Unbiased on lattice domain growth

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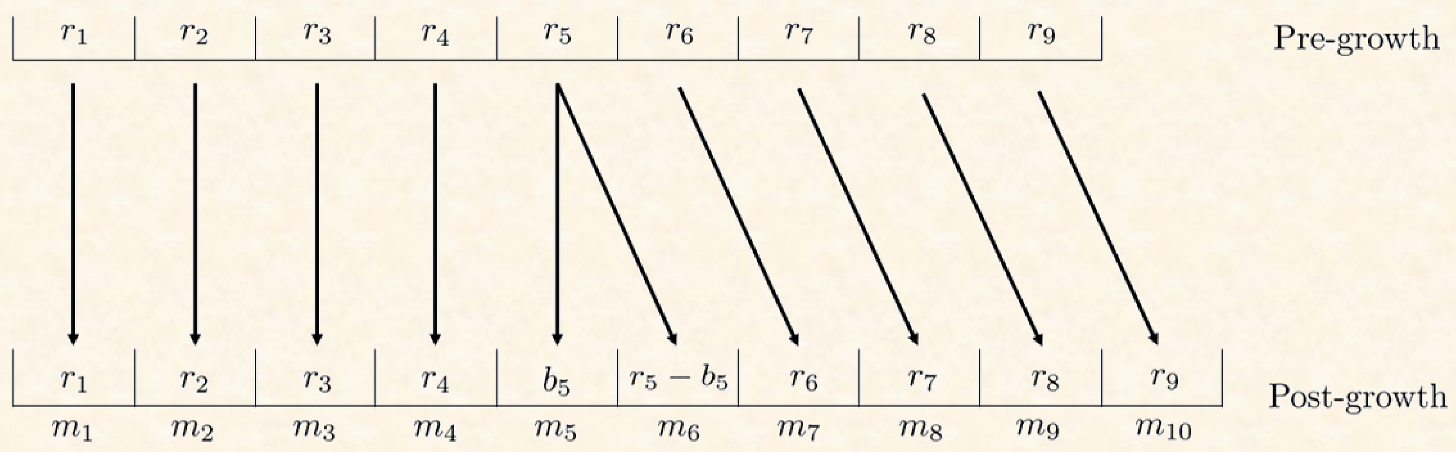
Motivation

Domain growth is an inherent feature of many biological systems. One such example is in the movement and proliferation of melanoblasts, the precursor to pigment producing melanocytes, on a growing embryo. If melanoblasts fail to fully populate the spatial domain, small regions of skin will contain no pigment [Mort *et al.*, 2016]. This disease is called piebaldism, a proxy for many neurocristopathies — a class of pathogies caused by the similar failure of neural crest cells to proliferate and migrate during embryonic growth. Models for domain growth are of importance in order to simulate and predict biological and physical systems such as that of piebaldism.

We demonstrate that a previously employed method for on-lattice domain growth causes a build up of particles at the boundaries of the spatial domain in "low-diffusion regimes".

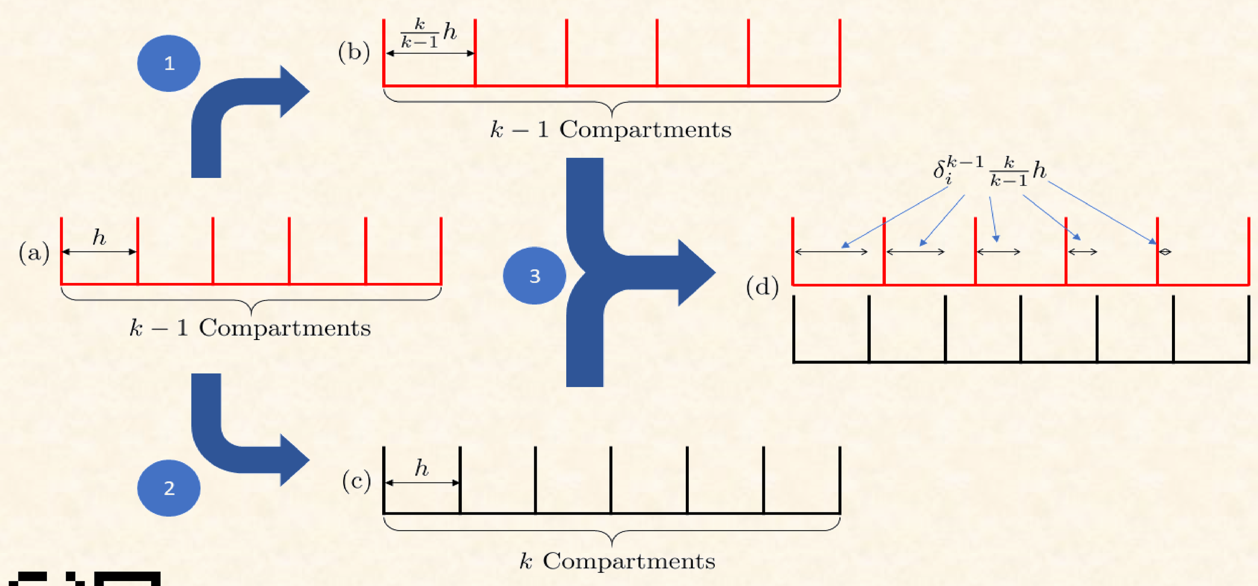
A piebald mouse with a white belly spot. Image reproduced with permission from Mort *et al*, 2016.

The original method: Baker *et al.*, 2010



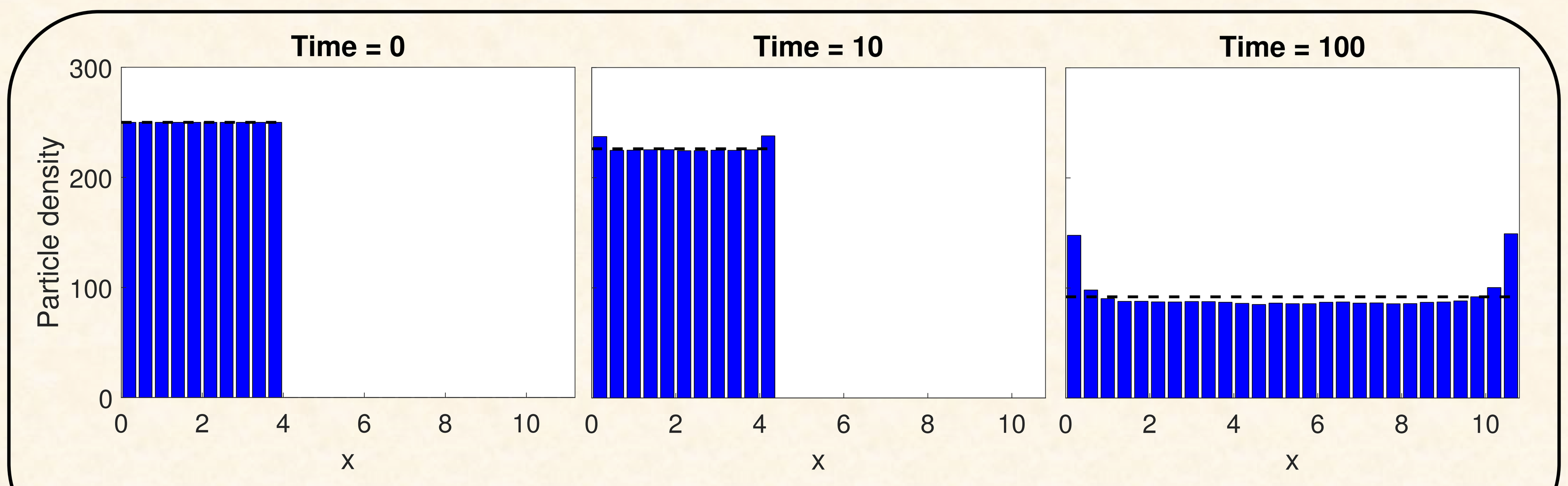
A schematic showing a possible splitting event when there are nine pre-growth compartments (compartments identified by the subscripts on the particle numbers). Pre-growth particle numbers are denoted r_i. In this case, compartment 5 is chosen to divide, and its contents are split binomially with probability of success 1/2 ($b_5 \sim Bin(r_5, 1/2)$) between the compartment in the original position (compartment 5 in this case) and the new one that is created to its right. The compartments originally numbered 6, 7, 8 and 9 are moved one position to the right and become compartments 7, 8, 9 and 10, respectively. Post-growth particle numbers are denoted by the m_i's.

The stretching method: Smith *et al.*, 2019

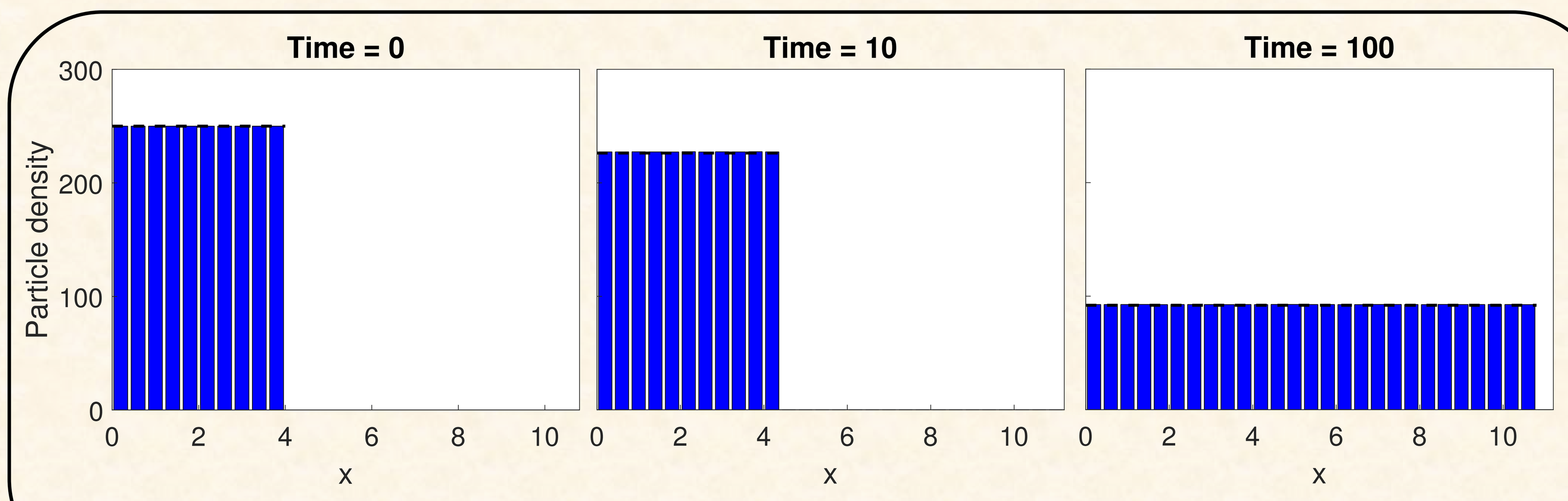


The process of domain growth for the stretching method. The initial domain (a) is lengthened in two ways: by stretching all compartments by a small amount (b) and by adding a new compartment (c), so that each domain is of the same length. Overlap values are calculated in (d) and used in order to redistribute the particles. Each overlap value gives the probability that a particle in the associated original compartment is placed in the new compartment which overlaps it on the left.

On-lattice domain growth can introduce unexpected particle accumulation at the boundaries



Results from 50,000 repeats of the original method. The blue bars are the solution of the original method, while the black dashed line is the mean-field solution.



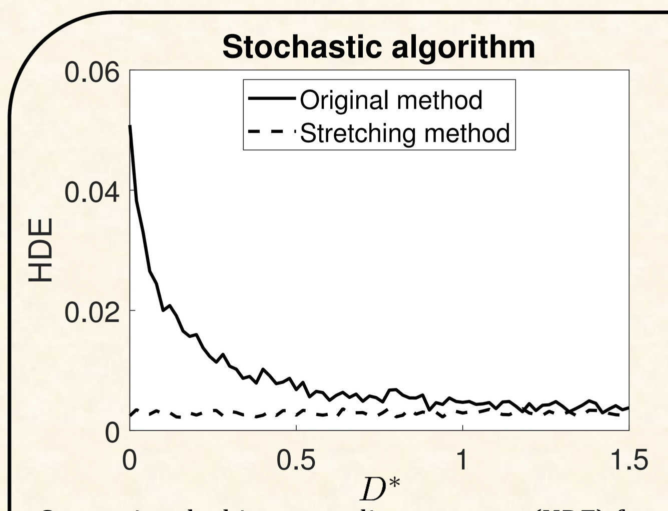
Results from 50,000 repeats of the stretching method. The blue bars and black dashed lines are the same as the original method plots.

Let M_i^k be the density of particles, with $M_1^1 = 1$. The recursion relationships are as follows.

$$M_i^{k+1} = M_i^k \frac{k-i+1/2}{k} + M_{i-1/2}^k \frac{i-2}{k} \Rightarrow M_i^k \approx \frac{\exp\{1/2\}}{\sqrt{\pi}} \prod_{j=2}^{i} \frac{2j-3}{2j-2} k^{-1/2}.$$

$$M_i^{k+1} = \delta_i^k M_i^k + \left(1-\delta_{i-1}^k\right) M_{i-1}^k \Rightarrow M_i^k = \frac{1}{k}.$$

Comparison



Comparing the histogram distance error (HDE) for a non-dimensional stochastic simulation of the original and stretching methods

When are the errors in the original method acceptable? We consider a heuristic argument. The mean squared displacement describes how the variance in position of a Brownian particle changes in time. If multiple particles are initialised at the origin and diffuse for a time, t, then $\langle x^2 \rangle = 2Dt$. If a particle is to diffuse over the entire domain before the domain grows, then the squared distance from the origin would be $x^2 \sim L_0^2$. Likewise, the typical time frame for growth is given by setting $t \sim 1/\rho$. Substituting these into the expression for the mean squared displacement yields $D \sim L_0^2 \rho$. Therefore, we say we are in a high diffusion parameter regime when $D > L_0^2 \rho$.

To the left is the result of several non-dimensional simulations of both the orignal and stretching methods, where the non-dimensional diffusion parameter is $D^* = D/(L_0^2 \rho)$. For $D^* > 1$, the two methods have similar histogram distance errors, which verifies the results of the heuristic argument.

References

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