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Markovianity in space and time

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Markovianity in Space and Time

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Dedicated to Professor Mike Keane
on the occasion of his 65th birthday

ABSTRACT

Markov chains in time, such as simple random walks, are at the heart of probability. In space, due to the absence of an obvious definition of past and future, a range of definitions of Markovianity have been proposed. In this paper, after a brief review, we introduce a new concept of Markovianity that aims to combine spatial and temporal conditional independence.

1. FROM MARKOV CHAIN TO MARKOV POINT PROCESS, AND BEYOND

Markov chains are one of the most fundamental and intensively studied processes in probability, see e.g. [2]. If we restrict ourselves to a bounded time horizon, say $0, 1, \ldots, N$ for some $N \in \mathbb{N}$, a discrete Markov chain is a random vector $(X_0, \ldots, X_N)$ with values in some denumerable set $L \neq \emptyset$ for which

$$\mathbb{P}(X_i = x_i \mid X_0 = x_0; \ldots; X_{i-1} = x_{i-1}) = \mathbb{P}(X_i = x_i \mid X_{i-1} = x_{i-1}) \qquad (1.1)$$

for all $1 \leq i \leq N$ and all $x_j \in L$, $j = 0, \ldots, i$. In words, the Markov property (1.1) states that the future and the past are conditionally independent given the present. The right hand side is referred to as the *transition probability* at time i from x_{i-1} to x_i. If $\mathbb{P}(X_i = x_i \mid X_{i-1} = x_{i-1}) = p(x_{i-1}, x_i)$ does not depend on i, the Markov chain is said to be *stationary*. By the product rule, the joint distribution can be factorised as

$$\mathbb{P}(X_0 = x_0; \ldots; X_N = x_N) = \mathbb{P}(X_0 = x_0) \prod_{i=1}^{N} p(x_{i-1}, x_i). \qquad (1.2)$$

For example, for the *simple random walk* on $L = \mathbb{Z}^2$, $p(x, y) = 1/4$ if x and y are horizontally or vertically adjacent in L, that is, $||x - y|| = 1$, and zero otherwise [25]. To tie in with a more general concept of Markovianity, the time slots $i - 1$, $i + 1$ (if within the finite horizon) may be called *neighbours* of i, $i \in \{0, \ldots, N\}$.

The concept of Markovianity plays an important role in space as well as in time, especially in image analysis and statistical physics. Since, in contrast to the setting in the previous paragraph, there is no natural order, a symmetric, reflexive *neighbourhood* relation $\sim$ must be defined on the domain of definition, which we assume to be a finite set I. The generic example is a rectangular grid $I \subseteq \mathbb{Z}^2$ with $i \sim j$ if and only if $||i - j|| \leq 1$. Then, a discrete *Markov random field* with respect to $\sim$ is a random vector $X = (X_i)_{i \in I}$, with values of the components X_i in some denumerable set $L \neq \emptyset$, that satisfies the *local Markov property*

$$\mathbb{P}(X_i = x_i \mid X_j = x_j, j \neq i) = \mathbb{P}(X_i = x_i \mid X_j = x_j, j \in \partial(i))$$

where $\partial(i) = \{j \in I \setminus \{i\} : j \sim i\}$ is the set of neighbours of i. The expression should be compared to (1.1); indeed a Markov chain is a Markov random field on $I = \{0, 1, \ldots, N\}$ with $i \sim j$ if and only if $|i - j| \leq 1$, $i, j \in I$. To state the analogue of (1.2), define a *clique* to be a set of sites C such that for all $i, j \in C$ these sites are neighbours, that is $i \sim j$. By default, the empty set is a clique. If we assume for simplicity that the joint probability mass function of the random vector X has no zeroes, it defines a Markov random field if and only if it can be factorised as

$$\mathbb{P}(X_0 = x_0; \ldots; X_N = x_N) = \prod_{\text{cliques } C} \varphi_C(x_j, j \in C) \tag{1.3}$$

for some *clique interaction functions* $\varphi_C(\cdot) > 0$. Models of this kind are very popular in statistical physics under the name *Gibbs random field*. An early example is the *Ising model* for spins in a magnetic field [15]. For this model on a 2D grid with horizontal and vertical neighbours, $L = \{-1, 1\}$ for the two spin types. The interaction functions are $\varphi_{\{i\}}(x_i) = e^{\alpha x_i}$ and $\varphi_{\{i,j\}}(x_i, x_j) = e^{\beta x_i x_j}$, with $\varphi_\emptyset$ set to the unique constant for which the right hand side of (1.3) is a probability mass function. The constant α reflects the external magnetic field and influences the frequencies of the two spin types. For $\beta > 0$, neighbouring sites tend to agree in spin, for $\beta < 0$, they tend to have different spins. The product form allows for easy interpretation and definition of new models. For further details, the reader is referred to [11].

The next step is to leave discrete domains and move into Euclidean space. Thus, let $D \subset \mathbb{R}^d$ be a disc, rectangle or other bounded set of positive volume. A realisation of a *Markov point process* on D is a subset $\mathbf{x} = \{x_1, \ldots, x_n\}$ of D with random, finite $n \geq 0$. Again define a reflexive, symmetric neighbourhood relation $\sim$, for instance by $x \sim y$ if and only if $||x - y|| \leq R$ for some $R > 0$. Note that each point has uncountably many potential neighbours, in contrast to the discrete case. Moreover, the probability of finding a point at any particular location $a \in D$ will usually be 0, so densities rather than probability mass functions are needed. A suitable dominating measure is the homogeneous Poisson process (see e.g. [17]), because of its lack of spatial interaction. Indeed, given such a Poisson process places n points in D, the locations are i.i.d. and uniformly distributed over D. If desirable, one could easily attach *marks* to the points, for example a measurement or type label of an object located at

the point. Doing so, the domain becomes $D \times M$, where M is the mark set, and each x_i can be written as (d_i, m_i). In this set-up, a *Markov point process* X is defined by a density $f(\cdot)$ that is hereditary in the sense that $f(\mathbf{x}) > 0 \Rightarrow f(\mathbf{y}) > 0$ for all configurations $\mathbf{y} \subseteq \mathbf{x}$ and satisfies [26, 18] the *local Markov condition*, that is, whenever $f(\mathbf{x}) > 0$ the ratio

$$\frac{f(\mathbf{x} \cup \{u\})}{f(\mathbf{x})} \tag{1.4}$$

depends only on u and $\{x_i : u \sim x_i\}$. Note that since realisations $\mathbf{x}$ of X are *sets* of (marked) points, $f(\cdot)$ is symmetric, i.e. invariant under permutations of the x_i that constitute $\mathbf{x}$. An example of a process satisfying the above condition is the *hard core model*, a homogeneous Poisson process conditioned to contain no pair of points that are closer than R to one another. A factorisation is provided by the *Hammersley–Clifford theorem* which states [1, 26] that a marked point process with density $f(\cdot)$ is Markov if and only if

$$f(\mathbf{x}) = \prod_{\text{cliques } \mathbf{y} \subseteq \mathbf{x}} \varphi(\mathbf{y}) \tag{1.5}$$

for some non-negative, measurable interaction functions $\varphi(\cdot)$. For the hard core model, $\varphi(\{x, y\}) = \mathbf{1}\{\|x - y\| > R\}$, $\varphi(\mathbf{y}) \equiv 1$ for singletons and configurations $\mathbf{y}$ containing three or more points. The interaction function for the empty set acts as normalising constant to make sure that $f(\cdot)$ integrates to unity.

Although Markov point processes are useful modelling tools [18], the assumption of permutation invariance may be too restrictive. For instance in image interpretation, occlusion of one object by another may be dealt with by an ordering of the objects in terms of proximity to the camera [20], or in scene modelling various kinds of alignment of the parts that make up an objects may be modelled by means of non-symmetric neighbour relations [22]. Non-symmetric densities also arise naturally when local scale and intensity is taken into account by transforming the conditional intensity of a homogeneous template process, see [14].

In stark contrast to the vast literature on spatial point processes, sequential patterns have not been studied much. Indeed, an analogue to the theory of Markov point processes does not exist in the non-symmetrical setting. The present paper fills this gap.

2. DEFINITIONS AND NOTATION

This paper is concerned with *finite sequential spatial processes*. Realisations of such a process at least consist of a finite sequence

$$\vec{\mathbf{x}} = (x_1, \ldots, x_n), \qquad n \in \mathbb{N}_0$$

of points in some bounded subset D of the plane. Additionally, to each point x_i, a mark m_i in some complete, separable metric space, say M, may be attached. The mark may be a discrete type label, a real valued measurement taken at each location, or a vector of shape parameters to represent an object located at x_i. Thus, we may write

$$\vec{\mathbf{y}} = (y_1, \ldots, y_n) = ((x_1, m_1), \ldots, (x_n, m_n)), \qquad n \in \mathbb{N}_0$$

for the configuration of marked points, and shall denote the family of all such configurations by N^{f}.

As an aside, the plane $\mathbb{R}^2$ may be replaced by $\mathbb{R}^d$ or any other complete separable metric space, equipped with the Borel σ-algebra and a finite diffuse Borel measure.

The distribution of a finite sequential spatial process may be defined as follows. Given a finite diffuse Borel measure $\mu(\cdot)$ on $(D, \mathcal{B}_D)$ so that $\mu(D) > 0$, usually Lebesgue measure, and a mark probability measure $\mu_M(\cdot)$ on M equipped with its Borel σ-algebra $\mathcal{M}$, specify

1. a probability mass function q_n, $n \in \mathbb{N}_0$, for the number of points in D;

2. for each n, a Borel measurable and $(\mu \times \mu_M)^n$-integrable joint probability density $p_n(y_1, \ldots, y_n)$ for the sequence of marked points $y_1, \ldots, y_n \in D \times M$, given it has length n.

Alternatively, a probability density $f(\cdot)$ may be specified directly on $N^{\mathrm{f}} = \cup_{n=0}^{\infty}(D \times M)^n$, the space of finite point configurations in D with marks in M, with respect to the reference measure

$$\nu(F) = \sum_{n=0}^{\infty} \frac{e^{-\mu(D)}}{n!} \int_D \int_M \cdots \int_D \int_M \mathbf{1}\left\{(y_1, \ldots, y_n) \in F\right\} d\mu \times \mu_M(y_1) \ldots d\mu \times \mu_M(y_n)$$

defined for F in the σ-algebra on finite marked point sequences generated by the product Borel σ-fields on $(D \times M)^n$. In words, $\nu(\cdot)$ corresponds to a random sequence of Poisson length with independent components distributed according to the normalised reference measure $\mu(\cdot)\,\mu_M(\cdot)/\mu(D)$.

It is readily observed that

$$q_n = \frac{e^{-\mu(D)}}{n!} \int_D \int_M \cdots \int_D \int_M f(y_1, \ldots, y_n)\, d\mu \times \mu_M(y_1) \ldots d\mu \times \mu_M(y_n)$$

$$p_n(\vec{y}) = \frac{e^{-\mu(D)}}{n!\,q_n} f(\vec{y})$$

for each $n \in \mathbb{N}$, and $q_0 = \exp(-\mu(D))\,f(\emptyset)$. Reversely, if the length $n(\vec{y})$ of $\vec{y}$ is n,

$$f(\vec{y}) = e^{\mu(D)}\,n!\,q_n\,p_n(\vec{y}).$$

Note that neither $f(\cdot)$ nor the $p_n(\cdot, \ldots, \cdot)$ are required to be symmetric [3, Ch. 5].

We are now ready to define and analyse a Markov concept for random sequences in the plane. To do so, we begin by defining the *sequential conditional intensity*

$$\lambda_i((x,m)|\vec{y}) := \frac{f(s_i(\vec{y}, (x,m)))}{(n+1)\,f(\vec{y})} \quad \text{if } f(\vec{y}) > 0$$

$$:= 0 \quad \text{otherwise} \tag{2.1}$$

for inserting $(x, m) \notin \vec{y}$ at position $i \in \{1, \ldots, n+1\}$ of $\vec{y} = (y_1, \ldots, y_n)$. Here $s_i(\vec{y}, (x,m)) = (y_1, \ldots, y_{i-1}, (x,m), y_i, \ldots, y_n)$. The overall conditional probability of a finding a marked

point at $du = d\mu \times \mu_M(u)$ in any position in the vector given that the remainder of the sequence equals $\vec{y}$ is given by

$$\sum_{i=1}^{n+1} \lambda_i(du|\vec{y}).$$

The expression should be compared to its classic counterpart (1.4). As for Markov chains, we are mostly interested in $\lambda_{n+1}(\cdot|\vec{y})$, but all $\lambda_i(\cdot|\cdot)$ are needed for the reversibility of the dynamic representation to be considered in Section 4.

Note that provided $f(\cdot)$ is hereditary in the sense that $f(\vec{y}) > 0$ implies $f(\vec{z}) > 0$ for all subsequences $\vec{z}$ of $\vec{y}$, then

$$f(y_1, \ldots, y_n) \propto n! \prod_{i=1}^{n} \lambda_i\left(y_i \mid \vec{y}_{<i}\right) \tag{2.2}$$

where $\vec{y}_{<i} = (y_1, \ldots, y_{i-1})$. This observation implies an alternative way of defining a sequential spatial process: by its conditional intensity. Some care has to be taken to make sure that the resulting density (2.2) is integrable with respect to $\nu(\cdot)$. A sufficient condition is that $\lambda_i\left(y_i \mid \vec{y}_{<i}\right) \le \beta/i$ for all choices of i, y_i, and $\vec{y}_{<i}$. It is important to note, though, that such an assumption does not imply that $f(s_j(\vec{y}, u))/f(\vec{y})$ is uniformly bounded in u and $\vec{y}$ for $j \ne n(\mathbf{y})$. The latter stronger assumption, which may be referred to as *local stability* in analogy with classic marked point processes, will be required in Section 4.

In order to generalise the concept of Ripley–Kelly Markovianity [26, 18] to random sequences, suppose a reflexive relation $\sim$ on $D \times M$ is given with the purpose of formalising the local interactions. In contrast to the point process context, we do not require $\sim$ to be symmetric. If $y \sim z$, the marked point z is said to be a *directed neighbour* of y.

Definition 1. *A sequential spatial process Y on a bounded Borel set $D \subseteq \mathbb{R}^2$ with marks in M defined by its density $f(\cdot)$ with respect to $\nu(\cdot)$ is said to be Markov with respect to the relation $\sim$ on $D \times M$ if*

- *$f(\vec{y}) > 0$ implies $f(\vec{z}) > 0$ for all subsequences $\vec{z}$ of $\vec{y}$;*

- *for all sequences $\vec{y}$ for which $f(\vec{y}) > 0$, the ratio $f((\vec{y}, u))/f(\vec{y})$ depends only on u and its directed neighbours $\{y_i \in \vec{y} : u \sim y_i\}$ in $\vec{y}$.*

In particular, $\lambda_{n(\vec{y})+1}(\cdot|\vec{y})$ is invariant under permutations of $\vec{y}$. In the sequel, we shall sometimes abuse notation somewhat and write $\lambda_{n(\mathbf{y})+1}(\cdot|\mathbf{y})$, where $\mathbf{y} = \{y_i \in \vec{y}\}$, and $n(\mathbf{y})$ is the cardinality of the set $\mathbf{y}$.

Due to the lack of symmetry, sequential spatial point processes are particularly useful for modelling inhomogeneous space-time processes. For instance, to obtain a complete packing of non-intersecting particles [28], a typical algorithm keeps adding particles randomly until this becomes impossible due to violation of the condition of no overlap, see e.g. the recent review papers [6, 27]. A related soft-core model for landslides was proposed by Fiksel and Stoyan [9].

Example 1. Simple Sequential Inhibition Let $\pi(\cdot)$ be a probability density with respect to Lebesgue measure on a bounded planar Borel set D of strictly positive area. Suppose a population of animals arrives in the region D to set up nests, and would like to pick locations according to $\pi(\cdot)$, that is those subregions with high π-mass are deemed the most suitable. However, as each animal needs its space, a newly arriving animal may not build its nest closer than some $r > 0$ to an existing nest location [4, 5]. Thus, if we write $d(z, \vec{\mathbf{x}}) = \min\{||z - x|| : x \in \vec{\mathbf{x}}\}$ for the minimal distance between $z \in D$ and the components of $\vec{\mathbf{x}}$,

$$p_n(x_1, \ldots, x_n) = \pi(x_1) \frac{\pi(x_2) \mathbf{1}\{d(x_2, x_1) > r\}}{\int_D \pi(z) \mathbf{1}\{d(z, x_1) > r\} \, dz} \cdots \frac{\pi(x_n) \mathbf{1}\{d(x_n, \vec{\mathbf{x}}_{<n}) > r\}}{\int_D \pi(z) \mathbf{1}\{d(z, \vec{\mathbf{x}}_{<n}) > r\} \, dz} \quad (2.3)$$

for $x_i \in D$, $i = 1, \ldots, n$. Some care has to be taken about division by zero. If n is larger than the packing number for balls of radius r in D, or $q_n = 0$ for some other reason, $p_n(\cdot, \ldots, \cdot)$ may be any probability density on D^n. For smaller n, or if $q_n > 0$, set $p_n(x_1, \ldots, x_n) = 0$ whenever some term in the denominator of (2.3) is zero. The total number of animals in D is either fixed – as in the formulation by [4] – or random according to some probability mass function q_n, $n \leq n_p$, the packing number. For example, for *Random Sequential Adsorption*[6, 27], q_n equals the probability that a jump process, starting from an empty vector, with transition rate $b(z, \mathbf{x}) = \pi(z) \mathbf{1}\{d(z, \vec{\mathbf{x}}) > r\}$ for a birth jump from $\vec{\mathbf{x}}$ to $(\vec{\mathbf{x}}, z)$ has exactly n jumps within a pre-fixed time horizon $T > 0$ (which can be expressed explicitly in terms of the convolution of exponential distributions with rates $B(\vec{\mathbf{x}}) = \int_D b(z, \vec{\mathbf{x}}) \, dz$). Because of the fact that given the current state is $\vec{\mathbf{x}}$ and a birth occurs, the new point is distributed according to $b(z, \vec{\mathbf{x}})/B(\vec{\mathbf{x}})$, the jump process interpretation described above leads to the conditional n-points density (2.3). Moreover, for large T, realisations tend to be concentrated on complete packings of D. Clearly generalisations are possible by considering other forms of $b(z, \vec{\mathbf{x}})$, see e.g. [6].

If n is fixed, that is $q_n = \mathbf{1}\{n = n_0\}$ for some $n_0 \in \mathbb{N}_0$, $f(\vec{\mathbf{x}})$ is not hereditary, therefore not Markovian in the sense of Definition 1. If $q_n > 0$ for $n \leq n_p$, and $\sum_{n=0}^{n_p} q_n = 1$, the density is hereditary. In that case, provided $f(x_1, \ldots, x_n) > 0$,

$$\lambda_{n+1}(u \mid (x_1, \ldots, x_n)) = \frac{q_{n+1}}{q_n} \frac{\pi(u) \mathbf{1}\{d(u, \vec{\mathbf{x}}) > r\}}{\int_D \pi(z) \mathbf{1}\{d(z, \vec{\mathbf{x}}) > r\} \, dz}.$$

The likelihood ratio is invariant under permutations of the components of $\vec{\mathbf{x}}$. However, it may depend on the sequence length through q_{n+1}/q_n, and, moreover, $\int_D \pi(z) \mathbf{1}\{d(z, \vec{\mathbf{x}}) > r\} \, dz$ may depend on the geometry of $\vec{\mathbf{x}}$, i.e. on the whole sequence. Hence, in general, $f(\cdot)$ is Markovian only with respect to the trivial relation in which each pair of points is related.

Example 2. Sequential Soft Core Further to example 1, suppose the animals have no locational preferences, but claim territory within a certain radius. The radius can depend deterministically on the location [14] (in fertile regions, less space is needed than in poorer ones), be random and captured by a mark, or a combination of both [1]. To be specific, suppose

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[1]Assume the mark space $(0, \infty)$, for concreteness, is equipped with a density $g(\cdot)$. By the transformation $h_{(c_1, c_2)}(x, m) = (c_1 x, c_2 m)$ for $c_1, c_2 > 0$, the Lebesgue intensity measure $\mu(\cdot)$ is scaled by c_1^{-2} on $c_1 D$, the new mark density is $c_2^{-1} g(m/c_2)$. Let $c(\cdot, \cdot)$ be a scaling function such that $0 < \underline{c} \leq c(u, m) \leq$

an animal settling at $x \in D$ claims the region within a radius m of x for itself that newcomers are persuaded to avoid. An appropriate density with respect to $\nu(\cdot)$ could be

$$f(\vec{\mathbf{y}}) \propto \beta^{n(\vec{\mathbf{y}})} \prod_{i=1}^{n(\vec{\mathbf{y}})} \gamma^{\sum_{j<i} \mathbf{1}\{\|x_i - x_j\| \le m_j\}},$$

$\vec{\mathbf{y}} \ni y_i = (x_i, m_i) \in D \times (0, \infty)$. Here $\beta > 0$ is an intensity parameter, and $0 \le \gamma < 1$ reflects the strength of persuasion, the smaller γ, the stronger the inhibition. Indeed, for $\gamma = 0$, no new arrival is allowed to enter the territory of well-settled animals. Alternatively, if invaders demand space according to their own mark, replace m_j by m_i in the exponent of γ.

Note that the ratio

$$(n(\vec{\mathbf{y}}) + 1)\, \lambda((x, m)|\vec{\mathbf{y}}) = \beta\, \gamma^{\sum_{j=1}^{n(\vec{\mathbf{y}})} \mathbf{1}\{\|x - x_j\| \le m_j\}}$$

depends only on those $y_j = (x_j, m_j)$ for which $\|x - x_j\| \le m_j$. Hence $f(\cdot)$ is Markov with respect to the relation $(x, r) \sim (y, s) \Leftrightarrow \|x - y\| \le s$.

3. Hammersley–Clifford factorisation

The goal of this section is to formulate and prove a factorisation theorem for sequential spatial processes in analogy with (1.2) and (1.5).

To do so, we need the notion of a directed clique interaction function. Indeed, for a marked point $z \in D \times M$, define the sequence $\vec{\mathbf{y}}$ to be a z-clique with respect to a reflexive relation $\sim$ on $D \times M$ if $\vec{\mathbf{y}}$ either has length zero or all its components $y \in \vec{\mathbf{y}}$ satisfy $z \sim y$. The definition is z-directed but otherwise permutation invariant, so we may identify $\vec{\mathbf{y}}$ with the set $\mathbf{y} \in \widetilde{N^{\mathrm{f}}}$, the family of unordered finite marked point configurations, obtained by ignoring the permutation.

Our main theorem is the following.

Theorem 1. *A sequential spatial process with density $f(\cdot)$ is Markov with respect to $\sim$ if and only if it can be factorised as*

$$f(y_1, \ldots, y_n) = f(\emptyset) \prod_{i=1}^{n} \prod_{\mathbf{z} \subseteq \mathbf{y}_{<i}} \varphi(y_i, \mathbf{z}) \tag{3.1}$$

for some non-negative, jointly measurable interaction function $\varphi : (D \times M) \times \widetilde{N^{\mathrm{f}}} \to [0, \infty)$ that vanishes except on cliques (i.e. $\varphi(u, \mathbf{z}) = 1$ if $\mathbf{z}$ is no u-clique with respect to $\sim$). Here $\mathbf{y}_{<i} = \{y_1, \ldots, y_{i-1}\}$.

$\bar{c} < \infty$ uniformly. Let Y be a template marked point process with hereditary density $f(\cdot)$, and define a sequential conditional intensity with respect to $d\mu_c(x, m) = c_1(u, m)^{-2} c_2(u, m)^{-1} g(m/c_2(u, m))$ by $\lambda_{Y_c}(u, m \mid \mathbf{y}) := \lambda\left(\frac{u}{c_1(u,m)}, \frac{m}{c_2(u,m)} \mid h_{c(u,m)}^{-1}(\mathbf{y})\right) / (n(\mathbf{y}) + 1)$. For example, the marked hard core density $f(\mathbf{y}) \propto \prod \mathbf{1}\{\|x_i - x_j\| > m_i + m_j\}$ is transformed in $f_{Y_c}(\vec{\mathbf{y}}) \propto \prod_{i<j} \mathbf{1}\left\{\|x_i - x_j\| > \frac{c_1(x_j, m_j)}{c_2(x_j, m_j)}(m_i + m_j)\right\}$. Intuitively, the resulting process Y_c looks like a scaling of Y at (u, m) by $c(u, m)$. Indeed, if Y is Markov with respect to $\sim$, then Y_c is Markov with respect to $(u, r) \sim_c (v, s) \Leftrightarrow \left(\frac{u}{c_1(u,r)}, \frac{r}{c_2(u,r)}\right) \sim \left(\frac{v}{c_1(u,r)}, \frac{s}{c_2(u,r)}\right)$ and the $\sim_c$-neighbourhood $\partial_c(u, m) = h_{c(u,m)}(\partial(h_{c(u,m)}^{-1}(u, m)))$ inherits from $\partial(\cdot)$ geometric properties such as convexity that are invariant under rescaling.

Proof: To show that any density of the given form is Markovian, suppose $f(\vec{\mathbf{y}}) > 0$ but $f(\vec{\mathbf{z}}) = 0$ for some subsequence $\vec{\mathbf{z}}$ of $\vec{\mathbf{y}}$. Then, with the notation $n(\vec{\mathbf{z}})$ for the length of $\vec{\mathbf{z}}$,

$$f(\emptyset) \prod_{i=1}^{n(\vec{\mathbf{z}})} \prod_{\mathbf{x} \subseteq \mathbf{z}_{<i}} \varphi(z_i, \mathbf{x}) = 0.$$

Hence some term $\varphi(z_i, \mathbf{x}) = 0$, but as it features in the factorisation (3.1) of $f(\vec{\mathbf{y}})$ too, $f(\vec{\mathbf{y}})$ must be 0 as well in contradiction with the assumption.

Assume that $f(\vec{\mathbf{y}}) > 0$. Now, $f((\vec{\mathbf{y}}, u))/f(\vec{\mathbf{y}}) = \prod_{\mathbf{z} \subseteq \mathbf{y}} \varphi(u, \mathbf{z})$ depends only on u and its directed neighbours in $\mathbf{y}$, as $\varphi(u, \mathbf{z}) = 1$ except if $\mathbf{z}$ is an u-clique.

Reversely, set $\varphi(y_1, \emptyset) := f(y_1)/f(\emptyset) = \lambda_1(y_1|\emptyset)$, and define putative interaction functions $\varphi(\cdot, \cdot)$ recursively as follows. If $\{y_1, \ldots, y_n\}$ is no y_{n+1}-clique, $\varphi(y_{n+1}, \{y_1, \ldots, y_n\}) = 1$; else

$$\varphi(y_{n+1}, \{y_1, \ldots, y_n\}) = \frac{(n+1)\,\lambda_{n+1}(y_{n+1}|\{y_1, \ldots, y_n\})}{\prod_{\mathbf{z}} \varphi(y_{n+1}, \mathbf{z})} \tag{3.2}$$

where the product ranges over all strict subsets $\{y_1, \ldots, y_n\} \neq \mathbf{z} \subset \{y_1, \ldots, y_n\}$. To deal with any zeroes, we set $0/0 = 0$.

We first show that $\varphi(\cdot, \cdot)$ is a well-defined interaction function. By the Markov assumption, $(n+1)\lambda_{n+1}(y_{n+1}|\{y_1, \ldots, y_n\})$ is invariant under permutations of $y_1, \ldots, y_n$, so a simple induction argument yields the permutation invariance of $\varphi(y_{n+1}, \{y_1, \ldots, y_n\})$ in its second argument. By definition, $\varphi(\cdot, \cdot)$ vanishes except on cliques, hence it is an interaction function. To show that if the denominator of (3.2) is zero, so is the numerator, note that if $f(\emptyset) = 0$, by the assumption that the process is hereditary, necessarily $f \equiv 0$ which contradicts the fact that $f(\cdot)$ is a probability density. Therefore $f(\emptyset) > 0$ and $\varphi(y_1, \emptyset)$ is well-defined. Suppose $\varphi(\cdot, \cdot)$ is well-defined for sets of cardinality at most $n - 1 \geq 0$ as its second argument. Let $\{y_1, \ldots, y_n\}$ be an y_{n+1}-clique and assume $\varphi(y_{n+1}, \mathbf{z}) = 0$ for some strict subset $\mathbf{z} \subset \{y_1, \ldots, y_n\}$. By the induction assumption, $\lambda_{n(\mathbf{z})+1}(y_{n+1}|\mathbf{z}) = 0$. Hence $f((\vec{\mathbf{z}}, y_{n+1})) = 0$, with the remark that if $f(\vec{\mathbf{z}}) = 0$ the Markov assumption that the process is hereditary implies $f((\vec{\mathbf{z}}, y_{n+1})) = 0$. A similar observation allows us to conclude that $f(y_1, \ldots, y_{n+1}) = 0 = \lambda_{n+1}(y_{n+1}|\{y_1, \ldots, y_n\})$, hence (3.2) is well-defined by induction.

It remains to show that φ satisfies the desired factorisation. To do so, we again proceed by induction. By definition, $f(y_1) = f(\emptyset)\,\varphi(y_1, \emptyset)$ for any $y_1 \in D \times M$, so the factorisation holds for sequences of length at most 1. Suppose (3.1) holds for all sequences that are at most $n \geq 1$ long, and consider any sequence $\vec{\mathbf{y}} = (y_1, \ldots, y_{n+1})$ with components in $D \times M$. If $f(y_1, \ldots, y_n) = 0$, by the assumption on hereditariness, $f(y_1, \ldots, y_{n+1}) = 0$. By the induction hypothesis, $f(y_1, \ldots, y_n) = f(\emptyset) \prod_{i=1}^{n} \prod_{\mathbf{z} \subseteq \mathbf{y}_{<i}} \varphi(y_i, \mathbf{z}) = 0$ which implies $f(\emptyset) \prod_{i=1}^{n+1} \prod_{\mathbf{z} \subseteq \mathbf{y}_{<i}} \varphi(y_i, \mathbf{z}) = 0 = f(y_1, \ldots, y_{n+1})$. Hence without loss of generality we may assume that $f(y_1, \ldots, y_n)$ is strictly positive. Then

$$
\begin{aligned}
f(y_1, \ldots, y_{n+1}) &= \frac{f(y_1, \ldots, y_{n+1})}{f(y_1, \ldots, y_n)}\, f(y_1, \ldots, y_n) \\
&= (n+1)\,\lambda_{n+1}(y_{n+1}|\{y_1, \ldots, y_n\})\, f(\emptyset) \prod_{i=1}^{n} \prod_{\mathbf{z} \subseteq \mathbf{y}_{<i}} \varphi(y_i, \mathbf{z}) \tag{3.3}
\end{aligned}
$$

because of the induction hypothesis. We shall distinguish several cases.

Firstly, suppose that $\{y_1, \ldots, y_n\}$ is an y_{n+1}-clique and recall that if the denominator in the right hand side of (3.2) is zero, then so are $\varphi(y_{n+1}, \{y_1, \ldots, y_n\})$ and $\lambda_{n+1}(y_{n+1}|\{y_1, \ldots, y_n\})$. Hence, in this case, formula (3.3) yields $f(y_1, \ldots, y_{n+1}) = 0$, so the desired factorisation holds. If, on the other hand, the denominator is strictly positive,

$$\lambda_{n+1}(y_{n+1}|\{y_1, \ldots, y_n\}) = \frac{1}{n+1} \prod_{\mathbf{z} \subseteq \{y_1, \ldots, y_n\}} \varphi(y_{n+1}, \mathbf{z})$$

and (3.1) holds by substitution in (3.3).

Secondly, assume $\{y_1, \ldots, y_n\}$ is no y_{n+1}-clique. Then, $y_{n+1} \not\sim y_i$ for some y_i, $i = 1, \ldots, n$. Now, if $f(y_1, \ldots, y_{i-1}, y_{i+1}, \ldots, y_n) > 0$, by the Markov assumption

$$
\begin{aligned}
(n+1)\,\lambda_{n+1}(y_{n+1}|\{y_1, \ldots, y_n\}) &= (n+1)\,\lambda_{n+1}(y_{n+1}|\{y_1, \ldots, y_{i-1}, y_{i+1}, \ldots, y_n\}) \\
&= \frac{f(y_1, \ldots, y_{i-1}, y_{i+1}, \ldots, y_{n+1})}{f(y_1, \ldots, y_{i-1}, y_{i+1}, \ldots, y_n)} \\
&= \prod_{\mathbf{z} \subseteq \{y_1, \ldots, y_{i-1}, y_{i+1}, \ldots, y_n\}} \varphi(y_{n+1}, \mathbf{z}) = \prod_{\mathbf{z} \subseteq \{y_1, \ldots, y_n\}} \varphi(y_{n+1}, \mathbf{z})
\end{aligned}
$$

where the last line is obtained by the induction hypothesis and the fact that $\varphi(y_{n+1}, \mathbf{z}) = 1$ whenever $\mathbf{z}$ contains y_i. Finally, if $f(y_1, \ldots, y_{i-1}, y_{i+1}, \ldots, y_n) = 0$, by the induction hypothesis, $\varphi(y_k, \mathbf{z}) = 0$ for some $i \neq k \leq n$ and $\mathbf{z} \subseteq \{y_1, \ldots, y_{k-1}\} \setminus \{y_i\}$. Since by assumption $f(\cdot)$ is Markov, $f(y_1, \ldots, y_{n+1}) = 0$ as well, the factorisation follows, and the proof is complete. $\square$

The factorisation (3.1) is similar to that of the finite distributions of a Markov chain, cf. (1.2). Indeed, the product of transition probabilities $p(x_{i-1}, x_i)$ from state x_{i-1} to x_i is replaced by a product of interaction functions $\prod_{\mathbf{z} \subseteq \mathbf{y}_{<i}} \varphi(y_i, \mathbf{z})$ over cliques of 'past' neighbours of y_i similar to (1.5).

Theorem 1 provides a third way of defining a sequential point process: by specifying its clique interaction functions. Of course one must verify integrability for each choice.

Example 1. (ctd) Recall that we need to assume $q_n > 0$ for $n \leq n_p$ and $q_n = 0$ for $n > n_p$ in order to be sure the simple sequential inhibition model (2.3) is hereditary. Then, the interaction functions can be computed iteratively by (3.2). Set $r_n := nq_n/q_{n-1}$ for $n = 1, 2, \ldots, n_p$, 0 otherwise, and $I(\mathbf{x}) := \int_D \pi(z)\,\mathbf{1}\{d(z, \mathbf{x}) > r\}\,dz$ for any finite set $\mathbf{x}$ of points in D, with $I(\emptyset) = 1$. Then

$$\phi(x, \emptyset) = r_1\,\pi(x);$$

$$\phi(x, \mathbf{y}) = \mathbf{1}\{d(x, \mathbf{y}) > r\} \exp\left[\sum_{\mathbf{z} \subseteq \mathbf{y}} (-1)^{n(\mathbf{y} \setminus \mathbf{z})} \log\left(\frac{r_{n(\mathbf{z})+1}}{I(\mathbf{z})} \right) \right]$$

for non-empty configurations $\mathbf{y}$. The expression can be verified by a computation of the likelihood ratios. Indeed for $\vec{\mathbf{x}} = (x_1, \ldots, x_n)$, $n \geq 1$,

$$\frac{f(s_{n+1}(\vec{\mathbf{x}}, x_{n+1}))}{f(\vec{\mathbf{x}})} = r_1\,\pi(x_{n+1}) \exp\left[\sum_{\emptyset \neq \mathbf{y} \subseteq \mathbf{x}} \sum_{\mathbf{z} \subseteq \mathbf{y}} (-1)^{n(\mathbf{y} \setminus \mathbf{z})} \log\left(\frac{r_{n(\mathbf{y})+1}}{I(\mathbf{y})} \right) \right] = \frac{r_{n+1}\,\pi(x_{n+1})}{I(\mathbf{x})}$$

provided $d(x_{n+1}, \{x_1, \ldots, x_n\}) > r$, which implies $d(x_{n+1}, \mathbf{y}) > r$ for any subset $\mathbf{y}$ of $\mathbf{x} = \{x_1, \ldots, x_n\}$, and zero otherwise. The last identity is a consequence of Newton's binomium.

Example 2. (ctd) For the sequential soft core model,

$$
\begin{aligned}
\varphi(y, \emptyset) &= \beta; \\
\varphi((x_1, m_1), (x_2, m_2)) &= \gamma^{1\{\|x_1 - x_2\| \le m_2\}}
\end{aligned}
$$

and 1 otherwise [2].

Example 3. Pairwise interaction models of the form

$$
f(\emptyset) \prod_{i=1}^{n} \left[\varphi(y_i, \emptyset) \prod_{j<i} \varphi(y_i, y_j) \right]
$$

are particularly convenient. Note that the sequential soft core model discussed in the previous example exhibits pairwise interactions only. It has a constant penalty term $\gamma \in [0, 1)$ for each pair $y_i \sim y_j$. It may be more natural to let the interaction vary with distance, for example quadratically as in

$$
\varphi((x, r), (y, s)) = 1 - (1 - \|x - y\|^2 / R_{r,s}^2)^2
$$

for $\|x - y\| \le R_{r,s}$. Here the range of interaction, $R_{r,s}$ may depend on the marks. A sufficient condition for the model to be integrable is that $\varphi(y_i, y_j)$ is bounded by 1. Thus, pairwise interaction models are particularly suitable for modelling repulsion between marked points.

4. DYNAMIC REPRESENTATION

Markov sequential spatial processes arise naturally as the limit distribution of a jump process [7] with transitions that add or remove one component of the sequence at a time. From a statistical point of view, it is then possible to obtain samples from some sequential spatial model of interest by running the pure jump process into equilibrium. Standard Markov chain Monte Carlo ideas [10] can than be applied to estimate model parameters by the maximum likelihood principle, to perform likelihood ratio tests to assess the goodness-of-fit of the model, to compute confidence regions, profile likelihoods and so on. Moreover, at least in principle, it is possible to determine exactly when equilibrium is reached, by applying the coupling ideas of Propp and Wilson [24] along the lines proposed in [8, 16, 19] and the references therein.

Below, we first propose a birth-and-death jump process, then develop a discrete time Metropolis–Hastings style sampler.

4.1 Spatial birth-and-death processes

A *spatial birth-and-death process* is a continuous time Markov process with state space N^{f}. Its only transitions are the insertion of a marked point in the current sequence (a *birth*), or

---

[2] The density of the scaled process Y_c of Example 2 can be factorised as $f_{Y_c}(\emptyset) \prod_{i=1}^{n(\mathbf{y})} \prod_{\mathbf{z} \subseteq \mathbf{y}_{<i}} \varphi \left(h_{c(y_i)}^{-1}(\mathbf{z}) \cup \{(\frac{x_i}{c_1(y_i)}, \frac{m_i}{c_2(y_i)})\} \right)$ if $\varphi(\cdot)$ denotes the interaction function of a template Markov marked point process Y.

the deletion of a component (a *death*). Suppose the current state is $\vec{\mathbf{y}}$, and write $b_i(\vec{\mathbf{y}}, u) \, d\mu \times \mu_M(u)$ for the birth rate of a new marked point in du, $u \in D \times M$, to be inserted at position i of $\vec{\mathbf{y}}$, and $d_i(\vec{\mathbf{y}})$ for the death rate of the reverse transition. Then the detailed balance equations are given by

$$\frac{e^{-\mu(D)}}{n!} \, f(\vec{\mathbf{y}}) \, b_i(\vec{\mathbf{y}}, u) = \frac{e^{-\mu(D)}}{(n+1)!} \, f(s_i(\vec{\mathbf{y}}, u)) \, d_i(s_i(\vec{\mathbf{y}}, u)).$$

If we take unit death rate for each marked point,

$$b_i(\vec{\mathbf{y}}, u) = \frac{f(s_i(\vec{\mathbf{y}}, u))}{(n+1) \, f(\vec{\mathbf{y}})} = \lambda_i(u | \vec{\mathbf{y}}), \tag{4.1}$$

again with the convention $0/0 = 0$. Note that if the jump process starts in the set $\{\vec{\mathbf{y}} \in N^{\mathrm{f}} : f(\vec{\mathbf{y}}) > 0\}$, it will almost surely never leave it. Clearly, for this choice of birth and death rates, $f(\cdot)$ is an invariant probability density.

Since our process evolves in continuous time, some care has to be taken to avoid explosion, that is, infinitely many transitions in finite time. Set

$$\mathcal{B}_n := \sup_{n(\vec{\mathbf{y}})=n} \sum_{i=1}^{n+1} \int_{D \times M} b_i(\vec{\mathbf{y}}, u) \, d\mu \times \mu_M(u)$$

for the upper bound on the total birth rate from sequences of length $n \geq 0$, and note that

$$\delta_n = \inf_{n(\vec{\mathbf{y}})=n} \sum_{i=1}^{n} d_i(\vec{\mathbf{y}}) = n.$$

By [23, Prop. 5.1, Thm. 7.1], sufficient conditions for the existence of a unique jump process with birth rates (4.1) and unit death rates with a unique invariant probability measure to which it converges in distribution regardless of the initial state are that $\delta_n > 0$ for all $n \geq 1$ and one of the following holds:

- $\mathcal{B}_n = 0$ for all sufficiently large $n \geq n_0 \geq 0$;

- $\mathcal{B}_n > 0$ for all $n \geq 1$ and

$$\sum_{n=1}^{\infty} \frac{\delta_1 \cdots \delta_n}{\mathcal{B}_1 \cdots \mathcal{B}_n} = \infty; \qquad \sum_{n=2}^{\infty} \frac{\mathcal{B}_1 \cdots \mathcal{B}_{n-1}}{\delta_1 \cdots \delta_n} < \infty.$$

For densities $f(\cdot)$ that satisfy

$$f(s_i(\vec{\mathbf{y}}, u)) \leq \beta f(\vec{\mathbf{y}}) \tag{4.2}$$

for some $\beta > 0$ and all $\vec{\mathbf{y}} \in N^{\mathrm{f}}$, $u \in D \times M$, $i = 1, \ldots, n(\vec{\mathbf{y}}) + 1$, the total birth rate is bounded by $\beta \, \mu(D)$, and it is easily verified that the Preston conditions hold. From a practical point of view, the jump process may be implemented by thinning the transitions of

a process with unit death rate and constant birth rate $\tilde{b}_i(\vec{\mathbf{y}}, \cdot) \equiv \beta/(n(\vec{\mathbf{y}}) + 1)$, which avoids having to compute explicitly the parameter

$$\sum_{i=1}^{n(\vec{\mathbf{y}})+1} \int_{D \times M} b_i(\vec{\mathbf{y}}, u) \, d\mu \times \mu_M(u) + n(\vec{\mathbf{y}})$$

of the exponentially distributed waiting times in between jumps. The retention probability of a transition from $\vec{\mathbf{y}}$ to $s_i(\vec{\mathbf{y}}, u)$ is given by

$$\frac{f(s_i(\vec{\mathbf{y}}, u))}{\beta \, f(\vec{\mathbf{y}})} = \frac{1}{\beta} \prod_{\mathbf{z} \subseteq \mathbf{y}_{<i}} \varphi(u, \mathbf{z}) \prod_{j=i}^{n(\vec{\mathbf{y}})} \prod_{\mathbf{z} \subseteq \mathbf{y}_{<j}} \varphi(y_j, \mathbf{z} \cup \{u\}).$$

The first term depends on the directed neighbours y_j of u ($u \sim y_j$) in $\mathbf{y}_{<i}$. The interaction functions in the last product reduce to 1 if $y_j \nsim u$.

4.2 A Metropolis–Hastings sampler

A popular, flexible and generally applicable technique for generating samples from a complex or high-dimensional probability density is the *Metropolis–Hastings method*, see e.g. [10]. Briefly, the method works by proposing an update according to a distribution that is convenient to sample from, and then to accept or reject this proposal with a probability that is chosen so as to make sure the detailed balance equations are satisfied.

In the context of this paper, two types of proposals are considered: births and deaths. More precisely, given the current state is $\vec{\mathbf{y}}$, with probability $1/2$ propose a birth, otherwise a death. In the first case, select a position i to insert and a new marked point u uniformly on $1, \ldots, n(\vec{\mathbf{y}}) + 1$ respectively $D \times M$ (w.r.t. $\mu \times \mu_M$), and accept the new state $s_i(\vec{\mathbf{y}}, u)$ with probability

$$\alpha(\vec{\mathbf{y}}, s_i(\vec{\mathbf{y}}, u)) := \min\left\{ 1, \frac{f(s_i(\vec{\mathbf{y}}, u)) \, \mu(D)}{f(\vec{\mathbf{y}}) \, (n(\vec{\mathbf{y}}) + 1)} \right\}.$$

In case a death is proposed, if $\vec{\mathbf{y}}$ is the empty sequence, do nothing; otherwise, select the position of the marked point to be removed uniformly, say i, and accept the transition with probability

$$\alpha(\vec{\mathbf{y}}, \vec{\mathbf{y}}_{(-i)}) := \min\left\{ 1, \frac{f(\vec{\mathbf{y}}_{(-i)}) \, n(\vec{\mathbf{y}})}{f(\vec{\mathbf{y}}) \, \mu(D)} \right\}$$

where $\vec{\mathbf{y}}_{(-i)}$ denotes the subsequence of $\vec{\mathbf{y}}$ obtained by removing the ith component. It is easily seen that $f(\cdot)$ is an invariant density. If we start the chain in a sequence $\vec{\mathbf{y}}$ for which $f(\vec{\mathbf{y}}) > 0$, the chain will never leave the set. Thus, we shall restrict the Markov chain to $H := \{\vec{\mathbf{y}} \in N^{\mathrm{f}} : f(\vec{\mathbf{y}}) > 0\}$ from now on.

In order to show that the Metropolis–Hastings chain Y_n, $n \in \mathbb{N}_0$, converges to $f(\cdot)$ in total variation from any initial state in H, we need to establish aperiodicity and Harris recurrence, that is *Harris ergodicity* [21]. Aperiodicity immediately follows from the fact that self-transitions occur. A sufficient condition for Harris recurrence (in fact for the even

stronger property of geometric ergodicity) is that there exist a function $V : N^{\mathrm{f}} \to [1, \infty)$, constants $b < \infty$ and $\gamma < 1$, and a measurable small set $C \subset N^{\mathrm{f}}$ such that

$$PV(\vec{\mathbf{y}}) := \mathbb{E}\left[V(X_{n+1}) | X_n = \vec{\mathbf{y}}\right] \leq \gamma V(\vec{\mathbf{y}}) + b\mathbf{1}\left\{\mathbf{y} \in C\right\}. \tag{4.3}$$

Recall that a set C is small if there exists a non-zero measure $\phi(\cdot)$ and an integer n such that the probability that the Metropolis–Hastings chain reaches any measurable subset B of N^{f} from $\vec{\mathbf{y}} \in C$ is at least as large as $\nu(B)$. See [21] for further details.

From now on, assume that (4.2) holds. Then, the drift condition (4.3) can be verified by an adaptation of the proof of [12, Prop.3.3] with $V(\vec{\mathbf{y}}) = A^{n(\vec{\mathbf{y}})}$ for some $A > 1$. Indeed, note that the acceptance probability for inserting $u \in D \times M$ at position i in $\vec{\mathbf{y}}$ is bounded by $\beta\mu(D)/(n(\vec{\mathbf{y}}) + 1)$, which does not exceed a prefixed constant $\epsilon > 0$ if $n(\vec{\mathbf{y}})$ is sufficiently large. Similarly, the acceptance probability for removing a component from the sequence $\vec{\mathbf{y}}$ reduces to 1 if $\vec{\mathbf{y}}$ is long enough. Now,

$$\begin{aligned}
PV(\vec{\mathbf{y}}) &= \frac{1}{2}V(\vec{\mathbf{y}}) \sum_{i=1}^{n(\vec{\mathbf{y}})+1} \int_D \int_M \frac{A-1}{\mu(D)\,(n(\vec{\mathbf{y}})+1)}\, \alpha(\vec{\mathbf{y}}, s_i(\mathbf{y}, u))\, d\mu \times \mu_M(u) \\
&+ \frac{1}{2}V(\vec{\mathbf{y}}) \sum_{i=1}^{n(\vec{\mathbf{y}})} \frac{A^{-1}-1}{n(\vec{\mathbf{y}})}\, \alpha(\vec{\mathbf{y}}, \vec{\mathbf{y}}_{(-i)}) + V(\vec{\mathbf{y}}).
\end{aligned} \tag{4.4}$$

Since for sufficiently long sequences of marked points, say $n(\vec{\mathbf{y}}) > N_\epsilon$, deaths are always accepted, $\alpha(\vec{\mathbf{y}}, s_i(\vec{\mathbf{y}}, u)) \leq \epsilon$ uniformly in its arguments, and $A > 1$, (4.4) is less than or equal to $\left[\frac{1}{2}(A-1)\epsilon + \frac{1}{2}(A^{-1}-1) + 1\right]V(\vec{\mathbf{y}})$. This and the uniform lower bound $1/(\beta\,\mu(D))$ on the acceptance probability for deaths yield the desired result by the same arguments in the proof of Propositions 3.2–3.3 in [12] with $C = \cup_{n=0}^{N_\epsilon}(D \times M)^n$.

4.3 Reversible jump Markov chains

The Metropolis–Hastings algorithm of the previous subsection is a special case of a so-called reversible jump Markov chain [13]. This is a proposal–acceptance/rejection scheme for moves between subspaces of different dimension. Suppose a target equilibrium distribution and a proposal probability for each move type are given. The aim is to define acceptance probabilities in such a way that the resulting Markov chain is well-defined and the detailed balance equations hold. In order to avoid singularities due to the different dimensions, for each move type, a symmetric dominating measure $\xi(\cdot, \cdot)$ on the product of the state space with itself is needed. It turns out [13] that acceptance probabilities that are ratios of the joint density of the target and proposal distributions with respect to $\xi(\cdot, \cdot)$ evaluated at the proposed and current state do the trick.

In the context of section 4.2, define, for measurable subsets A and B of N^{f},

$$\begin{aligned}
\xi(A \times B) &= \int_{N^{\mathrm{f}}} \mathbf{1}\left\{\vec{\mathbf{y}} \in A\right\} \frac{1}{n(\vec{\mathbf{y}})+1} \sum_{i=1}^{n(\vec{\mathbf{y}})+1} \int_{D \times M} \mathbf{1}\left\{s_i(\vec{\mathbf{y}}, u) \in B\right\} d\mu \times \mu_M(u)\, d\nu(\vec{\mathbf{y}}) \\
&+ \int_{N^{\mathrm{f}}} \mathbf{1}\left\{\vec{\mathbf{y}} \in A\right\} \sum_{i=1}^{n(\vec{\mathbf{y}})} \mathbf{1}\left\{\vec{\mathbf{y}}_{(-i)} \in B\right\}\, d\nu(\vec{\mathbf{y}}).
\end{aligned}$$

The measure is symmetric by the form of the reference measure $\nu(\cdot)$.

The joint bi-variate density of the product of the distribution to sample from and the birth proposal distribution with respect to $\xi(\cdot,\cdot)$ is given by $f(\vec{\mathbf{y}}, s_i(\vec{\mathbf{y}}, u)) = f(\vec{\mathbf{y}})/(2\,\mu(D))$. Similarly for death proposals we have $f(\vec{\mathbf{y}}, \vec{\mathbf{y}}_{(-i)}) = f(\vec{\mathbf{y}})/(2n(\vec{\mathbf{y}}))$. Hence, the acceptance probabilities for births and deaths, as given in the previous section, follow as ratios of joint bi-variate densities truncated at 1. Note that there is no need to worry about division by zero, as we had restricted the Metropolis–Hastings chain to the family of sequences having strictly positive density.

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