y* (or if your data are noiseless). Default value is None, which results in the <code>ZeroKernel</code> (noise specified elsewhere or not present).

```
diag_factor: float, optional
```

Factor of sys.float_info.epsilon which is added to the diagonal of the total *K* matrix to improve the stability of the Cholesky decomposition. If you are having issues, try increasing this by a factor of 10 at a time. Default is 1e2.

```
mu: MeanFunction instance
```

The mean function of the Gaussian process. Default is None (zero mean prior).

NOTE:

The following are all passed to add_data(), refer to its docstring.

 \mathbf{X} : array, (M, D), optional

M input values of dimension D. Default value is None (no data).

 \mathbf{y} : array, (M_1) , optional

M data target values. Default value is None (no data).

 err_y : array, (M_1) , optional

Error (given as standard deviation) in the M training target values. Default value is 0 (noiseless observations).

 \mathbf{n} : array, (M, D) or scalar float, optional

Non-negative integer values only. Degree of derivative for each target. If n is a scalar it is taken to be the value for all points in y. Otherwise, the length of n must equal the length of y. Default value is 0 (observation of target value). If non-integer values are passed, they will be silently rounded.

 \mathbf{T} : array, (M, N), optional

Linear transformation to get from latent variables to data in the argument y. When T is passed the argument y holds the transformed quantities y=TY(X) where y are the observed values of the transformed quantities, T is the transformation matrix and Y(X) is the underlying (untransformed) values of the function to be fit that enter into the transformation. When T is M-by-N and Y has Y elements, Y and Y will both be Y-by-Y. Default is None (no transformation).

Raises GPArgumentError:

Gave *X* but not *y* (or vice versa).

ValueError:

Training data rejected by add_data().

See also:

add_data Used to process *X*, *y*, *err_y* and to add data to the process.

Attributes

k	Kernel	The non-noise portion of the covariance kernel.
	instance	
noise_k	Kernel	The noise portion of the covariance kernel.
	instance	
X	array, (M, D)	The M training input values, each of which is of dimension D .
y	array, $(M,)$	The <i>M</i> training target values.
err_y	array, $(M,)$	The error in the <i>M</i> training input values.
n	array, (M, D)	The orders of derivatives that each of the M training points represent,
		indicating the order of derivative with respect to each of the D dimensions.
T	array, (M, N)	The transformation matrix applied to the data. If this is not None, X and n will
		be <i>N</i> -by- <i>D</i> .
K_up_to_	_d late ol	True if no data have been added since the last time the internal state was
		<pre>updated with a call to compute_K_L_alpha_11().</pre>
K	array, (M, M)	Covariance matrix between all of the training inputs.
noise_K	array, (M, M)	Noise portion of the covariance matrix between all of the training inputs. Only
		includes the noise from noise_k, not from err_y.
L	array, (M, M)	Cholesky decomposition of the combined covariance matrix between all of the
		training inputs.
alpha	array, $(M, 1)$	Solution to $K\alpha = y$.
11	float	Log-likelihood of the data given the model.
diag_fact	onfloat	The factor of sys.float_info.epsilon which is added to the diagonal
		of the <i>K</i> matrix to improve stability.
mu		nThe mean function.
	instance	

hyperprior

Combined hyperprior for the kernel, noise kernel and (if present) mean function.

fixed_params

params

param_bounds

param_names

free_params

free_param_bounds

free_param_names

 $add_data(X, y, err_y=0, n=0, T=None)$

Add data to the training data set of the GaussianProcess instance.

Parameters X: array, (M, D)

M input values of dimension D.

 \mathbf{y} : array, (M,)

M target values.

 err_y : array, (M,) or scalar float, optional

Non-negative values only. Error given as standard deviation) in the M target values. If err_y is a scalar, the data set is taken to be homoscedastic (constant error). Otherwise, the length of err_y must equal the length of y. Default value is 0 (noiseless observations).

\mathbf{n} : array, (M, D) or scalar float, optional

Non-negative integer values only. Degree of derivative for each target. If n is a scalar it is taken to be the value for all points in y. Otherwise, the length of n must equal the length of y. Default value is 0 (observation of target value). If non-integer values are passed, they will be silently rounded.

\mathbf{T} : array, (M, N), optional

Linear transformation to get from latent variables to data in the argument y. When T is passed the argument y holds the transformed quantities y=TY(X) where y are the observed values of the transformed quantities, T is the transformation matrix and Y(X) is the underlying (untransformed) values of the function to be fit that enter into the transformation. When T is M-by-N and Y has Y elements, Y and Y will both be Y-by-Y. Default is None (no transformation).

Raises ValueError:

Bad shapes for any of the inputs, negative values for *err_y* or *n*.

condense_duplicates()

Condense duplicate points using a transformation matrix.

This is useful if you have multiple non-transformed points at the same location or multiple transformed points that use the same quadrature points.

Won't change the GP if all of the rows of [X, n] are unique. Will create a transformation matrix T if necessary. Note that the order of the points in [X, n] will be arbitrary after this operation.

```
remove_outliers (thresh=3, **predict_kwargs)
```

Remove outliers from the GP.

Removes points that are more than *thresh* * *err_y* away from the GP mean. Note that this is only very rough in that it ignores the uncertainty in the GP mean at any given point. But you should only be using this as a rough way of removing bad channels, anyways!

Returns the values that were removed and a boolean array indicating where the removed points were.

Parameters thresh: float, optional

The threshold as a multiplier times *err_y*. Default is 3 (i.e., throw away all 3-sigma points).

**predict_kwargs : optional kwargs

All additional kwargs are passed to predict(). You can, for instance, use this to make it use MCMC to evaluate the mean. (If you don't use MCMC, then the current value of the hyperparameters is used.)

Returns X_bad: array

Input values of the bad points.

y_bad : array
Bad values.

err_y_bad : array

Uncertainties on the bad values.

n_bad: array

Derivative order of the bad values.

bad idxs: array

Array of booleans with the original shape of X with True wherever a point was taken to be bad and subsequently removed.

T_bad: array

Transformation matrix of returned points. Only returned if T is not None for the instance.

Optimize the hyperparameters by maximizing the log likelihood.

Leaves the GaussianProcess instance in the optimized state.

If scipy.optimize.minimize() is not available (i.e., if your scipy version is older than 0.11.0) then fmin_slsqp() is used independent of what you set for the *method* keyword.

Parameters method: str. optional

The method to pass to scipy.optimize.minimize(). Refer to that function's docstring for valid options. Default is 'SLSQP'. See note above about behavior with older versions of scipy.

```
opt_kwargs : dict, optional
```

Dictionary of extra keywords to pass to scipy.optimize.minimize(). Refer to that function's docstring for valid options. Note that if you use jac = True (i.e., optimization function returns Jacobian) you should also set args = (True,) to tell update_hyperparameters() to compute and return the Jacobian. Default is: {}.

verbose: bool, optional

Whether or not the output should be verbose. If True, the entire Result object from scipy.optimize.minimize() is printed. If False, status information is only printed if the *success* flag from minimize() is False. Default is False.

random_starts: non-negative int, optional

Number of times to randomly perturb the starting guesses (distributed uniformly within their bounds) in order to seek the global minimum. If None, then *num_proc* random starts will be performed. Default is None (do number of random starts equal to the number of processors allocated). Note that for *random_starts* != 0, the initial guesses provided are not actually used.

num_proc : non-negative int or None

Number of processors to use with random starts. If 0, processing is not done in parallel. If None, all available processors are used. Default is None (use all available processors).

The order of the derivative is given by n. The keyword *noise* sets whether or not noise is included in the prediction.

Parameters Xstar: array, (M, D)

M test input values of dimension D.

 \mathbf{n} : array, (M, D) or scalar, non-negative int, optional

Order of derivative to predict (0 is the base quantity). If n is scalar, the value is used for all points in Xstar. If non-integer values are passed, they will be silently rounded. Default is 0 (return base quantity).

noise: bool, optional

Whether or not noise should be included in the covariance. Default is False (no noise in covariance).

return std: bool, optional

Set to True to compute and return the standard deviation for the predictions, False to skip this step. Default is True (return tuple of (*mean*, *std*)).

return_cov: bool, optional

Set to True to compute and return the full covariance matrix for the predictions. This overrides the *return_std* keyword. If you want both the standard deviation and covariance matrix pre-computed, use the *full_output* keyword.

full_output : bool, optional

Set to True to return the full outputs in a dictionary with keys:

mea	mean of GP at requested points	
std	standard deviation of GP at requested points	
cov	covariance matrix for values of GP at requested points	
sam	random samples of GP at requested points (only if return_sample is	
	True)	

return_samples: bool, optional

Set to True to compute and return samples of the GP in addition to computing the mean. Only done if *full_output* is True. Default is False.

num_samples : int, optional

Number of samples to compute. If using MCMC this is the number of samples per MCMC sample, if using present values of hyperparameters this is the number of samples actually returned. Default is 1.

samp_kwargs : dict, optional

Additional keywords to pass to $draw_sample()$ if $return_samples$ is True. Default is $\{\}$.

use MCMC: bool, optional

Set to True to use $predict_MCMC()$ to evaluate the prediction marginalized over the hyperparameters.

full_MC: bool, optional

Set to True to compute the mean and covariance matrix using Monte Carlo sampling of the posterior. The samples will also be returned if full_output is True. Default is False (don't use full sampling).

rejection_func : callable, optional

Any samples where this function evaluates False will be rejected, where it evaluates True they will be kept. Default is None (no rejection). Only has an effect if *full_MC* is True.

ddof: int, optional

The degree of freedom correction to use when computing the covariance matrix when *full MC* is True. Default is 1 (unbiased estimator).

output_transform: array, ('L', 'M'), optional:

Matrix to use to transform the output vector of length M to one of length L. This can, for instance, be used to compute integrals.

**kwargs: optional kwargs

All additional kwargs are passed to predict_MCMC() if use_MCMC is True.

Returns mean: array, (M,)

Predicted GP mean. Only returned if full_output is False.

std: array, (M,)

Predicted standard deviation, only returned if *return_std* is True, *return_cov* is False and *full_output* is False.

 \mathbf{cov} : array, (M, M)

Predicted covariance matrix, only returned if return_cov is True and full_output is False.

full output: dict

Dictionary with fields for mean, std, cov and possibly random samples. Only returned if *full_output* is True.

Raises ValueError:

If n is not consistent with the shape of Xstar or is not entirely composed of non-negative integers.

plot (X=None, n=0, ax=None, envelopes=[1, 3], base_alpha=0.375, return_prediction=False, return_std=True, full_output=False, plot_kwargs={}, **kwargs)
Plots the Gaussian process using the current hyperparameters. Only for num_dim <= 2.</pre>

Parameters X: array-like (M,) or (M, num_dim) , optional

The values to evaluate the Gaussian process at. If None, then 100 points between the minimum and maximum of the data's X are used. Default is None (use 100 points between min and max).

n: int or list, optional

The order of derivative to compute. For num_dim=1, this must be an int. For num_dim=2, this must be a list of ints of length 2. Default is 0 (don't take derivative).

ax: axis instance, optional

Axis to plot the result on. If no axis is passed, one is created. If the string 'gca' is passed, the current axis (from plt.gca()) is used. If X_dim = 2, the axis must be 3d.

envelopes: list of float, optional:

+/-n*sigma envelopes to plot. Default is [1, 3].

base_alpha: float, optional

Alpha value to use for +/-1*sigma envelope. All other envelopes env are drawn with base_alpha/env. Default is 0.375.

return_prediction: bool, optional

If True, the predicted values are also returned. Default is False.

return std: bool, optional

If True, the standard deviation is computed and returned along with the mean when *return_prediction* is True. Default is True.

full_output: bool, optional

Set to True to return the full outputs in a dictionary with keys:

mea	mean of GP at requested points
std	standard deviation of GP at requested points
cov	covariance matrix for values of GP at requested points
sam	random samples of GP at requested points (only if <i>return_sample</i> is
	True)

plot_kwargs : dict, optional

The entries in this dictionary are passed as kwargs to the plotting command used to plot the mean. Use this to, for instance, change the color, line width and line style.

**kwargs: extra arguments for predict, optional

Extra arguments that are passed to predict ().

Returns ax: axis instance

The axis instance used.

mean: Array, (M,)

Predicted GP mean. Only returned if return_prediction is True and full_output is False.

std: Array, (M,)

Predicted standard deviation, only returned if *return_prediction* and *return_std* are True and *full_output* is False.

full_output : dict

Dictionary with fields for mean, std, cov and possibly random samples. Only returned if *return_prediction* and *full_output* are True.

 $\label{lem:draw_sample} \begin{array}{ll} \textbf{draw_sample} \ (\textit{Xstar}, & n=0, & num_samp=1, & rand_vars=None, & rand_type='standard & normal', \\ & diag_factor=1000.0, & method='cholesky', & num_eig=None, & mean=None, & cov=None, \\ & **kwargs) \end{array}$

Draw a sample evaluated at the given points *Xstar*.

Parameters Xstar: array, (M, D)

M test input values of dimension D.

 \mathbf{n} : array, (M, D) or scalar, non-negative int, optional

Derivative order to evaluate at. Default is 0 (evaluate value).

noise: bool, optional

Whether or not to include the noise components of the kernel in the sample. Default is False (no noise in samples).

num_samp : Positive int, optional

Number of samples to draw. Default is 1. Cannot be used in conjunction with $rand_vars$: If you pass both num_samp and $rand_vars$, num_samp will be silently ignored.

 $rand_vars$: array, (M, P), optional

Vector of random variables u to use in constructing the sample $y_* = f_* + Lu$, where $K = LL^T$. If None, values will be produced using numpy.random.multivariate_normal(). This allows you to use pseudo/quasi random numbers generated by an external routine. Default is None (use multivariate_normal() directly).

rand_type : {'standard normal', 'uniform'}, optional

Type of distribution the inputs are given with.

- 'standard normal': Standard (mu = 0, sigma = 1) normal distribution (this is the default)
- 'uniform': Uniform distribution on [0, 1). In this case the required Gaussian variables are produced with inversion.

diag_factor: float, optional

Number (times machine epsilon) added to the diagonal of the covariance matrix prior to computing its Cholesky decomposition. This is necessary as sometimes the decomposition will fail because, to machine precision, the matrix appears to not be positive definite. If you are getting errors from scipy.linalg.cholesky(), try increasing this an order of magnitude at a time. This parameter only has an effect when using rand vars. Default value is 1e3.

method: {'cholesky', 'eig'}, optional

Method to use for constructing the matrix square root. Default is 'cholesky' (use lower-triangular Cholesky decomposition).

- 'cholesky': Perform Cholesky decomposition on the covariance matrix: $K = LL^T$, use L as the matrix square root.
- 'eig': Perform an eigenvalue decomposition on the covariance matrix: $K=Q\Lambda Q^{-1}$, use $Q\Lambda^{1/2}$ as the matrix square root.

num_eig: int or None, optional

Number of eigenvalues to compute. Can range from 1 to *M* (the number of test points). If it is None, then all eigenvalues are computed. Default is None (compute all eigenvalues). This keyword only has an effect if *method* is 'eig'.

mean: array, (M,)

If you have pre-computed the mean and covariance matrix, then you can simply pass them in with the *mean* and *cov* keywords to save on having to call predict().

```
cov : array, (M, M)
```

If you have pre-computed the mean and covariance matrix, then you can simply pass them in with the *mean* and *cov* keywords to save on having to call predict ().

**kwargs: optional kwargs

All extra keyword arguments are passed to predict () when evaluating the mean and covariance matrix of the GP.

Returns samples: Array (M, P) or (M, num_samp)

Samples evaluated at the *M* points.

Raises ValueError:

If rand type or method is invalid.

update_hyperparameters (new_params, exit_on_bounds=True, inf_on_error=True)

Update the kernel's hyperparameters to the new parameters.

This will call compute_K_L_alpha_ll() to update the state accordingly.

Parameters new_params: Array or other Array-like, length dictated by kernel

New parameters to use.

exit on bounds: bool, optional

If True, the method will automatically exit if the hyperparameters are impossible given the hyperprior, without trying to update the internal state. This is useful during MCMC sampling and optimization. Default is True (don't perform update for impossible hyperparameters).

inf_on_error: bool, optional

If True, the method will return *scipy.inf* if the hyperparameters produce a linear algebra error upon trying to update the Gaussian process. Default is True (catch errors and return infinity).

Returns -1*ll: float

The updated log likelihood.

compute_K_L_alpha_11()

Compute K, L, alpha and log-likelihood according to the first part of Algorithm 2.1 in R&W.

Computes K and the noise portion of K using compute_Kij(), computes L using scipy.linalg.cholesky(), then computes alpha as L.T(L)y.

Only does the computation if K_up_to_date is False – otherwise leaves the existing values.

num_dim

The number of dimensions of the input data.

Returns num_dim: int:

The number of dimensions of the input data as defined in the kernel.

compute_Kij (Xi, Xj, ni, nj, noise=False, hyper_deriv=None)

Compute covariance matrix between datasets Xi and Xj.

Specify the orders of derivatives at each location with the ni, nj arrays. The $include_noise$ flag is passed to the covariance kernel to indicate whether noise is to be included (i.e., for evaluation of $K + \sigma I$ versus K_*).

If Xj is None, the symmetric matrix K(X, X) is formed.

Note that type and dimension checking is NOT performed, as it is assumed the data are from inside the instance and have hence been sanitized by add_data().

Parameters Xi: array, (M, D)

M input values of dimension D.

Xj: array, (P, D)

P input values of dimension D.

 \mathbf{ni} : array, (M_1) , non-negative integers

M derivative orders with respect to the Xi coordinates.

nj: array, (P,), non-negative integers

P derivative orders with respect to the Xj coordinates.

noise: bool, optional

If True, uses the noise kernel, otherwise uses the regular kernel. Default is False (use regular kernel).

hyper_deriv : None or non-negative int

Index of the hyperparameter to compute the first derivative with respect to. If None, no derivatives are taken. Default is None (no hyperparameter derivatives).

Returns Kij: array, (M, P)

Covariance matrix between Xi and Xj.

compute_ll_matrix (bounds, num_pts)

Compute the log likelihood over the (free) parameter space.

Parameters bounds: 2-tuple or list of 2-tuples with length equal to the number of free parameters

Bounds on the range to use for each of the parameters. If a single 2-tuple is given, it will be used for each of the parameters.

num_pts: int or list of ints with length equal to the number of free parameters

If a single int is given, it will be used for each of the parameters.

Returns ll_vals: Array

The log likelihood for each of the parameter possibilities.

param_vals [List of Array] The parameter values used.

Produce samples from the posterior for the hyperparameters using MCMC.

Returns the sampler created, because storing it stops the GP from being pickleable. To add more samples to a previous sampler, pass the sampler instance in the *sampler* keyword.

Parameters nwalkers: int, optional

The number of walkers to use in the sampler. Should be on the order of several hundred. Default is 200.

nsamp: int, optional

Number of samples (per walker) to take. Default is 500.

burn: int, optional

This keyword only has an effect on the corner plot produced when $plot_posterior$ is True and the flattened chain plot produced when $plot_chains$ is True. To perform computations with burn-in, see <code>compute_from_MCMC()</code>. The number of samples to discard at the beginning of the chain. Default is 0.

thin: int, optional

This keyword only has an effect on the corner plot produced when *plot_posterior* is True and the flattened chain plot produced when *plot_chains* is True. To perform computations with thinning, see <code>compute_from_MCMC()</code>. Every *thin-*th sample is kept. Default is 1.

num_proc : int or None, optional

Number of processors to use. If None, all available processors are used. Default is None (use all available processors).

sampler: Sampler instance

The sampler to use. If the sampler already has samples, the most recent sample will be used as the starting point. Otherwise a random sample from the hyperprior will be used.

plot_posterior: bool, optional

If True, a corner plot of the posterior for the hyperparameters will be generated. Default is False.

plot_chains : bool, optional

If True, a plot showing the history and autocorrelation of the chains will be produced.

sampler_type : str, optional

The type of sampler to use. Valid options are "ensemble" (affine- invariant ensemble sampler) and "pt" (parallel-tempered ensemble sampler).

ntemps: int, optional

Number of temperatures to use with the parallel-tempered ensemble sampler.

sampler_a: float, optional

Scale of the proposal distribution.

 $\begin{tabular}{ll} \textbf{compute_from_MCMC} (X, n=0, return_mean=True, return_std=True, return_cov=False, return_samples=False, num_samples=1, noise=False, samp_kwargs=\{\}, sampler=None, flat_trace=None, burn=0, thin=1, **kwargs) \\ Compute desired quantities from MCMC samples of the hyperparameter posterior. \\ \end{tabular}$

The return will be a list with a number of rows equal to the number of hyperparameter samples. The columns depend on the state of the boolean flags, but will be some subset of (mean, stddev, cov, samples), in that order. Samples will be the raw output of draw_sample(), so you will need to remember to convert to an array and flatten if you want to work with a single sample.

Parameters X: array-like (M,) or (M, num_dim)

The values to evaluate the Gaussian process at.

n: non-negative int or list, optional

The order of derivative to compute. For num_dim=1, this must be an int. For num_dim=2, this must be a list of ints of length 2. Default is 0 (don't take derivative).

return_mean: bool, optional

If True, the mean will be computed at each hyperparameter sample. Default is True (compute mean).

return_std: bool, optional

If True, the standard deviation will be computed at each hyperparameter sample. Default is True (compute stddev).

return cov: bool, optional

If True, the covariance matrix will be computed at each hyperparameter sample. Default is True (compute stddev).

return_samples: bool, optional

If True, random sample(s) will be computed at each hyperparameter sample. Default is False (do not compute samples).

num_samples : int, optional

Compute this many samples if *return_sample* is True. Default is 1.

noise: bool, optional

If True, noise is included in the predictions and samples. Default is False (do not include noise).

samp_kwargs: dict, optional

If $return_sample$ is True, the contents of this dictionary will be passed as kwargs to $draw_sample()$.

sampler: Sampler instance or None, optional

Sampler instance that has already been run to the extent desired on the hyperparameter posterior. If None, a new sampler will be created with sample_hyperparameter_posterior(). In this case, all extra kwargs will be passed on, allowing you to set the number of samples, etc. Default is None (create sampler).

flat trace: array-like (nsamp, ndim) or None, optional

Flattened trace with samples of the free hyperparameters. If present, overrides *sampler*. This allows you to use a sampler other than the ones from <code>emcee</code>, or to specify arbitrary values you wish to evaluate the curve at. Note that this WILL be thinned and burned according to the following two kwargs. "Flat" refers to the fact that you must have combined all chains into a single one. Default is None (use *sampler*).

burn: int, optional

The number of samples to discard at the beginning of the chain. Default is 0.

thin: int, optional

Every *thin*-th sample is kept. Default is 1.

num_proc: int, optional

The number of processors to use for evaluation. This is used both when calling the sampler and when evaluating the Gaussian process. If None, the number of available processors will be used. If zero, evaluation will proceed in parallel. Default is to use all available processors.

**kwargs : extra optional kwargs

All additional kwargs are passed to sample_hyperparameter_posterior().

Returns out : dict

A dictionary having some or all of the fields 'mean', 'std', 'cov' and 'samp'. Each entry is a list of array-like. The length of this list is equal to the number of hyperparameter samples used, and the entries have the following shapes:

mean	(M,)
std	(M,)
cov	(M,M)
samp	(M, num_samples)

predict_MCMC (X, ddof=1, full_MC=False, rejection_func=None, **kwargs)

Make a prediction using MCMC samples.

This is essentially a convenient wrapper of compute_from_MCMC(), designed to act more or less interchangeably with predict().

Computes the mean of the GP posterior marginalized over the hyperparameters using iterated expectations. If *return_std* is True, uses the law of total variance to compute the variance of the GP posterior marginalized over the hyperparameters. If *return_cov* is True, uses the law of total covariance to compute the entire covariance of the GP posterior marginalized over the hyperparameters. If both *return_cov* and *return_std* are True, then both the covariance matrix and standard deviation array will be returned.

Parameters X: array-like (M,) or (M, num_dim)

The values to evaluate the Gaussian process at.

ddof: int, optional

The degree of freedom correction to use when computing the variance. Default is 1 (standard Bessel correction for unbiased estimate).

return_std: bool, optional

If True, the standard deviation is also computed. Default is True.

full_MC: bool, optional

Set to True to compute the mean and covariance matrix using Monte Carlo sampling of the posterior. The samples will also be returned if full_output is True. Default is False (don't use full sampling).

rejection_func : callable, optional

Any samples where this function evaluates False will be rejected, where it evaluates True they will be kept. Default is None (no rejection). Only has an effect if *full_MC* is True.

ddof: int, optional

**kwargs: optional kwargs

All additional kwargs are passed directly to compute_from_MCMC().

class gptools.gaussian_process.Constraint $(gp, boundary_val=0.0, n=0, loc='min', type_='gt', bounds=None)$

Bases: object

Implements an inequality constraint on the value of the mean or its derivatives.

Provides a callable such as can be passed to SLSQP or COBYLA to implement the constraint when using scipy.optimize.minimize().

The function defaults implement a constraint that forces the mean value to be positive everywhere.

Parameters gp: GaussianProcess

The GaussianProcess instance to create the constraint on.

boundary_val: float, optional

Boundary value for the constraint. For $type_{-}$ = 'gt', this is the lower bound, for $type_{-}$ = 'lt', this is the upper bound. Default is 0.0.

n: non-negative int, optional

Derivative order to evaluate. Default is 0 (value of the mean). Note that non-int values are silently cast to int.

loc: {'min', 'max'}, float or Array-like of float (num_dim,), optional

Which extreme of the mean to use, or location to evaluate at.

- If 'min', the minimum of the mean (optionally over *bounds*) is used.
- If 'max', the maximum of the mean (optionally over bounds) is used.
- If a float (valid for *num_dim* = 1 only) or Array of float, the mean is evaluated at the given X value.

Default is 'min' (use function minimum).

type_: {'gt', 'lt'}, optional

What type of inequality constraint to implement.

- If 'gt', a greater-than-or-equals constraint is used.
- If 'lt', a less-than-or-equals constraint is used.

Default is 'gt' (greater-than-or-equals).

bounds: 2-tuple of float or 2-tuple Array-like of float (num_dim,) or None, optional

Bounds to use when *loc* is 'min' or 'max'.

- If None, the bounds are taken to be the extremes of the training data. For multivariate
 data, "extremes" essentially means the smallest hypercube oriented parallel to the
 axes that encapsulates all of the training inputs. (I.e., (gp.X.min(axis=0),
 gp.X.max(axis=0)))
- If *bounds* is a 2-tuple, then this is used as (*lower*, *upper*) where lower and *upper* are Array-like with dimensions (*num_dim*,).
- If *num_dim* is 1 then *lower* and *upper* can be scalar floats.

Default is None (use extreme values of training data).

Raises TypeError:

If gp is not an instance of Gaussian Process.

ValueError:

If *n* is negative.

ValueError:

If *loc* is not 'min', 'max' or an Array-like of the correct dimensions.

ValueError:

If *type*_ is not 'gt' or 'lt'.

ValueError:

If *bounds* is not None or length 2 or if the elements of bounds don't have the right dimensions.

```
___call___(params)
```

Returns a non-negative number if the constraint is satisfied.

Parameters params: Array-like, length dictated by kernel

New parameters to use.

Returns val: float

Value of the constraint. minimize will attempt to keep this non-negative.

4.1.5 gptools.gp_utils module

Provides convenient utilities for working with the classes and results from gptools.

This module specifically contains utilities that need to interact directly with the GaussianProcess object, and hence can present circular import problems when incorporated in the main utils submodule.

```
gptools.gp_utils.parallel_compute_ll_matrix(gp, bounds, num_pts, num_proc=None)

Compute matrix of the log likelihood over the parameter space in parallel.
```

Parameters bounds: 2-tuple or list of 2-tuples with length equal to the number of free parameters

Bounds on the range to use for each of the parameters. If a single 2-tuple is given, it will be used for each of the parameters.

num_pts: int or list of ints with length equal to the number of free parameters

The number of points to use for each parameters. If a single int is given, it will be used for each of the parameters.

num_proc: Positive int or None, optional

Number of processes to run the parallel computation with. If set to None, ALL available cores are used. Default is None (use all available cores).

Returns ll_vals : array

The log likelihood for each of the parameter possibilities.

param vals: list of array

The parameter values used.

```
gptools.gp_utils.slice_plot(*args, **kwargs)
```

Constructs a plot that lets you look at slices through a multidimensional array.

Parameters vals: array, (M, D, P, ...)

Multidimensional array to visualize.

 $x_vals_1 : array, (M,)$

Values along the first dimension.

 $x_vals_2 : array, (D,)$

Values along the second dimension.

 $x_vals_3 : array, (P,)$

Values along the third dimension.

...and so on. At least four arguments must be provided.

names: list of strings, optional

Names for each of the parameters at hand. If None, sequential numerical identifiers will be used. Length must be equal to the number of dimensions of *vals*. Default is None.

n: Positive int, optional

Number of contours to plot. Default is 100.

Returns f: Figure

The Matplotlib figure instance created.

Raises GPArgumentError:

If the number of arguments is less than 4.

```
gptools.gp_utils.arrow_respond(slider, event)
```

Event handler for arrow key events in plot windows.

Pass the slider object to update as a masked argument using a lambda function:

```
lambda evt: arrow_respond(my_slider, evt)
```

Parameters slider: Slider instance associated with this handler.

event: Event to be handled.

4.1.6 gptools.mean module

Provides classes for defining explicit, parametric mean functions.

To provide the necessary hooks to optimize/sample the hyperparameters, your mean function must be wrapped with MeanFunction before being passed to GaussianProcess. The function must have the calling fingerprint fun(X, n, p1, p2, ...), where X is an array with shape (M, N), n is a vector with length D and p1, p2, ... are the (hyper)parameters of the mean function, given as individual arguments.

Bases: object

Wrapper to turn a function into a form useable by GaussianProcess.

This lets you define a simple function fun(X, n, p1, p2, ...) that operates on an (M, D) array X, taking the derivatives indicated by the vector n with length D (one derivative order for each dimension). The function should evaluate this derivative at all points in X, returning an array of length M. MeanFunction takes care of looping over the different derivatives requested by GaussianProcess.

Parameters fun : callable

Must have fingerprint fun(X, n, p1, p2, ...) where X is an array with shape (M, D), n is an array of non-negative integers with length D representing the order of derivative orders to take for each dimension and p1, p2, ... are the parameters of the mean function.

num_params : Non-negative int, optional

Number of parameters in the model. Default is to determine the number of parameters by inspection of *fun* or the other arguments provided.

initial_params : Array, (num_params,), optional

Initial values to set for the hyperparameters. Default is None, in which case 1 is used for the initial values.

fixed_params: Array of bool, (num_params,), optional

Sets which hyperparameters are considered fixed when optimizing the log likelihood. A True entry corresponds to that element being fixed (where the element ordering is as defined in the class). Default value is None (no hyperparameters are fixed).

param_bounds: list of 2-tuples (*num_params*,), optional

List of bounds for each of the hyperparameters. Each 2-tuple is of the form (lower', *upper*). If there is no bound in a given direction, it works best to set it to something big like 1e16. Default is (0.0, 1e16) for each hyperparameter. Note that this is overridden by the *hyperprior* keyword, if present.

param_names : list of str (num_params,), optional

List of labels for the hyperparameters. Default is all empty strings.

enforce_bounds: bool, optional

If True, an attempt to set a hyperparameter outside of its bounds will result in the hyperparameter being set right at its bound. If False, bounds are not enforced inside the kernel. Default is False (do not enforce bounds).

hyperprior: JointPrior instance or list, optional

Joint prior distribution for all hyperparameters. Can either be given as a JointPrior instance or a list of *num_params* callables or rv_frozen instances from scipy.stats, in which case a IndependentJointPrior is constructed with these as the independent priors on each hyperparameter. Default is a uniform PDF on all hyperparameters.

```
\underline{\hspace{1cm}}call\underline{\hspace{1cm}}(X, n)
```

param_bounds

set_hyperparams (new_params)

Sets the free hyperparameters to the new parameter values in new_params.

Parameters new_params: Array or other Array-like, (len(self.params),)

New parameter values, ordered as dictated by the docstring for the class.

num_free_params

Returns the number of free parameters.

free param idxs

Returns the indices of the free parameters in the main arrays of parameters, etc.

free params

Returns the values of the free hyperparameters.

Returns free_params: Array

Array of the free parameters, in order.

free_param_bounds

Returns the bounds of the free hyperparameters.

Returns free_param_bounds: Array

Array of the bounds of the free parameters, in order.

free_param_names

Returns the names of the free hyperparameters.

Returns free_param_names: Array

Array of the names of the free parameters, in order.

```
gptools.mean.constant(X, n, mu)
```

Function implementing a constant mean suitable for use with MeanFunction.

```
class gptools.mean.ConstantMeanFunction(**kwargs)
```

```
Bases: gptools.mean.MeanFunction
```

Class implementing a constant mean function suitable for use with GaussianProcess.

All kwargs are passed to MeanFunction. If you do not pass *hyperprior* or *param_bounds*, the hyperprior for the mean is taken to be uniform over [-1e3, 1e3].

```
gptools.mean.mtanh(alpha, z)
```

Modified hyperbolic tangent function mtanh(z; alpha).

Parameters alpha: float

The core slope of the mtanh.

z: float or array

The coordinate of the mtanh.

```
gptools.mean.mtanh\_profile(X, n, x0, delta, alpha, h, b)
```

Profile used with the mtanh function to fit profiles, suitable for use with MeanFunction.

Only supports univariate data!

```
Parameters X: array, (M, 1)
```

The points to evaluate at.

n: array, (1,)

The order of derivative to compute. Only up to first derivatives are supported.

x0: float

Pedestal center

delta: float

Pedestal halfwidth

alpha: float

Core slope

h: float

Pedestal height

b : float

Pedestal foot

```
class gptools.mean.MtanhMeanFunction1d(**kwargs)
```

```
Bases: gptools.mean.MeanFunction
```

Profile with mtanh edge, suitable for use with GaussianProcess.

All kwargs are passed to MeanFunction. If *hyperprior* and *param_bounds* are not passed then the hyperprior is taken to be uniform over the following intervals:

x0	0.98	1.1
delta	0.0	0.1
alpha	-0.5	0.5
h	0	5
b	0	0.5

gptools.mean.linear(X, n, *args)

Linear mean function of arbitrary dimension, suitable for use with MeanFunction.

The form is $m_0 * X[:, 0] + m_1 * X[:, 1] + \cdots + b$.

Parameters X: array, (M, D)

The points to evaluate the model at.

 \mathbf{n} : array of non-negative int, (D)

The derivative order to take, specified as an integer order for each dimension in X.

*args: num_dim+1 floats

The slopes for each dimension, plus the constant term. Must be of the form m0, m1, ..., b

class gptools.mean.LinearMeanFunction(num_dim=1, **kwargs)

Bases: gptools.mean.MeanFunction

Linear mean function suitable for use with GaussianProcess.

Parameters num_dim: positive int, optional

The number of dimensions of the input data. Default is 1.

**kwargs : optional kwargs

All extra kwargs are passed to MeanFunction. If *hyperprior* and *param_bounds* are not specified, all parameters are taken to have a uniform hyperprior over [-1e3, 1e3].

4.1.7 gptools.utils module

Provides convenient utilities for working with the classes and results from gptools.

class gptools.utils.LessThanUniformPotential (l_idx, g_idx)

Bases: object

Class to implement a potential to enforce an inequality constraint.

Specifically lets you change the param with l_idx to have a uniform prior between its lower bound and the param with g_idx.

Returns log((ub-lb)/(theta[g_idx]-lb)) if theta[l_idx] <= theta[g_idx], double_min otherwise.

Parameters l_idx: int

Index of the parameter that is required to be lesser.

g_idx: int

Index of the parameter that is required to be greater.

 $_$ call $_$ (theta, k)

Return the log-density of the potential.

Parameters theta: array-like

Array of the hyperparameters.

```
k: Kernel instance
                      The kernel the hyperparameters apply to.
               Returns f: float
                      Returns log((ub-lb)/(theta[g_idx]-lb)) if the condition is met, -inf if not.
class gptools.utils.JeffreysPrior(idx, bounds)
     Bases: object
     Class to implement a Jeffreys prior over a finite range. Returns log-density.
           Parameters idx: int
                   The index this prior applies to.
               bounds: 2-tuple
                   The bounds for the parameter this prior corresponds to: (lb, ub).
     __call__(theta)
     interval (alpha)
class gptools.utils.LinearPrior(idx, bounds)
     Bases: object
     Class to implement a linear prior. Returns log-density.
           Parameters idx: int
                   The index this prior applies to.
               bounds: 2-tuple
                   The bounds for the parameter this prior corresponds to: (lb, ub).
       __call___(theta)
           Return the log-density of the uniform prior.
               Parameters theta: array-like, or float
                      Value of values of the hyperparameter.
               Returns f: Array or float
                      Returns log(2/(b-a)^2) + log(b-theta) if theta is in bounds, -inf if theta is out of bounds.
     interval (alpha)
class gptools.utils.UniformPrior(idx, bounds)
     Bases: object
     Class to implement a uniform prior. Returns log-density.
           Parameters idx: int
                   The index this prior applies to.
               bounds: 2-tuple
                   The bounds for the parameter this prior corresponds to: (lb, ub).
        _{\mathtt{call}} (theta)
           Return the log-PDF of the uniform prior.
               Parameters theta: array-like
                      Values of the hyperparameters.
```

Returns -log(ub - lb) if theta is scalar and in bounds, double_min if theta is scalar and out of bounds and an appropriately-shaped array if theta is array-like. interval (alpha) rvs (size=None) class gptools.utils.JointPrior Bases: object Abstract class for objects implementing joint priors over hyperparameters. _**call**___(*theta*) Evaluate the prior log-PDF at the given values of the hyperparameters, theta. **Parameters theta**: array-like, (num_params,) The hyperparameters to evaluate the log-PDF at. random_draw(size=None) Draw random samples of the hyperparameters. **Parameters size**: None, int or array-like, optional The number/shape of samples to draw. If None, only one sample is returned. Default is None. mul (other) Multiply two JointPrior instances together. class gptools.utils.CombinedBounds(<math>l1, l2) Bases: object Object to support reassignment of the bounds from a combined prior. __getitem__(pos) __setitem__(pos, value) __len__() invert () class gptools.utils.MaskedBounds(a, m)Bases: object Object to support reassignment of free parameter bounds. __getitem__(pos) __setitem__(pos, value) __len__() class gptools.utils.ProductJointPrior (p1, p2) Bases: gptools.utils.JointPrior Product of two independent priors. Parameters p1, p2: :py:class:'JointPrior' instances : The two priors to merge.

Returns f: Array or float

bounds

call (theta)

```
Evaluate the prior log-PDF at the given values of the hyperparameters, theta.
          The log-PDFs of the two priors are summed.
               Parameters theta: array-like, (num_params,)
                     The hyperparameters to evaluate the log-PDF at.
     random draw(size=None)
          Draw random samples of the hyperparameters.
          The outputs of the two priors are stacked vertically.
               Parameters size: None, int or array-like, optional
                     The number/shape of samples to draw. If None, only one sample is returned. Default is
class gptools.utils.UniformJointPrior (bounds)
     Bases: gptools.utils.JointPrior
     Uniform prior over the specified bounds.
          Parameters bounds: list of tuples, (num_params,)
                   The bounds for each of the random variables.
     ___call___(theta)
          Evaluate the prior log-PDF at the given values of the hyperparameters, theta.
               Parameters theta: array-like, (num params,)
                     The hyperparameters to evaluate the log-PDF at.
     random_draw(size=None)
          Draw random samples of the hyperparameters.
               Parameters size: None, int or array-like, optional
                     The number/shape of samples to draw. If None, only one sample is returned. Default is
                     None.
class gptools.utils.CoreEdgeJointPrior(bounds)
     Bases: gptools.utils.UniformJointPrior
     Prior for use with Gibbs kernel warping functions with an inequality constraint between the core and edge length
     scales.
       _call__(theta)
          Evaluate the prior log-PDF at the given values of the hyperparameters, theta.
               Parameters theta: array-like, (num params,)
                     The hyperparameters to evaluate the log-PDF at.
     random_draw(size=None)
          Draw random samples of the hyperparameters.
               Parameters size: None, int or array-like, optional
                     The number/shape of samples to draw. If None, only one sample is returned. Default is
class gptools.utils.CoreMidEdgeJointPrior(bounds)
     Bases: gptools.utils.UniformJointPrior
```

Prior for use with Gibbs kernel warping functions with an inequality constraint between the core, mid and edge length scales and the core-mid and mid-edge joins.

```
__call__(theta)
```

Evaluate the prior log-PDF at the given values of the hyperparameters, theta.

Parameters theta: array-like, (num_params,)

The hyperparameters to evaluate the log-PDF at.

```
random_draw (size=None)
```

Draw random samples of the hyperparameters.

Parameters size: None, int or array-like, optional

The number/shape of samples to draw. If None, only one sample is returned. Default is None.

class gptools.utils.IndependentJointPrior (univariate_priors)

```
Bases: gptools.utils.JointPrior
```

Joint prior for which each hyperparameter is independent.

Parameters univariate_priors: list of callables or rv_frozen, (num_params,)

The univariate priors for each hyperparameter. Entries in this list can either be a callable that takes as an argument the entire list of hyperparameters or a frozen instance of a distribution from scipy.stats.

```
__call__(theta)
```

Evaluate the prior log-PDF at the given values of the hyperparameters, theta.

Parameters theta: array-like, (num_params,)

The hyperparameters to evaluate the log-PDF at.

bounds

The bounds of the random variable.

```
random_draw(size=None)
```

Draw random samples of the hyperparameters.

Parameters size: None, int or array-like, optional

The number/shape of samples to draw. If None, only one sample is returned. Default is None.

class gptools.utils.NormalJointPrior(mu, sigma)

```
Bases: gptools.utils.JointPrior
```

Joint prior for which each hyperparameter has a normal prior with fixed hyper-hyperparameters.

Parameters mu: list of float, same size as sigma

Means of the hyperparameters.

sigma: list of float

Standard deviations of the hyperparameters.

```
__call__(theta)
```

Evaluate the prior log-PDF at the given values of the hyperparameters, theta.

Parameters theta: array-like, (num_params,)

The hyperparameters to evaluate the log-PDF at.

bounds

The bounds of the random variable.

```
random draw(size=None)
```

Draw random samples of the hyperparameters.

Parameters size: None, int or array-like, optional

The number/shape of samples to draw. If None, only one sample is returned. Default is None

class gptools.utils.LogNormalJointPrior (mu, sigma)

Bases: gptools.utils.JointPrior

Joint prior for which each hyperparameter has a log-normal prior with fixed hyper-hyperparameters.

Parameters mu: list of float, same size as sigma

Means of the logarithms of the hyperparameters.

sigma: list of float

Standard deviations of the logarithms of the hyperparameters.

```
___call___(theta)
```

Evaluate the prior log-PDF at the given values of the hyperparameters, theta.

Parameters theta: array-like, (num_params,)

The hyperparameters to evaluate the log-PDF at.

bounds

The bounds of the random variable.

```
random_draw(size=None)
```

Draw random samples of the hyperparameters.

Parameters size: None, int or array-like, optional

The number/shape of samples to draw. If None, only one sample is returned. Default is None.

```
class gptools.utils.GammaJointPrior (a, b)
```

Bases: gptools.utils.JointPrior

Joint prior for which each hyperparameter has a gamma prior with fixed hyper-hyperparameters.

Parameters \mathbf{a} : list of float, same size as b

Shape parameters.

b: list of float

Rate parameters.

```
__call__(theta)
```

Evaluate the prior log-PDF at the given values of the hyperparameters, theta.

Parameters theta: array-like, (num_params,)

The hyperparameters to evaluate the log-PDF at.

bounds

The bounds of the random variable.

$random_draw (size=None)$

Draw random samples of the hyperparameters.

Parameters size: None, int or array-like, optional

The number/shape of samples to draw. If None, only one sample is returned. Default is None.

gptools.utils.wrap_fmin_slsqp(fun, guess, opt_kwargs={})

Wrapper for fmin_slsqp() to allow it to be called with minimize()-like syntax.

This is included to enable the code to run with scipy versions older than 0.11.0.

Accepts *opt_kwargs* in the same format as used by scipy.optimize.minimize(), with the additional precondition that the keyword *method* has already been removed by the calling code.

Parameters fun: callable

The function to minimize.

guess: sequence

The initial guess for the parameters.

opt_kwargs: dict, optional

Dictionary of extra keywords to pass to <code>scipy.optimize.minimize()</code>. Refer to that function's docstring for valid options. The keywords 'jac', 'hess' and 'hessp' are ignored. Note that if you were planning to use jac = True (i.e., optimization function returns Jacobian) and have set args = (True,) to tell <code>update_hyperparameters()</code> to compute and return the Jacobian this may cause unexpected behavior. Default is: {}.

Returns Result: namedtuple

namedtuple that mimics the fields of the Result object returned by scipy.optimize.minimize(). Has the following fields:

status	int	Code indicating the exit mode of the optimizer (<i>imode</i> from
		<pre>fmin_slsqp())</pre>
suc-	bool	Boolean indicating whether or not the optimizer thinks a
cess		minimum was found.
fun	float	Value of the optimized function (-1*LL).
X	ndar-	Optimal values of the hyperparameters.
	ray	
mes-	str	String describing the exit state (<i>smode</i> from fmin_slsqp())
sage		
nit	int	Number of iterations.

Raises ValueError:

Invalid constraint type in *constraints*. (See documentation for scipy.optimize.minimize().)

gptools.utils.incomplete_bell_poly (n, k, x)

Recursive evaluation of the incomplete Bell polynomial $B_{n,k}(x)$.

Evaluates the incomplete Bell polynomial $B_{n,k}(x_1,x_2,\ldots,x_{n-k+1})$, also known as the partial Bell polynomial or the Bell polynomial of the second kind. This polynomial is useful in the evaluation of (the univariate) Faa di Bruno's formula which generalizes the chain rule to higher order derivatives.

The implementation here is based on the implementation in: sympy.functions.combinatorial.numbers.bell._be

$$B_{n,k}(x_1, x_2, \dots, x_{n-k+1}) = \sum_{m=1}^{n-k+1} x_m \binom{n-1}{m-1} B_{n-m,k-1}(x_1, x_2, \dots, x_{n-m-k})$$

Following that function's documentation, the polynomial is computed according to the recurrence formula:

The end cases are:

```
B_{0,0} = 1
```

$$B_{n,0}=0$$
 for $n\geq 1$

$$B_{0,k} = 0 \text{ for } k \ge 1$$

Parameters n: scalar int

The first subscript of the polynomial.

k: scalar int

The second subscript of the polynomial.

```
x: Array of floats, (p, n - k + 1)
```

p sets of n - k + 1 points to use as the arguments to $B_{n,k}$. The second dimension can be longer than required, in which case the extra entries are silently ignored (this facilitates recursion without needing to subset the array x).

Returns result: Array, (p,)

Incomplete Bell polynomial evaluated at the desired values.

```
gptools.utils.generate_set_partition_strings(n)
```

Generate the restricted growth strings for all of the partitions of an *n*-member set.

Uses Algorithm H from page 416 of volume 4A of Knuth's *The Art of Computer Programming*. Returns the partitions in lexicographical order.

Parameters n: scalar int, non-negative

Number of (unique) elements in the set to be partitioned.

Returns partitions: list of Array

List has a number of elements equal to the n-th Bell number (i.e., the number of partitions for a set of size n). Each element has length n, the elements of which are the restricted growth strings describing the partitions of the set. The strings are returned in lexicographic order.

```
gptools.utils.generate_set_partitions(set_)
```

Generate all of the partitions of a set.

This is a helper function that utilizes the restricted growth strings from generate_set_partition_strings(). The partitions are returned in lexicographic order.

Parameters set_: Array or other Array-like, (*m*,)

The set to find the partitions of.

Returns partitions: list of lists of Array

The number of elements in the outer list is equal to the number of partitions, which is the $len(m)^h$ Bell number. Each of the inner lists corresponds to a single possible partition. The length of an inner list is therefore equal to the number of blocks. Each of the arrays in an inner list is hence a block.

```
gptools.utils.powerset([1,2,3]) -> ()(1,)(2,)(3,)(1,2)(1,3)(2,3)(1,2,3)
```

From itertools documentation.

```
gptools.utils.unique_rows (arr, return_index=False, return_inverse=False)
```

Returns a copy of arr with duplicate rows removed.

From Stackoverflow "Find unique rows in numpy.array."

Parameters arr: Array, (m, n)

The array to find the unique rows of.

return_index: bool, optional

If True, the indices of the unique rows in the array will also be returned. I.e., unique = arr[idx]. Default is False (don't return indices).

return inverse: bool, optional:

If True, the indices in the unique array to reconstruct the original array will also be returned. I.e., arr = unique[inv]. Default is False (don't return inverse).

Returns unique: Array, (p, n) where $p \le m$

The array arr with duplicate rows removed.

Compute the average statistics (mean, std dev) for the given values.

Parameters vals: array-like, (M, D)

Values to compute the average statistics along the specified axis of.

check_nan: bool, optional

Whether or not to check for (and exclude) NaN's. Default is False (do not attempt to handle NaN's).

robust: bool, optional

Whether or not to use robust estimators (median for mean, IQR for standard deviation). Default is False (use non-robust estimators).

axis: int, optional

Axis to compute the statistics along. Presently only supported if *robust* is False. Default is 1.

plot_QQ : bool, optional

Whether or not a QQ plot and histogram should be drawn for each channel. Default is False (do not draw QQ plots).

bins: int, optional

Number of bins to use when plotting histogram (for plot_QQ=True). Default is 15

name: str, optional

Name to put in the title of the QQ/histogram plot.

Returns mean: ndarray, (M,)

Estimator for the mean of vals.

std: ndarray, (M,)

Estimator for the standard deviation of vals.

Raises NotImplementedError:

If axis != 1 when robust is True.

Not Implemented Error:

If *plot_QQ* is True.

```
gptools.utils.univariate_envelope_plot(x, mean, std, ax=None, base_alpha=0.375, en-
                                                       velopes=[1, 3], **kwargs)
     Make a plot of a mean curve with uncertainty envelopes.
qptools.utils.summarize sampler(sampler, burn=0, thin=1, ci=0.95)
     Create summary statistics of the flattened chain of the sampler.
     The confidence regions are computed from the quantiles of the data.
           Parameters sampler: emcee. Ensemble Sampler instance
                   The sampler to summarize the chains of.
               burn: int, optional
                   The number of samples to burn from the beginning of the chain. Default is 0 (no burn).
               thin: int, optional
                   The step size to thin with. Default is 1 (no thinning).
               ci: float, optional
                   A number between 0 and 1 indicating the confidence region to compute. Default is 0.95
                   (return upper and lower bounds of the 95% confidence interval).
           Returns mean: array, (num_params,)
                   Mean values of each of the parameters sampled.
               ci_l : array, (num_params,)
                   Lower bounds of the ci*100% confidence intervals.
               ci u : array, (num params,)
                   Upper bounds of the ci*100\% confidence intervals.
gptools.utils.plot_sampler(sampler, labels=None, burn=0, chain_mask=None)
     Plot the results of MCMC sampler (posterior and chains).
     Loosely based on triangle.py.
           Parameters sampler: emcee. Ensemble Sampler instance
                   The sampler to plot the chains/marginals of.
               labels: list of str, optional
                   The labels to use for each of the free parameters. Default is to leave the axes unlabeled.
               burn: int, optional
                   The number of samples to burn before making the marginal histograms. Default is zero
                   (use all samples).
               chain_mask : (index) array
                   Mask identifying the chains to keep before plotting, in case there are bad chains. Default
```

4.1.8 Module contents

gptools - Gaussian process regression with support for arbitrary derivatives

is to use all chains.

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