Module 4: *(Template)*

RENAME THE FILE TO INCLUDE YOUR COMPANY, GROUP NUMBER, AND LAST NAMES

E.G. KAMEN1_GROVES_MODULE_4.IPYNB

Team Members:

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Project Title:

SIR Model of Disease Spread

Project Goal:

This project seeks to establish a 'model' (using differential equations) that is able to accurately predict disease spread for a given population, using Euler approximation, Runge-Kutta approximation, and a SEIRS-type approach.

Disease Background:

Middle East respiratory syndrome coronavirus (MERS-CoV)

- Prevalence & incidence

MERS-Cov was first reported in Saudi Arabia in 2012. Since then, around 2600 laboratory-confirmed cases of MERS-CoV have been reported globally since 2012, across 27 countries including 12 countrires in the Middle Eastern region. Of these cases, 948 deaths have been reported.

Source: https://www.emro.who.int/health-topics/mers-cov/mers-outbreaks.html https://iris.who.int/server/api/core/bitstreams/276466de-a41a-427d-aa42-5d99cd15ecdc/content

- Economic burden

According to a study published on the NLM database, the average cost of managing a MERS case at Saudi hospitals ranged from $1278.41to$75,987.96 with a mean cost of $12,947.03\pm$19,923.14. Another study pubished on the same database reported that the MERS outbreak in 2015 was correlated "with a reduction of 2.1 million non-citizen visitors corresponding with US $2.6 billion in tourism loss for the ROK [Republic of Korea]."

Source: https://pmc.ncbi.nlm.nih.gov/articles/PMC6560634/ https://pmc.ncbi.nlm.nih.gov/articles/PMC6844224/

- Risk factors (genetic, lifestyle) & Societal determinants

Risk factors for MERS include old age, previous medical conditions (diabetes, kidney disease, cancer), a weakened immune system, smoking, exposure to camels, and poor hygiene. Societal determinants of MERS infection include socioeconomic status, occupation, location (Saudi Arabia), and access to healthcare.

Source: https://www.medicalnewstoday.com/articles/262538#symptoms https://bmcpublichealth.biomedcentral.com/articles/10.1186/s12889-018-5484-8

- Symptoms

Common symptoms of MERS include fever, cough, shortness of breath, diarrhea, nausea, or vomiting. Symptoms usually appear within 6 days of exposure, but some people experience very mild or no symptoms.

Source: https://www.cdc.gov/mers/about/index.html

- Diagnosis

To diagnose MERS, a healthcare provider will perform a normal clinical evaluation (travel history, contact with infected people, camel exposure) and a physical exam. They may also take a chest X-ray, blood tests, or a nasal/throat swab. Normally, MERS is officially diagnosed with a Reverse Transcription Polymerase Chain Reaction test, which detects MERS RNA.

Source: https://www.hopkinsmedicine.org/health/conditions-and-diseases/middle-east-respiratory-syndrome-mers

- Biological mechanisms (anatomy, organ physiology, cell & molecular physiology)

Anatomy/Organ Physiology: Targets lower respiratory tract, kidneys, and immune cells via DPP4 receptor. This receptor is found in alveolar epithelial cells, kidney cells, and immune cells, which explains why MERS can cause lung failure.

Cell & Molecular Physiology: Virus binds to DPP4 receptor, viral RNA enters the cytoplasm, replicates, blocks interferons (slow immune response), delays cytokine release, results in damaged lung tissue, cell death, fluid buildup, and organ damage.

Source: https://pmc.ncbi.nlm.nih.gov/articles/PMC7104727/#s0190 https://pmc.ncbi.nlm.nih.gov/articles/PMC7155742/

Dataset:

We are using the MERS Outbreaks dataset from 2012-2019, found on Kaggle. Each row contains a report from each region/location per day, while each column represents number of cases per country/region. From the dataset we are only looking at cases in Saudi Arabia to conduct our SIR model. The data is extracted from the World Health Organization. The GitHub repository contains two datasets, one with data unorganized, and a "cleaned" dataset with cases ordered from week 12 of 2012 onward. Cases for Saudi Arabia, South Korea, and "rest of world" are included.

https://www.kaggle.com/datasets/imdevskp/mers-outbreak-dataset-20122019/data Data extracted from: https://www.who.int/health-topics/middle-east-respiratory-syndrome-coronavirus-mers#tab=tab_1

(Describe the data set you will analyze. Cite the source(s) of the data. Describe how the data was collected -- What techniques were used? What units are the data measured in? Etc.)

Data Analyis:

Methods

We used Euler approximation, Runge-Kutta, and an attempted "improved" model that considered two different populations, South Korea (less infectious) and Saudi Arabia (more infectious), an approach similar in nature to a SEIRS model.

Analysis

We loaded the MERS Saudi Arabia dataset and converted the date column to a datetime format to analyze the data. We constructed cumulative case counts and daily new cases, which were plotted to visualize overall outbreak trends. Because SIR compartments were not directly available from just the CSV dataset, we used the convert_cumulative_to_SIR function to estimate the Susceptible, Infectious, and Recovered populations from cumulative cases, assuming a population of 30 million and a 14-day infectious period. We plotted the estimated S, I, and R curves to examine disease dynamics. Our initial model only uses Euler's method. Thus, to evaluate model performance, we computed the sum of squared errors (SSE) between the model-predicted and actual infectious populations and optimized the infection (beta) and recovery (gamma) rates to minimize SSE.

Following the SIR model fitting, we retrained our model on only the first half of data to find the SSE, or sum of squared errors, between the predicted and actual 1/2 value. This allowed us to test if our model was actually able to predict disease spread given a chunk of data it hasn't "seen" yet, i.e. we cut of the model's time period, thus how accurately it predict the future? After abtaining our SSE, we began the process of 'optimizing' our model, first using Runge-Kutta optimization through scipy.integrate.solve_ivp with method RK45. Our aim was to prove the hypothesis that using RK4 would result in a lower SSE score using the same 1/2 trainign split, thus acheiving a more 'accurate' model (dicussed more below). Finally, we tested to see if including more data would optimize our model further. Using data from South Korea, we changed our model to consider a high-infection country and a low-infection country (Saudi Arabia and South Korea, respectively). Thus let I_1 = Saudi Arabia, I_2 = South Korea, beta_1 = Saudi Arabia, beta_2 = South Korea, and (ideally) b_1 > b_2. Then I_total = I_1 + I_2. We then defined a new sum new_inf to take the sum of both infections and divide it by time steps. Then if most infections come from I_1, I_1 is the driving force for I_total at any given time t. We introduce a penalty coefficient to "force" the model to have b_1 > b_2 by adding 1e^9*(beta1-beta2)**2 to the penalty so that the optimizer reduces the score and thus keeps b_1 > b_2. This penalty allows us to divide I_0 evenly into I_10 and I_20 by assumption for our initial conditions, since the minimizer will "take care" of things as time t progresses. After running our model, we found that the 'optimal' b_1 =2, b_2 = 0, are the upper and lower bounds of beta, respectively, indicating that the model solely wanted to incorporate data from I_1, suggesting that transmission was contained to just one group (Saudi Arabia). Finally, the split test SSE for this approach was SSE = 1227599.4098615828, nearly double that of RK4 = 676477.9500418671, suggesting this approach is not a valid solution to optimizing our model.

1. Fitting the SIR Model

In [6]:
```
from main_functions import convert_cumulative_to_SIR
import pandas as pd
import matplotlib.pyplot as plt
import matplotlib.dates as mdates
import numpy as np

# Load the MERS dataset
data = pd.read_csv('MERS_Saudi_Arabia_data_2013_2014_new_cases.csv')
print(data.head())
print(data.columns)

# Ensure correct date format
data['date'] = pd.to_datetime(data['date'])

# Create cumulative case count (if raw new cases exist)
data['Cumulative_cases'] = data['confirmed_cases'].cumsum()

# Plot confirmed cases over time
plt.figure(figsize=(10, 6))
plt.plot(
    data['date'],
    data['confirmed_cases'],
    label='Daily Reported MERS Cases',
```

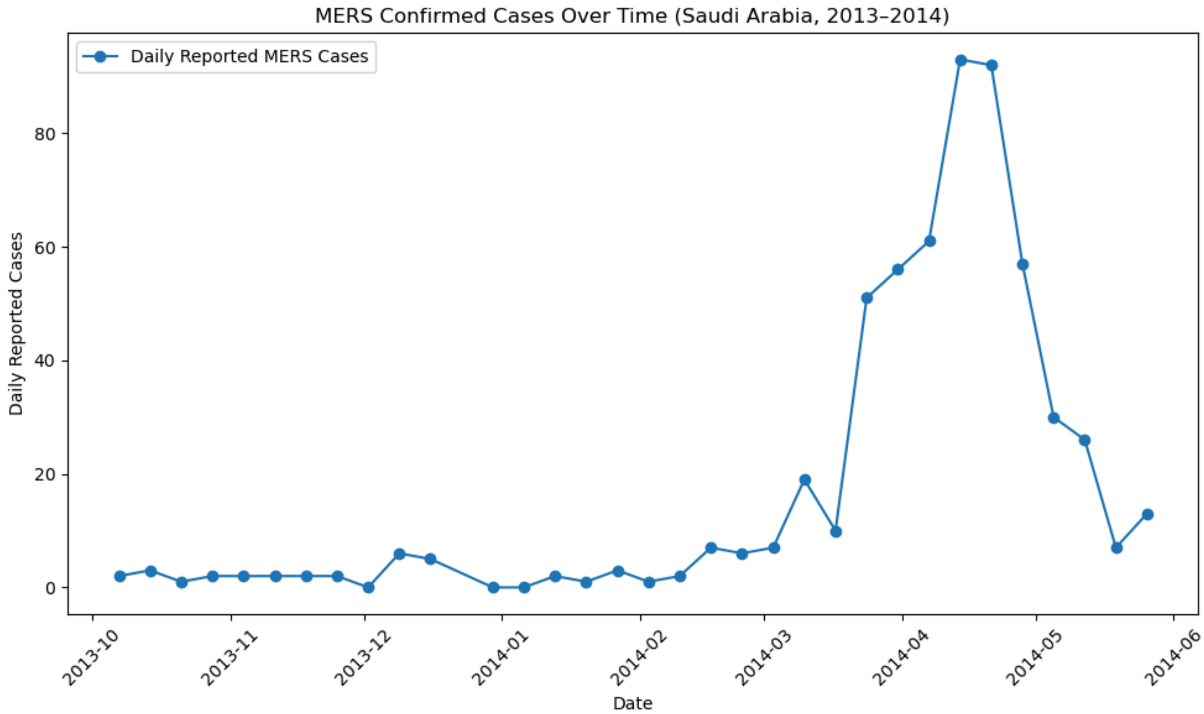
```
    marker="o"
)
plt.xlabel('Date')
plt.ylabel('Daily Reported Cases')
plt.title('MERS Confirmed Cases Over Time (Saudi Arabia, 2013–2014)')
plt.gca().xaxis.set_major_formatter(mdates.DateFormatter('%Y-%m'))
plt.gca().xaxis.set_major_locator(mdates.MonthLocator(interval=1))
plt.xticks(rotation=45)
plt.legend()
plt.tight_layout()
plt.show()

# Compute new cases per day
data['new_cases'] = data['confirmed_cases'].diff().fillna(0)

plt.figure(figsize=(10, 6))
plt.plot(
    data['date'],
    data['new_cases'],
    label='New MERS Cases Per Day',
    marker="o"
)
plt.xlabel('Date')
plt.ylabel('New Cases')
plt.title('Daily New MERS Cases Over Time')
plt.gca().xaxis.set_major_formatter(mdates.DateFormatter('%Y-%m'))
plt.gca().xaxis.set_major_locator(mdates.MonthLocator(interval=1))
plt.xticks(rotation=45)
plt.legend()
plt.tight_layout()
plt.show()

# Convert to SIR estimates
# Estimated Saudi Arabia population (~30 million around 2013–2014)
population = 30000000

data_sir = convert_cumulative_to_SIR(
    data,
    date_col='date',
    cumulative_col='Cumulative_cases',
    population=population,
    infectious_period=14,  # adjustable assumption
    new_case_col='new_cases',
    I_col='I_est',
    R_col='R_est',
    S_col='S_est'
)

# Plot infectious population estimate
plt.figure(figsize=(10, 6))
plt.plot(
    data_sir['date'],
    data_sir['I_est'],
    label='Estimated Infectious (I)',
    color='red'
)
```

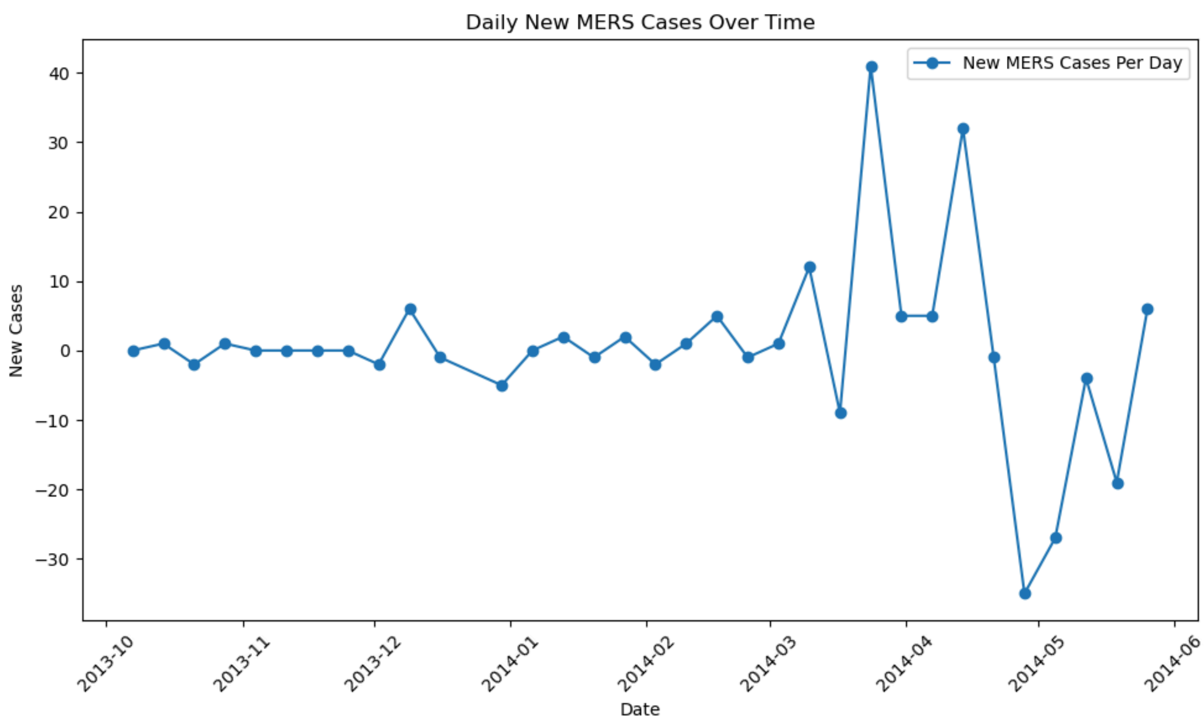
```
plt.xlabel('Date')
plt.ylabel('Estimated Infectious Individuals')
plt.title('Estimated MERS Infections Over Time (I(t))')
plt.gca().xaxis.set_major_formatter(mdates.DateFormatter('%Y-%m'))
plt.gca().xaxis.set_major_locator(mdates.MonthLocator(interval=1))
plt.xticks(rotation=45)
plt.legend()
plt.tight_layout()
plt.show()

# Plot SIR curves
plt.figure(figsize=(10, 6))
plt.plot(
    data_sir['date'],
    data_sir['S_est'],
    label='Susceptible (S)',
    color='blue'
)
plt.plot(
    data_sir['date'],
    data_sir['I_est'],
    label='Infectious (I)',
    color='red'
)
plt.plot(
    data_sir['date'],
    data_sir['R_est'],
    label='Recovered (R)',
    color='green'
)
plt.xlabel('Date')
plt.ylabel('Population Count')
plt.title('Approximated SIR Model for MERS (Saudi Arabia)')
plt.gca().xaxis.set_major_formatter(mdates.DateFormatter('%Y-%m'))
plt.gca().xaxis.set_major_locator(mdates.MonthLocator(interval=1))
plt.xticks(rotation=45)
plt.legend()
plt.tight_layout()
plt.show()


# Compare true and model I(t) using SSE
def euler_sir(beta, gamma, S0, I0, R0, t, N):
    """ Solve the SIR model using Euler's method.

    Parameters:
    - beta: Infection rate
    - gamma: Recovery rate
    - S0: Initial susceptible population
    - I0: Initial infected population
    - R0: Initial recovered population
    - t: Array of time points (days or weeks)
    - N: Total population

    Returns:
    - S: Array of susceptible population over time
```

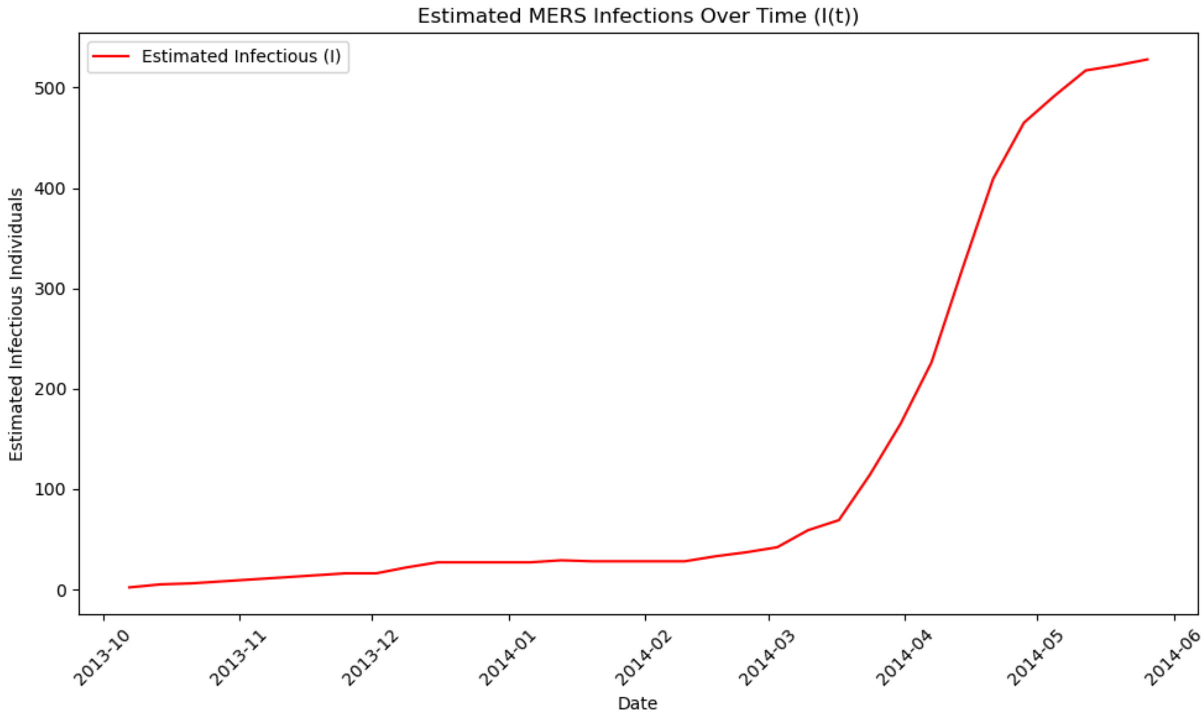
```
    - I: Array of infected population over time
    - R: Array of recovered population over time
    """
    S = np.empty(len(t), float)
    I = np.empty(len(t), float)
    R = np.empty(len(t), float)

    # Initial conditions
    S[0], I[0], R[0] = S0, I0, R0

    for n in range(len(t) - 1):
        dt = t[n + 1] - t[n]

        # Differential equations for SIR model
        dS = -beta * S[n] * I[n] / N
        dI = beta * S[n] * I[n] / N - gamma * I[n]
        dR = gamma * I[n]

        # Euler update steps
        S[n + 1] = S[n] + dS * dt
        I[n + 1] = I[n] + dI * dt
        R[n + 1] = R[n] + dR * dt

    return S, I, R


# find true I(t)
true_I = data_sir['I_est'].values
dates = data_sir['date'].values
N = population  # Saudi population

# initial conditions
I0 = true_I[0]
R0 = 0
S0 = N - I0

# time array
t = np.arange(len(true_I))

# run model with gamma and beta guesses
beta_guess = 0.3
gamma_guess = 0.1
S_model, I_model, R_model = euler_sir(beta_guess, gamma_guess, S0, I0, R0, t

# plot model I(t) vs. true I(t)
plt.figure(figsize=(10, 6))
plt.plot(dates, true_I, label="True I(t) (from data)", color="black")
plt.plot(dates, I_model, label="Model I(t)", color="red", linestyle="--")
plt.title(f"Initial SIR Model Fit (β={beta_guess}, γ={gamma_guess})")
plt.xlabel("Date")
plt.ylabel("Infectious Individuals")
plt.legend()
plt.xticks(rotation=45)
plt.show()
```

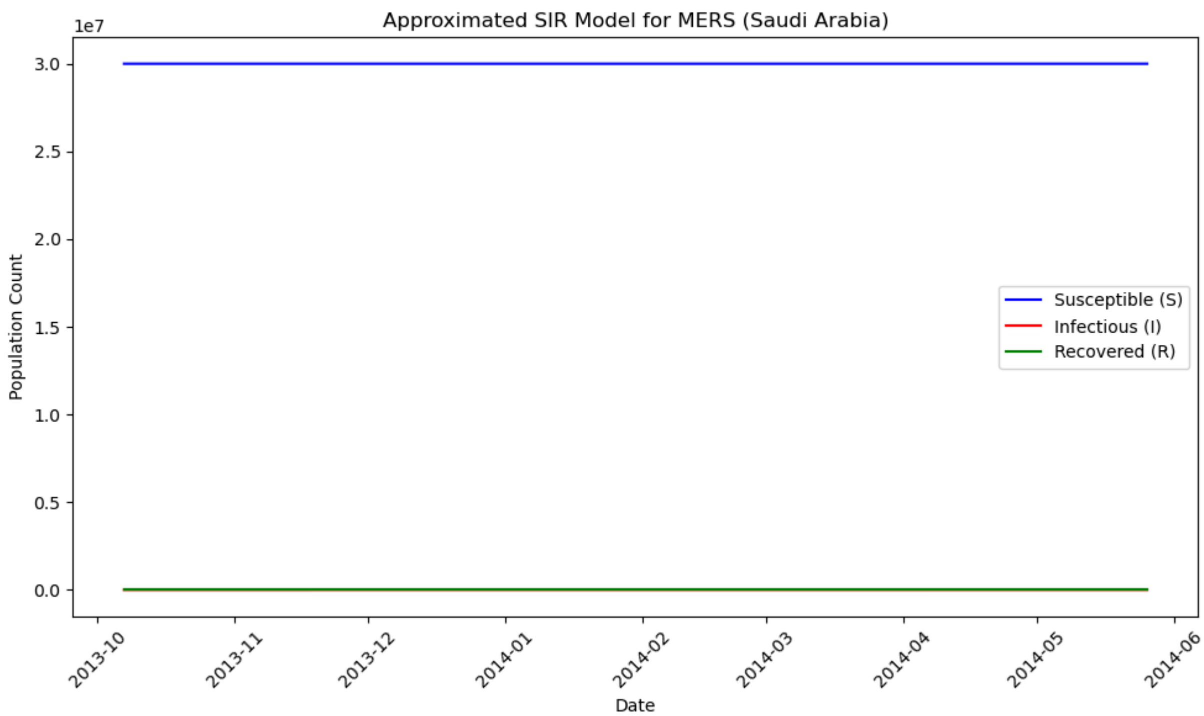
```python
# SSE function
def SSE(model_I, true_I):
    return np.sum((model_I - true_I) ** 2)


# fit gamma and beta to minimize SSE
from scipy.optimize import minimize


def objective(params):
    beta, gamma = params
    _, I_temp, _ = euler_sir(beta, gamma, S0, I0, R0, t, N)
    return SSE(I_temp, true_I)


initial_guess = [3, 5] # This is inputted by us (we can change it to see how
result = minimize(objective, initial_guess, bounds=[(0, 2), (0, 2)])
beta_opt, gamma_opt = result.x

print("Optimal beta:", beta_opt)
print("Optimal gamma:", gamma_opt)

# After computing I_model from Euler on the full dataset:

def SSE(model_I, true_I):
    return np.sum((model_I - true_I)**2)

sse_full = SSE(I_model, true_I)
print("Full-data SSE:", sse_full)
```

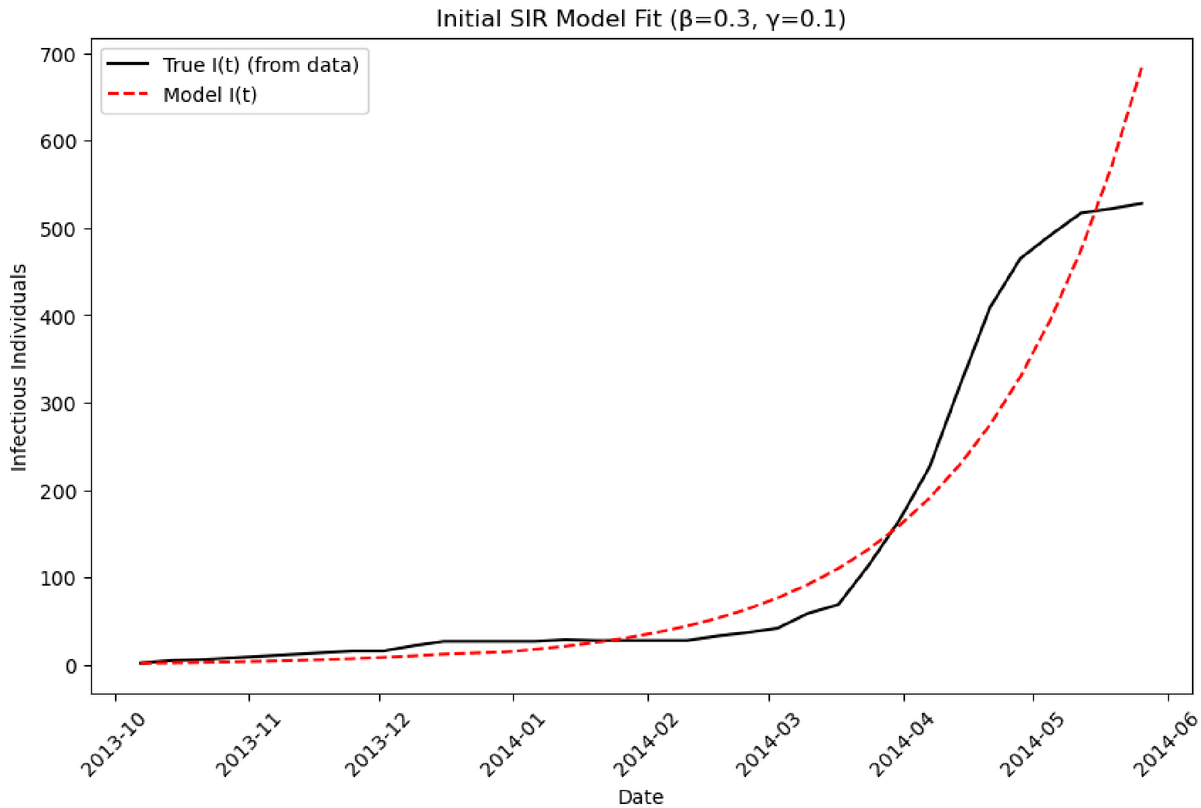
```
         date  confirmed_cases
0  2013-10-07                2
1  2013-10-14                3
2  2013-10-21                1
3  2013-10-28                2
4  2013-11-04                2
Index(['date', 'confirmed_cases'], dtype='object')
```


MERS Confirmed Cases Over Time (Saudi Arabia, 2013–2014)
Daily Reported MERS Cases
Daily Reported Cases
Date
0
20
40
60
80
2013-10
2013-11
2013-12
2014-01
2014-02
2014-03
2014-04
2014-05
2014-06


Daily New MERS Cases Over Time
New MERS Cases Per Day
New Cases
Date
40
30
20
10
0
−10
−20
−30
2013-10
2013-11
2013-12
2014-01
2014-02
2014-03
2014-04
2014-05
2014-06


Estimated MERS Infections Over Time (I(t))
Estimated Infectious (I)
Estimated Infectious Individuals
0
100
200
300
400
500
2013-10
2013-11
2013-12
2014-01
2014-02
2014-03
2014-04
2014-05
2014-06
Date


Approximated SIR Model for MERS (Saudi Arabia)
1e7
Population Count
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Susceptible (S)
Infectious (I)
Recovered (R)
2013-10
2013-11
2013-12
2014-01
2014-02
2014-03
2014-04
2014-05
2014-06
Date




```
Optimal beta: 2.0
Optimal gamma: 1.7998542365660475
Full-data SSE: 90089.37777766612
```

2. 1/2 Train/Test Split

In [3]:
```
from main_functions import convert_cumulative_to_SIR
import pandas as pd
import matplotlib.pyplot as plt
import matplotlib.dates as mdates
import numpy as np

# Load the MERS dataset
data = pd.read_csv('MERS_Saudi_Arabia_data_2013_2014_new_cases.csv')

print(data.head())
print(data.columns)

# Ensure correct date format
data['date'] = pd.to_datetime(data['date'])

# Create cumulative case count (if raw new cases exist)
data['Cumulative_cases'] = data['confirmed_cases'].cumsum()

# Plot confirmed cases over time
plt.figure(figsize=(10, 6))
plt.plot(
    data['date'],
    data['confirmed_cases'],
    label='Daily Reported MERS Cases',
    marker="o"
```

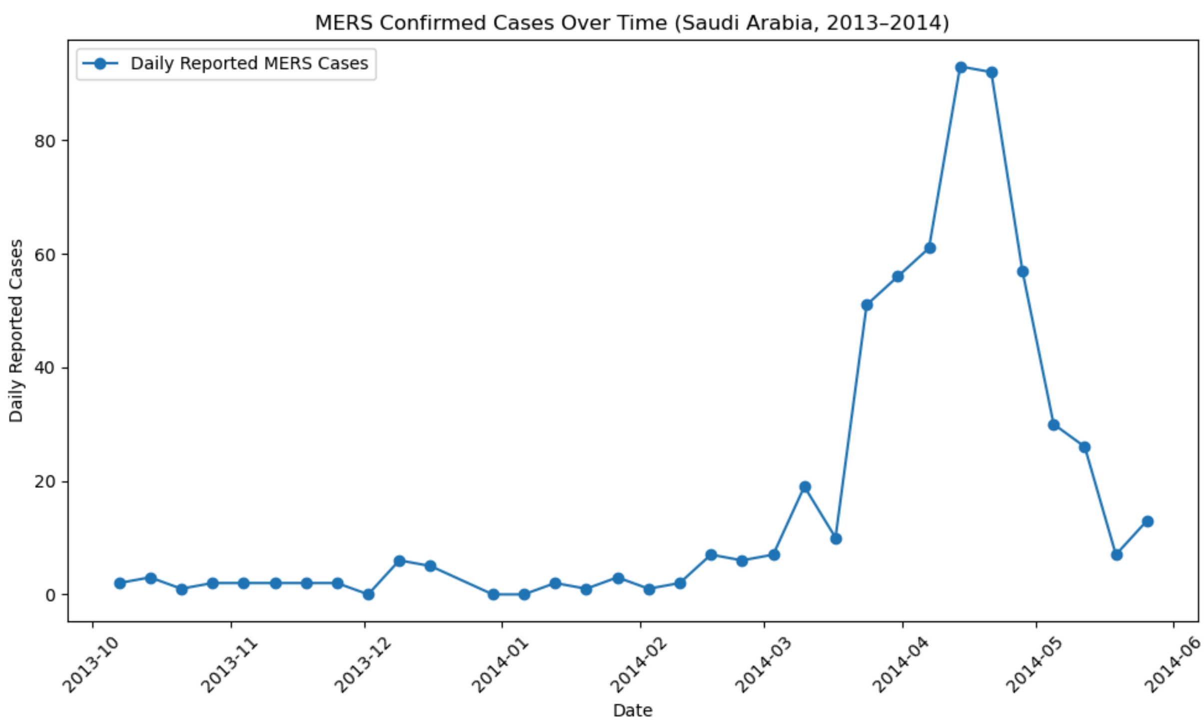
```python
)

plt.xlabel('Date')
plt.ylabel('Daily Reported Cases')
plt.title('MERS Confirmed Cases Over Time (Saudi Arabia, 2013–2014)')
plt.gca().xaxis.set_major_formatter(mdates.DateFormatter('%Y-%m'))
plt.gca().xaxis.set_major_locator(mdates.MonthLocator(interval=1))
plt.xticks(rotation=45)
plt.legend()
plt.tight_layout()
plt.show()

# Compute new cases per day
data['new_cases'] = data['confirmed_cases'].diff().fillna(0)

plt.figure(figsize=(10, 6))
plt.plot(
    data['date'],
    data['new_cases'],
    label='New MERS Cases Per Day',
    marker="o"
)

plt.xlabel('Date')
plt.ylabel('New Cases')
plt.title('Daily New MERS Cases Over Time')
plt.gca().xaxis.set_major_formatter(mdates.DateFormatter('%Y-%m'))
plt.gca().xaxis.set_major_locator(mdates.MonthLocator(interval=1))
plt.xticks(rotation=45)
plt.legend()
plt.tight_layout()
plt.show()

# Convert to SIR estimates
# Estimated Saudi Arabia population (~30 million around 2013–2014)
population = 30000000

data_sir = convert_cumulative_to_SIR(
    data,
    date_col='date',
    cumulative_col='Cumulative_cases',
    population=population,
    infectious_period=14,  # adjustable assumption
    new_case_col='new_cases',
    I_col='I_est',
    R_col='R_est',
    S_col='S_est'
)

# Plot infectious population estimate
plt.figure(figsize=(10, 6))
plt.plot(
    data_sir['date'],
    data_sir['I_est'],
    label='Estimated Infectious (I)',
    color='red'
```

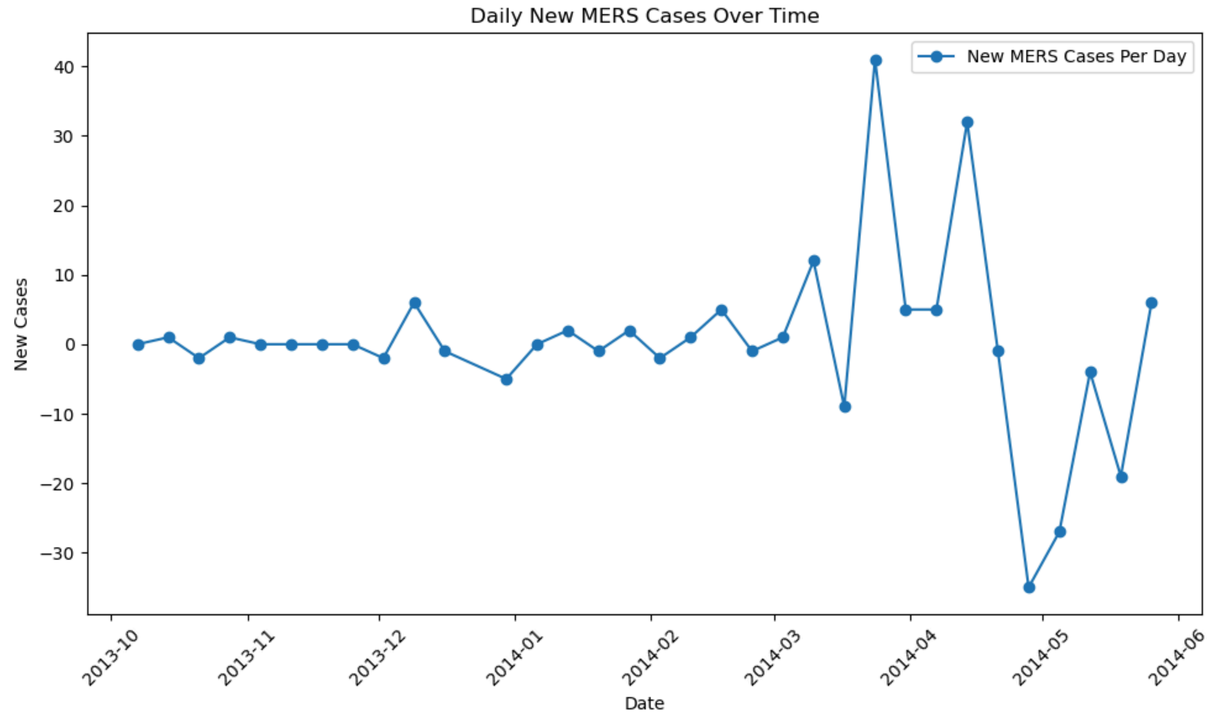
```
)

plt.xlabel('Date')
plt.ylabel('Estimated Infectious Individuals')
plt.title('Estimated MERS Infections Over Time (I(t))')
plt.gca().xaxis.set_major_formatter(mdates.DateFormatter('%Y-%m'))
plt.gca().xaxis.set_major_locator(mdates.MonthLocator(interval=1))
plt.xticks(rotation=45)
plt.legend()
plt.tight_layout()
plt.show()

# Plot SIR curves
plt.figure(figsize=(10, 6))

plt.plot(data_sir['date'], data_sir['S_est'], label='Susceptible (S)', color
plt.plot(data_sir['date'], data_sir['I_est'], label='Infectious (I)', color=
plt.plot(data_sir['date'], data_sir['R_est'], label='Recovered (R)', color='

plt.xlabel('Date')
plt.ylabel('Population Count')
plt.title('Approximated SIR Model for MERS (Saudi Arabia)')
plt.gca().xaxis.set_major_formatter(mdates.DateFormatter('%Y-%m'))
plt.gca().xaxis.set_major_locator(mdates.MonthLocator(interval=1))
plt.xticks(rotation=45)
plt.legend()
plt.tight_layout()
plt.show()

# Compare true and model I(t) using SSE

# Compare true and model I(t) using SSE

def euler_sir(beta, gamma, S0, I0, R0, t, N):
    """
    Solve the SIR model using Euler's method.
    """
    S = np.empty(len(t), float)
    I = np.empty(len(t), float)
    R = np.empty(len(t), float)

    # Initial conditions
    S[0], I[0], R[0] = S0, I0, R0

    for n in range(len(t) - 1):
        dt = t[n + 1] - t[n]

        # Differential equations for SIR model
        dS = -beta * S[n] * I[n] / N
        dI = beta * S[n] * I[n] / N - gamma * I[n]
        dR = gamma * I[n]

        # Euler update steps
        S[n + 1] = S[n] + dS * dt
        I[n + 1] = I[n] + dI * dt
        R[n + 1] = R[n] + dR * dt
```

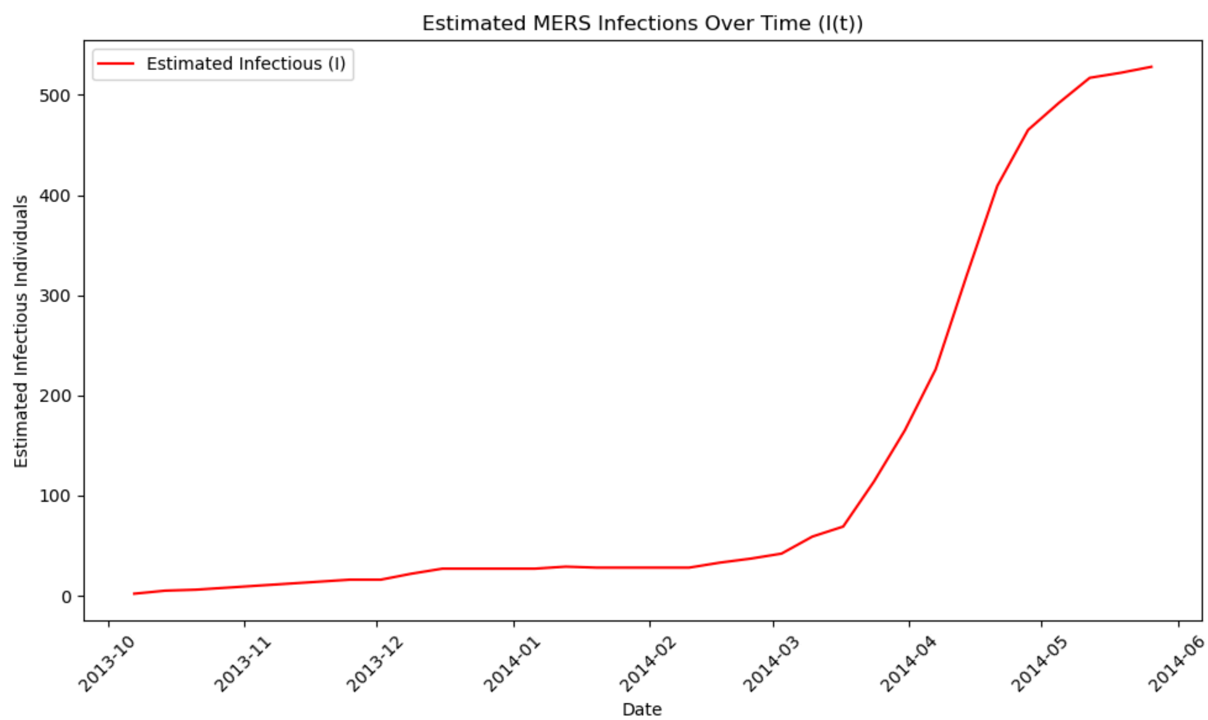
```python
    return S, I, R


# ---------- set up data & split into halves ----------

true_I = data_sir['I_est'].values
dates = data_sir['date'].values
N = population

# time array
t = np.arange(len(true_I))

n = len(true_I)
mid = n // 2  # index that splits first / second half

# first half = training
t_train = t[:mid]
I_train = true_I[:mid]
dates_train = dates[:mid]

# second half = testing
t_test = t[mid:]
I_test = true_I[mid:]
dates_test = dates[mid:]

# initial conditions based on first point in training data
I0 = I_train[0]
R0 = 0
S0 = N - I0


# ---------- SSE + fitting only on FIRST half ----------

def SSE(model_I, true_I_slice):
    return np.sum((model_I - true_I_slice) ** 2)

from scipy.optimize import minimize

def objective(params):
    beta, gamma = params
    _, I_temp, _ = euler_sir(beta, gamma, S0, I0, R0, t_train, N)
    return SSE(I_temp, I_train)

initial_guess = [5, 3]

result = minimize(objective, initial_guess, bounds=[(0, 2), (0, 2)])
beta_opt, gamma_opt = result.x

print("Optimal beta (train only):", beta_opt)
print("Optimal gamma (train only):", gamma_opt)


# ---------- run model on FULL time range with fitted params ----------

S_full, I_full, R_full = euler_sir(beta_opt, gamma_opt, S0, I0, R0, t, N)
```

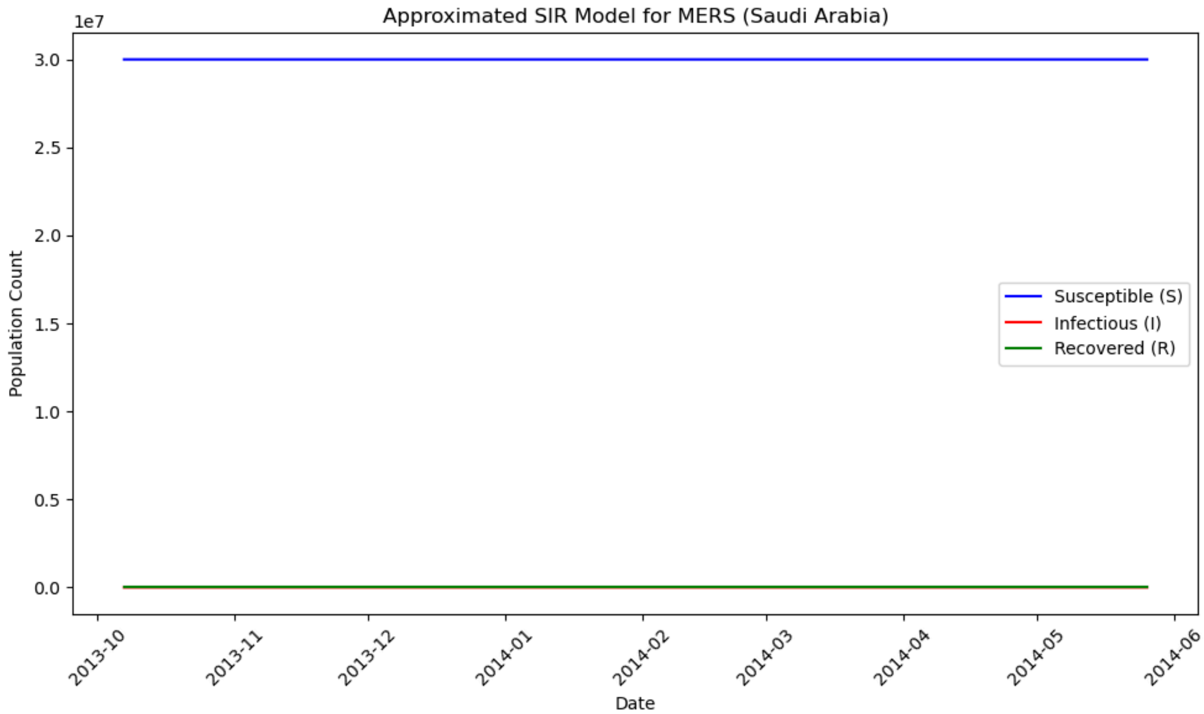
```python
# plot model vs true, with train/test split line
plt.figure(figsize=(10, 6))
plt.plot(dates, true_I, label="True I(t) (data)", color="black")
plt.plot(dates, I_full, label="Model I(t)", color="red", linestyle="--")
plt.axvline(dates[mid], color="gray", linestyle=":", label="Train/Test Split

plt.title(f"SIR Fit: train = first half (β={beta_opt:.3f}, γ={gamma_opt:.3f}
plt.xlabel("Date")
plt.ylabel("Infectious Individuals")
plt.legend()
plt.xticks(rotation=45)
plt.tight_layout()
plt.show()

# ---------- compute SSE on first and second halves ----------

sse_train = SSE(I_full[:mid], I_train)
sse_test  = SSE(I_full[mid:], I_test)

print("Train SSE (first half):", sse_train)
print("Test SSE (second half, Euler error):", sse_test)

sse_test_euler = sse_test  # save for comparison with RK4 later
```

```
         date  confirmed_cases
0  2013-10-07                2
1  2013-10-14                3
2  2013-10-21                1
3  2013-10-28                2
4  2013-11-04                2
Index(['date', 'confirmed_cases'], dtype='object')
```

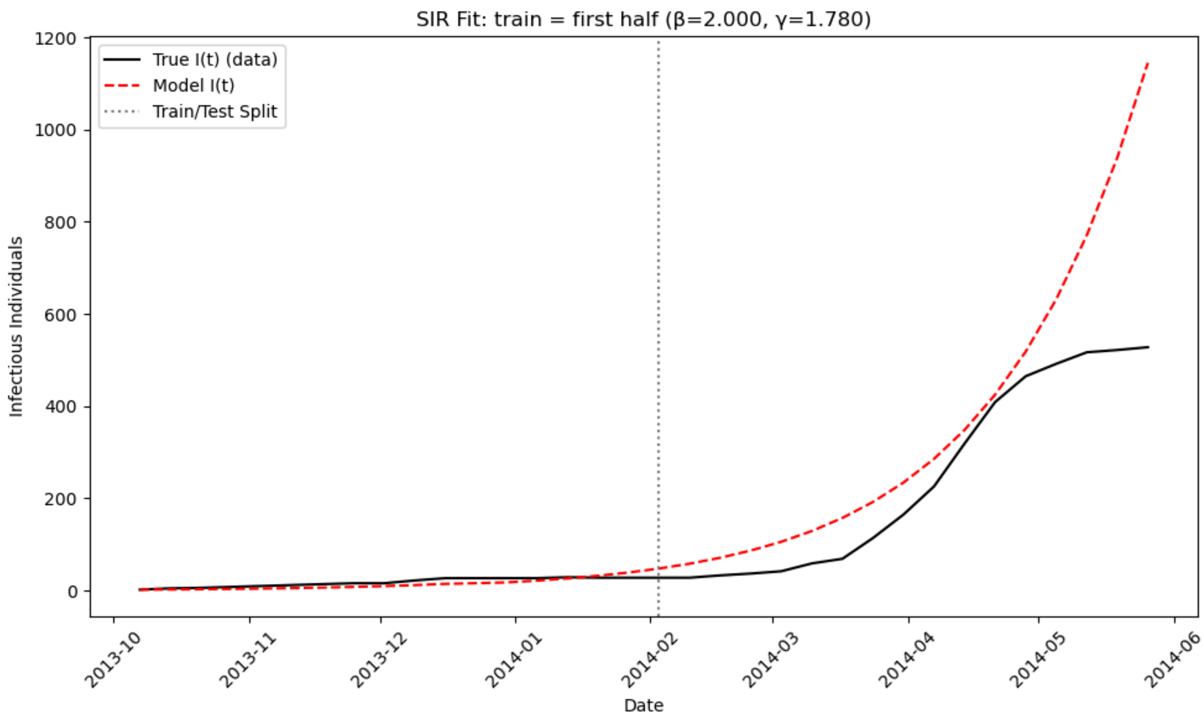



Daily New MERS Cases Over Time
New MERS Cases Per Day
New Cases
Date
40
30
20
10
0
−10
−20
−30
2013-10
2013-11
2013-12
2014-01
2014-02
2014-03
2014-04
2014-05
2014-06


Estimated MERS Infections Over Time (I(t))
Estimated Infectious (I)
Estimated Infectious Individuals
Date
500
400
300
200
100
0
2013-10
2013-11
2013-12
2014-01
2014-02
2014-03
2014-04
2014-05
2014-06




```
Optimal beta (train only): 2.0
Optimal gamma (train only): 1.7804042410853684
```




```
Train SSE (first half): 788.427015468611
Test SSE (second half, Euler error): 679393.5697174852
```

Using RK4 Method

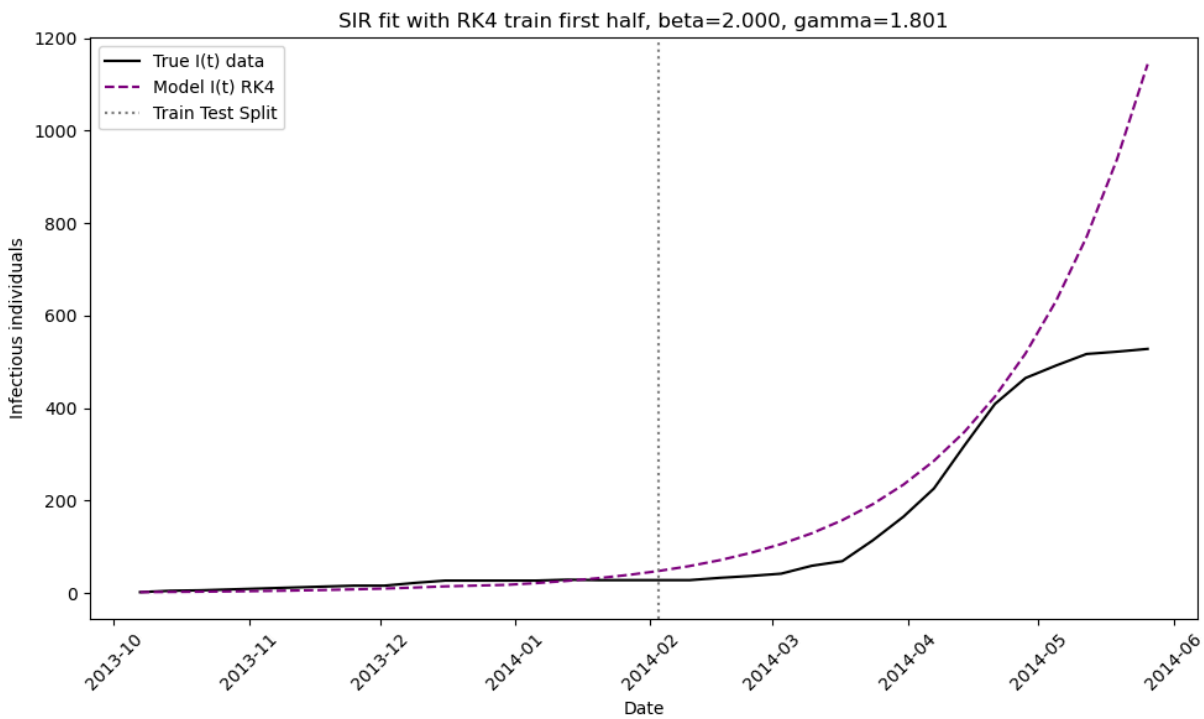
In [4]:

```
from scipy.integrate import solve_ivp

def sir_rhs(t, y, beta, gamma, N):
    # Right hand side for SIR ODEs
    S, I, R = y
```

```
    dSdt = -beta * S * I / N
    dIdt = beta * S * I / N - gamma * I
    dRdt = gamma * I
    return [dSdt, dIdt, dRdt]

def sir_solve_ivp(beta, gamma, S0, I0, R0, t, N):
    # Solve SIR using solve_ivp with RK45
    y0 = [S0, I0, R0]
    t_span = (t[0], t[-1])

    sol = solve_ivp(
        fun=lambda tau, y: sir_rhs(tau, y, beta, gamma, N),
        t_span=t_span,
        y0=y0,
        t_eval=t,
        method="RK45",
        rtol=1e-6,
        atol=1e-9
    )

    S = sol.y[0]
    I = sol.y[1]
    R = sol.y[2]
    return S, I, R

def objective_rk(params):
    # Objective for fitting beta and gamma on first half using RK4
    beta, gamma = params
    _, I_temp, _ = sir_solve_ivp(beta, gamma, S0, I0, R0, t_train, N)
    return SSE(I_temp, I_train)

initial_guess_rk = [5, 3]

result_rk = minimize(objective_rk, initial_guess_rk, bounds=[(0, 2), (0, 2)]
beta_rk, gamma_rk = result_rk.x

print("RK4 beta train only:", beta_rk)
print("RK4 gamma train only:", gamma_rk)

# Simulate over full time range with RK4 fit
S_rk_full, I_rk_full, R_rk_full = sir_solve_ivp(beta_rk, gamma_rk, S0, I0, R

plt.figure(figsize=(10, 6))
plt.plot(dates, true_I, label="True I(t) data", color="black")
plt.plot(dates, I_rk_full, label="Model I(t) RK4", color="purple", linestyle
plt.axvline(dates[mid], color="gray", linestyle=":", label="Train Test Split
plt.title(f"SIR fit with RK4 train first half, beta={beta_rk:.3f}, gamma={ga
plt.xlabel("Date")
plt.ylabel("Infectious individuals")
plt.legend()
plt.xticks(rotation=45)
plt.tight_layout()
plt.show()

# SSE on first and second halves for RK4
sse_train_rk = SSE(I_rk_full[:mid], I_train)
```

```
sse_test_rk = SSE(I_rk_full[mid:], I_test)

rmse_train_rk = np.sqrt(sse_train_rk / len(I_train))
rmse_test_rk = np.sqrt(sse_test_rk / len(I_test))

print("Train SSE RK4 first half:", sse_train_rk)
print("Test SSE RK4 second half:", sse_test_rk)
print("Train RMSE RK4 first half:", rmse_train_rk)
print("Test RMSE RK4 second half:", rmse_test_rk)

# Compare RK4 with Euler on second half
print("Euler test SSE second half:", sse_test_euler)
print("RK4   test SSE second half:", sse_test_rk)
```

```
RK4 beta train only: 2.0
RK4 gamma train only: 1.8014782540813967
```




```
Train SSE RK4 first half: 788.4061654248368
Test SSE RK4 second half: 676477.9500418671
Train RMSE RK4 first half: 7.019642821330178
Test RMSE RK4 second half: 199.48137905754027
Euler test SSE second half: 679393.5697174852
RK4   test SSE second half: 676477.9500418671
```

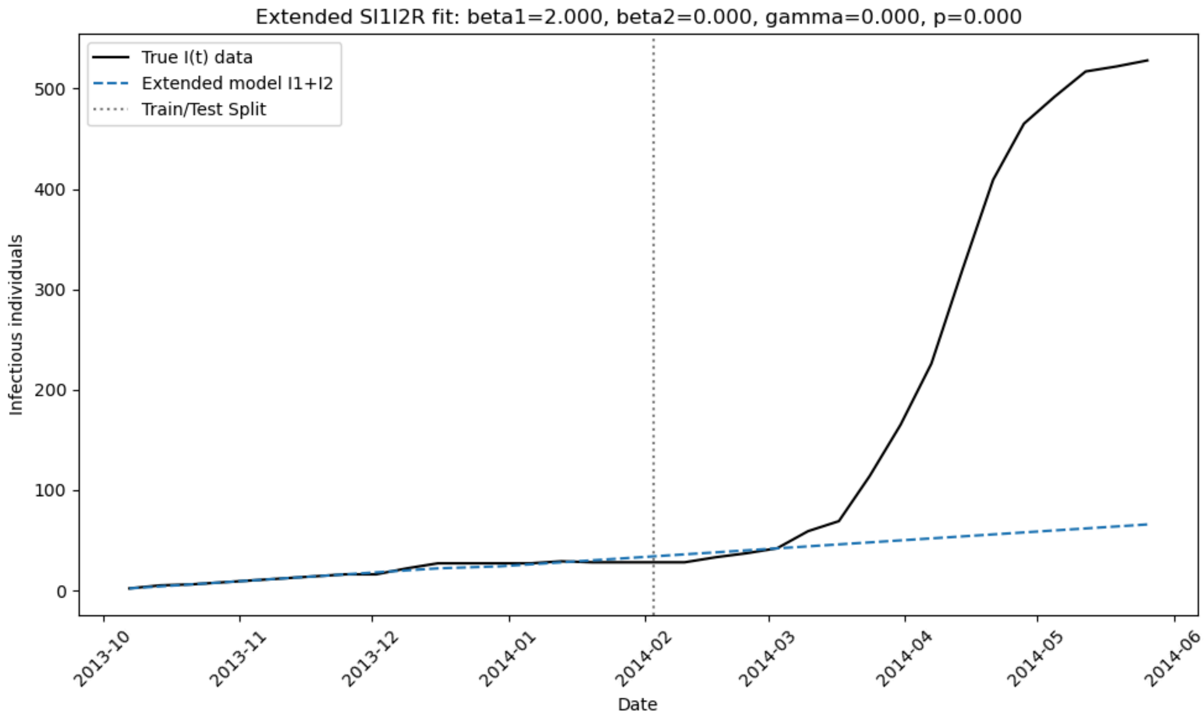
Extending the SIR model (incorporating South Korea data)

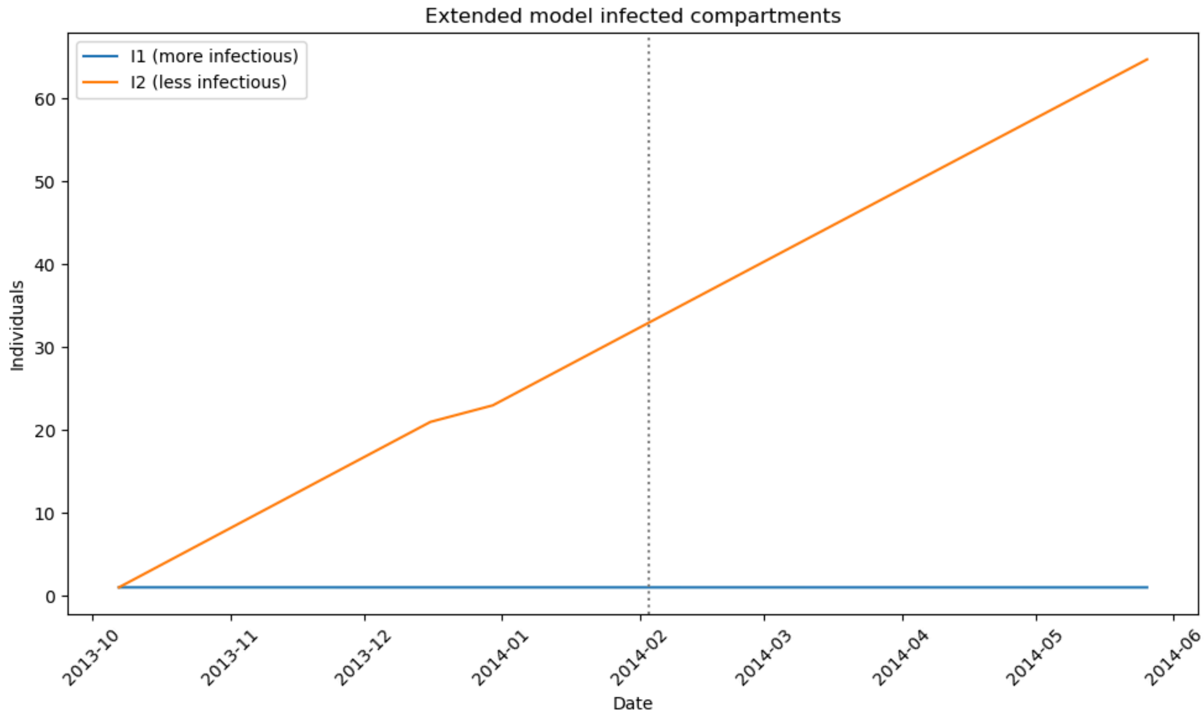
In [5]:
```
from scipy.integrate import solve_ivp

# -------- Extended model RHS: S, I1, I2, R --------
def si1i2r_rhs(t, y, beta1, beta2, gamma, p, N):
    S, I1, I2, R = y

    # force of infection uses both infected groups
```

```python
    new_inf = (beta1 * I1 + beta2 * I2) * S / N

    dS  = -new_inf
    dI1 =  p * new_inf - gamma * I1
    dI2 = (1 - p) * new_inf - gamma * I2
    dR  = gamma * (I1 + I2)

    return [dS, dI1, dI2, dR]

def si1i2r_solve_ivp(beta1, beta2, gamma, p, S0, I10, I20, R0, t, N):
    y0 = [S0, I10, I20, R0]
    t_span = (t[0], t[-1])

    sol = solve_ivp(
        fun=lambda tau, y: si1i2r_rhs(tau, y, beta1, beta2, gamma, p, N),
        t_span=t_span,
        y0=y0,
        t_eval=t,
        method="RK45",
        rtol=1e-6,
        atol=1e-9
    )

    S  = sol.y[0]
    I1 = sol.y[1]
    I2 = sol.y[2]
    R  = sol.y[3]
    I_total = I1 + I2
    return S, I1, I2, I_total, R

# -------- Objective: fit on first half --------
# split initial I0 into two groups (simple: 50/50)
I10 = 0.5 * I0
I20 = 0.5 * I0

def objective_ext(params):
    beta1, beta2, gamma, p = params

    # enforce beta1 >= beta2 (Saudi-like more infectious group vs less infec
    penalty = 0.0
    if beta1 < beta2:
        penalty += 1e9 * (beta2 - beta1)**2

    _, _, _, I_temp, _ = si1i2r_solve_ivp(beta1, beta2, gamma, p, S0, I10, I
    return SSE(I_temp, I_train) + penalty

init_guess = [1.0, 0.3, 0.2, 0.5]  # beta1, beta2, gamma, p
bounds = [(0, 2), (0, 2), (0, 2), (0, 1)]

res_ext = minimize(objective_ext, init_guess, bounds=bounds)
beta1_fit, beta2_fit, gamma_fit, p_fit = res_ext.x

print("EXT beta1 (more infectious):", beta1_fit)
print("EXT beta2 (less infectious):", beta2_fit)
print("EXT gamma:", gamma_fit)
print("EXT p:", p_fit)
```

```
print("beta1 > beta2 ?", beta1_fit > beta2_fit)

# -------- Simulate full with fitted params --------
S_ext, I1_ext, I2_ext, I_ext_full, R_ext = si1i2r_solve_ivp(
    beta1_fit, beta2_fit, gamma_fit, p_fit, S0, I10, I20, R0, t, N
)

# -------- SSE train/test --------
sse_train_ext = SSE(I_ext_full[:mid], I_train)
sse_test_ext  = SSE(I_ext_full[mid:],  I_test)

rmse_train_ext = np.sqrt(sse_train_ext / len(I_train))
rmse_test_ext  = np.sqrt(sse_test_ext  / len(I_test))

print("Train SSE EXT:", sse_train_ext)
print("Test SSE EXT:", sse_test_ext)
print("Train RMSE EXT:", rmse_train_ext)
print("Test RMSE EXT:", rmse_test_ext)

print("\nCompare test SSE:")
print("Baseline SIR test SSE:", sse_test_rk)   # from your Step 5 RK45 SIR
print("Extended  test SSE:", sse_test_ext)

# -------- Plot (total I + optional I1/I2 breakdown) --------
import matplotlib.pyplot as plt

plt.figure(figsize=(10, 6))
plt.plot(dates, true_I, label="True I(t) data", color="black")
plt.plot(dates, I_ext_full, label="Extended model I1+I2", linestyle="--")
plt.axvline(dates[mid], color="gray", linestyle=":", label="Train/Test Split
plt.title(f"Extended SI1I2R fit: beta1={beta1_fit:.3f}, beta2={beta2_fit:.3f
plt.xlabel("Date")
plt.ylabel("Infectious individuals")
plt.legend()
plt.xticks(rotation=45)
plt.tight_layout()
plt.show()

# Show the two infected groups separately
plt.figure(figsize=(10, 6))
plt.plot(dates, I1_ext, label="I1 (more infectious)")
plt.plot(dates, I2_ext, label="I2 (less infectious)")
plt.axvline(dates[mid], color="gray", linestyle=":")
plt.title("Extended model infected compartments")
plt.xlabel("Date")
plt.ylabel("Individuals")
plt.legend()
plt.xticks(rotation=45)
plt.tight_layout()
plt.show()
```

```
EXT beta1 (more infectious): 2.0
EXT beta2 (less infectious): 0.0
EXT gamma: 0.00013762514126407064
EXT p: 0.0
beta1 > beta2 ? True
Train SSE EXT: 64.98404843029954
Test SSE EXT: 1227599.4098615828
Train RMSE EXT: 2.015317103309978
Test RMSE EXT: 268.7224032191172

Compare test SSE:
Baseline SIR test SSE: 676477.9500418671
Extended  test SSE: 1227599.4098615828
```





Verify and validate your analysis:

Our initial model was tested on the entire dataset, and we found the SSE to be around 90089.38, using optimized beta and gamma of 5, and 3, respectively. When training the model again on only the second half of the data, we found an SSE of 788.41 which was be expected since it was trained well on a small amount of data. However, when we used this selection to predict the second half, our SSE exploded, resulting in a score of 679393.57, almost 7 times higher than the entire dataset run. This was expected as our original model was using the entire dataset while the 1/2 model was trying to predict the second half. The midpoint method samples the slope halfway through each step, which better represents the actual average slope. Therefore, each update is more accurate in our SIR model.

The RK4 SSE was slightly better than the Euler method, therefore we can use it to optimize our SIR model.

To extend our SIR model, we considered infection data from South Korea in addition to Saudia Arabia. In order to do this we first had to take the original file (found on Kaggle), then create a new CSV file that contained only data from South Korea from only specific dates that matched the Saudia Arabia data (since the file given was only for a subset of time). Since our results in the analysis are common signs of overfitting, we could assume that incorporating South Korea as another dataset to train our model is not optimal for predicting disease growth. However, this study (link below) discloses that "[regarding overfitting] it becomes increasingly important to develop models that can capture invariant relationships, which can be more effectively achieved by leveraging the diversity of populations within the training data." Thus further work should be done to determine whether there is a weak relationship between the infection rates of South Korea and Saudi Arabia, or if the datasets we used were too small to extrapolate a correlation.

Paper: text

Conclusions and Ethical Implications:

It is important to consider that because our model was on a relatively small dataset, it may be misleading or dangerous to use our model as a tool for predicting disease spread, especially in real-world contexts. Due to overfitting, our model may be over or under-estimating the potential growth, thus it is important for institutions using models such as ours to prepare for the ramifications of either scenario, regardless of a model's "accuracy." Finally, all prediction based models are, at best, still *predicting* future data, thus a model can never be fully accurate (The stock market is a great example).

Limitations and Future Work:

Given that our model was trained on an extremely small dataset, it is likely not accurate in general for larger (more realistic) datasets. This may also be a reason why the RK45 method did not significantly reduce the SSE for the 1/2 train/test split compared to the standard Euler SIR. In addition, our model was only trained on a single 'disease' (COVID MERS) in 1-2 regions, further limiting the validity of the model. Thus, more training should be done on larger datasets and potentially including different COVID strains, in order to enable a model to accurately "predict" future spread. Note: Since there exist many different factors that affect population growth and disease spread, there is no single "best" approach when it comes to approximating or predicting disease spread.

NOTES FROM YOUR TEAM:

N/A

QUESTIONS FOR YOUR TA:

N/A