RANDOM WALK DRIVEN ANISOTROPIC DIFFUSION

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Abstract. A spatially heterogeneous nonsymmetric random walk system is introduced when the walk length depends on space variables and walking direction. We derive an advection-diffusion equation related to such a random walk system which covers both isotropic and anisotropic dispersal. The resulting equation is similar to the ones obtained from a kinetic transport equation by Hillen *et al.* [4, 5]. The derived equation is applied to model anisotropic dispersal of fungus in vineyard. Monte-Carlo simulations are compared with the solution of model equations.

1. Spatially heterogeneous nonsymmetric random walk

The purpose of this paper is to introduce a space jump process based on a general random walk system and derive an anisotropic diffusion equation. Similar anisotropic diffusion models have been obtained using a velocity jump process based on a transport equation and the method of the paper gives an alternative model equation. We test the anisotropic diffusion models with Monte-Carlo simulations in the context of fungus spreading in a vineyard.

1.1. **Random walk in one space dimension.** We start with one space dimension. The notations of a random walk system and its illustration are given in Table 1 and Figure 1. There are a few differences of our random walk system in comparison with traditional ones. First, the parameters of the random walk system in Table 1 are all spatially heterogeneous, i.e., $\Delta x = \Delta x(\mathbf{x}), \Delta t = \Delta t(\mathbf{x})$, and so on. Hence, we cannot exchange the order of parameters and differential operators. We will consider a random walk system in the context of biological dispersal. Since biological organisms may stay or depart depending on the environment, we introduce departing probability $\gamma(\mathbf{x})$ (see [3]). However, for a comparison, we mostly take $\gamma = 1$, which is the case of Brownian particles.

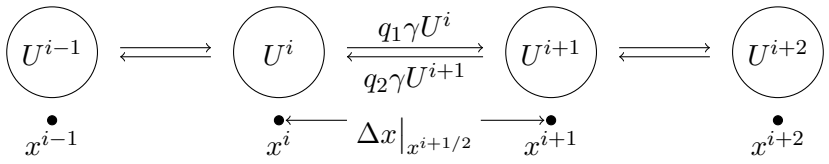

Figure 1. Diagram of a space-jump process of this paper in 1-D.

We assume that the probability for a particle to move to right is $q_1(\mathbf{x})$ and to left is $q_2(\mathbf{x})$, where $q_1(\mathbf{x}) + q_2(\mathbf{x}) = 1$. Hence, the particle flux that crosses the midpoint

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TABLE 1. Notation and parameters of the random system in $\mathbf{R}^1$.

notation	definition and meaning
x^i	grid point
$x^{i+1/2}$	midpoint between x^i and x^{i+1} $(x^{i+1/2} := (x^i + x^{i+1})/2)$
$\Delta x\big\vert_{x^i}$	mesh size $(\Delta x\big\vert_{x^i} = x^{i+1/2} - x^{1-1/2})$
$\Delta x\big\vert_{x^{i+1/2}}$	walk length $(\Delta x\big\vert_{x^{i+1/2}} = x^{i+1} - x^i)$
$\Delta t\big\vert_{x^{i+1/2}}$	jumping (or traveling) time from x^i to x^{i+1} or vice versa
U^i	population at x^i
u^i	population density at x^i $(u^i = U^i/\Delta x)$
γ	departing probability during the time period Δt
q_1, q_2	probability for a particle to move right and left, respectively
$\mathbf{f}\big\vert_{x^{i+1/2}}$	flux across a midpoint $x^{i+1/2}$

$x^{i+1/2}$ from left to right is $\frac{q_1\gamma U}{\Delta t}\big\vert_{x=x^i}$. Similarly, the flux from right to left is $\frac{q_2\gamma U}{\Delta t}\big\vert_{x=x^{i+1}}$. Therefore, in terms of particle density, $u = \frac{U}{\Delta x}$, the net flux across $x = x^{i+1/2}$ is given by

$$\mathbf{f}(x^{i+\frac{1}{2}}) = \frac{q_1\Delta x}{\Delta t}\gamma u\Big\vert_{x^i} - \frac{q_2\Delta x}{\Delta t}\gamma u\Big\vert_{x^{i+1}}.$$

Let $v := \frac{\Delta x}{\Delta t}$ be the particle speed and $\mu = \frac{1}{\Delta t}$ the turning frequency, which are functions of the space variable, i.e., $v = v(x)$ and $\mu = \mu(x)$. Then, the flux is approximated by

$$\begin{aligned}
\mathbf{f}(x^{i+\frac{1}{2}}) &= q_1 v\gamma u\big\vert_{x^i} - q_1 v\gamma u\big\vert_{x^{i+1}} + (q_1 - q_2)v\gamma u\big\vert_{x^{i+1}} \\
&= -\Delta x\big\vert_{x^{i+\frac{1}{2}}}\Big(\frac{q_1 v\gamma u\big\vert_{x^i} - q_1 v\gamma u\big\vert_{x^{i+1}}}{x^i \;-\; x^{i+1}}\Big) + (q_1 - q_2)v\gamma u\big\vert_{x^{i+1}} \\
&\cong -\frac{1}{\mu}v\frac{\partial}{\partial x}\big(q_1 v\gamma u\big)\big\vert_{x^{i+\frac{1}{2}}} + (q_1 - q_2)v\gamma u\big\vert_{x^{i+1}}.
\end{aligned}$$

Note that the first term, $-\frac{1}{\mu}v\frac{\partial}{\partial x}\big(q_1 v\gamma u\big)$, in the final approximation can be written as $-\frac{1}{\mu}\frac{\partial}{\partial x}\big(q_1 v^2\gamma u\big)$ only if v is constant. Otherwise, one of the velocities should stay outside.

1.2. **Random walk in $\mathbf{R}^n$.** Next we extend the one dimensional flux to multi-dimensions. We introduce notations in multi-dimensions and rewrite the flux in a multi-dimensional context. Denote

$$\mathbf{e}_1 = (1, 0, \cdots, 0),\ \cdots,\ \mathbf{e}_n = (0, \cdots, 0, 1),\ \mathbf{v}_1 := v\mathbf{e}_1,\ \text{and}\ \mathbf{v}_2 = -v\mathbf{e}_1.$$

Then, one can easily check that the first component of a vector,

$$\mathbf{f}(\mathbf{x}) \cong -\frac{1}{\mu}\mathbf{v}_1\nabla\cdot(q_1\mathbf{v}_1\gamma u)\big\vert_{\mathbf{x}} + (q_1\mathbf{v}_1 + q_2\mathbf{v}_2)\gamma u\big\vert_{\mathbf{x}+\frac{\varepsilon}{2}},$$

is same as the previous flux for one space dimension and all the other components are zero. If we swap the role of $q_1\mathbf{v}_1$ and $q_2\mathbf{v}_2$ and take $\varepsilon \to 0$, we obtain

$$\mathbf{f}(\mathbf{x}) \cong -\frac{1}{\mu}\mathbf{v}_2\nabla\cdot(q_2\mathbf{v}_2\gamma u)\big\vert_{\mathbf{x}} + (q_1\mathbf{v}_1 + q_2\mathbf{v}_2)\gamma u\big\vert_{\mathbf{x}}.$$

Add the two expressions and divide the sum by 2 to obtain

$$\mathbf{f}(\mathbf{x}) = -\frac{1}{2\mu}\sum_{i=1}^{2}\Big(\mathbf{v}_i\nabla\cdot(q_i\mathbf{v}_i\gamma u)\Big) + \sum_{i=1}^{2}(q_i\mathbf{v}_i)\gamma u.$$

This is the one dimensional random walk flux in multi-space dimensions. Note that both v_i's and q_i's are spatially heterogeneous here.

In one space dimension, there are basically two directions, $\pm\mathbf{e}_1$, which is why we only took two velocity vectors. However, in multi-dimensions, we cannot enjoy this simplicity. Let V be the collection of all possible velocities in $\mathbf{R}^n$ and $q(\mathbf{x},\mathbf{v})$ be the probability distribution measure that a particle moves with the velocity $\mathbf{v}$ at the position $\mathbf{x}$. Here, the spatial heterogeneity is in q and $\int_V q(\mathbf{x},\mathbf{v}) = 1$. The flux is similarly given by

$$\mathbf{f} = -\frac{1}{2\mu}\int_V \Big(\mathbf{v}\nabla\cdot(\mathbf{v}q(\mathbf{x},\mathbf{v})\gamma u)\Big)d\mathbf{v} + \gamma u\mathbf{E}, \quad \mathbf{E} := \int_V \mathbf{v}q(\mathbf{x},\mathbf{v})d\mathbf{v}.$$

The corresponding conservation law is

$$u_t + \nabla\cdot(\gamma u\mathbf{E}) = \nabla\cdot\Big(\frac{1}{2\mu}\int_V \Big(\mathbf{v}\nabla\cdot(\mathbf{v}q(\mathbf{x},\mathbf{v})\gamma u)\Big)\,d\mathbf{v}\Big). \tag{1}$$

If $|\mathbf{v}|$ = constant, the first part of the flux is written as

$$-\frac{1}{2\mu}\int_V \Big(\mathbf{v}\nabla\cdot(\mathbf{v}q(\mathbf{x},\mathbf{v})\gamma u)\Big)d\mathbf{v} = -\frac{1}{2\mu}\nabla\cdot(\mathcal{D}\gamma u), \quad \mathcal{D} = \int_V (\mathbf{v}\otimes\mathbf{v})q(\mathbf{x},\mathbf{v})d\mathbf{v}, \tag{2}$$

where $\mathbf{v}\otimes\mathbf{v}$ denotes tensor product. Then, Eq. (1) can be simplified as given in Table 2 depending on the parameters. Note that, if $q(\mathbf{x},-\mathbf{v}) = q(\mathbf{x},\mathbf{v})$, the advection part disappears since $\mathbf{E} = 0$.

TABLE 2. Three diffusion equations obtained from (1) when $\mathbf{E} = 0$. In (D2) we denote by $\nabla\nabla : (Du) = \sum_{i,j=1}^n \frac{\partial^2(D_{ij}u)}{\partial x_i \partial x_j}$.

	diffusion equation	diffusion tensor	parameter conditions
(D1)	$u_t = \nabla\cdot\big(\frac{1}{2\mu}\nabla\cdot\big(\mathcal{D}u\big)\big)$	$\mathcal{D} = \int_V(\mathbf{v}\otimes\mathbf{v})q(\mathbf{x},\mathbf{v})d\mathbf{v}$	$\gamma = 1$, $\lvert\mathbf{v}\rvert$ is constant
(D2)	$u_t = \nabla\nabla : \big(Du\big)$	$D = \frac{1}{2\mu}\int_V(\mathbf{v}\otimes\mathbf{v})q(\mathbf{x},\mathbf{v})d\mathbf{v}$	$\gamma = 1$, $\lvert\mathbf{v}\rvert$ and μ are constant
(D3)	$u_t = \nabla\cdot\big(D\nabla u\big)$	$D = \frac{1}{2\mu(\mathbf{x})}\int_V(\mathbf{v}\otimes\mathbf{v})q(\mathbf{v})d\mathbf{v}$	$\gamma = 1, q = q(\mathbf{v})$

Note that the diffusion tensor could be spatially heterogeneous, $D = D(\mathbf{x})$, for both cases of (D2) and (D3). However, the corresponding diffusion equations are different. A constant state is a steady state of (D3), but not necessarily of (D2). In other words, the spatial heterogeneity in turning frequency $\mu = \mu(\mathbf{x})$ and the one in probability distribution $q = q(\mathbf{x},\mathbf{v})$ gives different consequences.

1.3. **Diffusion scaling and examples.** Let $\gamma = 1$, the walk length Δx be of order ε, and the turning frequency $\frac{1}{\Delta t}$ of order μ. Then, the speed is of order $\varepsilon\mu$ and, hence, $\mathcal{D}$ and $\mathbf{E}$ are of orders $\varepsilon^2\mu^2$ and $\varepsilon\mu$, respectively. Therefore, the conservation law (1) is written as

$$u_t + \varepsilon\mu\nabla\cdot(u\mathbf{E}_0) = \nabla\cdot\frac{\varepsilon^2\mu}{2}\Big(\nabla\cdot(\mathcal{D}_0 u)\Big),$$

where $\mathbf{E}_0$ and $\mathcal{D}_0$ are the ones obtained with unit velocity vectors. Diffusion scaling is the one that keeps $\varepsilon^2\mu$ constant when taking $\varepsilon\to 0$ and $\mu\to\infty$. Such a scaling is meaningful only when $\mathbf{E} = 0$.[1] Now we consider two example cases. For simplicity we only consider cases without advection, i.e., $\mathbf{E} = 0$. If $\mathbf{E}\neq 0$, anisotropic dispersal theory of fungus in vineyard requires a study of systems of fungus and spores (see [8].)

[1]If $\tilde{D}_0$ and $\mathbf{E}_0$ are obtained and $\mathbf{E}_0 \neq 0$, then μ and ε can be computed by measuring the diffusivity and advection. This may provide an alternative method of measuring instantaneous speed of Brownian particles [6].

Example 1 (Isotropic diffusion)**.** *In a traditional random walk system in* $\mathbf{R}^n$ *particles walk to one of* $2n$ *directions,* $\pm\mathbf{e}_i$*, and* $\gamma = 1$*. Let* $\Delta x = \varepsilon$ *and* $\Delta t = 1/\mu$*. The corresponding velocity set is* $V = \{\pm\varepsilon\mu\mathbf{e}_i\}_{i=1}^n$ *with the uniform probability* $q = 1/2n$*. Then,* $\mathbf{E} = 0$ *and* $D = \frac{\varepsilon^2\mu}{2n}I$*, where* I *is the identity matrix. The corresponding diffusion equation is*

$$u_t = \frac{\varepsilon^2\mu}{2n}\Delta u. \tag{3}$$

Instead of taking directions along coordinates, we may take all possible directions. Let $n = 2$*,* $\gamma = 1$*,* $V = \{\varepsilon\mu(\cos\theta, \sin\theta) : 0 \le \theta < 2\pi\}$*, and* $q = \frac{1}{2\pi}d\theta$*. Then,* $\mathbf{E} = 0$ *and*

$$D = \frac{1}{2\mu}\int_V (\mathbf{v}\otimes\mathbf{v})q(\mathbf{x},\mathbf{v}) = \frac{\varepsilon^2\mu}{4\pi}\int_0^{2\pi}\begin{pmatrix}\cos^2\theta & \cos\theta\sin\theta\\ \cos\theta\sin\theta & \sin^2\theta\end{pmatrix}d\theta = \frac{\varepsilon^2\mu}{4}\mathbf{I}.$$

Therefore, we still obtain (3)*. Remember that it is enough to take a simplified random walk system of* $2n$ *orthogonal walking directions to cover an isotropic case.*

Example 2 (Anisotropic diffusion)**.** *We may generalize the isotropic random walk system by taking* $\Delta x = a_i\varepsilon$*,* $i = 1, \cdots, n$*. Then,* $V = \{\pm\varepsilon\mu a_i\mathbf{e}_i\}_{i=1}^n$*,* $q = 1/2n$*,* $\mathbf{E} = 0$*, and*

$$D = \frac{\varepsilon^2\mu}{2n}\begin{pmatrix}a_1^2 & \cdots & 0\\ \vdots & \ddots & \vdots\\ 0 & \cdots & a_n^2\end{pmatrix}.$$

Therefore, the corresponding diffusion equation is anisotropic, i.e.,

$$u_t = \frac{\varepsilon^2\mu}{2n}(a_1^2u_{x_1x_1} + \cdots + a_n^2u_{x_nx_n}).$$

Let $n = 2$*,* $\gamma = 1$*,* $V = \{\varepsilon\mu(0.5\cos\theta, \sin\theta) : 0 \le \theta < 2\pi\}$*, and* $q = \frac{1}{2\pi}d\theta$*. Then,* $\mathbf{E} = 0$ *and*

$$D = \frac{1}{2\mu}\int_V (\mathbf{v}\otimes\mathbf{v})q(\mathbf{x},\mathbf{v}) = \frac{\varepsilon^2\mu}{16\pi}\int_0^{2\pi}\begin{pmatrix}\cos^2\theta & 2\cos\theta\sin\theta\\ 2\cos\theta\sin\theta & 4\sin^2\theta\end{pmatrix}d\theta = \frac{\varepsilon^2\mu}{16}\begin{pmatrix}1 & 0\\ 0 & 4\end{pmatrix}.$$

Therefore, we obtain the same anisotropic diffusion equation as the case with $a_1 = 1/2$ *and* $a_2 = 1$*. Note that we may obtain the same anisotropic diffusion using a simplified random walk system of* $2n$ *orthogonal walking directions if the directions are eigenvectors. However, if the symmetry is broken, the situation becomes more complicate.*

1.4. **Derivation of anisotropic diffusion from a kinetic equation.** Similar anisotropic diffusion equations have been obtained using a velocity jump process based on a kinetic transport equation and used to model biological phenomena (see Hillen *et al.* [4, 5]). The model equation is written as

$$u_t = \nabla\cdot\Big(\frac{1}{\mu}\nabla\cdot\big(\mathcal{D}\bar{u}\big)\Big), \tag{4}$$

which takes the same $\mathcal{D}$ in (2). It is surprising that two different approaches end up in the same equations. However, there is not the factor $\frac{1}{2}$ in (4) which exists in the equation (D1). The reason for this difference seems to be related to the fact that Eq. (4) models a velocity jump process and the jumping time Δt is a random variable with mean $1/\mu$. For example, if Δt is a random variable taking 0 or $\frac{2}{\mu}$ with the equal probability, then the mean is $1/\mu$ and the diffusivity is the double of the one with fixed jumping time $\Delta t = 1/\mu$.

2. Anisotropic diffusion in a vineyard

We consider the dispersal in a vineyard as an example of the anisotropic diffusion. Population spreading in an anisotropic environment has been studied in two different contexts, where one is focused on the role of dispersal (see [1, 2]) and the other is of growth rate (see [7, 9]). We assume the fungus in a vineyard is spread by wind, where the wind speed is constant, its direction is changed with a constant frequency μ, and a new wind direction is given randomly, i.e., the distribution of wind is isotropic. However, the anisotropic dispersal in a vineyard comes up since wind is deflected by grapevine rows. The effective wind speed and direction in a vineyard should account for the structure of each vineyard.

We assume a linear relation,

$$\mathbf{v} = A\mathbf{u},$$

where $\mathbf{u}$ is the wind velocity outside of the vineyard, $\mathbf{v}$ is the effective one that carries spores, and A is a symmetric matrix. For simplicity, we assume that $|\mathbf{u}| = 1$, the vineyard rows are parallel to the y axis, and the effectiveness matrix is given by

$$A = \begin{pmatrix} 0.5 & 0 \\ 0 & 1 \end{pmatrix}.$$

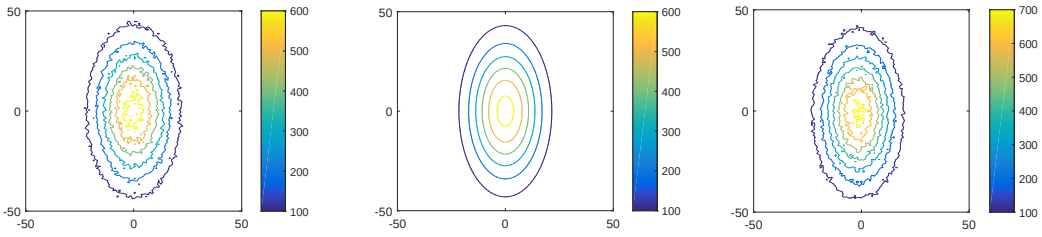
We set $\mathbf{u} = (\cos\theta, \sin\theta)$ for $0 \le \theta < 2\pi$. Then,

$$\mathbf{v} = A\mathbf{u} = \begin{pmatrix} 0.5 & 0 \\ 0 & 1 \end{pmatrix} \begin{pmatrix} \cos\theta \\ \sin\theta \end{pmatrix} = \begin{pmatrix} 0.5\cos\theta \\ \sin\theta \end{pmatrix}, \quad \text{and} \quad D = \frac{1}{16}\begin{pmatrix} 1 & 0 \\ 0 & 4 \end{pmatrix},$$

which is the case of Example 2 with $\varepsilon = \mu = \Delta t = 1$. Then, the anisotropic diffusion equation becomes

$$u_t = d_{11}u_{xx} + d_{22}u_{yy}, \quad d_{11} = 1/16, \ d_{22} = 1/4. \tag{5}$$

Now we are ready to do a Monte-Carlo simulation and compare it to the solution of the anisotropic diffusion equation. Each particle starts from the origin. Let p_n be the position of a particle after n steps. To take the next step, we choose an angle $0 \le \theta < 2\pi$ randomly and set $p_{n+1} = p_n + \mathbf{v}$ for $\mathbf{v} = (0.5\cos\theta, \sin\theta)$. Note that the jumping time is fixed by $\Delta t = 1$ in this simulation. In Figure 2(a) the contour map of the density distribution of a Monte-Carlo simulation of 10^6 particles is given when each of them finished 10^3 walks.



(a) Space jump ($t = 1000$). (b) Solution of the model. (c) Velocity jump ($t = 500$).

Figure 2. Contour maps of Monte-Carlo simulation and explicit solution (6).

The initial value for the diffusion equation (5) corresponding to the previous Monte-Carlo simulation is

$$u(\mathbf{x}, 0) = 10^6\delta(\mathbf{x}),$$

where $\delta(x)$ is the Dirac delta distribution. We can find the exact formula for the equation in terms of the heat kernel $\phi(\mathbf{x}, t)$ after changing variables

$$u(x, y, t) = \frac{10^6}{\sqrt{d_{11}d_{22}}} \times \phi(x/\sqrt{d_{11}}, y/\sqrt{d_{22}}, t) = \frac{10^6}{4\pi t\sqrt{d_{11}d_{22}}}\, e^{-(x^2/d_{11}+y^2/d_{22})/4t}. \tag{6}$$

Since the particles walked 10^3 steps and $\Delta t = \mu = 1$, the corresponding time is $t = 10^3$. The contour map of this explicit solution is given Figure 2(b). We can see that the solution of the anisotropic diffusion equation perfectly matches to the Monte-Carlo simulation. If one takes the diffusion equation (4), the corresponding diffusivity constants are $d_{11} = 1/8$ and $d_{22} = 1/2$. Therefore, to obtain the profile in Figure 2(b) using (4), one should compute the equation for $t = 500$. In Figure 2(c), a Monte-Carlo simulation of a velocity jumping process is given. In this simulation the jumping time Δt is not fixed, but $\ln(\Delta t)$ is a random variable which follows the normal distribution with a standard deviation $\sigma = 0.6$ and a mean zero. The final simulation time is $t = 500$ in this case.

3. Conclusion

There have been a lot of efforts to develop better biological diffusion models. Anisotropic diffusion is one of them which arises due to direction dependency in various mechanisms related to biological dispersal such as the probability to choose the direction, migration distance before making a turn, and the turning frequency itself. In this paper we have developed an anisotropic diffusion model (1) based on a general space jump process in multi-dimensions. This model covers a general case that the parameters may have spatial and temporal dependency and turns into simplified ones, (D1)–(D3), if parameters and the probability kernel are independent of the space variable. The Monte-Carlo simulation in Section 2 is developed as a simplest way to test anisotropic dispersal in a biology context. Its comparison to the exact solution shows that the diffusion equation explains anisotropic phenomenon correctly.

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