IVP

April 2, 2025

Initial Value Problems for Systems Modeling

This notebook summarizes 10 fundamental initial value problems (IVPs) used in mathematical modeling across biology, chemistry, and physics. Each IVP includes a differential equation and an initial condition.

1. Exponential Growth

This describes a process where the rate of change of a population (or quantity) is proportional to its current size.

IVP:

$$\frac{dP}{dt} = rP, \quad P(0) = P_0$$

Solution:

$$P(t) = P_0 e^{rt}$$

2. Logistic Growth

This introduces a carrying capacity which limits growth as the population increases.

IVP:

$$\frac{dP}{dt} = rP\left(1 - \frac{P}{K}\right), \quad P(0) = P_0$$

Solution:

$$P(t) = \frac{K}{1 + \left(\frac{K-P_0}{P_0}\right)e^{-rt}}$$

3. Pharmacokinetics (Drug Clearance)

Describes how a drug enters and is removed from the bloodstream.

IVP:

$$\frac{dC}{dt} = k_{\text{in}} - k_{\text{out}}C, \quad C(0) = C_0$$

Solution:

$$C(t) = \frac{k_{\text{in}}}{k_{\text{out}}} + \left(C_0 - \frac{k_{\text{in}}}{k_{\text{out}}}\right)e^{-k_{\text{out}}t}$$

4. SIR Epidemiological Model

Tracks susceptible (S), infected (I), and recovered (R) individuals.

System:

$$\frac{dS}{dt} = -\beta SI \quad \frac{dI}{dt} = \beta SI - \gamma I \quad \frac{dR}{dt} = \gamma I$$

Initial Conditions: $S(0) = S_0, \quad I(0) = I_0, \quad R(0) = R_0$

5. Predator-Prey Model (Lotka-Volterra)

Describes how predator and prey populations affect each other.

System:

$$\frac{dx}{dt} = ax - bxy \quad \frac{dy}{dt} = cxy - dy$$

Initial Conditions: $x(0) = x_0, \quad y(0) = y_0$

6. Enzyme Kinetics (Michaelis-Menten)

Describes how a substrate is consumed in an enzymatic reaction.

IVP:

$$\frac{dS}{dt} = -\frac{V_{\max} S}{K_m + S}, \quad S(0) = S_0$$

7. Genetic Circuit with Negative Feedback

A gene produces a protein that inhibits its own production.

IVP:

$$\frac{dP}{dt} = \frac{\alpha}{1 + P^n} - \beta P, \quad P(0) = P_0$$

8. Fick's Law (Diffusion)

Describes how a substance diffuses out of a cell or membrane.

IVP:

$$\frac{dC}{dt} = -kC, \quad C(0) = C_0$$

Solution:

$$C(t) = C_0 e^{-kt}$$

9. Tumor Growth Model (Gompertz)

Describes a tumor that grows fast early and slows as it reaches a max size.

IVP:

$$\frac{dT}{dt} = rT \ln\left(\frac{K}{T}\right), \quad T(0) = T_0$$

Solution:

$$T(t) = K \exp\left[\ln\left(\frac{T_0}{K}\right) e^{-rt}\right]$$

10. Calcium Dynamics in Neurons

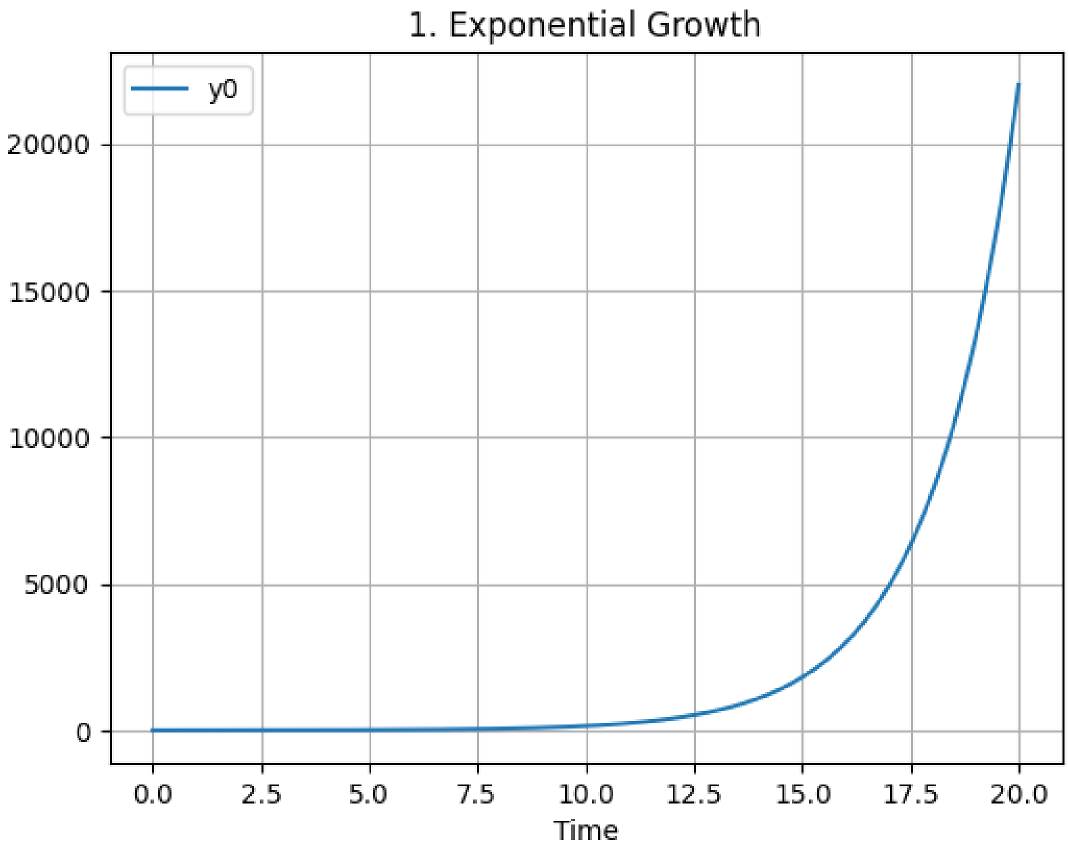
Describes how calcium concentration changes due to influx and removal.

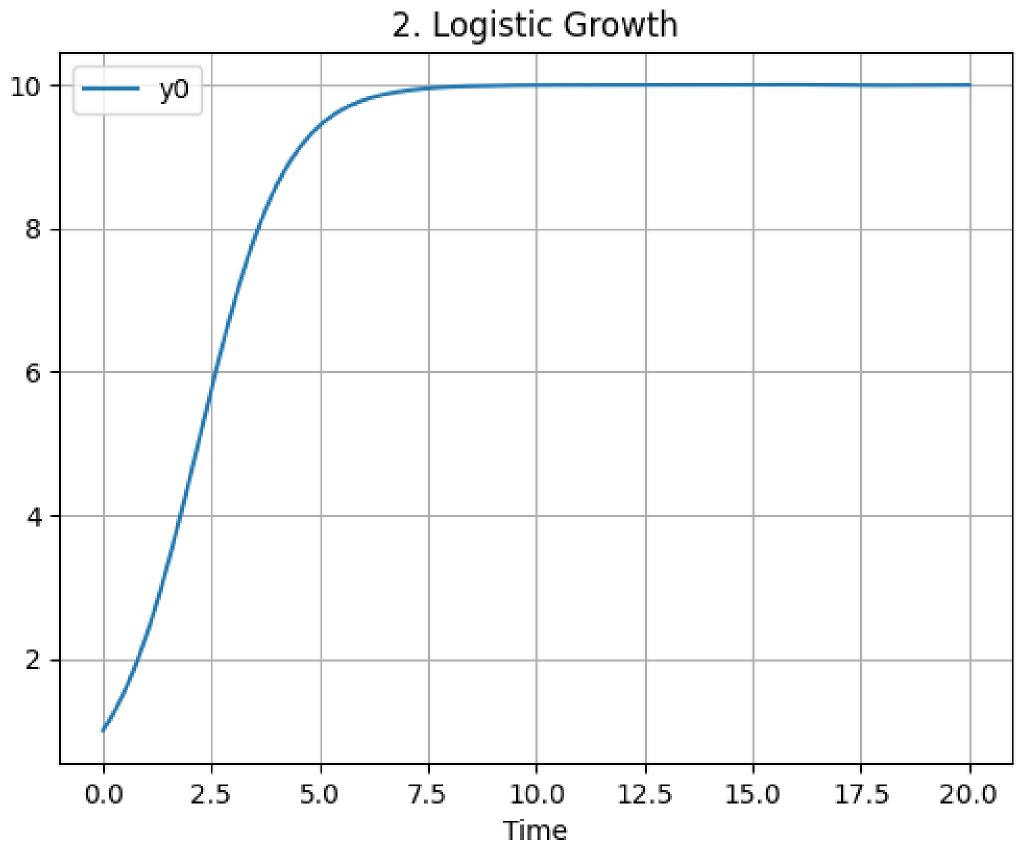
IVP (Same as Pharmacokinetics):

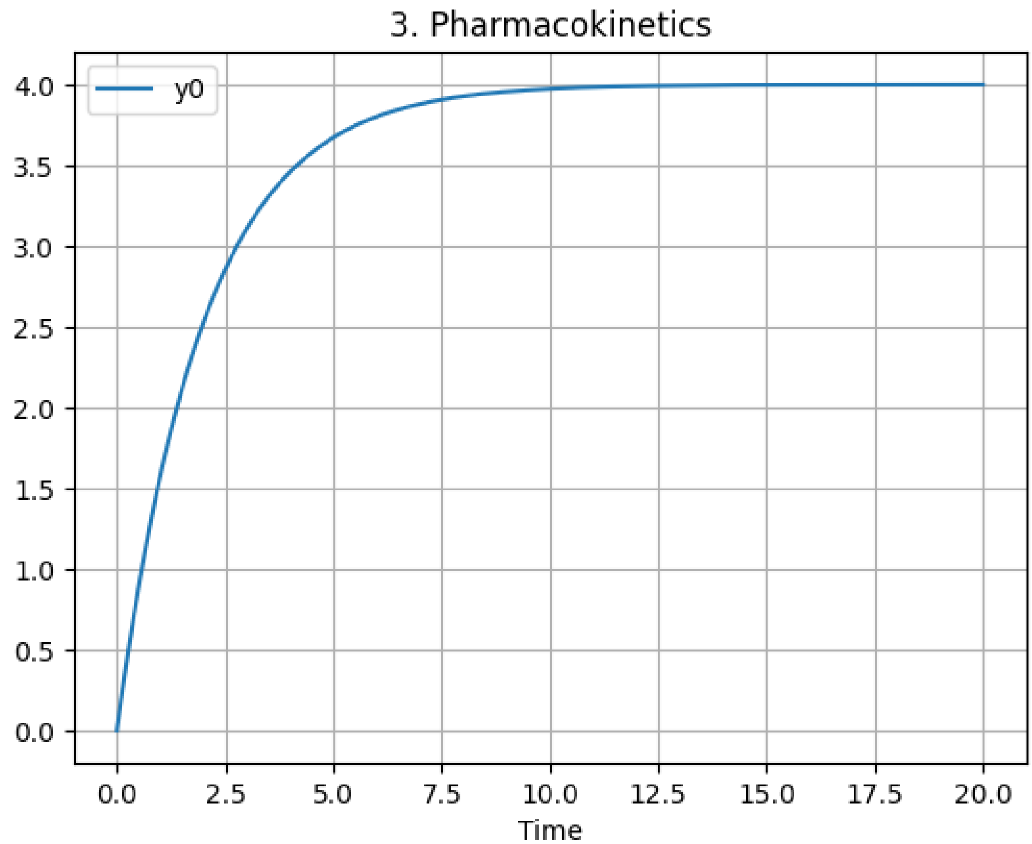
$$\frac{dC}{dt} = k_{\text{in}} - k_{\text{out}}C, \quad C(0) = C_0$$

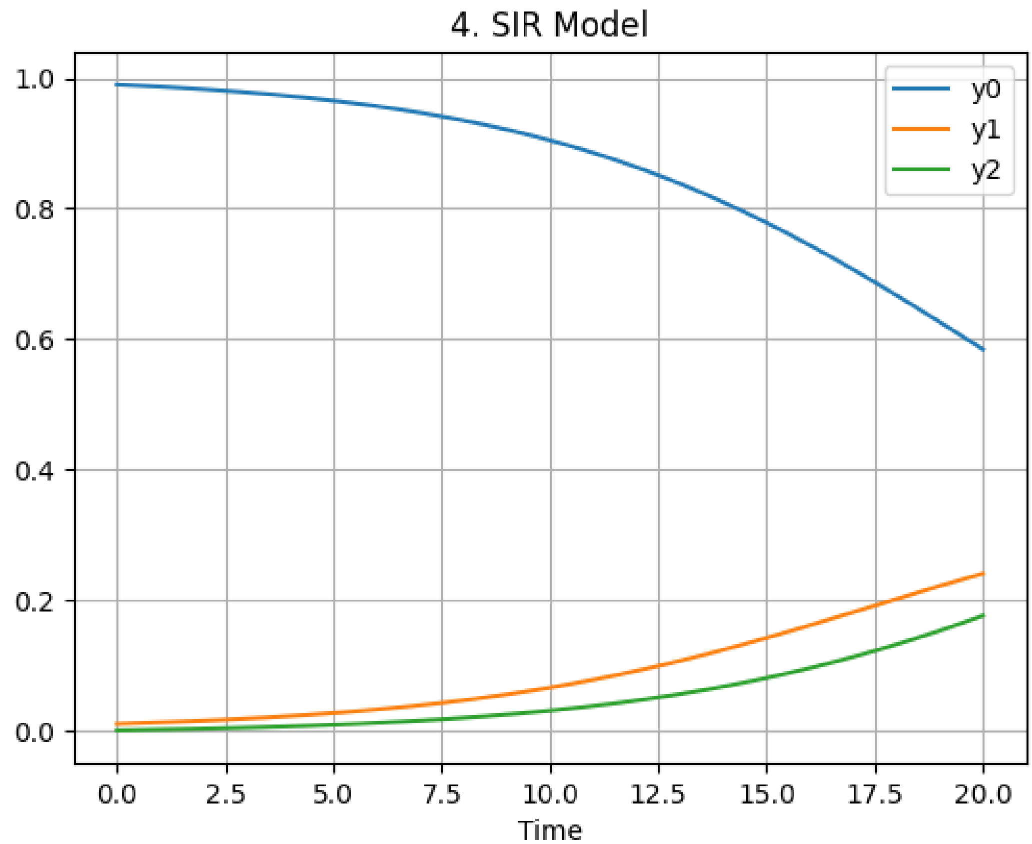
[2]:
```python
import numpy as np
import matplotlib.pyplot as plt
from scipy.integrate import solve_ivp

# Time range
t_span = (0, 20)
t_eval = np.linspace(*t_span, 300)

# 1. Exponential Growth
def exponential_growth(t, P, r):
    return r * P

# 2. Logistic Growth
def logistic_growth(t, P, r, K):
    return r * P * (1 - P / K)

# 3 & 10. Pharmacokinetics / Calcium Dynamics
def clearance_model(t, C, k_in, k_out):
    return k_in - k_out * C

# 4. SIR Model
def sir_model(t, y, beta, gamma):
    S, I, R = y
    dSdt = -beta * S * I
    dIdt = beta * S * I - gamma * I
    dRdt = gamma * I
    return [dSdt, dIdt, dRdt]

# 5. Predator-Prey
def predator_prey(t, y, a, b, c, d):
    x, y_pred = y
    dxdt = a * x - b * x * y_pred
    dydt = c * x * y_pred - d * y_pred
    return [dxdt, dydt]

# 6. Michaelis-Menten
def michaelis_menten(t, S, Vmax, Km):
    return -Vmax * S / (Km + S)

# 7. Genetic Circuit
```

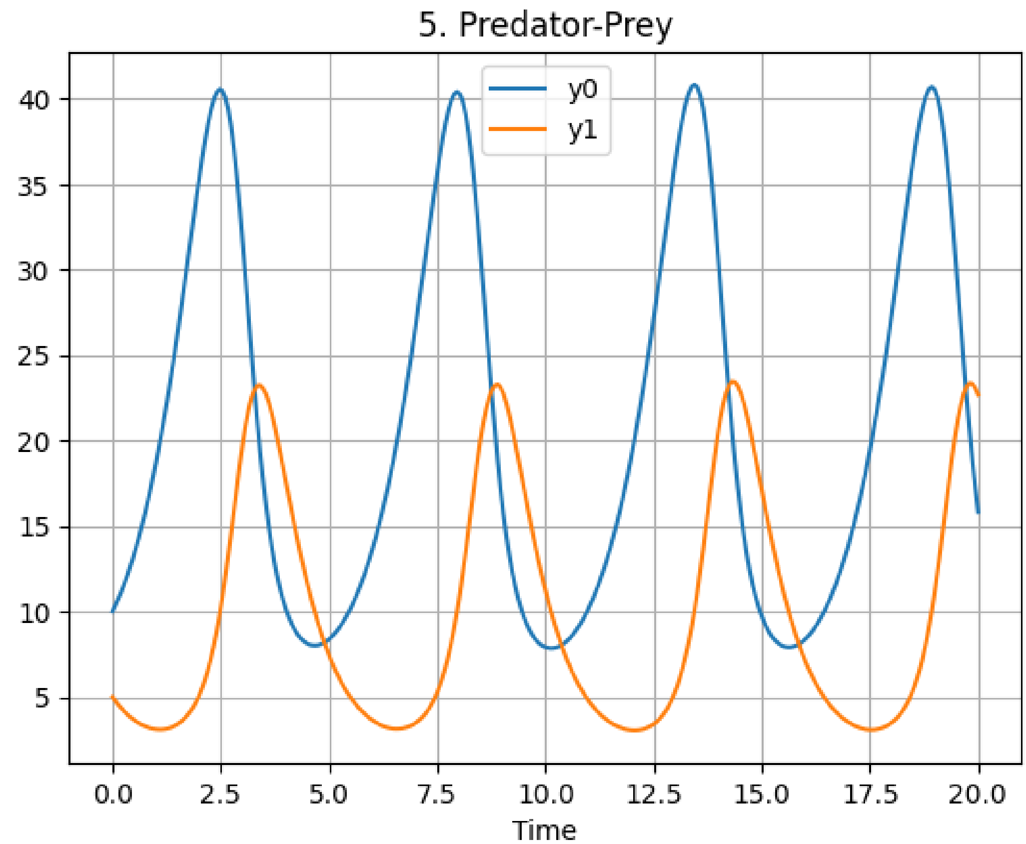
```python
def genetic_circuit(t, P, alpha, beta, n):
    return alpha / (1 + P**n) - beta * P

# 9. Gompertz Tumor Growth
def gompertz_growth(t, T, r, K):
    return r * T * np.log(K / T)

# Solver and plotter function
def solve_and_plot(model, y0, params, title):
    sol = solve_ivp(lambda t, y: model(t, y, *params), t_span, y0,␣
 ↪t_eval=t_eval)
    plt.plot(sol.t, sol.y.T)
    plt.title(title)
    plt.xlabel("Time")
    plt.legend([f"y{i}" for i in range(len(y0))])
    plt.grid(True)
    plt.show()

# Run and plot each model
solve_and_plot(exponential_growth, [1], [0.5], "1. Exponential Growth")
solve_and_plot(logistic_growth, [1], [1.0, 10], "2. Logistic Growth")
solve_and_plot(clearance_model, [0], [2.0, 0.5], "3. Pharmacokinetics")
solve_and_plot(lambda t, y: sir_model(t, y, 0.3, 0.1), [0.99, 0.01, 0], [], "4.␣
 ↪SIR Model")
solve_and_plot(lambda t, y: predator_prey(t, y, 1.0, 0.1, 0.075, 1.5), [10, 5],␣
 ↪[], "5. Predator-Prey")
solve_and_plot(michaelis_menten, [10], [2.0, 5.0], "6. Michaelis-Menten")
solve_and_plot(genetic_circuit, [1], [5.0, 1.0, 2], "7. Genetic Circuit")
solve_and_plot(clearance_model, [10], [0.0, 0.3], "8. Fick's Law")
solve_and_plot(gompertz_growth, [0.5], [1.0, 10.0], "9. Gompertz Tumor Growth")
solve_and_plot(clearance_model, [5], [1.5, 0.4], "10. Calcium Dynamics")
```

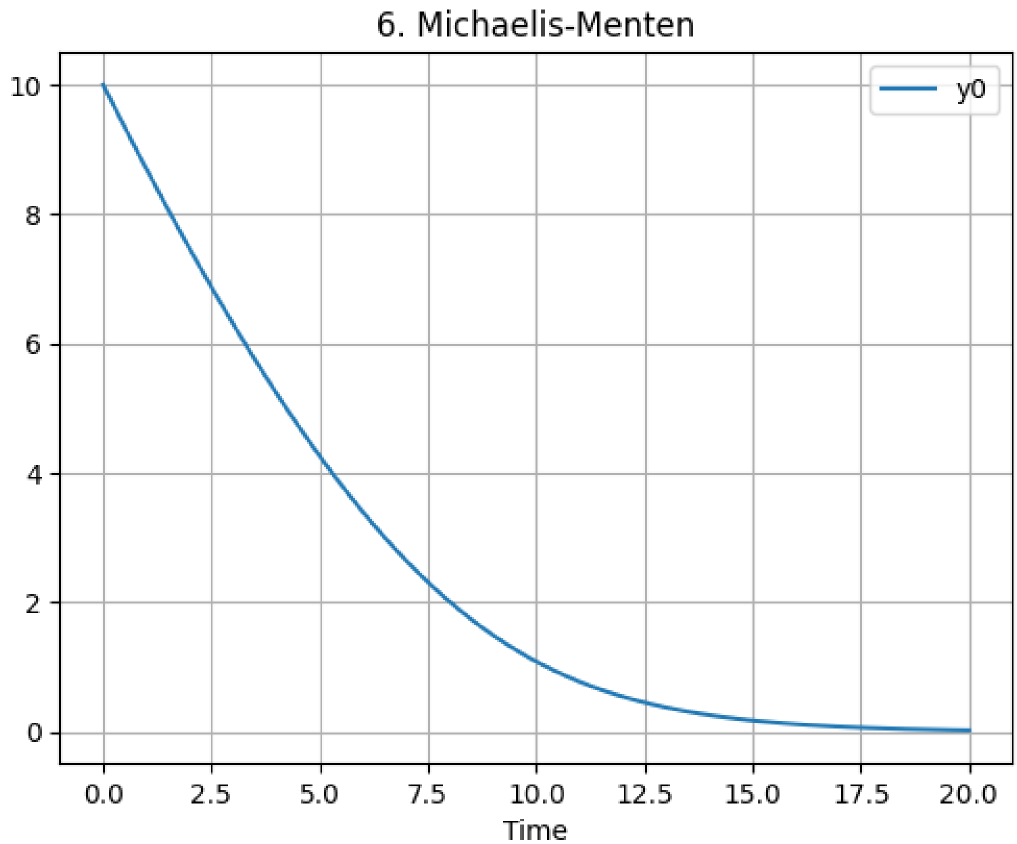

1. Exponential Growth
y0
20000
15000
10000
5000
0
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
Time

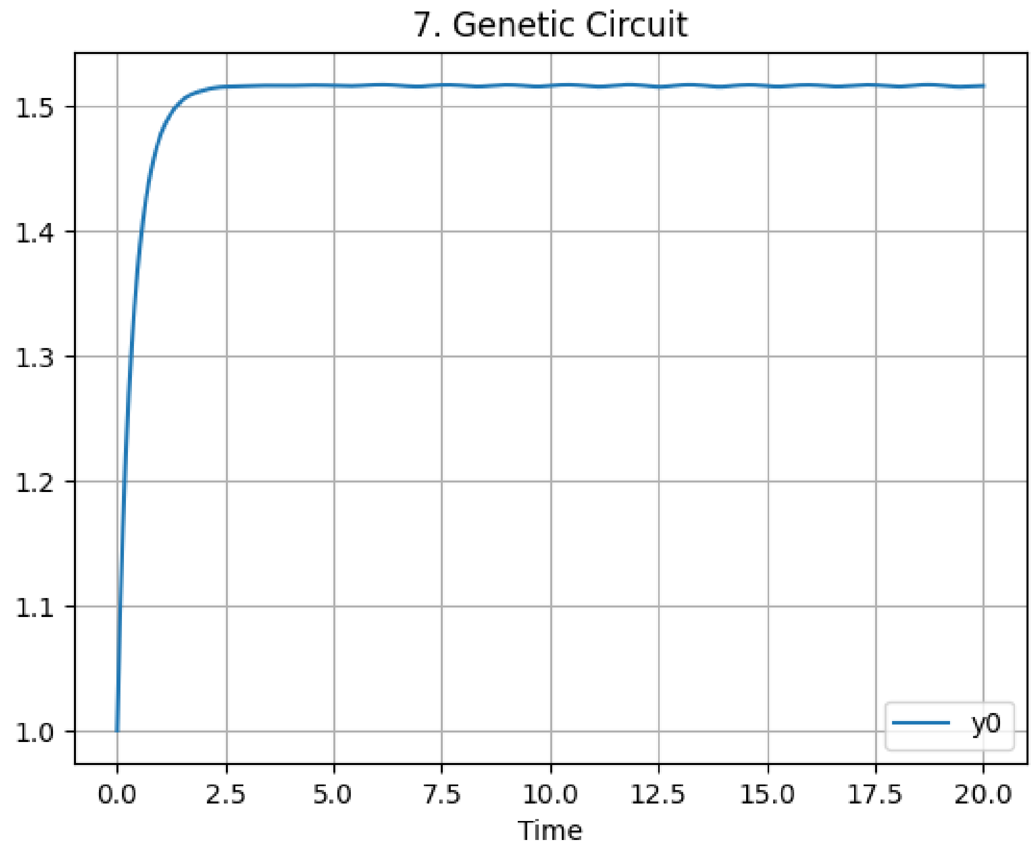

2. Logistic Growth
y0
10
8
6
4
2
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
Time

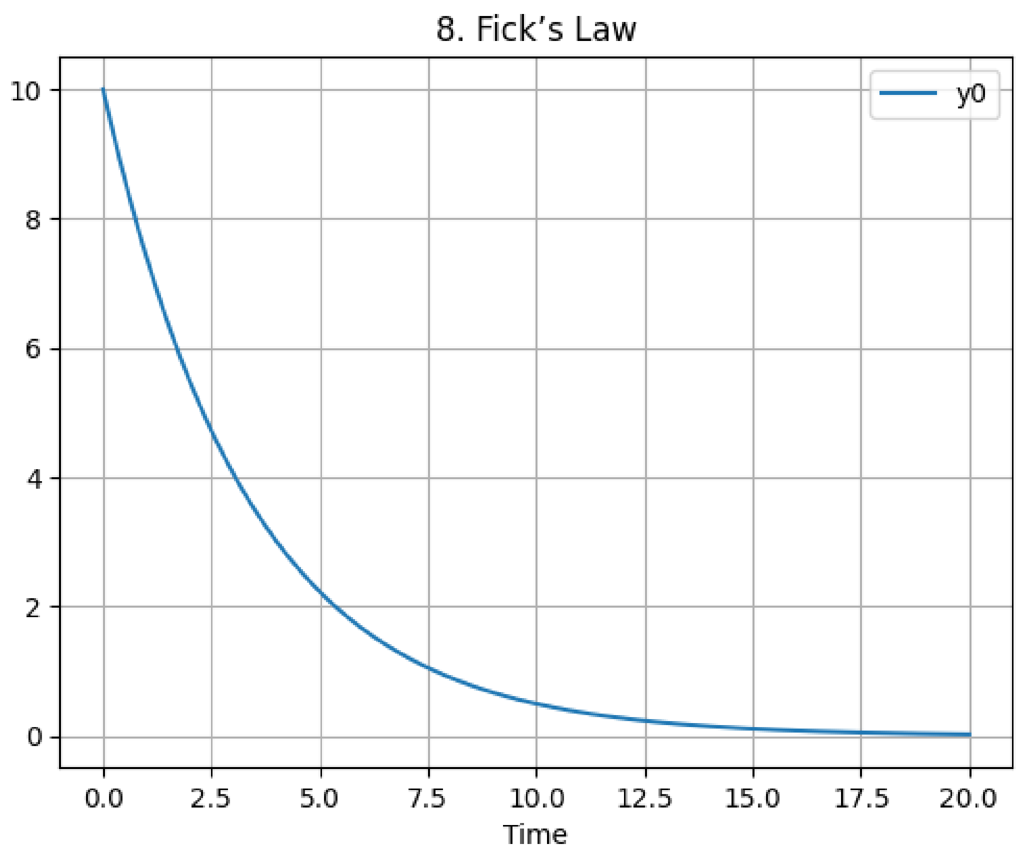

3. Pharmacokinetics
y0
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
Time

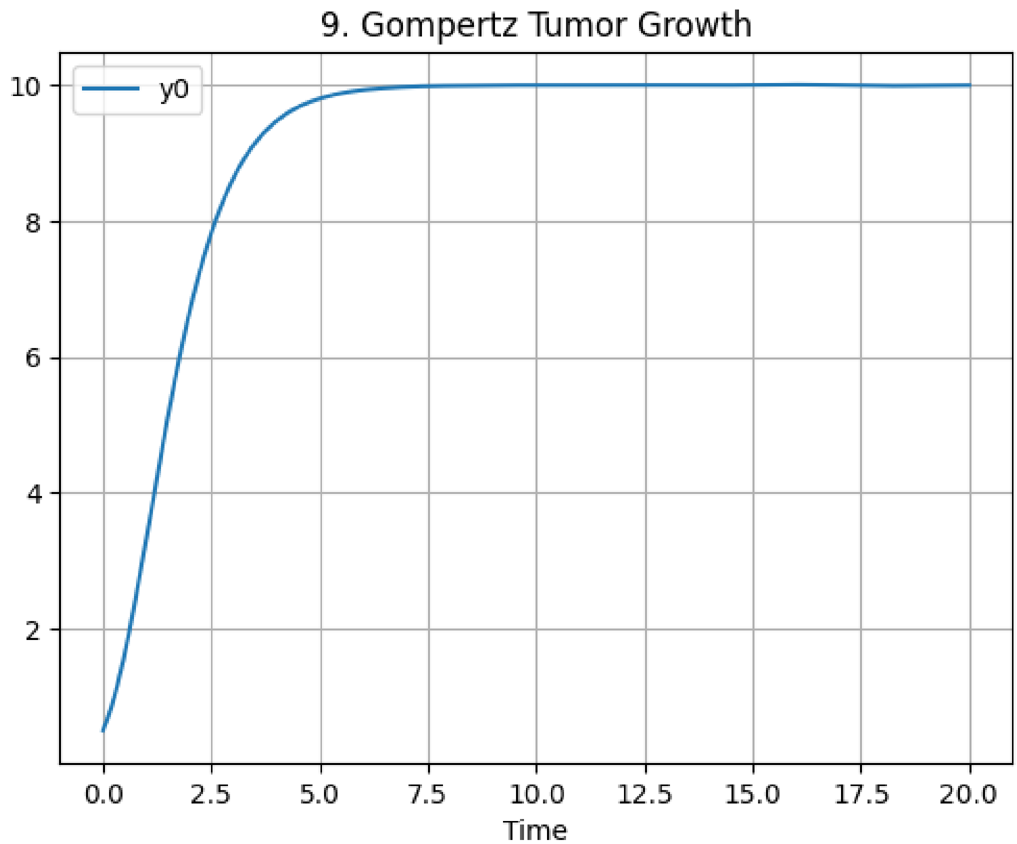

4. SIR Model
1.0
0.8
0.6
0.4
0.2
0.0
y0
y1
y2
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
Time

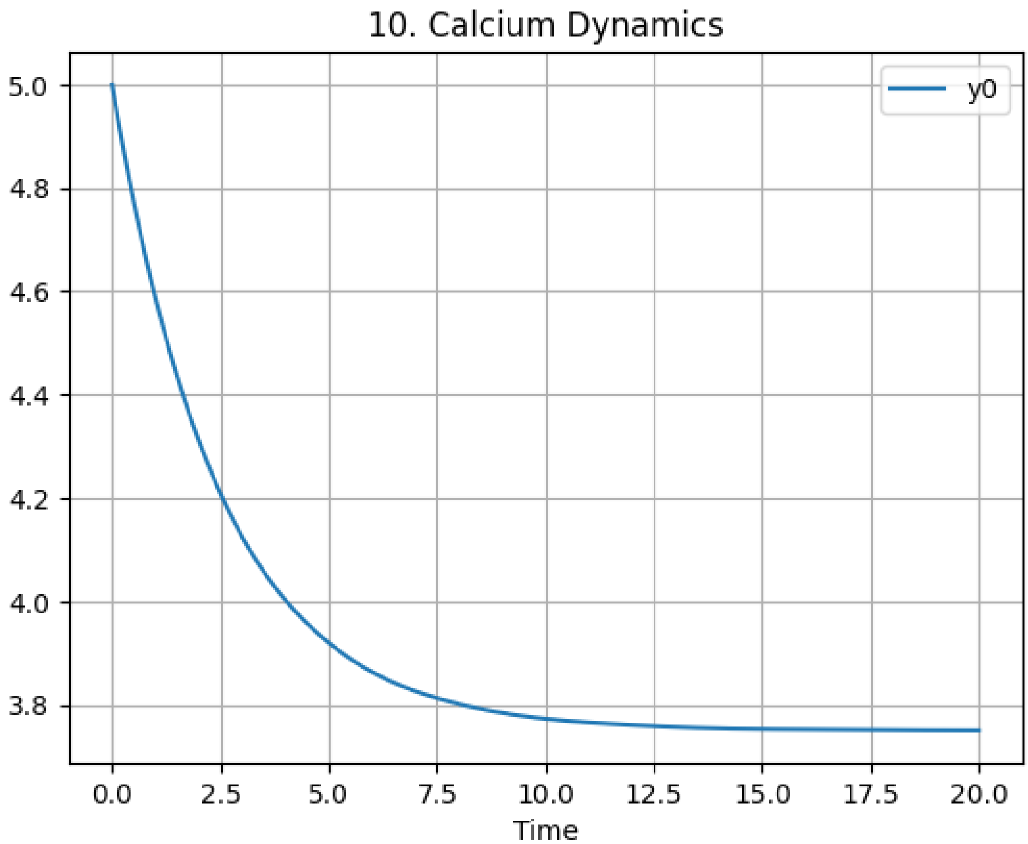

5. Predator-Prey
y0
y1
40
35
30
25
20
15
10
5
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
Time


6. Michaelis-Menten
y0
10
8
6
4
2
0
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
Time


7. Genetic Circuit
1.5
1.4
1.3
1.2
1.1
1.0
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
Time
y0


8. Fick’s Law
y0
10
8
6
4
2
0
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
Time


9. Gompertz Tumor Growth
y0
10
8
6
4
2
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
Time


10. Calcium Dynamics
y0
5.0
4.8
4.6
4.4
4.2
4.0
3.8
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0
Time