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Computer Generation of Points on a Plane

Treatment of Boundary Line Overlap in a Forest-Sampling Simulator

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COMPUTER GENERATION OF POINTS ON A PLANE

A statistical model for the generation of random, contagious, and uniform spatial patterns is developed. Points are located on the plane one at a time with each point modifying the probability matrix for the next point. For random patterns no change is made in the probabilities. For contagious patterns, location of a point increases the probability of locating another point near it. However, for uniform patterns the probability of locating another point near previously established points is reduced.

TREATMENT OF BOUNDARY LINE OVERLAP IN A FOREST-SAMPLING SIMULATOR

A procedure is given for treating boundary line overlap in computer *simulated sampling. This procedure, referred to as algo*rithm *EDGE,* insures that each point in the rectangular population has the same probability of being included in the sample, thereby eliminating possible edge-effect bias. The effectiveness of *EDGE* in producing a more realistic variance/plot size relationship is demonstrated by comparing the variance functions with uncorrected samples and samples corrected using a previously reported weighting scheme.

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Lee C. Wensel

Computer Generation of Points on a Plane[1]

INTRODUCTION

AN INCREASING NUMBER of researchers have been using mapped and artificially generated spatial populations as basic data for simulation models of various types. O'Regan and Palley (1965) Kulow (1966), Wensel and John (1969), Ek (1971), Aldred (1971) and others have used mapped stands to study the properties of various sampling estimators. Payandeh (1970) and Payandeh and Paine (1971) used both mapped stands and "computer redistributed" stands to examine the effect of differences in spatial pattern on the relative precision of systematic versus random sampling. Payandeh (1970) also used these mapped and computer redistributed stands to compare measures of stand contagion.

In order to simulate the operation of pulpwood harvesting machinery, Newnham (1968) has developed a general program for generating artificial populations of points on a plane. This program enables the user to generate, through trial and error, any one of a number of spatial patterns from clumped (contagious) through random to uniform. Uniform stands are generated by locating trees within grid squares, the exact location being stochastic and depending upon the degree of uniformity desired. Contagious populations of points are generated by first locating a number of clump centers. Then X and Y coordinates are randomly selected for each point to be located and the distance to its nearest clump center is reduced, thus yielding a new set of coordinates closer to the clump center in question.

For use in an even-aged forest management simulator, Dress (1970) generated randomly distributed artificial forest populations using a combined Poisson arrival (birth) and binomial removal (death) process for grid cells of equal areas. The actual coordinates of the tree within the cells were based upon randomly selected azimuths and distances from the center of the cell.

Of the methods of generating artificial populations of points on a plane, the method given by Newnham (1968) appears to be the more general. It is especially good for generating special distributions, such as those characterizing plantations of stands with infection centers (e.g., seed trees) or density gradients. Dress (1970) treats only even-aged stands which characteristically give either uniform or random spatial patterns. Payandeh's (1970) method requires data from previously mapped stands and thus is not as flexible as the others.

The present study develops a stochastic method for generating artificial populations of points in a plane that can be used to study the effects of the degree of contagion, randomness, or uniformity (over-dispersion) on the sampling efficiency of a number of sampling designs. Thus, the method of generating populations must make it possible to vary the degree of non-randomness in a continuous fashion. The generator should also

[1] Submitted for publication October 26, 1973.

be able to generate populations that are free from edge effect.[2] Because only relatively small (area) populations can be used in computer sampling simulators, possible edge effect bias may be significant (Wensel and John 1969).

This paper is followed by a paper (starting on page 143) that describes a procedure for eliminating bias from either boundary-line overlap or edge-effect.

An Appendix containing computer programs relative to both papers begins on page 147.

THE GENERATION PROCESS

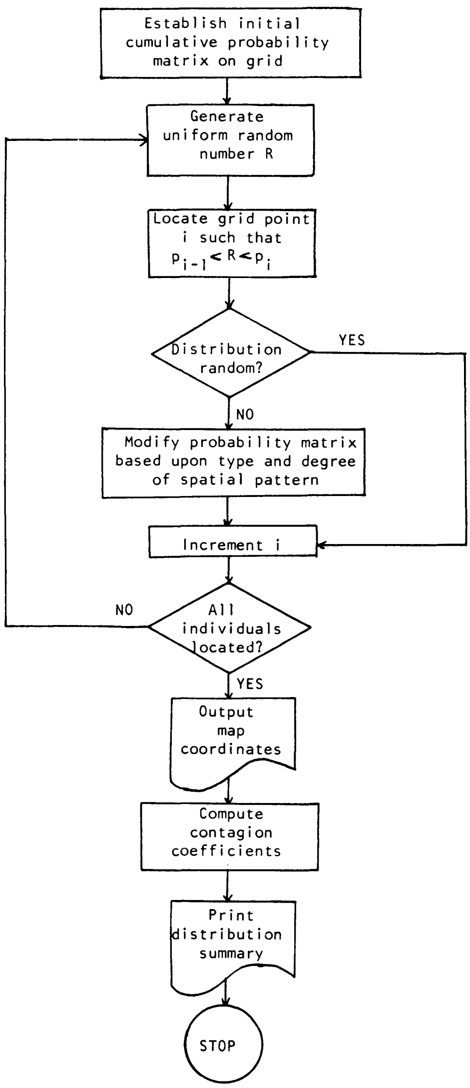


Fig. 1. Flow chart for spatial pattern generator STAND.

Figure 1 is an abbreviated flow chart of the process used to generate various spatial patterns. The principle used here is to start with a uniform grid of points, each of which could be the location on the grid of any one of the individuals in the pattern. Initially, each point has the same probability of being chosen as the location for an individual. However, as each individual in the pattern is located, the probability of selecting each remaining point on the next draw is modified to reflect the effect that the previous point had on the pattern. This process is repeated until all the individual points in the pattern have been located.

[2] As used here edge effect is the result of a population having different properties near the edge or border than it does in the interior.

INITIAL PROBABILITY MATRIX; RANDOM NUMBER GENERATOR

An initial cumulative probability matrix P is generated so that the probability of locating the first individual at any point is the same for all points. The initial values of the matrix P are given by

$$P_i = \frac{i}{n_{xy}} \quad i = 1, 2, \ldots, n_{xy}$$

where n_{xy} is the total number of points on the population grid.

In order to locate individuals on the probability grid, a uniform pseudo-random number R on the unit interval $(0 \leq R \leq 1)$ is generated using the function RANDOM. (Computer routines referred to here in upper case letters are given in the Appendix, starting on page 147.) This routine uses the multiplicative congruent method described by Hillier and Lieberman (1968); it has been tested by some authors (cf. Aldred 1971 and Kourtz 1970), but it does not work uniformly well for all seeds (starting values). Table 1 gives the four seeds used in the examples that follow. Standard tests of randomness were applied to numbers generated from these sequences and they failed to show any significant departures from randomness. Further, tests of randomness for spatial patterns resulting from these numbers failed to show significant departures from randomness (see below).

TABLE 1
SEEDS FOR RANDOM NUMBER GENERATOR RANDOM

Number	Seed (octal)
1	17164312635650214531
2	17166110231614303311
3	17175445572764662267
4	17161717553070425125

LOCATION OF SELECTED GRID POINTS

Subroutine LOCATE uses a search procedure to select the coordinate point k so that $P_{k-1} < R \leq P_k$ where $1 \leq k \leq n_{xy}$ and n_{xy} is the total number of points on the grid. The initial appoximation given by $k = Rn_{xy}$ was increased or decreased sucessively by 8, 4, 2 and 1 until the proper value of k was found. The use of this initial approximation (exact for random spatial patterns) reduced the total search time over the often-used binary search. Search time increases as P is modified by successive iterations.

MODIFICATION OF PROBABILITY MATRIX

After each individual is located on the grid, the probability mass for all points within a specified radius (defined below) of the point just selected is redistributed over these points. This redistribution of probability mass reflects the relative probability of observing an individual at the respective coordinate points in populations of the type being generated. For contagious populations, grid points near the point just selected would have their selection probabilities increased at the expense of points removed from the point. For uniform populations the reverse is true. The actual probabality modification is accomplished by multiplying the individual selection probabilities by a function that is greater than 1 or less than 1, depending upon whether the probability is to be increased or decreased, respectively.

Boundary line "slopover" bias is eliminated by projecting opposite sides of the population onto one another (subroutine LOCATE, Appendix) using the concepts embodied in the paper which follows (Wensel 1975).

FUNCTIONS FOR REDISTRIBUTING PROBABILITY MASS

The principle used here is that the modification procedure must not alter the total probability mass of the area affected. Thus the decrease in probability mass in one area must be offset by an equal increase in probability mass in another area. The functions used here are based upon a measure of the scaled distance, X, between the individual and the grid point being modified. The *type* of non-random pattern generated is determined by the modification function chosen and the *degree* of non-randomness is controlled by the parameters used in that function.

Regular spatial patterns

Most even-aged coniferous forest populations tend to be distributed in a uniform, regular or over-dispersed pattern. To generate these types of spatial patterns, consider the maximum value of the probability modification function (fig. 2) to be at the point $(1.0, H_m)$ with the function equal to 1.0 (no modification) at $X = x_o$ and at $X = (2.0 - x_o)$. Here H_m represents the maximum modification and $(x_o, 1.0)$ represents the point at which the probability modification changes from being less than 1.0, thus decreasing the probability, to being greater than 1.0, which increases the probability of the respective grid point being selected.

We now must find the equation of a line (fig. 2) that goes through the points $(0, 0)$, $(x_o, 1)$, $(1, H_m)$, and $(2-x_o, 1)$ as well as satisfying the condition that the total probability mass within the area affected is not changed. Equating the decrease in probability within the radius x_o to the increase in probability over the "donut" area from x_o to $(2-x_o)$ we have

(1)

$$\int_0^{2\pi} \int_0^{x_o} [1-f(x)]\ dx = \int_0^{\pi} \int_{x_o}^{1} [f(x) - 1]\ dx + \int_0^{2\pi} \int_1^{2-x_o} [f(2-x) - 1]\ dx.$$

The functional form

$$f(x) = kx^b(1-e^{-ax})$$

can be made to satisfy the above conditions.

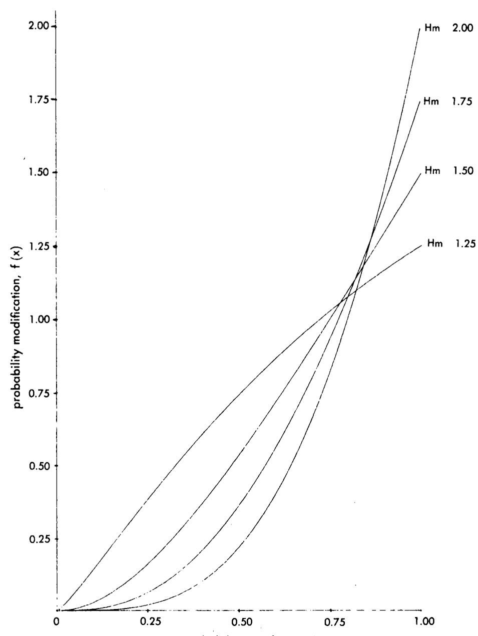


Fig. 2. Probability modification function for uniform patterns.

Using the points through which we know the curve must pass (above), we express k and b in terms of a as follows:

$$k = H_m / (1\text{-}e^{-a})$$

$$b = -\ (\log k + \log (1\text{-}e^{-ax_o})) \ / \log x_o$$

Given H_m an iterative procedure[a] is then used to find values of a and x_o that make the absolute value of the difference between the left- and right-hand sides of equation (1) less than ϵ, where ϵ is a small positive quality (10^{-5} as used here). Table 2 gives values of x_o, a, b, and k for selected values of H_m. The set of constants is not unique for each H_m, but within practical limits any two sets of constants that satisfy the above constraints will define the same line. Thus the degree of uniformity produced by the model is controlled by the value of H_m used (see below). Figure 2 illustrates the form of probability modifications functions for the set of constants given in table 2.

TABLE 2
COEFFICIENTS FOR PROBABILITY MODIFICATION FUNCTION
$f(x) = k\,x^b\,(1-e^{-ax})$

Hm	X_o	a	b	k
1.25	0.725	1.50	0.20	1.61
1.50	0.750	2.00	1.04	1.73
1.75	0.775	2.00	1.83	2.02
2.00	0.800	2.00	2.75	2.31

Contagious spatial patterns

The function used to modify the probabilities for contagious patterns cause the probabilities to increase for grid points within a distance of x_o and decrease for distances x_0 to x_1 as shown in figure 3. The constants a_1, b_1, a_2, and b_2 for the two linear functions

$$g(x) = \begin{cases} a_1 + b_1 x & 0 \leq x \leq 1 \\ a_2 + b_2 x & 1 < x \leq x \end{cases}$$

are obtained in a similar manner as was used in (a) above. Here the constants a_1, b_1, a_2, and b_2 are expressed in terms of H_m, x_o, and x_1 based upon the points that the lines must pass through. These points are $(0, H_m)$, $(x_o, 1)$, and $(x_1, 1)$. Then given H_m and x_1, x_o can be obtained by iteration so that the gain in

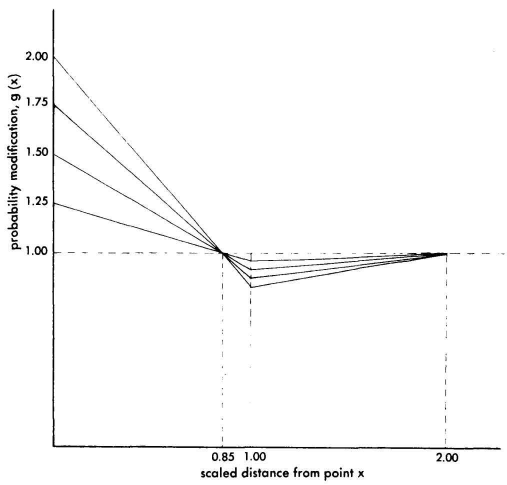


Fig. 3. Probability modification function for contagious patterns.

TABLE 3
PARAMETERS FOR CONTAGIOUS PROBABILITY MODIFICATION FUNCTION

hm	x_0	x_1	a_1	b_1	a_2	b_2
1.25	0.85	2.00	1.25	−0.29412	0.91176	0.04412
1.50	0.85	2.00	1.50	−0.58824	0.82353	0.08824
1.75	0.85	2.00	1.75	−0.88235	0.73529	0.13258
2.00	0.85	2.00	2.00	−1.17647	0.64706	0.17647

[a] A short computer program (VOLDIF) designed to solve this problem is available from the author.

probability from a radius of 0 to x_o is approximately equal to the loss in probability for the radius x_o to x_1[4]. Table 3 gives values of these constants for the functions plotted in figure 3.

For the example used here setting $H_m = 2.0$, $x_o = .85$, and $x_1 = 2.0$ yielded the equations

$$g(x) = \begin{cases} 2.0 - 1.176x & 0 \le x \le 1 \\ 0.647 + 0.176x & 1 < x \le x_1 \end{cases}$$

SCALING

The scale, S, of the grid used to represent the physical area A is given by

$$S = \sqrt{\frac{A}{n_{xy}}}$$

This scale is to be interpreted as the physical distance "on the ground" represented by the "distance" between grid points in the computer, where n_{xy} is the total number of grid points used. In order to conserve computer time it is better to choose S as large as possible without destroying the relationship being generated. In general, contagious patterns are more sensitive to increases in S (because their individuals tend to be grouped closer together) than are uniform patterns. It is suggested that several scales be tried to choose the optimum scale for a particular application.

The average number of grid points per individual is given by the ratio $\frac{(n_{xy})}{N}$, where N is the number of individuals generated. Because the area to be modified is circular, the radius (number of grid points) of the maximum modification, W, is given by

$$W = \sqrt{\left(\frac{4}{\pi}\right)\left(\frac{n_{xy}}{N}\right)}\,.$$

For W given, the number of individuals in the population is thus

$$N = \left(\frac{4}{\pi}\right)\left(\frac{n_{xy}}{W^2}\right).$$

The radius of probability modification, in terms of the number of computer grid points, for regular and contagious patterns is $W(2-x_0)$ and Wx_1, respectively, where W, x_o, and x_1 are defined above. Multiplying these radii by the scale factor S we have the "on the ground" radius R defined as:

$$R = \begin{cases} S\ W\ (2 - x_0) & \text{contagion pattern} \\ S\ W\ x_1 & \text{regular pattern} \end{cases}$$

Example:

Let an area of $A = 10$ acres be represented in the computer by $n_{xy} = 6400$ points. This gives the scale factor S as

$$S = \sqrt{\frac{(10 \text{ acres})\ (43{,}560 \text{ sq. ft./acre})}{6400 \text{ points}}}$$

$$= \sqrt{68.0625 \text{ ft.}^2\text{/point}}$$

$$= 8.25 \text{ feet/point}$$

For $W = 7$ points, we compute N, the number of individuals in the population to be generated, as

$$N = \left(\frac{4}{\pi}\right)\left(\frac{6400}{7^2}\right) = 166 \text{ individuals}$$

Letting $x_0 = 0.75$ $(X_1 = 1 - X_0 = 1.25)$ for regular patterns and $x_1 = 2.00$ for contagious patterns we have R, the radii of probability modification defined as

$$R = \begin{cases} (8.25)\ (7)\ (1.25) = 72.2 \text{ feet (regular)} \\ (8.25)\ (7)\ (2.00) = 115.5 \text{ feet (contagious)} \end{cases}$$

[4]A short computer program (CONTDIF) designed to obtain the quantities x_0, x_1, a_1, b_1, a_2, and b_2 is available from the author.

MEASURES OF SPATIAL PATTERN

Three measures of spatial pattern (Pielou, 1969) will be used here based upon (1) the distance from a randomly located point to the nearest individual

$$\alpha = D\frac{\Sigma d_1^2}{n-1}$$

(2) the distance from a random individual to its nearest neighbor

$$R = 2\sqrt{D}\frac{\Sigma d_2}{n}$$

and (3) Hopkins' measure of aggregation

$$A = \frac{\Sigma d_1^2}{\Sigma d_2^2}$$

where d_1 is the distance from a random point to the nearest individual, d_2 is the distance from a random individual to its nearest neighbor, D is the average number of individuals per unit area, and n is the number of samples taken. The measures α, R, and A are commonly referred to as the point-to-plant, plant-to-plant, and Hopkins' measures, respectively.

Table 4 gives the expected values of α, R, and A for contagious, random and regular patterns.

In comparing the measures α and R, Pielou (1969, p. 119) states that R is ... "possibly the best if one wishes to measure pattern intensity." In tests on actual and computer-redistributed populations, Payandeh (1970) found that α and R accurately detect departures from randomness but only α was sensitive to the degree and direction of this departure. Also, Payandeh found Hopkins' coefficient of aggregation, A, to be quite inaccurate.

TABLE 4
EXPECTED VALUES OF SPATIAL PATTERN MEASURES

Measure	Type of pattern		
	Contagious	Random	Uniform
α	>1	1	<1
R	<1	1	>1
A	>1	1	<1

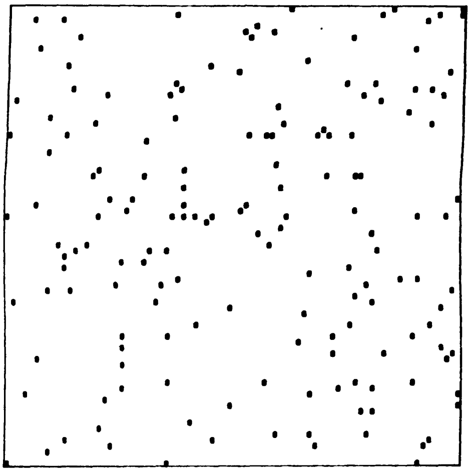
In the present study, Hopkins' measure of aggregation was found to be more accurate and more sensitive than either α or R. This is due to special characteristics of computer sampling which make it possible to take large samples. In addition, the usual sampling difficulties associated with these distance measures are not a problem when dealing with computer-generated populations. Both α and R require that the population density, D, be known. While additional (quadrat) sampling may be used to estimate the density in actual populations, the density of computer-generated populations is known. Further, randomly selecting individuals from the populations for measures R and A, while extremely expensive in field situations, is quite simple in the computer.

GENERATION RESULTS

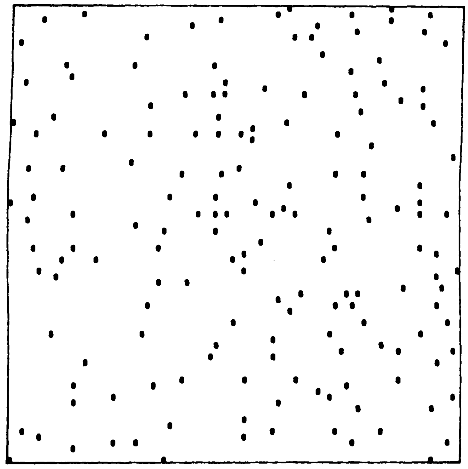
From an examination of the patterns that were generated it is quite evident that the generator was able to generate spatial patterns with increasing intensities of regularity and contagion. Thus this objective has been met and the generator can now be used to study the effect of spatial pattern on sampling efficiency and other management operations.

Random spatial patterns

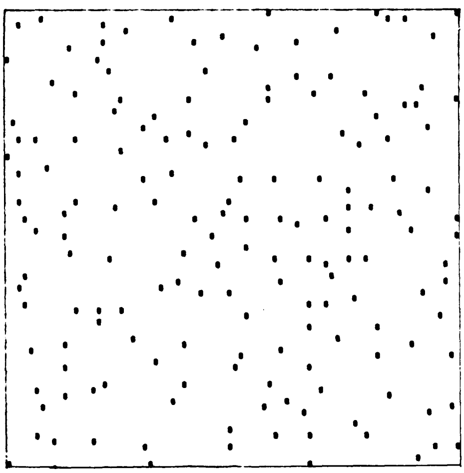
For random spatial patterns, no probability modification is made and hence, there is no limit to the number of individuals that can be generated, theoret-



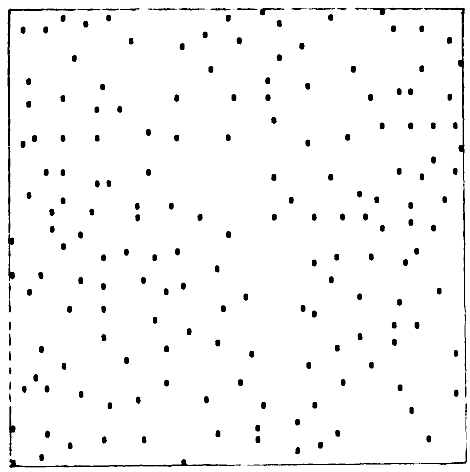
seed 2, hm = 1.00



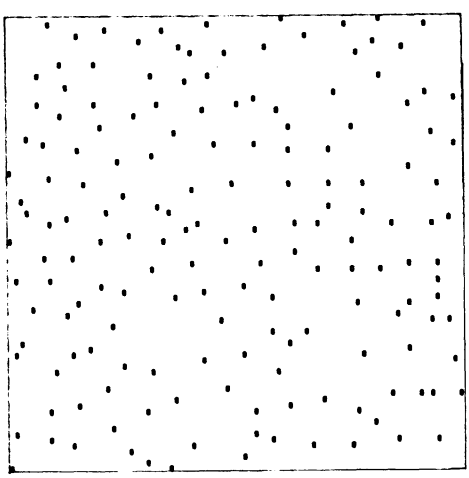
seed 2, hm = 1.25



seed 2, hm = 1.50



seed 2, hm = 1.75



seed 2, hm = 2.00

Fig. 4. Patterns with increasing degrees of uniformity, seed 2.

ically at least. For comparative purposes, however, random patterns were generated with the same number of individuals used in the uniform spatial patterns. For $n_{xy} = 6400$ points, and $N = 166$ individuals (see example above), the four seeds shown in table 1 were used to generate random patterns (no modification). The following values of A, Hopkins' measure of aggregation, were calculated for these populations: 0.926, 1.003, 0.818, and 1.088 with an average of 0.984. Using the transformation

$$x = \frac{A}{1 + A}$$

Pielou (1969, p. 116) has shown that,

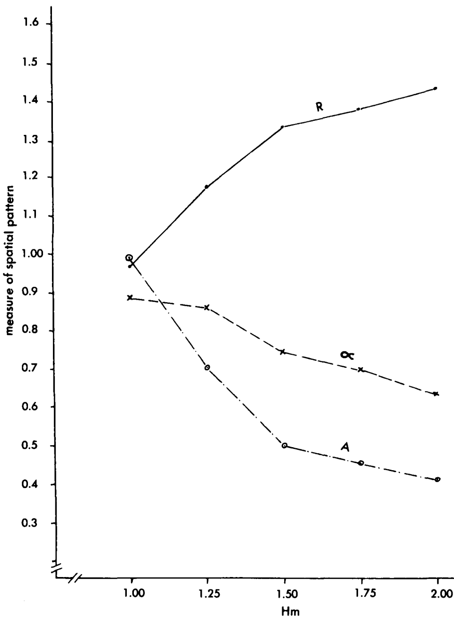


Fig. 5. Randomness indices for uniform spatial patterns.

for random populations, x is asymptotically normally distributed with E $[x]$ = ½ and $Var\ (x) = \frac{1}{4(2n+1)}$, where n is the number of samples taken. For n = 166 we have

$$Var\ (x) = \frac{1}{1332}$$

and $\sqrt{Var\ (x)} = 0.027$.

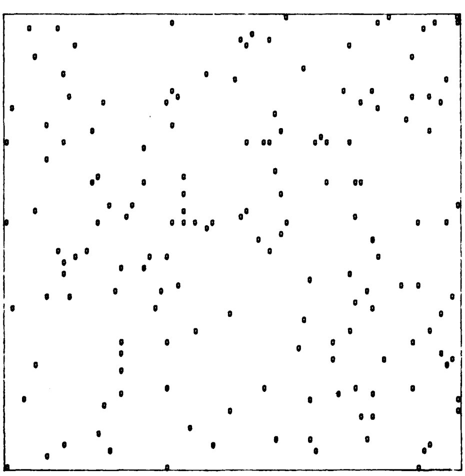
For the values of A given above, we have the following values of x: 0.481, 0.501, 0.450, and 0.521. None of these values is significantly different from $E\ [x] = ½$ at the 95 per cent level of confidence and thus none of the four patterns with $H_m = 1.00$ departs significantly from being random.

Regular spatial patterns

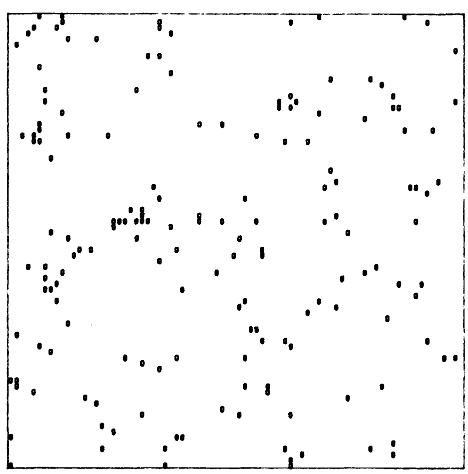
Figure 4 shows the spatial patterns that were generated by increasing the intensity of the probability modification for seed 2 (table 1) and using data given in the example above. Figure 5 shows averages of the three measures of spatial pattern for the four seeds used. Of the three measures of pattern used here, only Hopkins' measure is consistent in reflecting the increasing regularity of the patterns for individual seeds and between patterns generated with different seeds and different intensities.

Contagious spatial patterns

Using the same generation parameters as above, but changing to the contagious probability modification function, contagious patterns were generated for each of the four seeds. Figure 6 shows the patterns generated for seed 2. The increase in the contagion with increasing H_m is evident in both the pat-

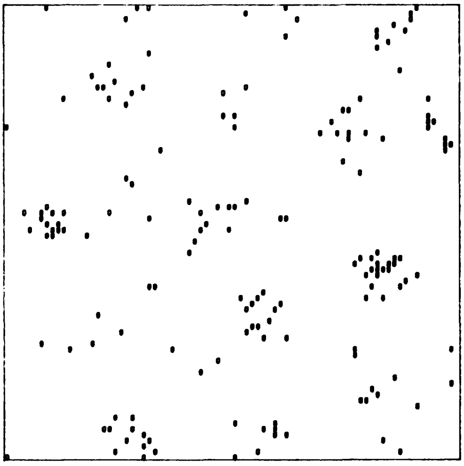


seed 2, hm = 1.00

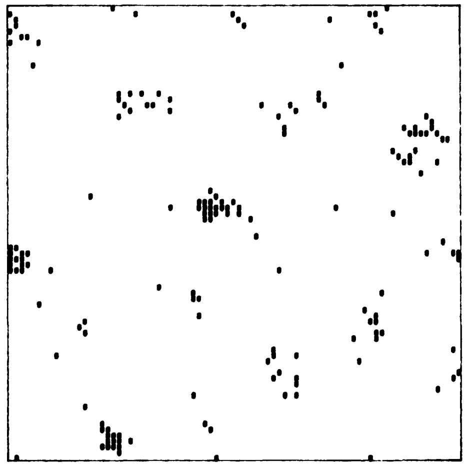


seed 2, hm = 1.25

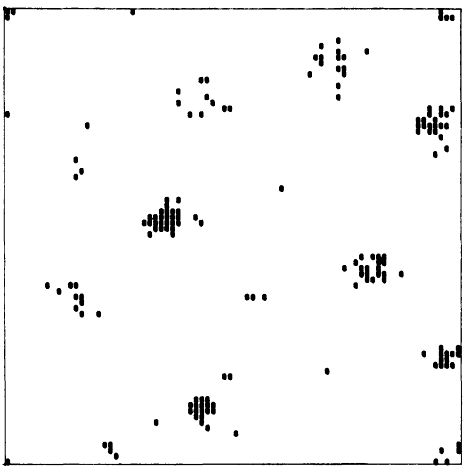
Fig. 6. (See next page for description.)



seed 2, hm = 1.50



seed 2, hm = 1.75



seed 2, hm = 2.00

Fig. 6. (Continued from page 139.) Patterns with increasing degrees of contagion, seed 2.

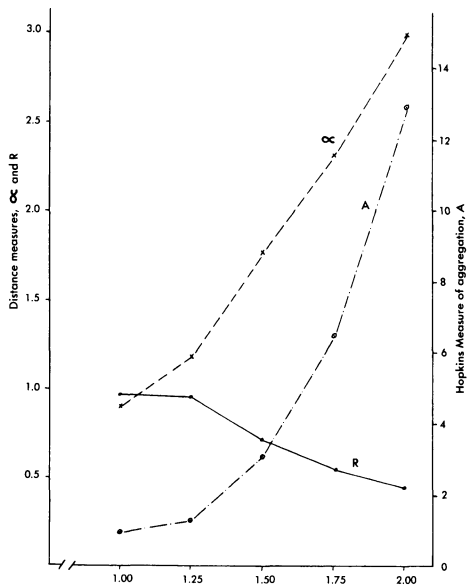


Fig. 7. (Immediately above.) Randomness indices for contagious spatial patterns.

terns shown in figure 6 for seed 2 and in the average measures of spatial pattern plotted in figure 7 for all four seeds.

As with regular patterns, Hopkins' measure of aggregation, A appears to more accurately reflect changes in the intensity of the pattern both within and between seeds for the various levels of intensity of the pattern.

OPERATION OF THE GENERATOR

Four control cards are necessary to set up the program STAND to generate a particular spatial pattern. Table 5 gives the READ and FORMAT statements for these cards, together with sample data cards. The variables listed in table 5 are defined as follows (with the sample values given in parentheses):

Card 1

NAMEFILE is an 80-character label used to identify the program output. (POPULATION 1, CONTAGIOUS)

Card 2

N is the number of individuals to be generated. If N is given as zero, a value is calculated using equation 10 above. (166)

NX, NY, and NXY are the number of grid points in the X and Y directions and the total number of grid points, respectively. (80, 80, 6400)

W is the scale used for the probability modification function. The radius of modification is given by W*X1, where X1 is defined on card 4. (7)

A is the physical area in square units (square feet, square meters, etc.) represented by the NXY grid points. (6400)

Card 3

NITER is the number of populations to be generated on this run. For each such population the same value of SEED1 is used but an additional parameter card, card 4, is supplied for each population. (1)

SEED1 is the starting seed for the pseudo-random number generator RANDOM. It is given as a 20-digit octal number. (17164312635650214531)

Card 4

ID is the code that indicates the type of pattern to be generated. The pattern is contagious, random, or uniform, depending upon whether ID is negative, zero, or positive, respectively. (−1)

HM is the maximum probability modification. (1.25)

X0 and X1 are the points (scaled) where the probability modification function is equal to 1.0. (0.725, 1.275)

BA, *BB*, *BK*, and *B*2 are the values *a*, *b*, *k*, and 0.0 for *ID* = −1 (uniform) and a_1, b_1, a_2, and b_2 if ID = +1 (contagious), (1.50, 0.2008, 1.609, 0.0). This card can be blank when generating random spatial patterns.

To generate additional populations

TABLE 5

STAND: FORTRAN INPUT SPECIFICATIONS WITH EXAMPLES

Read statements

```
READ 916, NAMFILE
READ 905, N, NX, NY, NXY, W, A
READ 910, NITER, SEED1
READ 906, ID, HM, XO, X1, BA, BB, BK, B2
```

Format specifications

```
916 FØRMAT (8A10)
905 FØRMAT (4I10, 2F10.0)
910 FØRMAT (I3, 2X, ø20)
906 FØRMAT (I10, 7F10.0)
```

Example input

```
---------------------------------------card columns---------------------------------------
0        1        2        3        4        5        6        7        8
1        0        0        0        0        0        0        0        0
------------------------------------------------------------------------------------------
 POPULATION 1, REGULAR WITH HM = 1.25, W = 7, AND N = 166
        100       80       80     6400        7     6400
1  17164312635650214531
         -1     1.25    0.725    1.275     1.50   0.2008    1.609      0.0
```

with all parameters the same except for those given on card 4, NITER is increased and additional card 4's are supplied. Alternatively, the order of the READ statements may be changed in the program to gain further flexibility in stacking problems. For example, interchanging the order of cards 3 and 4 and their respective READ statements will permit the user to generate, on a single run, several populations having the same parameters but with different seeds.

All programs and subroutines necessary to operate STAND are listed in the Appendix and are available from the author, with the exception of the sort program TSORTR. This routine is available in COMPASS for use on Control Data computers. For other computers, the user may substitute another sort routine.

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