Spatial Statistics

PM569 Lecture 9: Point Pattern 2

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Point Pattern Data

Review of point processes

- Simple stochastic models for point patterns do not have tractable distributions.
- To test models against data we use Monte Carlo tests (simulation-based).
- Monte Carlo steps:
  - Let u_1 be the observed value of a statistic U
  - Let u_i be the values of the statistic U generated by independent random sampling from the distribution of U under a simple hypothesis H$_0$ (the null hypothesis)
  - Let $u_{(j)}$ denote the jth largest among the u_i, $i = 1, ..., s$
  - Then, under H$_0$, $P\{u_1 = u_{(j)}\} = s^{-1}, j = 1, ..., s$ and rejection of H$_0$ on the basis that u_1 ranks kth largest or higher gives an exact one sided test of size k/s

Point Pattern Data

Review of point processes

- Monte Carlo methods are not precisely replicable since they rely on simulated data.
- An independent set of simulated realizations will result in a different estimated p-value than the first set of realizations.
- The larger number of simulations the more stable the resulting estimates.
- We use Monte Carlo methods to test whether our observations are a CSR with homogeneous or inhomogeneous Poisson process, cluster process, regular process.

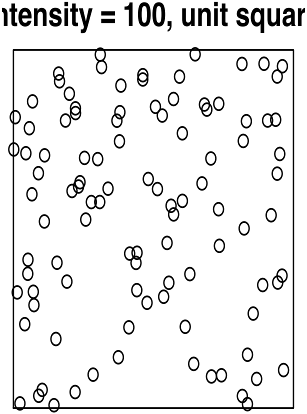
Point Pattern Data

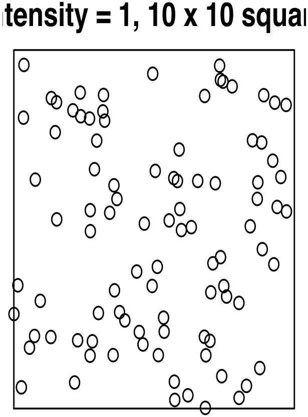
Review of point processes

- Testing for CSR:
  - Often want to adjust for edge effects.
  - We test for CSR with Ripley's K, which involves a search window with bandwidth h.
  - We test for CSR based on inter-event distances being less than a threshold δ with H(h).
  - We test for for CSR based on nearest-neighbour distances with G(h).
- The types of spatial processes where the Poisson processes is the building block are:
  - Homogeneous Poisson process (constant intensity), used for testing CSR.
  - Inhomogeneous Poisson process (intensity varies across domain), used for testing CSR.
  - Poisson Cluster process (intensity varies for parents and/or children forming clusters), used for testing clustered patterns.
  - Simple inhibition processes, Markovian processes (Strauss and pairwise interaction), used for testing regular patterns.

Point Pattern Data

Homogeneous Poisson Process (CSR)





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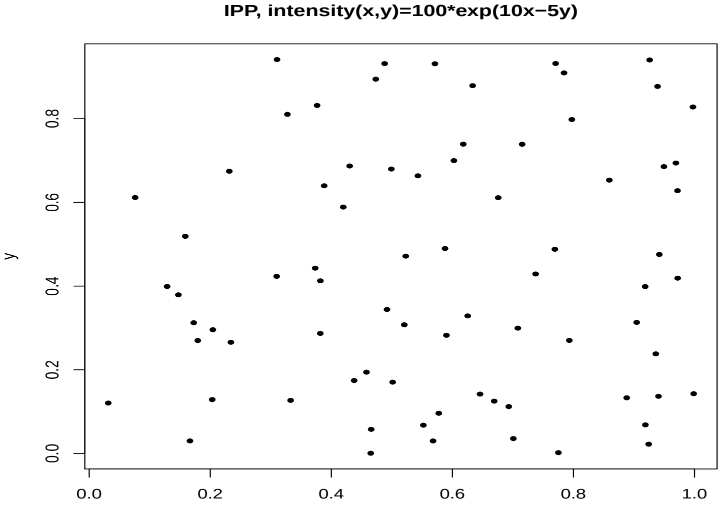
Inhomogeneous Poisson Process



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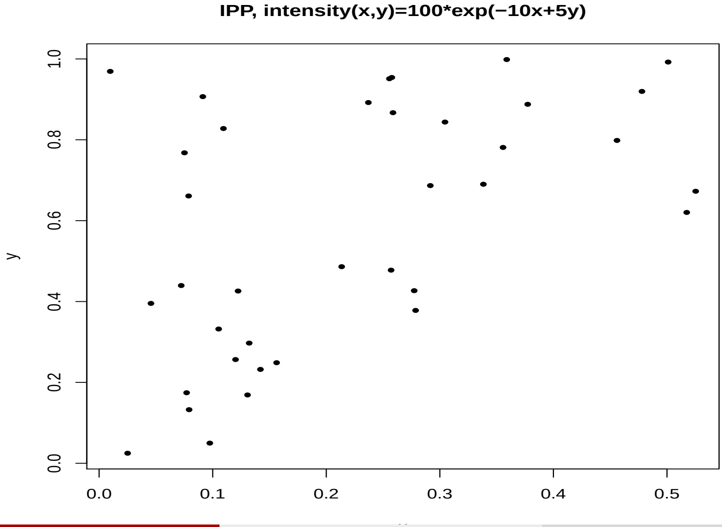
Inhomogeneous Poisson Process



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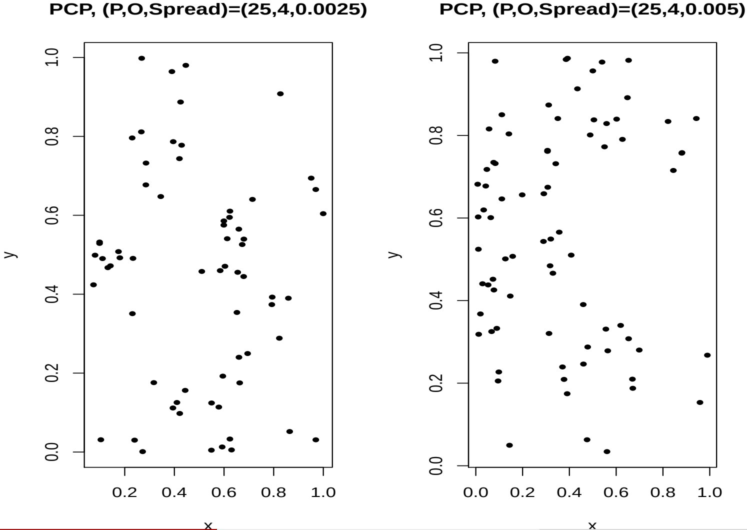
Poisson Clustered Process

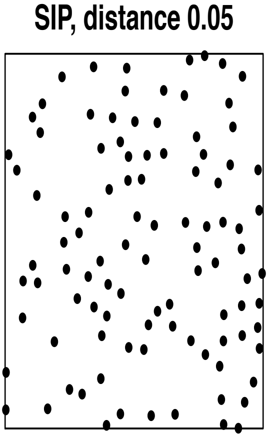


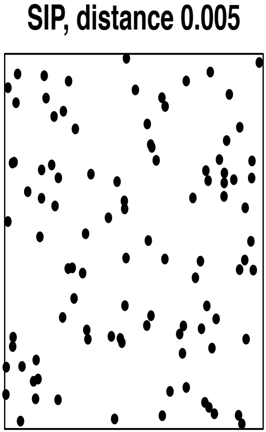
PCP, (P,O,Spread)=(25,4,0.0025)

PCP, (P,O,Spread)=(25,4,0.005)

Point Pattern Data

Simple Inhibition Process





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- Inhomogeneous Point Processes, where the intensity, λ, is not constant.
- Properties of a spatial point process in terms of the intensity function.
  - First order properties are described by the intensity function.

$$\lambda(x) = \lim_{|dx| \to 0} \frac{E[N(dx)]}{|dx|}$$

  - The first order properties are the mean properties of the random process, describing the expcted density of events in any location of the region.
  - Clusters appear in areas of high intensity
  - Under IPP and CPC, clusters occur due to heterogeneities in the intensity function and individual event locations remain independent of one another.

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- First order properties are described by the intensity function
- Example: consider the constant risk hypothesis
  - Each person has the same risk of disease, but we expect more cases in areas with more people at risk
  - Clusters of cases in high population areas will violate CSR but not the constant risk hypothesis
  - We are interested in clustering of disease events after accounting for known variations in population density
  - This requires a generalization of the intensity where we define it as a spatially varying function over the study area
  - As population size increases, so should the expected number of cases

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Inhomogeneous Poisson Process intensity function

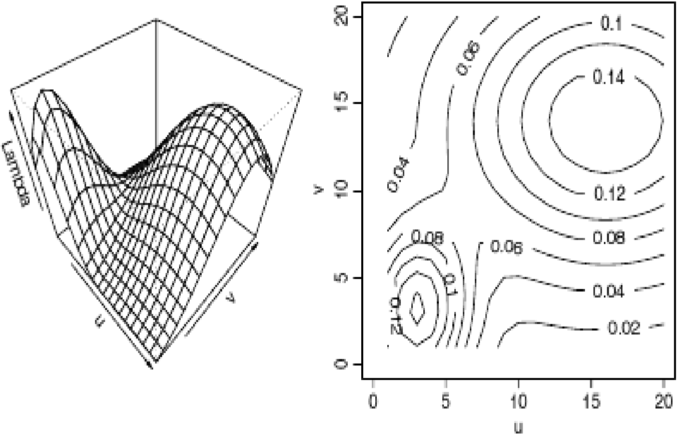

FIG. 5.5 Example intensity function, $\lambda(s)$, for a heterogeneous Poisson point process defined for $s = (u, v)$ and $u, v \in (0, 20)$.

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- The inhomogeneous Poisson process shows lack of events between the modes
- More events around the mode (16,14) and a narrower peaked area around (3,3)
- Collections of events suggest areas of higher intensity
- Single realizations make it hard to identify the specific areas of these modes
- Useful to simulate multiple realizations of the process

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- Second order properties are described by the inter-relationships between events

$$\lambda(x, y) = \lim_{|dx|,|dy| \to 0} \frac{E[N(dx)N(dy)]}{|dx||dy|}$$

- This allows us to describe how often events occur within a given distance of other events
- The second order properties are similar to variance/covariance of the process
- Allows us to summarize the spatial dependence between events over a wide range of possible spatial scales
- The Ripley's K function is a second-order statistic

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- Recall the K function for distance h:

$$K(h) = \frac{E[\# \text{ events within h of randomly chosen event}]}{\lambda}$$

- The second order properties gives us insight into the global aspects of the point pattern
- Are there general patterns of clustering or regularity with respect to CSR or another pattern?

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Cox processes

- Spatial clustering with a spatially varying intensity function of the inhomogeneous Poisson process
- Varying $\lambda(x)$ and $\lambda(x)$ is a realization of a stochastic process
- Property 1) it is a non-negative valued stochastic process

$$\{\Lambda(x); x \in \Re^2\}$$

- Property 2) the events for an inhomogenous Poisson process (IPP) with intensity function $\lambda(x)$

$$\{\Lambda(x) = \lambda(x); x \in \Re^2\}$$

Point Pattern Data

Cox processes

- The Cox process is homogeneous iff $\Lambda(x)$is homogeneous:

$$E[\Lambda(x)] = \lambda \forall x$$

$$E[\Lambda(x)\Lambda(x+h)]\text{depends only on}||h||$$

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Cox processes

- The Cox process is linked to the clustered Poisson process
- Aggregation into clusters may be a result of environmental heterogeneity
- Clusters of events in regions of high intensity
- Cox processes are considered doubly stochastic, intensity is heterogeneous but also may be a random quantity
- $\lambda(x)$ can be drawn from some probability distribution of possible intensity functions over the study area

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Cox processes

$$\Lambda(x) = \mu \sum_{i=1}^{\infty} h(x - X_i)$$

- $\mu > 0$, $h(\cdot)$ is a bivariate pdf, and X_i are points from a Poisson process
- The Cox process can also be thought of as a specific case of a Poisson cluster process with number of offspring having intensity μ and dispersion around parents with pdf $h(\cdot)$

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Cox processes

- The log-Gaussian Cox process is another form of the Cox process

$$\Lambda(x) = \exp(Z(x))$$

- $Z(x)$ is a Gaussian process.
- If $Z(x)$ is stationary with mean μ, variance σ^2 and correlation $\rho(h)$:
  - $\lambda = \exp(\mu + 0.5\sigma^2)$
  - $\gamma(h) = \exp(\sigma\rho(h))$
- The log-Gaussian Cox process can be fit in R spatstat with the rLGCP() function

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Simple Inhibition Process

- This process is used to describe regular patterns
- Often related to interactions or contagions where the occurrence of an event raises or lowers the probability of subsequent events nearby
- Useful for modeling the spread of infectious disease (contagion) or an application where an event precludes the occurrence of other events in a nearby area such as animal territories (inhibition)
- **Contagion** typically refers to the increased likelihood of events occurring near other events
- **Inhibition** may be absolute, where there is a specified distance around which *no* other events may occur, or it may be probabilistic where there is small but positive probability of an event occurring near other events

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Simple Inhibition Process

- Models for inhibition or contagion processes are Markov point processes or Gibbs processes
- The general idea is to take a CSR and "delete" points within a distance less than a threshold δ
- Under a Markov process, the existence of an event in a region depends on the locations of events in a neighbourhood (where neighbourhoods are within regions)
- There are two ways to do this: 1) to simulate CSR then delete all within a distance δ, and 2) to simulate CSR, record when event was simulated, then delete an event if it is within distance δ of an older event

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Simple Inhibition Process

- We use the packing intensity to describe simple inhibition processes:

$$\tau = \lambda \pi (\delta/2)^2$$

  Where λ is the intensity, giving τ to be the proportion of the region A covered by non-overlapping discs of diameter δ

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Simple Inhibition Process

- For simple inhibition process 1) we take a a Poisson process with intensity ρ and thin it by the deletion of pairs of events that are less than δ apart
- In this case, the probability that an event "survives" is $\exp(-\pi\rho\delta^2)$ giving the intensity of a simple inhibition process as:

$$\lambda = \rho \exp(-\pi\rho\delta^2)$$

- The second order properties can be expressed as:

$$\lambda(h) = \rho^2 \exp(-\rho U_\delta(h)) \qquad\qquad h \geq \delta$$

- $\lambda(h) = 0$ when $0 < h < \delta$, and $U_\delta(h)$ is the area of the union of two discs with equal radius δ and centers distance h apart

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Simple Inhibition Process

- For simple inhibition process 2) we take a a Poisson process with intensity ρ and thin it by the deletion of pairs of "older" events that are less than δ apart
- The expressions are the same as for process 1) but with the addition of the sequential piece (this process is referred to as the simple sequential inhibition process)
- Let X_i be a sequence of n events in A, and $d(x, y)$ be the distance between two points x and y. Then:
  - X_1 is simulated from a uniform distribution in A
  - Given (past) $\{X_j = x_j, j = 1, ...(i-1)\}$, then X_i (present) is uniformly distributed on the intersection of A with $\{y : d(y, x_j) \geq \delta j = 1, ...(i-1)\}$
- So the simple sequential inhibition process has packing intensity:

$$\tau = \frac{n\pi(\delta/2^2)}{|A|}$$

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- In R (spatstat), the functions for thinning processes 1) and 2) described above are called rMaternI and rMaternII
- The simple sequential inhibition process, called rSSI is similar but slightly different:
  - Each new point is generated uniformly in the window and independently of preceding points
  - If a new point lies within distance δ from an existing point then it is rejected and another random point is generated
  - The SSI process ends when no points can be added

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Markov point processes

- The general idea of a Markov point process lies in conditioning, whereby the existence of an event in a finite region A depends on the locations of events in a neighbourhood
- Inhibition processes are a special form of Markov process: the conditional intensity of an event at a point x given the realization of the process in the remainder of the region A depends on the existence (or otherwise) of an event within distance δ of x
- General Markov processes were introduced by Ripley and Kelly (1977)
- Markov point processes are characterized by the likelihood ratio with respect to a Poisson process of unit intensity

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Markov point processes

- Let's call the likelihood ratio $f(\cdot)$
- If $\mathbf{X} = \{x_1, ..., x_n\}$ denotes a finite set of points in A then $f(\mathbf{X})$ indicates how much more likely is the configuration of events $\mathbf{X}$ than a homogeneous point process (with unit intensity)
- We can factorize the likelihood ratio to:

$$f(\mathbf{X}) = \alpha \prod_{i=1}^{n} g_i(x_i) \prod_{j>i} g_{ij}(x_i, x_j) ... g_{12...n}(x_1, x_2, ..., x_n)$$

- Where α is a normalizing constant
- We also define two points x and y in A to be neighbours if $d(x, y) < \delta$ for some $\delta > 0$ where $d(x, y)$ is the distance between x and y
- We also define a clique (recall areal data) as a set of mutual neighbours, and the neighbourhood of x to be the set of points $\{y \in A : 0 < d(x, y), \delta\}$

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Markov point processes

- The point process with these definitions is Markov with range δ if the conditional intensity at the point x given the configuration of the other events in A depends only on the configuration in the neighbourhood of x
- The g-functions from the above equation are unity *unless* the x form a clique

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Examples of Markov point processes: the Strauss process

$$f(\mathbf{X}) = \alpha\beta^n\gamma^p$$

- Where α is the normalizing constant, β is the intensity of the process, γ is the interaction between neighbours, and p is the number of distinct pairs of neighbours in **X**
- If $\gamma = 1$ then the Strauss process gives a Poisson process with intensity β
- if $\gamma = 0$ then the Strauss process gives a simple inhibition process because no two events may be neighbours
- In R spatstat, the Strauss process is simulated with `rStrauss`

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Examples of Markov point processes: the pairwise interaction process

$$f(\mathbf{X}) = \alpha\beta^n \prod_{i \neq j} h\{d(x_i, x_j)\}$$

- Where α is the normalizing constant, β is the intensity of the process, $h(d)$ is non-negative for all distances and the product is over all pairs of distinct points in **X**
- The additional restriction is that $h(d)$ is bounded and that $h(d) = 0$ for all distances less than some $\delta > 0$
- This restriction limits the number of events in A by imposing a minimum allowable distance δ between any two events
- The pairwise interaction process may be fit in R `spatstat` using the `rmh` function

Examples of Markov point processes: the pairwise interaction process

- The pairwise interaction process may be simulated using the following steps (MCMC):
    1. For the initial realization, consider n points $\{x_1, ...x_n\}$
    2. Delete one of the points in $\{x_1, ...x_n\}$
    3. Generate a point y from a uniform distribution in A, and accept y with probability $p(y)$
    4. Repeat 2-3 until the MCMC converges

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Review of point processes

- Testing for CSR:
  - Adjusting for edge effect
  - Testing for CSR with Ripley's K.
  - Testing for CSR based on inter-event distances, H(h).
  - Testing for CSR based on nearest-neighbour distances, G(h).
- Spatial processes, Poisson processes are the building block:
  - Homogeneous Poisson process (constant intensity).
  - Inhomogeneous Poisson process (intensity varies across domain).
  - Poisson Cluster process (intensity varies for parents and/or children forming clusters), Cox process when the cluster intensity is spatially varying.
  - Simple inhibition processes, Markovian processes (Strauss and pairwise interaction) for regular patterns.
- In this lecture we will focus on fitting point process models and on methods for detecting clusters.

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Fitting point process models

- Given our set of observed point events $\{x_1, ...x_n\}$ in region A we wish to fit a model (which is stationary and isotropic)
- Model fitting is approached by estimating the parameters of the particular process
  - Example: fitting the parameters ρ, μ and σ^2 of a clustered process
  - Example: fitting a parametric form of the intensity of an inhomogeneous Poisson process
- We use familiar fitting methods: Least squares, Maximum Likelihood and non-parametric methods.

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Fitting point process models: Least Squares

- We start with $K(h)$ and the estimator $\hat{K}(h)$ (or L, or G, or H) for parameter fitting
- This is useful when the mathematical form of $K(h)$ is known either explicitly or as an integral (which is true for some point processes)
- If $K(h)$ is not known we use the simulated realizations
- Example, to fit a homogeneous poisson cluster process we have parameters $\theta = (\rho, \sigma)$ and the Ripley's K function is:

$$K(h, \theta) = \pi h^2 + \frac{1}{\rho}(1 - \exp(-h^2/(4\sigma^2)))$$

- And we estimate $\hat{K}(h)$ from the data

Fitting point process models: Least Squares

- Given the theoretical K-function and the estimator $\hat{K}(h)$ we minimize the deviance:

$$D(\theta) = \int_0^{h_0} [(\hat{K}(h))^c - (K(h,\theta))^c]^2 dh$$

- Where h_0 is the maximum distance which is typically chosen as 1/3 to 1/2 of the width of a rectangular region, and c is the power transformation
- The power transformation controls the sampling fluctuations in $\hat{K}(h)$ which can increase with h and have influence on $\hat{\theta}$ (i.e. it is a variance stabilizer)
- Examples of c are c=0.5 for a pattern that is not too different from CSR, c=0.25 for cluster patters. However, choose a variety of c values in practice in order to see how sensitive the results are

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Fitting point process models: Least Squares Estimation Steps

1. Compute the edge corrected $\hat{K}(h)$

$$\hat{K}(h) = \frac{|A|}{n^2} \sum_{i=1}^{n} \sum_{j \neq i} I(h_{i,j} \leq h)$$

2. Choose a theoretical model for $K(h, \theta)$ where θ are the parameters of the model
3. Find $\hat{\theta}$ that minimizes the deviance for a given c

$$D(\theta) = \int_0^{h_0} [(\hat{K}(h))^c - (K(h,\theta))^c]^2 dh$$

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Fitting point process models: Least Squares Estimation

- When $K(h, \theta)$ is unknown because there is no closed form, use the simulated method (for s simulations):

$$\bar{K}_s(h, \theta) = \frac{1}{n} \sum_{i=1}^{s} \hat{K}_i(h, \theta)$$

- Finding $\bar{K}_s(h, \theta)$ for each value of θ can be prohibitive computationally
  1. Start with a small number of simulations, s
  2. Find a first approximation of $\hat{\theta}$
  3. Repeat with a larger value for s

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Fitting point process models: Least Squares Estimation Steps

- A weighted version of the deviance, shown to have asymptotic properties (consistency and asymptotic normality), is often used:

$$D(\theta) = \int_0^{h_0} w(h)[(\hat{K}(h))^c - (K(h,\theta))^c]^2 dh$$

- The weight $w(h)$ is a weight on the distance also controls the variance
- When $c = 0.5$ and $w(h) = 1$ we have the Poisson cluster process
- See Guam and Sherman, J R Stat Soc (2007) for asymptotic properties

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Fitting point process models: Least Squares Estimation

- In R `spatstat`, cluster or Cox point process models are fit with least squares estimation through the `kppm` function with the `method="mincontrast"` option
- To fit a log-Gaussian Cox point process, use the function `lgcp.estK`
- To fit the Matern cluster process (type I or II), use the function `matclust.estK`

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Fitting point process models: Maximum Likelihood

- To fit inhomogeneous Poisson, Strauss and pairwise interaction processes we need to rely on likelihood methods
- Recall for the inhomogeneous Poisson process:
  - $N(A)$ is Poisson with mean $\int_A \lambda(x)dx$
  - Conditional on $N(A) = n$, the n events in A form an independent random sample from A with a probability distribution function proportional to $\lambda(x)$
- We can define the process based on its conditional intensity
- Namely, the conditional probability of finding a point of the process inside an infinitesimal neighbourhood du of the location u given the complete point pattern **x** is $\lambda(u, \mathbf{x})du$

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Fitting point process models: Conditional Intensity

- For example, CSR has conditional intensity $\lambda(u, \mathbf{x}) = \lambda$
- The IPP has conditional intensity $\lambda(u, \mathbf{x}) = \lambda(u)$
- Sometimes the IPP trend is denoted as $\beta(u)$ and indicates "spatial trend"
- The Strauss process has conditional intensity $\lambda(u, \mathbf{x}) = \beta^n \gamma^p$ where β is the intensity, γ is the interaction parameter, and p is the number of points of **x** that lie within a distance δ of u (i.e. pairs of neighbours)
- For example, the Strauss process with $\gamma < 1$ dependence between points is reflected in the fact that the conditional probability of finding a point of the process at the location u is reduced if other points of the process are present within a distance δ. And when $\gamma = 0$, the conditional probability of finding a point at u is zero if there are any other points of the process within a distance δ of this location.

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Fitting point process models: Pseudolikelihood

- Because maximum likelihood is difficult for point process models, the log of the pseudolikelihood is maximized, using the conditional intensity
- For a point process governed by parameter θ the pseudolikelihood is:

$$PL(\theta; x) = \prod_{i=1}^{n} \lambda_\theta(x_i; x) \exp(\int_A \lambda_\theta(u; x) du)$$

- The maximum pseudolikelihood estimate of θ minimizes the above equation

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Fitting point process models: Pseudolikelihood

- We need to take the log of the pseudolikelihood equation and approximate the integral using a "quadrature" scheme (see Berman and Turner, 1992)

$$\int_A \lambda_\theta(u;x)du \approx \sum_{j=1}^{m} \lambda_\theta(u_j,x)w_j$$

- Where u_j are "quadrature points" in A and $w_j \geq 0$ are the "quadrature weights"

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Fitting point process models: Pseudolikelihood

- The quadrature points can be chosen as all data points, x_i and the addition of some dummy points u_j, i.e. $\{x_1, ..., x_n\} \subset \{u_1, ..., u_m\}$
- Then the log pseudolikelihood can be written:

$$\log PL(\theta; x) = \sum_{j=1}^{m} z_j \log \lambda_\theta(u_j; x) - w_j \lambda_\theta(u_j; x)$$

- Where $z_j = 1$ if u_j is a data point, and $z_j = 0$ if u_j is a dummy point

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Fitting point process models in R

- In R `spatstat` the function `ppm` fits models by pseudolikelihood based on the conditional intensity $\lambda_\theta(u, x)$
- The model must be loglinear in the parameters θ
- For example, the Strauss process can be written:

$$\log \lambda(u, x) = \log \beta + \log \gamma p$$

- So $\theta = (\log \beta, \log \gamma)$ are the "regular parameters" and the parameter driving the interaction, p is the "irregular parameter"

Point Pattern Data

Fitting point process models in R

- Thus in `spatstat ppm` the conditional intensity is split into first and higher order terms:

$$\log \lambda_\theta(u, x) = \eta S(u) + \phi V(u, x)$$

- The first order term $S(u)$ describes the spatial inhomogeneity of the intensity (including covariate effects) and the higher order term $V(u, x)$ describes the interactions between points

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Fitting point process models in R

- The general form of ppm is `ppm(X, trend, interaction,...)`
- The trend argument specifies any spatial trend or covariate effects and is written as an R formula
- The default trend formula is ~ 1, which indicates $\lambda(u) = 1$, corresponding to a process without spatial trend or covariate effects. The formula $\sim x$ indicates the vector statistic $\lambda(x, y) = (1, x)$ corresponding to a spatial trend of the form $\exp(\alpha + \beta x)$, where α, β are coefficient parameters to be estimated, while $\sim x + y$ indicates $\lambda(x, y) = (1, x, y)$ corresponding to $\exp(\alpha + \beta x + \gamma y)$

Point Pattern Data

Fitting point process models in R

- The general form of ppm is `ppm(X, trend, interaction,...)`
- The interaction term represents the interaction function $V(u, x)$
- For example, the Strauss function with interaction distance $\delta = 0.1$ is fit with `ppm(X,  1, Strauss(r=0.1))`
- Note that the ppm with a specified higher order term calls the first order term for the intensity β rather than λ
- `spatstat` automatically creates a quadrature scheme but it can be controlled by the user through the function `quadscheme`

Point Pattern Data: Detecting Clusters

- So far we have simulated point processes, found statistics that indicate a global measure of what pattern there may be, and fit models to specific types of point patterns.
- If we want to find where clusters of observations are located, we need a different set of tools called scan statistics.
- Goals of scan statistics:
  - To determine areas where the number of events is inconsistent with the number observed over the rest of the study area.
  - Compare local rates of events (or case/control ratios) to detect clusters.

Point Pattern Data: Detecting Clusters

- First attempts at cluster detection methods were developed in the 1980s: geographical analysis machine and the cluster evaluation permutation procedure.
- Early cluster detection methods:
  - Graphical in nature
  - Divides the region up into a fine grid
  - Uses a search window, which is a circle of predefined radius, larger than the grid spacing in order for circles to overlap
  - Centers the circle over each grid cell, then moves across the region
  - The number of cases occurring within the search window are counted
  - The circle is drawn on the map if the count observed within the circle exceeds some tolerance level
  - The tolerance level may be defined as the observed count exceeding all of the counts associated with that circle under random selection (N=499)

Point Pattern Data: Detecting Clusters

- The circle in these cases is considered a circular uniform kernel
- In kernel estimation, the kernel is centered on the data locations, in scan statistics, the circle is centered on the grid

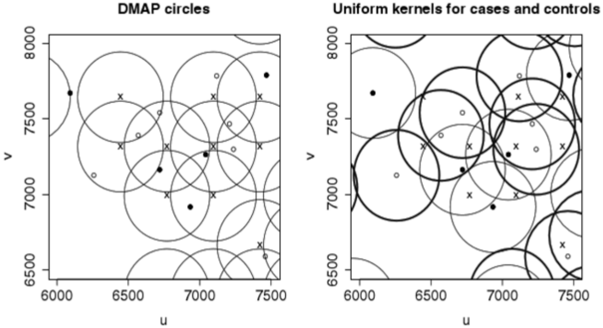


FIG. 6.8 Equivalence between the case/control ratio within circles surrounding grid points (left-hand plot) and the ratio of intensity (density) functions based on circular uniform kernels (right-hand plot). Case locations appear as filled small circles, control locations as open small circles, and grid points as "×" symbols. In the left-hand plot, large circles represent radii of 300 units around each grid point. In the right-hand plot, dark circles represent control kernel radii, and lighter circles represent control kernel radii (both 300 units).

Point Pattern Data: Spatial Scan Statistics

- A scan statistics involves the definition of a moving window and a statistical comparison measurement (count or rate) within the window to the same measurement outside the window.
- Kulldorff (1995, 1997) defines a spatial scan statistic that is similar to the geographical analysis machine, but with an inferential framework.
- Scan statistics tend to consider circular windows with variable radii ranging from the smallest distance between a pair of cases to the user-defined upper bound.
- The circles can be centered on either grid locations (like earlier methods)or the set of locations. Different results will be seen depending on what is chosen.

Point Pattern Data: Spatial Scan Statistics

Setup:
Let $N_{1,in}$ represent the number of case locations and $N_{in} = N_{0,in} + N_{1,in}$ be the total number of people at risk (or number of case and control locations) inside a particular window.
Let $N_{1,out}$ represent the number of case locations and $N_{out} = N_{0,out} + N_{1,out}$ be the total number of people at risk (or number of case and control locations) outside the window.
The test statistic is:

$$T_{scan} = \max(\frac{N_{1,in}}{N_{in}})^{N_{1,in}}(\frac{N_{1,out}}{N_{out}})^{N_{1,out}} I(\frac{N_{1,in}}{N_{in}} > \frac{N_{1,out}}{N_{out}})$$

I(.) is the indicator function (i.e. we only maximize over windows where the observed rate inside the window exceeds that outside the window)

Point Pattern Data: Spatial Scan Statistics

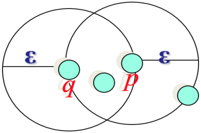
- The maximum observed likelihood ratio statistic provides a test of overall general clustering and an indication of the most likely clusters with significance determined by Monte Carlo testing of the constant risk hypothesis.
- SaTScan is a software package that enables this.
- There is also a new R package called scanstatistics that looks promising `https://cran.r-project.org/web/packages/scanstatistics/vignettes/introduction.html`

Point Pattern Data: Density Based Clustering

- Density-based spatial clustering is a data clustering algorithm that falls under "machine learning" techniques.
- It was popularly implemented in 1996 by Ester et al as "DBSCAN" (Proceedings of the Second International Conference on Knowledge Discovery and Data Mining (KDD-96): A density-based algorithm for discovering clusters in large spatial databases with noise).
- Density-based approaches like DBSCAN model clusters as high-density clumps of points.
- It is different than other clustering algorithms such as k-means clustering:
  - In k-means clustering, each cluster is represented by a centroid, and points are assigned to whichever centroid they are closest to.
  - In DBSCAN, there are no centroids, and clusters are formed by linking nearby points to one another.
  - In k-means you have to choose the number of clusters before running the algorithm.
  - In DBSCAN you choose the minimum number of points that must be in a cluster of radius ϵ to consider it a cluster.
  - Clusters from density-based algorithms are arbitrary in shape.

Point Pattern Data: Density Based Clustering

The ϵ defines the neighbourhood, where points within ϵ radius from another point are considered part of a cluster as long as it fulfills that there are a certain number of MinPts.



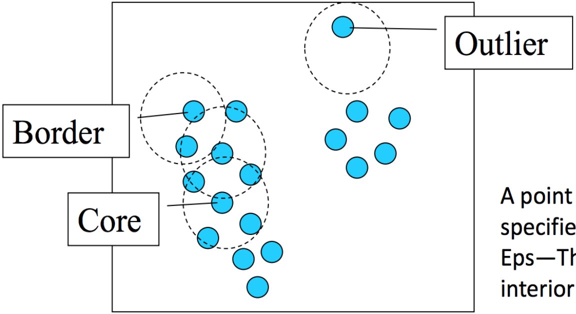
ε-Neighborhood of *p*

ε-Neighborhood of *q*

Density of p is “high” (MinPts = 4)

Density of q is “low” (MinPts = 4)

Point Pattern Data: Density Based Clustering



ε = 1unit, MinPts = 5

Given ε and *MinPts*, categorize the objects into three exclusive groups.

A point is a core point if it has more than a specified number of points (MinPts) within Eps—These are points that are at the interior of a cluster.

A border point has fewer than MinPts within Eps, but is in the neighborhood of a core point.

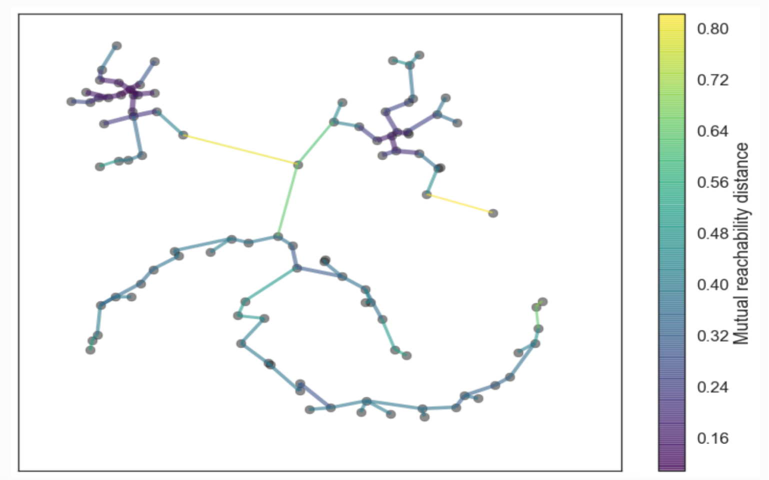
A noise point is any point that is not a core point nor a border point.

Point Pattern Data: Density Based Clustering

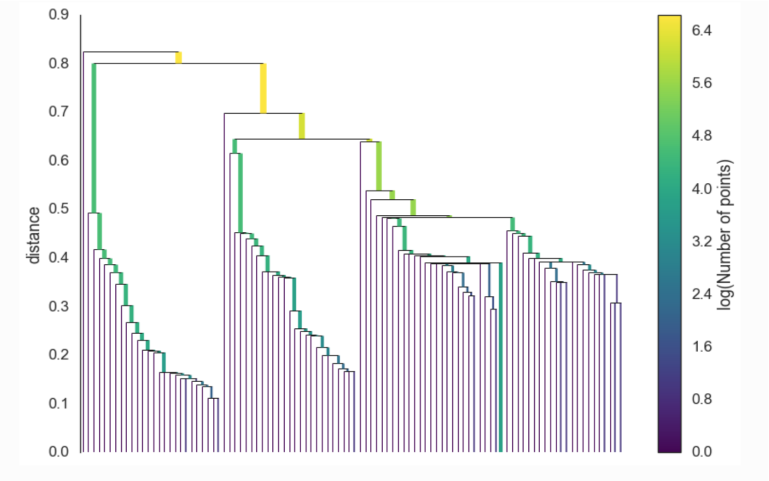
Here is a good visualization of DBSCAN results:
https://www.naftaliharris.com/blog/visualizing-dbscan-clustering/
A better version in Hierarchical DBSCAN, where we do not need to set the ϵ neighbourhood. With HDBSCAN we do set the minimum number of points that we wish to have in a cluster (2 to n). A larger MinPts means larger clusters.

- HDBSCAN uses the concept of mutual reachability, where we look at distances that connect all of the points
- A tree (hierarchy) is formed based on these distances

Point Pattern Data: Density Based Clustering



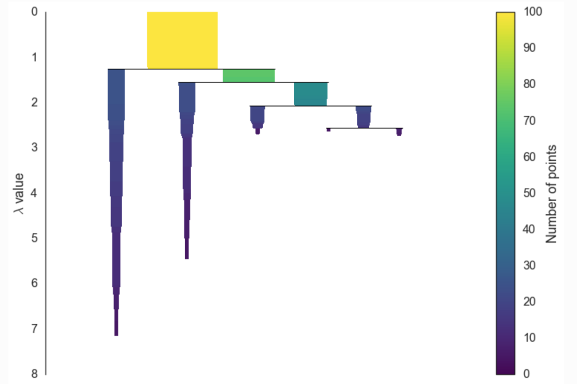
Point Pattern Data: Density Based Clustering



If we cut the tree at a given distance (ϵ) that is giving us the same estimate as DBSCAN

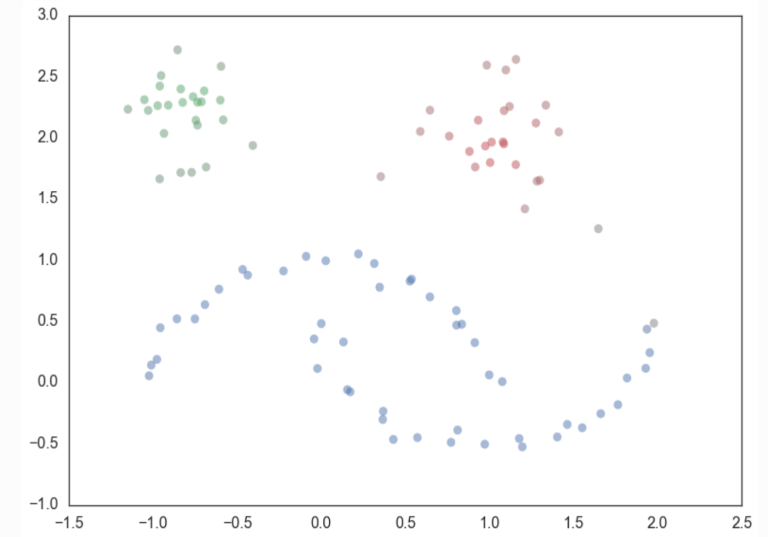
Point Pattern Data: Density Based Clustering

The tree has to be condensed somehow and provide us the main clusters. Using the minimum cluster size the algorithm walks through the hierarchy and at each split asks if one of the new clusters created by the split has fewer points than the minimum cluster size.



Point Pattern Data: Density Based Clustering

In this example with min number of points of 5, there are 3 clusters chosen


3.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
2.0
2.5