

```
In [ ]: import numpy as np
from matplotlib import pyplot as plt
from functools import partial
from scipy.optimize import least_squares
import pandas as pd
import re
```

Let's find the beginning date t_0 which $V(t_0) > V_{min}$ ($V_{min} = 5$) and do some preprocessing here.

```
In [ ]: df = pd.read_csv('project10_data.csv')

# First to clean the table with only the time series data
col_list = []
for col in df.columns:
    if re.search("[0-9]+", col):
        col_list.append(col)

# df_clean symbolizing all dates with given data
df_clean = df[col_list]
df_clean.columns = pd.to_datetime(df_clean.columns, format="%m/%d/%y")

# find t0 as the starting time for the simulation
for i in range(len(df_clean.columns)):
    if df_clean.iloc[0, i] >= 5:
        t0 = i
        break

print(t0)
print(df_clean.columns[i].date())
```

```
45
2020-03-07
```

```
In [ ]: # Get population
population = df["Population"][0]
# Get the V(t): detected infection
accumulated_cases = np.array(df_clean.iloc[0])
# Get the Y(t): the cumulative number of deaths
accumulated_deaths = np.array(df_clean.iloc[1])

T_max = 119
I = np.zeros(T_max + 1)

# Get the I(t)
for t in range(0, T_max + 1):
    I[t] = accumulated_cases[t + t0 + 7] - accumulated_cases[t + t0 - 7]
```

```
# When accumulated_deaths > 5, the simulation starts
t_deaths_0 = np.argwhere(accumulated_deaths > 5)[1, 0]
```

Exercise 1

This problem asks you to implement and run the Meta-Algorithm for SIR Calibration using the time series of cumulative number of detected infection $V(t)$ and the cumulative number of deaths $Y(t)$. Use initialization $S(0) = N$, $I(0)$ from the data set, $R(0) = 0$. Use the following parameters: $T_{max} = 119$ (i.e., a total of 120 time samples), $V_{min} = 5$, $\tau_0 = 7$, $p = 1, 2, \infty$ (check all three values), $\lambda = 1$. For the set Ω write nested loops over α , R_0 , and N by searching over the following intervals: $\alpha \in [0.05, 0.2]$, $R_0 \in [1.5, 1.9]$, $N/Population \in [2\%, 10\%]$.

Recall $\beta = R_0\alpha$, and P opulation is extracted from your data set.

The first step is to generate a set of potential simulation params. In this case, we sampled 10 for each of the 3 parameters. We then generated a set of 1000 simulations using these parameters.

```
In [ ]: # Exercise 1

omegas = []
for alpha in np.linspace(0.05, 0.2, 10):
    for r0 in np.linspace(1.5, 1.9, 10):
        beta = alpha * r0
        for p in np.linspace(0.02, 0.1, 10):
            omegas.append((alpha, beta, r0, p * population))

print(f"Number of simulations: {len(omegas)}")
```

Number of simulations: 1000

Then, let's implement the SIR model following our PPT. We also need to implement an ode solver. We will use the Euler method here.

```
In [ ]: def SIR_simulation(x, return_all=False):
    # S, I, R
    alpha, beta, N = x
    y_0 = [N-I[0], I[0], 0] # Susceptible, Infected, Recovered
    T = 0.01

    results = [
        y_0,
    ]

    # Euler method
    for t in np.arange(start=1, stop=T_max+1, step=0.01):
```

```

    y_0 = [
        y_0[0] - beta * y_0[0] * y_0[1]/N * T,
        y_0[1] + beta * y_0[0] * y_0[1]/N * T - alpha * y_0[1] * T,
        y_0[2] + alpha * y_0[1] * T
    ]
    results.append(y_0)

results = np.array(results)
results = results[:,100]

if return_all:
    return results[:, 0], results[:, 1], results[:, 2]

return I - results[:, 1]

```

Question (1)

Find and print the minimum of the objective function J . Print the optimal values of $\hat{\alpha}$, $\hat{\beta}$, \hat{R}_0 , \hat{N} and $\hat{\gamma}$ ($\hat{\gamma}$ is obtained by implementing the minimization of $\|Y - \gamma R_{sim}\|_p$ over γ).

Question (2)

Visualize the 2D surface (function) $(\alpha, \beta) \rightarrow J = J(\alpha, \beta, \hat{N}, \hat{\gamma})$ at the optimal values \hat{N} and $\hat{\gamma}$ obtained before. You should obtain one plot for each p .

Question (3)

Plot on the same graph the simulated I_{sim} and the preprocessed rate of detected infections $I(t) = V(t + t_0 + \tau_0) - V(t + t_0 - \tau_0)$. Plot on the same graph the predicted number of deaths $Y_{sim} = \hat{\gamma} R_{sim}$ and the observed number of deaths $Y(t)$ from your data set. You should obtain two plots for each value of p .

We run SIR simulations for all questions (Sub question 1 to 3).

```

In [ ]: ps = [1, 2, np.inf]

for p in ps:
    lambda_ = 1
    minimum = None
    all_results = []

    for alpha, beta, r0, N in omegas:

```

```

S_sim, I_sim, R_sim = SIR_simulation((alpha, beta, N), return_all=True)
gamma = least_squares(lambda x: np.linalg.norm(accumulated_deaths[:T_max+1] - x * R_sim, ord=p), 1, bounds=(0, 1))
gamma = gamma.x[0]

if p != np.inf:
    J = np.sum((I - I_sim) ** 2) + lambda_ * np.sum((accumulated_deaths[:T_max+1] - gamma * R_sim) ** 2)
else:
    J = np.max(np.abs(I - I_sim)) + lambda_ * np.max(np.abs(accumulated_deaths[:T_max+1] - gamma * R_sim))

if minimum is None or J < minimum[0]:
    minimum = (J, alpha, beta, r0, N, gamma)

all_results.append((J, alpha, beta, r0, N, gamma))

J, alpha, beta, r0, N, gamma = minimum
all_results = np.array(all_results)

print(f"[p={p}] alpha: {alpha}, beta: {beta}, r0: {r0}, N: {N}, gamma: {gamma}, J: {J}")

# Sub Question (2)
plt.figure()
fig, (ax1, ax2, ax3) = plt.subplots(1, 3, figsize=(20, 5))
plt.suptitle(f"p={p}")

temp = ax1.scatter(all_results[:, 1], all_results[:, 2], c=all_results[:, 0])
ax1.scatter(alpha, beta, c="red", marker="x")
ax1.set_xlabel("alpha")
ax1.set_ylabel("beta")
ax1.set_title("J vs alpha and beta")
fig.colorbar(temp, ax=ax1)

# Sub Question (3)
S_sim, I_sim, R_sim = SIR_simulation((alpha, beta, N), return_all=True)

ax2.plot(I_sim, label="I_sim")
ax2.plot(I, label="I")
ax2.legend()
ax2.set_xlabel("Time (days)")
ax2.set_ylabel("Count")
ax2.set_title("Infected vs Time")

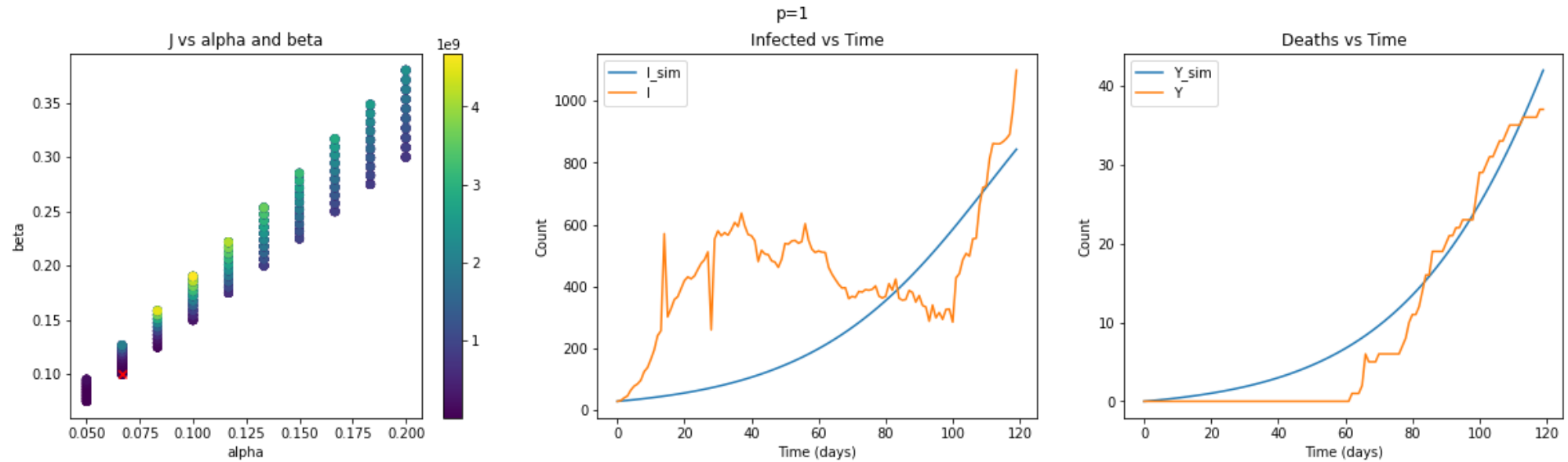
ax3.plot(gamma * R_sim, label="Y_sim")
ax3.plot(accumulated_deaths[:T_max+1], label="Y")
ax3.legend()
ax3.set_xlabel("Time (days)")
ax3.set_ylabel("Count")
ax3.set_title("Deaths vs Time")

```

```
plt.show()
```

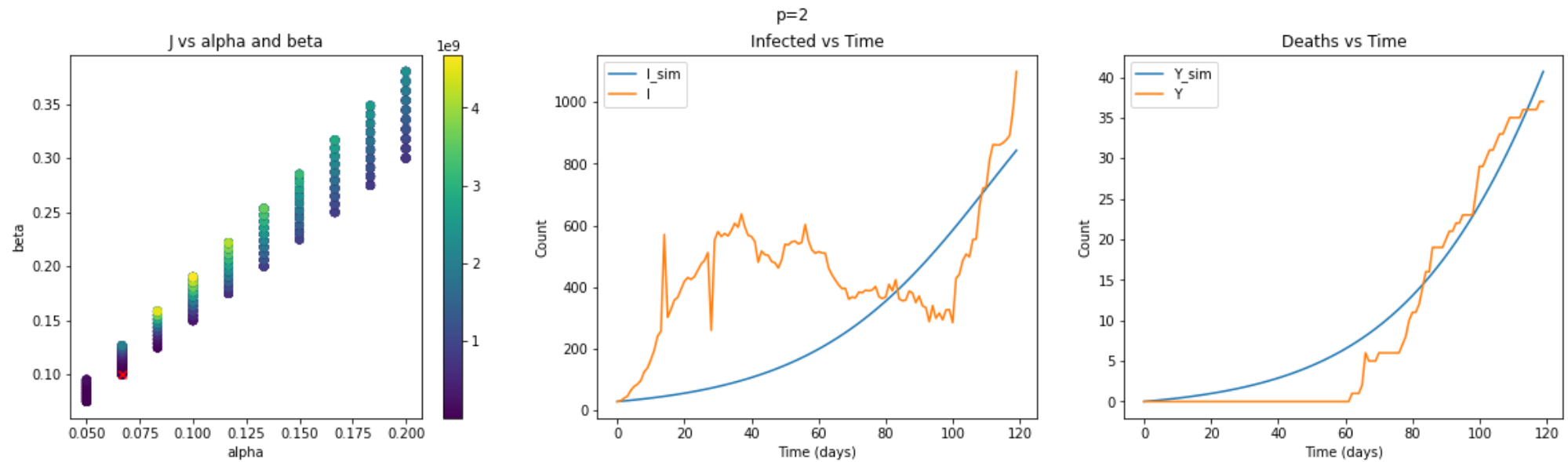
[p=1] alpha: 0.06666666666666668, beta: 0.10000000000000002, r0: 1.5, N: 17630.98, gamma: 0.018719402293418983, J: 9082436.290154533

<Figure size 432x288 with 0 Axes>



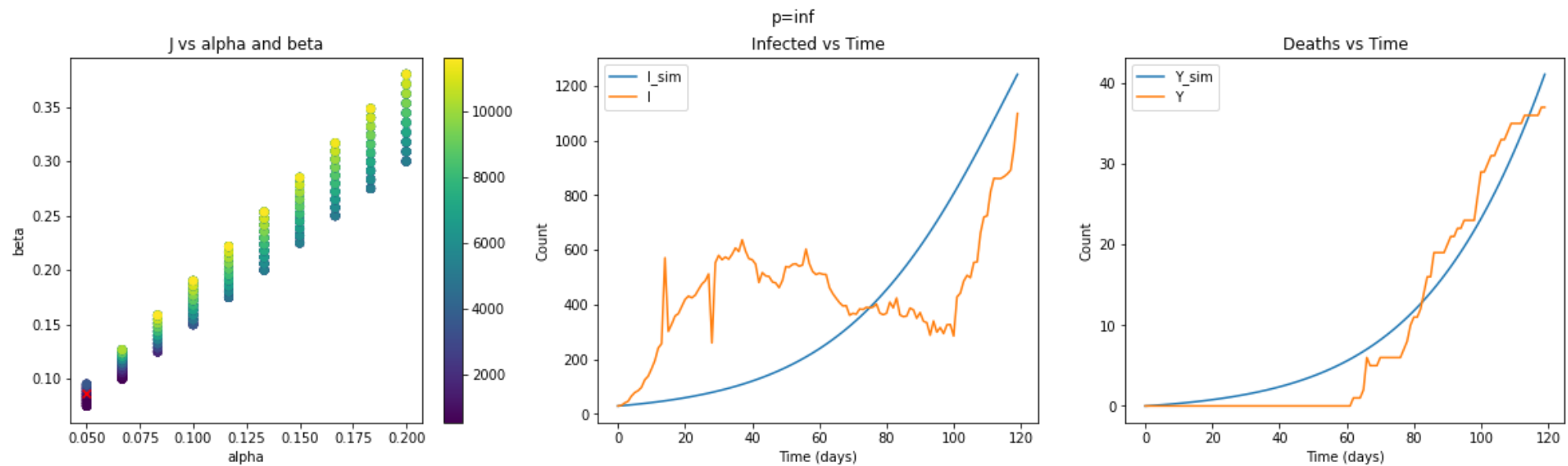
[p=2] alpha: 0.06666666666666668, beta: 0.10000000000000002, r0: 1.5, N: 17630.98, gamma: 0.018153494262134962, J: 9082407.231795408

<Figure size 432x288 with 0 Axes>



[p=inf] alpha: 0.05, beta: 0.08611111111111111, r0: 1.722222222222222, N: 17630.98, gamma: 0.01846782732175221, J: 534.5574042873181

<Figure size 432x288 with 0 Axes>



Question (4)

If you are asked to improve the estimates, what would be your refined range of parameters?

The above data shows that the expected α is between 0.05 and 0.075, while the expected β is between 0.09 to 0.11 ($R_0 = 1.5$).

Since the above graphs look good, we probably rerun the experiments with $\alpha \in [0.05, 0.075]$ and $R_0 \in [1.4, 1.6]$.

Exercise 2

This problem asks you to implement and run the Meta-Algorithm for *SEIR* Calibration using the time series of cumulative number of detected infection $V(t)$ and the cumulative number of deaths $Y(t)$.

Use the same parameters as in Problem 1 with the following initialization: $S(0) = N$, $E(0) = I(0)$ to match the data set value $V(t_0 + \tau_0) - V(t_0 - \tau_0)$, $R(0) = 0$. For the set Ω write nested loops over α , R_0 , and N by searching over the following intervals: $\alpha \in [0.05, 0.4]$, $\delta \in [0.05, 0.4]$, $R_0 \in [1.5, 1.9]$, $N/Population \in [2\%, 10\%]$.

Recall $\beta = R_0\alpha$, and P opulation is extracted from your data set.

The first step is to generate a set of potential simulation params. In this case, we sampled 7 for each of the 4 parameters. We then generated a set of 2401 simulations using these parameters.

```
In [ ]: ## Similar to 1

omegas = []
for alpha in np.linspace(0.05, 0.4, 7):
    for delta in np.linspace(0.05, 0.4, 7):
        for r0 in np.linspace(1.5, 1.9, 7):
            beta = alpha * r0
            for p in np.linspace(0.02, 0.1, 7):
                omegas.append((alpha, beta, delta, r0, p * population))

print(f"Number of simulations: {len(omegas)}")
```

Number of simulations: 2401

Then, let's implement the SEIR model following our PPT. We also need to implement an ode solver. We will use the Euler method here.

```
In [ ]: def SEIR_simulation(x, return_all=False):
    # S, E, I, R
    alpha, beta, delta, N = x
    y_0 = [N-I[0], I[0], I[0], 0] # Susceptible, Exposed, Infected, Recovered
    T = 0.01

    results = [
        y_0,
    ]

    # Euler method
    for t in np.arange(start=1, stop=T_max+1, step=0.01):
        y_0 = [
            y_0[0] - beta * y_0[0] * y_0[2]/N * T,
            y_0[1] + beta * y_0[0] * y_0[2]/N * T - delta * y_0[1] * T,
            y_0[2] + delta * y_0[1] * T - alpha * y_0[2] * T,
            y_0[3] + alpha * y_0[2] * T
        ]
        results.append(y_0)

    results = np.array(results)
    results = results[:,100]

    if return_all:
        return results[:, 0], results[:, 1], results[:, 2], results[:, 3]

    return I - results[:, 2]
```

Question (1)

Find and print the minimum of the objective function J . Print the optimal values of $\hat{\alpha}$, $\hat{\beta}$, $\hat{\delta}$, \hat{R}_0 , \hat{N} and $\hat{\gamma}$ ($\hat{\gamma}$ is obtained by implementing the minimization of $\|Y - \gamma R_{sim}\|_p$ over γ).

Question (2)

Visualize the 2D surfaces (functions):

- $(\alpha, \beta) \rightarrow J = J(\alpha, \beta, \hat{\delta}, \hat{N}, \hat{\gamma})$ at the optimal values $\hat{\delta}$, \hat{N} and $\hat{\gamma}$ obtained before. You should obtain one plot for each p .
- $(\alpha, \delta) \rightarrow J = J(\alpha, \hat{\beta}, \delta, \hat{N}, \hat{\gamma})$ at the optimal values $\hat{\beta}$, \hat{N} and $\hat{\gamma}$ obtained before. You should obtain one plot for each p .
- $(\beta, \delta) \rightarrow J = J(\hat{\alpha}, \beta, \delta, \hat{N}, \hat{\gamma})$ at the optimal values $\hat{\alpha}$, \hat{N} and $\hat{\gamma}$ obtained before. You should obtain one plot for each p .

Question (3)

Plot on the same graph the simulated I_{sim} and the preprocessed rate of detected infections $I(t) = V(t + t_0 + \tau_0) - V(t + t_0 - \tau_0)$ Plot on the same graph the predicted number of deaths $Y_{sim} = \hat{\gamma} R_{sim}$ and the observed number of deaths $Y(t)$ from your data set. You should obtain two plots for each value of p .

We run *SEIR* simulations for all questions (Subquestion 1 to 3).

```
In [ ]: ps = [1, 2, np.inf]

for p in ps:
    lambda_ = 1
    minimum = None
    all_results = []

    for alpha, beta, delta, r0, N in omegas:
        S_sim, E_sim, I_sim, R_sim = SEIR_simulation((alpha, beta, delta, N), return_all=True)
        gamma = least_squares(lambda x: np.linalg.norm(accumulated_deaths[:T_max+1] - x * R_sim, ord=p), 1, bounds=(0, 1))
        gamma = gamma.x[0]

        if p != np.inf:
            J = np.sum((I - I_sim) ** 2) + lambda_ * np.sum((accumulated_deaths[:T_max+1] - gamma * R_sim) ** 2)
        else:
            J = np.max(np.abs(I - I_sim)) + lambda_ * np.max(np.abs(accumulated_deaths[:T_max+1] - gamma * R_sim))
```



```

    if minimum is None or J < minimum[0]:
        minimum = (J, alpha, beta, delta, r0, N, gamma)

    all_results.append((J, alpha, beta, delta, r0, N, gamma))

J, alpha, beta, delta, r0, N, gamma = minimum
all_results = np.array(all_results)

print(f"[p={p}] alpha: {alpha}, beta: {beta}, delta: {delta}, r0: {r0}, N: {N}, gamma: {gamma}, J: {J}")

# Sub Question (2)
plt.figure()
fig, (ax1, ax2, ax3) = plt.subplots(1, 3, figsize=(20, 5))
plt.suptitle(f"2D graphs for p={p}")

temp = ax1.scatter(all_results[:, 1], all_results[:, 2], c=all_results[:, 0])
ax1.scatter(alpha, beta, c="red", marker="x")
ax1.set_xlabel("alpha")
ax1.set_ylabel("beta")
ax1.set_title("J vs alpha and beta")
fig.colorbar(temp, ax=ax1)

temp = ax2.scatter(all_results[:, 1], all_results[:, 3], c=all_results[:, 0])
ax2.scatter(alpha, delta, c="red", marker="x")
ax2.set_xlabel("alpha")
ax2.set_ylabel("delta")
ax2.set_title("J vs alpha and delta")
fig.colorbar(temp, ax=ax2)

temp = ax3.scatter(all_results[:, 2], all_results[:, 3], c=all_results[:, 0])
ax3.scatter(beta, delta, c="red", marker="x")
ax3.set_xlabel("beta")
ax3.set_ylabel("delta")
ax3.set_title("J vs beta and delta")
fig.colorbar(temp, ax=ax3)

plt.show()

# Sub Question (3)
S_sim, E_sim, I_sim, R_sim = SEIR_simulation((alpha, beta, delta, N), return_all=True)

plt.figure()
fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(14, 5))
plt.suptitle(f"Infected and Deaths for p={p}")

ax1.plot(I_sim, label="I_sim")
ax1.plot(I, label="I")

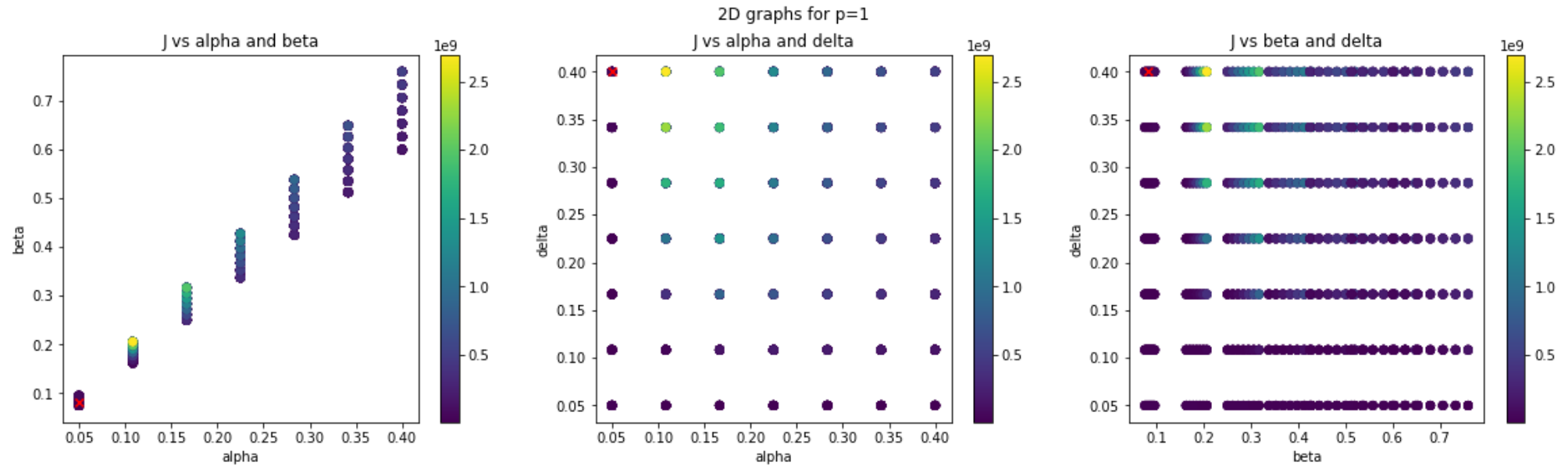
```

```
ax1.legend()
```

```
ax2.plot(gamma * R_sim, label="Y_sim")
ax2.plot(accumulated_deaths[:T_max+1], label="Y")
ax2.legend()
plt.show()
```

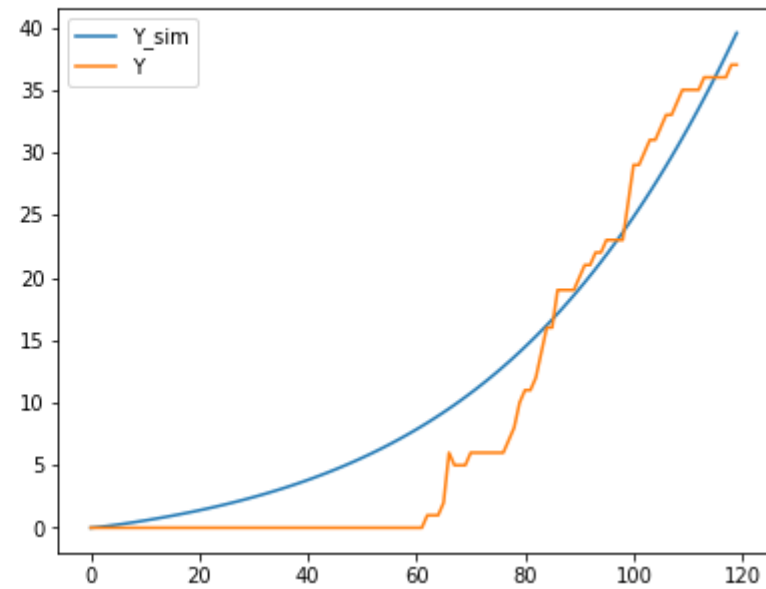
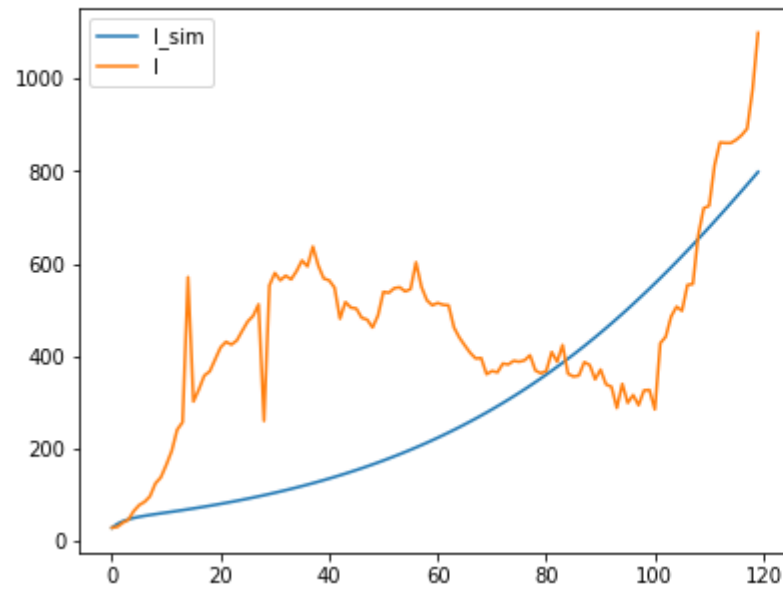
[p=1] alpha: 0.05, beta: 0.08166666666666667, delta: 0.4, r0: 1.6333333333333333, N: 17630.98, gamma: 0.022946439211738816, J: 7946520.418773221

<Figure size 432x288 with 0 Axes>



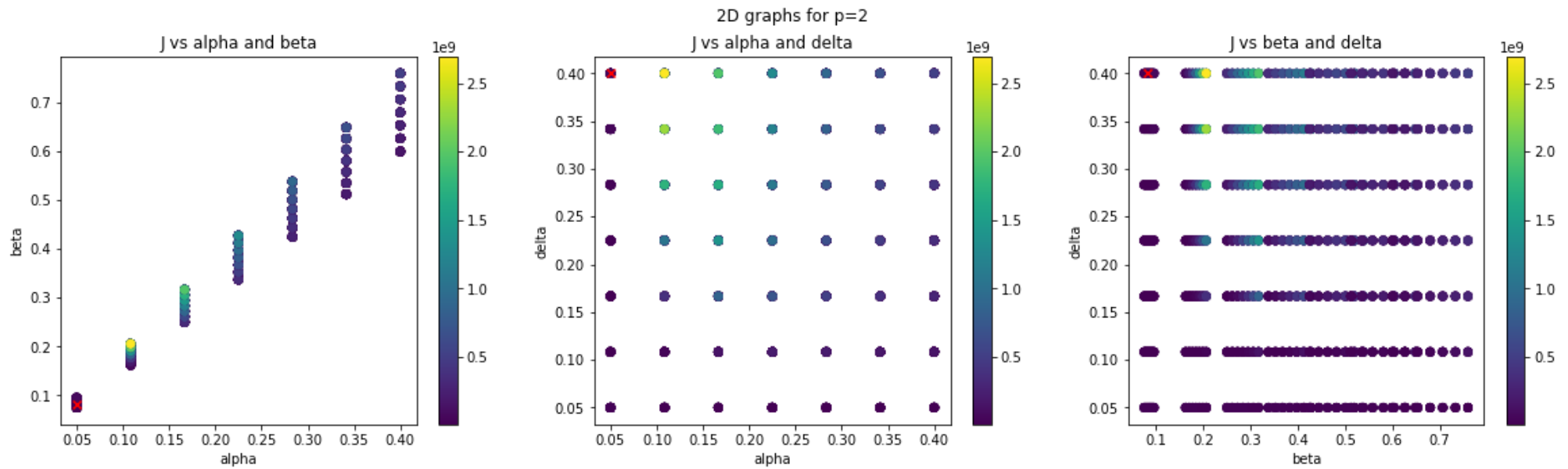
<Figure size 432x288 with 0 Axes>

Infected and Deaths for p=1



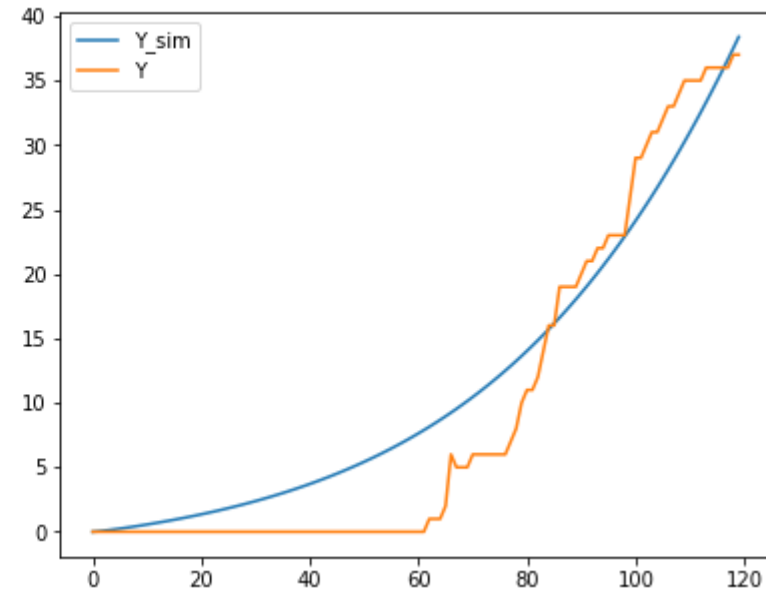
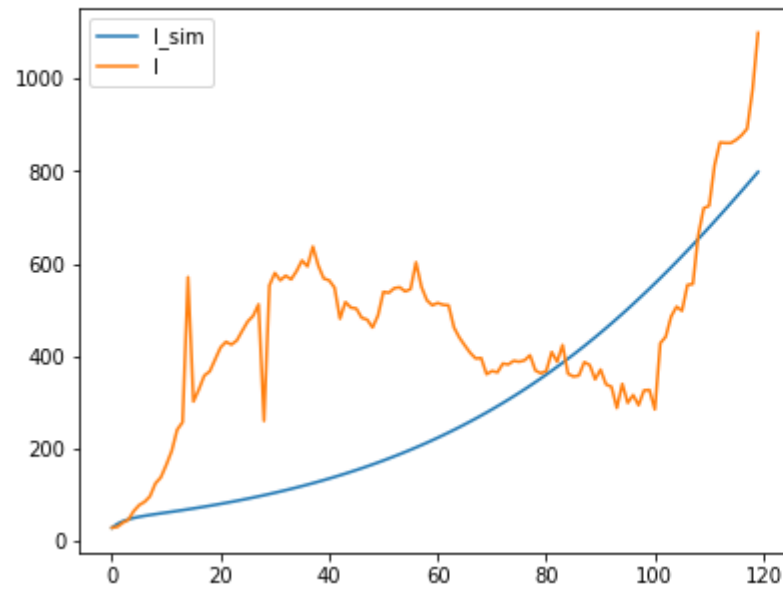
[p=2] alpha: 0.05, beta: 0.08166666666666667, delta: 0.4, r0: 1.6333333333333333, N: 17630.98, gamma: 0.022269691829954686, J: 7946493.282757058

<Figure size 432x288 with 0 Axes>

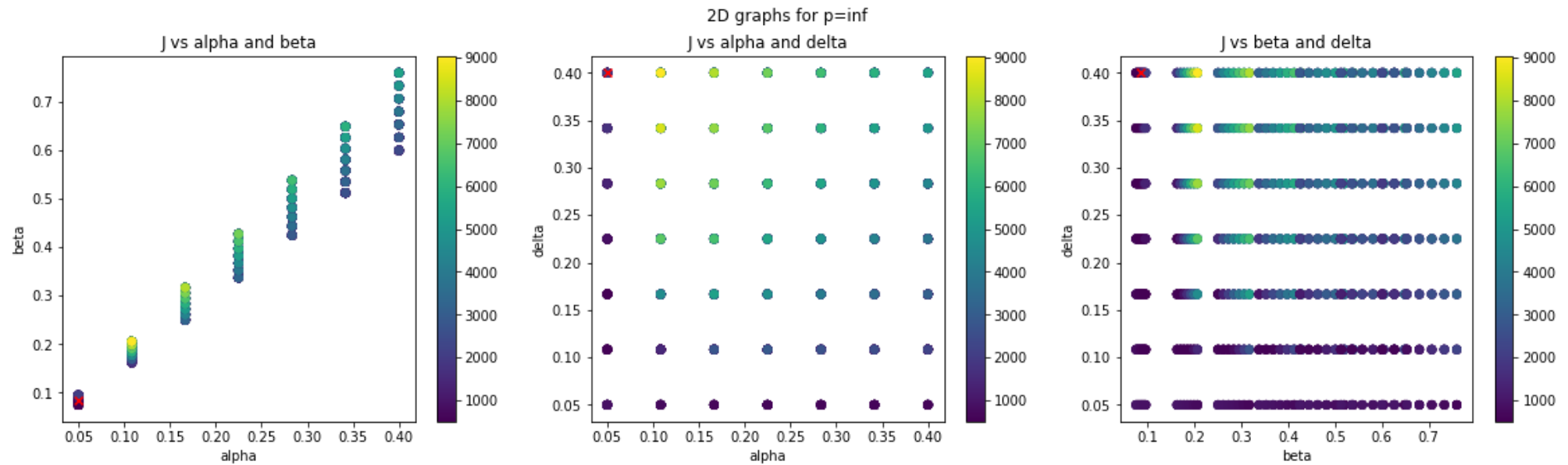


<Figure size 432x288 with 0 Axes>

Infected and Deaths for $p=2$

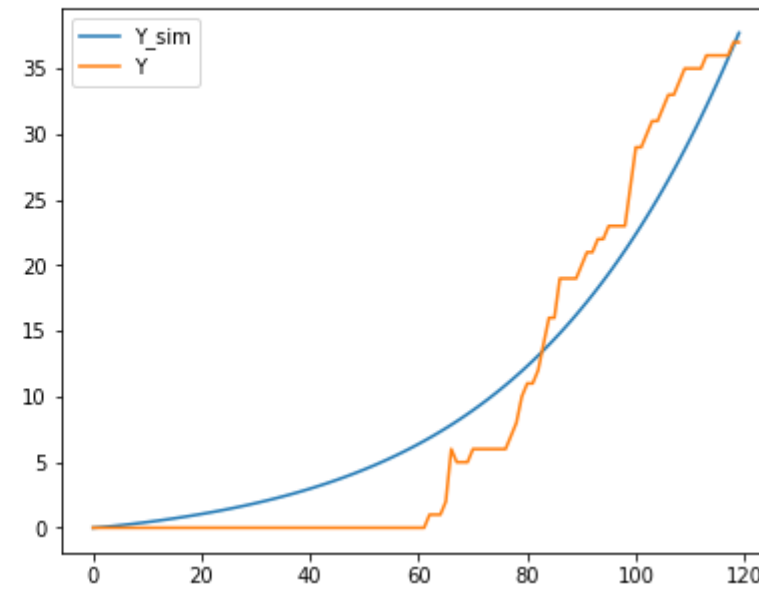
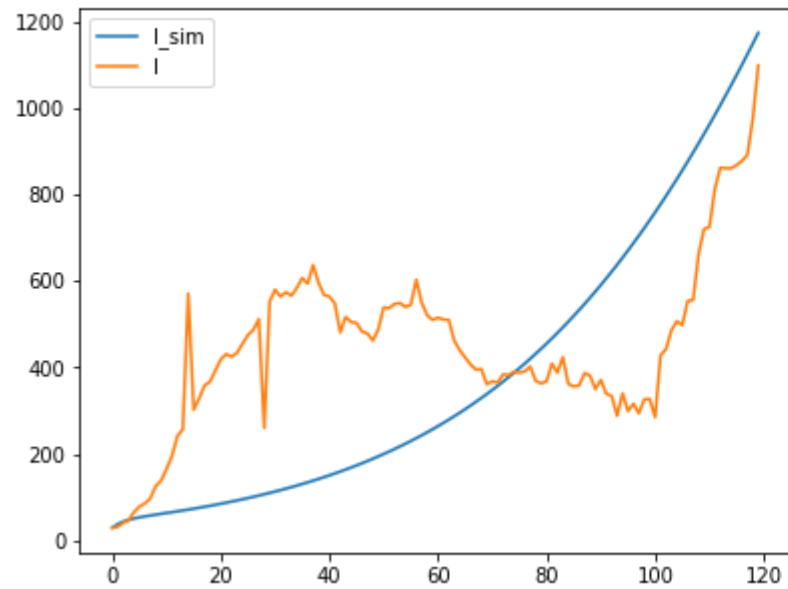


[$p=\text{inf}$] α : 0.05, β : 0.085, δ : 0.4, r_0 : 1.7, N : 29384.966666666667, γ : 0.01687606295482428, J : 506.548849860189
 <Figure size 432x288 with 0 Axes>



<Figure size 432x288 with 0 Axes>

Infected and Deaths for $p=\text{inf}$



Question (4)

If you are asked to improve the estimates, what would be your refined range of parameters?

The above data shows that the expected α is 0.05 (on the very left), while the expected β is between 0.05 to 0.1 ($R_0 = 1.5$).

The δ is on the very top, so we probably need to improve the sampling range.

We probably rerun the experiments with $\alpha \in [0.04, 0.075]$, $R_0 \in [1.4, 1.6]$, and $\delta \in [0.35, 0.5]$.