Hyperparameter Tuning Cookbook

A guide for scikit-learn, PyTorch, river, and spotpython

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Preface

This document provides a comprehensive guide to hyperparameter tuning using spotpython for scikit-learn, scipy-optimize, River, and PyTorch. The first part introduces fundamental ideas from optimization. The second part discusses numerical issues and introduces spotpython's surrogate model-based optimization process. The thirs part focuses on hyperparameter tuning. Several case studies are presented, including hyperparameter tuning for sklearn models such as Support Vector Classification, Random Forests, Gradient Boosting (XGB), and K-nearest neighbors (KNN), as well as a Hoeffding Adaptive Tree Regressor from river. The integration of spotpython into the PyTorch and PyTorch Lightning training workflow is also discussed. With a hands-on approach and step-by-step explanations, this cookbook serves as a practical starting point for anyone interested in hyperparameter tuning with Python. Highlights include the interplay between Tensorboard, PyTorch Lightning, spotpython, spotriver, and River. This publication is under development, with updates available on the corresponding webpage.

> ❗ Important: This book is still under development.
>
> The most recent version of this book is available at https://sequential-parameter-optimization.github.io/Hyperparameter-Tuning-Cookbook/

Book Structure

This document is structured in three parts. The first part presents an introduction to optimization. The second part describes numerical methods, and the third part presents hyperparameter tuning.

> 💡 Hyperparameter Tuning Reference
>
> - The open access book Bartz et al. (2022) provides a comprehensive overview of hyperparameter tuning. It can be downloaded from https://link.springer.com/book/10.1007/978-981-19-5170-1.

> **Note**
>
> The `.ipynb` notebook (Bartz-Beielstein 2023) is updated regularly and reflects updates and changes in the `spotpython` package. It can be downloaded from https://github.com/sequential-parameter-optimization/spotpython/blob/main/notebooks/14_spot_ray_hpt_torch_cifar10.ipynb.

Software Used in this Book

scikit-learn is a Python module for machine learning built on top of SciPy and is distributed under the 3-Clause BSD license. The project was started in 2007 by David Cournapeau as a Google Summer of Code project, and since then many volunteers have contributed.

PyTorch is an optimized tensor library for deep learning using GPUs and CPUs. Lightning is a lightweight PyTorch wrapper for high-performance AI research. It allows you to decouple the research from the engineering.

River is a Python library for online machine learning. It is designed to be used in real-world environments, where not all data is available at once, but streaming in.

spotpython ("Sequential Parameter Optimization Toolbox in Python") is the Python version of the well-known hyperparameter tuner SPOT, which has been developed in the R programming environment for statistical analysis for over a decade. The related open-access book is available here: Hyperparameter Tuning for Machine and Deep Learning with R—A Practical Guide.

spotriver provides an interface between spotpython and River.

Citation

If this document has been useful to you and you wish to cite it in a scientific publication, please refer to the following paper, which can be found on arXiv: https://arxiv.org/abs/2307.10262.

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@ARTICLE{bart23iArXiv,
      author = {{Bartz-Beielstein}, Thomas},
      title = "{Hyperparameter Tuning Cookbook:
          A guide for scikit-learn, PyTorch, river, and spotpython}",
     journal = {arXiv e-prints},
    keywords = {Computer Science - Machine Learning,
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Part I

Optimization

1 Introduction: Optimization

1.1 Optimization, Simulation, and Surrogate Modeling

- We will consider the interplay between
  - mathematical models,
  - numerical approximation,
  - simulation,
  - computer experiments, and
  - field data
- Experimental design will play a key role in our developments, but not in the classical regression and response surface methodology sense
- Challenging real-data/real-simulation examples benefiting from modern surrogate modeling methodology
- We will consider the classical, response surface methodology (RSM) approach, and then move on to more modern approaches
- All approaches are based on surrogates

1.2 Surrogates

- Gathering data is **expensive**, and sometimes getting exactly the data you want is impossible or unethical
- **Surrogate**: substitute for the real thing
- In statistics, draws from predictive equations derived from a fitted model can act as a surrogate for the data-generating mechanism
- Benefits of the surrogate approach:
  - Surrogate could represent a cheaper way to explore relationships, and entertain "what ifs?"
  - Surrogates favor faithful yet pragmatic reproduction of dynamics:
    - interpretation,
    - establishing causality, or
    - identification
  - Many numerical simulators are **deterministic**, whereas field observations are noisy or have measurement error

1.2.1 Costs of Simulation

- Computer simulations are generally cheaper (but not always!) than physical observation
- Some computer simulations can be just as expensive as field experimentation, but computer modeling is regarded as easier because:
  - the experimental apparatus is better understood
  - more aspects may be controlled.

1.2.2 Mathematical Models and Meta-Models

- Use of mathematical models leveraging numerical solvers has been commonplace for some time
- Mathematical models became more complex, requiring more resources to simulate/solve numerically
- Practitioners increasingly relied on **meta-models** built off of limited simulation campaigns

1.2.3 Surrogates = Trained Meta-models

- Data collected via expensive computer evaluations tuned flexible functional forms that could be used in lieu of further simulation to
  - save money or computational resources;
  - cope with an inability to perform future runs (expired licenses, off-line or over-impacted supercomputers)
- Trained meta-models became known as **surrogates**

1.2.4 Computer Experiments

- **Computer experiment**: design, running, and fitting meta-models.
  - Like an ordinary statistical experiment, except the data are generated by computer codes rather than physical or field observations, or surveys
- **Surrogate modeling** is statistical modeling of computer experiments

1.2.5 Limits of Mathematical Modeling

- Mathematical biologists, economists and others had reached the limit of equilibrium-based mathematical modeling with cute closed-form solutions
- **Stochastic simulations replace deterministic solvers** based on FEM, Navier–Stokes or Euler methods
- Agent-based simulation models are used to explore predator-prey (Lotka–Voltera) dynamics, spread of disease, management of inventory or patients in health insurance markets
- Consequence: the distinction between surrogate and statistical model is all but gone

1.2.6 Example: Why Computer Simulations are Necessary

- You can't seed a real community with Ebola and watch what happens
- If there's (real) field data, say on a historical epidemic, further experimentation may be almost entirely limited to the mathematical and computer modeling side
- Classical statistical methods offer little guidance

1.2.7 Simulation Requirements

- Simulation should
  - enable rich **diagnostics** to help criticize that models
  - **understanding** its sensitivity to inputs and other configurations
  - providing the ability to **optimize** and
  - refine both **automatically** and with expert intervention
- And it has to do all that while remaining **computationally tractable**
- One perspective is so-called **response surface methods** (RSMs):
- a poster child from industrial statistics' heyday, well before information technology became a dominant industry

> **!** Goals
>
> - How to choose models and optimizers for solving real-world problems
> - How to use simulation to understand and improve processes

1.3 Jupyter Notebook

> **Note**
>
> - The Jupyter-Notebook of this lecture is available on GitHub in the Hyperparameter-Tuning-Cookbook Repository

2 Aircraft Wing Weight Example

2.1 AWWE Equation

- Example from Forrester et al.
- Understand the **weight** of an unpainted light aircraft wing as a function of nine design and operational parameters:

$$W = 0.036 S_W^{0.758} \times W_{fw}^{0.0035} \left(\frac{A}{\cos^2 \Lambda} \right)^{0.6} \times q^{0.006} \times \lambda^{0.04}$$
$$\times \left(\frac{100 R_{tc}}{\cos \Lambda} \right)^{-0.3} \times (N_z W_{dg})^{0.49}$$

2.2 AWWE Parameters and Equations (Part 1)

Table 2.1: Aircraft Wing Weight Parameters

Symbol	Parameter	Baseline	Minimum	Maximum
S_W	Wing area (ft^2)	174	150	200
W_{fw}	Weight of fuel in wing (lb)	252	220	300
A	Aspect ratio	7.52	6	10
Λ	Quarter-chord sweep (deg)	0	-10	10
q	Dynamic pressure at cruise (lb/ft^2)	34	16	45
λ	Taper ratio	0.672	0.5	1
R_{tc}	Aerofoil thickness to chord ratio	0.12	0.08	0.18
N_z	Ultimate load factor	3.8	2.5	6
W_{dg}	Flight design gross weight (lb)	2000	1700	2500
W_p	paint weight (lb/ft^2)	0.064	0.025	0.08

The study begins with a baseline Cessna C172 Skyhawk Aircraft as its reference point. It aims to investigate the impact of wing area and fuel weight on the overall weight of the aircraft. Two crucial parameters in this analysis are the aspect ratio (A), defined as the ratio of the wing's length to the average chord (thickness of the airfoil), and the

taper ratio (λ), which represents the ratio of the maximum to the minimum thickness of the airfoil or the maximum to minimum chord.

It's important to note that the equation used in this context is not a computer simulation but will be treated as one for the purpose of illustration. This approach involves employing a true mathematical equation, even if it's considered unknown, as a useful tool for generating realistic settings to test the methodology. The functional form of this equation was derived by "calibrating" known physical relationships to curves obtained from existing aircraft data, as referenced in Raymer 2012. Essentially, it acts as a surrogate for actual measurements of aircraft weight.

Examining the mathematical properties of the AWWE (Aircraft Weight With Wing Area and Fuel Weight Equation), it is evident that the response is highly nonlinear concerning its inputs. While it's common to apply the logarithm to simplify equations with complex exponents, even when modeling the logarithm, which transforms powers into slope coefficients and products into sums, the response remains nonlinear due to the presence of trigonometric terms. Given the combination of nonlinearity and high input dimension, simple linear and quadratic response surface approximations are likely to be inadequate for this analysis.

2.3 Goals: Understanding and Optimization

The primary goals of this study revolve around understanding and optimization:

1. **Understanding**: One of the straightforward objectives is to gain a deep understanding of the input-output relationships in this context. Given the global perspective implied by this setting, it becomes evident that a more sophisticated model is almost necessary. At this stage, let's focus on this specific scenario to establish a clear understanding.
2. **Optimization**: Another application of this analysis could be optimization. There may be an interest in minimizing the weight of the aircraft, but it's likely that there will be constraints in place. For example, the presence of wings with a nonzero area is essential for the aircraft to be capable of flying. In situations involving (constrained) optimization, a global perspective and, consequently, the use of flexible modeling are vital.

The provided Python code serves as a genuine computer implementation that "solves" a mathematical model. It accepts arguments encoded in the unit cube, with defaults used to represent baseline settings, as detailed in the table labeled as Table **??**. To map values from the interval $[a, b]$ to the interval $[0, 1]$, the following formula can be employed:

$$y = f(x) = \frac{x - a}{b - a}.$$

To reverse this mapping and obtain the original values, the formula

$$g(y) = a + (b - a)y$$

can be used.

```
import numpy as np

def wingwt(Sw=0.48, Wfw=0.4, A=0.38, L=0.5, q=0.62, l=0.344,  Rtc=0.4, Nz=0.37, Wdg=0.38):
    # put coded inputs back on natural scale
    Sw = Sw * (200 - 150) + 150
    Wfw = Wfw * (300 - 220) + 220
    A = A * (10 - 6) + 6
    L = (L * (10 - (-10)) - 10) * np.pi/180
    q = q * (45 - 16) + 16
    l = l * (1 - 0.5) + 0.5
    Rtc = Rtc * (0.18 - 0.08) + 0.08
    Nz = Nz * (6 - 2.5) + 2.5
    Wdg = Wdg*(2500 - 1700) + 1700
    # calculation on natural scale
    W = 0.036 * Sw**0.758 * Wfw**0.0035 * (A/np.cos(L)**2)**0.6 * q**0.006
    W = W * l**0.04 * (100*Rtc/np.cos(L))**(-0.3) * (Nz*Wdg)**(0.49)
    return(W)
```

2.4 Properties of the Python "Solver"

The compute time required by the "wingwt" solver is extremely short and can be considered trivial in terms of computational resources. The approximation error is exceptionally small, effectively approaching machine precision, which indicates the high accuracy of the solver's results.

To simulate time-consuming evaluations, a deliberate delay is introduced by incorporating a `sleep(3600)` command, which effectively synthesizes a one-hour execution time for a particular evaluation.

Moving on to the AWWE visualization, plotting in two dimensions is considerably simpler than dealing with nine dimensions. To aid in creating visual representations, the code provided below establishes a grid within the unit square to facilitate the generation of sliced visuals. This involves generating a "meshgrid" as outlined in the code.

```
import numpy as np
x = np.linspace(0, 1, 3)
y = np.linspace(0, 1, 3)
```

```
X, Y = np.meshgrid(x, y)
zp = zip(np.ravel(X), np.ravel(Y))
list(zp)
```

```
[(0.0, 0.0),
 (0.5, 0.0),
 (1.0, 0.0),
 (0.0, 0.5),
 (0.5, 0.5),
 (1.0, 0.5),
 (0.0, 1.0),
 (0.5, 1.0),
 (1.0, 1.0)]
```

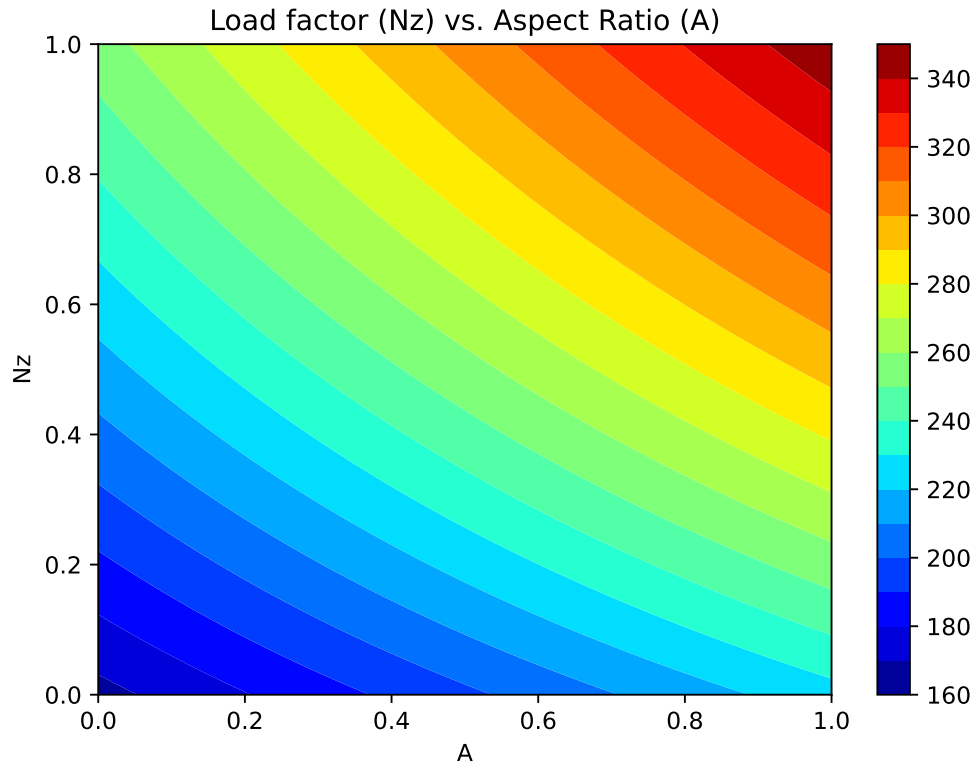
The coding used to transform inputs from natural units is largely a matter of taste, so long as it's easy to undo for reporting back on original scales

```
%matplotlib inline
import matplotlib.pyplot as plt
# plt.style.use('seaborn-white')
import numpy as np
x = np.linspace(0, 1, 100)
y = np.linspace(0, 1, 100)
X, Y = np.meshgrid(x, y)
```

2.5 Plot 1: Load Factor (N_z) and Aspect Ratio (A)

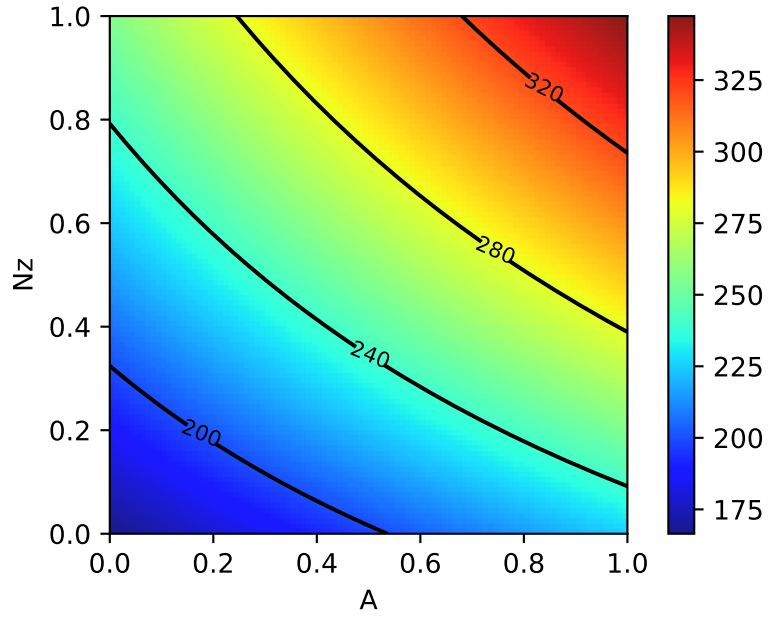
We will vary N_z and A, with other inputs fixed at their baseline values.

```
z = wingwt(A = X, Nz = Y)
fig = plt.figure(figsize=(7., 5.))
plt.contourf(X, Y, z, 20, cmap='jet')
plt.xlabel("A")
plt.ylabel("Nz")
plt.title("Load factor (Nz) vs. Aspect Ratio (A)")
plt.colorbar()
plt.show()
```



Contour plots can be refined, e.g., by adding explicit contour lines as shown in the following figure.

```
contours = plt.contour(X, Y, z, 4, colors='black')
plt.clabel(contours, inline=True, fontsize=8)
plt.xlabel("A")
plt.ylabel("Nz")

plt.imshow(z, extent=[0, 1, 0, 1], origin='lower',
           cmap='jet', alpha=0.9)
plt.colorbar()
```



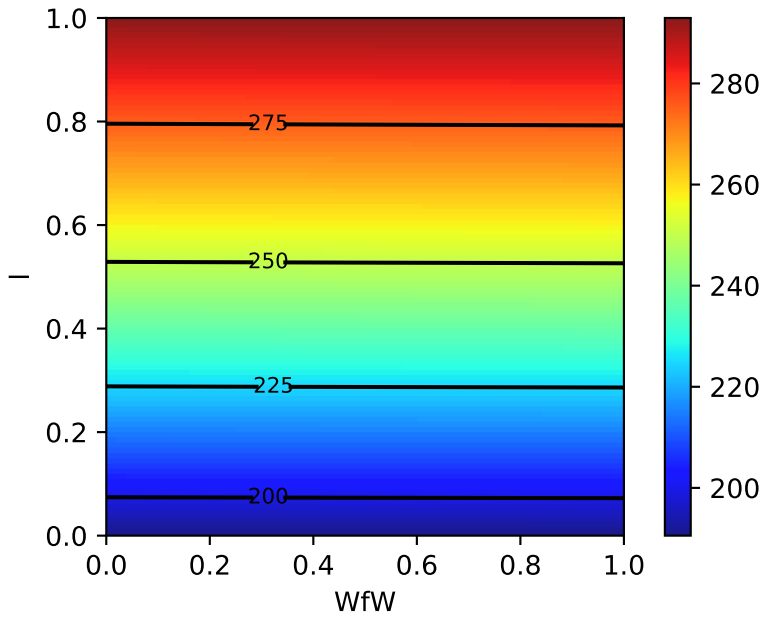
The interpretation of the AWWE plot can be summarized as follows:

- The figure displays the weight response as a function of two variables, N_z and A, using an image-contour plot.
- The slight curvature observed in the contours suggests an interaction between these two variables.
- Notably, the range of outputs depicted in the figure, spanning from approximately 160 to 320, nearly encompasses the entire range of outputs observed from various input settings within the full 9-dimensional input space.
- The plot indicates that aircraft wings tend to be heavier when the aspect ratios (A) are high.
- This observation aligns with the idea that wings are designed to withstand and accommodate high gravitational forces (g-forces, large N_z), and there may be a compounding effect where larger values of N_z contribute to increased wing weight.
- It's plausible that this phenomenon is related to the design considerations of fighter jets, which cannot have the efficient and lightweight glider-like wings typically found in other types of aircraft.

2.6 Plot 2: Taper Ratio and Fuel Weight

- The same experiment for two other inputs, e.g., taper ratio λ and fuel weight W_{fw}

```
z = wingwt(Wfw = X,  Nz = Y)
contours = plt.contour(X, Y, z, 4, colors='black')
plt.clabel(contours, inline=True, fontsize=8)
plt.xlabel("WfW")
plt.ylabel("l")

plt.imshow(z, extent=[0, 1, 0, 1], origin='lower',
           cmap='jet', alpha=0.9)
plt.colorbar();
```



- Interpretation of Taper Ratio (l) and Fuel Weight (W_{fw})
  - Apparently, neither input has much effect on wing weight:
    - with λ having a marginally greater effect, covering less than 4 percent of the span of weights observed in the $A \times N_z$ plane
  - There's no interaction evident in $\lambda \times W_{fw}$

2.7 The Big Picture: Combining all Variables

```
pl = ["Sw", "Wfw", "A", "L", "q", "l",  "Rtc", "Nz", "Wdg"]
```

```
import math

Z = []
Zlab = []
l = len(pl)
# lc = math.comb(l,2)
for i in range(l):
    for j in range(i+1, l):
    # for j in range(l):
        # print(pl[i], pl[j])
        d = {pl[i]: X, pl[j]: Y}
        Z.append(wingwt(**d))
        Zlab.append([pl[i],pl[j]])
```

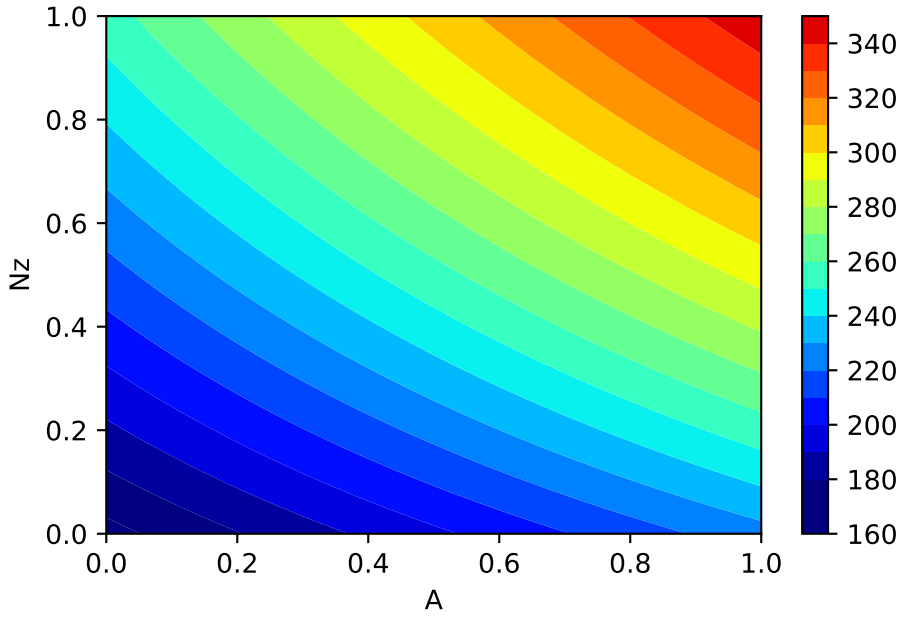
Now we can generate all 36 combinations, e.g., our first example is combination `p = 19`.

```
p = 19
Zlab[p]
```

```
['A', 'Nz']
```

To help interpret outputs from experiments such as this one—to level the playing field when comparing outputs from other pairs of inputs—code below sets up a color palette that can be re-used from one experiment to the next. We use the arguments `vmin=180` and `vmax =360` to implement comparibility

```
plt.contourf(X, Y, Z[p], 20, cmap='jet', vmin=180, vmax=360)
plt.xlabel(Zlab[p][0])
plt.ylabel(Zlab[p][1])
plt.colorbar()
```

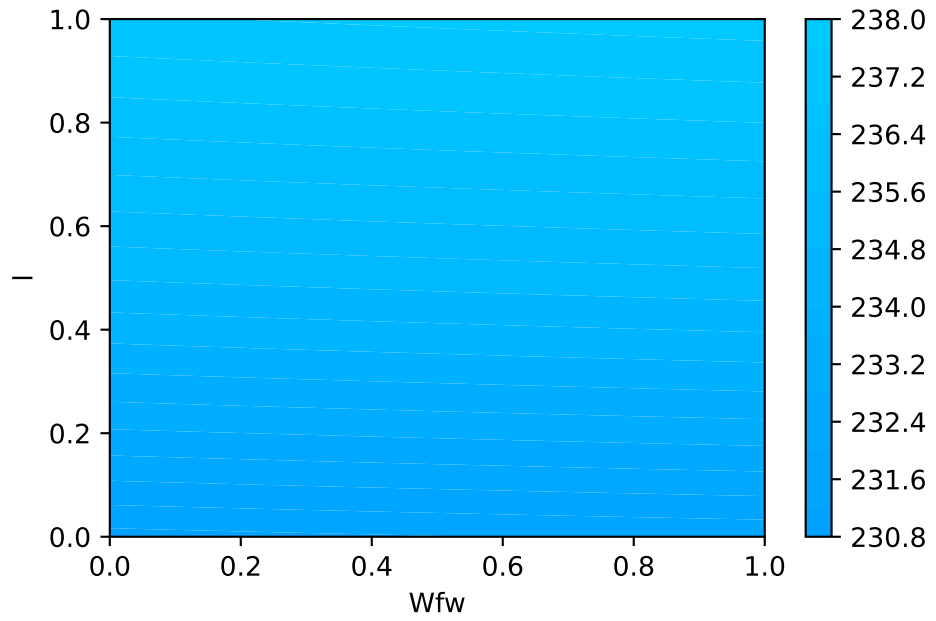


- Let's plot the second example, taper ratio λ and fuel weight W_{fw}
- This is combination 11:

```
p = 11
Zlab[p]
```

```
['Wfw', 'l']
```

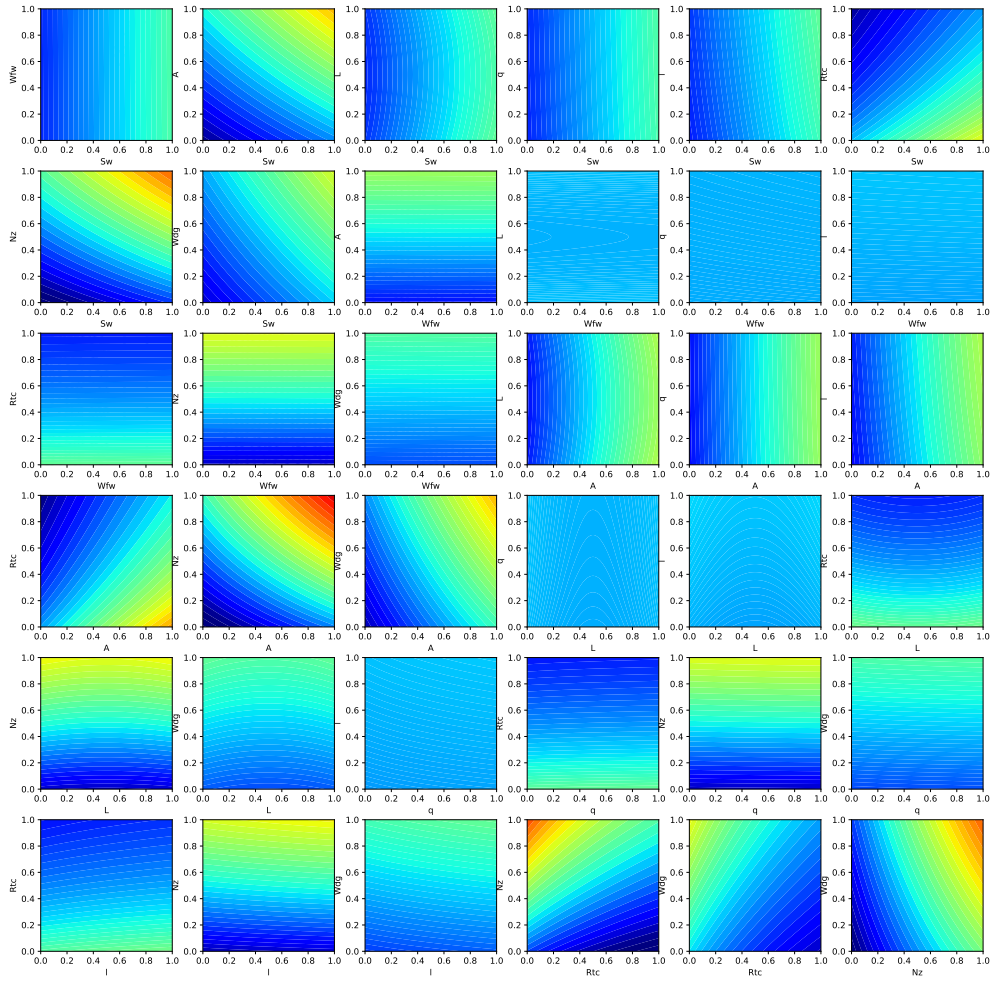
```
plt.contourf(X, Y, Z[p], 20, cmap='jet', vmin=180, vmax=360)
plt.xlabel(Zlab[p][0])
plt.ylabel(Zlab[p][1])
plt.colorbar()
```



- Using a global colormap indicates that these variables have minor effects on the wing weight.
- Important factors can be detected by visual inspection
- Plotting the Big Picture: we can plot all 36 combinations in one figure.

```
import matplotlib.pyplot as plt
from mpl_toolkits.axes_grid1 import ImageGrid
import numpy as np

fig = plt.figure(figsize=(20., 20.))
grid = ImageGrid(fig, 111,  # similar to subplot(111)
                 nrows_ncols=(6,6),  # creates 2x2 grid of axes
                 axes_pad=0.5,  # pad between axes in inch.
                 share_all=True,
                 label_mode="all",
                 )
i = 0
for ax, im in zip(grid, Z):
    # Iterating over the grid returns the Axes.
    ax.set_xlabel(Zlab[i][0])
    ax.set_ylabel(Zlab[i][1])
    # ax.set_title(Zlab[i][1] + " vs. " + Zlab[i][0])
    ax.contourf(X, Y, im, 30, cmap = "jet",  vmin = 180, vmax = 360)
```

```
    i = i + 1

plt.show()
```



2.8 AWWE Landscape

- Our Observations

    1. The load factor N_z, which determines the magnitude of the maximum aerodynamic load on the wing, is very active and involved in interactions with other variables.

  - Classic example: the interaction of N_z with the aspect ratio A indicates a heavy wing for high aspect ratios and large g-forces
  - This is the reaon why highly manoeuvrable fighter jets cannot have very efficient, glider wings)
2. Aspect ratio A and airfoil thickness to chord ratio R_{tc} have nonlinear interactions.
3. Most important variables:
  - Ultimate load factor N_z, wing area S_w, and flight design gross weightW_{dg}.
4. Little impact: dynamic pressure q, taper ratio l, and quarter-chord sweep L.

- Expert Knowledge
  - Aircraft designers know that the overall weight of the aircraft and the wing area must be kept to a minimum
  - the latter usually dictated by constraints such as required stall speed, landing distance, turn rate, etc.

2.9 Summary of the First Experiments

- First, we considered two pairs of inputs, out of 36 total pairs
- Then, the "Big Picture":
  - For each pair we evaluated `wingwt` 10,000 times
- Doing the same for all pairs would require 360K evaluations:
  - not a reasonable number with a real computer simulation that takes any non-trivial amount of time to evaluate
  - Only 1s per evaluation: $>$ 100 hours
- Many solvers take minutes/hours/days to execute a single run
- And: three-way interactions?
- Consequence: a different strategy is needed

2.10 Exercise

2.10.1 Adding Paint Weight

- Paint weight is not considered.
- Add Paint Weight W_p to formula (the updated formula is shown below) and update the functions and plots in the notebook.

$$W = 0.036 S_W^{0.758} \times W_{fw}^{0.0035} \times \left(\frac{A}{\cos^2 \Lambda} \right)^{0.6} \times q^{0.006} \times \lambda^{0.04} \times \left(\frac{100 R_{tc}}{\cos \Lambda} \right)^{-0.3} \times (N_z W_{dg})^{0.49} + S_w W_p$$

2.11 Jupyter Notebook

> **Note**
>
> - The Jupyter-Notebook of this lecture is available on GitHub in the Hyperparameter-Tuning-Cookbook Repository

3 Introduction to `scipy.optimize`

SciPy provides algorithms for optimization, integration, interpolation, eigenvalue problems, algebraic equations, differential equations, statistics and many other classes of problems. SciPy is a collection of mathematical algorithms and convenience functions built on NumPy. It adds significant power to Python by providing the user with high-level commands and classes for manipulating and visualizing data.

SciPy optimize provides functions for minimizing (or maximizing) objective functions, possibly subject to constraints. It includes solvers for nonlinear problems (with support for both local and global optimization algorithms), linear programing, constrained and nonlinear least-squares, root finding, and curve fitting.

In this notebook, we will learn how to use the `scipy.optimize` module to solve optimization problems. See: https://docs.scipy.org/doc/scipy/tutorial/optimize.html

> **Note**
>
> - This content is based on information from the scipy.optimize package.
> - The `scipy.optimize` package provides several commonly used optimization algorithms. A detailed listing is available in `scipy.optimize` (can also be found by `help(scipy.optimize)`).

Common functions and objects, shared across different SciPy optimize solvers, are shown in Table **??**.

Table 3.1: Common functions and objects, shared across different SciPy optimize solvers

Function or Object	Description
show_options([solver, method, disp])	Show documentation for additional options of optimization solvers.
OptimizeResult	Represents the optimization result.
OptimizeWarning	Warning issued by solvers.

We will introduce unconstrained minimization of multivariate scalar functions in this chapter. The minimize function provides a common interface to unconstrained and constrained minimization algorithms for multivariate scalar functions in `scipy.optimize`.

To demonstrate the minimization function, consider the problem of minimizing the Rosenbrock function of N variables:

$$f(J) = \sum_{i=1}^{N-1} 100(x_{i+1} - x_i^2)^2 + (1 - x_i)^2$$

The minimum value of this function is 0, which is achieved when (x_i = 1).

Note that the Rosenbrock function and its derivatives are included in `scipy.optimize`. The implementations shown in the following sections provide examples of how to define an objective function as well as its Jacobian and Hessian functions. Objective functions in `scipy.optimize` expect a numpy array as their first parameter, which is to be optimized and must return a float value. The exact calling signature must be `f(x, *args)`, where `x` represents a numpy array, and `args` is a tuple of additional arguments supplied to the objective function.

3.1 Derivative-free Optimization Algorithms

Section ?? and Section ?? present two approaches that do not need gradient information to find the minimum. They use function evaluations to find the minimum.

3.1.1 Nelder-Mead Simplex Algorithm

`method='Nelder-Mead'`: In the example below, the `minimize` routine is used with the *Nelder-Mead* simplex algorithm (selected through the `method` parameter):

```
import numpy as np
from scipy.optimize import minimize

def rosen(x):
    """The Rosenbrock function"""
    return sum(100.0 * (x[1:] - x[:-1]**2.0)**2.0 + (1 - x[:-1])**2.0)

x0 = np.array([1.3, 0.7, 0.8, 1.9, 1.2])
res = minimize(rosen, x0, method='nelder-mead',
               options={'xatol': 1e-8, 'disp': True})

print(res.x)
```

```
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 339
         Function evaluations: 571
[1. 1. 1. 1. 1.]
```

The simplex algorithm is probably the simplest way to minimize a well-behaved function. It requires only function evaluations and is a good choice for simple minimization problems. However, because it does not use any gradient evaluations, it may take longer to find the minimum.

3.1.2 Powell's Method

Another optimization algorithm that needs only function calls to find the minimum is *Powell*'s method, which can be selected by setting the `method` parameter to `'powell'` in the `minimize` function.

To demonstrate how to supply additional arguments to an objective function, let's consider minimizing the Rosenbrock function with an additional scaling factor a and an offset b:

$$f(J, a, b) = \sum_{i=1}^{N-1} a(x_{i+1} - x_i^2)^2 + (1 - x_i)^2 + b$$

You can achieve this using the `minimize` routine with the example parameters $a = 0.5$ and $b = 1$:

```
def rosen_with_args(x, a, b):
    """The Rosenbrock function with additional arguments"""
    return sum(a * (x[1:] - x[:-1]**2.0)**2.0 + (1 - x[:-1])**2.0) + b

x0 = np.array([1.3, 0.7, 0.8, 1.9, 1.2])
res = minimize(rosen_with_args, x0, method='nelder-mead',
               args=(0.5, 1.), options={'xatol': 1e-8, 'disp': True})

print(res.x)
```

```
Optimization terminated successfully.
         Current function value: 1.000000
         Iterations: 319
         Function evaluations: 525
[1.         1.         1.         1.         0.99999999]
```

As an alternative to using the `args` parameter of `minimize`, you can wrap the objective function in a new function that accepts only `x`. This approach is also useful when it is necessary to pass additional parameters to the objective function as keyword arguments.

```
def rosen_with_args(x, a, *, b):  # b is a keyword-only argument
    return sum(a * (x[1:] - x[:-1]**2.0)**2.0 + (1 - x[:-1])**2.0) + b

def wrapped_rosen_without_args(x):
    return rosen_with_args(x, 0.5, b=1.)  # pass in `a` and `b`

x0 = np.array([1.3, 0.7, 0.8, 1.9, 1.2])
res = minimize(wrapped_rosen_without_args, x0, method='nelder-mead',
               options={'xatol': 1e-8,})

print(res.x)
```

```
[1.         1.         1.         1.         0.99999999]
```

Another alternative is to use `functools.partial`.

```
from functools import partial

partial_rosen = partial(rosen_with_args, a=0.5, b=1.)
res = minimize(partial_rosen, x0, method='nelder-mead',
               options={'xatol': 1e-8,})

print(res.x)
```

```
[1.         1.         1.         1.         0.99999999]
```

3.2 Gradient-based optimization algorithms

3.2.1 An Introductory Example: Broyden-Fletcher-Goldfarb-Shanno Algorithm (BFGS)

This section introduces an optimization algorithm that uses gradient information to find the minimum. The Broyden-Fletcher-Goldfarb-Shanno (BFGS) algorithm (selected by setting `method='BFGS'`) is an optimization algorithm that aims to converge quickly to the solution. This algorithm uses the gradient of the objective function. If the gradient is not provided by the user, it is estimated using first-differences. The

BFGS method typically requires fewer function calls compared to the simplex algorithm, even when the gradient needs to be estimated.

Example 3.1 (BFGS)**.** To demonstrate the BFGS algorithm, let's use the Rosenbrock function again. The gradient of the Rosenbrock function is a vector described by the following mathematical expression:

$$\frac{\partial f}{\partial x_j} = \sum_{i=1}^{N} 200(x_i - x_{i-1}^2)(\delta_{i,j} - 2x_{i-1}\delta_{i-1,j}) - 2(1 - x_{i-1})\delta_{i-1,j} \tag{3.1}$$

$$= 200(x_j - x_{j-1}^2) - 400x_j(x_{j+1} - x_j^2) - 2(1 - x_j) \tag{3.2}$$

This expression is valid for interior derivatives, but special cases are:

$$\frac{\partial f}{\partial x_0} = -400x_0(x_1 - x_0^2) - 2(1 - x_0)$$

$$\frac{\partial f}{\partial x_{N-1}} = 200(x_{N-1} - x_{N-2}^2)$$

Here's a Python function that computes this gradient:

```
def rosen_der(x):
    xm = x[1:-1]
    xm_m1 = x[:-2]
    xm_p1 = x[2:]
    der = np.zeros_like(x)
    der[1:-1] = 200*(xm-xm_m1**2) - 400*(xm_p1 - xm**2)*xm - 2*(1-xm)
    der[0] = -400*x[0]*(x[1]-x[0]**2) - 2*(1-x[0])
    der[-1] = 200*(x[-1]-x[-2]**2)
    return der
```

You can specify this gradient information in the minimize function using the jac parameter as illustrated below:

```
res = minimize(rosen, x0, method='BFGS', jac=rosen_der,
               options={'disp': True})

print(res.x)
```

```
Optimization terminated successfully.
         Current function value: 0.000000
         Iterations: 25
         Function evaluations: 30
         Gradient evaluations: 30
[1.00000004 1.0000001  1.00000021 1.00000044 1.00000092]
```

3.2.2 Background and Basics for Gradient-based Optimization

3.2.3 Gradient

The gradient $\nabla f(J)$ for a scalar function $f(J)$ with n different variables is defined by its partial derivatives:

$$\nabla f(J) = \left[\frac{\partial f}{\partial x_1}, \frac{\partial f}{\partial x_2}, \ldots, \frac{\partial f}{\partial x_n}\right]$$

3.2.4 Jacobian Matrix

The Jacobian matrix $J(J)$ for a vector-valued function $F(J) = [f_1(J), f_2(J), \ldots, f_m(J)]$ is defined as:

$$J(J) = \begin{bmatrix} \frac{\partial f_1}{\partial x_1} & \frac{\partial f_1}{\partial x_2} & \cdots & \frac{\partial f_1}{\partial x_n} \\ \frac{\partial f_2}{\partial x_1} & \frac{\partial f_2}{\partial x_2} & \cdots & \frac{\partial f_2}{\partial x_n} \\ \vdots & \vdots & \ddots & \vdots \\ \frac{\partial f_m}{\partial x_1} & \frac{\partial f_m}{\partial x_2} & \cdots & \frac{\partial f_m}{\partial x_n} \end{bmatrix}$$

It consists of the first order partial derivatives and gives therefore an overview about the gradients of a vector valued function.

Example 3.2 (acobian matrix)**.** Consider a vector-valued function $f : \mathbb{R}^2 \to \mathbb{R}^3$ defined as follows:

$$f(J) = \begin{bmatrix} x_1^2 + 2x_2 \\ 3x_1 - \sin(x_2) \\ e^{x_1 + x_2} \end{bmatrix}$$

Let's compute the partial derivatives and construct the Jacobian matrix:

$\frac{\partial f_1}{\partial x_1} = 2x_1, \quad \frac{\partial f_1}{\partial x_2} = 2$

$\frac{\partial f_2}{\partial x_1} = 3, \quad \frac{\partial f_2}{\partial x_2} = -\cos(x_2)$

$\frac{\partial f_3}{\partial x_1} = e^{x_1+x_2}, \quad \frac{\partial f_3}{\partial x_2} = e^{x_1+x_2}$

So, the Jacobian matrix is:

$$J(J) = \begin{bmatrix} 2x_1 & 2 \\ 3 & -\cos(x_2) \\ e^{x_1+x_2} & e^{x_1+x_2} \end{bmatrix}$$

This Jacobian matrix provides information about how small changes in the input variables x_1 and x_2 affect the corresponding changes in each component of the output vector.

3.2.5 Hessian Matrix

The Hessian matrix $H(J)$ for a scalar function $f(J)$ is defined as:

$$H(J) = \begin{bmatrix} \frac{\partial^2 f}{\partial x_1^2} & \frac{\partial^2 f}{\partial x_1 \partial x_2} & \cdots & \frac{\partial^2 f}{\partial x_1 \partial x_n} \\ \frac{\partial^2 f}{\partial x_2 \partial x_1} & \frac{\partial^2 f}{\partial x_2^2} & \cdots & \frac{\partial^2 f}{\partial x_2 \partial x_n} \\ \vdots & \vdots & \ddots & \vdots \\ \frac{\partial^2 f}{\partial x_n \partial x_1} & \frac{\partial^2 f}{\partial x_n \partial x_2} & \cdots & \frac{\partial^2 f}{\partial x_n^2} \end{bmatrix}$$

So, the Hessian matrix consists of the second order dervatives of the function. It provides information about the local curvature of the function with respect to changes in the input variables.

Example 3.3 (Hessian matrix)**.** Consider a scalar-valued function:

$$f(J) = x_1^2 + 2x_2^2 + \sin(x_1 x_2)$$

The Hessian matrix of this scalar-valued function is the matrix of its second-order partial derivatives with respect to the input variables:

$$H(J) = \begin{bmatrix} \frac{\partial^2 f}{\partial x_1^2} & \frac{\partial^2 f}{\partial x_1 \partial x_2} \\ \frac{\partial^2 f}{\partial x_2 \partial x_1} & \frac{\partial^2 f}{\partial x_2^2} \end{bmatrix}$$

Let's compute the second-order partial derivatives and construct the Hessian matrix:

$$\frac{\partial^2 f}{\partial x_1^2} = 2 + \cos(x_1 x_2) x_2^2 \tag{3.3}$$

$$\frac{\partial^2 f}{\partial x_1 \partial x_2} = 2x_1 x_2 \cos(x_1 x_2) - \sin(x_1 x_2) \tag{3.4}$$

$$\frac{\partial^2 f}{\partial x_2 \partial x_1} = 2x_1 x_2 \cos(x_1 x_2) - \sin(x_1 x_2) \tag{3.5}$$

$$\frac{\partial^2 f}{\partial x_2^2} = 4x_2^2 + \cos(x_1 x_2) x_1^2 \tag{3.6}$$

So, the Hessian matrix is:

$$H(J) = \begin{bmatrix} 2 + \cos(x_1 x_2) x_2^2 & 2x_1 x_2 \cos(x_1 x_2) - \sin(x_1 x_2) \\ 2x_1 x_2 \cos(x_1 x_2) - \sin(x_1 x_2) & 4x_2^2 + \cos(x_1 x_2) x_1^2 \end{bmatrix}$$

3.2.6 Gradient for Optimization

In optimization, the goal is to find the minimum or maximum of a function. Gradient-based optimization methods utilize information about the gradient (or derivative) of the function to guide the search for the optimal solution. This is particularly useful when dealing with complex, high-dimensional functions where an exhaustive search is impractical.

The gradient descent method can be divided in the following steps:

- **Initialize:** start with an initial guess for the parameters of the function to be optimized.
- **Compute Gradient:** Calculate the gradient (partial derivatives) of the function with respect to each parameter at the current point. The gradient indicates the direction of the steepest increase in the function.
- **Update Parameters:** Adjust the parameters in the opposite direction of the gradient, scaled by a learning rate. This step aims to move towards the minimum of the function:
  - $x_{k+1} = x_k - \alpha \times \nabla f(x_k)$
  - x_x is current parameter vector or point in the parameter space.
  - α is the learning rate, a positive scalar that determines the step size in each iteration.
  - $\nabla f(x)$ is the gradient of the objective function.
- **Iterate:** Repeat the above steps until convergence or a predefined number of iterations. Convergence is typically determined when the change in the function value or parameters becomes negligible.

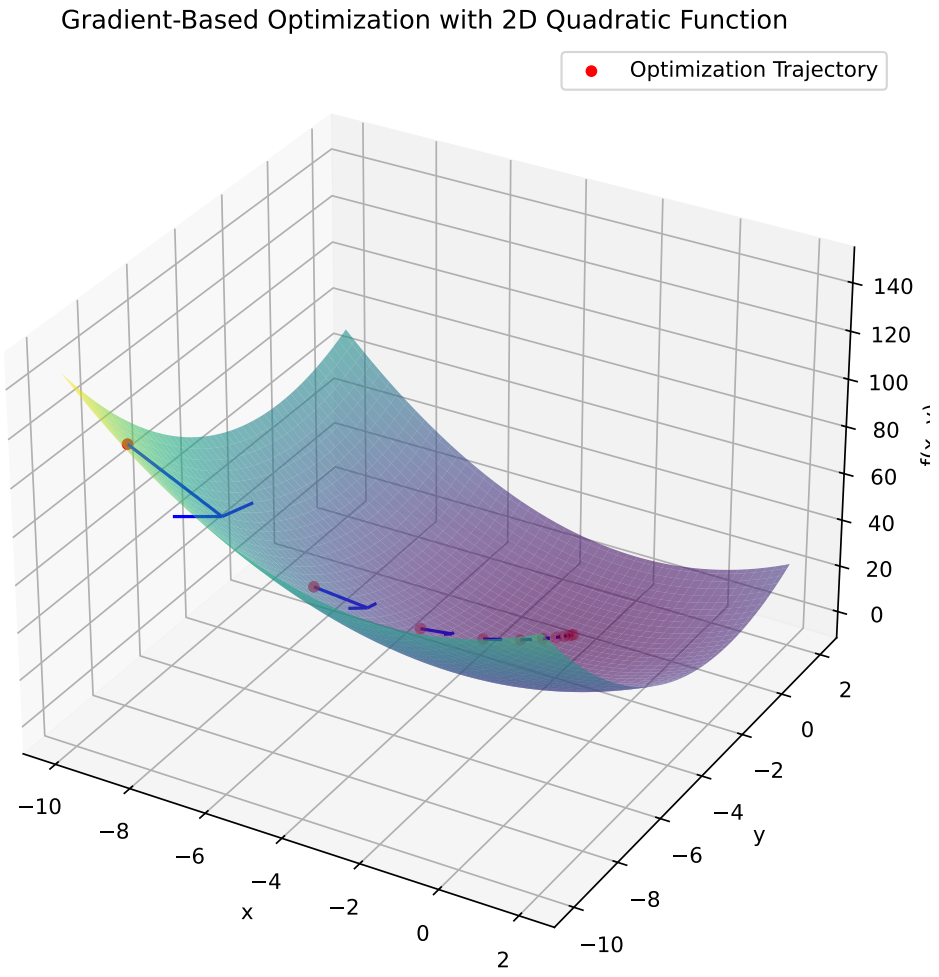
Example 3.4 (Gradient Descent)**.** We consider a simple quadratic function as an example:

$$f(x) = x^2 + 4x + y^2 + 2y + 4.$$

We'll use gradient descent to find the minimum of this function.

```
import numpy as np
import matplotlib.pyplot as plt
from mpl_toolkits.mplot3d import Axes3D

# Define the quadratic function
def quadratic_function(x, y):
    return x**2 + 4*x + y**2 + 2*y + 4

# Define the gradient of the quadratic function
def gradient_quadratic_function(x, y):
    grad_x = 2*x + 4
    grad_y = 2*y + 2
    return np.array([grad_x, grad_y])

# Gradient Descent for optimization in 2D
def gradient_descent(initial_point, learning_rate, num_iterations):
    points = [np.array(initial_point)]
    for _ in range(num_iterations):
        current_point = points[-1]
        gradient = gradient_quadratic_function(*current_point)
        new_point = current_point - learning_rate * gradient
        points.append(new_point)
    return points

# Visualization of optimization process with 3D surface and consistent arrow sizes
def plot_optimization_process_3d_consistent_arrows(points):
    fig = plt.figure(figsize=(10, 8))
    ax = fig.add_subplot(111, projection='3d')

    x_vals = np.linspace(-10, 2, 100)
    y_vals = np.linspace(-10, 2, 100)
    X, Y = np.meshgrid(x_vals, y_vals)
    Z = quadratic_function(X, Y)

    ax.plot_surface(X, Y, Z, cmap='viridis', alpha=0.6)
    ax.scatter(*zip(*points), [quadratic_function(*p) for p in points], c='red', label='Optimizatior

    for i in range(len(points) - 1):
        x, y = points[i]
```

```
        dx, dy = points[i + 1] - points[i]
        dz = quadratic_function(*(points[i + 1])) - quadratic_function(*points[i])
        gradient_length = 0.5

        ax.quiver(x, y, quadratic_function(*points[i]), dx, dy, dz, color='blue', leng

    ax.set_title('Gradient-Based Optimization with 2D Quadratic Function')
    ax.set_xlabel('x')
    ax.set_ylabel('y')
    ax.set_zlabel('f(x, y)')
    ax.legend()
    plt.show()

# Initial guess and parameters
initial_guess = [-9.0, -9.0]
learning_rate = 0.2
num_iterations = 10

# Run gradient descent in 2D and visualize the optimization process with 3D surface ar
trajectory = gradient_descent(initial_guess, learning_rate, num_iterations)
plot_optimization_process_3d_consistent_arrows(trajectory)
```



3.2.7 Newton Method

Initialization: Start with an initial guess for the optimal solution: x_0.

Iteration: Repeat the following three steps until convergence or a predefined stopping criterion is met:

1. Calculate the gradient (∇) and the Hessian matrix (∇^2) of the objective function at the current point:

$$\nabla f(x_k) \quad \text{and} \quad \nabla^2 f(x_k)$$

2. Update the current solution using the Newton-Raphson update formula

$$x_{k+1} = x_k - [\nabla^2 f(x_k)]^{-1} \nabla f(x_k),$$

where

```
* $\nabla f(x_k)$ is the gradient (first derivative) of the objective function wi
```

- $\nabla^2 f(x_k)$: The Hessian matrix (second derivative) of the objective function with respect to x, evaluated at the current solution x_k.
- x_k: The current solution or point in the optimization process.
- $\nabla^2 f(x_k)]^{-1}$: The inverse of the Hessian matrix at the current point, representing the approximation of the curvature of the objective function.
- x_{k+1}: The updated solution or point after applying the Newton-Raphson update.

3. Check for convergence.

Example 3.5 (Newton Method)**.** We want to optimize the Rosenbrock function and use the Hessian and the Jacobian (which is equal to the gradient vector for scalar objective function) to the `minimize` function.

```
def rosenbrock(x):
    return 100 * (x[1] - x[0]**2)**2 + (1 - x[0])**2

def rosenbrock_gradient(x):
    dfdx0 = -400 * x[0] * (x[1] - x[0]**2) - 2 * (1 - x[0])
    dfdx1 = 200 * (x[1] - x[0]**2)
    return np.array([dfdx0, dfdx1])

def rosenbrock_hessian(x):
    d2fdx0 = 1200 * x[0]**2 - 400 * x[1] + 2
    d2fdx1 = -400 * x[0]
    return np.array([[d2fdx0, d2fdx1], [d2fdx1, 200]])

def classical_newton_optimization_2d(initial_guess, tol=1e-6, max_iter=100):
    x = initial_guess.copy()

    for i in range(max_iter):
        gradient = rosenbrock_gradient(x)
        hessian = rosenbrock_hessian(x)

        # Solve the linear system H * d = -g for d
        d = np.linalg.solve(hessian, -gradient)

        # Update x
```

```
        x += d

        # Check for convergence
        if np.linalg.norm(gradient, ord=np.inf) < tol:
            break

    return x

# Initial guess
initial_guess_2d = np.array([0.0, 0.0])

# Run classical Newton optimization for the 2D Rosenbrock function
result_2d = classical_newton_optimization_2d(initial_guess_2d)

# Print the result
print("Optimal solution:", result_2d)
print("Objective value:", rosenbrock(result_2d))
```

```
Optimal solution: [1. 1.]
Objective value: 0.0
```

3.2.8 BFGS-Algorithm

BFGS is an optimization algorithm designed for unconstrained optimization problems. It belongs to the class of quasi-Newton methods and is known for its efficiency in finding the minimum of a smooth, unconstrained objective function.

3.2.9 Procedure:

1. **Initialization:**
   - Start with an initial guess for the parameters of the objective function.
   - Initialize an approximation of the Hessian matrix (inverse) denoted by H.

2. **Iterative Update:**
   - At each iteration, compute the gradient vector at the current point.
   - Update the parameters using the BFGS update formula, which involves the inverse Hessian matrix approximation, the gradient, and the difference in parameter vectors between successive iterations:

$$x_{k+1} = x_k - H_k^{-1} \nabla f(x_k).$$

- Update the inverse Hessian approximation using the BFGS update formula for the inverse Hessian.

$$H_{k+1} = H_k + \frac{\Delta x_k \Delta x_k^T}{\Delta x_k^T \Delta g_k} - \frac{H_k g_k g_k^T H_k}{g_k^T H_k g_k},$$

  where:
- x_k and x_{k+1} are the parameter vectors at the current and updated iterations, respectively.
- $\nabla f(x_k)$ is the gradient vector at the current iteration.
- $\Delta x_k = x_{k+1} - x_k$ is the change in parameter vectors.
- $\Delta g_k = \nabla f(x_{k+1}) - \nabla f(x_k)$ is the change in gradient vectors.

3. **Convergence:**

   - Repeat the iterative update until the optimization converges. Convergence is typically determined by reaching a sufficiently low gradient or parameter change.

Example 3.6 (BFGS for Rosenbrock)**.**

```
import numpy as np
from scipy.optimize import minimize

# Define the 2D Rosenbrock function
def rosenbrock(x):
    return (1 - x[0])**2 + 100 * (x[1] - x[0]**2)**2

# Initial guess
initial_guess = np.array([0.0, 0.0])

# Minimize the Rosenbrock function using BFGS
minimize(rosenbrock, initial_guess, method='BFGS')
```

```
  message: Optimization terminated successfully.
  success: True
   status: 0
      fun: 2.843987518235081e-11
        x: [ 1.000e+00  1.000e+00]
      nit: 19
      jac: [ 3.987e-06 -2.844e-06]
 hess_inv: [[ 4.948e-01  9.896e-01]
            [ 9.896e-01  1.984e+00]]
     nfev: 72
     njev: 24
```

3.2.10 Visualization BFGS for Rosenbrock

A visualization of the BFGS search process on Rosenbrock's function can be found here: https://upload.wikimedia.org/wikipedia/de/f/ff/Rosenbrock-bfgs-animation.gif

Tasks

- In which situations is it possible to use algorithms like BFGS, but not the classical Newton method?
- Investigate the Newton-CG method
- Use an objective function of your choice and apply Newton-CG
- Compare the Newton-CG method with the BFGS. What are the similarities and differences between the two algorithms?

3.3 Gradient- and Hessian-based Optimization Algorithms

Section **??** presents an optimization algorithm that uses gradient and Hessian information to find the minimum. Section **??** presents an optimization algorithm that uses gradient and Hessian information to find the minimum. Section **??** presents an optimization algorithm that uses gradient and Hessian information to find the minimum.

The methods Newton-CG, trust-ncg and trust-krylov are suitable for dealing with large-scale problems (problems with thousands of variables). That is because the conjugate gradient algorithm approximately solve the trust-region subproblem (or invert the Hessian) by iterations without the explicit Hessian factorization. Since only the product of the Hessian with an arbitrary vector is needed, the algorithm is specially suited for dealing with sparse Hessians, allowing low storage requirements and significant time savings for those sparse problems.

3.3.1 Newton-Conjugate-Gradient Algorithm

Newton-Conjugate Gradient algorithm is a modified Newton's method and uses a conjugate gradient algorithm to (approximately) invert the local Hessian.

3.3.2 Trust-Region Newton-Conjugate-Gradient Algorithm

3.3.3 Trust-Region Truncated Generalized Lanczos / Conjugate Gradient Algorithm

3.4 Global Optimization

Global optimization aims to find the global minimum of a function within given bounds, in the presence of potentially many local minima. Typically, global minimizers efficiently search the parameter space, while using a local minimizer (e.g., minimize) under the hood.

3.4.1 Local vs Global Optimization

3.4.1.1 Local Optimizater:

- Seeks the optimum in a **specific region** of the search space
- Tends to **exploit** the local environment, to find solutions in the immediate area
- Highly **sensitive to initial conditions**; may converge to different local optima based on the starting point
- Often **computationally efficient for low-dimensional problems** but may struggle with high-dimensional or complex search spaces
- Commonly used in situations where the objective is to refine and improve existing solutions

3.4.1.2 Global Optimizer:

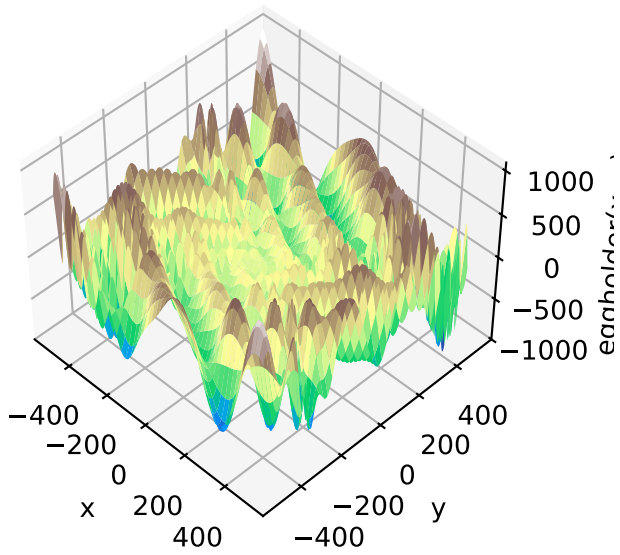
- Explores the **entire search space** to find the global optimum
- Emphasize **exploration over exploitation**, aiming to search broadly and avoid premature convergence to local optima
- Aim to **mitigate the risk of premature convergence** to local optima by employing strategies for global exploration
- **Less sensitive to initial conditions**, designed to navigate diverse regions of the search space
- Equipped to handle **high-dimensional** and **complex** problems, though computational demands may vary depending on the specific algorithm
- Preferred for applications where a comprehensive search of the solution space is crucial, such as in parameter tuning, machine learning, and complex engineering design

3.4.2 Global Optimizers in SciPy

SciPy contains a number of good global optimizers. Here, we'll use those on the same objective function, namely the (aptly named) eggholder function:

```
def eggholder(x):
    return (-(x[1] + 47) * np.sin(np.sqrt(abs(x[0]/2 + (x[1]  + 47))))
            -x[0] * np.sin(np.sqrt(abs(x[0] - (x[1]  + 47)))))

bounds = [(-512, 512), (-512, 512)]
```

```
import matplotlib.pyplot as plt
from mpl_toolkits.mplot3d import Axes3D

x = np.arange(-512, 513)
y = np.arange(-512, 513)
xgrid, ygrid = np.meshgrid(x, y)
xy = np.stack([xgrid, ygrid])

fig = plt.figure()
ax = fig.add_subplot(111, projection='3d')
ax.view_init(45, -45)
ax.plot_surface(xgrid, ygrid, eggholder(xy), cmap='terrain')
ax.set_xlabel('x')
ax.set_ylabel('y')
ax.set_zlabel('eggholder(x, y)')
plt.show()
```



We now use the global optimizers to obtain the minimum and the function value at the minimum. We'll store the results in a dictionary so we can compare different optimization results later.

```
from scipy import optimize
results = dict()
results['shgo'] = optimize.shgo(eggholder, bounds)
results['shgo']
```

```
 message: Optimization terminated successfully.
 success: True
     fun: -935.3379515605789
    funl: [-9.353e+02]
       x: [ 4.395e+02  4.540e+02]
      xl: [[ 4.395e+02  4.540e+02]]
     nit: 1
    nfev: 45
   nlfev: 40
   nljev: 10
   nlhev: 0
```

```
results['DA'] = optimize.dual_annealing(eggholder, bounds)
results['DA']
```

```
 message: ['Maximum number of iteration reached']
```

```
 success: True
  status: 0
     fun: -888.9491252694841
       x: [ 3.473e+02  4.994e+02]
     nit: 1000
    nfev: 4061
    njev: 20
    nhev: 0
```

All optimizers return an `OptimizeResult`, which in addition to the solution contains information on the number of function evaluations, whether the optimization was successful, and more. For brevity, we won't show the full output of the other optimizers:

```
results['DE'] = optimize.differential_evolution(eggholder, bounds)
results['DE']
```

```
             message: Optimization terminated successfully.
             success: True
                 fun: -935.3379515542147
                   x: [ 4.395e+02  4.540e+02]
                 nit: 26
                nfev: 831
          population: [[ 4.398e+02  4.542e+02]
                       [ 4.377e+02  4.513e+02]
                       ...
                       [ 4.405e+02  4.547e+02]
                       [ 4.422e+02  4.556e+02]]
 population_energies: [-9.353e+02 -9.335e+02 ... -9.351e+02 -9.334e+02]
                 jac: [ 3.411e-05  2.274e-05]
```

`shgo` has a second method, which returns all local minima rather than only what it thinks is the global minimum:

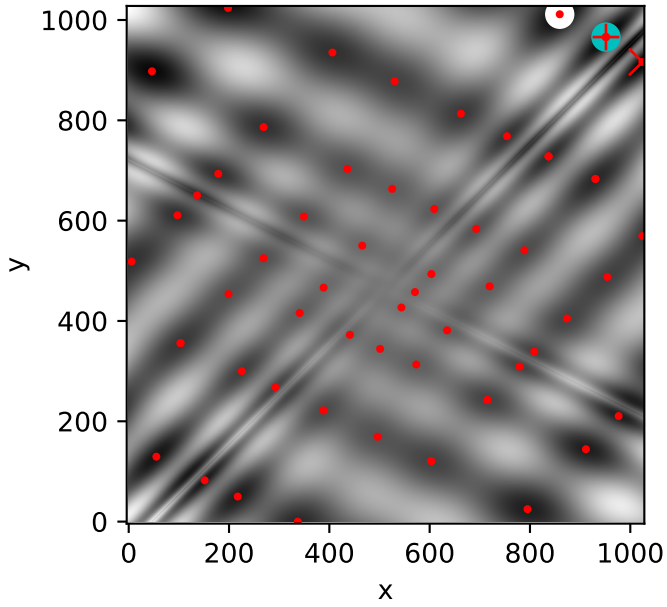
```
results['shgo_sobol'] = optimize.shgo(eggholder, bounds, n=200, iters=5,
                                      sampling_method='sobol')
results['shgo_sobol']
```

```
 message: Optimization terminated successfully.
 success: True
     fun: -959.640662720831
    funl: [-9.596e+02 -9.353e+02 ... -6.591e+01 -6.387e+01]
       x: [ 5.120e+02  4.042e+02]
      xl: [[ 5.120e+02  4.042e+02]
```

```
           [ 4.395e+02  4.540e+02]
           ...
           [ 3.165e+01 -8.523e+01]
           [ 5.865e+01 -5.441e+01]]
     nit: 5
    nfev: 3529
   nlfev: 2327
   nljev: 634
   nlhev: 0
```

We'll now plot all found minima on a heatmap of the function:

```
fig = plt.figure()
ax = fig.add_subplot(111)
im = ax.imshow(eggholder(xy), interpolation='bilinear', origin='lower',
               cmap='gray')
ax.set_xlabel('x')
ax.set_ylabel('y')

def plot_point(res, marker='o', color=None):
    ax.plot(512+res.x[0], 512+res.x[1], marker=marker, color=color, ms=10)

plot_point(results['DE'], color='c')  # differential_evolution - cyan
plot_point(results['DA'], color='w')  # dual_annealing.        - white

# SHGO produces multiple minima, plot them all (with a smaller marker size)
plot_point(results['shgo'], color='r', marker='+')
plot_point(results['shgo_sobol'], color='r', marker='x')
for i in range(results['shgo_sobol'].xl.shape[0]):
    ax.plot(512 + results['shgo_sobol'].xl[i, 0],
            512 + results['shgo_sobol'].xl[i, 1],
            'ro', ms=2)

ax.set_xlim([-4, 514*2])
ax.set_ylim([-4, 514*2])
plt.show()
```



3.4.3 Dual Annealing Optimization

This function implements the Dual-Annealing optimization, which is a variant of the famous simulated annealing optimization.

Simulated Annealing is a **probabilistic** optimization algorithm inspired by the annealing process in metallurgy. The algorithm is designed to find a good or optimal **global** solution to a problem by exploring the solution space in a controlled and adaptive manner.

> **i** Annealing in Metallurgy
>
> Simulated Annealing draws inspiration from the physical process of annealing in metallurgy. Just as metals are gradually cooled to achieve a more stable state, Simulated Annealing uses a similar approach to explore solution spaces in the digital world.

Heating Phase: In metallurgy, a metal is initially heated to a high temperature. At this elevated temperature, the atoms or molecules in the material become more energetic and chaotic, allowing the material to overcome energy barriers and defects.

Analogy Simulated Annealing (Exploration Phase): In Simulated Annealing, the algorithm starts with a high "temperature," which encourages exploration of the

solution space. At this stage, the algorithm is more likely to accept solutions that are worse than the current one, allowing it to escape local optima and explore a broader region of the solution space.

Cooling Phase: The material is then gradually cooled at a controlled rate. As the temperature decreases, the atoms or molecules start to settle into more ordered and stable arrangements. The slow cooling rate is crucial to avoid the formation of defects and to ensure the material reaches a well-organized state.

Analogy Simulated Annealing (Exploitation Phase): As the algorithm progresses, the temperature is gradually reduced over time according to a cooling schedule. This reduction simulates the cooling process in metallurgy. With lower temperatures, the algorithm becomes more selective and tends to accept only better solutions, focusing on refining and exploiting the promising regions discovered during the exploration phase.

3.4.3.1 Key Concepts

Temperature: The temperature is a parameter that controls the likelihood of accepting worse solutions. We start with a high temperature, allowing the algorithm to explore the solution space braodly. The temperature decreases with the iterations of the algorithm.

Cooling Schedule: The temperature parameter is reduced according to this schedule. The analogy to the annealing of metals: a slower cooling rate allows the material to reach a more stable state.

Neighborhood Exploration: At each iteration, the algorithm explores the neighborhood of the current solution. The neighborhood is defined by small perturbations or changes to the current solution.

Acceptance Probability: The algorithm evaluates the objective function for the new solution in the neighborhood. If the new solution is better, it is accepted. If the new solution is worse, it may still be accepted with a certain probability. This probability is determined by both the difference in objective function values and the current temperature.

For minimization: If:

$$f(x_t) > f(x_{t+1})$$

Then:

$$P(accept\_new\_point) = 1$$

If:

$$f(x_t) < f(x_{t+1})$$

Then:

$$P(accept\_new\_point) = e^{-(\frac{f(x_{t+1})-f(x_t)}{Tt})}$$

Termination Criterion: The algorithm continues iterations until a termination condition is met. This could be a fixed number of iterations, reaching a specific temperature threshold, or achieving a satisfactory solution.

3.4.3.2 Steps

1. Initialization: Set an initial temperature (T_0) and an initial solution ($f(x_0)$). The temperature is typically set high initially to encourage exploration.

2. Generate a Neighbor: Perturb the current solution to generate a neighboring solution. The perturbation can be random or follow a specific strategy.

3. Evaluate the Neighbor: Evaluate the objective function for the new solution in the neighborhood.

4. Accept or Reject the Neighbor: + If the new solution is better (lower cost for minimization problems or higher for maximization problems), accept it as the new current solution. + If the new solution is worse, accept it with a probability determined by an acceptance probability function as mentioned above. The probability is influenced by the difference in objective function values and the current temperature.

5. Cooling: Reduce the temperature according to a cooling schedule. The cooling schedule defines how fast the temperature decreases over time. Common cooling schedules include exponential or linear decay.

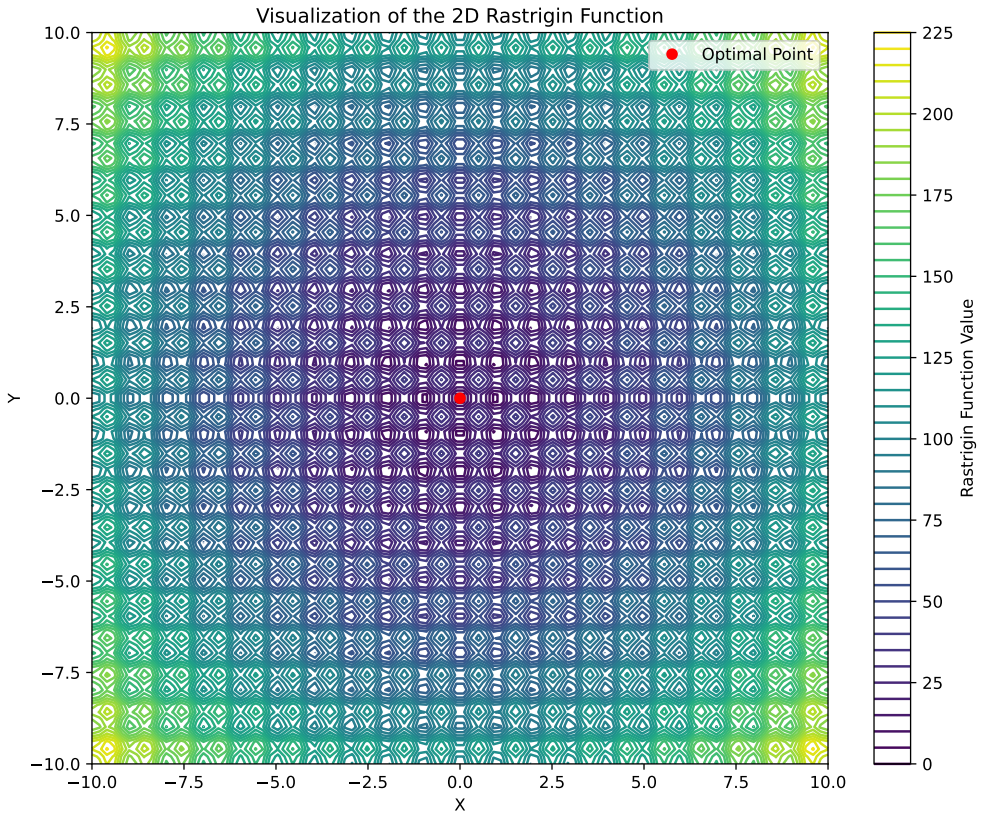
6. Termination Criterion: Repeat the iterations (2-5) until a termination condition is met. This could be a fixed number of iterations, reaching a specific temperature threshold, or achieving a satisfactory solution.

3.4.3.3 Scipy Implementation of the Dual Annealing Algorithm

In Scipy, we utilize the Dual Annealing optimizer, an extension of the simulated annealing algorithm that is versatile for both discrete and continuous problems.

```
import numpy as np
import matplotlib.pyplot as plt
from scipy.optimize import dual_annealing

def rastrigin_function(x):
    return 20 + x[0]**2 - 10 * np.cos(2 * np.pi * x[0]) + x[1]**2 - 10 * np.cos(2 * np.pi * x[1])

# Define the Rastrigin function for visualization
def rastrigin_visualization(x, y):
    return 20 + x**2 - 10 * np.cos(2 * np.pi * x) + y**2 - 10 * np.cos(2 * np.pi * y)
```

```
# Create a meshgrid for visualization
x_vals = np.linspace(-10, 10, 100)
y_vals = np.linspace(-10, 10, 100)
x_mesh, y_mesh = np.meshgrid(x_vals, y_vals)
z_mesh = rastrigin_visualization(x_mesh, y_mesh)

# Visualize the Rastrigin function
plt.figure(figsize=(10, 8))
contour = plt.contour(x_mesh, y_mesh, z_mesh, levels=50, cmap='viridis')
plt.colorbar(contour, label='Rastrigin Function Value')
plt.title('Visualization of the 2D Rastrigin Function')

# Optimize the Rastrigin function using dual annealing
result = dual_annealing(func = rastrigin_function,
                        x0=[5.0,3.0],                        #Initial Guess
                        bounds= [(-10, 10), (-10, 10)],
                        initial_temp = 5230,                 #Intial Value for temperat
                        restart_temp_ratio = 2e-05,          #Temperature schedule
                        seed=42)

# Plot the optimized point
optimal_x, optimal_y = result.x
plt.plot(optimal_x, optimal_y, 'ro', label='Optimal Point')

# Set labels and legend
plt.xlabel('X')
plt.ylabel('Y')
plt.legend()

# Show the plot
plt.show()

# Display the optimization result
print("Optimal parameters:", result.x)
print("Minimum value of the Rastrigin function:", result.fun)
```




```
Optimal parameters: [-4.60133247e-09 -4.31928660e-09]
Minimum value of the Rastrigin function: 7.105427357601002e-15
```

```
result
```

```
 message: ['Maximum number of iteration reached']
 success: True
  status: 0
     fun: 7.105427357601002e-15
       x: [-4.601e-09 -4.319e-09]
     nit: 1000
    nfev: 4088
    njev: 29
    nhev: 0
```

3.4.3.4 Example of Comparison Table:

Function	Algorithm	Best Objective Function Value	Number of Iterations	Number of Evaluations	Local/Global Optimizer	Gradient-Based/Free Algorithm	Other Comments
Rastrigin	Algorithm 1	1.23	1000	5000	Global	Free	?
Rastrigin	Algorithm 2	0.95	800	4000	Local	Gradient-Based	?
Rastrigin	Algorithm 3	1.45	1200	6000	Global	Free	?
Rosenbrock	Algorithm 1	2.56	1500	7500	Local	Gradient-Based	?
Rosenbrock	Algorithm 2	2.12	1200	6000	Global	Free	?
Rosenbrock	Algorithm 3	2.73	1800	9000	Local	Gradient-Based	?

3.4.4 Differential Evolution

Differential Evolution is an algorithm used for finding the global minimum of multivariate functions. It is stochastic in nature (does not use gradient methods), and can search large areas of candidate space, but often requires larger numbers of function evaluations than conventional gradient based techniques.

Differential Evolution (DE) is a versatile and global optimization algorithm inspired by natural selection and evolutionary processes. Introduced by Storn and Price in 1997, DE mimics the survival-of-the-fittest principle by evolving a population of candidate solutions through iterative mutation, crossover, and selection operations. This nature-inspired approach enables DE to efficiently explore complex and non-linear solution spaces, making it a widely adopted optimization technique in diverse fields such as engineering, finance, and machine learning.

3.4.5 Procedure

The procedure boils down to the following steps:

1. **Initialization:**
    - Create a population of candidate solutions randomly within the specified search space.
2. **Mutation:**

- For each individual in the population, select three distinct individuals (vectors) randomly.
- Generate a mutant vector `V` by combining these three vectors with a scaling factor.

3. **Crossover:**
    - Perform the crossover operation between the target vector `U` and the mutant vector `V`. Information from both vectors is used to create a trial vector `U´`

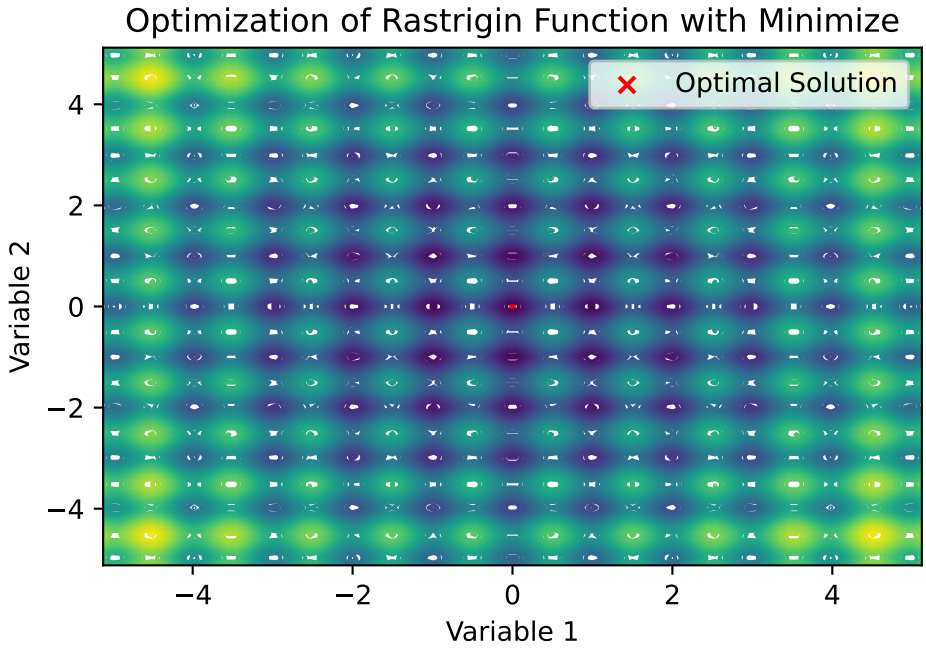
> **i** Cross-Over Strategies in DE
>
> - There are several crossover strategies in the literature. Two examples are:
>
> **Binominal Crossover:**
> In this strategy, each component of the trial vector is selected from the mutant vector with a probability equal to the crossover rate (CR). This means that each element of the trial vector has an independent probability of being replaced by the corresponding element of the mutant vector.
>
> $$U_i' = \begin{cases} V_i, & \text{if a random number } \sim U(0,1) \leq CR \text{ (Crossover Rate)} \\ U_i, & \text{otherwise} \end{cases}$$
>
> **Exponential Crossover:**
> In exponential crossover, the trial vector is constructed by selecting a random starting point and copying elements from the mutant vector with a certain probability. The probability decreases exponentially with the distance from the starting point. This strategy introduces a correlation between neighboring elements in the trial vector.

4. **Selection:**
    - Evaluate the fitness of the trial vector obtained from the crossover.
    - Replace the target vector with the trial vector if its fitness is better.
5. **Termination:**
    - Repeat the mutation, crossover, and selection steps for a predefined number of generations or until convergence criteria are met.
6. **Result:**
    - The algorithm returns the best-found solution after the specified number of iterations.

The key parameters in DE include the population size, crossover probability, and the scaling factor. Tweak these parameters based on the characteristics of the optimization problem for optimal performance.

```python
import numpy as np
import matplotlib.pyplot as plt
from scipy.optimize import minimize

# Define the Rastrigin function
def rastrigin(x):
    A = 10
    return A * len(x) + sum([(xi**2 - A * np.cos(2 * np.pi * xi)) for xi in x])

# Create a grid for visualization
x_vals = np.linspace(-5.12, 5.12, 100)
y_vals = np.linspace(-5.12, 5.12, 100)
X, Y = np.meshgrid(x_vals, y_vals)
Z = rastrigin(np.vstack([X.ravel(), Y.ravel()]))

# Reshape Z to match the shape of X and Y
Z = Z.reshape(X.shape)

# Plot the Rastrigin function
plt.contour(X, Y, Z, levels=50, cmap='viridis', label='Rastrigin Function')

# Initial guess (starting point for the optimization)
initial_guess = (4,3,4,2)

# Define the bounds for each variable in the Rastrigin function
bounds = [(-5.12, 5.12)] * 4  # 4D problem, each variable has bounds (-5.12, 5.12)

# Run the minimize function
result = minimize(rastrigin, initial_guess, bounds=bounds, method='L-BFGS-B')

# Extract the optimal solution
optimal_solution = result.x

# Plot the optimal solution
plt.scatter(optimal_solution[0], optimal_solution[1], color='red', marker='x', label=

# Add labels and legend
plt.title('Optimization of Rastrigin Function with Minimize')
plt.xlabel('Variable 1')
plt.ylabel('Variable 2')
plt.legend()

# Show the plot
plt.show()
```

```
# Print the optimization result
print("Optimal Solution:", optimal_solution)
print("Optimal Objective Value:", result.fun)
```




```
Optimal Solution: [-2.52869119e-08 -2.07795060e-08 -2.52869119e-08 -1.62721002e-08]
Optimal Objective Value: 3.907985046680551e-13
```

3.4.6 DIRECT

DIviding RECTangles (DIRECT) is a deterministic global optimization algorithm capable of minimizing a black box function with its variables subject to lower and upper bound constraints by sampling potential solutions in the search space

3.4.7 SHGO

SHGO stands for "simplicial homology global optimization". It is considered appropriate for solving general purpose NLP and blackbox optimization problems to global optimality (low-dimensional problems).

3.4.8 Basin-hopping

Basin-hopping is a two-phase method that combines a global stepping algorithm with local minimization at each step. Designed to mimic the natural process of energy minimization of clusters of atoms, it works well for similar problems with "funnel-like, but rugged" energy landscapes

3.5 Project: One-Mass Oscillator Optimization

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from scipy.optimize import minimize
```

3.5.1 Introduction

In this project, you will apply various optimization algorithms to fit a one-mass oscillator model to real-world data. The objective is to minimize the sum of the squared residuals between the model predictions and the observed amplitudes of a one-mass oscillator system across different frequencies.

3.5.2 One-Mass Oscillator Model

The one-mass oscillator is characterized by the following equation, representing the amplitudes of the system:

$$V(\omega) = \frac{F}{\sqrt{(1-\nu^2)^2 + 4D^2\nu^2}}$$

Here, ω represents the angular frequency of the system, ν is the ratio of the excitation frequency to the natural frequency, i.e.,

$$\nu = \frac{\omega_{\text{err}}}{\omega_{\text{eig}}},$$

D is the damping ratio, and F is the force applied to the system.

The goal of the project is to determine the optimal values for the parameters ω_{eig}, D, and F that result in the best fit of the one-mass oscillator model to the observed amplitudes.

3.5.3 The Real-World Data

There are two different measurements. `J` represents the measured frequencies, and `N` represents the measured amplitudes.

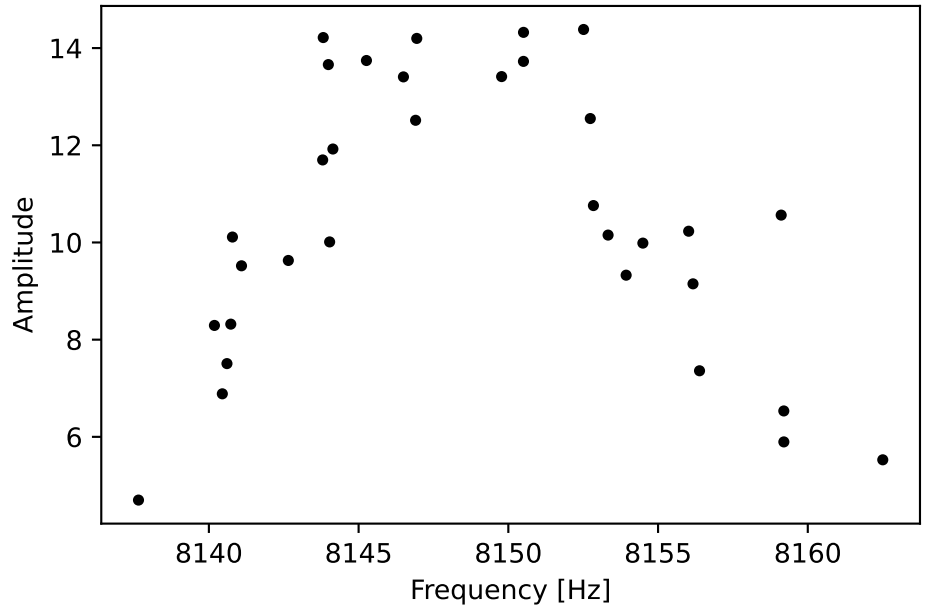
```
df1 = pd.read_pickle("./data/Hcf.d/df1.pkl")
df2 = pd.read_pickle("./data/Hcf.d/df2.pkl")
df1.describe()
```

	J	N
count	33.000000	33.000000
mean	8148.750252	10.430887
std	6.870023	2.846469
min	8137.649210	4.698761
25%	8143.799766	8.319253
50%	8146.942295	10.152119
75%	8153.934051	13.407260
max	8162.504002	14.382749

```
df1.head()
```

	J	N
14999	8162.504002	5.527511
15011	8156.384831	7.359789
15016	8159.199238	6.532958
15020	8159.200889	5.895933
15025	8153.934051	9.326749

```
# plot the data, i.e., the measured amplitudes as a function of the measured frequencies
plt.scatter(df1["J"], df1["N"], color="black", label="Spektralpunkte", zorder=5, s=10)
plt.xlabel("Frequency [Hz]")
plt.ylabel("Amplitude")
plt.show()
```



Note: Low amplitudes distort the fit and are negligible therefore we define a lower threshold for N.

```
threshold = 0.4
df1.sort_values("N")
max_N = max(df1["N"])
df1 = df1[df1["N"]>=threshold*max_N]
```

We extract the frequency value for maximum value of the amplitude. This serves as the initial value for one decision variable.

```
df_max=df1[df1["N"]==max(df1["N"])]
initial_Oeig = df_max["J"].values[0]
max_N = df_max["N"].values[0]
```

We also have to define the other two initial guesses for the damping ratio and the force, e.g.,

```
initial_D = 0.006
initial_F = 0.120
initial_values = [initial_Oeig, initial_D, initial_F]
```

Additionally, we define the bounds for the decision variables:

```
min_Oerr = min(df1["J"])
max_Oerr = max(df1["J"])
```

```
bounds = [(min_Oerr, max_Oerr), (0, 0.03), (0, 1)]
```

3.5.4 Objective Function

Then we define the objective function:

```
def one_mass_oscillator(params, Oerr) -> np.ndarray:
    # returns amplitudes of the system
    # Defines the model of a one mass oscilator
    Oeig, D, F = params
    nue = Oerr / Oeig
    V = F / (np.sqrt((1 - nue**2) ** 2 + (4 * D**2 * nue**2)))
    return V
```

```
def objective_function(params, Oerr, amplitudes) -> np.ndarray:
    # objective function to compare calculated and real amplitudes
    return np.sum((amplitudes - one_mass_oscillator(params, Oerr)) ** 2)
```

We define the options for the optimzer and start the optimization process:

```
options = {
    "maxfun": 100000,
    "ftol": 1e-9,
    "xtol": 1e-9,
    "stepmx": 10,
    "eta": 0.25,
    "gtol": 1e-5}
```

```
J = np.array(df1["J"]) # measured frequency
N = np.array(df1["N"]) # measured amplitude
```

```
result = minimize(
    objective_function,
    initial_values,
    args=(J, N),
    method='Nelder-Mead',
    bounds=bounds,
    options=options)
```

3.5.5 Results

We can observe the results:

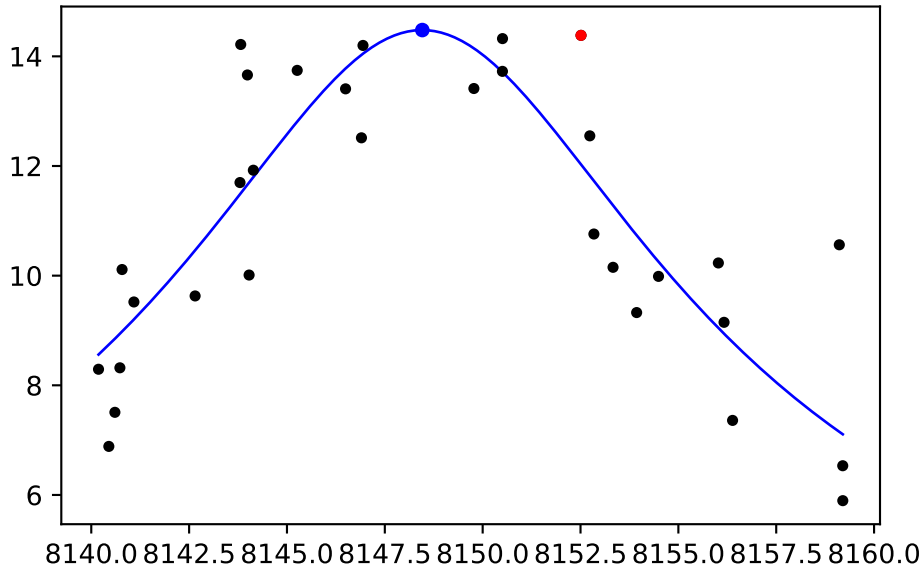
```
# map optimized values to variables
resonant_frequency = result.x[0]
D = result.x[1]
F = result.x[2]
# predict the resonant amplitude with the fitted one mass oscillator.
X_pred = np.linspace(min_Oerr, max_Oerr, 1000)
ypred_one_mass_oscillator = one_mass_oscillator(result.x, X_pred)
resonant_amplitude = max(ypred_one_mass_oscillator)
print(f"result: {result}")
```

```
result:        message: Optimization terminated successfully.
       success: True
        status: 0
           fun: 53.54144061205875
             x: [ 8.148e+03  7.435e-04  2.153e-02]
           nit: 93
          nfev: 169
 final_simplex: (array([[ 8.148e+03,  7.435e-04,  2.153e-02],
                        [ 8.148e+03,  7.435e-04,  2.153e-02],
                        [ 8.148e+03,  7.435e-04,  2.153e-02],
                        [ 8.148e+03,  7.435e-04,  2.153e-02]]), array([ 5.354e+01,  5.3
```

Finally, we can plot the optimized fit and the real values:

```
plt.scatter(
    df1["J"],
    df1["N"],
    color="black",
    label="Spektralpunkte filtered",
    zorder=5,
    s=10,
)
# color the max amplitude point red
plt.scatter(
    initial_Oeig,
    max_N,
    color="red",
    label="Max Amplitude",
    zorder=5,
    s=10,
```

```
)

plt.plot(
        X_pred,
        ypred_one_mass_oscillator,
        label="Alpha",
        color="blue",
        linewidth=1,
    )
plt.scatter(
    resonant_frequency,
    resonant_amplitude,
    color="blue",
    label="Max Curve Fit",
    zorder=10,
    s=20,
)
```



3.5.6 Tasks

- Investigate the trust region Conjugate Gradient method
- Investigate the Differential Evolution Algorithm

- Compare all the methods we introduced for the Rosenbrock (4d) and Rastrigin (2d) function

3.5.7 Task for the Project Work

> **Task**
>
> - Experiment with various optimizers to identify the optimal parameter setup for the one-mass oscillator model and both data frames.
> - Please explain your thoughts and ideas, and subsequently compare the results obtained from different optimizers.

3.6 Jupyter Notebook

> **Note**
>
> - The Jupyter-Notebook of this lecture is available on GitHub in the Hyperparameter-Tuning-Cookbook Repository

4 Sequential Parameter Optimization: Using `scipy` Optimizers

As a default optimizer, `spotpython` uses `differential_evolution` from the `scipy.optimize` package. Alternatively, any other optimizer from the `scipy.optimize` package can be used. This chapter describes how different optimizers from the `scipy optimize` package can be used on the surrogate. The optimization algorithms are available from https://docs.scipy.org/doc/scipy/reference/optimize.html

```
import numpy as np
from math import inf
from spotpython.fun.objectivefunctions import analytical
from spotpython.spot import spot
from scipy.optimize import shgo
from scipy.optimize import direct
from scipy.optimize import differential_evolution
from scipy.optimize import dual_annealing
from scipy.optimize import basinhopping
from spotpython.utils.init import fun_control_init, design_control_init, optimizer_control_init, sur
```

4.1 The Objective Function Branin

The `spotpython` package provides several classes of objective functions. We will use an analytical objective function, i.e., a function that can be described by a (closed) formula. Here we will use the Branin function. The 2-dim Branin function is

$$y = a(x_2 - bx_1^2 + cx_1 - r)^2 + s(1-t)\cos(x_1) + s,$$

where values of a, b, c, r, s and t are: $a = 1$, $b = 5.1/(4\pi^2)$, $c = 5/\pi$, $r = 6$, $s = 10$ and $t = 1/(8\pi)$.

It has three global minima: $f(x) = 0.397887$ at $(-\pi, 12.275)$, $(\pi, 2.275)$, and $(9.42478, 2.475)$.

Input Domain: This function is usually evaluated on the square $x_1 \in [-5, 10] \times x_2 \in [0, 15]$.

```
from spotpython.fun.objectivefunctions import analytical
lower = np.array([-5,-0])
upper = np.array([10,15])
fun = analytical(seed=123).fun_branin
```

4.2 The Optimizer

Differential Evolution (DE) from the `scikit.optimize` package, see https://docs.scipy.org/doc/scipy/reference/generated/scipy.optimize.differential_evolution.html#scipy.optimize.differential_evolution is the default optimizer for the search on the surrogate. Other optimiers that are available in `spotpython`, see https://docs.scipy.org/doc/scipy/reference/optimize.html#global-optimization.

- `dual_annealing`
- `direct`
- `shgo`
- `basinhopping`

These optimizers can be selected as follows:

```
from scipy.optimize import differential_evolution
optimizer = differential_evolution
```

As noted above, we will use `differential_evolution`. The optimizer can use `1000` evaluations. This value will be passed to the `differential_evolution` method, which has the argument `maxiter` (int). It defines the maximum number of generations over which the entire differential evolution population is evolved, see https://docs.scipy.org/doc/scipy/reference/generated/scipy.optimize.differential_evolution.html#scipy.optimize.differential_evolution

> **TensorBoard**
>
> Similar to the one-dimensional case, which is discussed in Section **??**, we can use TensorBoard to monitor the progress of the optimization. We will use a similar code, only the prefix is different:

```
fun_control=fun_control_init(
                    lower = lower,
                    upper = upper,
                    fun_evals = 20,
                    PREFIX = "04_DE_"
                    )
surrogate_control=surrogate_control_init(
                    n_theta=len(lower))
```

```
spot_de = spot.Spot(fun=fun,
                    fun_control=fun_control,
                    surrogate_control=surrogate_control)
spot_de.run()
```

```
spotpython tuning: 3.8004550038787155 [######----] 55.00%
spotpython tuning: 3.8004550038787155 [######----] 60.00%
spotpython tuning: 3.1588579885698627 [######----] 65.00%
spotpython tuning: 3.1342382932317037 [#######---] 70.00%
spotpython tuning: 2.8956615907630585 [########--] 75.00%
spotpython tuning: 0.42052429574482275 [########--] 80.00%
spotpython tuning: 0.4013351867835322 [########--] 85.00%
spotpython tuning: 0.399265616254338 [#########-] 90.00%
spotpython tuning: 0.399265616254338 [##########] 95.00%
spotpython tuning: 0.399265616254338 [##########] 100.00% Done...
```

```
<spotpython.spot.spot.Spot at 0x103e12ae0>
```

4.2.1 TensorBoard

If the `prefix` argument in `fun_control_init()`is not `None` (as above, where the `prefix` was set to `04_DE_`) , we can start TensorBoard in the background with the following command:

```
tensorboard --logdir="./runs"
```

We can access the TensorBoard web server with the following URL:

```
http://localhost:6006/
```

The TensorBoard plot illustrates how spotpython can be used as a microscope for the internal mechanisms of the surrogate-based optimization process. Here, one important parameter, the learning rate θ of the Kriging surrogate is plotted against the number of optimization steps.

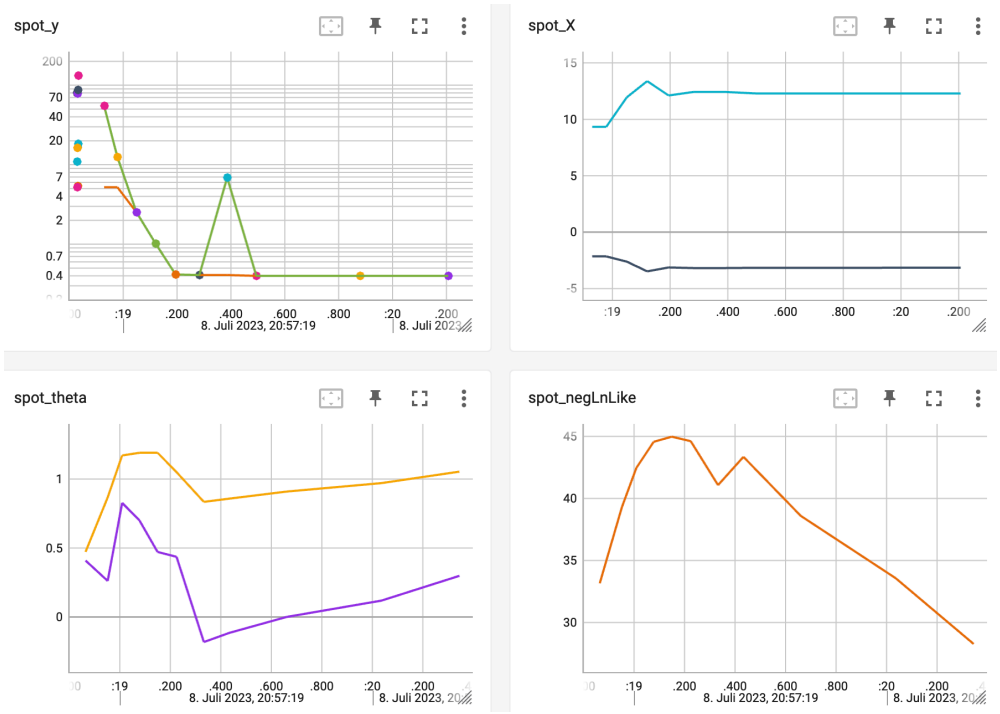


Figure 4.1: TensorBoard visualization of the spotpython optimization process and the surrogate model.

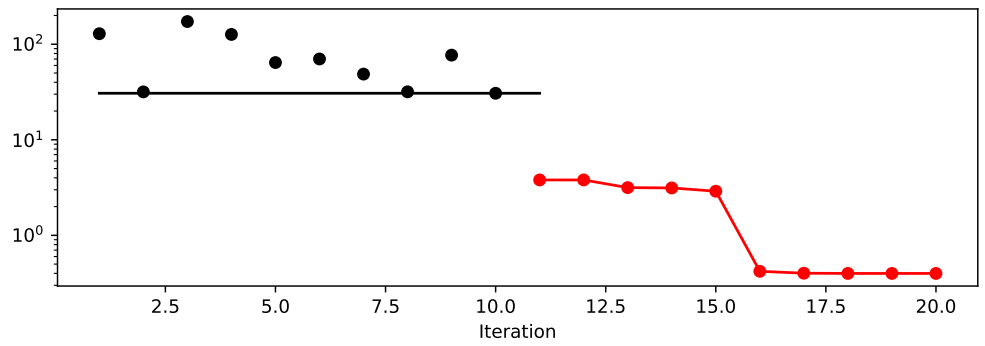
4.3 Print the Results

```
spot_de.print_results()
```

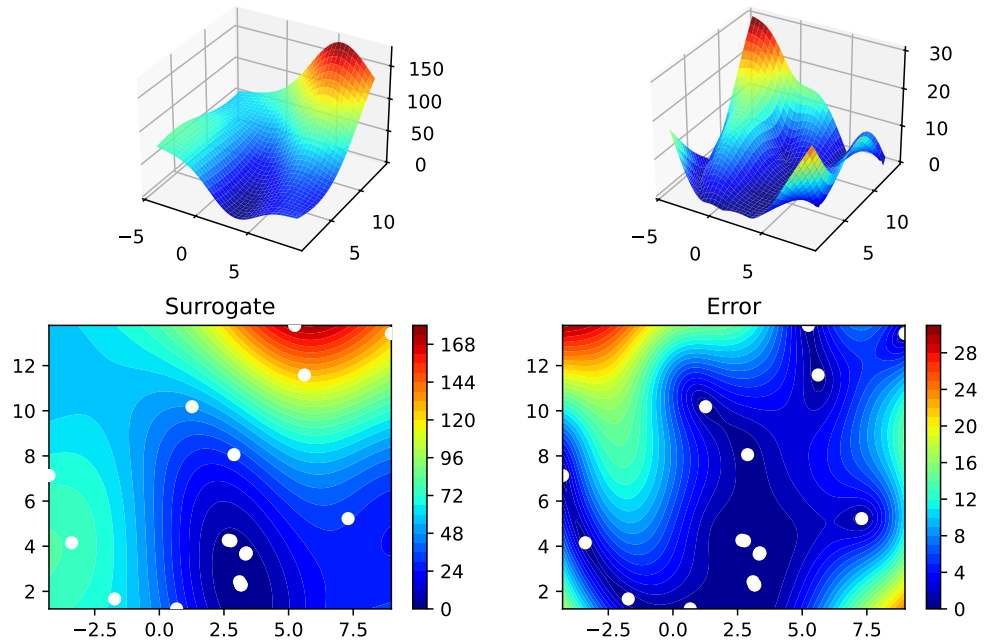
```
min y: 0.399265616254338
x0: 3.151170754781285
x1: 2.2981660114765448

[['x0', 3.151170754781285], ['x1', 2.2981660114765448]]
```

4.4 Show the Progress

```
spot_de.plot_progress(log_y=True)
```




```
spot_de.surrogate.plot()
```



4.5 Exercises

4.5.1 dual_annealing

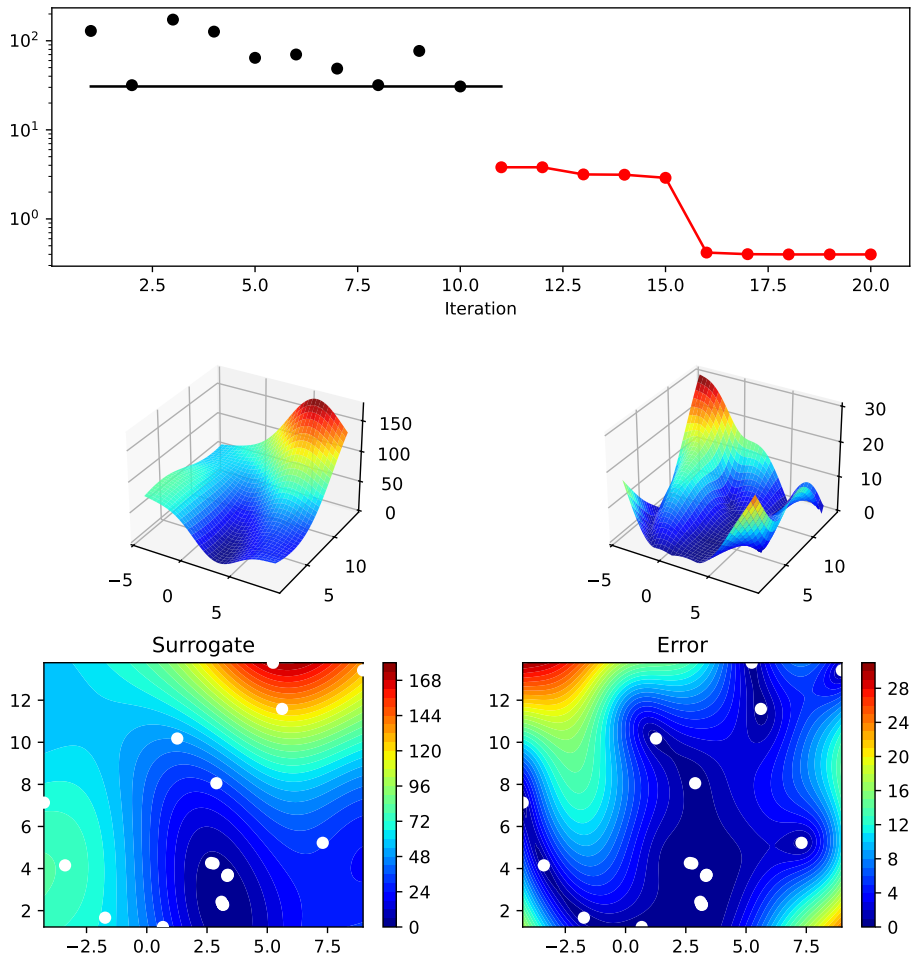
- Describe the optimization algorithm, see scipy.optimize.dual_annealing.
- Use the algorithm as an optimizer on the surrogate.

Tip: Selecting the Optimizer for the Surrogate

We can run spotpython with the dual_annealing optimizer as follows:

```
spot_da = spot.Spot(fun=fun,
                    fun_control=fun_control,
                    optimizer=dual_annealing,
                    surrogate_control=surrogate_control)
spot_da.run()
spot_da.print_results()
spot_da.plot_progress(log_y=True)
spot_da.surrogate.plot()
```

```
spotpython tuning: 3.8004480172281534 [######----] 55.00%
spotpython tuning: 3.8004480172281534 [######----] 60.00%
spotpython tuning: 3.158996247273234 [######----] 65.00%
spotpython tuning: 3.134218255713952 [#######---] 70.00%
spotpython tuning: 2.8926591957342467 [########--] 75.00%
spotpython tuning: 0.4189006494820333 [########--] 80.00%
spotpython tuning: 0.4019392204560983 [########--] 85.00%
spotpython tuning: 0.39922543271904765 [#########-] 90.00%
spotpython tuning: 0.39922543271904765 [##########] 95.00%
spotpython tuning: 0.39922543271904765 [##########] 100.00% Done...

min y: 0.39922543271904765
x0: 3.1506699177492252
x1: 2.298631597428197
```



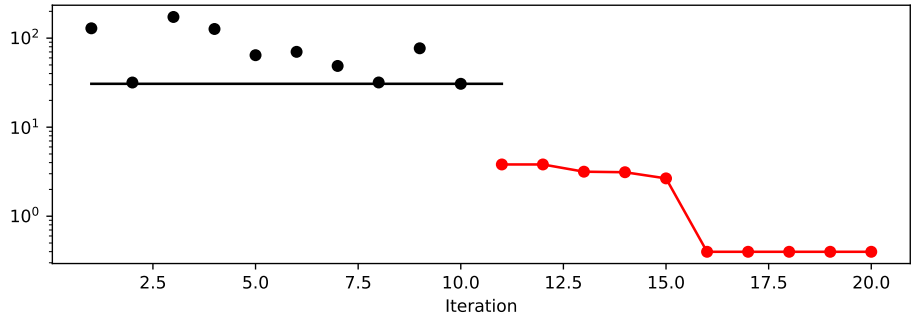
4.5.2 `direct`

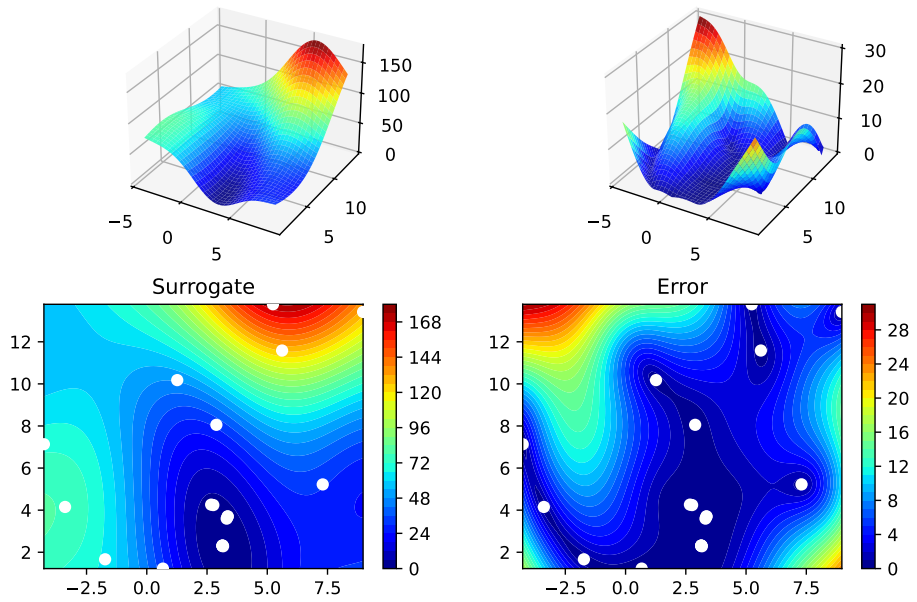
- Describe the optimization algorithm
- Use the algorithm as an optimizer on the surrogate

> Tip: Selecting the Optimizer for the Surrogate
>
> We can run spotpython with the `direct` optimizer as follows:

```
spot_di = spot.Spot(fun=fun,
                    fun_control=fun_control,
                    optimizer=direct,
                    surrogate_control=surrogate_control)
spot_di.run()
spot_di.print_results()
spot_di.plot_progress(log_y=True)
spot_di.surrogate.plot()
```

```
spotpython tuning: 3.812970247994418 [######----] 55.00%
spotpython tuning: 3.812970247994418 [######----] 60.00%
spotpython tuning: 3.162514679816068 [######----] 65.00%
spotpython tuning: 3.1189615135325983 [#######---] 70.00%
spotpython tuning: 2.6597698275013038 [########--] 75.00%
spotpython tuning: 0.3984917773445744 [########--] 80.00%
spotpython tuning: 0.3984917773445744 [########--] 85.00%
spotpython tuning: 0.3984917773445744 [#########-] 90.00%
spotpython tuning: 0.3984917773445744 [##########] 95.00%
spotpython tuning: 0.3984917773445744 [##########] 100.00% Done...

min y: 0.3984917773445744
x0: 3.137860082304525
x1: 2.3010973936899863
```





4.5.3 shgo

- Describe the optimization algorithm
- Use the algorithm as an optimizer on the surrogate

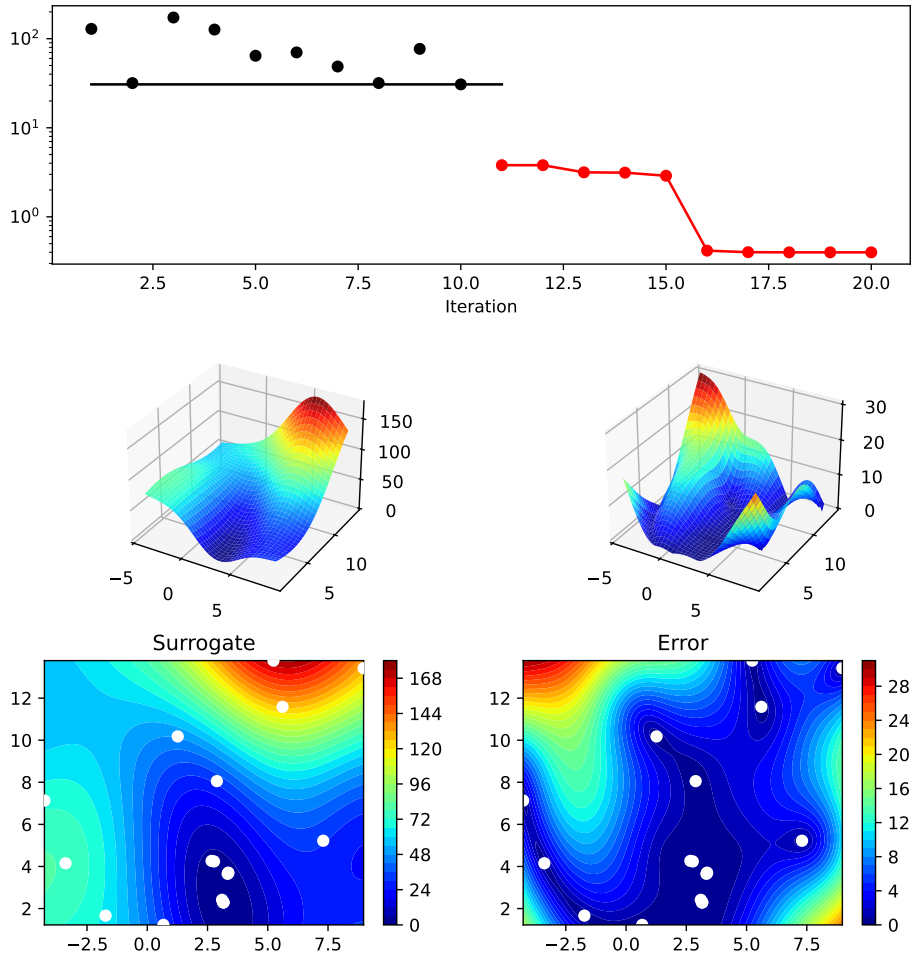
Tip: Selecting the Optimizer for the Surrogate

We can run spotpython with the `direct` optimizer as follows:

```
spot_sh = spot.Spot(fun=fun,
                    fun_control=fun_control,
                    optimizer=shgo,
                    surrogate_control=surrogate_control)
spot_sh.run()
spot_sh.print_results()
spot_sh.plot_progress(log_y=True)
spot_sh.surrogate.plot()
```

```
spotpython tuning: 3.8004562736456844 [######----] 55.00%
spotpython tuning: 3.8004562736456844 [######----] 60.00%
spotpython tuning: 3.158996879015902 [######----] 65.00%
```

```
spotpython tuning: 3.1341298968229996 [#######---] 70.00%
spotpython tuning: 2.8919915800445954 [########--] 75.00%
spotpython tuning: 0.4173165753511867 [########--] 80.00%
spotpython tuning: 0.40097732409794773 [########--] 85.00%
spotpython tuning: 0.3993020098909934 [#########-] 90.00%
spotpython tuning: 0.3993020098909934 [##########] 95.00%
spotpython tuning: 0.3993020098909934 [##########] 100.00% Done...

min y: 0.3993020098909934
x0: 3.1510894339439672
x1: 2.298936853041466
```



4.5.4 basinhopping

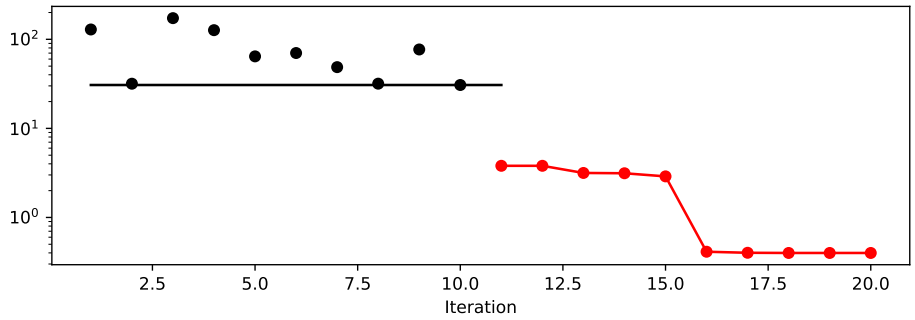
- Describe the optimization algorithm
- Use the algorithm as an optimizer on the surrogate

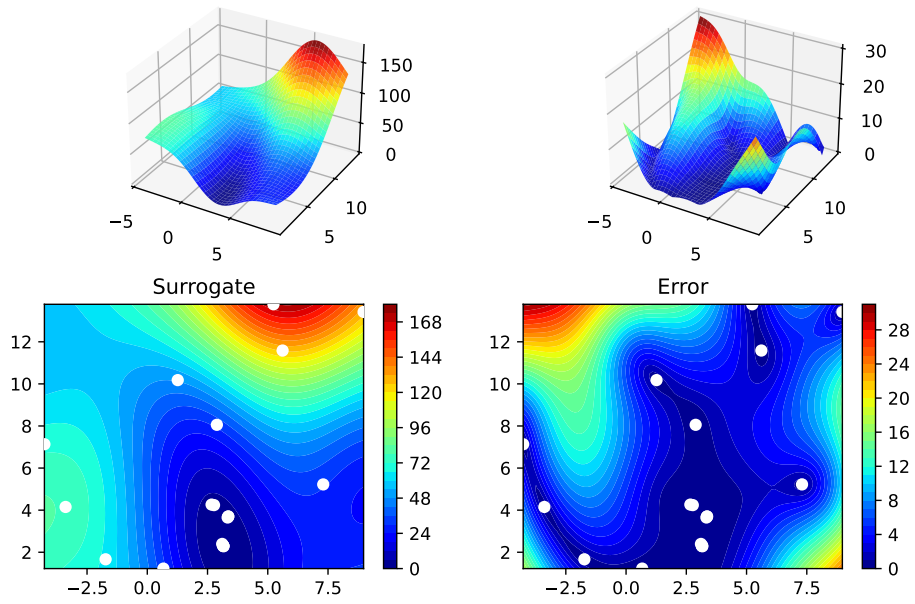
Tip: Selecting the Optimizer for the Surrogate

We can run spotpython with the `direct` optimizer as follows:

```
spot_bh = spot.Spot(fun=fun,
                    fun_control=fun_control,
                    optimizer=basinhopping,
                    surrogate_control=surrogate_control)
spot_bh.run()
spot_bh.print_results()
spot_bh.plot_progress(log_y=True)
spot_bh.surrogate.plot()
```

```
spotpython tuning: 3.800453600053931 [######----] 55.00%
spotpython tuning: 3.800453600053931 [######----] 60.00%
spotpython tuning: 3.1590141837294237 [######----] 65.00%
spotpython tuning: 3.1341341806066314 [#######---] 70.00%
spotpython tuning: 2.8914331943522242 [########--] 75.00%
spotpython tuning: 0.41214245125719984 [########--] 80.00%
spotpython tuning: 0.40113843843078634 [########--] 85.00%
spotpython tuning: 0.3992327747775164 [#########-] 90.00%
spotpython tuning: 0.3992327747775164 [##########] 95.00%
spotpython tuning: 0.3992327747775164 [##########] 100.00% Done...

min y: 0.3992327747775164
x0: 3.15016404734246
x1: 2.2998320162156896
```





4.5.5 Performance Comparison

Compare the performance and run time of the 5 different optimizers:

- `differential_evolution`
- `dual_annealing`
- `direct`
- `shgo`
- `basinhopping`.

The Branin function has three global minima:

- $f(x) = 0.397887$ at
  - $(-\pi, 12.275)$,
  - $(\pi, 2.275)$, and
  - $(9.42478, 2.475)$.

- Which optima are found by the optimizers?
- Does the `seed` argument in `fun = analytical(seed=123).fun_branin` change this behavior?

4.6 Jupyter Notebook

> **Note**
>
> - The Jupyter-Notebook of this chapter is available on GitHub in the Hyperparameter-Tuning-Cookbook Repository

Part II

Numerical Methods

5 Introduction: Numerical Methods

This part deals with numerical implementations of optimization methods. The goal is to understand the implementation of optimization methods and to solve real-world problems numerically and efficiently. We will focus on the implementation of surrogate models, because they are the most efficient way to solve real-world problems.

Starting point is the well-established response surface methodology. It will be extended to the design and analysis of computer experiments (DACE). The DACE methodology is a modern extension of the response surface methodology. It is based on the use of surrogate models, which are used to replace the real-world problem with a simpler problem. The simpler problem is then solved numerically. The solution of the simpler problem is then used to solve the real-world problem.

> ! Numerical methods: Goals
>
> - Understand implementation of optimization methods
> - Solve real-world problems numerically and efficiently

5.1 Response Surface Methods: What is RSM?

Response Surface Methods (RSM) refer to a collection of statistical and mathematical tools that are valuable for developing, improving, and optimizing processes. The overarching theme of RSM involves studying how input variables that control a product or process can potentially influence a response that measures performance or quality characteristics.

The advantages of RSM include a rich literature, well-established methods often used in manufacturing, the importance of careful experimental design combined with a well-understood model, and the potential to add significant value to scientific inquiry, process refinement, optimization, and more. However, there are also drawbacks to RSM, such as the use of simple and crude surrogates, the hands-on nature of the methods, and the limitation of local methods.

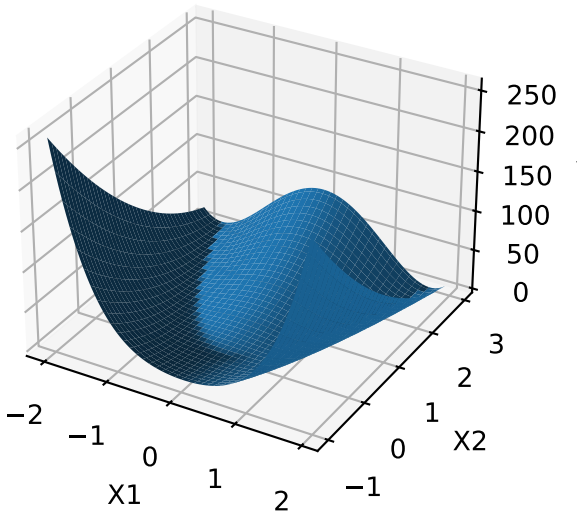
RSM is related to various fields, including Design of Experiments (DoE), quality management, reliability, and productivity. Its applications are widespread in industry and manufacturing, focusing on designing, developing, and formulating new products and

improving existing ones, as well as from laboratory research. RSM is commonly applied in domains such as materials science, manufacturing, applied chemistry, climate science, and many others.

An example of RSM involves studying the relationship between a response variable, such as yield (y) in a chemical process, and two process variables: reaction time (ξ_1) and reaction temperature (ξ_2). The provided code illustrates this scenario, following a variation of the so-called "banana function."

In the context of visualization, RSM offers the choice between 3D plots and contour plots. In a 3D plot, the independent variables ξ_1 and ξ_2 are represented, with y as the dependent variable.

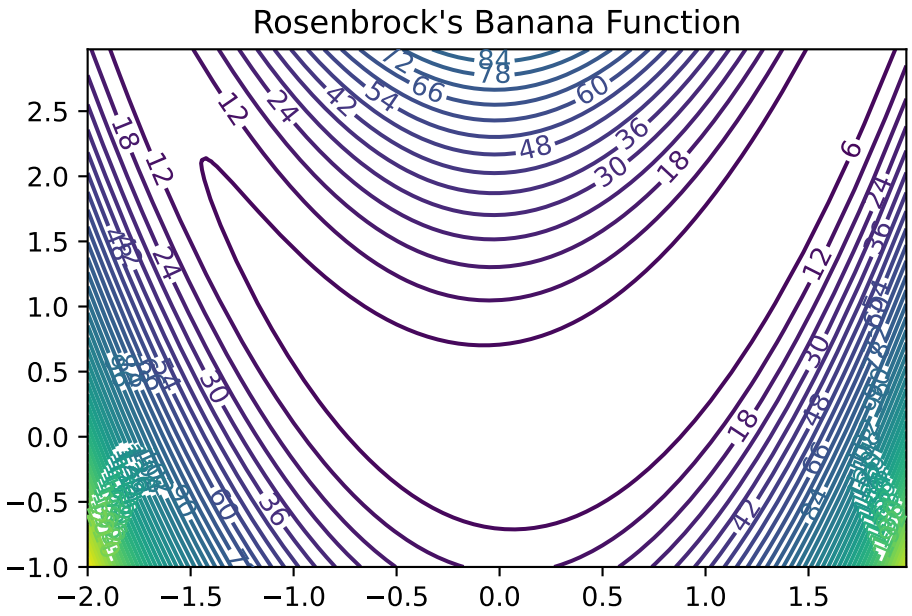
```
import numpy as np
import matplotlib.pyplot as plt

def fun_rosen(x1, x2):
    b = 10
    return (x1-1)**2 + b*(x2-x1**2)**2

fig = plt.figure()
ax = fig.add_subplot(111, projection='3d')
x = np.arange(-2.0, 2.0, 0.05)
y = np.arange(-1.0, 3.0, 0.05)
X, Y = np.meshgrid(x, y)
zs = np.array(fun_rosen(np.ravel(X), np.ravel(Y)))
Z = zs.reshape(X.shape)

ax.plot_surface(X, Y, Z)

ax.set_xlabel('X1')
ax.set_ylabel('X2')
ax.set_zlabel('Y')

plt.show()
```



- contour plot example:
  - x_1 and x_2 are the independent variables
  - y is the dependent variable

```
import numpy as np
import matplotlib.cm as cm
import matplotlib.pyplot as plt

delta = 0.025
x1 = np.arange(-2.0, 2.0, delta)
x2 = np.arange(-1.0, 3.0, delta)
X1, X2 = np.meshgrid(x1, x2)
Y = fun_rosen(X1, X2)
fig, ax = plt.subplots()
CS = ax.contour(X1, X2, Y , 50)
ax.clabel(CS, inline=True, fontsize=10)
ax.set_title("Rosenbrock's Banana Function")
```

```
Text(0.5, 1.0, "Rosenbrock's Banana Function")
```



- Visual inspection: yield is optimized near $(\xi_1.\xi_2)$

5.1.1 Visualization: Problems in Practice

- True response surface is unknown in practice
- When yield evaluation is not as simple as a toy banana function, but a process requiring care to monitor, reconfigure and run, it's far too expensive to observe over a dense grid
- And, measuring yield may be a noisy/inexact process
- That's where stats (RSM) comes in

5.1.2 RSM: Strategies

- RSMs consist of experimental strategies for
- **exploring** the space of the process (i.e., independent/input) variables (above ξ_1 and $\xi 2$)
- empirical statistical **modeling** targeted toward development of an appropriate approximating relationship between the response (yield) and process variables local to a study region of interest

- **optimization** methods for sequential refinement in search of the levels or values of process variables that produce desirable responses (e.g., that maximize yield or explain variation)
- RSM used for fitting an Empirical Model
- True response surface driven by an unknown physical mechanism
- Observations corrupted by noise
- Helpful: fit an empirical model to output collected under different process configurations
- Consider response Y that depends on controllable input variables $\xi_1, \xi_2, \ldots, \xi_m$
- RSM: Equations of the Empirical Model
  - $Y = f(\xi_1, \xi_2, \ldots, \xi_m) + \epsilon$
  - $\mathbb{E}\{Y\} = \eta = f(\xi 1_1, \xi_2, \ldots, \xi_m)$
  - ϵ is treated as zero mean idiosyncratic noise possibly representing
    - inherent variation, or
    - the effect of other systems or
    - variables not under our purview at this time

5.1.3 RSM: Noise in the Empirical Model

- Typical simplifying assumption: $\epsilon \sim N(0, \sigma^2)$
- We seek estimates for f and σ^2 from noisy observations Y at inputs ξ

5.1.4 RSM: Natural and Coded Variables

- Inputs $\xi_1, \xi_2, \ldots, \xi_m$ called **natural variables**:
  - expressed in natural units of measurement, e.g., degrees Celsius, pounds per square inch (psi), etc.
- Transformed to **coded variables** $x_1, x_2, \ldots, x_m$:
  - to mitigate hassles and confusion that can arise when working with a multitude of scales of measurement
- Typical **Transformations** offering dimensionless inputs $x_1, x_2, \ldots, x_m$
  - in the unit cube, or
  - scaled to have a mean of zero and standard deviation of one, are common choices.
- Empirical model becomes $\eta = f(x_1, x_2, \ldots, x_m)$

5.1.5 RSM Low-order Polynomials

- Low-order polynomial make the following simplifying Assumptions
  - Learning about f is lots easier if we make some simplifying approximations
  - Appealing to **Taylor's theorem**, a low-order polynomial in a small, localized region of the input (x) space is one way forward
  - Classical RSM:
    - disciplined application of **local analysis** and
    - **sequential refinement** of locality through conservative extrapolation
  - Inherently a **hands-on process**

5.2 First-Order Models (Main Effects Model)

- **First-order model** (sometimes called main effects model) useful in parts of the input space where it's believed that there's little curvature in f:

$$\eta = \beta_0 + \beta_1 x_1 + \beta_2 x_2$$

- For example:

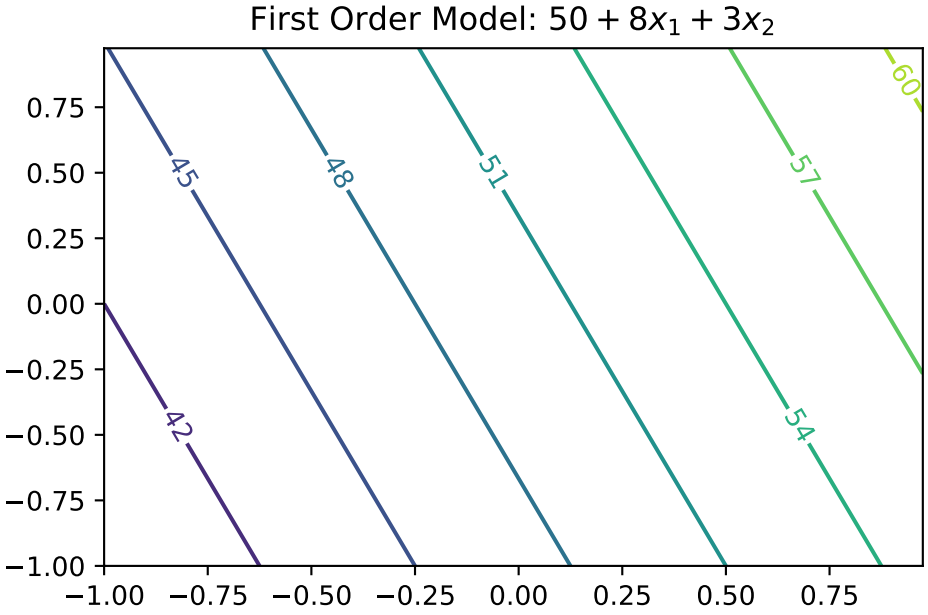
$$\eta = 50 + 8x_1 + 3x_2$$

- In practice, such a surface would be obtained by fitting a model to the outcome of a designed experiment
- First-Order Model in python Evaluated on a Grid
- Evaluate model on a grid in a double-unit square centered at the origin
- Coded units are chosen arbitrarily, although one can imagine deploying this approximating function nearby $x^{(0)} = (0, 0)$

```
def fun_1(x1,x2):
    return 50 + 8*x1 + 3*x2
```

```
import numpy as np
import matplotlib.cm as cm
import matplotlib.pyplot as plt

delta = 0.025
x1 = np.arange(-1.0, 1.0, delta)
x2 = np.arange(-1.0, 1.0, delta)
X1, X2 = np.meshgrid(x1, x2)
Y = fun_1(X1,X2)
fig, ax = plt.subplots()
CS = ax.contour(X1, X2, Y)
ax.clabel(CS, inline=True, fontsize=10)
ax.set_title('First Order Model: $50 + 8x_1 + 3x_2$')
```

```
Text(0.5, 1.0, 'First Order Model: $50 + 8x_1 + 3x_2$')
```



5.2.1 First-Order Model Properties

- First-order model in 2d traces out a **plane** in $y \times (x_1, x_2)$ space
- Only be appropriate for the most trivial of response surfaces, even when applied in a highly localized part of the input space
- Adding **curvature** is key to most applications:
  - First-order model with **interactions** induces limited degree of curvature via different rates of change of y as x_1 is varied for fixed x_2, and vice versa:

$$\eta = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_{12} x_{12}$$

- For example $\eta = 50 + 8x_1 + 3x_2 - 4x_1 x_2$

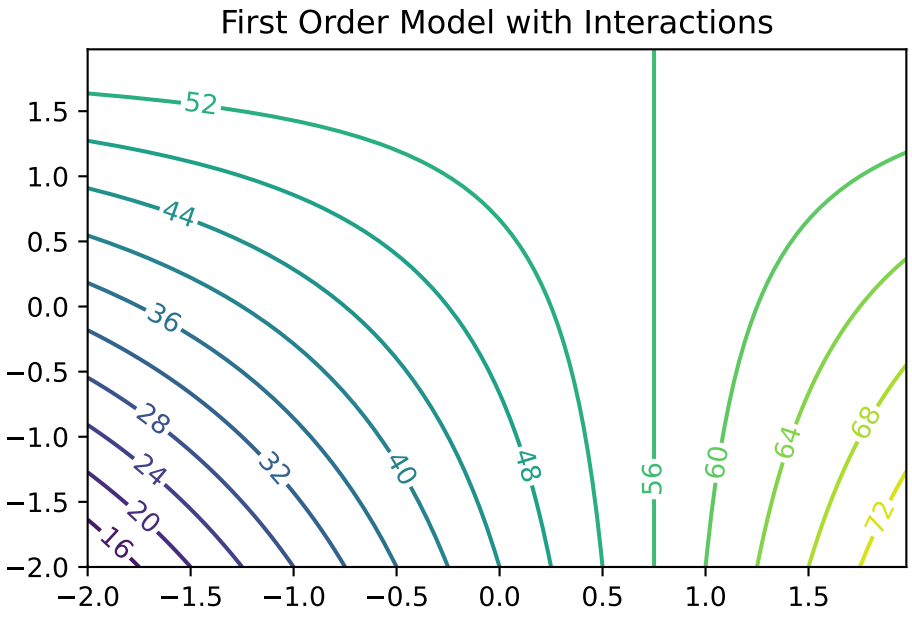
5.2.2 First-order Model with Interactions in python

- Code below facilitates evaluations for pairs (x_1, x_2)
- Responses may be observed over a mesh in the same double-unit square

```
def fun_11(x1,x2):
    return 50 + 8 * x1 + 3 * x2 - 4 * x1 * x2
```

```
import numpy as np
import matplotlib.cm as cm
import matplotlib.pyplot as plt

delta = 0.025
x1 = np.arange(-2.0, 2.0, delta)
x2 = np.arange(-2.0, 2.0, delta)
X1, X2 = np.meshgrid(x1, x2)
Y = fun_11(X1,X2)
fig, ax = plt.subplots()
CS = ax.contour(X1, X2, Y, 20)
ax.clabel(CS, inline=True, fontsize=10)
ax.set_title('First Order Model with Interactions')
```

```
Text(0.5, 1.0, 'First Order Model with Interactions')
```



5.2.3 Observations: First-Order Model with Interactions

- Mean response η is increasing marginally in both x_1 and x_2, or conditional on a fixed value of the other until x_1 is 0.75
- Rate of increase slows as both coordinates grow simultaneously since the coefficient in front of the interaction term x_1x_2 is negative
- Compared to the first-order model (without interactions): surface is far more useful locally
- Least squares regressions often flag up significant interactions when fit to data collected on a design far from local optima

5.3 Second-Order Models

- Second-order model may be appropriate near local optima where f would have substantial curvature:

$$\eta = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_{11} x_1^2 + \beta_{22} x^2 + \beta_{12} x_1 x_2$$

- For example

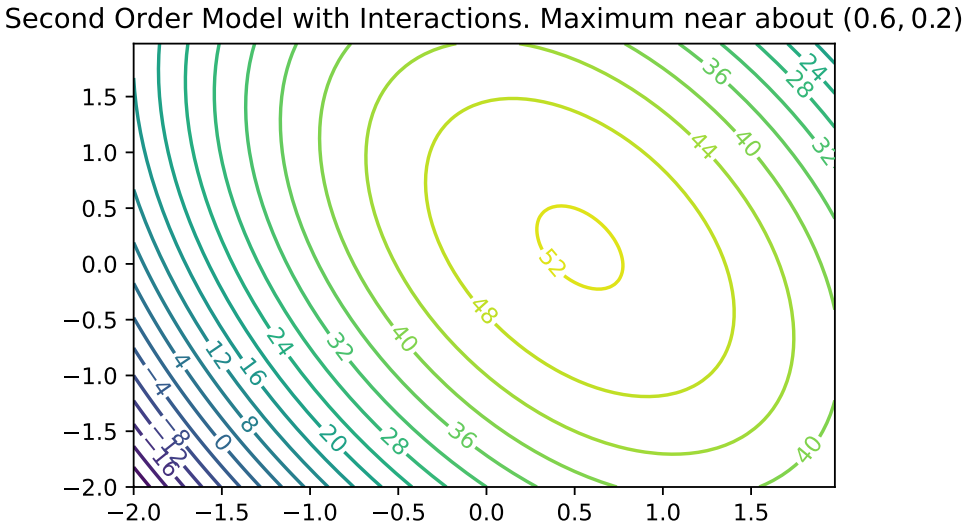
$$\eta = 50 + 8x_1 + 3x_2 - 7x_1^2 - 3x_2^2 - 4x_1 x_2$$

- Implementation of the Second-Order Model as `fun_2()`.

```
def fun_2(x1,x2):
    return 50 + 8 * x1 + 3 * x2 - 7 * x1**2 - 3*x2**2 - 4 * x1 * x2
```

```
import numpy as np
import matplotlib.cm as cm
import matplotlib.pyplot as plt

delta = 0.025
x1 = np.arange(-2.0, 2.0, delta)
x2 = np.arange(-2.0, 2.0, delta)
X1, X2 = np.meshgrid(x1, x2)
Y = fun_2(X1,X2)
fig, ax = plt.subplots()
CS = ax.contour(X1, X2, Y, 20)
ax.clabel(CS, inline=True, fontsize=10)
ax.set_title('Second Order Model with Interactions. Maximum near about $(0.6,0.2)$')
```

```
Text(0.5, 1.0, 'Second Order Model with Interactions. Maximum near about $(0.6,0.2)$')
```



5.3.1 Second-Order Models: Properties

- Not all second-order models would have a single stationary point (in RSM jargon called "a simple maximum")
- In "yield maximizing" setting we're presuming response surface is **concave** down from a global viewpoint
  - even though local dynamics may be more nuanced
- Exact criteria depend upon the eigenvalues of a certain matrix built from those coefficients
- Box and Draper (2007) provide a diagram categorizing all of the kinds of second-order surfaces in RSM analysis, where finding local maxima is the goal

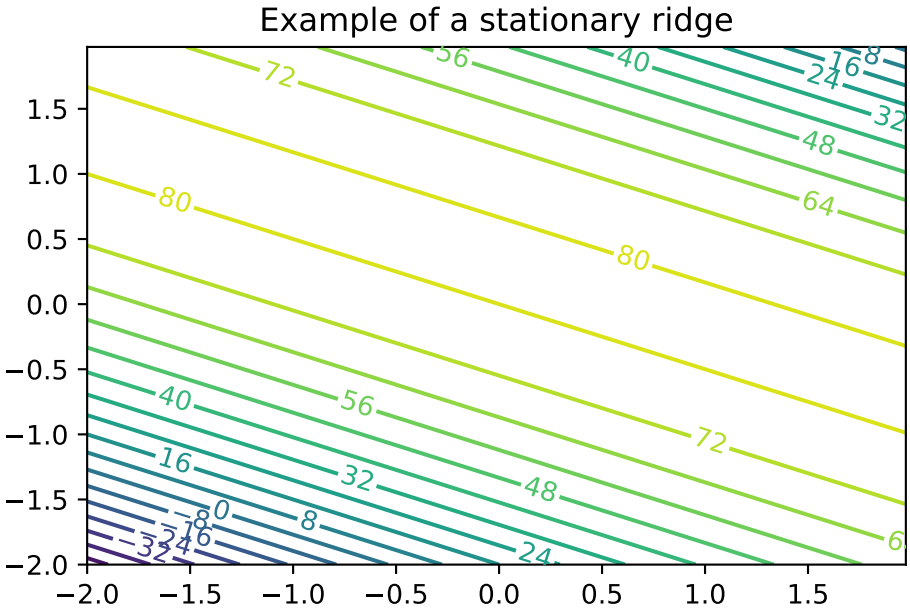
5.3.2 Example: Stationary Ridge

- Example set of coefficients describing what's called a **stationary ridge** is provided by the code below

```
def fun_ridge(x1, x2):
    return 80 + 4*x1 + 8*x2 - 3*x1**2 - 12*x2**2 - 12*x1*x2
```

```
import numpy as np
import matplotlib.cm as cm
import matplotlib.pyplot as plt

delta = 0.025
x1 = np.arange(-2.0, 2.0, delta)
x2 = np.arange(-2.0, 2.0, delta)
X1, X2 = np.meshgrid(x1, x2)
Y = fun_ridge(X1,X2)
fig, ax = plt.subplots()
CS = ax.contour(X1, X2, Y, 20)
ax.clabel(CS, inline=True, fontsize=10)
ax.set_title('Example of a stationary ridge')
```

```
Text(0.5, 1.0, 'Example of a stationary ridge')
```



5.3.3 Observations: Second-Order Model (Ridge)

- **Ridge**: a whole line of stationary points corresponding to maxima
- Situation means that the practitioner has some flexibility when it comes to optimizing:

– can choose the precise setting of (x_1, x_2) either arbitrarily or (more commonly) by consulting some tertiary criteria

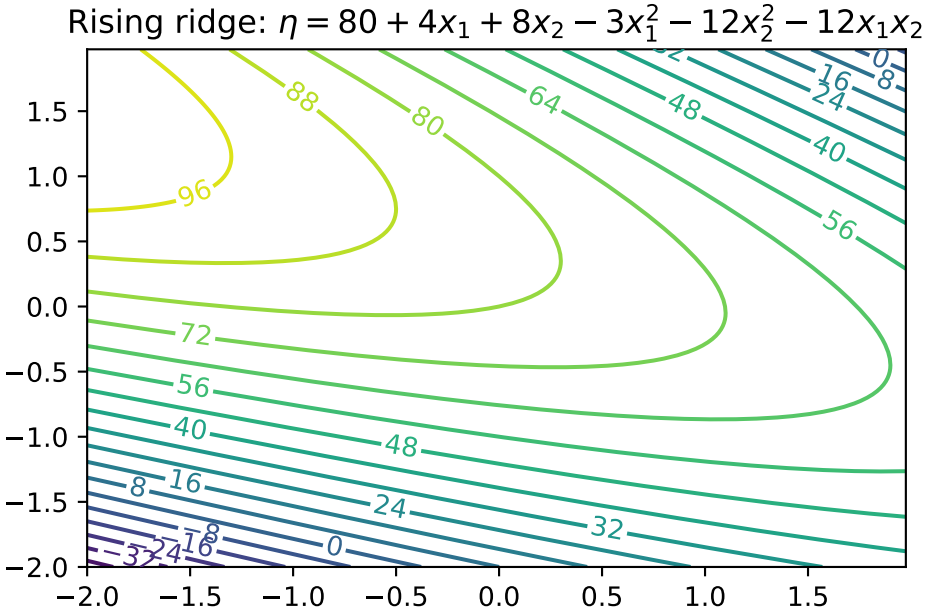
5.3.4 Example: Rising Ridge

- An example of a rising ridge is implemented by the code below.

```
def fun_ridge_rise(x1, x2):
     return 80 - 4*x1 + 12*x2 - 3*x1**2 - 12*x2**2 - 12*x1*x2
```

```
import numpy as np
import matplotlib.cm as cm
import matplotlib.pyplot as plt

delta = 0.025
x1 = np.arange(-2.0, 2.0, delta)
x2 = np.arange(-2.0, 2.0, delta)
X1, X2 = np.meshgrid(x1, x2)
Y = fun_ridge_rise(X1,X2)
fig, ax = plt.subplots()
CS = ax.contour(X1, X2, Y, 20)
ax.clabel(CS, inline=True, fontsize=10)
ax.set_title('Rising ridge: $\\eta = 80 + 4x_1 + 8x_2 - 3x_1^2 - 12x_2^2 - 12x_1x_2$')
```

```
Text(0.5, 1.0, 'Rising ridge: $\\eta = 80 + 4x_1 + 8x_2 - 3x_1^2 - 12x_2^2 - 12x_1x_2$')
```



5.3.5 Summary: Rising Ridge

- The stationary point is remote to the study region
- Ccontinuum of (local) stationary points along any line going through the 2d space, excepting one that lies directly on the ridge
- Although estimated response will increase while moving along the axis of symmetry toward its stationary point, this situation indicates
  - either a poor fit by the approximating second-order function, or
  - that the study region is not yet precisely in the vicinity of a local optima—often both.

5.3.6 Falling Ridge

- Inversion of a rising ridge is a falling ridge
- Similarly indicating one is far from local optima, except that the response decreases as you move toward the stationary point
- Finding a falling ridge system can be a back-to-the-drawing-board affair.

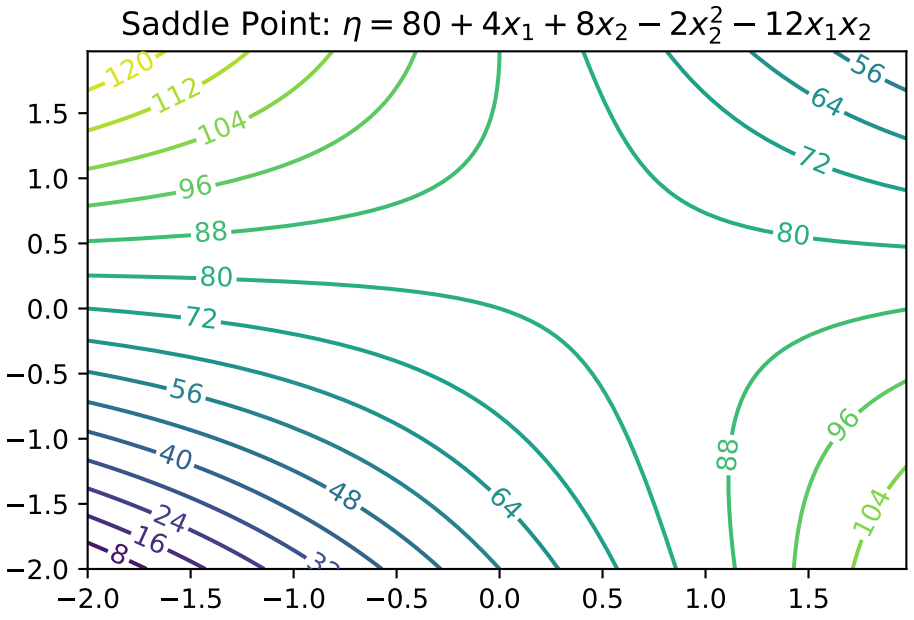
5.3.7 Saddle Point

- Finally, we can get what's called a saddle or minimax system.

```
def fun_saddle(x1, x2):
    return 80 + 4*x1 + 8*x2 - 2*x2**2 - 12*x1*x2
```

```
import numpy as np
import matplotlib.cm as cm
import matplotlib.pyplot as plt

delta = 0.025
x1 = np.arange(-2.0, 2.0, delta)
x2 = np.arange(-2.0, 2.0, delta)
X1, X2 = np.meshgrid(x1, x2)
Y = fun_saddle(X1,X2)
fig, ax = plt.subplots()
CS = ax.contour(X1, X2, Y, 20)
ax.clabel(CS, inline=True, fontsize=10)
ax.set_title('Saddle Point: $\\eta = 80 + 4x_1 + 8x_2 - 2x_2^2 - 12x_1x_2$')
```

```
Text(0.5, 1.0, 'Saddle Point: $\\eta = 80 + 4x_1 + 8x_2 - 2x_2^2 - 12x_1x_2$')
```



5.3.8 Interpretation: Saddle Points

- Likely further data collection, and/or outside expertise, is needed before determining a course of action in this situation

5.3.9 Summary: Ridge Analysis

- Finding a simple maximum, or stationary ridge, represents ideals in the spectrum of second-order approximating functions
- But getting there can be a bit of a slog
- Using models fitted from data means uncertainty due to noise, and therefore uncertainty in the type of fitted second-order model
- A ridge analysis attempts to offer a principled approach to navigating uncertainties when one is seeking local maxima
- The two-dimensional setting exemplified above is convenient for visualization, but rare in practice
- Complications compound when studying the effect of more than two process variables

5.4 General RSM Models

- General **first-order model** on m process variables $x_1, x_2, \cdots, x_m$ is

$$\eta = \beta_0 + \beta_1 x_1 + \cdots + \beta_m x_m$$

- General **second-order model** on m process variables

$$\eta = \beta_0 + \sum_{j=1}^{m} + \sum_{j=1}^{m} x_j^2 + \sum_{j=2}^{m} \sum_{k=1}^{j} \beta_{kj} x_k x_j.$$

5.4.1 Ordinary Least Squares

- Inference from data is carried out by **ordinary least squares** (OLS)
- For an excellent review including R examples, see Sheather (2009)
- OLS and maximum likelihood estimators (MLEs) are in the typical Gaussian linear modeling setup basically equivalent

5.5 Designs

- Important: Organize the data collection phase of a response surface study carefully
- **Design**: choice of x's where we plan to observe y's, for the purpose of approximating f
- Analyses and designs need to be carefully matched
- When using a first-order model, some designs are preferred over others
- When using a second-order model to capture curvature, a different sort of design is appropriate
- Design choices often contain features enabling modeling assumptions to be challenged
  - e.g., to check if initial impressions are supported by the data ultimately collected

5.5.1 Different Designs

- **Screening desings**: determine which variables matter so that subsequent experiments may be smaller and/or more focused
- Then there are designs tailored to the form of model (first- or second-order, say) in the screened variables
- And then there are more designs still

5.6 RSM Experimentation

5.6.1 First Step

- RSM-based experimentation begins with a **first-order model**, possibly with interactions
- Presumption: current process operating **far from optimal** conditions
- Collect data and apply **method of steepest ascent** (gradient) on fitted surfaces to move to the optimum

5.6.2 Second Step

- Eventually, if all goes well after several such carefully iterated refinements, **second-order models** are used on appropriate designs in order to zero-in on ideal operating conditions
- Careful analysis of the fitted surface:
  - Ridge analysis with further refinement using gradients of, and

  - standard errors associated with, the fitted surfaces, and so on

5.6.3 Third Step

- Once the practitioner is satisfied with the full arc of
  - design(s),
  - fit(s), and
  - decision(s):
- A small experiment called **confirmation test** may be performed to check if the predicted optimal settings are realizable in practice

5.7 RSM: Review and General Considerations

- First Glimpse, RSM seems sensible, and pretty straightforward as quantitative statistics-based analysis goes
- But: RSM can get complicated, especially when input dimensions are not very low
- Design considerations are particularly nuanced, since the goal is to obtain reliable estimates of main effects, interaction, and curvature while minimizing sampling effort/expense
- RSM Downside: Inefficiency
  - Despite intuitive appeal, several RSM downsides become apparent upon reflection
  - Problems in practice
  - Stepwise nature of sequential decision making is inefficient:
    * Not obvious how to re-use or update analysis from earlier phases, or couple with data from other sources/related experiments
- RSM Downside: Locality
  - In addition to being local in experiment-time (stepwise approach), it's local in experiment-space
  - Balance between
    * exploration (maybe we're barking up the wrong tree) and
    * exploitation (let's make things a little better) is modest at best
- RSM Downside: Expert Knowledge

  - Interjection of expert knowledge is limited to hunches about relevant variables (i.e., the screening phase), where to initialize search, how to design the experiments
  - Yet at the same time classical RSMs rely heavily on constant examination throughout stages of modeling and design and on the instincts of seasoned practitioners

- RSM Downside: Replicability

  - Parallel analyses, conducted according to the same best intentions, rarely lead to the same designs, model fits and so on
  - Sometimes that means they lead to different conclusions, which can be cause for concern

5.7.1 Historical Considerations about RSM

- In spite of those criticisms, however, there was historically little impetus to revise the status quo
- Classical RSM was comfortable in its skin, consistently led to improvements or compelling evidence that none can reasonably be expected
- But then in the late 20th century came an explosive expansion in computational capability, and with it a means of addressing many of those downsides

5.7.2 Status Quo

- Nowadays, field experiments and statistical models, designs and optimizations are coupled with with mathematical models
- Simple equations are not regarded as sufficient to describe real-world systems anymore
- Physicists figured that out fifty years ago; industrial engineers followed, biologists, social scientists, climate scientists and weather forecasters, etc.
- Systems of equations are required, solved over meshes (e.g., finite elements), or stochastically interacting agents
- Goals for those simulation experiments are as diverse as their underlying dynamics
- Optimization of systems is common, e.g., to identify worst-case scenarios

5.7.3 The Role of Statistics

- Solving systems of equations, or interacting agents, requires computing
- Statistics involved at various stages:

  - choosing the mathematical model

  - solving by stochastic simulation (Monte Carlo)
  - designing the computer experiment
  - smoothing over idiosyncrasies or noise
  - finding optimal conditions, or
  - calibrating mathematical/computer models to data from field experiments

5.7.4 New RSM is needed: DACE

- Classical RSMs are not well-suited to any of those tasks, because
  - they lack the fidelity required to model these data
  - their intended application is too local
  - they're also too hands-on.
- Once computers are involved, a natural inclination is to automate—to remove humans from the loop and set the computer running on the analysis in order to maximize computing throughput, or minimize idle time
- **Design and Analysis of Computer Experiments** as a modern extension of RSM
- Experimentation is changing due to advances in machine learning
- **Gaussian process** (GP) regression is the canonical surrogate model
- Origins in geostatistics (gold mining)
- Wide applicability in contexts where prediction is king
- Machine learners exposed GPs as powerful predictors for all sorts of tasks:
- from regression to classification,
- active learning/sequential design,
- reinforcement learning and optimization,
- latent variable modeling, and so on

5.8 Exercises

1. Generate 3d Plots for the Contour Plots in this notebook.
2. Write a `plot_3d` function, that takes the objective function `fun` as an argument.

- It should provide the following interface: `plot_3d(fun)`.

3. Write a `plot_contour` function, that takes the objective function `fun` as an argument:

- It should provide the following interface: `plot_contour(fun)`.

4. Consider further arguments that might be useful for both function, e.g., ranges, size, etc.

5.9 Jupyter Notebook

> **Note**
>
> - The Jupyter-Notebook of this lecture is available on GitHub in the Hyperparameter-Tuning-Cookbook Repository

6 Kriging (Gaussian Process Regression)

6.1 DACE and RSM

Mathematical models implemented in computer codes are used to circumvent the need for expensive field data collection. These models are particularly useful when dealing with highly nonlinear response surfaces, high signal-to-noise ratios (which often involve deterministic evaluations), and a global scope. As a result, a new approach is required in comparison to Response Surface Methodology (RSM), which was discussed in Section **??**.

With the improvement in computing power and simulation fidelity, researchers gain higher confidence and a better understanding of the dynamics in physical, biological, and social systems. However, the expansion of configuration spaces and increasing input dimensions necessitates more extensive designs. High-performance computing (HPC) allows for thousands of runs, whereas previously only tens were possible. This shift towards larger models and training data presents new computational challenges.

Research questions for DACE (Design and Analysis of Computer Experiments) include how to design computer experiments that make efficient use of computation and how to meta-model computer codes to save on simulation effort. The choice of surrogate model for computer codes significantly impacts the optimal experiment design, and the preferred model-design pairs can vary depending on the specific goal.

The combination of computer simulation, design, and modeling with field data from similar real-world experiments introduces a new category of computer model tuning problems. The ultimate goal is to automate these processes to the greatest extent possible, allowing for the deployment of HPC with minimal human intervention.

One of the remaining differences between RSM and DACE lies in how they handle noise. DACE employs replication, a technique that would not be used in a deterministic setting, to separate signal from noise. Traditional RSM is best suited for situations where a substantial proportion of the variability in the data is due to noise, and where the acquisition of data values can be severely limited. Consequently, RSM is better suited for a different class of problems, aligning with its intended purposes.

Two very good texts on computer experiments and surrogate modeling are Santner, Williams, and Notz (2003) and Forrester, Sóbester, and Keane (2008). The former

is the canonical reference in the statistics literature and the latter is perhaps more popular in engineering.

Example 6.1 (Example: DACE and RSM)**.** Imagine you are a chemical engineer tasked with optimizing a chemical process to maximize yield. You can control temperature and pressure, but repeated experiments show variability in yield due to inconsistencies in raw materials.

- Using RSM: You would use RSM to design a series of experiments varying temperature and pressure. You would then fit a response surface (a mathematical model) to the data, helping you understand how changes in temperature and pressure affect yield. Using this model, you can identify optimal conditions for maximizing yield despite the noise.
- Using DACE: If instead you use a computational model to simulate the chemical process and want to account for numerical noise or uncertainty in model parameters, you might use DACE. You would run simulations at different conditions, possibly repeating them to assess variability and build a surrogate model that accurately predicts yields, which can be optimized to find the best conditions.

6.1.1 Noise Handling in RSM and DACE

Noise in RSM: In experimental settings, noise often arises due to variability in experimental conditions, measurement errors, or other uncontrollable factors. This noise can significantly affect the response variable, Y. Replication is a standard procedure for handling noise in RSM. In the context of computer experiments, noise might not be present in the traditional sense since simulations can be deterministic. However, variability can arise from uncertainty in input parameters or model inaccuracies. DACE predominantly utilizes advanced interpolation to construct accurate models of deterministic data, sometimes considering statistical noise modeling if needed.

6.2 Background: Expectation, Mean, Standard Deviation

The distribution of a random vector is characterized by some indexes. These are the expectation, the mean, and the standard deviation. The expectation is a measure of the central tendency of a random variable, while the standard deviation quantifies the spread of the distribution. These indexes are essential for understanding the behavior of random variables and making predictions based on them.

Definition 6.1 (Random Variable)**.** A random variable X is a mapping from the sample space of a random experiment to the real numbers. It assigns a numerical value to each outcome of the experiment. Random variables can be either:

- Discrete: If X takes on a countable number of distinct values.
- Continuous: If X takes on an uncountable number of values.

Mathematically, a random variable is a function $X : \Omega \to \mathbb{R}$, where Ω is the sample space.

Definition 6.2 (Probability Distribution)**.** A probability distribution describes how the values of a random variable are distributed. It is characterized for a discrete random variable X by the probability mass function (PMF) $p_X(x)$ and for a continuous random variable X by the probability density function (PDF) $f_X(x)$.

Definition 6.3 (Probability Mass Function (PMF))**.** $p_X(x) = P(X = x)$ gives the probability that X takes the value x.

Definition 6.4 (Probability Density Function (PDF):)**.** $f_X(x)$ is a function such that for any interval $[a, b]$, the probability that X falls within this interval is given by the integral $\int_a^b f_X(x)\mathrm{d}x$.

The distribution function must satisfy:

$$\sum_{x \in D_X} p_X(x) = 1$$

for discrete random variables, where D_X is the domain of X and

$$\int_{-\infty}^{\infty} f_X(x)\mathrm{d}x = 1$$

for continuous random variables.

With these definitions in place, we can now introduce the definition of the expectation, which is a fundamental measure of the central tendency of a random variable.

Definition 6.5 (Expectation)**.** The expectation or expected value of a random variable X, denoted $E[X]$, is defined as follows:

For a discrete random variable X:

$$E[X] = \sum_{x \in D_X} x p_X(x) \quad \text{if } X \text{ is discrete.}$$

For a continuous random variable X:

$$E[X] = \int_{x \in D_X} x f_X(x)\mathrm{d}x \quad \text{if } X \text{ is continuous.}$$

The mean, μ, of a probability distribution is a measure of its central tendency or location. That is, $E(X)$ is defined as the average of all possible values of X, weighted by their probabilities.

Example 6.2 (Expectation)**.** Let X denote the number produced by rolling a fair die. Then

$$E(X) = 1 \times 1/6 + 2 \times 1/6 + 3 \times 1/6 + 4 \times 1/6 + 5 \times 1/6 + 6 \times 1/6 = 3.5.$$

Definition 6.6 (Sample Mean)**.** The sample mean is an important estimate of the population mean. The sample mean of a sample $\{x_i\}$ $(i = 1, 2, ..., n)$ is defined as

$$\overline{x} = \frac{1}{n} \sum_i x_i.$$

While both the expectation of a random variable and the sample mean provide measures of central tendency, they differ in their context, calculation, and interpretation.

- The expectation is a theoretical measure that characterizes the average value of a random variable over an infinite number of repetitions of an experiment. The expectation is calculated using a probability distribution and provides a parameter of the entire population or distribution. It reflects the long-term average or central value of the outcomes generated by the random process.
- The sample mean is a statistic. It provides an estimate of the population mean based on a finite sample of data. It is computed directly from the data sample, and its value can vary between different samples from the same population. It serves as an approximation or estimate of the population mean. It is used in statistical inference to make conclusions about the population mean based on sample data.

If we are trying to predict the value of a random variable X by its mean $\mu = E(X)$, the error will be $X - \mu$. In many situations it is useful to have an idea how large this deviation or error is. Since $E(X - \mu) = E(X) - \mu = 0$, it is necessary to use the absolute value or the square of $(X - \mu)$. The squared error is the first choice, because the derivatives are easier to calculate. These considerations motivate the definition of the variance:

Definition 6.7 (Variance)**.** The variance of a random variable X is the mean squared deviation of X from its expected value $\mu = E(X)$.

$$Var(X) = E[(X - \mu)^2]. \tag{6.1}$$

The variance is a measure of the spread of a distribution. It quantifies how much the values of a random variable differ from the mean. A high variance indicates that the values are spread out over a wide range, while a low variance indicates that the values are clustered closely around the mean.

Definition 6.8 (Standard Deviation)**.** Taking the square root of the variance to get back to the same scale of units as X gives the standard deviation. The standard deviation of X is the square root of the variance of X.

$$sd(X) = \sqrt{Var(X)}. \tag{6.2}$$

6.2.1 Calculation of the Standard Deviation with Python

The function `numpy.std` returns the standard deviation, a measure of the spread of a distribution, of the array elements. The argument `ddof` specifies the Delta Degrees of Freedom. The divisor used in calculations is `N - ddof`, where `N` represents the number of elements. By default `ddof` is zero, i.e., `std` uses the formula

$$\sqrt{\frac{1}{N}\sum_i (x_i - \bar{x})^2} \qquad \text{with} \qquad \bar{x} = \sum_{i=1}^{N} x_i/N.$$

Example 6.3 (Standard Deviation with Python)**.** Consider the array $[1, 2, 3]$: Since $\bar{x} = 2$, the following value is computed:

$$\sqrt{1/3 \times ((1-2)^2 + (2-2)^2 + (3-2)^2)} = \sqrt{2/3}.$$

```
import numpy as np
a = np.array([[1, 2, 3]])
np.std(a)
```

```
0.816496580927726
```

The empirical standard deviation (which uses $N-1$), $\sqrt{1/2 \times ((1-2)^2 + (2-2)^2 + (3-2)^2)} = \sqrt{2/2}$, can be calculated in Python as follows:

```
np.std(a, ddof=1)
```

```
1.0
```

6.2.2 The Argument "axis"

When you compute `np.std` with `axis=0`, it calculates the standard deviation along the vertical axis, meaning it computes the standard deviation for each column of the array. On the other hand, when you compute `np.std` with `axis=1`, it calculates the standard deviation along the horizontal axis, meaning it computes the standard deviation for each row of the array. If the axis parameter is not specified, `np.std` computes the standard deviation of the flattened array, i.e., it calculates the standard deviation of all the elements in the array.

Example 6.4 (Axes along which the standard deviation is computed)**.**

```
A = np.array([[1, 2], [3, 4]])
A
```

```
array([[1, 2],
       [3, 4]])
```

First, we calculate the standard deviation of all elements in the array:

```
np.std(A)
```

```
1.1180339887498895
```

Setting `axis=0` calculates the standard deviation along the vertical axis (column-wise):

```
np.std(A, axis=0)
```

```
array([1., 1.])
```

Finally, setting `axis=1` calculates the standard deviation along the horizontal axis (row-wise):

```
np.std(A, axis=1)
```

```
array([0.5, 0.5])
```

6.3 Data Types and Precision in Python

The float16 data type in numpy represents a half-precision floating point number. It uses 16 bits of memory, which gives it a precision of about 3 decimal digits.

The float32 data type in numpy represents a single-precision floating point number. It uses 32 bits of memory, which gives it a precision of about 7 decimal digits. On the other hand, float64 represents a double-precision floating point number. It uses 64 bits of memory, which gives it a precision of about 15 decimal digits.

The reason float16 and float32 show fewer digits is because it has less precision due to using less memory. The bits of memory are used to store the sign, exponent, and fraction parts of the floating point number, and with fewer bits, you can represent fewer digits accurately.

Example 6.5 (16 versus 32 versus 64 bit)**.**

```
import numpy as np

# Define a number
num = 0.123456789123456789

num_float16 = np.float16(num)
num_float32 = np.float32(num)
num_float64 = np.float64(num)

print("float16: ", num_float16)
print("float32: ", num_float32)
print("float64: ", num_float64)
```

```
float16:  0.1235
float32:  0.12345679
float64:  0.12345678912345678
```

6.4 Distributions and Random Numbers in Python

Results from computers are deterministic, so it sounds like a contradiction in terms to generate random numbers on a computer. Standard computers generate pseudo-randomnumbers, i.e., numbers that behave as if they were drawn randomly.

> **i** Deterministic Random Numbers
>
> - Idea: Generate deterministically numbers that **look** (behave) as if they were drawn randomly.

6.4.1 The Uniform Distribution

Definition 6.9 (The Uniform Distribution)**.** The probability density function of the uniform distribution is defined as:

$$f_X(x) = \frac{1}{b-a} \qquad \text{for } x \in [a, b].$$

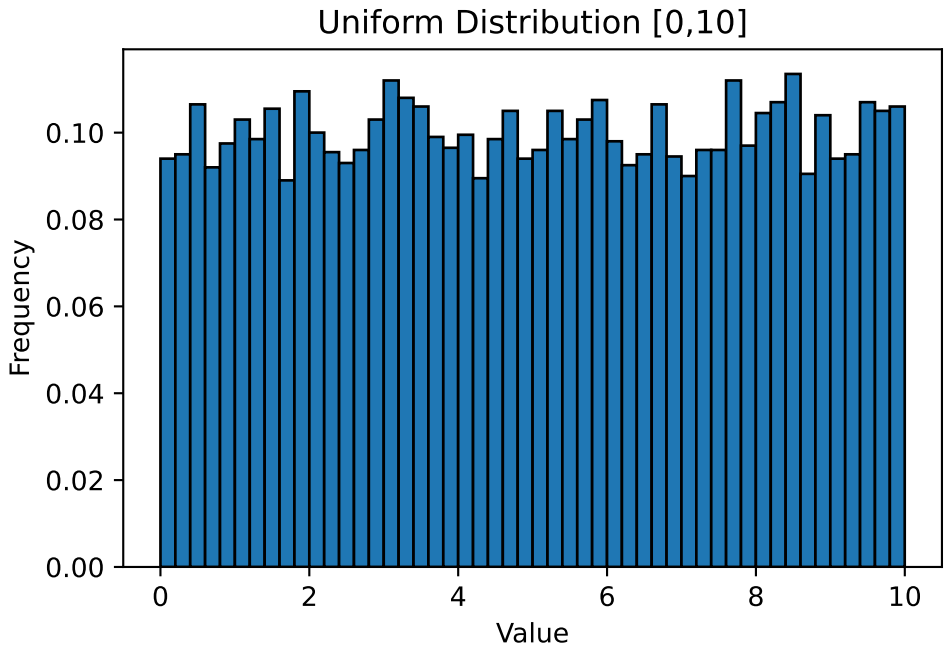
Generate 10 random numbers from a uniform distribution between $a = 0$ and $b = 1$:

```
import numpy as np
# Initialize the random number generator
rng = np.random.default_rng(seed=123456789)
n = 10
x = rng.uniform(low=0.0, high=1.0, size=n)
x
```

```
array([0.02771274, 0.90670006, 0.88139355, 0.62489728, 0.79071481,
       0.82590801, 0.84170584, 0.47172795, 0.95722878, 0.94659153])
```

Generate 10,000 random numbers from a uniform distribution between 0 and 10 and plot a histogram of the numbers:

```
import numpy as np
import matplotlib.pyplot as plt

# Initialize the random number generator
rng = np.random.default_rng(seed=123456789)

# Generate random numbers from a uniform distribution
x = rng.uniform(low=0, high=10, size=10000)

# Plot a histogram of the numbers
plt.hist(x, bins=50, density=True, edgecolor='black')
plt.title('Uniform Distribution [0,10]')
plt.xlabel('Value')
plt.ylabel('Frequency')
plt.show()
```



6.4.2 The Normal Distribution

A normally distributed random variable is a random variable whose associated probability distribution is the normal (or Gaussian) distribution. The normal distribution is a continuous probability distribution characterized by a symmetric bell-shaped curve.

The distribution is defined by two parameters: the mean μ and the standard deviation σ. The mean indicates the center of the distribution, while the standard deviation measures the spread or dispersion of the distribution.

This distribution is widely used in statistics and the natural and social sciences as a simple model for random variables with unknown distributions.

Definition 6.10 (The Normal Distribution)**.** The probability density function of the normal distribution is defined as:

$$f_X(x) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{1}{2}\left(\frac{x-\mu}{\sigma}\right)^2\right), \tag{6.3}$$

where: μ is the mean; σ is the standard deviation.

To generate ten random numbers from a normal distribution, the following command can be used.

```
import numpy as np
rng = np.random.default_rng()
n = 10
mu, sigma = 2, 0.1
x = rng.normal(mu, sigma, n)
x
```

```
array([2.05096474, 1.88443323, 1.77796221, 2.09220806, 2.14259863,
       2.07164316, 2.09841223, 1.88488905, 1.93211818, 1.96653543])
```

Verify the mean:

```
abs(mu - np.mean(x))
```

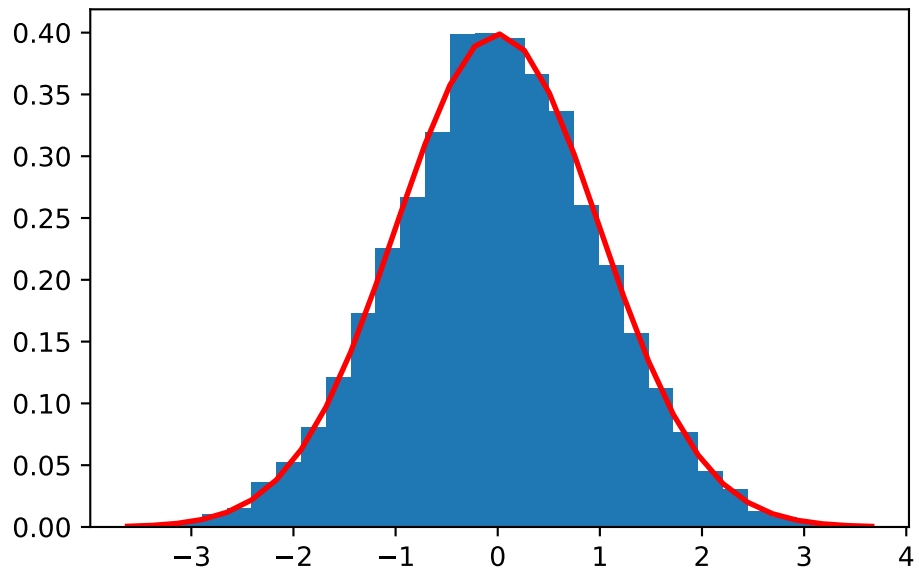
```
0.009823507167880496
```

Note: To verify the standard deviation, we use `ddof = 1` (empirical standard deviation):

```
abs(sigma - np.std(x, ddof=1))
```

```
0.018753528024255325
```

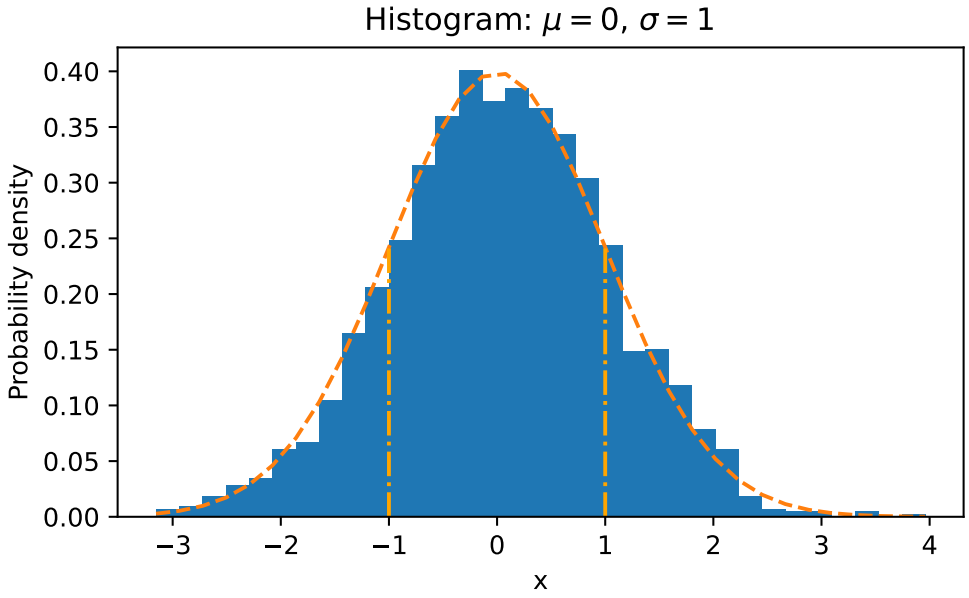
```
plot_normal_distribution(mu=0, sigma=1, num_samples=10000)
```



6.4.3 Visualization of the Standard Deviation

The standard deviation of normal distributed can be visualized in terms of the histogram of X:

- about 68% of the values will lie in the interval within one standard deviation of the mean
- 95% lie within two standard deviation of the mean
- and 99.9% lie within 3 standard deviations of the mean.



6.4.4 Standardization of Random Variables

To compare statistical properties of random variables which use different units, it is a common practice to transform these random variables into standardized variables.

Definition 6.11 (Standard Units)**.** If a random variable X has expectation $E(X) = \mu$ and standard deviation $sd(X) = \sigma > 0$, the random variable

$$X^* = (X - \mu)/\sigma$$

is called X in standard units. It has $E(X^*) = 0$ and $sd(X^*) = 1$.

6.4.5 Realizations of a Normal Distribution

Realizations of a normal distribution refers to the actual values that you get when you draw samples from a normal distribution. Each sample drawn from the distribution is a realization of that distribution.

Example 6.6 (Realizations of a Normal Distribution)**.** If you have a normal distribution with a mean of 0 and a standard deviation of 1, each number you draw from that distribution is a realization. Here is a Python example that generates 10 realizations of a normal distribution with a mean of 0 and a standard deviation of 1:

```
import numpy as np
mu = 0
sigma = 1
realizations = np.random.normal(mu, sigma, 10)
print(realizations)
```

```
[ 0.48951662  0.23879586 -0.44811181 -0.610795   -2.02994507  0.60794659
 -0.35410888  0.15258149  0.50127485 -0.78640277]
```

In this code, `np.random.normal` generates ten realizations of a normal distribution with a mean of 0 and a standard deviation of 1. The realizations array contains the actual values drawn from the distribution.

6.4.6 The Multivariate Normal Distribution

The multivariate normal, multinormal, or Gaussian distribution serves as a generalization of the one-dimensional normal distribution to higher dimensions. We will consider k-dimensional random vectors $X = (X_1, X_2, \dots, X_k)$. When drawing samples from this distribution, it results in a set of values represented as $\{x_1, x_2, \dots, x_k\}$. To fully define this distribution, it is necessary to specify its mean μ and covariance matrix Σ. These parameters are analogous to the mean, which represents the central location, and the variance (squared standard deviation) of the one-dimensional normal distribution introduced in Equation **??**.

Definition 6.12 (The Multivariate Normal Distribution)**.** The probability density function (PDF) of the multivariate normal distribution is defined as:

$$f_X(x) = \frac{1}{\sqrt{(2\pi)^n \det(\Sigma)}} \exp\left(-\frac{1}{2}(x-\mu)^T \Sigma^{-1}(x-\mu)\right),$$

where: μ is the $k \times 1$ mean vector; Σ is the $k \times k$ covariance matrix. The covariance matrix Σ is assumed to be positive definite, so that its determinant is strictly positive.

In the context of the multivariate normal distribution, the mean takes the form of a coordinate within an k-dimensional space. This coordinate represents the location where samples are most likely to be generated, akin to the peak of the bell curve in a one-dimensional or univariate normal distribution.

Definition 6.13 (Covariance of two random variables)**.** For two random variables X and Y, the covariance is defined as the expected value (or mean) of the product of their deviations from their individual expected values:

$$\operatorname{cov}(X, Y) = \mathrm{E}\left[(X - \mathrm{E}[X])(Y - \mathrm{E}[Y])\right]$$

For discrete random variables, covariance can be written as:

$$\operatorname{cov}(X, Y) = \frac{1}{n} \sum_{i=1}^{n} (x_i - E(X))(y_i - E(Y)).$$

The covariance within the multivariate normal distribution denotes the extent to which two variables vary together. The elements of the covariance matrix, such as Σ_{ij}, represent the covariances between the variables x_i and x_j. These covariances describe how the different variables in the distribution are related to each other in terms of their variability.

Example 6.7 (The Bivariate Normal Distribution with Positive Covariances)**.** Figure **??** shows draws from a bivariate normal distribution with $\mu = \begin{pmatrix} 0 \\ 0 \end{pmatrix}$ and $\Sigma = \begin{pmatrix} 9 & 4 \\ 4 & 9 \end{pmatrix}$.

The covariance matrix of a bivariate normal distribution determines the shape, orientation, and spread of the distribution in the two-dimensional space.

The diagonal elements of the covariance matrix (σ_1^2, σ_2^2) are the variances of the individual variables. They determine the spread of the distribution along each axis. A larger variance corresponds to a greater spread along that axis.

The off-diagonal elements of the covariance matrix (σ_{12}, σ_{21}) are the covariances between the variables. They determine the orientation and shape of the distribution. If the covariance is positive, the distribution is stretched along the line $y = x$, indicating that the variables tend to increase together. If the covariance is negative, the distribution is stretched along the line $y = -x$, indicating that one variable tends to decrease as the other increases. If the covariance is zero, the variables are uncorrelated and the distribution is axis-aligned.

In Figure **??**, the variances are identical and the variables are correlated (covariance is 4), so the distribution is stretched along the line $y = x$.

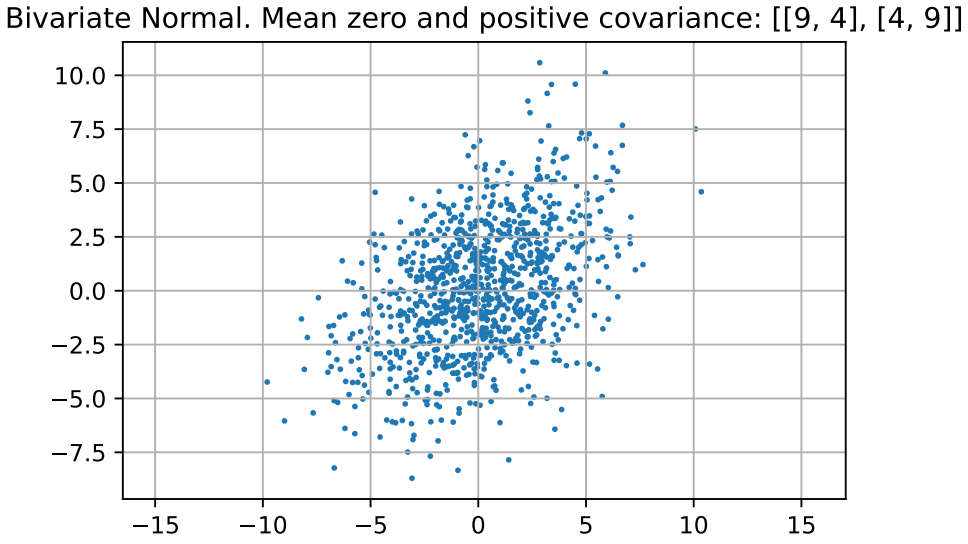


Figure 6.1: Bivariate Normal. Mean zero and covariance $\Sigma = \begin{pmatrix} 9 & 4 \\ 4 & 9 \end{pmatrix}$

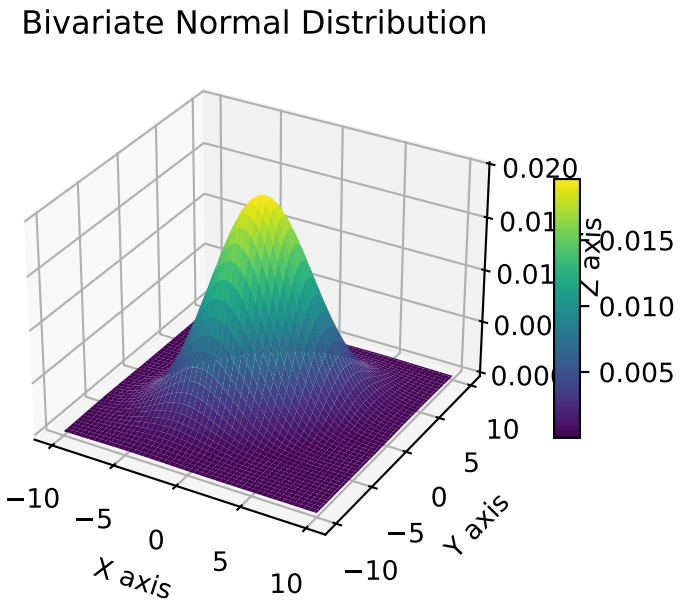


Figure 6.2: Bivariate Normal. Mean zero and covariance $\Sigma = \begin{pmatrix} 9 & 4 \\ 4 & 9 \end{pmatrix}$.

Example 6.8 (The Bivariate Normal Distribution with Mean Zero and Zero Covariances)**.** The Bivariate Normal Distribution with Mean Zero and Zero Covariances $\sigma_{12} = \sigma_{21} = 0$.

$$\Sigma = \begin{pmatrix} 9 & 0 \\ 0 & 9 \end{pmatrix}$$

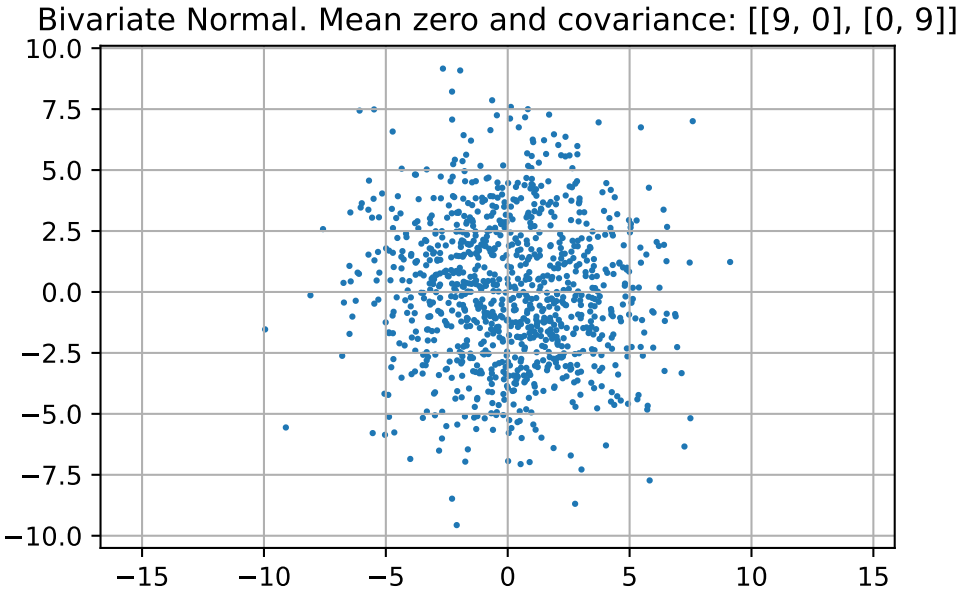


Figure 6.3: Bivariate Normal. Mean zero and covariance $\Sigma = \begin{pmatrix} 9 & 0 \\ 0 & 9 \end{pmatrix}$

Example 6.9 (The Bivariate Normal Distribution with Mean Zero and Negative Covariances)**.** The Bivariate Normal Distribution with Mean Zero and Negative Covariances $\sigma_{12} = \sigma_{21} = -4$.

$$\Sigma = \begin{pmatrix} 9 & -4 \\ -4 & 9 \end{pmatrix}$$

6.5 Covariance

In statistics, understanding the relationship between random variables is crucial for making inferences and predictions. Two common measures of such relationships are covariance and correlation. Covariance is a measure of how much two random variables change together. If the variables tend to show similar behavior (i.e., when one increases,

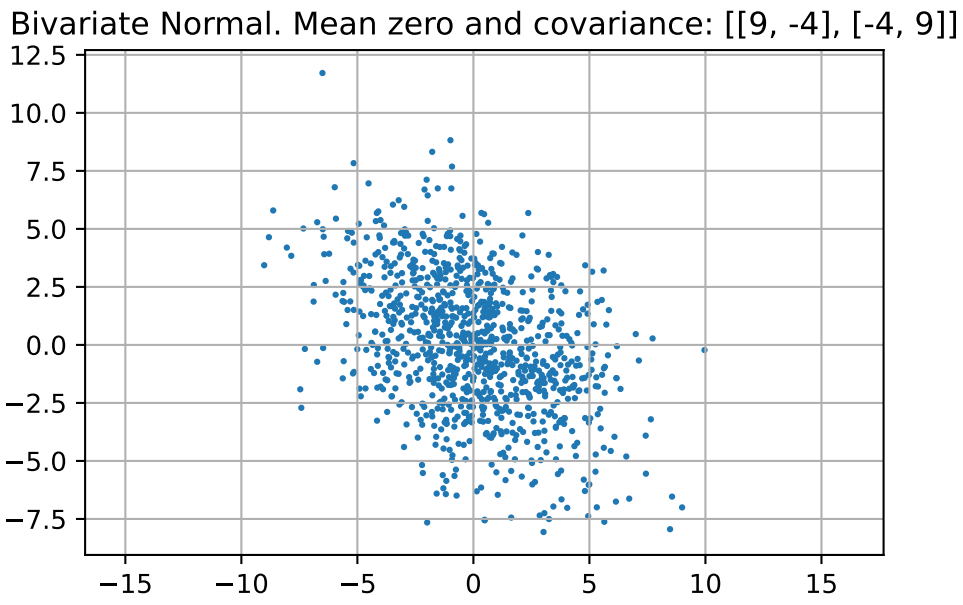


Figure 6.4: Bivariate Normal. Mean zero and covariance $\Sigma = \begin{pmatrix} 9 & -4 \\ -4 & 9 \end{pmatrix}$

the other tends to increase), the covariance is positive. Conversely, if they tend to move in opposite directions, the covariance is negative.

Definition 6.14 (Covariance)**.** Covariance is calculated as:

$$\text{Cov}(X, Y) = E[(X - E[X])(Y - E[Y])] = E[XY] - E[X]E[Y]$$

Here, $E[X]$ and $E[Y]$ are the expected values (means) of X and Y, respectively. Covariance has units that are the product of the units of X and Y.

For a vector of random variables $\mathbf{Y} = \left(Y^{(1)}, \ldots, Y^{(n)}\right)^T$, the covariance matrix Σ encapsulates the covariances between each pair of variables:

$$\Sigma = \text{Cov}(\mathbf{Y}, \mathbf{Y}) = \begin{pmatrix} \text{Var}(Y^{(1)}) & \text{Cov}(Y^{(1)}, Y^{(2)}) & \ldots \\ \text{Cov}(Y^{(2)}, Y^{(1)}) & \text{Var}(Y^{(2)}) & \ldots \\ \vdots & \vdots & \ddots \end{pmatrix}$$

The diagonal elements represent the variances, while the off-diagonal elements are the covariances.

6.6 Correlation

6.6.1 Definitions

Definition 6.15 ((Pearson) Correlation Coefficient)**.** The Pearson correlation coefficient, often denoted by ρ for the population or r for a sample, is calculated by dividing the covariance of two variables by the product of their standard deviations.

$$\rho_{XY} = \frac{\text{Cov}(X, Y)}{\sigma_X \sigma_Y}, \tag{6.4}$$

where $\text{Cov}(X, Y)$ is the covariance between variables X and Y, and σ_X and σ_Y are the standard deviations of X and Y, respectively.

Correlation, specifically the correlation coefficient, is a normalized measure of the linear relationship between two variables. It provides a value ranging from -1 to 1, which is scale-free, making it easier to interpret:

- -1: Perfect negative correlation, indicating that as one variable increases, the other decreases.
- 0: No correlation, indicating no linear relationship between the variables.
- 1: Perfect positive correlation, indicating that both variables increase together.

The correlation matrix Ψ provides a way to quantify the linear relationship between multiple variables, extending the notion of the correlation coefficient beyond just pairs of variables. It is derived from the covariance matrix Σ by normalizing each element with respect to the variances of the relevant variables.

Definition 6.16 (The Correlation Matrix Ψ)**.** Given a set of random variables $X_1, X_2, \ldots, X_n$, the covariance matrix Σ is:

$$\Sigma = \begin{pmatrix} \sigma_{11} & \sigma_{12} & \cdots & \sigma_{1n} \\ \sigma_{21} & \sigma_{22} & \cdots & \sigma_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ \sigma_{n1} & \sigma_{n2} & \cdots & \sigma_{nn} \end{pmatrix},$$

where $\sigma_{ij} = \operatorname{cov}(X_i, X_j)$ is the covariance between the i^{th} and j^{th} variables. The correlation matrix Ψ is then defined as:

$$\Psi = (\rho_{ij}) = \left(\frac{\sigma_{ij}}{\sqrt{\sigma_{ii}\sigma_{jj}}}\right),$$

where:

- ρ_{ij} is the correlation coefficient between the i^{th} and j^{th} variables.
- σ_{ii} is the variance of the i^{th} variable, i.e., σ_i^2.
- $\sqrt{\sigma_{ii}}$ is the standard deviation of the i^{th} variable, denoted as σ_i.

Thus, Ψ can also be expressed as:

$$\Psi = \begin{pmatrix} 1 & \frac{\sigma_{12}}{\sigma_1\sigma_2} & \cdots & \frac{\sigma_{1n}}{\sigma_1\sigma_n} \\ \frac{\sigma_{21}}{\sigma_2\sigma_1} & 1 & \cdots & \frac{\sigma_{2n}}{\sigma_2\sigma_n} \\ \vdots & \vdots & \ddots & \vdots \\ \frac{\sigma_{n1}}{\sigma_n\sigma_1} & \frac{\sigma_{n2}}{\sigma_n\sigma_2} & \cdots & 1 \end{pmatrix}$$

The correlation matrix Ψ has the following properties:

- The matrix Ψ is symmetric, meaning $\rho_{ij} = \rho_{ji}$.
- The diagonal elements are all 1, as $\rho_{ii} = \frac{\sigma_{ii}}{\sigma_i\sigma_i} = 1$.
- Each off-diagonal element is constrained between -1 and 1, indicating the strength and direction of the linear relationship between pairs of variables.

6.6.2 Computations

Example 6.10 (Computing a Correlation Matrix)**.** Suppose you have a dataset consisting of three variables: X, Y, and Z. You can compute the correlation matrix as follows:

1. Calculate the covariance matrix Σ, which contains covariances between all pairs of variables.
2. Extract the standard deviations for each variable from the diagonal elements of Σ.
3. Use the standard deviations to compute the correlation matrix Ψ.

Suppose we have two sets of data points:

- $X = [1, 2, 3]$
- $Y = [4, 5, 6]$

We want to compute the correlation matrix Ψ for these variables. First, calculate the mean of each variable.

$$\bar{X} = \frac{1+2+3}{3} = 2$$

$$\bar{Y} = \frac{4+5+6}{3} = 5$$

Second, compute the covariance between X and Y. The covariance is calculated as:

$$\text{Cov}(X, Y) = \frac{1}{n-1} \sum_{i=1}^{n} (X_i - \bar{X})(Y_i - \bar{Y})$$

For our data:

$$\text{Cov}(X, Y) = \frac{1}{3-1} \left[(1-2)(4-5) + (2-2)(5-5) + (3-2)(6-5)\right]$$

$$= \frac{1}{2} \left[1 + 0 + 1\right] = 1$$

Third, calculate the variances of X and Y. Variance is calculated as:

$$\text{Var}(X) = \frac{1}{n-1} \sum_{i=1}^{n} (X_i - \bar{X})^2$$