Module 4:

Team Members:

Maggie Novak, Gabby Holohan

Project Title:

Predicting cases of COVID in Italy using various models

Project Goal:

This project seeks to use, optimize, and compare models to predict the future cases of COVID in Italy.

Disease Background:

Using your assigned disease, fill in the following bullet points.

- Prevalence & incidence: 25,603,510 confirmed cases in Italy. Averaging 3808 new cases per day in the last week (as of 11-20-2025). https://coronavirus.jhu.edu/region/italy. The infection length is 7-14 days, which is an average of 11 days.
- Economic burden: Globally, the economic burden of COVID-19 was estimated to be between US $77billionandUS$2.7 trillion in 2019. https://pmc.ncbi.nlm.nih.gov/articles/PMC10870589/#:~:text=Globally%2C%20the%20econ
- Risk factors (genetic, lifestyle) & Societal determinants: A main risk factor for COVID is age, with older individuals being more likely to experience a severe outcome. Certain underlying medical conditions and lack of vaccination are also risk factors for severe COVID cases.The risk of death is 25 times higher in those ages 50–64 years, 60 times higher in those ages 65–74 years, 140 times higher in those ages 75–84 years, and 340 times higher in those ages 85+ years. (From deaths in the US) Data has shown that compared to non-Hispanic White people, people from racial and ethnic minority groups are more likely to be infected with SARS-CoV-2 (the virus that causes COVID-19). Once infected, people from racial and ethnic minority groups are more likely to be hospitalized, be admitted to the ICU, and die from COVID-19 at younger ages. https://www.cdc.gov/covid/hcp/clinical-care/underlying-conditions.html#:~:text=Providers%20should%20consider%20the%20patient's%20age%2C
- Symptoms: Fever, chills, cough, shortness of breath/difficulty breathing, sore throat, congestion/runny nose, loss of tase/smell, fatigue, muscle or body aches, headache, nausea, diarrhea https://www.cdc.gov/covid/signs-symptoms/index.html

- Diagnosis: Molecular tests (PCR/NAAT): These are the most accurate tests and look for the virus's genetic material. They are typically processed in a lab and can be done at home or by a healthcare professional. Antigen tests: Also known as rapid tests, these detect viral proteins called antigens and are useful for quick results. They are less accurate than PCR tests, especially if you don't have symptoms. https://www.mayoclinic.org/diseases-conditions/coronavirus/diagnosis-treatment/drc-20479976#:~:text=COVID%2D19%20tests%20use%20a,Another%20test%20isn't%20needed
- Biological mechanisms (anatomy, organ physiology, cell & molecular physiology): Viral structural proteins and genomic RNA synthesized at the replication site are then translocated through an unknown mechanism to the ER–Golgi intermediate compartment (ERGIC), where virus assembly and budding occur. The S protein, assembled as a trimer, giving the appearance of a crown (corona), mediates major entry steps, including receptor binding and membrane fusion. During biosynthesis and maturation in the infected cell, the S protein is cleaved by furin or furin-like proprotein convertase in the Golgi apparatus into the S1 and S2 subunits, which remain associated. Assembled viruses bud into the ERGIC lumen and reach the plasma membrane via the secretory pathway, where they are released into the extracellular space after virus-containing vesicles fuse with the plasma membrane. FP, fusion peptide.https://www.nature.com/articles/s41580-021-00418-x
- R0 = R0 of COVID-19 as initially estimated by the World Health Organization (WHO) was between 1.4 and 2.4
- R0 = R0 of COVID-19 is best estimated between 2-4 in early 2020, we will use a starting value of 3.0

- https://pmc.ncbi.nlm.nih.gov/articles/PMC7074654/; https://pmc.ncbi.nlm.nih.gov/articles/PMC7280807/

Dataset:

This dataset has dates between March and July of 2020, paired with the number of confirmed cases of COVID in Italy. Each row is a day. It comes from a Repository by the Center for Systems Science and Engineering at Johns Hopkins University. The Regions compile the data of reported cases into an application. The Ministry of Health checks and sends the data fo the Department of Civil Protection. After quality control and dataset processing, it is published publically, which is where our dataset comes from. The step size of the dataset is days and the numbers are number of cases. Sources:Civil Protection Department: https://github.com/pcm-dpc/COVID-19/tree/master/,Ministry of Health: http://www.salute.gov.it/nuovocoronavirus

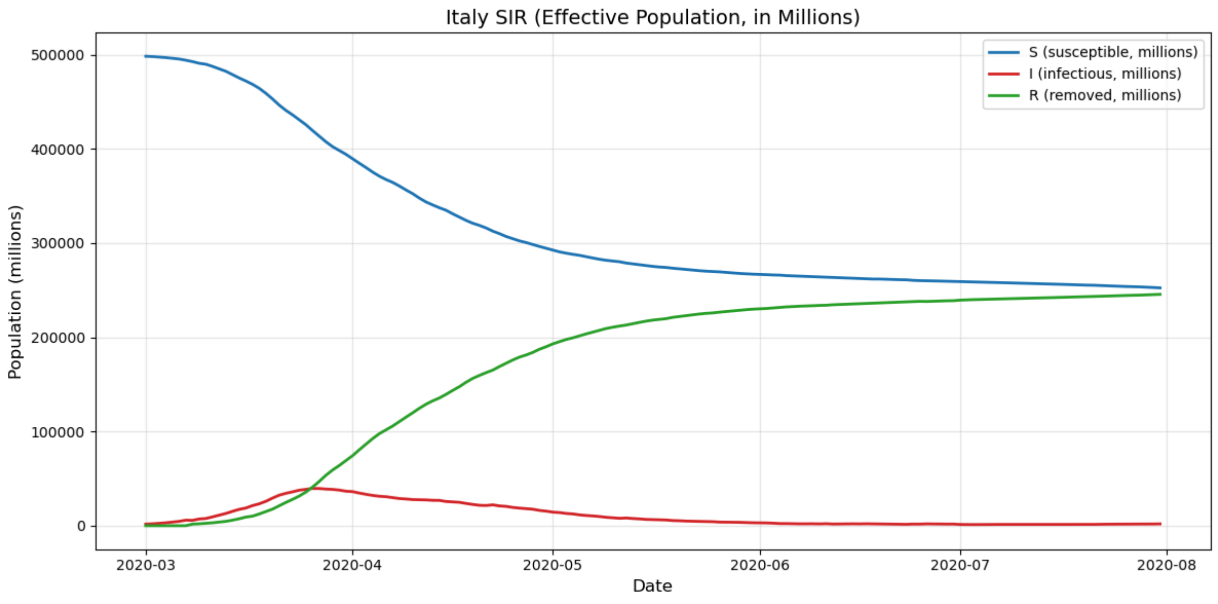
In [5]:

```
## LOAD YOUR DATASET HERE.

import numpy as np
```

```python
import pandas as pd
import matplotlib.pyplot as plt

# ================================================================
# 1. Load Italy Data
# ================================================================
df_full = pd.read_csv("covid_italy_data_march_july_2020_cumulative.csv")

df_full['date'] = pd.to_datetime(df_full['date'])
df_full['confirmed_cases'] = pd.to_numeric(df_full['confirmed_cases'], errors='coer

# ================================================================
# 2. Conversion: Cumulative → S, I, R Estimates
#    (Same method used in your US model)
# ================================================================
def convert_cumulative_to_SIR(df, date_col='date', cumulative_col='cumulative_cases
                              population=None, infectious_period=7, recovered_col=N
                              new_case_col='new_cases', I_col='I_est', R_col='R_est
    """
    Convert cumulative reported cases into S, I, R estimates for SIR modeling.
    - new_cases = diff(cumulative)
    - I_est = rolling sum(new_cases, window=infectious_period)
    - R_est = cumulative shifted by infectious_period (or user-provided recovered_c
    - S_est = population - I_est - R_est (if population provided)

    Returns a copy of the dataframe with the added columns.
    """
    df = df.copy()
    # Ensure date column sorted if present
    if date_col in df.columns:
        df[date_col] = pd.to_datetime(df[date_col])
        df = df.sort_values(date_col).reset_index(drop=True)

    if cumulative_col not in df.columns:
        raise ValueError(f"Column '{cumulative_col}' not found in dataframe.")

    # Compute new cases (incident)
    df[new_case_col] = df[cumulative_col].diff().fillna(
        df[cumulative_col].iloc[0])
    df[new_case_col] = df[new_case_col].clip(lower=0)

    # Estimate I(t) as rolling sum over infectious_period
    if infectious_period <= 0:
        raise ValueError("infectious_period must be positive integer.")
    df[I_col] = df[new_case_col].rolling(
        window=infectious_period, min_periods=1).sum()

    # Estimate R(t)
    if recovered_col and recovered_col in df.columns:
        df[R_col] = df[recovered_col].fillna(0)
    else:
        df[R_col] = df[cumulative_col].shift(infectious_period).fillna(0)

    # Compute S(t) if population provided
    if population is not None:
        df[S_col] = population - df[I_col] - df[R_col]
        df[S_col] = df[S_col].clip(lower=0)
    else:
        df[S_col] = np.nan

    # Ensure numeric and non-negative
    for col in [new_case_col, I_col, R_col]:
        df[col] = df[col].astype(float).clip(lower=0)
    if population is not None:
        df[S_col] = df[S_col].astype(float)

    return df

# Apply conversion
df_full = convert_cumulative_to_SIR(
    df_full,
    cumulative_col='confirmed_cases',
    population=500000,   # IMPORTANT: the raw Italy population (just like US code)
    infectious_period=7
)
print(df_full['I_est'])
# ================================================================
# 3. Effective Population Scaling
#    (This is the SAME trick used in the US code)
# ================================================================
# f = 8_000_000 / 60_000_000   # example: effective population ~8M

# df_full['S_eff'] = df_full['S_est'] * f
# df_full['I_eff'] = df_full['I_est'] * f
# df_full['R_eff'] = df_full['R_est'] * f

# # Convert to millions (just like your US file)
# df_full['S_m'] = df_full['S_eff'] / 1e6
# df_full['I_m'] = df_full['I_eff'] / 1e6
# df_full['R_m'] = df_full['R_eff'] / 1e6

# ================================================================
# 4. Euler SIR Solver
# ================================================================
def euler_sir(beta, gamma, S0, I0, R0, t, N):
    S = np.zeros(len(t))
    I = np.zeros(len(t))
    R = np.zeros(len(t))

    S[0], I[0], R[0] = S0, I0, R0

    for n in range(len(t)-1):
        dt = t[n+1] - t[n]
        dSdt = -(beta/N) * S[n] * I[n]
        dIdt = (beta/N) * S[n] * I[n] - gamma * I[n]
        dRdt = gamma * I[n]

        S[n+1] = S[n] + dSdt * dt
        I[n+1] = I[n] + dIdt * dt
        R[n+1] = R[n] + dRdt * dt

    return S, I, R
```

```
#Plot S, I, R over time.
plt.figure(figsize=(12, 6))
plt.plot(df_full['date'], df_full['S_est'], label='S (susceptible, millions)', colo
plt.plot(df_full['date'], df_full['I_est'], label='I (infectious, millions)', color
plt.plot(df_full['date'], df_full['R_est'], label='R (removed, millions)', color='#

plt.title('Italy SIR (Effective Population, in Millions)', fontsize=14)
plt.xlabel('Date', fontsize=12)
plt.ylabel('Population (millions)', fontsize=12)
plt.legend()
plt.grid(True, alpha=0.3)

# Format x-axis dates nicely
plt.tight_layout()
plt.show()
```

```
0      1694.0
1      2036.0
2      2502.0
3      3089.0
4      3858.0
        ...
148    1662.0
149    1736.0
150    1744.0
151    1820.0
152    1947.0
Name: I_est, Length: 153, dtype: float64
```



Data Analyis:

Methods

IN A SUMMARY, DESCRIBE THE METHODS YOU USED TO ANALYZE AND MODEL THE DATA.

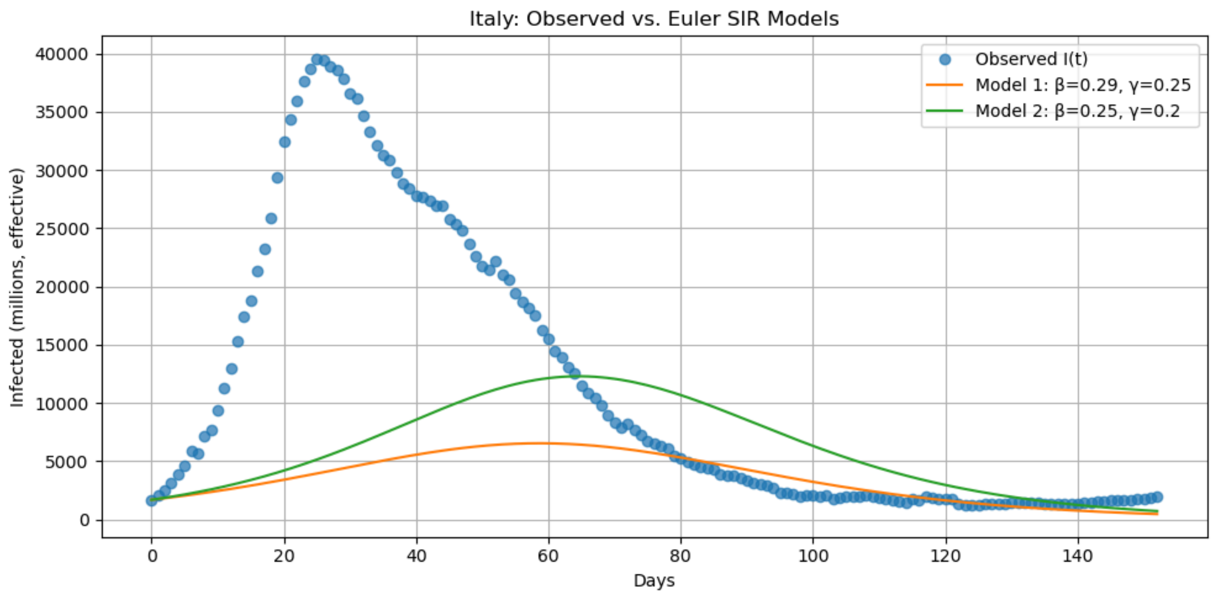
Analysis

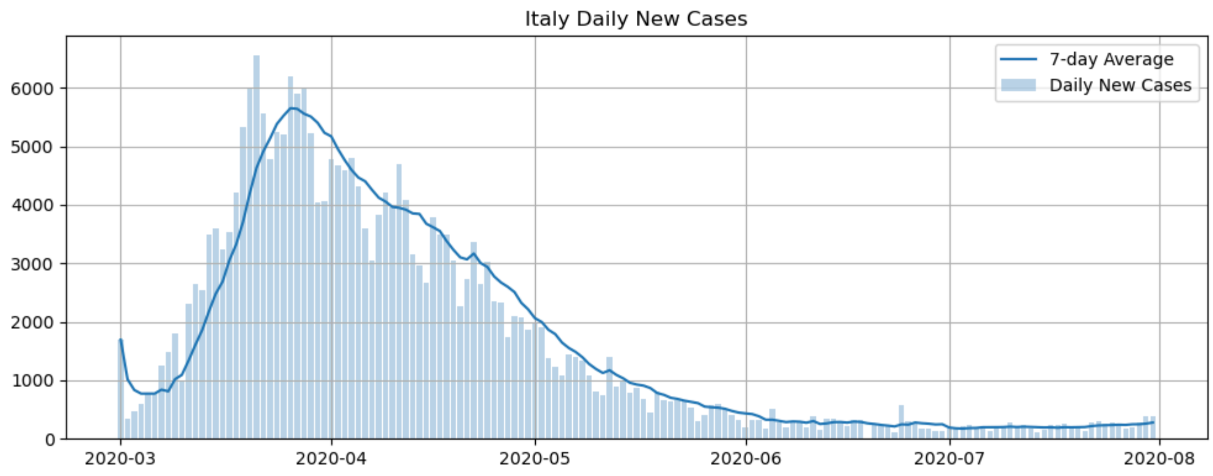
(Describe how you analyzed the data. This is where you should intersperse your Python code so that anyone reading this can run your code to perform the analysis that you did, generate your figures, etc.)

1. Fitting the SIR Model

In [6]:
```python
# Plug in guesses for gamma and beta, plot the model predictions against the data,
# ================================================================
#  Prepare Arrays for Modeling
# ================================================================
dates = df_full['date'].values
I_obs = df_full['I_est'].values
S_obs = df_full['S_est'].values
R_obs = df_full['R_est'].values

t = np.arange(len(I_obs))
N_eff = 500000

I0 = I_obs[0]
S0 = S_obs[0]
R0 = R_obs[0]

# ================================================================
# Run Two SIR Models
# ================================================================
beta1, gamma1 = 0.29, 1/4
beta2, gamma2 = 0.25, 1/5
S1, I1, R1 = euler_sir(beta1, gamma1, S0, I0, R0, t, 500000)
S2, I2, R2 = euler_sir(beta2, gamma2, S0, I0, R0, t, 500000)

# ================================================================
# PLOTS
# ================================================================

# ---- I(t) Model Comparison ----
plt.figure(figsize=(10,5))
plt.plot(t, I_obs, 'o', label="Observed I(t)", alpha=0.7)
plt.plot(t, I1, label=f"Model 1: β={beta1}, γ={gamma1}")
plt.plot(t, I2, label=f"Model 2: β={beta2}, γ={gamma2}")
plt.xlabel("Days")
plt.ylabel("Infected (millions, effective)")
plt.title("Italy: Observed vs. Euler SIR Models")
plt.legend()
plt.grid(True)
plt.tight_layout()
plt.show()

# ---- Daily Cases ----
daily = df_full["new_cases"]
roll = daily.rolling(7, min_periods=1).mean()
```

```
plt.figure(figsize=(10,4))
plt.bar(dates, daily, alpha=0.3, label="Daily New Cases")
plt.plot(dates, roll, label="7-day Average")
plt.legend()
plt.grid(True)
plt.title("Italy Daily New Cases")
plt.tight_layout()
plt.show()

# --- SSE and RMSE for I(t) ---
sse_I1 = np.sum((I_obs - I1)**2)
sse_I2 = np.sum((I_obs - I2)**2)

print(f"SSE (I) - Model 1: {sse_I1:,.4f}")
print(f"SSE (I) - Model 2: {sse_I2:,.4f}")
```



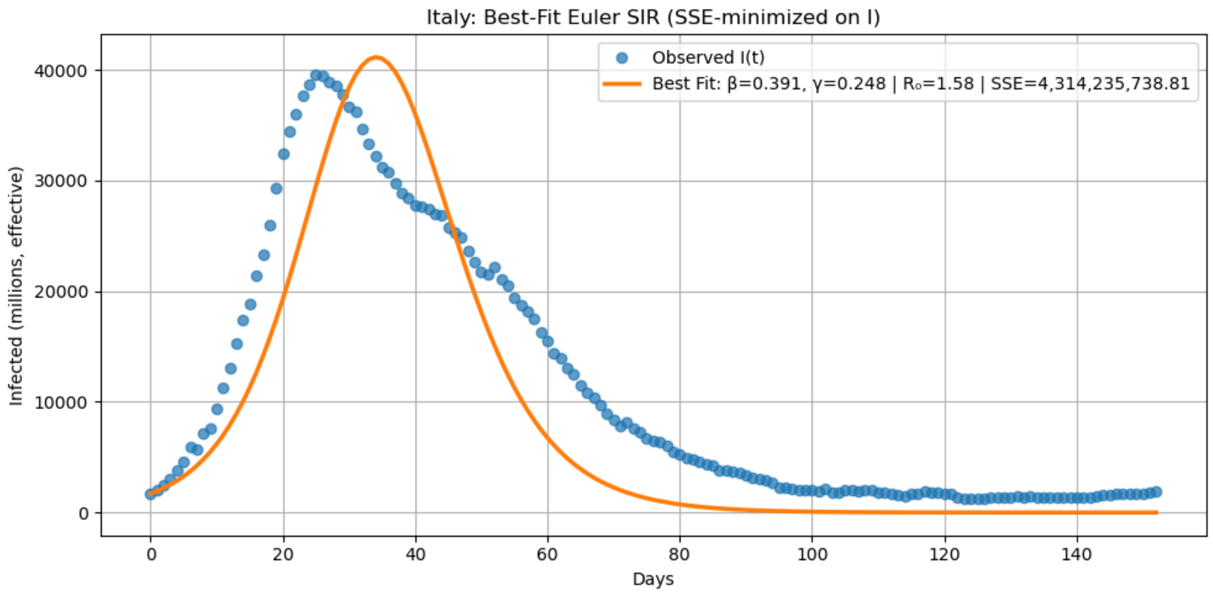


```
SSE (I) - Model 1: 27,833,798,374.5203
SSE (I) - Model 2: 23,898,946,207.0571
```

In [7]:
```
# optimize the beta and gamma parameters using grid search to minimize SSE

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

```python
# ----------------------------
# 1) Objective (SSE) function
# ----------------------------
def sse_params(beta, gamma, S0, I0, R0, t, N_eff,
               I_obs=None, S_obs=None, R_obs=None,
               target='I', weights=(1.0, 1.0, 1.0)):
    """
    Returns SSE for the chosen target:
      - target='I'  : fit I(t) only against I_obs
      - target='SIR': fit S, I, R jointly with weights (wS, wI, wR)
    All inputs should be in consistent units (e.g., millions).
    """
    # Simulate with given parameters
    S, I, R = euler_sir(beta, gamma, S0, I0, R0, t, N_eff)

    if target == 'I':
        # SSE on I(t) only
        return np.sum((I_obs - I)**2)

    elif target == 'SIR':
        # Weighted total SSE across S, I, R
        wS, wI, wR = weights
        return (wS * np.sum((S_obs - S)**2) +
                wI * np.sum((I_obs - I)**2) +
                wR * np.sum((R_obs - R)**2))

    else:
        raise ValueError("target must be 'I' or 'SIR'")

# -----------------------------------
# 2) Coarse + fine grid search driver
# -----------------------------------
def fit_sir_grid(S0, I0, R0, t, N_eff,
                 I_obs, S_obs=None, R_obs=None,
                 target='I', weights=(1.0, 1.0, 1.0),
                 beta_range=(0.05, 0.6), gamma_range=(1/14, 1/3),
                 coarse_n=60, fine_n=60, fine_span=0.30):
    """
    Grid search to minimize SSE over (beta, gamma).
    - coarse_n: number of points per axis in the coarse grid
    - fine_n  : points per axis in the fine grid around the best coarse point
    - fine_span: ±fraction around the best coarse value to search (e.g., 0.30 = ±30

    Returns:
        best_beta, best_gamma, best_sse
    """
    b_min, b_max = beta_range
    g_min, g_max = gamma_range

    # --- Coarse grid over beta & gamma ---
    beta_vals = np.linspace(b_min, b_max, coarse_n)
    gamma_vals = np.linspace(g_min, g_max, coarse_n)

    best_sse = np.inf
    best_beta, best_gamma = None, None
    for beta in beta_vals:
        for gamma in gamma_vals:
            sse = sse_params(beta, gamma, S0, I0, R0, t, N_eff,
                             I_obs=I_obs, S_obs=S_obs, R_obs=R_obs,
                             target=target, weights=weights)
            if sse < best_sse:
                best_sse = sse
                best_beta, best_gamma = beta, gamma

    # --- Fine grid around the best coarse point ---
    b_lo = max(b_min, best_beta * (1 - fine_span))
    b_hi = min(b_max, best_beta * (1 + fine_span))
    g_lo = max(g_min, best_gamma * (1 - fine_span))
    g_hi = min(g_max, best_gamma * (1 + fine_span))

    beta_vals_fine = np.linspace(b_lo, b_hi, fine_n)
    gamma_vals_fine = np.linspace(g_lo, g_hi, fine_n)

    for beta in beta_vals_fine:
        for gamma in gamma_vals_fine:
            sse = sse_params(beta, gamma, S0, I0, R0, t, N_eff,
                             I_obs=I_obs, S_obs=S_obs, R_obs=R_obs,
                             target=target, weights=weights)
            if sse < best_sse:
                best_sse = sse
                best_beta, best_gamma = beta, gamma

    return best_beta, best_gamma, best_sse

# ---------------------------
# 3) Run the fit (I-only default)
# ---------------------------
target = 'I'
weights = (1.0, 1.0, 1.0)  # used only if target='SIR'

best_beta, best_gamma, best_sse = fit_sir_grid(
    S0, I0, R0, t, N_eff,
    I_obs=I_obs, S_obs=S_obs, R_obs=R_obs,
    target=target, weights=weights,
    beta_range=(0.05, 0.6),
    gamma_range=(1/14, 1/3),
    coarse_n=60, fine_n=60, fine_span=0.30
)

# Simulate with best parameters
S_best, I_best, R_best = euler_sir(best_beta, best_gamma, S0, I0, R0, t, N_eff)

# Report only SSE (no RMSE)
R0_est = best_beta / best_gamma
print(f"Best fit → β={best_beta:.4f}, γ={best_gamma:.4f}, R0={R0_est:.2f}")
print(f"SSE (target={target}): {best_sse:,.4f}")

# ---------------------------
# 4) Plot I(t) with best model
# ---------------------------
plt.figure(figsize=(10, 5))
plt.plot(t, I_obs, 'o', label="Observed I(t)", alpha=0.7)
plt.plot(t, I_best, linewidth=2.5,
         label=f"Best Fit: β={best_beta:.3f}, γ={best_gamma:.3f} | R₀={R0_est:.2f}

# Optional: add baseline models if you computed them earlier
# (Comment these out if not defined to avoid NameError)
# plt.plot(t, I1, label=f"Model 1: β={beta1}, γ={gamma1}", alpha=0.6)
# plt.plot(t, I2, label=f"Model 2: β={beta2}, γ={gamma2}", alpha=0.6)

plt.xlabel("Days")
plt.ylabel("Infected (millions, effective)")
plt.title("Italy: Best-Fit Euler SIR (SSE-minimized on I)")
plt.legend()
plt.grid(True)
plt.tight_layout()
```

```
Best fit → β=0.3915, γ=0.2483, R0=1.58
SSE (target=I): 4,314,235,738.8106
```



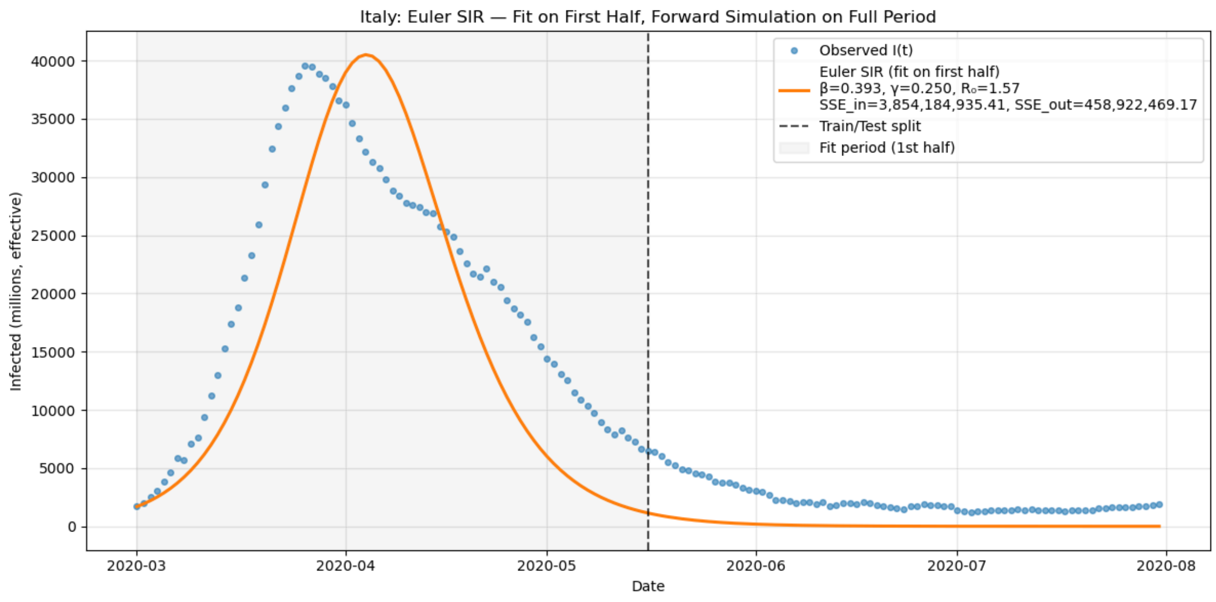
2. Predict "the future" with your fit SIR model

In [8]:
```
# Use euler's method and your optimization routine above to find new gamma and beta
# FIRST HALF of the data, then simulate the SIR model forward in time using those p
# ------------------------------------------------------------
# 0) Split the data into first half (fit) and second half (test)
# ------------------------------------------------------------
n = len(I_obs)
n_split = n // 2  # first half length
dates_fit = dates[:n_split]
dates_full = dates  # for plotting

# Observed subsets for fitting
S_fit = S_obs[:n_split]
I_fit = I_obs[:n_split]
R_fit = R_obs[:n_split]

# Time grids (dt = 1 day)
t_fit = np.arange(n_split)
```

```python
t_full = np.arange(n)

# Initial conditions (from the first observed point)
S0 = S_obs[0]
I0 = I_obs[0]
R0 = R_obs[0]

# Effective population (consistent with 'millions' units)
N_eff = S0 + I0 + R0

# ------------------------------------------------------------
# 1) Objective (SSE) function
# ------------------------------------------------------------
def sse_params(beta, gamma, S0, I0, R0, t, N_eff,
               I_obs=None, S_obs=None, R_obs=None,
               target='I', weights=(1.0, 1.0, 1.0)):
    """
    Returns SSE for the chosen target:
      - target='I'  : fit I(t) only against I_obs
      - target='SIR': fit S, I, R jointly with weights (wS, wI, wR)
    All arrays must be aligned with 't'. Units should be consistent (e.g., millions
    """
    S, I, R = euler_sir(beta, gamma, S0, I0, R0, t, N_eff)

    # Numerical safety: clamp small negatives to 0
    S = np.clip(S, 0, None)
    I = np.clip(I, 0, None)
    R = np.clip(R, 0, None)

    if target == 'I':
        return np.sum((I_obs - I)**2)
    elif target == 'SIR':
        wS, wI, wR = weights
        return (wS * np.sum((S_obs - S)**2) +
                wI * np.sum((I_obs - I)**2) +
                wR * np.sum((R_obs - R)**2))
    else:
        raise ValueError("target must be 'I' or 'SIR'")

# ------------------------------------------------------------
# 2) Coarse + fine grid search over (beta, gamma)
# ------------------------------------------------------------
def fit_sir_grid(S0, I0, R0, t, N_eff,
                 I_obs, S_obs=None, R_obs=None,
                 target='I', weights=(1.0, 1.0, 1.0),
                 beta_range=(0.05, 0.6), gamma_range=(1/14, 1/3),
                 coarse_n=60, fine_n=60, fine_span=0.30):
    """
    Grid search to minimize SSE over (beta, gamma).
    - coarse_n: points per axis in the coarse grid
    - fine_n  : points per axis in the fine grid around best coarse point
    - fine_span: ±fraction around the best coarse value to search (e.g., 0.30 = ±30

    Returns:
        best_beta, best_gamma, best_sse
    """
    b_min, b_max = beta_range
    g_min, g_max = gamma_range

    # --- Coarse grid over beta & gamma ---
    beta_vals = np.linspace(b_min, b_max, coarse_n)
    gamma_vals = np.linspace(g_min, g_max, coarse_n)

    best_sse = np.inf
    best_beta, best_gamma = None, None

    for beta in beta_vals:
        for gamma in gamma_vals:
            sse = sse_params(beta, gamma, S0, I0, R0, t, N_eff,
                             I_obs=I_obs, S_obs=S_obs, R_obs=R_obs,
                             target=target, weights=weights)
            if sse < best_sse:
                best_sse = sse
                best_beta, best_gamma = beta, gamma

    # --- Fine grid around the best coarse point ---
    b_lo = max(b_min, best_beta * (1 - fine_span))
    b_hi = min(b_max, best_beta * (1 + fine_span))
    g_lo = max(g_min, best_gamma * (1 - fine_span))
    g_hi = min(g_max, best_gamma * (1 + fine_span))

    beta_vals_fine = np.linspace(b_lo, b_hi, fine_n)
    gamma_vals_fine = np.linspace(g_lo, g_hi, fine_n)

    for beta in beta_vals_fine:
        for gamma in gamma_vals_fine:
            sse = sse_params(beta, gamma, S0, I0, R0, t, N_eff,
                             I_obs=I_obs, S_obs=S_obs, R_obs=R_obs,
                             target=target, weights=weights)
            if sse < best_sse:
                best_sse = sse
                best_beta, best_gamma = beta, gamma

    return best_beta, best_gamma, best_sse

# --------------------------------------------------------------
# 3) Fit on FIRST HALF (default: target='I')
# --------------------------------------------------------------
target = 'I'
weights = (1.0, 1.0, 1.0)  # used only if target='SIR'

best_beta, best_gamma, sse_in = fit_sir_grid(
    S0, I0, R0, t_fit, N_eff,
    I_obs=I_fit, S_obs=S_fit, R_obs=R_fit,
    target=target, weights=weights,
    beta_range=(0.05, 0.6),
    gamma_range=(1/14, 1/3),
    coarse_n=60, fine_n=60, fine_span=0.30
)

R0_est = best_beta / best_gamma
```

```
print(f"[Fit on first half] β={best_beta:.4f}, γ={best_gamma:.4f}, R₀={R0_est:.2f}"
print(f"SSE (in-sample, I): {sse_in:,.4f}")

# ------------------------------------------------------------
# 4) Simulate forward across FULL horizon using fitted params
# ------------------------------------------------------------
S_pred_full, I_pred_full, R_pred_full = euler_sir(best_beta, best_gamma, S0, I0, R0
S_pred_full = np.clip(S_pred_full, 0, None)
I_pred_full = np.clip(I_pred_full, 0, None)
R_pred_full = np.clip(R_pred_full, 0, None)

# Out-of-sample SSE on second half
sse_out = np.sum((I_obs[n_split:] - I_pred_full[n_split:])**2)
print(f"SSE (out-of-sample, I on second half): {sse_out:,.4f}")

# ------------------------------------------------------------
# 5) Plot: Observed vs. simulated; mark the split
# ------------------------------------------------------------
date_split = dates[n_split]  # first day of the second half

plt.figure(figsize=(12, 6))
plt.plot(dates_full, I_obs, 'o', ms=4, alpha=0.6, label="Observed I(t)")
plt.plot(dates_full, I_pred_full, '-', lw=2.2,
         label=(f"Euler SIR (fit on first half)\n"
                f"β={best_beta:.3f}, γ={best_gamma:.3f}, R₀={R0_est:.2f}\n"
                f"SSE_in={sse_in:,.2f}, SSE_out={sse_out:,.2f}"))

# Visual cue for split
plt.axvline(date_split, color='k', linestyle='--', alpha=0.7, label="Train/Test spl
plt.gca().axvspan(dates_full[0], date_split, color='gray', alpha=0.08, label="Fit p

plt.title("Italy: Euler SIR — Fit on First Half, Forward Simulation on Full Period"
plt.xlabel("Date")
plt.ylabel("Infected (millions, effective)")
plt.legend(loc='upper right')
plt.grid(True, alpha=0.3)
plt.tight_layout()
plt.show()
```

```
[Fit on first half] β=0.3929, γ=0.2503, R₀=1.57
SSE (in-sample, I): 3,854,184,935.4082
SSE (out-of-sample, I on second half): 458,922,469.1703
```



Is the new gamma and beta close to what you found on the full dataset? Is the fit much worse? What is the SSE calculated for the second half of the data? Yes, they are very close. The new beta is only about 9% different and the new gamma is only about 0.6% different. They both stay right around 0.3 on a scale of typically 0.1 to 0.5 for something like this. Based on visuals, the fit for the first half is better but the fit for the second half (the prediction) is much worse. The SSE calculated for the second half of the data is 0.02

Key Point:
The error you calculate is a *combination* of two sources:

1. the error associated with Euler's method (i.e. it is an imperfect numerical approximation to the true solution of the SIR model)
2. the error associated with comparing real-world data to a model with limitations.

First we will try to address the numerical error, and second we will address the limitations of the model.

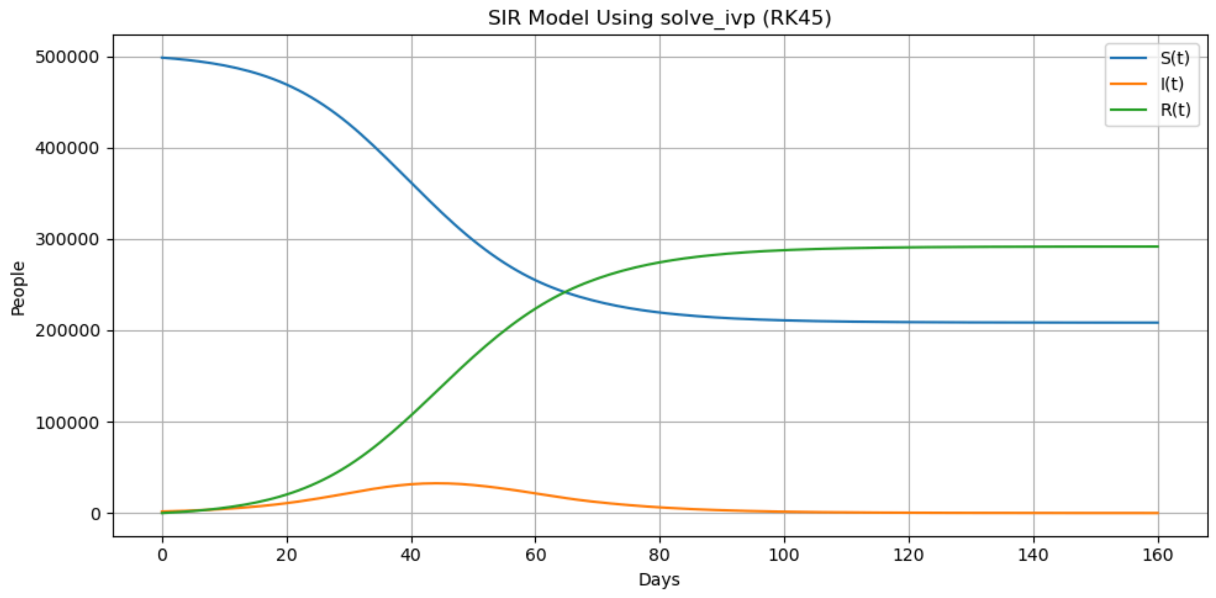
Describe how using a different method like the midpoint method might lower the numerical error.

The midpoint method can lower numerical error by using the slope in the middle of a step. Euler's method uses the slope at the beginning of a step to approximate the slope across the whole step. It might be a better approximation of the slope across the step to use the slope at the midpoint of the step, thus lowering numerical error.

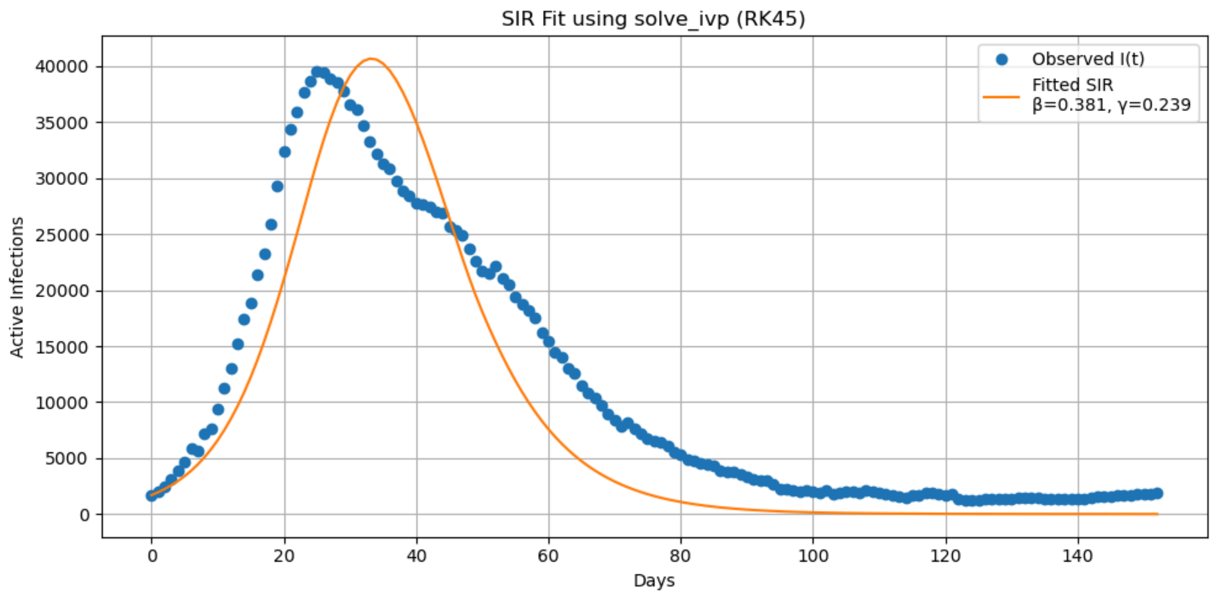
3. Decreasing numerical error with the RK4 Method

In [25]:
```python
# Using scipy's solve_ivp (RK45) to fit beta and gamma for the SIR model

import numpy as np
```

```python
from scipy.integrate import solve_ivp
from scipy.optimize import minimize
import matplotlib.pyplot as plt

# We assume you already defined these earlier:
# S_obs, I_obs, R_obs

t_obs = np.arange(len(I_obs))

# Initial conditions
S0 = S_obs[0]
I0 = I_obs[0]
R0 = R_obs[0]

# Total population
N = 500000


# --------------------------------------------------
# 1. Correct SIR ODE (must be f(t, y, beta, gamma))
# --------------------------------------------------
def SIR_ode(t, y, beta, gamma):
    S, I, R = y
    dSdt = -(beta/N) * S * I
    dIdt = (beta/N) * S * I - gamma * I
    dRdt = gamma * I
    return [dSdt, dIdt, dRdt]


# --------------------------------------------------
# 2. Simulate once (just to test)
# --------------------------------------------------
t_eval = np.arange(0, 161, 1)

sol = solve_ivp(
    lambda t, y: SIR_ode(t, y, 0.3, 0.2),
    [0, 160],
    [S0, I0, R0],
    t_eval=t_eval,
    method="RK45"
)

S_sim = sol.y[0]
I_sim = sol.y[1]
R_sim = sol.y[2]

plt.figure(figsize=(10,5))
plt.plot(sol.t, S_sim, label="S(t)")
plt.plot(sol.t, I_sim, label="I(t)")
plt.plot(sol.t, R_sim, label="R(t)")
plt.xlabel("Days")
plt.ylabel("People")
plt.title("SIR Model Using solve_ivp (RK45)")
plt.legend()
plt.grid(True)
plt.tight_layout()
plt.show()


# --------------------------------------------------
# 3. Function to simulate SIR with given beta, gamma
# --------------------------------------------------
def run_sir(beta, gamma):
    sol = solve_ivp(
        lambda t, y: SIR_ode(t, y, beta, gamma),
        [t_obs[0], t_obs[-1]],
        [S0, I0, R0],
        t_eval=t_obs,
        method="RK45"
    )
    return sol.y[1]   # return I(t)


# --------------------------------------------------
# 4. Objective function (fit to I_obs)
# --------------------------------------------------
def objective(params):
    beta, gamma = params
    I_pred = run_sir(beta, gamma)
    return np.sum((I_pred - I_obs)**2)


# --------------------------------------------------
# 5. Fit β and γ
# --------------------------------------------------
initial_guess = [0.3, 0.2]
bounds = [(0.0001, 2.0), (0.0001, 2.0)]

result = minimize(
    objective,
    initial_guess,
    bounds=bounds,
    method='L-BFGS-B'
)

beta_fit, gamma_fit = result.x
print("β_fit =", beta_fit)
print("γ_fit =", gamma_fit)


# --------------------------------------------------
# 6. Plot fitted vs observed
# --------------------------------------------------
I_fit = run_sir(beta_fit, gamma_fit)

plt.figure(figsize=(10,5))
plt.plot(t_obs, I_obs, 'o', label="Observed I(t)")
plt.plot(t_obs, I_fit, '-', label=f"Fitted SIR\nβ={beta_fit:.3f}, γ={gamma_fit:.3f}
plt.xlabel("Days")
plt.ylabel("Active Infections")
plt.title("SIR Fit using solve_ivp (RK45)")
plt.legend()
plt.grid(True)
plt.tight_layout()
plt.show()

# --- Re-run RK4 model over full time range ---
sol_RK4 = solve_ivp(
    lambda t, y: SIR_ode(t, y, beta_fit, gamma_fit),
    [t_obs[0], t_obs[-1]],
    [S0, I0, R0],
    t_eval=t_obs,
    method="RK45"
)

I_pred_full = sol_RK4.y[1]

# --- FULL DATA SSE ---
SSE_full = np.sum((I_pred_full - I_obs)**2)
print("SSE RK4 (full data):", SSE_full)

# --- SECOND HALF SSE ---
mid = len(I_obs) // 2

I_pred_second_half = I_pred_full[mid:]
I_obs_second_half  = I_obs[mid:]

SSE_second_half = np.sum((I_pred_second_half - I_obs_second_half)**2)
print("SSE RK4 (second half):", SSE_second_half)
```



```
β_fit = 0.3805893239100764
γ_fit = 0.23932343748122598
```



```
SSE RK4 (full data): 3454869899.633416
SSE RK4 (second half): 413975864.4383489
```

Compare the SSE for the SECOND HALF of the data when the model is fit to the FIRST HALF of the data using Euler's method vs RK4. Did RK4 do a better job? Why or why not?

The RK4 method did a better job, indicated by a lower SSE value. This is because RK4 is a fourth-order method while Euler's is a first order method. This results in a smaller error as RK4 evaluates the slope at several points inside each step size, reducing lower-order errors.

In [23]:
```
# SSE comparison between Euler's method and RK4 (solve_ivp) on the SECOND HALF of t
if (SSE_second_half<sse_out):
    print("RK4 estimation produces a lower out-of-sample SSE for the second half of
else:
    print("Euler's estimation produces a lower out-of-sample SSE for the second hal
```

```
RK4 estimation produces a lower out-of-sample SSE for the second half of the data.
```

4. Improving model fit by overcoming model limitations

Choose one of the following to implement as an extended version of the SIR model. Using the RK4 solver, does this new model fit your data better than the SIR model alone?

Options to overcome limitations (choose ONE to implement):

1. Include births in the model as described in reading.
2. Include deaths in the model as described in reading.
3. Include an exposed compartment (SEIR model).
4. Include loss of immunity (i.e. R population can go back to S population).
5. Include at least two I populations with varying degrees of infectiousness.
6. Include at least two age brackets with varying degress of infectiousness and recovery times.

Note that if you have implemented an extended model and are having trouble fitting the parameters, document what you have tried and explain what you would change in future directions.

```
In [24]: # Extended model implementation, parameter fitting, and plotting.
```

Verify and validate your analysis:

(Describe how you checked to see that your analysis gave you an answer that you believe (verify). Describe how your determined if your analysis gave you an answer that is supported by other evidence (e.g., a published paper).

Conclusions and Ethical Implications:

(Think about the answer your analysis generated, draw conclusions related to your overarching question, and discuss the ethical implications of your conclusions.

Limitations and Future Work:

(Think about the answer your analysis generated, draw conclusions related to your overarching question, and discuss the ethical implications of your conclusions. use assumptions of SIR model here

NOTES FROM YOUR TEAM:

- Both partners were absent from class on Tuesday. Maggie came on Thursday and did the dataset background. Worked separately on the digital notebook and emailed to establish a line of communication and a GitHub repository.
- week 2, part 1: Maggie filled in section 2 and the optimizing from section 1. Gabby did the base code and most of section 1. Maggie filled in dataset background during class on Tuesday.

QUESTIONS FOR YOUR TA:

Are these graphs the desired output?