sir_llm_hackathon_final

March 3, 2026

1 AI-Guided SIR Modeling Hackathon (2 Hours)

This notebook is the **workshop skeleton** for the **AI-Guided SIR Modeling Hackathon**.

- Dataset: **Niamey, Niger measles outbreaks** (biweekly case counts; communities A/B/C)
- Tooling: **Google Colab + Python + ChatGPT**
- Time unit: **biweeks**
- Key modeling shortcut: infectious period   **2 weeks**   **1 per biweek**

1.1 How to use this notebook

Each section contains: 1) A **ChatGPT prompt** (Markdown) you can copy into ChatGPT
2) A **starter code cell** (often with TODOs) to run in Colab

Rule of thumb: Always request **plots + sanity checks** when you ask ChatGPT for help.

1.2 0. Setup

1.2.1 ChatGPT Prompt (copy/paste)

```
Persona:
You are an expert epidemiological modeler and Python educator.

Task:
- Write a Colab-ready setup cell: imports, basic plotting config, and a helper for reproducibil
- If any package is missing show me how to run pip install

Constraints:
- Use numpy, scipy, pandas, matplotlib only

Verification:
- Print library versions and a simple "ready" message.
```

[1]:
```
# ========================
# Colab Setup Cell
# ========================

# --- If running in Colab and any package is missing, uncomment and run ---
# !pip install numpy scipy pandas matplotlib
```

```python
# Core scientific stack
import numpy as np
import pandas as pd
import scipy
from scipy import integrate, optimize
import matplotlib.pyplot as plt

# -------------------------
# Reproducibility helper
# -------------------------
def set_seed(seed: int = 42):
    """
    Set random seed for reproducibility.
    Works for numpy-based simulations and optimization.
    """
    np.random.seed(seed)

set_seed(42)

# -------------------------
# Basic plotting config
# -------------------------
plt.rcParams.update({
    "figure.figsize": (8, 5),
    "figure.dpi": 120,
    "axes.grid": True,
    "axes.spines.top": False,
    "axes.spines.right": False,
    "axes.labelsize": 11,
    "axes.titlesize": 12,
    "legend.frameon": False,
    "font.size": 11,
})

# -------------------------
# Version check
# -------------------------
print("Library versions:")
print(f"  numpy      : {np.__version__}")
print(f"  pandas     : {pd.__version__}")
print(f"  scipy      : {scipy.__version__}")
print(f"  matplotlib : {plt.matplotlib.__version__}")

print("\nSetup complete - ready  ")
```

```
Library versions:
  numpy      : 2.0.2
  pandas     : 2.2.2
  scipy      : 1.16.3
  matplotlib : 3.10.0

Setup complete - ready
```

Chat GPT Prompt to generate code to load data

```
Persona:
You are an expert epidemiological modeler and Python educator.

Task:
- Write a Colab-ready python code to:
  - Create `data` folder if it is not exists
  - Download the csv file `https://github.com/merlinvn/ai-guided-modeling-hackathon/raw/refs/he
```

[2]:
```python
import os
import requests

# Define the folder and file details
data_folder = 'data'
file_url = 'https://github.com/merlinvn/ai-guided-modeling-hackathon/raw/refs/
 ↪heads/main/data/niamey.csv'
file_name = os.path.join(data_folder, 'niamey.csv')

# Create the data folder if it doesn't exist
if not os.path.exists(data_folder):
    os.makedirs(data_folder)
    print(f"Folder '{data_folder}' created.")
else:
    print(f"Folder '{data_folder}' already exists.")

# Download the CSV file
response = requests.get(file_url)
response.raise_for_status()  # Raise an exception for HTTP errors

with open(file_name, 'wb') as f:
    f.write(response.content)

print(f"'{file_name}' downloaded successfully.")
```

```
Folder 'data' created.
'data/niamey.csv' downloaded successfully.
```

1.3 1. Explore the Niamey Measles Data:

1.3.1 Load the dataset and compute basic statistics

ChatGPT Prompt (copy/paste)

```
Persona:
You are an expert epidemiological modeler and Python educator.

Context:
- Dataset contains biweekly measles case counts from Niamey, Niger
- File path: data/niamey.csv

Task:
Write Python code to:
1. Load data/niamey.csv store it to `measles_df`
2. Display the first few rows
3. Print column names and basic information about the dataset
4. Show basic statistics about dataset

Constraints
- Use pandas only
- Keep code simple and readable
```

[3]:
```python
import pandas as pd

# 1. Load the dataset
measles_df = pd.read_csv("data/niamey.csv")

# 2. Display the first few rows
print("First 5 rows of the dataset:")
print(measles_df.head())

# 3. Print column names and basic information
print("\nColumn names:")
print(measles_df.columns.tolist())

print("\nDataset information:")
print(measles_df.info())

# 4. Show basic statistics (numeric columns)
print("\nBasic statistics:")
print(measles_df.describe())

# 5. Show unique values for categorical columns
categorical_columns = measles_df.select_dtypes(include=["object", "category"]).
 ↪columns

if len(categorical_columns) > 0:
    print("\nCategorical columns and their unique values:")
    for col in categorical_columns:
        print(f"\n{col}:")
        print(measles_df[col].unique())
```

```
else:
    print("\nNo categorical columns found.")
```

```
First 5 rows of the dataset:
   biweek community  measles
0       1         A     22.0
1       2         A     27.0
2       3         A     64.0
3       4         A     84.0
4       5         A    116.0

Column names:
['biweek', 'community', 'measles']

Dataset information:
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 48 entries, 0 to 47
Data columns (total 3 columns):
 #   Column     Non-Null Count  Dtype  
---  ------     --------------  -----  
 0   biweek     48 non-null     int64  
 1   community  48 non-null     object 
 2   measles    47 non-null     float64
dtypes: float64(1), int64(1), object(1)
memory usage: 1.3+ KB
None

Basic statistics:
          biweek      measles
count  48.000000    47.000000
mean    8.500000   232.531915
std     4.658554   316.792200
min     1.000000     0.000000
25%     4.750000    13.500000
50%     8.500000    81.000000
75%    12.250000   251.500000
max    16.000000  1041.000000

Categorical columns and their unique values:

community:
['A' 'B' 'C']
```

1.3.2 Exercise

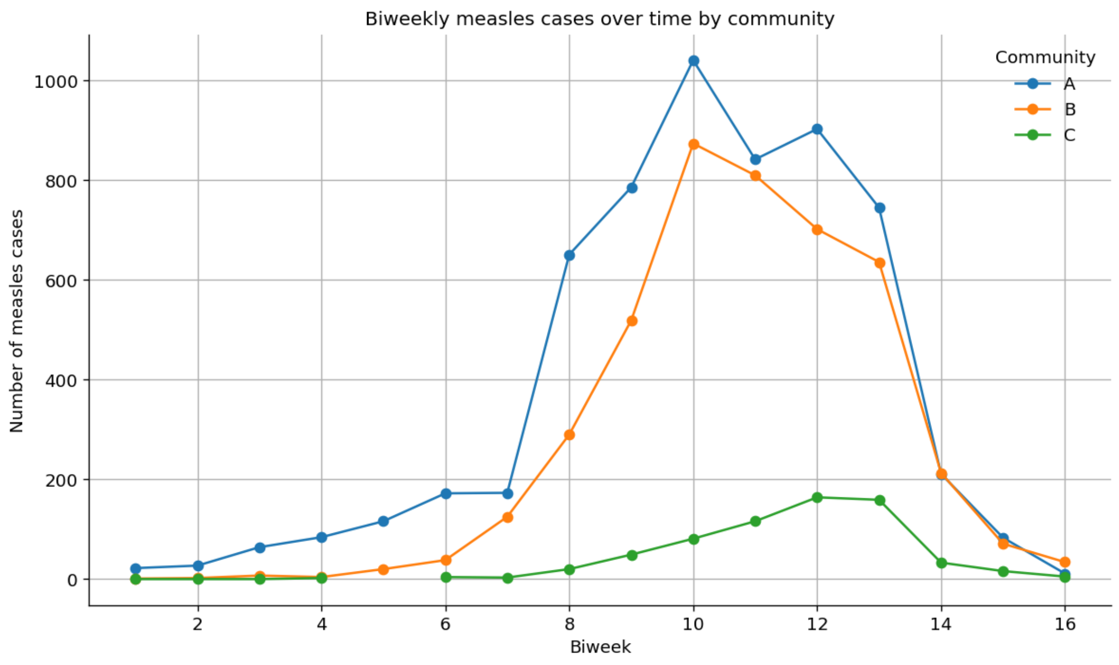
// TODO: Participants write a prompt to explain the results in plain language

1.3.3 Basic Plot

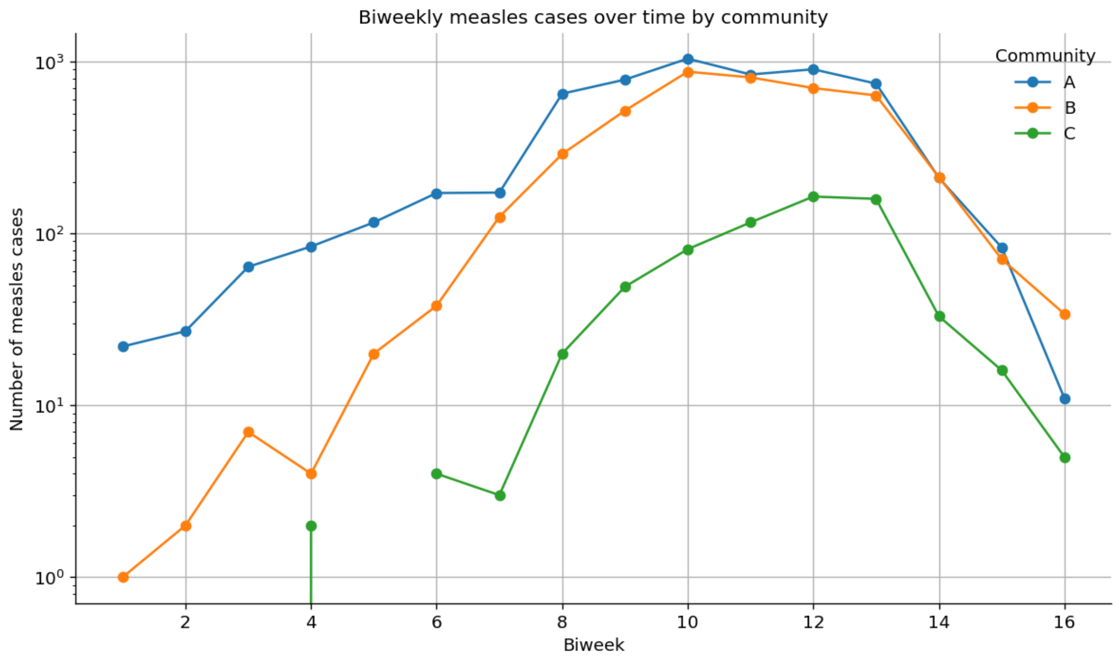
ChatGPT Prompt (copy/paste)

```
Persona:
You are an expert epidemiological modeler and Python educator.

Context:
- Dataset is already loaded into a DataFrame called `measles_df`
- Columns: biweek, community, measles

Task:
- Plot measles cases over time for each community
- Use one time-series plot
- Label axes and include a legend
- Briefly explain what biweekly case counts mean for epidemic modeling
```

[4]:
```python
import matplotlib.pyplot as plt

# Plot measles cases over time for each community
plt.figure(figsize=(10, 6))

for community, df_group in measles_df.groupby("community"):
    plt.plot(
        df_group["biweek"],
        df_group["measles"],
        marker="o",
        label=community
    )

# Labels and legend
plt.xlabel("Biweek")
plt.ylabel("Number of measles cases")
plt.title("Biweekly measles cases over time by community")
plt.legend(title="Community")

plt.tight_layout()
plt.show()
```



```
[5]: import matplotlib.pyplot as plt

     # Plot measles cases over time for each community
     plt.figure(figsize=(10, 6))

     for community, df_group in measles_df.groupby("community"):
         plt.plot(
             df_group["biweek"],
             df_group["measles"],
             marker="o",
             label=community
         )
     plt.yscale("log")
     # Labels and legend
     plt.xlabel("Biweek")
     plt.ylabel("Number of measles cases")
     plt.title("Biweekly measles cases over time by community")
     plt.legend(title="Community")

     plt.tight_layout()
     plt.show()
```



1.4 2. Feature-Based Estimation: Early Growth (Quick R)

We estimate early exponential growth using a semi-log regression: - Choose an early window where cases grow roughly exponentially. - Fit `log(cases)` vs time.

1.4.1 ChatGPT Prompt (copy/paste)

```
## Persona

You are an **expert in infectious disease modeling**, with experience in early-outbreak analys

## Context

* **Disease:** Measles
* **Community:** A
* **Data:** Biweekly reported case counts
* **Epidemic phase:** Early outbreak (first ~8-10 biweeks), where case counts exhibit **expone
* **Dataset:** Already loaded as `measles_df`

### Dataset structure

`
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 48 entries, 0 to 47
Columns:
- biweek     (int64)
- community  (object)
- measles    (float64, 47 non-null)
`

## Task

Estimate the **early exponential growth rate** of the outbreak by:

1. Selecting an appropriate **early biweek window** (  8-10 biweeks)
2. Fitting a **log-linear model**: log(measles cases) vs. time
3. Producing a **semi-log plot** showing observed data and fitted exponential growth
4. Converting the estimated growth rate to an **approximate basic reproduction number (R )**, a

   * Infectious removal rate: **  = 1 per biweek**

## Constraints

* Use **NumPy** and **SciPy** only (Matplotlib for plotting is acceptable)
* Clearly **state and explain modeling assumptions**
* Print key **statistical results** (e.g., slope, confidence intervals if available, R )
* **Output code only** (do not execute)

## Verification / Expected Output

* A **semi-log plot** of measles cases with the fitted exponential curve
* Printed values for:

  * Estimated **growth rate (slope)**
  * Corresponding **R  estimate**
```

[6]:

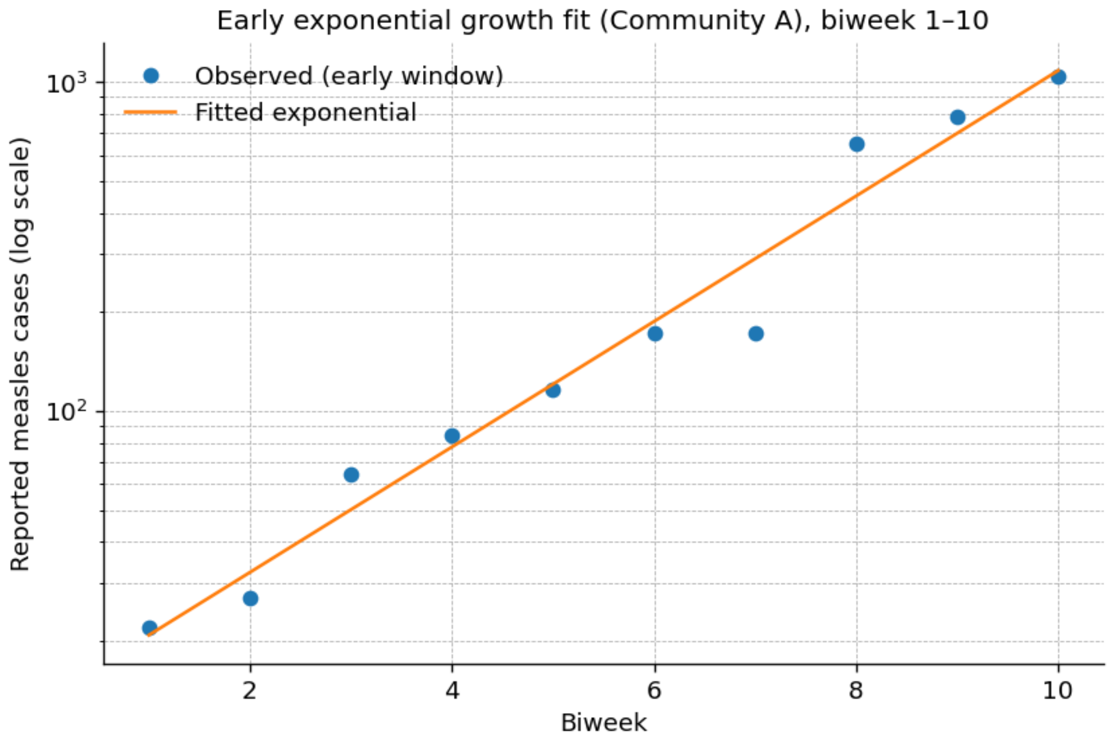
```python
# Early exponential growth estimation for measles (Community A)
# Constraints: NumPy + SciPy only (Matplotlib OK). Code-only, no execution.

import numpy as np
import matplotlib.pyplot as plt
from scipy import stats

# -----------------------------
# User-adjustable settings
# -----------------------------
COMMUNITY = "A"

# Choose the early window length (in biweeks) OR explicit biweek range.
# Option 1 (recommended): first N biweeks from the first nonzero case
EARLY_N_BIWEEKS = 10          # try 8-10
START_AT_FIRST_POSITIVE = True
```

```
# Option 2: explicit inclusive biweek indices (overrides Option 1 if not None)
EARLY_BIWEEK_MIN = None      # e.g., 0
EARLY_BIWEEK_MAX = None      # e.g., 9

# Handling zeros / missing
MIN_CASES = 1.0              # exclude cases < MIN_CASES (avoids log(0))
ALPHA = 0.05                 # 95% CI

# R0 conversion assumption
GAMMA_PER_BIWEEK = 1.0       # infectious removal rate   (per biweek)

# -----------------------------
# 1) Subset early window data
# -----------------------------
dfA = measles_df.loc[measles_df["community"] == COMMUNITY, ["biweek",␣
↪"measles"]].copy()
dfA = dfA.dropna(subset=["measles"])

# Keep only positive (or >= MIN_CASES) counts for log fit
dfA = dfA.loc[dfA["measles"] >= MIN_CASES].copy()
dfA = dfA.sort_values("biweek")

if dfA.empty:
    raise ValueError("No data points with measles >= MIN_CASES in the selected␣
↪community/window.")

# Determine early-window biweek bounds
if (EARLY_BIWEEK_MIN is not None) and (EARLY_BIWEEK_MAX is not None):
    bw_min, bw_max = int(EARLY_BIWEEK_MIN), int(EARLY_BIWEEK_MAX)
else:
    if START_AT_FIRST_POSITIVE:
        bw_min = int(dfA["biweek"].iloc[0])
    else:
        bw_min = int(dfA["biweek"].min())
    bw_max = bw_min + int(EARLY_N_BIWEEKS) - 1

early = dfA.loc[(dfA["biweek"] >= bw_min) & (dfA["biweek"] <= bw_max)].copy()
early = early.sort_values("biweek")

if early.shape[0] < 3:
    raise ValueError(
        f"Need at least 3 points to fit a log-linear model; got {early.
↪shape[0]} "
        f"in window biweek [{bw_min}, {bw_max}]."
    )

# Use time in "biweeks since window start" for interpretability
```

```
t = (early["biweek"].to_numpy(dtype=float) - float(bw_min))
y = early["measles"].to_numpy(dtype=float)
logy = np.log(y)

# -----------------------------
# 2) Fit log-linear model: log(y) = a + r * t + error
#    r is the exponential growth rate per biweek
# -----------------------------
# stats.linregress uses ordinary least squares and returns slope, intercept,␣
 ↪etc.
fit = stats.linregress(t, logy)
r_hat = float(fit.slope)         # growth rate per biweek
a_hat = float(fit.intercept)     # log-scale intercept
r_se = float(fit.stderr)         # standard error of slope (if available)
n = t.size
df = n - 2

# 95% CI for slope using Student-t
tcrit = stats.t.ppf(1 - ALPHA / 2, df)
r_ci = (r_hat - tcrit * r_se, r_hat + tcrit * r_se)

# -----------------------------
# 3) Convert growth rate to approximate R0
#    Assumption: SIR-like early phase with S ~ 1, growth rate r    -  ,
#    so R0 =  /   (r +  )/  = 1 + r/
# -----------------------------
gamma = float(GAMMA_PER_BIWEEK)
R0_hat = 1.0 + (r_hat / gamma)
R0_ci = (1.0 + (r_ci[0] / gamma), 1.0 + (r_ci[1] / gamma))

# -----------------------------
# 4) Plot: semi-log (y on log-scale) with fitted exponential curve
# -----------------------------
# Smooth curve over the early window
t_grid = np.linspace(t.min(), t.max(), 200)
y_fit = np.exp(a_hat + r_hat * t_grid)

plt.figure(figsize=(8, 5))
plt.semilogy(early["biweek"], y, "o", label="Observed (early window)")
plt.semilogy(bw_min + t_grid, y_fit, "-", label="Fitted exponential")

plt.title(f"Early exponential growth fit (Community {COMMUNITY}), biweek␣
 ↪{bw_min}-{bw_max}")
plt.xlabel("Biweek")
plt.ylabel("Reported measles cases (log scale)")
plt.grid(True, which="both", linestyle="--", linewidth=0.5)
plt.legend()
```

```
# ------------------------------
# Print key results + assumptions
# ------------------------------
print("=== Early Exponential Growth (log-linear) ===")
print(f"Community: {COMMUNITY}")
print(f"Early window biweeks: [{bw_min}, {bw_max}]")
print(f"Points used (after dropping NA and < {MIN_CASES}): n = {n}")
print("")
print("Model: log(cases_t) = a + r * t + error, where t is biweeks since window␣
  ↪start")
print(f"Estimated growth rate r (per biweek): {r_hat:.6f}")
print(f"95% CI for r: [{r_ci[0]:.6f}, {r_ci[1]:.6f}]")
print(f"R-squared: {fit.rvalue**2:.4f}")
print(f"p-value (slope): {fit.pvalue:.3e}")
print("")
print("R0 approximation:")
print("Assumption: early phase S 1 and SIR-like growth r    -  , so R0 = /   1␣
  ↪+ r/ ")
print(f"Using   = {gamma:.3f} per biweek")
print(f"Estimated R0: {R0_hat:.4f}")
print(f"95% CI for R0 (from slope CI): [{R0_ci[0]:.4f}, {R0_ci[1]:.4f}]")

# If running in a notebook, show the plot:
# plt.show()
```

```
=== Early Exponential Growth (log-linear) ===
Community: A
Early window biweeks: [1, 10]
Points used (after dropping NA and < 1.0): n = 10

Model: log(cases_t) = a + r * t + error, where t is biweeks since window start
Estimated growth rate r (per biweek): 0.439208
95% CI for r: [0.373936, 0.504481]
R-squared: 0.9678
p-value (slope): 2.963e-07

R0 approximation:
Assumption: early phase S 1 and SIR-like growth r    -  , so R0 = /   1 + r/
Using   = 1.000 per biweek
Estimated R0: 1.4392
95% CI for R0 (from slope CI): [1.3739, 1.5045]
```



Goal Assess how sensitive the estimated basic reproduction number (**R**) is to the choice of early-outbreak window length.

Method (brief) For a sequence of increasing early-outbreak windows (measured in biweeks):

- Fit a log-linear model to early reported measles cases to estimate the exponential growth rate.
- Convert the growth rate to **R** assuming a fixed infectious removal rate (= 1 per biweek).
- Compute a 95% confidence interval for **R** from the regression uncertainty.
- Visualize **R** and its uncertainty as a function of the window length.

Interpretation Stable **R** estimates across window lengths suggest a robust early-growth signal, while strong variation indicates sensitivity to window choice or departures from exponential growth.

1.4.2 Continue with the this prompt

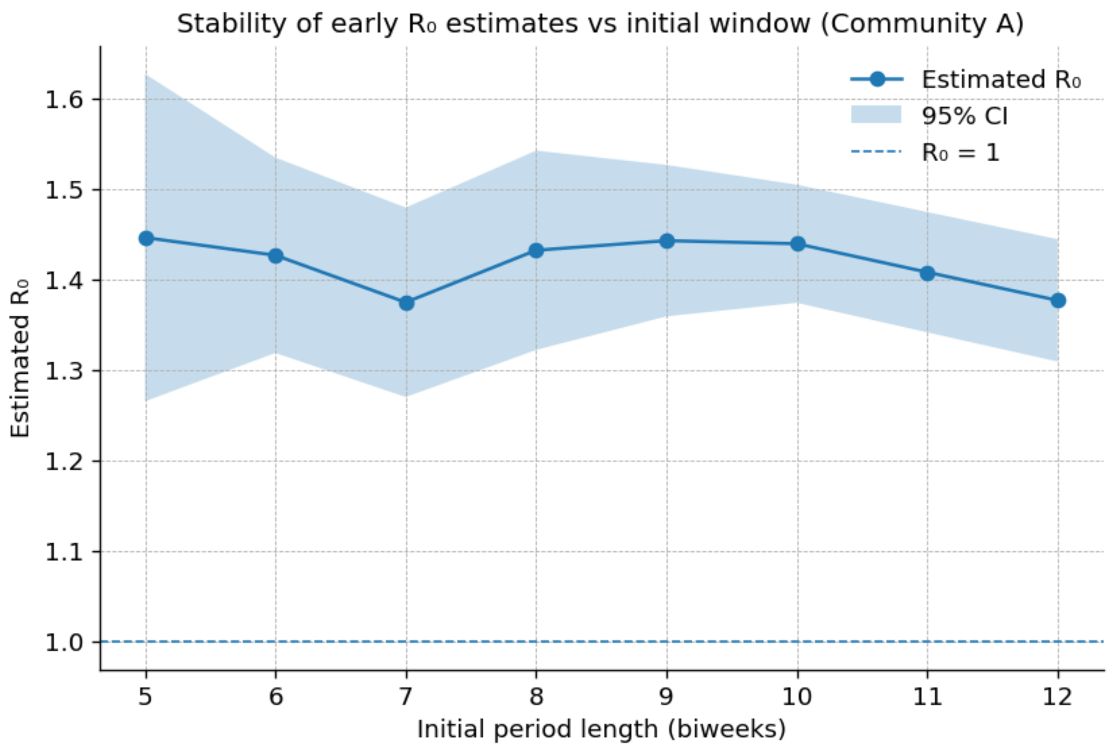
`For a range of early-outbreak window lengths, plot the estimated R (derived from exponential g`

[7]:
```
# Plot estimated R0 (with CI) versus initial-period length (number of biweeks)
# Constraints respected: NumPy, SciPy, Matplotlib only. Code-only.

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

```
# -----------------------------
# User-adjustable settings
# -----------------------------
COMMUNITY = "A"
MIN_CASES = 1.0
GAMMA_PER_BIWEEK = 1.0    #
ALPHA = 0.05              # 95% CI

# Range of early-window lengths to evaluate (in biweeks)
WINDOW_LENGTHS = np.arange(5, 13)   # e.g., 5-12 biweeks

# -----------------------------
# Prepare data
# -----------------------------
dfA = measles_df.loc[measles_df["community"] == COMMUNITY, ["biweek",␣
 ↪"measles"]].copy()
dfA = dfA.dropna(subset=["measles"])
dfA = dfA.loc[dfA["measles"] >= MIN_CASES].copy()
dfA = dfA.sort_values("biweek")

if dfA.shape[0] < WINDOW_LENGTHS.max():
    raise ValueError("Not enough positive observations to cover the largest␣
 ↪window length.")

# Start window at first positive case
bw_start = int(dfA["biweek"].iloc[0])

# Storage
R0_hat_list = []
R0_lo_list = []
R0_hi_list = []

# -----------------------------
# Loop over window lengths
# -----------------------------
for L in WINDOW_LENGTHS:
    bw_end = bw_start + int(L) - 1
    early = dfA.loc[(dfA["biweek"] >= bw_start) & (dfA["biweek"] <= bw_end)].
 ↪copy()
    early = early.sort_values("biweek")

    if early.shape[0] < 3:
        R0_hat_list.append(np.nan)
        R0_lo_list.append(np.nan)
        R0_hi_list.append(np.nan)
        continue
    t = (early["biweek"].to_numpy(dtype=float) - float(bw_start))
    y = early["measles"].to_numpy(dtype=float)
    logy = np.log(y)

    fit = stats.linregress(t, logy)
    r_hat = float(fit.slope)
    r_se = float(fit.stderr)
    df = t.size - 2
    tcrit = stats.t.ppf(1 - ALPHA / 2, df)

    r_ci = (r_hat - tcrit * r_se, r_hat + tcrit * r_se)

    # R0   1 + r /
    R0_hat = 1.0 + r_hat / GAMMA_PER_BIWEEK
    R0_ci = (1.0 + r_ci[0] / GAMMA_PER_BIWEEK,
             1.0 + r_ci[1] / GAMMA_PER_BIWEEK)

    R0_hat_list.append(R0_hat)
    R0_lo_list.append(R0_ci[0])
    R0_hi_list.append(R0_ci[1])

R0_hat_arr = np.array(R0_hat_list)
R0_lo_arr = np.array(R0_lo_list)
R0_hi_arr = np.array(R0_hi_list)

# -----------------------------
# Plot R0 vs initial-period length
# -----------------------------
plt.figure(figsize=(8, 5))

plt.plot(WINDOW_LENGTHS, R0_hat_arr, marker="o", label="Estimated R ")
plt.fill_between(
    WINDOW_LENGTHS,
    R0_lo_arr,
    R0_hi_arr,
    alpha=0.25,
    label="95% CI"
)

plt.axhline(1.0, linestyle="--", linewidth=1, label="R  = 1")

plt.xlabel("Initial period length (biweeks)")
plt.ylabel("Estimated R ")
plt.title(f"Stability of early R  estimates vs initial window (Community␣
  ↪{COMMUNITY})")
plt.grid(True, linestyle="--", linewidth=0.5)
plt.legend()
```

```python
# If running interactively:
# plt.show()

# ------------------------------
# Print table of results
# ------------------------------
print("Initial window (biweeks) | R0_hat | R0_CI_low | R0_CI_high")
for L, r0, lo, hi in zip(WINDOW_LENGTHS, R0_hat_arr, R0_lo_arr, R0_hi_arr):
    print(f"{L:>23d} | {r0:6.3f} | {lo:10.3f} | {hi:11.3f}")
```

```
Initial window (biweeks) | R0_hat | R0_CI_low | R0_CI_high
                      5 |  1.446 |      1.265 |       1.627
                      6 |  1.426 |      1.319 |       1.534
                      7 |  1.374 |      1.270 |       1.479
                      8 |  1.432 |      1.322 |       1.542
                      9 |  1.443 |      1.359 |       1.526
                     10 |  1.439 |      1.374 |       1.504
                     11 |  1.408 |      1.341 |       1.474
                     12 |  1.377 |      1.309 |       1.444
```



1.5 3. Implement the SIR Model (Biweekly Units)

We use a **closed SIR** model for a single outbreak wave: - S(t): susceptible - I(t): infectious - R(t): recovered

Time unit = **biweeks**.

1.5.1 ChatGPT Prompt (copy/paste)

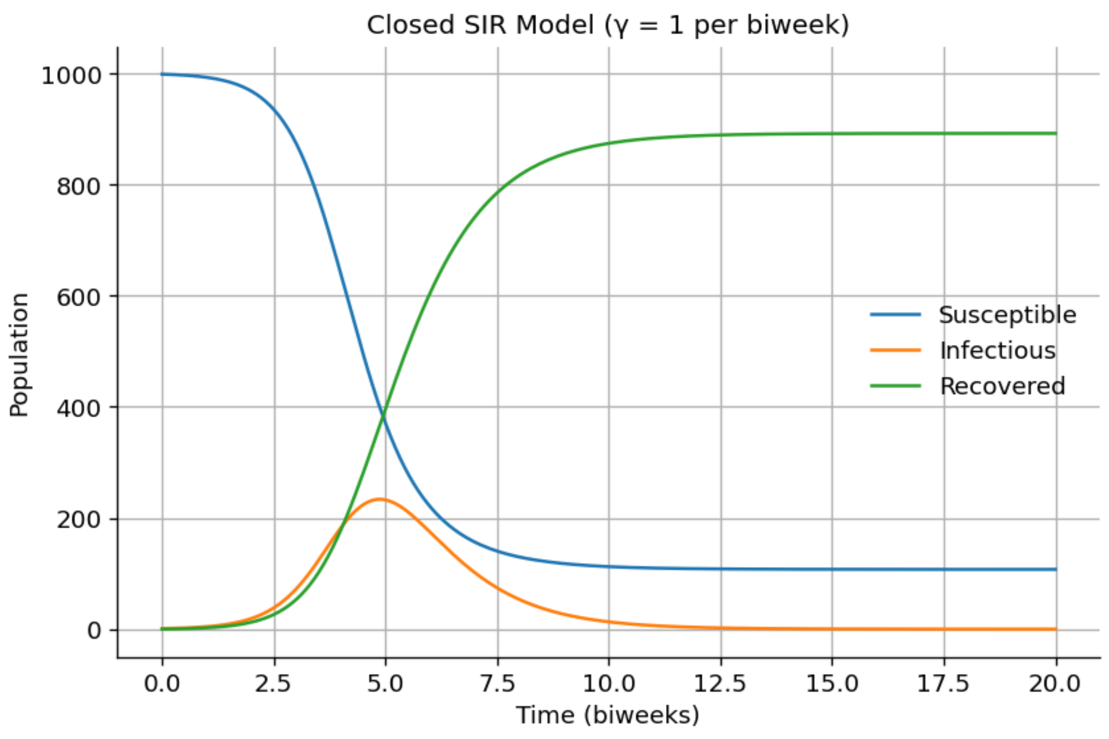
```
Persona:
You are an expert epidemiological modeler and Python educator.

Context:
- Closed SIR model (no birth or death)
- Time unit: biweeks
- Infectious period   2 weeks (gamma   1 per biweek)

Task:
Implement an SIR model using SciPy ODE solving:
- Define the SIR equations, the function name should be `sir_rhs`
- Solve over a biweekly time grid, put it in the function `simulate_sir`
- Plot S, I, R over time

Constraints:
- Use scipy.integrate.solve_ivp
- Keep code readable and commented

Verification:
- Plot S, I, R
- Verify S + I + R   N
```

[8]:

```python
import numpy as np
import matplotlib.pyplot as plt
from scipy.integrate import solve_ivp


def sir_rhs(t, y, beta, gamma, N):
    """
    Right-hand side of the closed SIR model.

    Parameters
    ----------
    t : float
        Time (in biweeks)
    y : array-like
        Current state vector [S, I, R]
    beta : float
        Transmission rate (per biweek)
    gamma : float
```

```
        Recovery rate (per biweek)
    N : float
        Total population size (constant)

    Returns
    -------
    dydt : list
        Time derivatives [dS/dt, dI/dt, dR/dt]
    """
    S, I, R = y

    dSdt = -beta * S * I / N
    dIdt = beta * S * I / N - gamma * I
    dRdt = gamma * I

    return [dSdt, dIdt, dRdt]


def simulate_sir(
    N=1000,
    I0=1,
    R0=0,
    beta=2.5,    # example: R0_basic = beta / gamma = 2.5
    gamma=1.0,   # infectious period   1 biweek
    t_max=20
):
    """
    Simulate the SIR model over a biweekly time grid.

    Returns
    -------
    t : array
        Time grid (biweeks)
    S, I, R : arrays
        Time series of compartments
    """
    # Initial susceptible population
    S0 = N - I0 - R0

    # Initial condition vector
    y0 = [S0, I0, R0]

    # Time grid (biweekly resolution)
    t_eval = np.linspace(0, t_max, 200)

    # Solve ODE system
    sol = solve_ivp(
        fun=lambda t, y: sir_rhs(t, y, beta, gamma, N),
        t_span=(0, t_max),
        y0=y0,
        t_eval=t_eval,
        vectorized=False
    )

    S, I, R = sol.y
    t = sol.t

    return t, S, I, R


# ==========================
# Run simulation
# ==========================

t, S, I, R = simulate_sir()

# ==========================
# Verification: Mass balance
# ==========================

N_total = S + I + R
print("Maximum deviation from N:",
      np.max(np.abs(N_total - N_total[0])))

# ==========================
# Plot results
# ==========================

plt.figure()
plt.plot(t, S, label="Susceptible")
plt.plot(t, I, label="Infectious")
plt.plot(t, R, label="Recovered")

plt.xlabel("Time (biweeks)")
plt.ylabel("Population")
plt.title("Closed SIR Model (  = 1 per biweek)")
plt.legend()
plt.show()
```

```
Maximum deviation from N: 2.2737367544323206e-13
```



1.6 4. Map Model Output to Observations (Incidence via ΔH)

Observed data are **biweekly case counts**, not the state `I(t)`.
We model **incidence** using an accumulator:

- Add `H(t)` with **dH/dt = S I / N**
- Predicted biweekly counts **ΔH** over each biweek interval

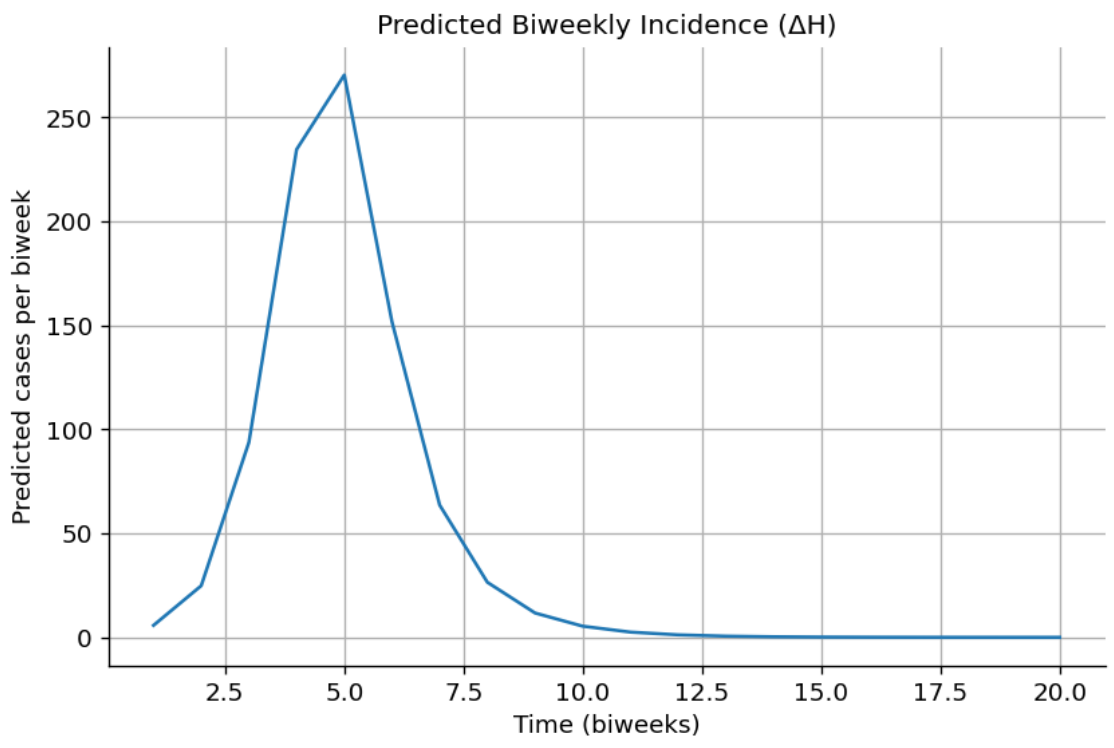
1.6.1 ChatGPT Prompt

```
Persona:
You are an expert epidemic modeler.

Context:
- Observed data are biweekly case counts (incidence)
- SIR model outputs states

Task:
Extend the SIR model by:
- Adding H(t) with dH/dt = beta*S*I/N
- Computing predicted biweekly cases as ΔH aligned to biweeks

Constraints:
```

```
- Keep code minimal and readable

Verification:
- Plot predicted ΔH
```

[9]:

```python
import numpy as np
import matplotlib.pyplot as plt
from scipy.integrate import solve_ivp


def sir_with_incidence_rhs(t, y, beta, gamma, N):
    """
    SIR model with cumulative incidence H.

    y = [S, I, R, H]
    """
    S, I, R, H = y

    infection_rate = beta * S * I / N

    dSdt = -infection_rate
    dIdt = infection_rate - gamma * I
    dRdt = gamma * I
    dHdt = infection_rate  # cumulative infections

    return [dSdt, dIdt, dRdt, dHdt]


def simulate_sir_with_incidence(
    N=1000,
    I0=1,
    R0=0,
    beta=2.5,
    gamma=1.0,
    t_max=20
):
    """
    Simulate SIR model and compute biweekly predicted cases.
    """

    S0 = N - I0 - R0
    H0 = 0

    y0 = [S0, I0, R0, H0]

    # Biweekly grid (matches reporting interval)
    t_eval = np.arange(0, t_max + 1)
    sol = solve_ivp(
        fun=lambda t, y: sir_with_incidence_rhs(t, y, beta, gamma, N),
        t_span=(0, t_max),
        y0=y0,
        t_eval=t_eval
    )

    S, I, R, H = sol.y
    t = sol.t

    # Predicted biweekly cases = change in cumulative infections
    delta_H = np.diff(H)

    return t, S, I, R, H, delta_H


# ======================
# Run simulation
# ======================

t, S, I, R, H, delta_H = simulate_sir_with_incidence()

# ======================
# Plot predicted biweekly incidence
# ======================

plt.figure()
plt.plot(t[1:], delta_H)
plt.xlabel("Time (biweeks)")
plt.ylabel("Predicted cases per biweek")
plt.title("Predicted Biweekly Incidence (ΔH)")
plt.show()
```



Continue with this prompt to plot the data

```
I have biweekly measles incidence data for Community A:

measles_df = pd.read_csv("data/niamey.csv")

dfA = (
    measles_df
    .loc[measles_df["community"] == "A", ["biweek", "measles"]]
    .dropna(subset=["measles"])
    .copy()
)


- dfA["biweek"] contains the biweekly time index

- dfA["measles"] contains observed biweekly incidence (number of cases)

I also have an SIR model that returns simulated incidence:

def simulate_sir_with_incidence(
    N=1000,
    I0=1,
    R0=0,
    beta=2.5,
    gamma=1.0,
    t_max=20
):
    ...
    return t, S, I, R, H, delta_H
```

Where:

t → model time points (in biweeks)

delta_H → simulated biweekly incidence (new infections per biweek)

H → cumulative infections

What I want to do

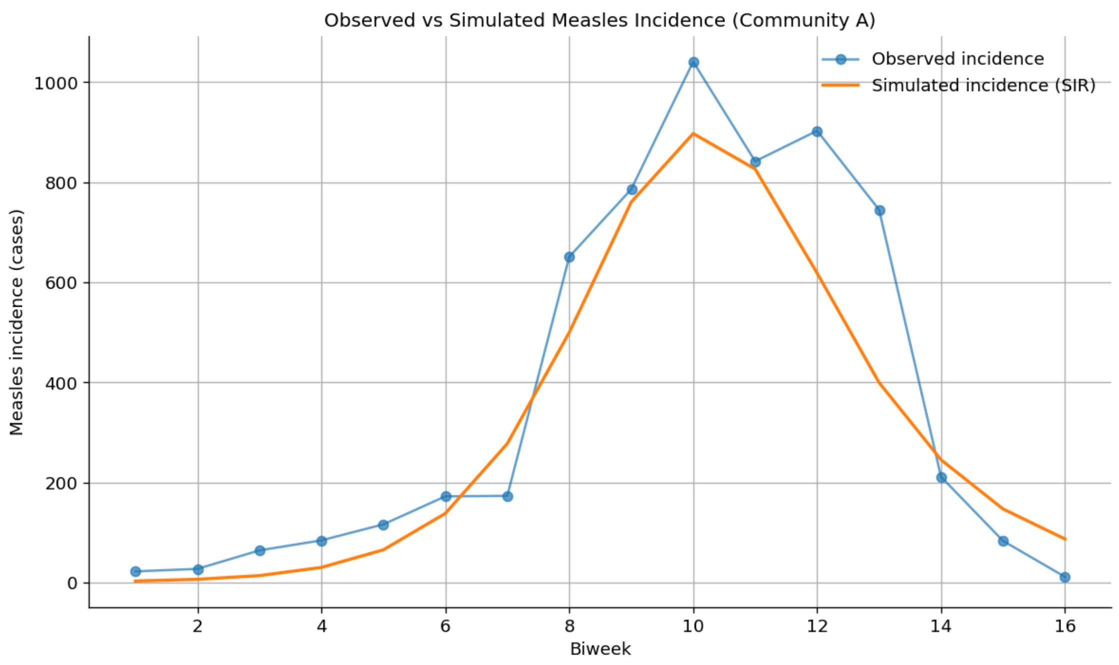
- Plot observed measles incidence (dfA["measles"])

- Overlay simulated biweekly incidence (delta_H) on the same figure

- Use t[1:] when plotting delta_H as len(t) is different from len(delta_h) by 1 unit

[10]:
```
# ----------------------------------------
# Get observed data for community A
# ----------------------------------------

measles_df = pd.read_csv("data/niamey.csv")
dfA = measles_df.loc[
    measles_df["community"] == "A",
    ["biweek", "measles"]
].copy()

dfA = dfA.dropna(subset=["measles"])
# Run simulation
t, S, I, R, H, delta_H = simulate_sir_with_incidence(
    N=7000,
    I0=1,
    R0=0,
    beta=1.8,
    gamma=1.0,
    t_max=dfA["biweek"].max()
)
import matplotlib.pyplot as plt

plt.figure(figsize=(10, 6))
```

```
# Observed measles incidence
plt.plot(
    dfA["biweek"],
    dfA["measles"],
    'o-',
    label="Observed incidence",
    alpha=0.7
)

# Simulated incidence
plt.plot(
    t[1:],            # shift because delta_H is one shorter
    delta_H,
    '-',
    label="Simulated incidence (SIR)",
    linewidth=2
)

plt.xlabel("Biweek")
plt.ylabel("Measles incidence (cases)")
plt.title("Observed vs Simulated Measles Incidence (Community A)")
plt.legend()
plt.grid(True)
plt.tight_layout()
plt.show()
```



1.7 5. Fit Parameters by Least Squares

We fit parameters by minimizing squared error between observed counts and predicted ΔH.

1.7.1 ChatGPT Prompt (copy/paste)

```
##  Persona

You are an **expert in numerical optimization for epidemic models**, with experience fitting co

---

##  Data

We have **biweekly measles incidence data** for **Community A**:

measles_df = pd.read_csv("data/niamey.csv")

dfA = (
    measles_df
    .loc[measles_df["community"] == "A", ["biweek", "measles"]]
    .dropna(subset=["measles"])
    .copy()
)

* `dfA["biweek"]` → biweekly time index
* `dfA["measles"]` → observed biweekly incidence (case counts)

---

##  Model

We use an SIR model that returns simulated incidence:

def simulate_sir_with_incidence(
    N=1000,
    I0=1,
    R0=0,
    beta=2.5,
    gamma=1.0,
    t_max=20
):
    ...
    return t, S, I, R, H, delta_H
```

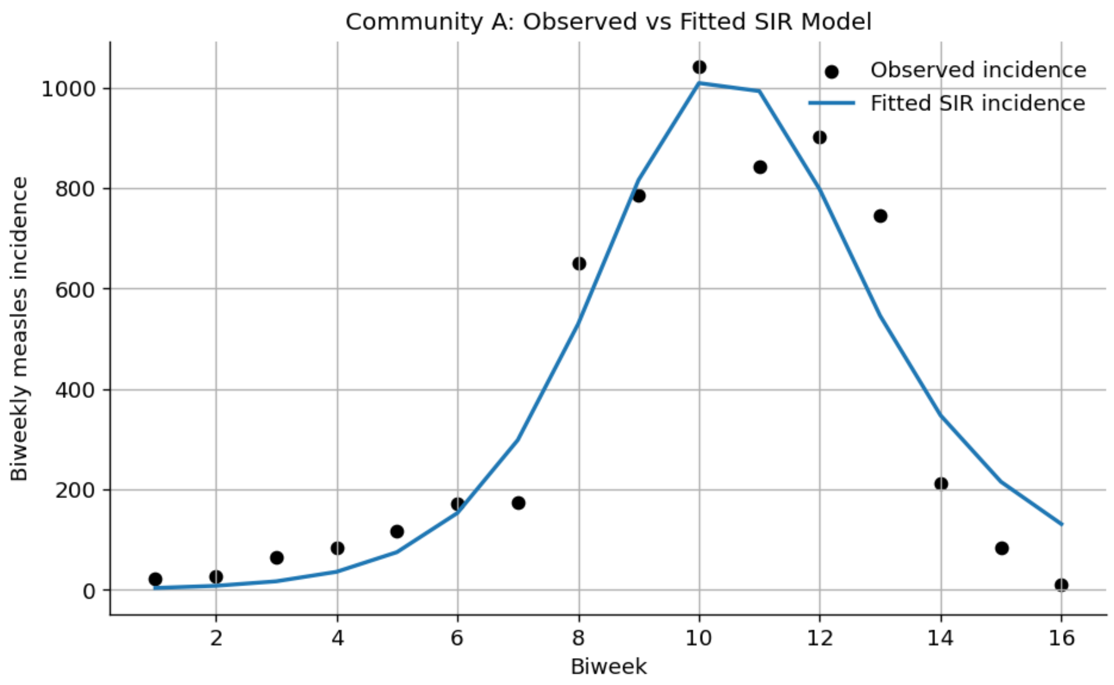
```
Where:

* `t` → model time points (in biweeks)
* `delta_H` → simulated **biweekly incidence** (new infections per biweek)
* Use `t[1:]` to align with `delta_H` (since incidence is computed between time steps)

---

##   Objective

Fit model parameters to the observed incidence data using **nonlinear least squares**.

### Parameters to estimate:

* `N` (population size)
* `beta` (transmission rate)
* Optional: `I0` (initial infected)

### Fixed parameter:

* `gamma = 1.0`

---

##   Initialization Strategy

Use an early-growth estimate:

* Estimated basic reproduction number:

  [
  R_0 = 1.443
  ]

* Since ( R_0 = \beta / \gamma ), initialize:

  [
  \beta_0 = 1.443
  ]

Choose reasonable initial guesses and bounds:

* `N` within plausible community size range
* `beta > 0`
* `I0   1`

---
```

```
##  Optimization Requirements

* Use `scipy.optimize.least_squares`
* Fit by minimizing:

[
\text{SSE} = \sum ( \text{Observed} - \text{Predicted} )^2
]

* Ensure runtime is suitable for a workshop (avoid heavy MCMC or expensive methods)

---

##  Verification & Output

After fitting:

1. Overlay observed and fitted incidence curves
2. Print:

   * Best-fit parameter values
   * Sum of squared errors (SSE)

---

##  Expected Deliverables

* Residual function definition
* Call to `least_squares`
* Overlay plot (observed vs fitted)
* Printed parameter estimates and SSE
* Clean, reproducible workshop-ready code
```

[11]:
```python
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from scipy.optimize import least_squares

# Load data
measles_df = pd.read_csv("data/niamey.csv")

dfA = (
    measles_df
    .loc[measles_df["community"] == "A", ["biweek", "measles"]]
    .dropna(subset=["measles"])
    .copy()
)
```

```python
# Observed time & incidence
t_obs = dfA["biweek"].values
y_obs = dfA["measles"].values


def residuals(params, t_obs, y_obs):
    """
    params = [N, beta, I0]
    """
    N, beta, I0 = params
    gamma = 1.0

    # Simulate model
    t_model, S, I, R, H, delta_H = simulate_sir_with_incidence(
        N=N,
        I0=I0,
        R0=0,
        beta=beta,
        gamma=gamma,
        t_max=max(t_obs)
    )

    # Model incidence aligned to t[1:]
    t_inc = t_model[1:]

    # Interpolate to observed biweeks
    y_model = np.interp(t_obs, t_inc, delta_H)

    return y_obs - y_model


# Initial guesses
N0 = 7000
beta0 = 1.433
I00 = 5

x0 = [N0, beta0, I00]

# Bounds
lower_bounds = [1000, 0.1, 1]
upper_bounds = [10000, 5.0, 200]

bounds = (lower_bounds, upper_bounds)


result = least_squares(
    residuals,
    x0,
    args=(t_obs, y_obs),
    bounds=bounds,
    method="trf"   # stable for bounded problems
)

N_hat, beta_hat, I0_hat = result.x

print(result.x)

# Compute SSE
SSE = np.sum(result.fun**2)
print(f"SSE = {SSE}")


gamma = 1.0

t_fit, S_fit, I_fit, R_fit, H_fit, delta_H_fit = simulate_sir_with_incidence(
    N=N_hat,
    I0=I0_hat,
    R0=0,
    beta=beta_hat,
    gamma=gamma,
    t_max=max(t_obs)
)

t_inc_fit = t_fit[1:]

plt.figure(figsize=(8,5))

plt.scatter(t_obs, y_obs, label="Observed incidence", color="black")
plt.plot(t_inc_fit, delta_H_fit, label="Fitted SIR incidence", linewidth=2)

plt.xlabel("Biweek")
plt.ylabel("Biweekly measles incidence")
plt.legend()
plt.title("Community A: Observed vs Fitted SIR Model")
plt.tight_layout()
plt.show()
```

```
[8.60920993e+03 1.75821976e+00 1.42764944e+00]
SSE = 163890.02506195556
```



1.8 6. Poisson Likelihood Inference (Counts)

For count data: - (y_t Poisson(_t)) - (_t =   H_t)

where   is a reporting/ascertainment fraction.

1.8.1 ChatGPT Prompt (copy/paste)

```
#  Persona

You are an **expert in numerical optimization for epidemic models**, with experience fitting co

---

#  Data

We have **biweekly measles incidence data** for **Community A**:

measles_df = pd.read_csv("data/niamey.csv")

dfA = (
    measles_df
    .loc[measles_df["community"] == "A", ["biweek", "measles"]]
    .dropna(subset=["measles"])
    .copy()
)
```

```
t_obs = dfA["biweek"].values
y_obs = dfA["measles"].values
```

* `t_obs` → biweekly time index
* `y_obs` → observed biweekly incidence (case counts)

# Model

We use an SIR model that returns simulated incidence:

```
def simulate_sir_with_incidence(
    N=1000,
    I0=1,
    R0=0,
    beta=2.5,
    gamma=1.0,
    t_max=20
):
    ...
    return t, S, I, R, H, delta_H
```

Where:

* `t` → model time points (in biweeks)
* `delta_H` → simulated **biweekly incidence**
* Use `t[1:]` to align with `delta_H`

# Objective

Fit model parameters to the observed incidence data using **maximum likelihood under a Poisson

Assume:

[
Y_t \sim \text{Poisson}(\lambda_t)
]

where:

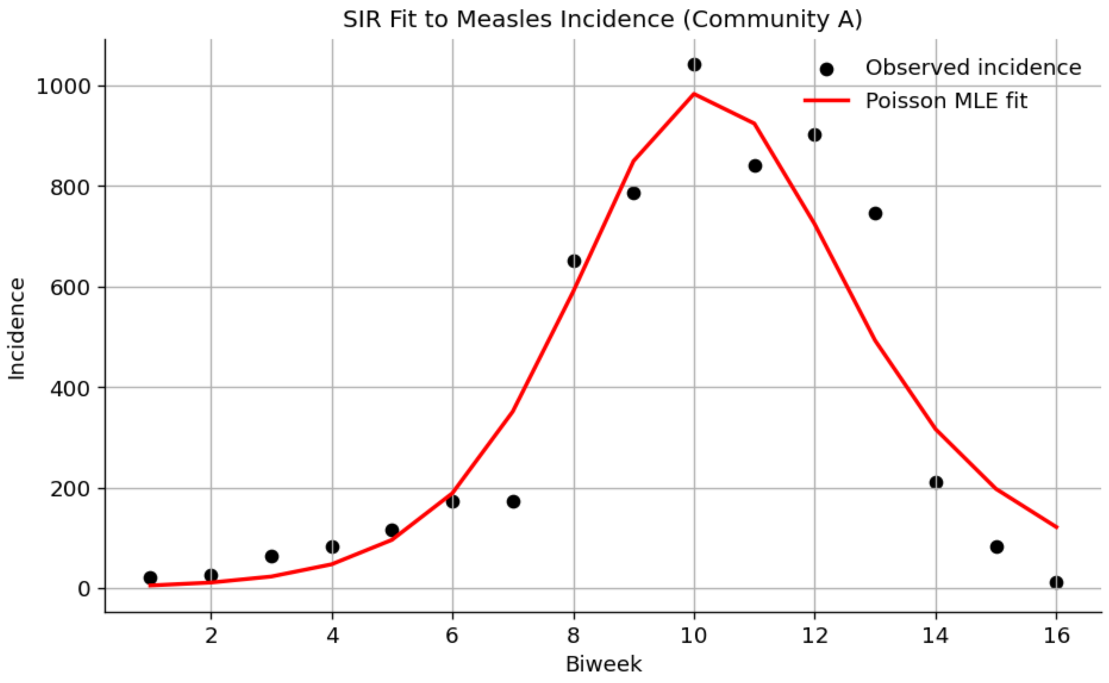
* (Y_t) = observed incidence
* (\lambda_t) = model-predicted incidence (`delta_H`)

```
---

#   Parameters to Estimate

* `N` (population size)
* `beta` (transmission rate)
* Optional: `I0` (initial infected)

### Fixed parameter:

* `gamma = 1.0`

---

#   Initialization Strategy

Use early-growth estimate:

[
R_0 = 1.443
]

Since:

[
R_0 = \beta / \gamma
]

Initialize:

[
\beta_0 = 1.443
]

Use reasonable bounds:

* `N` within plausible community size range
* `beta > 0`
* `I0   1`

---

#   Optimization Requirements

Use `scipy.optimize.minimize` (or `least_squares` minimizing -log-likelihood).

Minimize the **negative Poisson log-likelihood**:
```

```
[
\mathcal{L}(\theta)
===================

\sum_t \left(
\lambda_t - y_t \log(\lambda_t)
\right)
]

(omit constant (\log(y_t!)) term)

Add small epsilon to avoid `log(0)`.

Ensure runtime is suitable for a workshop (no MCMC).

---

#   Verification & Output

After fitting:

1. Overlay observed and fitted incidence curves
2. Print:

   * Best-fit parameter values
   * Final negative log-likelihood
3. (Optional) Compare visually against least-squares fit

---

#   Expected Deliverables

* Negative log-likelihood function definition
* Call to optimizer
* Overlay plot (observed vs fitted incidence)
* Printed parameter estimates
* Clean, reproducible workshop-ready code
* Proper numerical safeguards (`epsilon` for stability)
```

[12]:
```python
import numpy as np
from scipy.optimize import minimize
import matplotlib.pyplot as plt

epsilon = 1e-8

def neg_poisson_loglik(theta, t_obs, y_obs, gamma=1.0):
    """
    Negative Poisson log-likelihood for SIR incidence fit.

    theta = [N, beta, I0]
    """
    N, beta, I0 = theta

    # Enforce positivity (soft safeguard)
    if N <= 0 or beta <= 0 or I0 < 1:
        return np.inf

    # Simulate model
    t, S, I, R, H, delta_H = simulate_sir_with_incidence(
        N=N,
        I0=I0,
        R0=0,
        beta=beta,
        gamma=gamma,
        t_max=int(max(t_obs))
    )

    # Align times
    t_model = t[1:]

    # Interpolate model incidence at observed times
    lambda_t = np.interp(t_obs, t_model, delta_H)

    # Numerical safeguard
    lambda_t = np.maximum(lambda_t, epsilon)

    # Negative Poisson log-likelihood
    nll = np.sum(lambda_t - y_obs * np.log(lambda_t))

    return nll


# Initial guesses
N0 = 1000
beta0 = 1.443
I00 = 5

theta0 = [N0, beta0, I00]

# Bounds
bounds = [
    (200, 20000),    # N
    (1e-3, 10.0),   # beta
    (1, 50)         # I0
]


result = minimize(
    neg_poisson_loglik,
    theta0,
    args=(t_obs, y_obs),
    method="L-BFGS-B",
    bounds=bounds
)

N_hat, beta_hat, I0_hat = result.x
final_nll = result.fun

print("===== MLE RESULTS =====")
print(f"N      = {N_hat:.2f}")
print(f"ˆ      = {beta_hat:.4f}")
print(f"I0     = {I0_hat:.2f}")
print(f"Final NLL = {final_nll:.2f}")
print(f"Converged: {result.success}")

# Simulate using fitted parameters
t_fit, S_fit, I_fit, R_fit, H_fit, delta_H_fit = simulate_sir_with_incidence(
    N=N_hat,
    I0=I0_hat,
    R0=0,
    beta=beta_hat,
    gamma=1.0,
    t_max=int(max(t_obs))
)

t_model = t_fit[1:]
lambda_fit = np.interp(t_obs, t_model, delta_H_fit)


plt.figure(figsize=(8, 5))

plt.scatter(t_obs, y_obs, color="black", label="Observed incidence")
plt.plot(t_obs, lambda_fit, color="red", linewidth=2, label="Poisson MLE fit")

plt.xlabel("Biweek")
plt.ylabel("Incidence")
plt.title("SIR Fit to Measles Incidence (Community A)")
plt.legend()
plt.tight_layout()
plt.show()
```

```
===== MLE RESULTS =====
N      = 8635.31
^      = 1.7336
I0     = 2.10
Final NLL = -31799.00
Converged: True
```



1.9 7. Quick Uncertainty: Profile Likelihood for (Optional)

1.9.1 ChatGPT Prompt (copy/paste, continue with the likelihood chat)

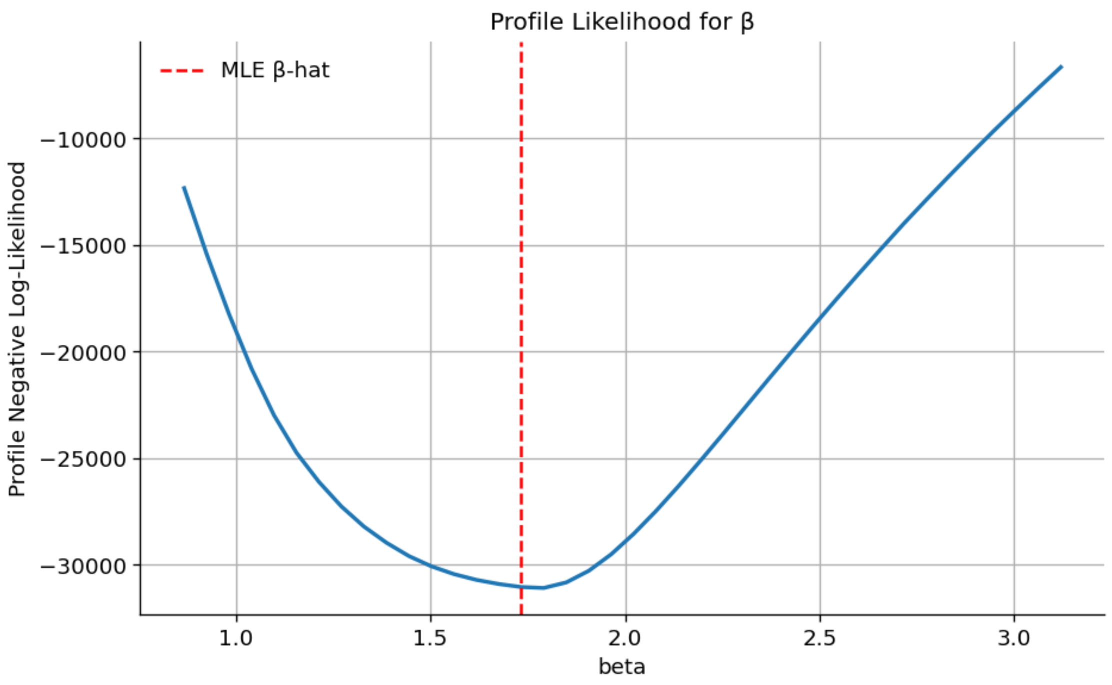
```
Persona:
You are an expert in likelihood-based inference.

Context:
- We already have a Poisson likelihood fit
- We want uncertainty for beta

Task:
Create a profile likelihood for beta:
1) Fix beta over a grid
2) Optimize I0 and rho for each beta
3) Plot profile NLL(beta)

Constraints:
- Keep runtime reasonable for a workshop
```

```
Verification:
- Profile plot
- Explain how to interpret the uncertainty
```

[13]:
```python
import numpy as np
from scipy.optimize import minimize
import matplotlib.pyplot as plt

epsilon = 1e-8

def neg_poisson_loglik(theta, beta_fixed, t_obs, y_obs, gamma=1.0):
    """
    NLL with beta fixed.
    theta = [N, I0]
    """
    N, I0 = theta

    # Hard constraints
    if N <= 0 or I0 < 1:
        return np.inf

    # Simulate
    t, S, I, R, H, delta_H = simulate_sir_with_incidence(
        N=N,
        I0=I0,
        R0=0,
        beta=beta_fixed,
        gamma=gamma,
        t_max=int(max(t_obs))
    )

    lambda_t = np.interp(t_obs, t[1:], delta_H)
    lambda_t = np.maximum(lambda_t, epsilon)

    nll = np.sum(lambda_t - y_obs * np.log(lambda_t))
    return nll
# Around previously estimated beta_hat
beta_hat = result.x[1]
print(beta_hat)

beta_grid = np.linspace(
    0.5 * beta_hat,
    1.8 * beta_hat,
    40   # workshop-friendly
)

profile_nll = []
```

```
# Initial guesses
N_init = result.x[0]
I0_init = result.x[2]

for beta_val in beta_grid:

    res = minimize(
        neg_poisson_loglik,
        x0=[N_init, I0_init],
        args=(beta_val, t_obs, y_obs),
        method="L-BFGS-B",
        bounds=[(200, 5000), (1, 50)]
    )

    profile_nll.append(res.fun)

    # Warm start next iteration
    N_init, I0_init = res.x

profile_nll = np.array(profile_nll)


plt.figure(figsize=(8,5))
plt.plot(beta_grid, profile_nll, linewidth=2)
plt.axvline(beta_hat, color='red', linestyle='--', label='MLE  -hat')

plt.xlabel("beta")
plt.ylabel("Profile Negative Log-Likelihood")
plt.title("Profile Likelihood for  ")
plt.legend()
plt.tight_layout()
plt.show()
```

```
1.7335681871869875
```



1.10 8. Generate a Markdown Summary (Hackathon Report Cell)

1.10.1 ChatGPT Prompt (copy/paste)

[13]:

```
```