Testing for Network and Spatial Autocorrelation

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Abstract. Testing for dependence has been a well-established component of spatial statistical analyses for decades. In particular, several popular test statistics have desirable properties for testing for the presence of spatial autocorrelation in continuous variables. In this paper we propose two contributions to the literature on tests for autocorrelation. First, we propose a new test for autocorrelation in categorical variables. While some methods currently exist for assessing spatial autocorrelation in categorical variables, the most popular method is unwieldy, somewhat ad hoc, and fails to provide grounds for a single omnibus test. Second, we discuss the importance of testing for autocorrelation in data sampled from the nodes of a network, motivated by social network applications. We demonstrate that our proposed statistic for categorical variables can both be used in the spatial and network setting.

Keywords: Social networks, Statistical dependence, Spatial autocorrelation, Peer effects

1 Introduction

In studies using spatial data, researchers routinely test for spatial dependence before proceeding with statistical analysis [17, 20, 8]. Spatial dependence is usually assumed to have an autocorrelation structure, whereby pairwise correlations between data points are a function of the geographic distance between the two observations [5, 26]. Because autocorrelation is a violation of the assumption of independent and identically distributed (i.i.d.) observations or residuals required by most standard statistical models and hypothesis tests [17, 1, 18], testing for spatial autocorrelation is a necessary step for valid statistical inference using spatial data.

Taking temporal dependence into account is also widely practiced in time series settings. But other kinds of statistical dependence are routinely ignored. In many public health and social science studies, observations are collected from individuals who are members of one or a small number of social networks within the target population, often for reasons of convenience or expense. For example, individuals may be sampled from one or a small number of schools, institutions, or online communities, where they may be connected by ties such as being related to one another; being friends, neighbors, acquaintances, or coworkers; or sharing...
the same teacher or medical provider. If individuals in a sample are related
to one another in these ways, they may not furnish independent observations,
and yet most statistical analyses in the literature use i.i.d. data methods [16].
This failure to account for dependence can result in anticonservative inference:
inflated false positive rates and artificially small p-values.

In the literature on spatial and temporal dependence, dependence is often
implicitly assumed to be the result of latent traits that are more similar for
observations that are close than for distant observations. This latent variable
dependence [24] is likely to be present in many network contexts as well. In net-
works, ties often present opportunities to transmit traits or information from
one node to another, and such direct transmission will result in dependence due
to direct transmission [24] that is informed by the underlying network structure.

In general, both of these sources of dependence result in positive pairwise corre-
lations that tend to be larger for pairs of observations from nodes that are close
in the network and smaller for observations from nodes that are distant in the
network. Network distance is usually measured by geodesic distance, which is a
count of the number of edges along the shortest path between two nodes. This
is analogous to spatial and temporal dependence, which are generally thought
to be inversely related to (Euclidean) distance.

Despite increasing interest in and availability of social network data, there
is a dearth of valid statistical methods to account for network dependence. Al-
though many statistical methods exist for dealing with dependent data, almost
all of these methods are intended for spatial or temporal data, or more broadly, for
observations with positions in \( \mathbb{R}^k \) and dependence that is related to Euclidean
distance between pairs of points. The topology of a network is very different
from that of Euclidean space, and many of the methods that have been de-
veloped to accommodate Euclidean dependence are not appropriate for network
dependence. The most important difference is the distribution of pairwise dis-
tances which, in Euclidean settings, is usually assumed to skew towards larger
distances as the sample grows, with the maximum distance tending to infinity
with sample size \( n \). In social networks, on the other hand, pairwise distances
tend to be concentrated on shorter distances and may be bounded from above.
However, as we elaborate in Section 2, methods that have been used to test for
spatial dependence can be adapted and applied to network data.

The most popular tests for spatial autocorrelation use Moran’s I statistic [23]
and Geary’s C statistic [13] for continuous random variables. In a companion
paper, we show that Moran’s I provides valid tests of network dependence whenever
the dependence is inversely related to a measure of network distance [16].
For categorical random variables, however, available tests based on join count
analysis [6] are unwieldy and fail to provide a single omnibus test of dependence.
Categorical random variables are especially important in social network settings,
where group affiliations are often of interest [15, 19, 35]. Join count analysis has
been recently used for testing autocorrelation in categorical outcomes sampled
from social network nodes (e.g. [21]). Farber et al. [9] proposed a more elegant
test for categorical network data and explored its performance in data generated
from linear spatial autoregression (SAR) models \cite{14, 20}, which are parametric models for network data \cite{9, 12}. As far as we are aware, all of the previous work on testing for network dependence in categorical variables assumes that the data were generated from SAR models, and none of this previous work has considered the performance of autocorrelation tests for more general network settings. Although SAR models are often used to model network dependent data, there is very little evidence that most social network data truly conform to these models. In particular, these models cannot capture general forms of latent variable dependence or of dependence due to direct transmission.

In this paper we propose a new test statistic that generalizes Moran’s $I$ for categorical random variables. We demonstrate that both Moran’s $I$ and our new test for categorical data can be used to test for dependence among observations sampled from a single social network (or a small number of networks). We assume that any dependence is monotonically inversely related to the pairwise distance between nodes, but otherwise we make no assumptions about the structure of the dependence, and we do not require any parametric assumptions. These tests allow researchers to assess the validity of i.i.d statistical methods, and are therefore the first step towards correcting the practice of defaulting to i.i.d. methods even when data may exhibit network dependence.

2 Methods

2.1 Moran’s $I$

Moran’s $I$ takes as input an $n$-vector of continuous random variables and an $n \times n$ weighted distance matrix $W$, where entry $w_{ij}$ is a non-negative, non-increasing function of the Euclidean distance between observations $i$ and $j$. Moran’s $I$ is expected to be large when pairs of observations with greater $w$ values (i.e. closer in space) have larger correlations than observations with smaller $w$ values (i.e. farther in space). The choice of non-increasing function used to construct $W$ is informed by background knowledge about how dependence decays with distance; it affects the power but not the validity of tests of independence based on Moran’s $I$.

Let $Y$ be a continuous variable of interest and $y_i$ be its realized observation for each of $n$ units ($i = 1, 2, \ldots, n$). Each observation is associated with a location, traditionally in space but we will extend this to networks. Let $W$ be a weight matrix signifying closeness between the units, e.g. a matrix of pairwise Euclidean distances for spatial data or an adjacency matrix for network data. (The entries $A_{ij}$ in the adjacency matrix $A$ for a network are indicators of whether nodes $i$ and $j$ share a tie.) Then Moran’s $I$ is defined as follows:

$$I = \frac{\sum_{i=1}^{n} \sum_{j=1}^{n} w_{ij} (y_i - \bar{y})(y_j - \bar{y})}{S_0 \sum_{i=1}^{n} (y_i - \bar{y})^2 / n}, \quad (1)$$
where \( S_0 = \sum_{i=1}^{n} (w_{ij} + w_{ji})/2 \) and \( \bar{y} = \sum_{i=1}^{n} y_i/n \). Under independence, the pairwise products \((y_i - \bar{y})(y_j - \bar{y})\) are each expected to be close to zero. On the other hand, under network dependence adjacent pairs are more likely to have similar values than non-adjacent pairs, and \((y_i - \bar{y})(y_j - \bar{y})\) will tend to be relatively large for the upweighted adjacent pairs; therefore, Moran’s \( I \) is expected to be larger in the presence of network dependence than under the null hypothesis of independence.

### 2.2 New methods for categorical random variables

For a \( K \)-level categorical random variable, join count statistics compare the number of adjacent pairs falling into the same category to the expected number of such pairs under independence, essentially performing \( K \) separate hypothesis tests. As the number of categories increases, join count analyses become quite cumbersome. Furthermore, they only consider adjacent observations, thereby throwing away potentially informative pairs of observations that are non-adjacent but may still exhibit dependence. Finally, the \( K \) separate hypothesis tests required for a join count analysis are non-independent and it is not entirely clear how to correct for multiple testing. To overcome this last limitation, Farber et al. [10] proposed a single test statistic that combines the \( K \) separate joint count statistics.

Instead of extending join count analysis, we propose a new statistic for categorical observations using the logic of Moran’s \( I \). This has two advantages over the proposal of [10]: it incorporates information from discordant, in addition to concordant, pairs, and it weights pairs according to their probability under the null, allowing more “surprising” pairs to contribute more information to the test. To illustrate, under network dependence adjacent nodes are more likely to have concordant outcomes – and less likely to have discordant outcomes – than they would be under independence. We operationalize independence as random distribution of the outcome across the network, holding fixed the marginal probabilities of each category. The less likely a concordant pair (under independence), the more evidence it provides for network dependence, and the less likely a discordant pair (under independence), the more evidence it provides against network dependence. Using this rationale, a test statistic should put higher weight on more unlikely observations. The following is our proposed test statistic:

\[
\Phi = \left\{ \sum_{i=1}^{n} \sum_{j=1}^{n} w_{ij} \left\{ 2I(y_i = y_j) - 1 \right\} / p_{yi} p_{yj} \right\} / S_0,
\]

where \( p_{yi} = P(Y = y_i) \), \( p_{yj} = P(Y = y_j) \), and \( S_0 = \sum_{i=1}^{n} (w_{ij} + w_{ji})/2 \). The term \( 2I(y_i = y_j) - 1 \) ∈ \{-1, 1\} allows concordant pairs to provide evidence for dependence and discordant pairs to provide evidence against dependence. The product of the proportions \( p_{yi} \) and \( p_{yj} \) in the denominator ensures that
more unlikely pairs contribute more to the statistic. As the true population proportion is generally unknown, \( \{p_k : k = 1, \ldots, K\} \) should be estimated by sample proportions for each category.

The first and second moment of \( \Phi \) are derived in the Appendix A.1. Asymptotic normality of the statistic \( \Phi \) under the null can also be proven based on the asymptotic behavior of statistics defined as weighted sums under some constraints. For more details see Appendix A.2. For binary observations, which can be viewed as categorical or continuous, our proposed statistic has the desirable property that the standardized version of \( \Phi \) is equivalent to the standardized Moran’s \( I \). Tests can be derived based on the asymptotic normal distribution of \( \Phi \) under the null, but tests based on the permutation distribution of \( \Phi \) when node labels are permuted but the adjacency matrix is held fixed may have better performance in finite sample sizes.

### 2.3 Choosing the weight matrix \( W \)

Tests for spatial dependence take Euclidean distances (usually in \( \mathbb{R}^2 \) or \( \mathbb{R}^3 \)) as inputs into the weight matrix \( W \). In networks, the entries in \( W \) can be comprised of any non-increasing function of geodesic (or other) distance, but for robustness we use the adjacency matrix \( A \) for \( W \), where \( A_{ij} \) is an indicator of nodes \( i \) and \( j \) sharing a tie. The choice of \( W = A \) puts weight 1 on pairs of observations at a distance of 1 and weight 0 otherwise. In many spatial settings, subject matter expertise can facilitate informed choices of weights for \( W \) (e.g. [33, 27]), and if researchers have concrete information about how dependence decays with geodesic network distance then a more informed choice of \( W \) can improve the power of the test.

### 3 Simulations

In Section 3.1, we demonstrate the validity and performance of our new statistic, \( \Phi \), for testing spatial autocorrelation in categorical variables. In Section 3.2, we demonstrate the performance of \( \Phi \) for testing for network dependence.

#### 3.1 Testing for spatial autocorrelation in categorical variables

We replicated one of the data generating settings used by Farber et al. [10] and implemented permutation tests of spatial dependence using \( \Phi \). First, we generated a binary weight matrix \( W \) with entries \( w_{ij} \) indicating whether regions \( i \) and \( j \) are adjacent. The number of neighbors \( (q_i) \) for each site \( i \) was randomly generated through \( q_i = 1 + \text{Binomial}(2(d-1), 0.5) \) for a fixed parameter \( d \) that controls the expected number of neighbors. We simulated 500 independent replicates of \( n = 100 \) observations under each of four different settings, varying the values of \( d = 3, 5, 7, 10 \). We then used \( W \) to generate a continuous, autocorrelated variable:

\[
Y^* = (I_n - \rho W)^{-1} \epsilon, \quad \epsilon = \{\epsilon_i \sim N(0, 1) : i = 1, \ldots, n\},
\]
where $I_n$ is an $n \times n$ identity matrix and $\rho$ controls the amount of dependence. When $\rho = 0$, $Y^*$'s are i.i.d. while positive $\rho$ induces some dependence among $Y^*$'s informed by $W$. Since $Y^*$ is continuous, we applied cutoffs based on the $(0.25, 0.5, 0.75)$ quantiles of each simulated dataset to convert $Y^*$ into categorical observations $Y = (Y_1, Y_2, \ldots, Y_n)$ having $K = 4$ categories.

Figure 1 presents the simulation results. It shows that under the null ($\rho = 0$), the rejection rate is close to the nominal level of $\alpha = 0.05$ and that the power to detect dependence increases with $\rho$. Moreover, as the expected number of adjacent neighbors, $d$, increases, power tends to increase at fixed $\rho$ when $\rho$ is relatively small ($\rho < 0.6$). This relationship is reversed when $\rho \geq 0.6$. This can be explained by the fact that, when $\rho$ and $d$ are large relative to $n$, all of the data points tend to look similar to one another, leading to smaller contrasts between pairs of data points that are close and pairs that are distant, i.e. to weaker evidence for dependence. This is an inevitable feature of any test of dependence that does not rely heavily on a parametric data-generating model.

### 3.2 Testing for network dependence

To illustrate the performance of $\Phi$, we simulated categorical outcomes $Y$ associated with nodes in a single interconnected network and with dependence structure informed by the network ties. $Y$ had five levels and marginal probabilities $(p_1, p_2, p_3, p_4, p_5) = (0.1, 0.2, 0.3, 0.25, 0.15)$: we seeded each node with independent outcomes and then induced dependence due to direct transmission by running a contagious process across the nodes over several time steps; details are provided in the Appendix. The number of time steps, $t$, indexes the amount
of dependence induces, with $t = 0$ indexing i.i.d. observations. To demonstrate the consequences of using i.i.d. inference in the presence of dependence, as is currently standard practice for network data, we calculated simultaneous 95% confidence intervals for estimates of $p_1$ through $p_5$ (using the method proposed in [32]). We tested for network dependence using permutation tests based on $\Phi$ and report power as the percentage of 500 simulations in which the test rejected the null.

| $t$   | 95% CI coverage rate | % of p-values($z$) $\leq$ 0.05 | % of p-values(permutation) $\leq$ 0.05 |
|-------|----------------------|-------------------------------|----------------------------------|
| 0     | 0.94                 | 5.40                          | 4.80                             |
| 1     | 0.81                 | 39.40                         | 36.20                            |
| 2     | 0.63                 | 67.80                         | 65.00                            |
| 3     | 0.43                 | 85.40                         | 83.40                            |

Table 1 summarizes the simulation results. As dependence increases, coverage rates of the 95% confidence intervals that were estimated under the i.i.d. assumption decrease, representing anticonservative inference. The power of $\Phi$ to reject the null simultaneously increases. These results indicate (a) that the common practice of using i.i.d. data for network data may be invalid, and (b) that tests based on $\Phi$ can operate as a good screening process for settings in which i.i.d. models are especially problematic.

The netdep R package for testing network dependence and generating network dependent observations is available through Github (github.com/youjin1207/netdep).

4 Applications

4.1 Spatial data

In this section we apply $\Phi$ to spatial data on a categorical variable describing the race/ethnicity of populations immediately surrounding 473 U.S. power generating facilities [28]. We compare the results to standard analyses using join count statistics.
Fig. 2: Panel (a): Proportion of race/ethnicity groups around 473 power-producing facilities across the U.S. Applying Moran’s I separately to each proportion, all of the tests reject the null hypothesis of independence at the $\alpha = 0.05$ level. Panel (b): Most populous group (left) and categories defined by having $\leq 10\%$ or $>10\%$ Hispanic or African American residents (right). Omnibus tests of dependence based on $\Phi$ reject the null hypothesis of independence at the $\alpha = 0.05$ level for both variables.

Figure 2a depicts the composition of the population living within a 100 km radius of each power generating facility, with the shade of each dot representing the proportion of the population falling into each race/ethnicity category (White/Hispanic/African American). We can apply Moran’s I separately to data on each of the three categories, but Moran’s I cannot provide a single aggregate test statistic. Figure 2b depicts the distributions of two alternative categorical summaries of the information from Figure 2a: a 3-level variable indicating the most populous group in the area surrounding each facility, and a 4-level variable indicating whether more than 10% of the population is Hispanic and African American, respectively. Using each of these categorical variables, we can perform an omnibus test for dependence using $\Phi$. We observe greater evidence of dependence in the second categorization ($\Phi : 22.72$) than the first categorization ($\Phi : 9.17$). This direct comparison is possible using $\Phi$ but would not be possible using join count statistics. The join count statistics for these two categorical variables are given in Table 2 and Table 3. The statistics themselves count the frequency of concordant neighboring pairs for each category and standardize it; the p-values are derived from a permutation test that permutes the location of each observation while holding the values fixed. Join count analysis requires a notion of adjacency; we specified a neighborhood size of 15, meaning that obser-
vation \( j \) is considered to be adjacent to \( i \) if \( j \) is one of \( i \)'s closest 15 neighbors in Euclidean distance.

Table 2: Permutation tests of dependence based on join count statistics applied to the most populous group.

| Most populous group | White | Hispanic | African-American |
|---------------------|-------|----------|------------------|
| \( n \)             | 446   | 13       | 14               |
| Join count statistic | 212.63| 0.97     | 0.77             |
| P-value (permutation)| < 0.01| < 0.01   | < 0.01           |

Table 3: Permutation tests of dependence based on join count statistics applied to four different population categories, defined by having \( \leq 10\% \) or \( > 10\% \) Hispanic or African American residents.

| AA \( \leq 10\% \), HP \( > 10\% \) | AA \( > 10\% \), HP \( \leq 10\% \) | AA \( > 10\% \), HP \( > 10\% \) | AA \( \leq 10\% \), HP \( \leq 10\% \) |
|------------------------------------|---------------------------------|---------------------------------|---------------------------------|
| \( n \)                            | 52                              | 106                             | 98                              |
| Join-count statistic               | 7.07                            | 26.63                           | 30.30                           |
| P-value (permutation)              | < 0.01                          | < 0.01                          | < 0.01                          | < 0.01                          |

4.2 Network data

The Framingham Heart Study, initiated in 1948, is an ongoing cohort study of participants from the town of Framingham, Massachusetts that was originally designed to identify risk factors for cardiovascular disease. The study has grown over the years to include five cohorts. For decades, FHS has been one of the most successful and influential epidemiologic cohort studies in existence. It is arguably the most important source of data on cardiovascular epidemiology. It has been analyzed using i.i.d. statistical models (as is standard practice for cohort studies) in over 3,400 peer-reviewed publications since 1950: to study cardiovascular disease etiology (e.g. [2, 7]), risks for developing obesity (e.g. [34]), factors affecting mental health (e.g. [29, 30]), and many other outcomes.

In addition to being a very prominent cohort study, more recently FHS has played a uniquely influential role in the study of social networks and social contagion. Researchers reconstructed the (partial) social network underlying the cohort and used this network to study social contagion and peer influence for a variety of outcomes in a series of highly influential papers [3, 4, 11]. However, even these analyses use methods that assume independence across subjects [22, 16]. In a companion paper we test for dependence in continuous and binary variables in the FHS data, and discuss the implications of network dependence for the body of research that relies on i.i.d. analyses these data. Here we illustrate that dependence in these data may extend beyond continuous and binary variables
to categorical variables, which previous methods would not have been able to ascertain. We analyzed \( n = 1,033 \) subjects with 690 undirected social network ties from the Offspring Cohort at Exam 5, which was conducted between 1991 and 1995.

![Network dependence test](image)

Fig. 3: Network dependence test for categorical variables with three levels (left) and four levels (right) using \( \Phi \).

We tested for dependence in two different categorical random variables using \( \Phi \): employment status and preferred method of making coffee. Figure 3 shows the distribution of these two variables over the largest connected component of the network. We found significant evidence of network dependence for both variables, resulting \( p \)-value of \(< 0.01 \) in both variables.

5 Concluding Remarks

In this paper, we proposed a simple test for dependence among categorical observations sampled from geographic space or from a network. We demonstrated the performance of our proposed test in simulations under both spatial and network dependence, and applied it to spatial data on U.S. power producing facilities and to social network data from the Framingham Heart Study.

Under network dependence, adjacent pairs are expected to exhibit the greatest correlations, and for robustness we used the adjacency matrix as the weight matrix for calculating the test statistic, thereby restricting our analysis to adjacent pairs; if researchers have substantive knowledge of the dependence mechanism other weights may increase power and efficiency.

Researchers should be aware of the possibility of dependence in their observations, both when studying social networks explicitly and when observations are sampled from a single community for reasons of convenience. As we have seen
in the classic Framingham Heart Study example, such observations can be dependence, potentially rendering i.i.d. statistical methods invalid. In a companion paper [16], we delve deeper into the consequences of assuming that observations are independent when they may in fact exhibit network dependence. That paper focuses on continuous and binary variables, but similar conclusions hold for the categorical variables that we addressed in this paper.

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**A Appendix**

**A.1 Moments of $\Phi$**

Here we derive $\mu_\Phi := E[\Phi]$ and $E[\Phi^2]$, the first and second moments of $\Phi$. Based on these moments, we can derive the variance of $\Phi$, $\sigma^2_\Phi := E[\Phi^2] - \mu^2_\Phi$.

When $K$ is the number of categories and $p_j$ is the proportion of $Y$ in category $j$ ($j = 1, 2, \ldots, K$),

$$
\mu_\Phi = \frac{1}{n(n-1)} \{ n^2 K (2 - k) - nQ_1 \},
$$

$$
E[\Phi^2] = \frac{1}{S_0^2} \left[ \frac{S_1}{n(n-1)} (n^2 Q_{22} - nQ_3) 
+ \frac{S_2 - 2S_1}{n(n-1)(n-2)} ((K-4)K + 4)n^3 Q_1 + n(n((2K-4)Q_2 - Q_{22}) + 2Q_3) 
+ \frac{S_0^2 - S_2 + S_1}{n(n-1)(n-2)(n-3)} \left\{ n(-4Q_3 + 2nQ_{22} - 6KnQ_2 + 12nQ_2 
- 3K^2n^2Q_1 + 14Kn^2Q_1 - 16n^2Q_1 + K^4n^3 - 4K^3n^3 + 4K^2n^3) 
- ((2K-4)n^2Q_2 + n^2(Kn(2Q_1 - KQ_1) - Q_{22}) + 2nQ_3) \right\} \right],
$$

where $Q_m := \sum_{i=1}^K 1/p_i^m$, $(m = 1, 2, 3)$; $Q_{22} := \sum_{i=1}^K \sum_{u=1}^K 1/p_i p_u$ ; $S_0 = \sum_{i=1}^n \sum_{j=1}^n (w_{ij} + w_{ji})/2$; $S_1 = \sum_{i=1}^n \sum_{j=1}^n (w_{ij} + w_{ji})^2/2$; $S_2 = \sum_{i=1}^n (w_{ii} + w_{i.})^2$. 


A.2 Asymptotic distribution of $\Phi$ under the null

Shapiro and Hubert [31] proved the asymptotic normality of permutation statistics of the form $H_n$ for i.i.d. random variables $Y_1, Y_2, \ldots, Y_n$ under some conditions:

$$H_n = \sum_{i=1}^{n} \sum_{j=1, j \neq i}^{n} d_{ij} h(Y_i, Y_j),$$

where $h(\cdot, \cdot)$ is a symmetric real valued function with $E[h^2(Y_i, Y_j)] < \infty$ and $D := \{d_{ij}; i, j = 1, \ldots, n\}$ is an $n \times n$ symmetric, nonzero matrix of which all diagonal terms must be zero. In the context of $\Phi$, $h(Y_i, Y_j) = (2I(Y_i = Y_j) - 1)/(p_Y p_Y)$ and $D = \mathbf{W}$. Requirements for asymptotic normality include

$$n \sum_{i,j=1, i \neq j}^{n} d_{ij}^2 \to 0 \quad \text{and} \quad \max_{1 \leq i \leq n} d_{ii}^2 / \sum_{i=1}^{n} d_{ii}^2 \to 0 \quad \text{as} \quad n \to 0,$$

where $d_{ii}$ is the degree of node $i$. More details can be found in [31]; see also [25].

B Simulation of categorical observations over network

B.1 Direct transmission simulations

We specify the starting probability that each observation falls into one of $K$ categories, $\{p_1, p_2, \ldots, p_K\} : \sum_{j=1}^{K} p_k = 1$. We then simulate initial outcomes from a multinomial distribution, and generate outcomes at subsequent time points iteratively:

$$Y_1^0, Y_2^0, \ldots, Y_n^0 \overset{i.i.d.}{\sim} \text{Multinomial}(\{p_1, p_2, \ldots, p_K\}),$$

$$Y_i^t = \begin{cases} 
Z_i^t \sim \text{Multinomial}(\{\hat{p}_{1t}, \hat{p}_{2t}, \ldots, \hat{p}_{Kt}\}) & \text{with probability } q \\
Y_i^{t-1} & \text{with probability } 1 - q
\end{cases}$$

where $\hat{p}_{mt} := \sum_{j=1}^{n} w_{ij} I(y_j^{t-1} = m) / \sum_{j=1}^{n} w_{ij} ; \quad m = 1, \ldots, K ; \quad 0 < q \leq 1$. At each time point, with probability $q$, a node’s outcome is updated as a draw from a new multinomial with probabilities influenced by the proportion of adjacent nodes falling into each category at the previous time. The amount of influence from adjacent peers can be controlled by pre-specified maximum susceptibility probability $q_m(0 \leq q_m \leq 1)$, where $q \in [0, q_m]$, and we set $q_m = 0.4$. 
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