

Estimation and edge correction in the Renshaw-Särkkä model

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- The process
- Simulations
- Estimation
- Data
- Edge effects
- Future work

The process - birth and growth

- New individuals **arrive** to the region of interest, $W \subseteq \mathbb{R}^d$, according to a **Poisson process** with intensity $\nu(W)\alpha$.
- Each individual is assigned a **position** $\mathbf{x}_i \sim \text{Uni}(W)$ together with an **initial size (mark)** $m_i(t_0^i) = \varepsilon_i$ ($t_0^i =$ arrival time of individual i).
- An individual **changes its size**, deterministically, according to

$$dm_i(t) = f(m_i(t); \Theta)dt + \sum_{\substack{j \neq i \\ j \in \Omega_t}} h(m_i(t), m_j(t), \|\mathbf{x}_i - \mathbf{x}_j\|; \Theta)dt$$

where

- Ω_t index set comprising the individuals alive at time t
- $f(\cdot)$ individual growth function
- $h(\cdot)$ spatial interaction function ($\|\cdot\|$ Euclidean distance)
- Θ set of model parameters

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Possible death scenarios in the model:

- Individuals **die naturally** according to a **death process** with intensity $\mu(m_i(t))$, $i \in \Omega_t$, i.e.

$$\mathbb{P}[\text{Individual } i \text{ dies naturally in } (t, t + dt) | m_i(t)] = \mu(m_i(t)) dt + o(dt)$$

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The process - model modifications

One possibility is to consider interactive death to occur when $m_i(t) < 0$.

Other options:

- $dm_i(t) < 0 \Rightarrow$ individual is considered **dead** through competition
- $dm_i(t) < 0 \Rightarrow$ individual **loses its individual growth** and is considered dead through competition when $m_i(t) < 0$.

Some natural suggestions for the natural death:

- $\mu(m_i(t)) \equiv \mu$
- $\mu(m_i(t)) = \mu \frac{m_i(t)}{1+m_i(t)}$
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Individual growth functions:

- **Linear growth:** $f(m_i(t), \lambda_i, K_i) = \lambda_i \left(1 - \frac{m_i(t)}{K_i}\right)$
- **Logistic growth:** $f(m_i(t), \lambda_i, K_i) = \lambda_i m_i(t) \left(1 - \frac{m_i(t)}{K_i}\right)$

where λ_i is the **growth rate** and K_i is the **carrying capacity**.

The process - interaction functions

Interaction functions:

- **Symmetric interaction:**

$$h(m_i(t), m_j(t), \|\mathbf{x}_i - \mathbf{x}_j\|, \Theta) = -c \mathbb{I} \{ \|\mathbf{x}_i - \mathbf{x}_j\| < r(m_i(t) + m_j(t)) \}$$

where $\Theta = \{r, c\}$, $r > 0$ and $\mathbb{I}\{\cdot\}$ denotes the indicator function.

- **Area interaction:**

$$h(m_i(t), m_j(t), \|\mathbf{x}_i - \mathbf{x}_j\|, \Theta) = -c \frac{\nu [B(\mathbf{x}_i, rm_i(t)) \cap B(\mathbf{x}_j, rm_j(t))]}{\pi r^2 m_i(t)^2}$$

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 $x_i \sim \text{Uni}(a, b)$ and $y_i \sim \text{Uni}(c, d)$
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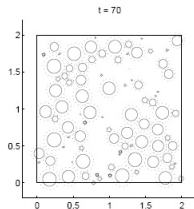
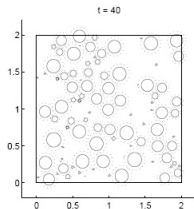
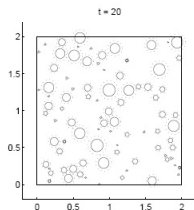
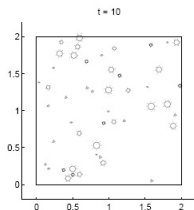
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Realisation:

$\alpha = 1.5$, $\mu = 0.02$, $\lambda = 0.2$, $K = 0.1$, $c = 0.1$, $r = 1.5$,
 $\varepsilon_i = 0.01$, $dt = 0.01$

The dotted rings are the **influence zones** $B(\mathbf{x}_i, r m_i(t))$.



Estimation: α and μ

Let $N_t = \#\{\text{individuals observed up until } t\}$ and T the final sample point of the process. Then

$$\hat{\alpha} = \frac{N_T}{\nu(W) T}$$

- If $\mu(m_i(t)) \equiv \mu$ then we use the ML estimator

$$\hat{\mu} = n_T / \left(\sum_{i=1}^{n_T} t_i + \sum_{j=1}^{m_T} s_j \right)$$

where t_1, \dots, t_{n_T} and s_1, \dots, s_{m_T} denote, respectively, the recorded lifetimes of the n_T individuals who **died from natural causes** by time T and the m_T individuals **still alive** at time T .

- If $\mu(m_i(t)) = \mu \frac{1}{1+m_i(t)}$ we numerically maximize

$$\begin{aligned} \log L(\mu) &\approx \sum_{i=1}^{n_t} \log \left\{ \int_0^{\infty} \mu \frac{1}{1+x} e^{-\frac{\mu}{1+x} t_i} \widehat{f_{m(t_i)}(x)} dx \right\} \\ &+ \sum_{j=1}^{m_t} \log \left\{ \int_0^{\infty} e^{-\frac{\mu}{1+x} s_j} \widehat{f_{m(T)}(x)} dx \right\} \end{aligned}$$

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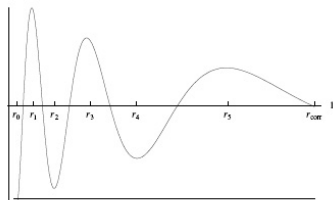
Determine the least squares estimates $\hat{\lambda}$, \hat{K} , \hat{r} , and \hat{c} by minimizing

$$S(\lambda, K, r, c) := \sum_{t=1}^{T-1} \sum_{i \in \Omega_t} [\tilde{m}_i(t+1; \lambda, K, r, c) - m_i(t+1)]^2$$

with respect to λ , K , r , and c (Naturally the time increments do not need to have size 1). $\tilde{m}_i(t+1; \lambda, K, r, c)$ is the predicted value of $m_i(t+1)$ based on $m_i(t)$ and $dm_i(t)$.

The pair correlation function

The (planar) **pair correlation function** $g(r) = \frac{K'(r)}{2\pi r}$ has the typical appearance



- r_0 = minimum inter-point distance; hard core distance
- r_1 = range of most frequent short inter-point distance; distance from typical point to near neighbours
- r_2 = distance from typical point to regions with a small number of points beyond the nearest neighbours
- r_3 = range of most frequent longer inter-point distance; distance from typical point to regions with further

Bounds and starting values

From $h(m_i(t), m_j(t), \|\mathbf{x}_i - \mathbf{x}_j\|, r, c) = -c \frac{\nu(B(\mathbf{x}_i, rm_i(t)) \cap B(\mathbf{x}_j, rm_j(t)))}{\pi r^2 m_i(t)^2}$ one can see that r and c are correlated which causes biased estimates.

For some fixed t a typical influence zone radius is given by $r\mathbb{E}[m_i(t)]$. So

$$2r\mathbb{E}[m_i(t)] + \mathbb{E}[m_i(t)] \leq r_3 \quad \implies \quad r \leq \frac{r_3 - \mathbb{E}[m_i(t)]}{2\mathbb{E}[m_i(t)]}$$

Since two trees do not intersect we get that $1 < r \leq \frac{r_3 - \mathbb{E}[m_i(t)]}{2\mathbb{E}[m_i(t)]}$. We use as starting values in our estimation (data sampled at t_1, \dots, t_n)

$$\hat{r}_0 = \left(\frac{r_3 - \mathbb{E}[m_i(t)]}{2\mathbb{E}[m_i(t)]} + 1 \right) / 2$$

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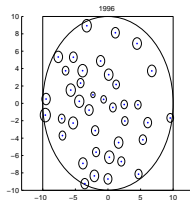
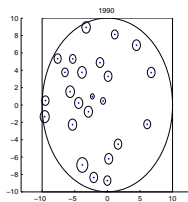
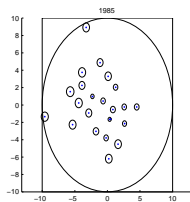
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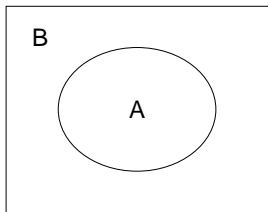
Data: Swedish pines (data set under investigation)



Correcting for edge effects

Data $\mathbb{X} = \left\{ \mathbf{x}_1(t_j), \dots, \mathbf{x}_{n_{t_j}}(t_j) \right\}_{j=1}^n$ is sampled in the circular region A .

$B = A^c$ represents the rest of our region of interest.



Correcting for edge effects: Rotations

- 1 Estimate parameters from \mathbb{X} to generate the parameter set $\hat{\Theta}_* = \{\hat{\mu}_*, \hat{\alpha}_*, \hat{\lambda}_*, \hat{K}_*, \hat{r}_*, \hat{c}_*\}$.
- 2 Simulate the process on $W = A \cup B$, based on $\hat{\Theta}_*$ and t_1, \dots, t_n (where W is wrapped onto a torus).
- 3 For t_1, \dots, t_n , remove what has been simulated in A .
- 4 For the angles $\theta_1, \dots, \theta_k$, $0 \leq \theta_i < 2\pi$, $\forall i = 1, \dots, k$, perform counterclockwise rotations of \mathbb{X} around the center of A to get $\mathbb{X}_{\theta_1}, \dots, \mathbb{X}_{\theta_k}$.
- 5 For each $i = 1, \dots, k$, put together the data simulated in B with \mathbb{X}_{θ_i} and perform estimation based on \mathbb{X}_{θ_i} only, but still letting the individuals in B affect the ones in \mathbb{X}_{θ_i} and vice versa (where W is wrapped onto a torus).
This gives us the estimates $\hat{\Theta}_i$, $i = 1, \dots, k$.
- 6 Let our final estimates be given by
$$\hat{\Theta} = \text{median} \left(\hat{\Theta}_{\theta_1}, \dots, \hat{\Theta}_{\theta_k} \right).$$

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Correcting for edge effects: Simultaneous growth

- 1 Estimate parameters from \mathbb{X} to generate the parameter set $\hat{\Theta}_* = \{\hat{\mu}_*, \hat{\alpha}_*, \hat{\lambda}_*, \hat{K}_*, \hat{r}_*, \hat{c}_*\}$.
- 2 For each time interval $(t_{j-1}, t_j]$ we get n_j new individuals. Simulate $Uni(t_{j-1}, t_j)$ -distributed birth times $b_1^j < \dots, b_{n_j}^j$ and assign these to the individuals which have arrived in $(t_{j-1}, t_j]$ in such an order that the largest individual gets the smallest time, going upwards until the smallest individual has received the largest time.
- 3 Simulate the process on $W = A \cup B$, based on $\hat{\Theta}_*$ and t_1, \dots, t_n (where W is wrapped onto a torus) where we let each data individual enter at its birth time and grow linearly until its death time, if it dies before T , or until T , if it is still alive at T .
- 4 Remove everything found in A at all the sample times (we are left with what has been simulated in B) and replace it by \mathbb{X} .
- 5 Estimate from \mathbb{X} (i.e. from A) but let the individuals in B and A affect each other.

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- ① Estimation/edge correction of multiple (homogeneous) data sets simultaneously
- ② Maximum likelihood estimation
- ③ Individual (stochastic) parameters
- ④ Incorporation of other individual growth functions