Discrete-time Stochastic Simulation of Chemical Reaction Networks



based on Furusawa & Kaneko's model in PRL 90.088102

Tuan Pham

Niels Bohr Institute Biocomplexity Department





Algorithm

* 0) Creating a vector of k components, denoted by x and assign to each of its component a random integer $\in [1,N]$. Let's keep the total number of molecules less than equal 2N before anything happens, i.e. $\sum x_i$ (initial time) = $\alpha N, \alpha \in (0,2)$, note that this is not important as a constraint as long as the initial condition, if set close to 2N, i.e α close to 2, will reach step 4 FASTER.

- * 1) Generating the chemical reaction network G with k species (nodes) and a probability ρ for i and j being connected and producing *l* as specified by $i + j \rightarrow l + j$, note ρ is independent from the pair *i* and *j*
- * 2) At every trial, choose a pair of species *i* and *j* at random with probability proportional to the product of their current abundances and if $i + j \rightarrow l + j$, $x_i \rightarrow x_i - 1$ and $x_l \rightarrow x_l + 1$
- * 3) After every *D* of such trials, let a *fixed* nutrient come in with probability 1 and go out with probability proportional to its concentration inside the cell. For simplicity, incoming makes $x_{nutrient} \rightarrow x_{nutrient} + 1$, whereas outgoing makes $x_{\text{nutrient}} \rightarrow x_{\text{nutrient}} - 1$,

* 4) Cell division happens if $\sum_{i=1}^{k} x_i = 2N$, use $x = (1 - p)x^{(1)} + px^{(2)}$, where p = rand(), keep one among the two $x^{(1)}$ and $x^{(2)}$

- Once step 4 is completed, go back to 2 and keep repeating this cycle 2-3-4-2 (for the same *G* that is generated at step 1) for a total number of cell_div



random integer to specify the reaction $i + j \rightarrow l + j$.

* Note ρ is independent of the pair *i* and *j*



* 1) Generating the chemical reaction network G with k species (nodes) and a probability ρ for *i* and *j* being connected and producing *l* that is chosen as a







import random from tqdm.auto import tqdm

while *True*:

Repeat each node index by its edge degree to get the list of edges edges = np.repeat(nodes, edge_degrees)

return G

```
* 1) Generating the chemical reaction network G with k species (nodes) and a
                     probability \rho for i and j being connected and producing l as specified by
                    i + j \rightarrow l + j. A_{ij} = 0, 1 D {ii} = product . random integer. G {ii}=A {ii}D {ii} find the set of the set
```

```
import matplotlib.pyplot as plt
```

```
def random_reaction_network(rho, k):
    """Generates a random reaction network with k nodes and density rho."""
    # Create an array of nodes indices
    nodes = np_arange(k)
```

```
# Keep generating edge degrees until the sum is even
    edge_degrees = np.random.poisson(rho * k, size=k)
    if sum(edge_degrees) % 2 == 0:
        break
```

```
# Shuffle the edges and reshape into a 2D array
np random shuffle(edges)
Is, Js = edges.reshape((2, -1))
```

Assign a random reaction product to each edge and store in a dictionary G = {(i, j): np.random.randint(k) for i, j in zip(Is, Js)}



- Diffusion
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- * 3) After every *D* of such trials, let a *fixed* nutrient come in with probability 1 and go out with probability proportional to its concentration inside the cell. For simplicity, incoming makes $x_{nutrient} \rightarrow x_{nutrient} + 1$, whereas outgoing makes $x_{\text{nutrient}} \rightarrow x_{\text{nutrient}} - 1$,
- * Cell division, 4) Cell division happens if $\sum x_i = 2N$, use $x = (1 p)x^{(1)} + px^{(2)}$, where
- p = rand(), keep one among the two $x^{(1)}$ and $x^{(2)}$





* Diffusion

Cell division

```
time = 0
r = np_array(list(G_keys()))
P = x[r[:,0]] * x[r[:,1]]
P = P / P_sum()
for division in tqdm(range(celldivision)):
    # If the total number of molecules exceeds 2N, divi
    print('Division count: ', division)
    while np_sum(x) < 2 * N:
        # Choose two random nodes
        index = np.random.choice(len(r), p=P)
        i, j = tuple(r[index])
        # If they are connected by a reaction and both
        if ((i, j) in G) and (x[i] > 0) and (x[j] > 0):
            time += 1
            l = G[(i, j)]
            x[i] -= 1
            x[l] += 1
            # Every D iterations, add a nutrient molecu
            if time % D == 0:
               x[0] += 1
               leaking_out = x[0] / np_sum(x)
               if np.random.random() < leaking_out:</pre>
                  x[0] -= 1
            P = x[r[:,0]] * x[r[:,1]]
            P = P / P_sum()
    x = x // np_random_randint(2, 10)
```



