Simulation of Typical Modulated Poisson-Voronoi Cells with Applications to Telecommunication Network Modelling

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Consider telecommunication networks on nationwide scales => population intensities

Estimation of population intensities in Germany
Motivation

- Models needed that can reflect a great variety of scenarios
- First step analysis of modulated poisson point processes w.r.t.
  - corresponding Voronoi tessellation
  - simulation of typical cell
  - cost analysis
- Voronoi cells can reflect serving zones in the access network
- Points might also be considered as locations of antennas in a mobile scenario
Modulated Poisson-Voronoi tessellations

Based on a Boolean model $\Psi$ that has circular grains with fixed radii

Realisation of a Poisson process
Modulated Poisson-Voronoi tessellations

Based on a Boolean model $\Psi$ that has circular grains with fixed radii

Realisation of a Boolean model $\Psi$
Consider a (planar) Cox point process \( X \) with (random) intensity measure \( \Lambda_X(.) \) given by

\[
\Lambda_X(dx) = \begin{cases} 
\lambda_1 dx & \text{if } x \in \Psi \\
\lambda_2 dx & \text{if } x \notin \Psi 
\end{cases}
\]

\( X \) is called a \( \Psi \)-modulated Poisson process.

Consider corresponding Voronoi tessellation \( \tau_X \).

Stationary model

Allows modelling instationarities
Modulated Poisson-Voronoi tessellations

Realisations of modulated Poisson-Voronoi tessellations
Modulated Poisson-Voronoi tessellations

- 4 model parameters
  - Intensity $\beta$ of the germs of $\Psi$
  - Radius $R$ of the circular grains of $\Psi$
  - Intensities $\lambda_1$ and $\lambda_2$ of $X$

- Derived characteristics ($\Psi$ stationary)
  - Coverage probability
    \[ p = P(0 \in \Psi) = 1 - \exp(\beta \pi E(R^2)) \]
  - Intensity of the modulated Poisson process
    \[ \lambda_X = p\lambda_1 + (1-p)\lambda_2 \]
Modulated Poisson-Voronoi tessellations

Scaling invariance

- Initial model has 4 parameters \((\lambda_1, \lambda_2, \beta, R)\)
- These 4 parameters can be reduced to 3 parameters
  \(\kappa = (\kappa_1, \kappa_2, \kappa_3)^t\) using scaling invariance properties
  \(\kappa_1 = p\)
  \(\kappa_2 = \lambda_1 / \beta\)
  \(\kappa_3 = \lambda_2 / \beta\)

Same random structure but different scale
Modulated Poisson-Voronoi tessellations

Some special cases

- Poisson-Voronoi \((\lambda_1 = \lambda_2)\)
or \(p = 0\) or \(p = 1\)

- Swiss-cheese \((\lambda_1 = 0)\)
Modulated Poisson-Voronoi tessellations

Some special cases

- Inner-city ($\lambda_2 = 0$)
Simulation of Typical Cell

- Typical (Voronoi-)cell $\Xi^*$ is drawn uniformly from all cells
- Some functionals of interest
  - Area $\nu_2(\Xi^*)$
  - Perimeter $\nu_1(\partial \Xi^*)$
  - Number of vertices $\eta(\Xi^*)$
- Cost functional(s)
  - $c(\Xi^*) = \int_{\Xi^*} ||u|| \, du$
  - $c'(\Xi^*) = \lambda_X \int_{\Xi^*} ||u|| \, du$
- Moments and distribution
Simulation of Typical Cell

- Advantages compared to large sampling window methods
  - No edge effect problems
  - Simulation easily partitionable (=> parallelisation)
  - No memory problems

- Drawbacks
  - Simulation not clear
  - Efficient stopping criteria needed
    - Initial cell
    - Typical cell
Simulation of Typical Cell

Algorithm

- Simulation based on representation of typical cell
  - \( P_o = \delta\delta_o \ast P_{Q_o} \)
  - \( \delta\delta_o \) distribution of a (deterministic) point in \( o \)
  - \( Q_o \) Palm distribution of \( \Lambda_X \) at \( o \)
  - \( P_{Q_o} \) distribution of a Cox process with measure \( Q_o \)

- Additional point is added to \( X \) in \( o \)
- Coverage probability \( p_c = P(o \in \Psi || o \in X) \neq p \)
  - \( p_c = \frac{p\lambda_1}{p\lambda_1 + (1-p)\lambda_2} \)

- Alternating radial simulation of \( X \) and \( \Psi \)
  - For \( X_i \in X \) it must be known if \( X_i \in \Psi \)
  - \( \Rightarrow \) Simulate \( \Psi_j \) until \( ||\Psi_j|| > ||X_i|| + R \)
Simulation of Typical Cell

Algoirthm

1. Put point $X_0 \in X$ in $o$

2. Determine if $o \in \Psi$ using $p_c$

3. Simulate grains $\Psi_j$ of $\Psi$
   - Germ radially Poisson (intensity $\beta$)
   - Conditional to $o \in \Psi$ for $\Psi_o$

4. Simulate points $X_i \in X$
   - Radially Poisson simulation
   - Intensity $\lambda_{max} = \max \{\lambda_1, \lambda_2\}$
   - Thinning by $\lambda_2/\lambda_1$ or by $\lambda_1/\lambda_2$
Point $X_0$ in origin
Simulation of Typical Cell

Algorithm

First grain with midpoint $\Psi_0$
Simulation of Typical Cell

Algorithm

For $X_2$ more information about $\Psi$ is needed
Simulation of Typical Cell

Algorithm

Further alternating simulation of $X$ and $\Psi$
Simulation of Typical Cell

Algorithm

Stopping criterion for initial cell
Construction of initial cell using bisectors
Simulation of Typical Cell

Alteration of Initial Cell

Initial modulated Cox-Voronoi cell
First alteration of initial cell
Simulation of Typical Cell

Alteration of Initial Cell

Second alteration of initial cell
Realisation of typical cell
Consider $R \sim U[r - \delta, r + \delta]$ instead of $R$ fixed

Algorithm has to be modified slightly w.r.t.

- simulation of $\Psi_0$
- amount of information about $\Psi$ needed for $X_i$

Similar modifications possible for other distributions of $R$ (finite support)
Tests in this context means testing of software with random outputs

- Deterministic (classical) tests hardly usable
- Random tests based on statistical test methods

Tests based on known theoretical formulae

- \( E(\nu_2(\Xi^*)) = \frac{1}{\lambda_X} \)
- \( E(\eta(\Xi^*)) = 6 \)
- \( E(c(\Xi^*)) = \frac{1}{2^{\frac{3}{2}}\lambda^\frac{3}{4}} \) in the Poisson-Voronoi case

Tests based on scaling invariance properties
Numerical Results

- Several scenarios
  - Poisson-Voronoi
  - Swiss-cheese
  - Random radii

- Functionals considered
  - Area, perimeter, number of vertices

- Cost functional(s)
  - $c(\Xi^*) = \int_{\Xi^*} \|u\| \, du$
  - $c'(\Xi^*) = \frac{1}{E(\nu_2(\Xi^*))} \int_{\Xi^*} \|u\| \, du = \lambda_X \int_{\Xi^*} \|u\| \, du$
Numerical Results

Transition to Swiss Cheese

- We simulated $n = 2000000$ typical cells for each case
- Parameter values
  - $p = 0.6, \beta = 0.2 \Rightarrow R = 1.20761$
  - $\lambda_X = 12$
  - $\lambda_1 \to 0$
  - $\lambda_2 = \frac{\lambda_X - p\lambda_1}{1 - p} = 30 - \frac{3}{2}\lambda_1$
- $\lambda_X = 12 \Rightarrow E(\nu_2(\Xi^*)) = \frac{1}{12}$ constant
Numerical Results

Transition to Swiss Cheese

\[ \lambda_1 = 10, \lambda_2 = 15 \]

\[ \lambda_1 = 0, \lambda_2 = 30 \]
### Numerical Results

**Transition to Swiss Cheese**

<table>
<thead>
<tr>
<th>$\lambda_1$</th>
<th>$\lambda_2$</th>
<th>$\hat{E}c'(\Xi^*)$</th>
<th>$\hat{E}c(\Xi^*)$</th>
<th>$\hat{E}\nu_2(\Xi^*)$</th>
<th>$\hat{E}\nu_1(\partial\Xi^*)$</th>
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<tr>
<td>12</td>
<td>12</td>
<td>0.14437</td>
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<td>0.47946</td>
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<td>1.03903</td>
</tr>
</tbody>
</table>

Estimates of first moments for $\lambda_1 \rightarrow 0$
Numerical Results

Transition to Swiss Cheese

\[
\lambda_1 = 12, \quad \lambda_2 = 12
\]

\[
\lambda_1 = 6, \quad \lambda_2 = 21
\]

Perimeter of the typical cell
Numerical Results
Transition to Swiss Cheese

$\lambda_1 = 0.05, \lambda_2 = 29.95$

$\lambda_1 = 0, \lambda_2 = 30$

Perimeter of the typical cell
First step towards modelling of nationwide scale networks

Modifications
- Grain shapes
- Random grain parameter
- Finite support
- Other distributions
- Germ distribution
Variable population densities

Equipment and population placed according to two modulated Poisson process $X_H$ and $X_L$ with same underlying Boolean model $\Psi$

Cost functional mean distance to the nearest nuclei

Usage of Neveu’s formula

$$c^*_{LH} = \mathbb{E}_{X_L}(||\tilde{X}_n - N(\tilde{X}_n)||) = \frac{\lambda H}{\lambda_L} \mathbb{E}_{X_H} \int_{\Xi^*} ||u|| \Lambda_L(du)$$
Summary and Outlook

Extensions

- Multi-modulated Poisson-Voronoi
- Boolean models $\Psi_1, \ldots, \Psi_n$
- Corresponding intensity measures $\Lambda_1, \ldots, \Lambda_n$
- Larger variability

- Modulated Poisson-Voronoi connected with line-based Cox-Voronoi
  - Equipment based on line segments
  - According to linear Poisson processes
  - Segments inside Boolean model
  - Inter-city connections
Modulated Poisson-Delaunay (=> connection length between neighboring Voronoi cells)
