

# Critical Thresholds and Sensitivity Dynamics of Percolation

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## Abstract

Neutral landscape models were introduced as a method for comparing the quantifiable characteristics of disparate landscapes. Tests of observed landscapes against replicate random maps reveal the degree of differences due to the structure and hypothesized underlying processes. A related central concept, percolation theory, is used to define and characterize relationships between patterns and probability values ( $p$ ) with the existence of a critical threshold value of  $p$  ( $p_c$ ). Changes in critical threshold values in neutral models can reflect significant changes in landscape function and integrity or may erroneously mask or create change when none exists. Therefore, statistical methods used to define such thresholds need to be explored. This paper reproduces historical percolation studies, which tested the influence of neighborhood configuration on spanning cluster creation. This research advances percolation theory and demonstrates the significant influence that small changes in model parameters near a critical threshold may result in disproportionately large changes in degrees of landscape fragmentation and its surrogate, connectivity.

## 1. Introduction

Ecological systems are extraordinarily complex and combine far too many elements for exhaustive, completely specified deterministic models. However, creating generalizable models using landscape patterns and processes introduces significant statistical violations. Neutral landscape models were introduced as a method for comparing the quantifiable characteristics of disparate landscapes (Gardner et al., 1987). Tests of observed landscapes against replicate random maps revealed the degree of differences due to the structure and hypothesized underlying processes (e.g., Qi, 1996; Boswell et al., 1998; Saura and Millan, 2000). A central concept, percolation theory, is used to define and characterize relationships between patterns and probability values ( $p$ ) with the

existence of a critical threshold value of  $p$  ( $p_c$ ) (Stauffer, 1985; Orbach, 1986; With, 1997). As maps are generated with successively greater values of  $p$ , the process of cluster formation is nonlinear, and a single cluster that extends or percolates from one edge of the map to the other is ultimately formed (Turner, 1989; With and Crist, 1995; Turner et al., 2001). Although, many papers study patterns, processes, and how “spanning cluster” formation occurs over landscapes using neutral models, the critical values that were used and specific thresholds are rarely known (Homan, et al., 2004). In addition, changes in critical threshold values in neutral models may reflect significant changes in landscape function and integrity or may erroneously mask or create change when none exists (Turner et al, 1989). Therefore, statistical methods used to define such thresholds need to be explored. One oft cited number for spanning cluster formation is a critical threshold value of  $p$  ( $p_c$ ) 0.5928. This critical  $p$  represents the scenario where 59.28% of an extent is occupied by a single common value. This might be a forest cover in a single landscape for example. However, as demonstrated here, this number represents confidence in a distribution of spanning cluster probabilities and not an absolute. Thus, this paper reproduces historical percolation studies, which tested the influence of neighborhood configuration on spanning cluster creation. This study advances percolation theory specifically exploring threshold sensitivity with respect to changes in extent, grain, neighborhood configuration, and origin on spanning cluster generation. We hypothesize that all parameters are important, each with its own sensitivity as  $p$  approaches a critical threshold. This research is broadly applicable and also generalizable. In particular, this research demonstrates the significant influence that small changes in model parameters near a critical threshold may result in disproportionately large changes in degrees of landscape fragmentation, connectivity and other measurable, comparable characteristics.

## **2. Methods**

The effects of changes in extent, grain, neighborhood configuration, and origin were tested with pseudo-random neutral model based data. Analyses were performed to test whether critical thresholds exist where sudden changes in landscape patterns might occur due to variations in exogenous experimental parameters. Thus, spanning cluster dynamics were characterized based on critical thresholds and changes in the basic parameters of spanning cluster calculations. Random neutral landscapes and the examination of changes in extent, grain, neighborhood configuration, and origin with different values of  $p$  were created with a series of programs developed using the Interactive Data Language (IDL) software. Next, critical threshold values where spanning cluster formation occurs were investigated. Fifty realizations were generated for each experimental parameter. Every modified landscape used a new neutral model. Statistical tests were used to test the observed frequencies and the expected values and to identify critical threshold values.

### **2.1 Interactive Data Language (IDL) program code**

#### **2.1.1 Extent**

```
;Test the spanning cluster has Pcrit of 0.5928
```

```
;Change extent
```

```
pro changeextent
```

```

simu = 50 ;the number of simulation
ptest = [0.5928] ;1) change the tested pcrit value
n = N_ELEMENTS(ptest)
arr_judge = BYTARR(simu,n) ;judge results (0=not percorate, 1=percorate)
FOR i=0,n-1 DO BEGIN
FOR j=0,simu-1,1 DO BEGIN
    ;change extent here
    extent = 5000
    arrayu = randomu(s, extent, extent)
    ne_array = arrayu LE ptest[i]
    ne_clump = LABEL_REGION(ne_array, /ulong )
    ;find the largest patch index(max_index)
    histo = histogram(ne_clump)
    max_area = max(histo[1:*])
    max_index = where(histo EQ max_area)
    ;print,'largest patch area is:', max_area
    ;print,'largest patch index is:', max_index
    ;convert to the binary data (binary) (non-lagest patch = 0)
    new_index = where(ne_clump NE max_index[0])
    ;ERROR MESSAGE:When the extent > 10000
    ;"% Unable to allocate memory: to make array"
    binary = ne_clump
    binary[new_index] = 0
    ;print, binary
    ;3) test the percolation!
    c_left = max(binary[1,*]) ;indicates all elements in the second column
    c_right = max(binary[5000-2,*])
    r_left = max(binary[*],1) ;indicates all elements in the second row
    r_right = max(binary[*],5000-2)
    IF ((c_left*c_right) EQ 0) THEN c=0 ELSE c=1
    IF ((r_left*r_right) EQ 0) THEN r=0 ELSE r=1
    IF (c EQ 0) AND (r EQ 0) THEN judge=0 ELSE judge=1
    arr_judge[j,i]=judge
ENDFOR
    print,'Pcrit judge result of ', ptest[i], ' is:',arr_judge[*],i]
ENDFOR
;the total number of percolated image within the 50 times simulation
vec_total = MAKE_ARRAY(n,/INTEGER)
vec_total = total(arr_judge,1) ;sum each of the rows
print,'total number of percolated image is:', vec_total
end

```

### 2.1.2 Grain

```

;Test the spanning cluster has Pcrit of 0.5928
;Change grain size

```

```

pro changegrain
simu = 50 ;the number of simulation
ptest = [0.5928] ;1) change the tested pcrit value
n = N_ELEMENTS(ptest)
arr_judge = BYTARR(simu,n) ;judge results (0=not percorate, 1=percorate)
FOR i=0,n-1 DO BEGIN
FOR j=0,simu-1,1 DO BEGIN
    ;create the clump image(ne_clump)
    extent = 5000
    arrayu = randomu(s, extent, extent)
    ;2) change grain here
    new = congrid(arrayu, 1000, 1000, /interp)
    ne_array = new LE ptest[i]
    ne_clump = LABEL_REGION(ne_array, /ulong )
    ;find the largest patch index(max_index)
    histo = histogram(ne_clump)
    max_area = max(histo[1:*])
    max_index = where(histo EQ max_area)
    ;print,'largest patch area is:', max_area
    ;print,'largest patch index is:', max_index
    ;convert to the binary data (binary) (non-lagest patch = 0)
    new_index = where(ne_clump NE max_index[0])
    ;ERROR MESSAGE:When the extent > 10000
    ;"% Unable to allocate memory: to make array"
    binary = ne_clump
    binary[new_index] = 0
    ;print, binary
    ;3) test the percolation!
    c_left = max(binary[1,*]) ;indicates all elements in the second column
    c_right = max(binary[1000-2,*])
    r_left = max(binary[*],1) ;indicates all elements in the second row
    r_right = max(binary[*],1000-2)
    IF ((c_left*c_right) EQ 0) THEN c=0 ELSE c=1
    IF ((r_left*r_right) EQ 0) THEN r=0 ELSE r=1
    IF (c EQ 0) AND (r EQ 0) THEN judge=0 ELSE judge=1
    arr_judge[j,i]=judge
ENDFOR
    print,'Pcrit judge result of ', ptest[i], ' is:',arr_judge[*],i]
ENDFOR
;the total number of percolated image within the 50 times simulation
vec_total = MAKE_ARRAY(n,/INTEGER)
vec_total = total(arr_judge,1) ;sum each of the rows
print,'total number of percolated image is:', vec_total
end

```

### 2.1.3 Change neighborhood configuration

;Test the spanning cluster has Pcrit of 0.5928

;Change neighborhood configuration

```
pro changeneighbor
simu = 50 ;the number of simulation
ptest = [0.5928] ;1) change the tested pcr it value
n = N_ELEMENTS(ptest)
arr_judge = BYTARR(simu,n) ;judge results (0=not percorate, 1=percorate)
FOR i=0,n-1 DO BEGIN
FOR j=0,simu-1,1 DO BEGIN
    extent = 1000
    arrayu = randomu(s, extent, extent)
    ne_array = arrayu LE ptest[i]
    ;change neighborhood configuration here
    ne_clump = LABEL_REGION(ne_array, /all_neighbors, /ulong )
    ;find the largest patch index(max_index)
    histo = histogram(ne_clump)
    max_area = max(histo[1: *])
    max_index = where(histo EQ max_area)
    ;print,'largest patch area is:', max_area
    ;print,'largest patch index is:', max_index
    ;convert to the binary data (binary) (non-lagest patch = 0)
    new_index = where(ne_clump NE max_index[0])
    ;ERROR MESSAGE:When the extent > 10000
    ;"% Unable to allocate memory: to make array"
    binary = ne_clump
    binary[new_index] = 0
    ;print, binary
    ;3) test the percolation!
    c_left = max(binary[1, *]) ;indicates all elements in the second column
    c_right = max(binary[1000-2, *])
    r_left = max(binary[*, 1]) ;indicates all elements in the second row
    r_right = max(binary[*, 1000-2])
    IF ((c_left*c_right) EQ 0) THEN c=0 ELSE c=1
    IF ((r_left*r_right) EQ 0) THEN r=0 ELSE r=1
    IF (c EQ 0) AND (r EQ 0) THEN judge=0 ELSE judge=1
    arr_judge[j,i]=judge
ENDFOR
    print,'Pcrit judge result of ', ptest[i], ' is:',arr_judge[*,i]
ENDFOR
;the total number of percolated image within the 50 times simulation
vec_total = MAKE_ARRAY(n,/INTEGER)
vec_total = total(arr_judge,1) ;sum each of the rows
print,'total number of percolated image is:', vec_total
end
```

### 2.1.4 Origin

;Test the spanning cluster has Pcrit of 0.5928

;Change the Origin

pro changeorigin

simu = 50 ;the number of simulation

ptest = [0.5928] ;1) change the tested pcr it value

n = N\_ELEMENTS(ptest)

arr\_judge = BYTARR(simu,n) ;judge results (0=not percorate, 1=percorate)

FOR i=0,n-1 DO BEGIN

FOR j=0,simu-1,1 DO BEGIN

  ;create the clump image(ne\_clump)

  extent = 100

  arrayu = randomu(s, extent, extent)

  ne\_array = arrayu LE ptest[i]

  ne\_clump = LABEL\_REGION(ne\_array, /ulong )

  b = make\_array(200, 200)

  b[100,100] = ne\_clump

  tvsc1, b

  ;find the largest patch index(max\_index)

  histo = histogram(b)

  max\_area = max(histo[1:\*])

  max\_index = where(histo EQ max\_area)

  ;print,'largest patch area is:', max\_area

  ;print,'largest patch index is:', max\_index

  ;convert to the binary data (binary) (non-lagest patch = 0)

  new\_index = where(b NE max\_index[0])

  ;ERROR MESSAGE:When the extent > 10000

  ;"% Unable to allocate memory: to make array"

  ;3) test the percolation!

  c\_left = max(binary[\*],101) ;indicates all elements in the second column

  c\_right = max(binary[\*],200-2)

  r\_left = max(binary[101,\*]) ;indicates all elements in the second row

  r\_right = max(binary[200-2,\*])

  IF ((c\_left\*c\_right) EQ 0) THEN c=0 ELSE c=1

  IF ((r\_left\*r\_right) EQ 0) THEN r=0 ELSE r=1

  IF (c EQ 0) AND (r EQ 0) THEN judge=0 ELSE judge=1

  arr\_judge[j,i]=judge

ENDFOR

  print,'Pcrit judge result of ' , ptest[i], ' is:',arr\_judge[\*],i

ENDFOR

;the total number of percolated image within the 50 times simulation

  vec\_total = MAKE\_ARRAY(n,/INTEGER)

  vec\_total = total(arr\_judge,1) ;sum each of the rows

  print,'total number of percolated image is:', vec\_total

end

## 2.2 Extent, Grain, Neighborhood configuration, and Origin on spanning cluster generation

The different extent sizes: 10, 50, 100, 500, 1000, were independently tested for 50 realizations. The 4-neighborhood structure was used to label regions. Grain remained constant throughout the process. Probability values from 0.2 to 0.9 where spanning cluster formation occurs were investigated. Next, random neutral landscapes were created with different grain sizes. Grain size of 1\*1 unit was created with an extent of 5000 \* 5000. The extent remained constant throughout the process. The grain size was adjusted by using the IDL CONGRID command. Pixels were morphed using adjustments of 2\*2, 5\*5, 10\*10, and 50\*50.

To test the effects of neighborhood structure, a data set with an extent of 1000 \* 1000 was created. Different neighborhood were modeled using the LABEL\_REGION function from IDL to consecutively label all members of the set of non-zero pixels within the neighborhood around the pixel under examination with 4 and 8 neighborhood configurations. To test for origin shifts, a random map structure of 200\*200 was created. The different of origins, (0,0), (100,0), (0,100), and (100, 100), were tested for common spanning cluster generation. Probability values from 0.2 to 0.9 where spanning cluster formation occurs were investigated for all the experiments.

The Chi-square tests were used in these experiments to define thresholds. The expected values were based on the assumption that all random maps have a spanning cluster.

The  $\chi^2$  test first calculates a  $\chi^2$  statistic and then sums the differences of actual values from the expected values. The equation for this function is  $CHITEST = p( X > \chi^2 )$ , where:

$$\chi^2 = \sum_{i=1}^r \sum_{j=1}^c \frac{(A_{ij} - E_{ij})^2}{E_{ij}}$$

and where:

$A_{ij}$  = actual frequency in the i-th row, j-th column

$E_{ij}$  = expected frequency in the i-th row, j-th column

r = number of rows

c = number of columns

CHITEST returns the probability for a  $\chi^2$  statistic and degrees of freedom, df, where  $df = (r - 1)(c - 1)$ .

## 3. Results and Discussion

### 3.1 Extent and spanning cluster generation

Table 1 illustrates that when the extent equal to 1000\*1000 and 500\*500, the probability 0.59 gave the Chi-square result more than 0.95. The number of spanning clusters generated was not significantly different from the expected result at the alpha 0.05. This can be interpreted that at least 95 percent that the spanning clusters will occur in random maps of probability 0.59. The random maps of probability of 0.6 or greater all produced

spanning clusters with all 50 realizations. For the extent 100\*100, the Chi-square result was more than 0.95 when probability of neutral model was equal or greater than 0.58. Notably, as the extent decreased, the critical probability value of the random map creating a spanning cluster also decreased.

The hypothesized critical point should be the probability where the spanning cluster always manifests. However, as shown in Table 1, the critical point can be at  $P = 0.59$  or  $0.6$  for the extent 1000\*1000 or  $0.55$  for the extent 10\*10 depending on definition of the critical point. The results demonstrate that the critical threshold is sensitive to changes in extent.

Table 1: The number of the occurrence of spanning clusters and the results from Chi-square test with the given probability when changing extent.

Probability	Extent = 1000*1000 # Spanning cluster/Chi-sq. prob.		Extent = 500*500 # Spanning cluster/Chi-sq. prob.		Extent = 100*100 # Spanning cluster/Chi-sq. prob.		Extent = 50*50 # Spanning cluster/Chi-sq. prob.		Extent = 10*10 # Spanning cluster/Chi-sq. prob.	
	#	prob.	#	prob.	#	prob.	#	prob.	#	prob.
0.2	0	0.433	0	0.433	0	0.433	0	0.433	0	0.433
0.3	0	0.433	0	0.433	0	0.433	0	0.433	1	0.473
0.4	0	0.433	0	0.433	0	0.433	0	0.433	6	0.676
0.5	0	0.433	0	0.433	0	0.433	0	0.433	13	0.917
0.55	0	0.433	0	0.433	0	0.433	7	0.714	24	0.997
0.56	0	0.433	0	0.433	3	0.555	11	0.873	28	1.000
0.57	0	0.433	0	0.433	9	0.785	19	0.979	30	1.000
0.575	0	0.433	0	0.433	12	0.873	22	0.993	30	1.000
0.58	0	0.433	3	0.555	20	0.985	21	0.990	32	1.000
0.585	0	0.433	8	0.750	26	0.999	25	0.998	33	1.000
0.59	17	0.961	23	0.996	31	1.000	26	0.999	34	1.000
0.591	17	0.961	27	0.999	32	1.000	28	1.000	34	1.000
0.5928	31	0.999	34	1.000	34	1.000	29	1.000	33	1.000
0.594	36	0.999	38	1.000	35	1.000	31	1.000	32	1.000
0.595	45	1.000	39	1.000	34	1.000	32	1.000	33	1.000
0.60	50	1.000	50	1.000	41	1.000	33	1.000	35	1.000
0.61	50	1.000	50	1.000	47	1.000	38	1.000	36	1.000
0.62	50	1.000	50	1.000	50	1.000	46	1.000	40	1.000
0.65	50	1.000	50	1.000	50	1.000	49	1.000	43	1.000
0.7	50	1.000	50	1.000	50	1.000	50	1.000	49	1.000
0.9	50	1.000	50	1.000	50	1.000	50	1.000	50	1.000

### 3.2 Grain and spanning cluster generation

Grain size of 1\*1 unit was created with an extent of 5000 \* 5000 units. The extent was the same through the process. Table 2 shows the results when the original grid was rescaled to 2\*2, 5\*5, 10\*10, and 50\*50 of the original. The Chi-square result for grain



1\*1 shifted from 0.5 to 1 with the probability map equal to 0.5928. The result also indicated the same critical point for grain 2\*2. For grain 5\*5, the critical pointed shifted to the probability map of 0.591. While grain size equal to 50\*50, the Chi-square shows that the critical point shifted to 0.58. These indicated that when the grain size increased the critical value would be less than 0.5928. The results imply that the critical threshold is sensitive to changes in grain size.

Table 2: The number of the occurrence of spanning clusters and the results from Chi-square test with the given probability when changing grain.

Probability	Grain = 1*1		Grain = 2*2		Grain = 5*5		Grain = 10*10		Grain = 50*50	
	# Spanning cluster	Chi-sq. prob.	# Spanning cluster	Chi-sq. prob.	# Spanning cluster	Chi-sq. prob.	# Spanning cluster	Chi-sq. prob.	# Spanning cluster	Chi-sq. prob.
0.2	0	0.433	0	0.433	0	0.433	0	0.433	0	0.433
0.3	0	0.433	0	0.433	0	0.433	0	0.433	0	0.433
0.4	0	0.433	0	0.433	0	0.433	0	0.433	0	0.433
0.5	0	0.433	0	0.433	0	0.433	0	0.433	0	0.433
0.55	0	0.433	0	0.433	0	0.433	0	0.433	1	0.473
0.56	0	0.433	0	0.433	0	0.433	0	0.433	4	0.595
0.57	0	0.433	0	0.433	0	0.433	0	0.433	9	0.785
0.575	0	0.433	0	0.433	0	0.433	0	0.433	12	0.873
0.58	0	0.433	0	0.433	0	0.433	0	0.433	21	0.990
0.585	0	0.433	0	0.433	0	0.433	8	0.750	27	0.999
0.59	1	0.473	2	0.473	14	0.917	23	0.996	33	1.000
0.591	2	0.514	9	0.785	17	0.961	29	1.000	34	1.000
0.5928	33	1.000	31	1.000	31	1.000	37	1.000	35	1.000
0.594	49	1.000	44	1.000	41	1.000	40	1.000	37	1.000
0.595	50	1.000	50	1.000	45	1.000	45	1.000	38	1.000
0.60	50	1.000	50	1.000	50	1.000	49	1.000	38	1.000
0.61	50	1.000	50	1.000	50	1.000	50	1.000	49	1.000
0.62	50	1.000	50	1.000	50	1.000	50	1.000	50	1.000
0.65	50	1.000	50	1.000	50	1.000	50	1.000	50	1.000
0.7	50	1.000	50	1.000	50	1.000	50	1.000	50	1.000
0.9	50	1.000	50	1.000	50	1.000	50	1.000	50	1.000

### 3.3 Neighborhood configuration and spanning cluster generation

For the neighborhood configuration experiments, the extent of 1000\*1000 was held constant. The results show that the spanning cluster occurred more frequently with the lower probability of neutral map for 8-neighbor than 4-neighbor. This is because the diagonal neighbors in 8-neighborhood structures will be counted for cluster membership. Obviously, the 8-neighbor structures will form cluster more readily than the 4-neighbor structure at a given  $p$ , and form a spanning cluster at a lower  $p$ . The critical threshold for 8-neighborhood configuration was 0.405. The chi-square test gave the Chi-square

probability of 0.990. The number of spanning clusters per 50 run tests was not significantly different from the expected result at the alpha 0.05. This can be interpreted that 99 percent that the spanning clusters will occur in random maps of probability 0.405. The results demonstrate that the critical threshold is sensitive to changes in neighborhood configuration.

Table 3: The number of spanning clusters and the Chi-square results given probability p when changing Neighborhood configuration.

<b>Probability</b>	<b>4-neighbors # Spanning cluster/Chi- sq. prob.</b>		<b>8-neighbors # Spanning cluster/Chi- sq. prob.</b>	
0.2	0	0.433	0	0.433
0.3	0	0.433	0	0.433
0.4	0	0.433	3	0.555
0.405	0	0.433	21	0.990
0.4075	0	0.433	37	1.000
0.40875	0	0.433	42	1.000
0.41	0	0.433	46	1.000
0.410625	0	0.433	47	1.000
0.41125	0	0.433	49	1.000
0.4125	0	0.433	50	1.000
0.415	0	0.433	50	1.000
0.42	0	0.433	50	1.000
0.5	0	0.433	50	1.000
0.59	17	0.961	50	1.000
0.591	17	0.961	50	1.000
0.5928	31	0.999	50	1.000
0.594	36	0.999	50	1.000
0.595	45	1.000	50	1.000
0.60	50	1.000	50	1.000
0.9	50	1.000	50	1.000

### 3.4 Origin and spanning cluster generation

The basic extent in this model was 200\*200 with an internal adjusting structure of 100\*100. The results show that the number of spanning clusters generated is very similar to others when changing the origin. The critical thresholds were between 0.58 and 0.585. The Chi-square result shows that 95 percent the spanning cluster will occur at the alpha 0.05. The results imply that the critical threshold is not sensitive to changes in origin. This result is as expected given a random neutral landscape as input.

Table 4: The number of the occurrence of spanning clusters and the results from Chi square test with the given probability when changing origin.

Probability	Origin=(0,0)		Origin=(100,0)		Origin=(0,100)		origin=(100,100)	
	#Spanning cluster/Chi-sq. prob.		#Spanning cluster/Chi-sq. prob.		#Spanning cluster/Chi-sq. prob.		#Spanning cluster/Chi-sq. prob.	
0.2	0	0.433	0	0.433	0	0.433	0	0.433
0.3	0	0.433	0	0.433	0	0.433	0	0.433
0.4	0	0.433	0	0.433	0	0.433	0	0.433
0.5	0	0.433	0	0.433	0	0.433	0	0.433
0.55	0	0.433	0	0.433	0	0.433	0	0.433
0.56	3	0.555	5	0.636	5	0.636	1	0.473
0.57	9	0.785	10	0.817	8	0.750	5	0.636
0.575	12	0.873	15	0.934	14	0.917	12	0.873
0.58	20	0.985	15	0.934	19	0.979	21	0.990
0.585	26	0.999	21	0.990	21	0.990	21	0.990
0.59	31	1.000	26	0.999	26	0.999	28	1.000
0.591	32	1.000	29	1.000	29	1.000	30	1.000
0.5928	34	1.000	34	1.000	33	1.000	32	1.000
0.594	35	1.000	34	1.000	33	1.000	34	1.000
0.595	34	1.000	34	1.000	34	1.000	35	1.000
0.60	41	1.000	39	1.000	38	1.000	37	1.000
0.61	47	1.000	45	1.000	46	1.000	46	1.000
0.62	50	1.000	50	1.000	50	1.000	50	1.000
0.65	50	1.000	50	1.000	50	1.000	50	1.000
0.7	50	1.000	50	1.000	50	1.000	50	1.000
0.9	50	1.000	50	1.000	50	1.000	50	1.000

#### 4. Conclusion

It is common in landscape ecology research to represent spatial data with a rectangular lattice composed of a large number of equal-sized grid cells. These geographically referenced, topologically constrained grid cells are often used with different extents, grain sizes, neighborhood configurations, and origins. To advance our understanding in spatial patterns and processes of ecosystems, therefore, it is critical to understand how changing these spatial parameters affect the results of spatial analysis of landscape patterns and influence hypothesis generating activities. This research was specifically motivated by scientific literature setting spanning cluster thresholds that simply do not hold for all circumstances or parameter adjustments. Consequently, this research specifically investigated landscape sensitivity with respect to changes in extent, grain, neighborhood configuration, and origin on spanning cluster generation. Focusing on neutral landscape models, changing extent, grain, or neighborhood methods does affect critical thresholds. In contrast, changing origins does not affect critical thresholds. Consider, however, that origin shifts are frequently used with autocorrelated, real world

spatial data, and it is likely that such shifts would also result in a distribution of critical thresholds.

This research demonstrates the significant influence that small changes in model parameters near a critical threshold may result in disproportionately large changes in degrees of landscape connectivity as measured by spanning cluster formation. Thus, the results of all spatial analyses employing pattern metrics, generally, and percolation, specifically, should be presented with explicit specification of the extent, grain, and neighborhood configuration on which the study is conducted. Other measurable, comparable characteristics, though not explicitly tested here are quite likely to be influenced equally given the colinearity of most pattern metrics. In general, landscape pattern analysis of any metric set at a specific grain, extent, neighborhood or origin will provide useful information, but examinations that include multiple metrics across a range of lattice configurations are most desirable.

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