

Assignment 10

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Ornstein-Uhlenbeck Maximum Likelihood Estimate

The analytical problem is to derive the maximum likelihood estimate for the Ornstein-Uhlenbeck process. This is Exercise 11.4 from (Särkkä and Solin 2019), and we are guided by the authors' instructions. The Ornstein-Uhlenbeck process is defined as follows:

$$dx = -\lambda x dt + d\beta, \quad x(0) = x_0, \quad (1)$$

where λ is unknown and β has an unknown diffusion constant q . Thus, we define the unknown parameters as the vector $\theta = (\lambda, q)$. The authors also previously provided the transition density:

$$p(x(t + \Delta t) | x(t)) = N\left(x(t + \Delta t) | \exp(-\lambda \Delta t)x(t), \frac{q}{2\lambda} [1 - \exp(-2\lambda \Delta t)]\right) \quad (2)$$

The negative log-likelihood is:

$$\ell(\lambda, q) = \sum_{k=0}^{T-1} \left[\frac{1}{2} \log \left(2\pi \frac{q}{2\lambda} [1 - \exp(-2\lambda \Delta t)] \right) + \frac{\lambda}{q [1 - \exp(-2\lambda \Delta t)]} (x(t_{k+1}) - \exp(-\lambda \Delta t)x(t_k))^2 \right] \quad (3)$$

and using this change of variables:

$$a = \exp(-\lambda \Delta t) \quad (4)$$

$$\Sigma = \frac{q}{2\lambda} [1 - \exp(-2\lambda \Delta t)] \quad (5)$$

we arrive at:

$$\ell(a, \Sigma) = \sum_{k=0}^{T-1} \left[\frac{1}{2} \log(2\pi \Sigma) + \frac{1}{2\Sigma} (x(t_{k+1}) - ax(t_k))^2 \right] \quad (6)$$

To find the maximum likelihood, we find where ℓ has a gradient of 0.

$$\frac{\partial \ell}{\partial a} = -\frac{1}{\Sigma} \sum_{k=0}^{T-1} (x(t_{k+1}) - ax(t_k)) x(t_k) = 0 \quad (7)$$

$$\implies 0 = \sum_{k=0}^{T-1} x(t_{k+1})x(t_k) - a \sum_{k=1}^{T-1} (x(t_k))^2 \quad (8)$$

$$\implies a_{\text{ML}} = \frac{\sum_{k=0}^{T-1} x(t_{k+1})x(t_k)}{\sum_{k=1}^{T-1} (x(t_k))^2} \quad (9)$$

$$(10)$$

$$\frac{\partial \ell}{\partial \Sigma} = \sum_{k=0}^{T-1} \left[\frac{1}{2\Sigma} - \frac{1}{2\Sigma^2} (x(t_{k+1}) - ax(t_k))^2 \right] = 0 \quad (11)$$

$$0 = \frac{T}{2\Sigma} - \frac{1}{2\Sigma^2} \sum_{k=0}^{T-1} (x(t_{k+1}) - ax(t_k))^2 \quad (12)$$

$$\implies \frac{T}{2\Sigma} = \frac{1}{2\Sigma^2} \sum_{k=0}^{T-1} (x(t_{k+1}) - ax(t_k))^2 \quad (13)$$

$$\implies T\Sigma = \sum_{k=0}^{T-1} (x(t_{k+1}) - ax(t_k))^2 \quad (14)$$

$$\implies \Sigma_{\text{ML}} = \frac{1}{T} \sum_{k=0}^{T-1} (x(t_{k+1}) - a_{\text{ML}}x(t_k))^2 \quad (15)$$

And to reverse the change of variables, we used:

$$a_{\text{ML}} = \exp(-\lambda_{\text{ML}}\Delta t) \quad (16)$$

$$\Sigma_{\text{ML}} = \frac{q_{\text{ML}}}{2\lambda} [1 - \exp(-2\lambda_{\text{ML}}\Delta t)] \quad (17)$$

which gives

$$a_{\text{ML}} = \frac{\sum_{k=0}^{T-1} x(t_{k+1})x(t_k)}{\sum_{k=1}^{T-1} (x(t_k))^2} \quad (18)$$

$$\exp(-\lambda_{\text{ML}}\Delta t) = \frac{\sum_{k=0}^{T-1} x(t_{k+1})x(t_k)}{\sum_{k=1}^{T-1} (x(t_k))^2} \quad (19)$$

$$\lambda_{\text{ML}} = -\frac{1}{\Delta t} \log \left[\frac{\sum_{k=0}^{T-1} x(t_{k+1})x(t_k)}{\sum_{k=1}^{T-1} (x(t_k))^2} \right] \quad (20)$$

$$(21)$$

$$\Sigma_{\text{ML}} = \frac{1}{T} \sum_{k=0}^{T-1} (x(t_{k+1}) - a_{\text{ML}}x(t_k))^2 \quad (22)$$

$$\frac{q_{\text{ML}}}{2\lambda} [1 - \exp(-2\lambda_{\text{ML}}\Delta t)] = \frac{1}{T} \sum_{k=0}^{T-1} (x(t_{k+1}) - a_{\text{ML}}x(t_k))^2 \quad (23)$$

$$\implies q_{\text{ML}} = \frac{2\lambda_{\text{ML}}}{T [1 - \exp(-2\lambda_{\text{ML}}\Delta t)]} \sum_{k=0}^{T-1} (x(t_{k+1}) - \exp(-\lambda_{\text{ML}}\Delta t)x(t_k))^2 \quad (24)$$

Computational Problem

This is problem 11.9 from (Särkkä and Solin 2019) and concerns a model where two parameters θ_1 and θ_2 are unknown:

$$dx = \theta_1 \sin(x - \theta_2) + d\beta, \quad x(0) = x_0, \quad (25)$$

where β is a standard Brownian motion (i.e. the diffusion coefficient $q = 1$).

I was restricted in the number of time steps based on the product required to calculate the negative log-likelihood. I also only sampled one path. As a result, the numerical method did not find the true parameters very well.

First, I'll show the Euler-Maruyama approximation of the true function. Then I will show the optimal parameters based on the maximum likelihood method based on one sample path.

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

# -- Plotting Tools --
def low_buff(y_values):
    span = y_values.max() - y_values.min()
    return y_values.min() - 0.1 * span

def plot_on_axis(ax, time, pos, cols, title, color_map, with_mean=False):
    for idx, col in enumerate(cols):
        ax.plot(time, pos[:, col], c=color_map[idx], alpha=0.5)
    ax.set_title(title)
    if with_mean:
        ax.plot(time, pos.mean(axis=1), color='black',
                label=r'Sample Mean $(n=\{n\})$'.format(pos.shape[1]), linewidth=2)
        ax.plot(time, pos.mean(axis=1) + 2* pos.std(axis=1), color='black',
                linestyle='dashed')
        ax.plot(time, pos.mean(axis=1) - 2* pos.std(axis=1), color='black',
                linestyle='dashed', label='Sample Two Std. Dev.')
    ax.legend()

# -- Brownian Motion --
def multiple_brownian_motion(end_time=1., num_tsteps=500, n_trials=1000):
    """Creates multiple 1-D Brownian motion with time as the row index and
    each column as a separate path of Brownian motion.

    This assumes that all Brownian motion starts at 0. Currently only
    implements one-dimensional Brownian motion. This also assumes all
    step sizes are the same size.

    The steps of Brownian motion, ``dw``, are modeled with a Gaussian
    distribution with mean 0 and variance ``sqrt(dt)``, where ``dt``
    is the constant time step size.

    Parameters
```

```

-----
end_time : float

num_tsteps : int
    The number of steps to take. Will calculate the step
    size dt internally. The number of rows in the output of
    Brownian motion will be num_tsteps + 1.

n_trials : int
    The number of sample paths to create. This will be the number
    of columns in the output.

Returns
-----
t : ndarray
    One-dimensional time ndarray from 0 to ``end_time`` with
    shape ``(num_tsteps+1,)``

w : ndarray
    Two-dimensional ndarray representing ``n_trials`` number of
    sample paths of one-dimensional Brownian motion.
    This will be of shape ``(num_tsteps+1, n_trials)``.

dt : float
    The value indicating the step size of t. This is only implemented
    with constant step size.

dw : ndarray
    Two-dimensional ndarray representing the steps of Brownian motion.
    The first row is all zeros. Each i-th row of ``dw``, ie. dw[i, :]
    indicates the change in ``w`` from w[i-1, :] to w[i, :]
    This will be the same shape as ``w``, ``(num_tsteps+1, n_trials)``.

"""

dt = (end_time - 0) / num_tsteps
dw = np.random.normal(scale=np.sqrt(dt), size=(num_tsteps+1, n_trials))
# Brownian motion must start at time 0 with value 0
dw[0] = np.zeros_like(dw[0])
w = dw.cumsum(axis=0)
# t is not used in calculations, but returned to allow user to keep track
# of points in time
t = np.linspace(0, end_time, num=num_tsteps+1).reshape((num_tsteps+1, 1))
assert w.shape[0] == t.shape[0], ('time and position arrays are not the '
                                  'same length. w.shape[0] - t.shape[0] = '
                                  f'{w.shape[0] - t.shape[0]}')
assert w.shape == dw.shape, ('position and velocity arrays are not the '
                              'same shape: '
                              f'w.shape: {w.shape}    dw.shape: {dw.shape}')

return t, w, dt, dw

def euler_maruyama_nonlinear_vec(f, g, x0, t, dt, dw, M):
    """

```

calculates the EM approximation on the nonlinear one-dimensional SDE, vectorized for multiple trials based on the shape of ``dw``.

SDE is of the form:

$$dX = f(X)dt + G(X)dW; X(0) = X_0$$

*:param f: shift function in SDE. Must be passed as a function of x
:param g: drift/dispersion function in SDE
:param x0: Initial condition
:param t: time one dimensional nd-array
:param dt: step size of time array, float
:param dw: White noise associated with the Brownian motion, ndarray
:param M: multiple of dt for Euler-Maruyama step size. Do not make this too large.
:return: time array and solution x array
"""*

```
if M < 1:
    raise ValueError('M must be greater than or equal to 1')

Dt = M * dt # EM step size
L = (t.shape[0] - 1) / M # number of EM steps

if not L.is_integer():
    raise ValueError('Cannot handle Step Size that is not a multiple of M')

L = int(L) # needed for range below

x = [np.full((dw.shape[1],), x0)]
T = [0]
for i in range(1, L+1):
    # DW is the step of Brownian motion for EM step size
    DW = (dw[M * (i - 1) + 1:M * i + 1, :]).sum(axis=0).reshape(dw.shape[1], )
    x.append(x[i-1] + Dt * f(x[i-1]) + g(x[i-1]) * DW)
    T.append(T[i-1] + Dt)

return np.array(T), np.array(x)
```

```
def approx_llh(sample, dt, f, g, theta):
    loc = sample[:-1] + f(sample[:-1], theta) * dt
    scale = np.sqrt(g(sample[:-1], theta) * dt)
    return norm(loc=loc, scale=scale).pdf(sample[1:]).prod()
```

```
def ell(theta, llh, sample, dt, f, g):
    return - (np.log(llh(sample, dt, f, g, theta))).sum()
```

== INPUT DECK ==

-- True Process --

"""

True Process:

$$dx = \text{THETA}_1 \sin(x - \text{THETA}_2)dt + dB$$

```
needs to be in the form:
dx = f(x) dt + g(x) dB
"""
```

```
## '\nTrue Process:\ndx = THETA_1 sin(x - THETA_2)dt + dB\nneeds to be in the form:\ndx = f(x) dt + g(x)
```

```
THETA_1 = 1.5
THETA_2 = np.pi/4

def f(x, theta):
    theta_1 = theta[0]
    theta_2 = theta[1]
    return theta_1 * np.sin(x - theta_2)

def g(x, theta):
    del x, theta # unused
    return 1

def known_f(x):
    return f(x, (THETA_1, THETA_2))

def known_g(x):
    return g(x, (THETA_1, THETA_2))

# Initial Condition
x0 = 1

# Only one trial for the sample, but creating multiple trials
# to study the true solution
END_TIME = 2
NUM_TSTEPS = 100
N_TRIALS = 1000
M = 1

# -- Plotting Variables
viridis_em = plt.get_cmap('viridis', lut=N_TRIALS)

# -- Start run --
# -- Generate Samples using Euler-Maruyama Method
t, w, dt, dw = multiple_brownian_motion(END_TIME, NUM_TSTEPS, N_TRIALS)
t_em, x_em = euler_maruyama_nonlinear_vec(known_f, known_g, x0, t, dt, dw, M)
fig, ax = plt.subplots(nrows=2, sharex=True, sharey=True, figsize=(7, 6.5))
plot_on_axis(ax[0], t_em, x_em, np.arange(N_TRIALS), 'Euler Maruyama Approximation\n'
                                                    r'$n=' f'{N_TRIALS}'+r'$',
                                                    color_map=viridis_em, with_mean=True)
```

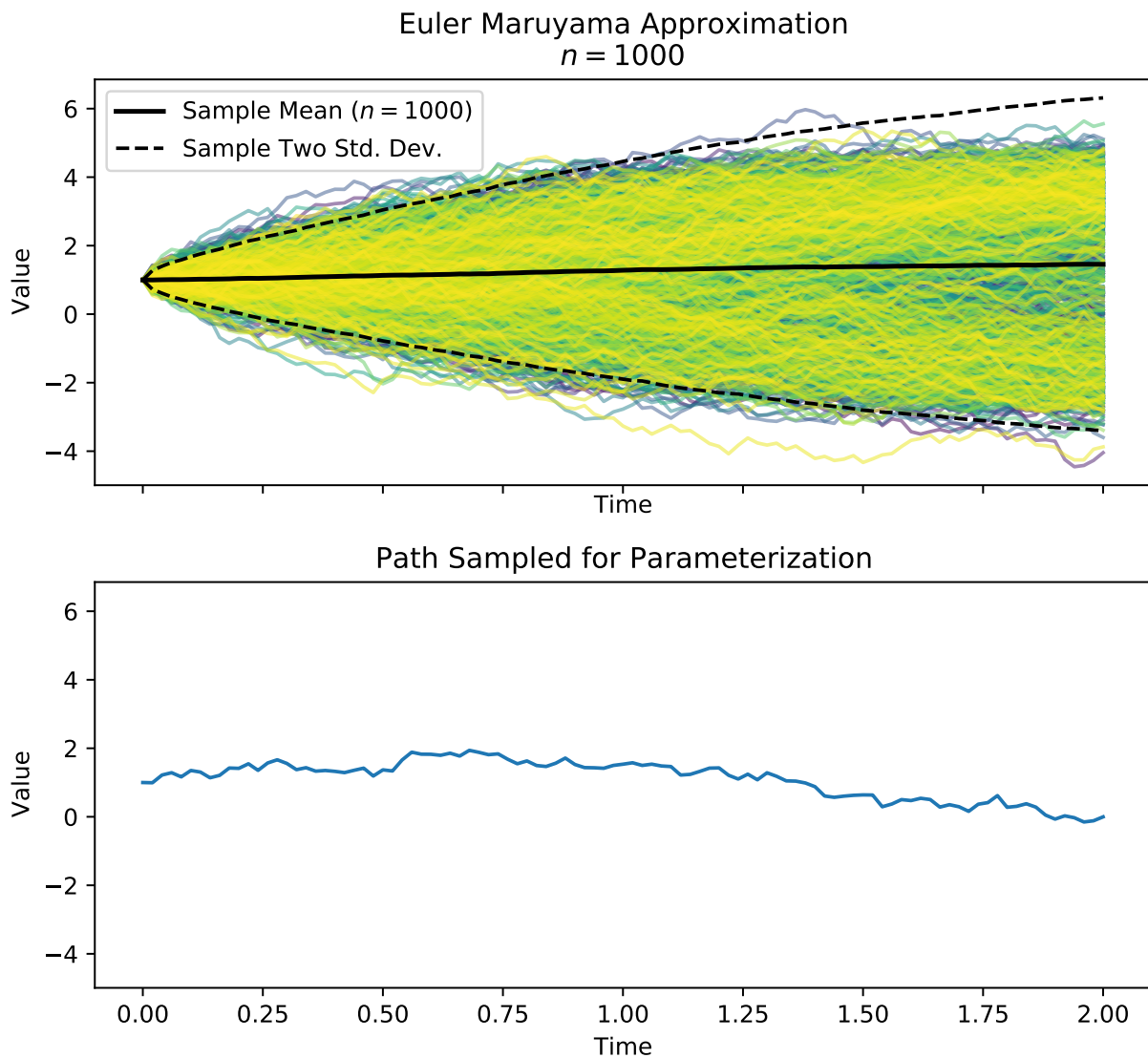
```

ax[0].set_xlabel('Time')
ax[0].set_ylabel('Value')

ax[1].plot(t_em, x_em[:, 1])
ax[1].set_title('Path Sampled for Parameterization')
ax[1].set_xlabel('Time')
ax[1].set_ylabel('Value')

fig.tight_layout()
plt.show()

```



```

sample_time = t_em
sample_value = x_em[:, 1].copy()

```

-- Approximate Likelihood

```

def approx_ell(theta):
    return ell(theta, approx_llh, sample_value, dt, f, g)

ml_res = minimize(approx_ell, x0=(0.5, 3), bounds=[(0, 5), (0, 5)])

plt.figure()
plot_theta_1 = np.linspace(0, 5, 100)
plot_theta_2 = np.linspace(0, 5, 100)
th_1_xx, th_2_yy = np.meshgrid(plot_theta_1, plot_theta_2)
plot_likelihood = np.zeros_like(th_2_yy)

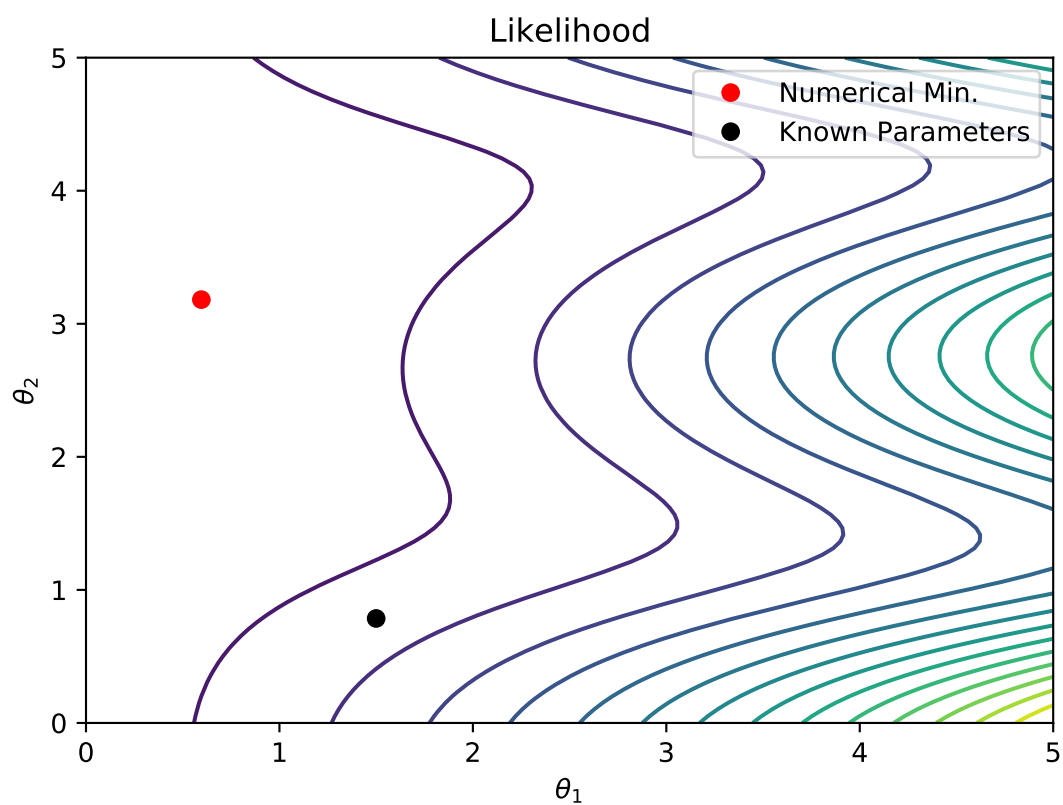
for x_idx, th_1 in enumerate(plot_theta_1):
    for y_idx, th_2 in enumerate(plot_theta_2):
        plot_likelihood[y_idx, x_idx] = approx_ell((th_1, th_2))

plt.contour(th_1_xx, th_2_yy, plot_likelihood, levels=20)

## <matplotlib.contour.QuadContourSet object at 0x1249bb8b0>

plt.xlabel(r'$\theta_1$')
plt.ylabel(r'$\theta_2$')
plt.plot(ml_res.x[0], ml_res.x[1], 'ro', label='Numerical Min.')
plt.plot(THETA_1, THETA_2, 'ko', label='Known Parameters')
plt.legend()
plt.title('Likelihood')

```

References

Särkkä, Simo, and Arno Solin. 2019. *Applied Stochastic Differential Equations*. Vol. 10. Cambridge University Press.