

Computational methods

Assignment 4

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```
# Imports
import numpy as np
import matplotlib.pyplot as plt
import sys

sys.path.append(
    "c:\\Programming\\Projects\\BioInf-Master\\Computational_methods\\Lab_5\\
    Assignment_4"
)
import gillespy
from scipy.integrate import solve_ivp
```

Stochastic model

Use/encode this stochastic model.

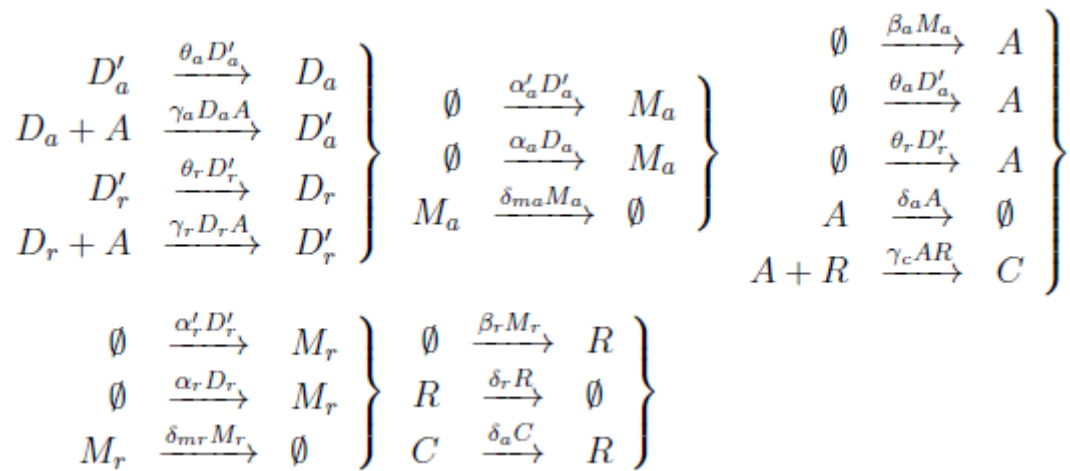


Figure 1: Stochastic model

a)

Reproduce Figure 2, c & d, from the article.

Constants and initial values

```

# Constants
alpha = [
    50, # a_A
    0.01, # a_R
    500, # a_prim_A
    50, # a_prim_R
]
beta = [
    50, # b_A
    5, # b_R
]
gamma = [
    1, # g_A
    1, # g_R
    2, # g_C
]
delta = [
    1, # d_A
    0.2, # d_R
    10, # d_MA
    0.5, # d_MR
]
theta = [
    50, # t_A
    100, # t_R
]
coeff = {"alpha": alpha, "beta": beta, "gamma": gamma, "delta": delta,
"theta": theta}

# Initial values
y_0 = [
    1, # D_A
    0, # Dprim_A
    1, # D_R
    0, # Dprim_R
    0, # M_A
    0, # M_R
    0, # A
    0, # R
    0, # C
]

```

Propensity function

```

def prop(Y, coeff):
    # Unpacking Y
    D_A = Y[0] # dD_A/dt
    Dprim_A = Y[1] # dDprim_A/dt

```

```

D_R = Y[2] # dD_R/dt
Dprim_R = Y[3] # dDprim_R/dt
M_A = Y[4] # dM_A/dt
M_R = Y[5] # dM_R/dt
A = Y[6] # dA/dt
R = Y[7] # dR/dt
C = Y[8] # dC/dt

# Unpacking constants
a_A, a_R, a_prim_A, a_prim_R = coeff["alpha"]
b_A, b_R = coeff["beta"]
g_A, g_R, g_C = coeff["gamma"]
d_A, d_R, d_MA, d_MR = coeff["delta"]
t_A, t_R = coeff["theta"]

# Propensity vector
prop = [
    t_A * Dprim_A,
    g_A * D_A * A,
    t_R * Dprim_R,
    g_R * D_R * A,
    #
    a_prim_A * Dprim_A,
    a_A * D_A,
    d_MA * M_A,
    #
    b_A * M_A,
    t_A * Dprim_A,
    t_R * Dprim_R,
    d_A * A,
    g_C * A * R,
    #
    a_prim_R * Dprim_R,
    a_R * D_R,
    d_MR * M_R,
    #
    b_R * M_R,
    d_R * R,
    d_A * C,
]

return prop

```

Stoichiometry matrix

```

stoch = np.array(
    [
        # D_A, Dprim_A, D_R, Dprim_R, M_A, M_R, A, R, C

```

```

        [ 1, -1, 0, 0, 0, 0, 0, 0], # t_A * Dprim_A
        [-1, 1, 0, 0, 0, 0, -1, 0], # g_A * D_A * A
        [ 0, 0, 1, -1, 0, 0, 0, 0], # t_R * Dprim_R
        [ 0, 0, -1, 1, 0, 0, -1, 0], # g_R * D_R * A
        #
        [ 0, 0, 0, 0, 1, 0, 0, 0], # a_prim_A *
Dprim_A
        [ 0, 0, 0, 0, 1, 0, 0, 0], # a_A * D_A
        [ 0, 0, 0, 0, -1, 0, 0, 0], # d_MA * M_A
        #
        [ 0, 0, 0, 0, 0, 0, 1, 0], # b_A * M_A
        [ 0, 0, 0, 0, 0, 0, 1, 0], # t_A * Dprim_A
        [ 0, 0, 0, 0, 0, 0, 1, 0], # t_R * Dprim_R
        [ 0, 0, 0, 0, 0, 0, -1, 0], # d_A * A
        [ 0, 0, 0, 0, 0, 0, -1, 1], # g_C * A * R
        #
        [ 0, 0, 0, 0, 0, 1, 0, 0], # a_prim_R *
Dprim_R
        [ 0, 0, 0, 0, 0, 1, 0, 0], # a_R * D_R
        [ 0, 0, 0, 0, 0, -1, 0, 0], # d_MR * M_R
        #
        [ 0, 0, 0, 0, 0, 0, 1, 0], # b_R * M_R
        [ 0, 0, 0, 0, 0, 0, -1, 0], # d_R * R
        [ 0, 0, 0, 0, 0, 0, 1, -1], # d_A * C
    ]
)

```

Time span

```

# Time span
t_0 = 0
t_stop = 400
times = np.arange(t_0, t_stop, 0.1)

```

Run SSA

```

t, Y = gillespy.SSA(
    prop = prop,
    stoch = stoch,
    X0 = y_0,
    tspan = (t_0, t_stop),
    coeff = coeff
)

```

Run the ODE for comparison

```

def ode_rhs(t, y, coeff):
    # Unpacking y
    D_A = y[0] # dD_A/dt
    Dprim_A = y[1] # dDprim_A/dt
    D_R = y[2] # dD_R/dt
    Dprim_R = y[3] # dDprim_R/dt
    M_A = y[4] # dM_A/dt
    M_R = y[5] # dM_R/dt
    A = y[6] # dA/dt
    R = y[7] # dR/dt
    C = y[8] # dC/dt

    # Unpacking constants
    a_A, a_R, a_prim_A, a_prim_R = coeff["alpha"]
    b_A, b_R = coeff["beta"]
    g_A, g_R, g_C = coeff["gamma"]
    d_A, d_R, d_MA, d_MR = coeff["delta"]
    t_A, t_R = coeff["theta"]

    # Equation system
    yt = [
        t_A * Dprim_A - g_A * D_A * A, # dD_A/dt
        g_A * D_A * A - t_A * Dprim_A, # dDprim_A/dt
        t_R * Dprim_R - g_R * D_R * A, # dD_R/dt
        g_R * D_R * A - t_R * Dprim_R, # dDprim_R/dt
        a_prim_A * Dprim_A + a_A * D_A - d_MA * M_A, # dM_A/dt
        a_prim_R * Dprim_R + a_R * D_R - d_MR * M_R, # dM_R/dt
        b_A * M_A
        + t_A * Dprim_A
        + t_R * Dprim_R
        - A * (g_A * D_A + g_R * D_R + g_C * R + d_A), # dA/dt
        b_R * M_R - g_C * A * R + d_A * C - d_R * R, # dR/dt
        g_C * A * R - d_A * C, # dC/dt
    ]

    return yt

```

```

sol = solve_ivp(ode_rhs, (t_0, t_stop), y_0, args=(coeff, ), t_eval=times,
method="BDF")

```

Results

The results from the SSA is largely the same as the ODE. The SSA is a less smooth due to the introduced randomness.

```

plt.figure(1)
plt.subplot(4, 1, 1)

```

```

plt.plot(sol.t, sol.y[5], color="blue")
plt.ylabel("A (ODE)")

plt.subplot(4, 1, 2)
plt.plot(sol.t, sol.y[7], color="orange")
plt.ylabel("R (ODE)")

plt.subplot(4, 1, 3)
plt.plot(t, Y[:, 6], color="green")
plt.ylabel("A (SSA)")

plt.subplot(4, 1, 4)
plt.plot(t, Y[:, 7], color="purple")
plt.ylabel("R (SSA)")
plt.xlabel("time [hr]")
plt.show()

```

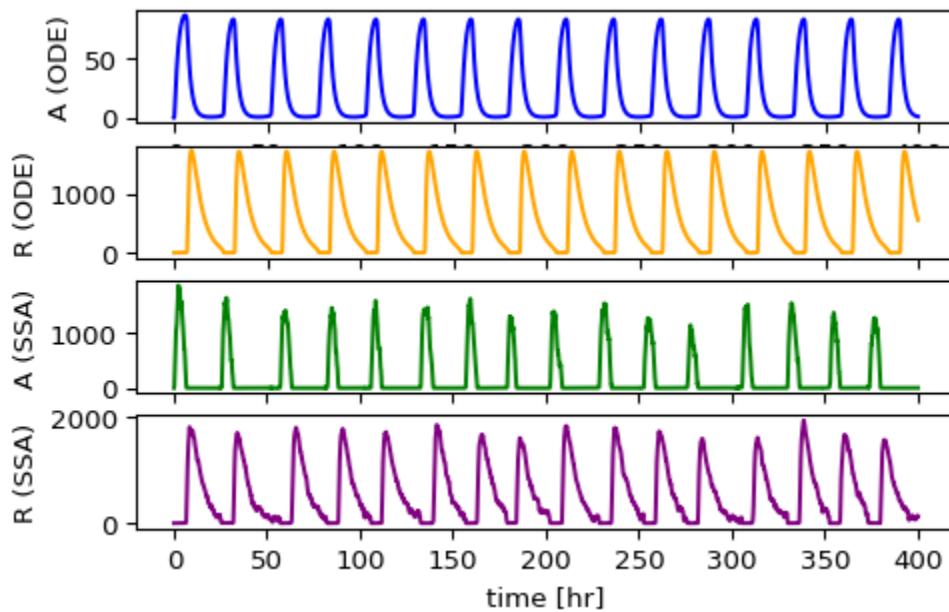


Figure 2: Recreation of Figure 2 from the article.

b)

We change the parameter $\delta_R = 0.2h^{-1}$ to $\delta_R = 0.05h^{-1}$ and compare the ODE to the SSA for R.

```

coeff["delta"][1] = 0.05 # d_R

```

```

sol = solve_ivp(
    ode_rhs,

```

```

    (t_0, t_stop),
    y_0,
    args=(coeff,),
    t_eval=times,
    method="BDF",
)

t, Y = gillespy.SSA(prop=prop, stoch=stoch, X0=y_0, tspan=(t_0, t_stop),
coeff=coeff)

```

Results

In the deterministic model, R sinks to near zero and never recovers while the SSA model retains the cyclic spikes. Showing that stochastic models are more robust when modeling biological processes.

```

plt.figure(2)
plt.subplot(2, 1, 1)
plt.plot(sol.t, sol.y[7], color="orange")
plt.ylabel("R (ODE)")

plt.subplot(2, 1, 2)
plt.plot(t, Y[:, 7], color="purple")
plt.ylabel("R (SSA)")
plt.xlabel("time [hr]")
plt.show()

```

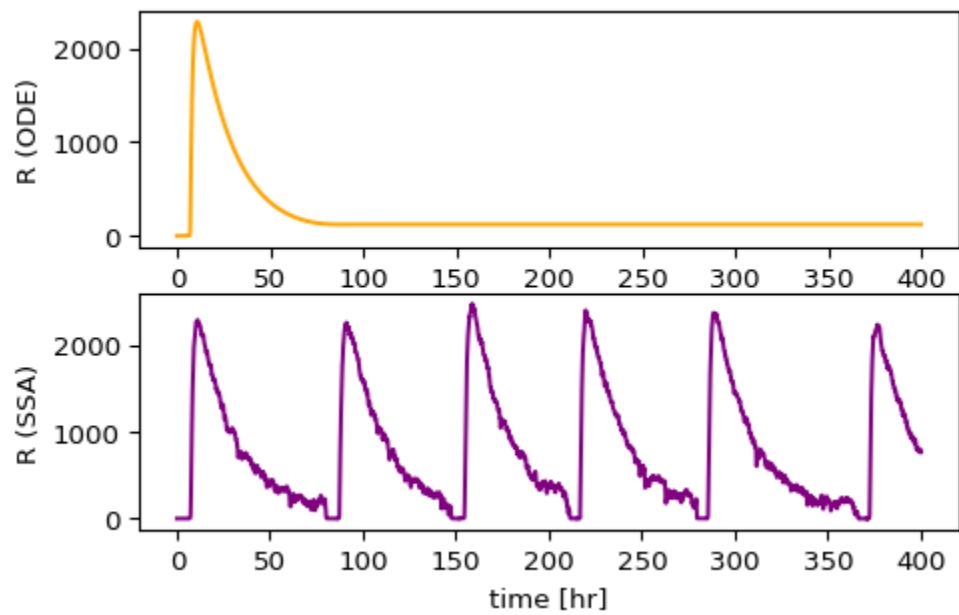


Figure 3: Comparison of ODE vs SSA showing that stochastic models sometimes handle biological processes better.