Spatio-temporal dynamic statistical modeling in practice: an introduction

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Reference Material

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INVITED PAPER

A general science-based framework for dynamical spatio-temporal models

Christopher K. Wikle · Mevin B. Hooten

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Abstract Spatio-temporal statistical models are increasingly being used across a wide variety of scientific disciplines to describe and predict spatially-explicit processes that evolve over time. Correspondingly, in recent years there has been a significant amount of research on new statistical methodology for such models. Although descriptive models that approach the problem from the second-order (covariance) perspective are important, and innovative work is being done in this regard, many real-world processes are dynamic, and it can be more efficient in some cases to characterize the associated spatio-temporal dependence by the use of dynamical models. The chief challenge with the specification of such dynamical models has been related to the curse of dimensionality. Even in fairly simple linear, first-order Markovian, Gaussian error settings, statistical models are often over parameterized. Hierarchical models have proven invaluable in their ability to deal to some extent with this issue by allowing dependency among groups of parameters. In addition, this framework has allowed for the specification of science based parameterizations (and associated prior distributions) in which classes of deterministic dynamical models (e.g., partial differential equations (PDEs), integro-difference equations (IDEs), matrix models, and agent-based models) are used to guide specific parameterizations. Most of the focus for the application of such models in statistics has been in the linear case. The problems mentioned above with linear dynamic models are com-

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Communicated by Domingo Morales.

This invited paper is discussed in the comments available at doi:10.1007/s11749-010-0210-6, doi:10.1007/s11749-010-0211-5, doi:10.1007/s11749-010-0212-4, doi:10.1007/s11749-010-0213-3.

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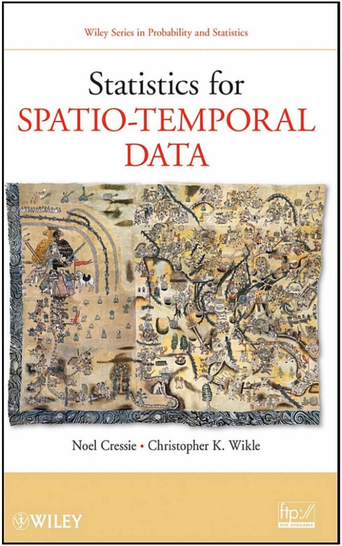

Wiley Series in Probability and Statistics

Statistics for
SPATIO-TEMPORAL
DATA

Noel Cressie • Christopher K. Wikle

WILEY

MOTIVATION

Objective

"The over-reaching goal of spatio-temporal modeling in statistics is related to the characterization of the *process of interest* in the presence of uncertain and (often) incomplete observations and system knowledge."[1]

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[1] Wikle and Hooten (2010), Test 19:418.

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- Prediction in space (interpolation)

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- Prediction in time (forecasting)
- Assimilate data and deterministic model output

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- Prediction in space (interpolation)
- Prediction in time (forecasting)
- Assimilate data and deterministic model output
- Inference on controlling parameters of the process

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[1] Wikle and Hooten (2010), Test 19:418.

Everything occurs in space and time

“no History without Geography” (Cressie and Wikle 2011, p. 1)

- Unrealistic to marginalize over space (i.e., time series) or time (i.e., spatial models)

<Cackling goose photo> <Subsistence hunter photo>

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- e.g., cackling geese

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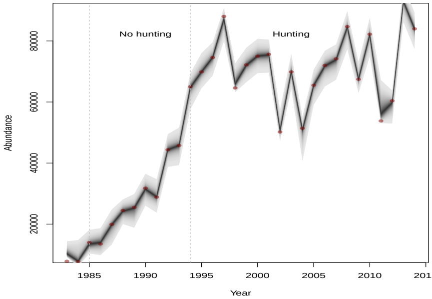

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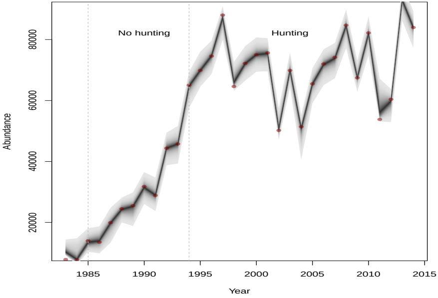

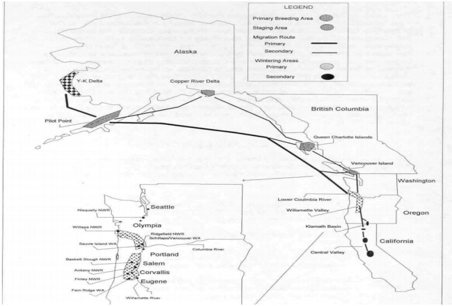

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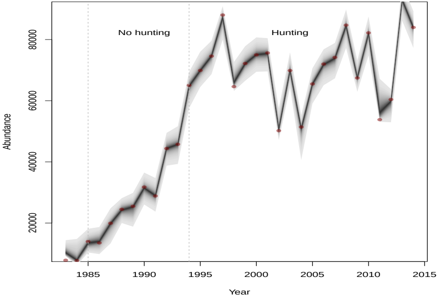

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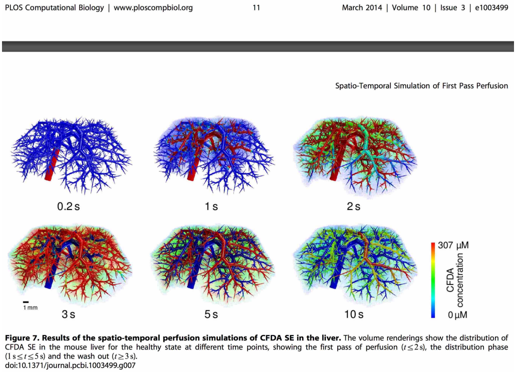
Everything occurs in space and time

- Relevant to most/all fields (human biology, epidemiology, city planning, economics)



PLOS Computational Biology | www.ploscompbiol.org 11 March 2014 | Volume 10 | Issue 3 | e1003499

Spatio-Temporal Simulation of First Pass Perfusion

Figure 7. Results of the spatio-temporal perfusion simulations of CFDA SE in the liver. The volume renderings show the distribution of CFDA SE in the mouse liver for the healthy state at different time points, showing the first pass of perfusion ($t \le 2\,\mathrm{s}$), the distribution phase ($1\,\mathrm{s} \le t \le 5\,\mathrm{s}$) and the wash out ($t \ge 3\,\mathrm{s}$).
doi:10.1371/journal.pcbi.1003499.g007

Everything occurs in space and time

- Relevant to most/all fields (human biology, epidemiology, city planning, economics)

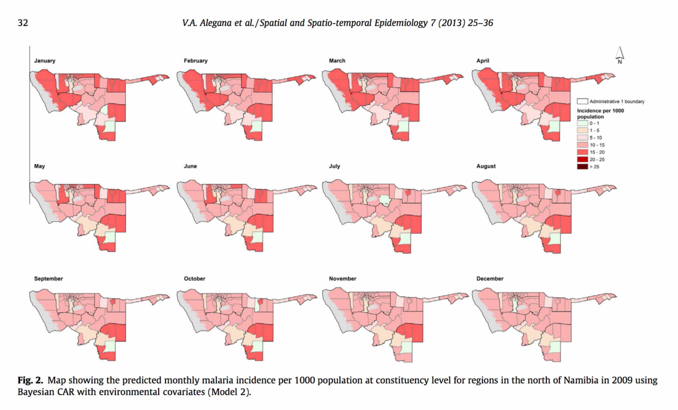
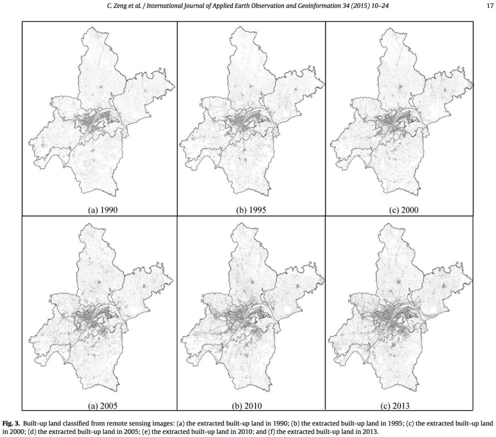

32 *V.A. Alegana et al./Spatial and Spatio-temporal Epidemiology 7 (2013) 25–36*

Fig. 2. Map showing the predicted monthly malaria incidence per 1000 population at constituency level for regions in the north of Namibia in 2009 using Bayesian CAR with environmental covariates (Model 2).

Everything occurs in space and time

- Relevant to most/all fields (human biology, epidemiology, city planning, economics)



C. Zeng et al. / International Journal of Applied Earth Observation and Geoinformation 34 (2015) 10–24 17

Fig. 3. Built-up land classified from remote sensing images: (a) the extracted built-up land in 1990; (b) the extracted built-up land in 1995; (c) the extracted built-up land in 2000; (d) the extracted built-up land in 2005; (e) the extracted built-up land in 2010; and (f) the extracted built-up land in 2013.

Addressing uncertainty

Observational uncertainty

- Measurement error
- False negatives/positives


Photo: Jamie Womble


Photo: P. Williams

Addressing uncertainty

Process uncertainty

- Model uncertainty
- Discretization

<Process uncertainty photo>

A science-based framework

- Incorporate knowledge obtained throughout the development of the subject-matter science at hand

<Stack of books photo>

Outline

In this module:

- Motivation
- Descriptive vs. dynamic spatio-temporal models
- PDEs
- Hierarchical modeling
- Dynamic spatio-temporal statistical models

Outline

Remaining modules:

2. Intro to finite differencing methods (PDE solvers)
3. Example 1: spread of disease in a wildlife population using binary spatio-temporal data
4. Example 2: spread of a population using wildlife survey data while accounting for measurement error

Spatio-temporal models: descriptive vs. dynamic

Two approaches for modeling spatio-temporal processes:

- Descriptive (aka *marginal*, *phenomenological*)
  - Characterize mean and covariance of the process

- Dynamic (aka *conditional*, *mechanistic*)
  - The process at a location evolves based on past values of the process at nearby locations in space and time

- Sometimes related through covariance function

- Neither approach is “new”

Descriptive spatio-temporal modeling

Simple example:

$$u(\mathsf{s}, t) = \mathbf{X}(\mathsf{s}, t)\boldsymbol{\beta} + \eta(\mathsf{s}) + \epsilon(t) + \delta(\mathsf{s}, t)$$

Descriptive spatio-temporal modeling

Simple example:

$$u(\mathbf{s}, t) = \mathbf{X}(\mathbf{s}, t)\boldsymbol{\beta} + \eta(\mathbf{s}) + \epsilon(t) + \delta(\mathbf{s}, t)$$

$$\begin{aligned}
\mathrm{cov}(\eta(\mathbf{s}), \eta(\mathbf{x})) &\equiv C_\eta(\mathbf{s}, \mathbf{x}) \equiv \sigma_\eta^2 \mathbf{I} \\
\mathrm{cov}(\epsilon(t), \epsilon(r)) &\equiv C_\epsilon(t, r) \equiv \sigma_\epsilon^2 \mathbf{I} \\
\mathrm{cov}(\delta(\mathbf{s}, t), \delta(\mathbf{x}, r)) &\equiv C_\delta(\mathbf{s}, \mathbf{x}; t, r) \equiv \sigma_\delta^2 \mathbf{I} \\
\mathrm{cov}(u(\mathbf{s}, t), u(\mathbf{x}, r)) &= \begin{cases} \sigma_\eta^2 + \sigma_\epsilon^2 + \sigma_\delta^2, & \text{if } \mathbf{s} = \mathbf{x}, t = r \\ \sigma_\eta^2, & \text{if } \mathbf{s} = \mathbf{x}, t \neq r \\ \sigma_\epsilon^2, & \text{if } \mathbf{s} \neq \mathbf{x}, t = r \\ 0, & \text{if } \mathbf{s} \neq \mathbf{x}, t \neq r \end{cases}
\end{aligned}$$

$$u(\mathbf{s}, t) \ \sim \ \mathrm{N}(\mathbf{X}(\mathbf{s}, t)\boldsymbol{\beta}, \mathrm{cov}(u(\mathbf{s}, t), u(\mathbf{x}, r)))$$

Descriptive spatio-temporal modeling

Advantages/Disadvantages of descriptive approach:

- Can be flexible, but requires non-negative definite covariance function (not always easy)
- Succinct, but informative summary of random processes in space and time
- Difficult to look at covariance function and understand spatio-temporal process
- Useful when understanding of the process is limited
- Available covariance functions often unrealistic for spatio-temporal processes (e.g., separable covariance functions)
- Dominated spatio-temporal statistics until the 21st century

Dynamic spatio-temporal modeling

Alternatively:

- Dependence motivated by evolution of process through time and in space
- Incorporate our knowledge of process evolution
- Use PDEs (or other mechanistic models; e.g., IDE) to motivate dynamics
- Nonnegative definite covariance function for free
- Natural framework for forecasting
- Computationally intensive

PARTIAL DIFFERENTIAL EQUATIONS

PDEs

What are they?

- Models with multiple variables, expressed in terms of changes in those variables (e.g., time, space, or space-time).
- When involving time and space, these are *dynamic spatio-temporal models* (DSTMs).

PDEs

What are they?

- Models with multiple variables, expressed in terms of changes in those variables (e.g., time, space, or space-time).
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Environmental:

- Movement of gases and fluids.

Ecology:

- Movement of organisms in environment.

Epidemiology:

- Movement of disease through living systems.

PDE Model

One example:

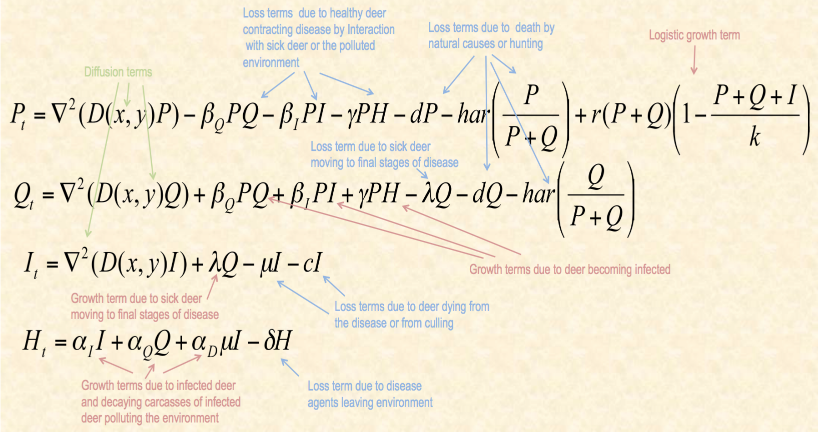
- Reaction-diffusion model (dispersal and growth):

$$\frac{\partial u}{\partial t} = \underbrace{\frac{\partial}{\partial x}\left(\delta(x,y)\frac{\partial u}{\partial x}\right) + \frac{\partial}{\partial y}\left(\delta(x,y)\frac{\partial u}{\partial y}\right)}_{\text{spread in space}} + \underbrace{g(r,k,\mathbf{u})}_{\text{growth}}$$

- The rate of change of the process u equals the spread of u in space plus the (potentially non-linear) growth which can depend on parameters r, and k

PDE for Chronic Wasting Disease

Another example:[1]



Diffusion terms

Loss terms due to healthy deer contracting disease by Interaction with sick deer or the polluted environment

Loss terms due to death by natural causes or hunting

Logistic growth term

$$P_t = \nabla^2(D(x,y)P) - \beta_Q PQ - \beta_I PI - \gamma PH - dP - har\left(\frac{P}{P+Q}\right) + r(P+Q)\left(1 - \frac{P+Q+I}{k}\right)$$

Loss term due to sick deer moving to final stages of disease

$$Q_t = \nabla^2(D(x,y)Q) + \beta_Q PQ + \beta_I PI + \gamma PH - \lambda Q - dQ - har\left(\frac{Q}{P+Q}\right)$$

$$I_t = \nabla^2(D(x,y)I) + \lambda Q - \mu I - cI$$

Growth terms due to deer becoming infected

Growth term due to sick deer moving to final stages of disease

Loss terms due to deer dying from the disease or from culling

$$H_t = \alpha_I I + \alpha_Q Q + \alpha_D \mu I - \delta H$$

Growth terms due to infected deer and decaying carcasses of infected deer polluting the environment

Loss term due to disease agents leaving environment

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[1] Garlick et al. (2013), Journal of Mathematical Biology 69:369–399

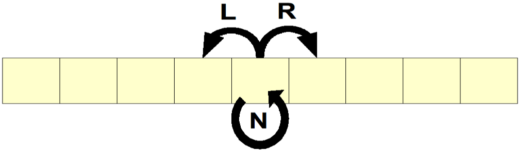
Ecological diffusion

$$\frac{\partial u(\mathbf{s},t)}{\partial t} = \left(\frac{\partial^2}{\partial s_1^2} + \frac{\partial^2}{\partial s_2^2}\right)[\delta(\mathbf{s},t)u(\mathbf{s},t)] + \gamma(\mathbf{s})u(\mathbf{s},t)$$

How do PDEs arise in nature?

Example: Diffusion-approximation model for a population of organisms moving according to an uncorrelated random walk in a heterogeneous environment (congregating in desirable habitat)

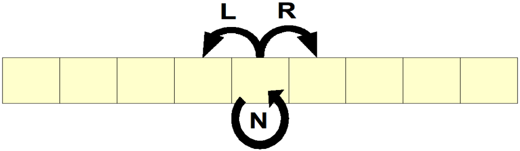
- Move left with $p_L(x, t)$.
- Move right with $p_R(x, t)$.
- Move nowhere with $p_N(x, t)$.
- $p(x, t)$: Probability of animal at location x and time t.



Lagrangian Model: uncorrelated random walk

Recurrence Equation:

$$
\begin{aligned}
p(x,t) = {} & p_L(x+\Delta x, t-\Delta t)p(x+\Delta x, t-\Delta t) \\
& + p_R(x-\Delta x, t-\Delta t)p(x-\Delta x, t-\Delta t) \\
& + p_N(x, t-\Delta t)p(x, t-\Delta t)
\end{aligned}
$$



We seek a differential model on $p(x,t)$, thus we need to get rid of Δx and Δt.

Taylor Series Expansion[1]

$$
\begin{aligned}
p(x, t-\Delta t) &= p - \Delta t \frac{\partial p}{\partial t} + \cdots \\
p(x-\Delta x, t-\Delta t) &= p - \Delta t \frac{\partial p}{\partial t} - \Delta x \frac{\partial p}{\partial x} + \frac{\Delta x^2}{2} \frac{\partial^2 p}{\partial x^2} + \cdots \\
p(x+\Delta x, t-\Delta t) &= p - \Delta t \frac{\partial p}{\partial t} + \Delta x \frac{\partial p}{\partial x} + \frac{\Delta x^2}{2} \frac{\partial^2 p}{\partial x^2} + \cdots
\end{aligned}
$$

---

[1] Turchin (1998), Quantitative Analysis of Movement

Substitution

$$
\begin{aligned}
p = {} & (p_L + p_N + p_R)p - \Delta t \frac{\partial p}{\partial t}(p_L + p_N + p_R) - \Delta t p \frac{\partial}{\partial t}(p_L + p_N + p_R) \\
& - \Delta x \frac{\partial p}{\partial x}(p_R - p_L) - \Delta x p \frac{\partial}{\partial t}(p_R - p_L) \\
& + \frac{\Delta x^2}{2} \frac{\partial^2 p}{\partial x^2}(p_L + p_R) + \Delta x^2 \frac{\partial p}{\partial x} \frac{\partial}{\partial x}(p_L + p_R) + p \frac{\Delta x^2}{2} \frac{\partial^2}{\partial x^2}(p_L + p_R) \\
& + \cdots
\end{aligned}
$$

Eulerian Equation

$$\frac{\partial p}{\partial t} = -\frac{\partial}{\partial x}(\beta p) + \frac{\partial^2}{\partial x^2}(\delta p)$$

- $\beta = \Delta x(p_R - p_L)/\Delta t$
- $\delta = \Delta x^2(p_R + p_L)/2\Delta t$

Ecological Diffusion

With N organisms $u(x,t) \equiv Np(x,t)$:

$$\frac{\partial u}{\partial t} = \frac{\partial^2}{\partial x^2}(\delta u)$$

Ecological Diffusion

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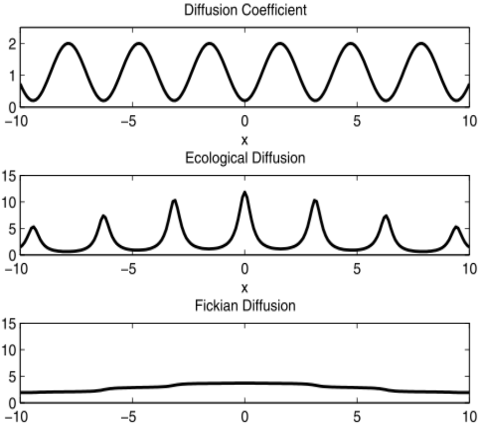
$$\frac{\partial u}{\partial t} = \frac{\partial^2}{\partial x^2}(\delta u)$$

Note, other forms of diffusion:

$$\begin{aligned} \frac{\partial u}{\partial t} &= \frac{\partial}{\partial x}\delta\frac{\partial}{\partial x}u \quad \text{(Fickian)} \\ \frac{\partial u}{\partial t} &= \delta\frac{\partial}{\partial x^2}u \qquad \text{(Plain)} \end{aligned}$$

Types of Diffusion[1]



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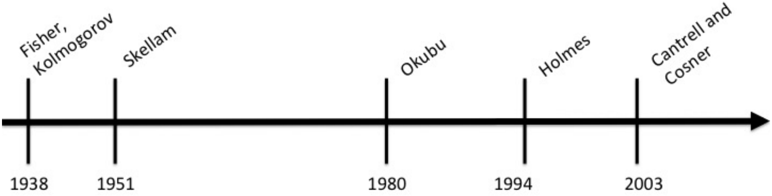
[1] Garlick et al. (2010), Bulletin of Mathematical Biology 73:2088–2108

Deterministic dynamic spatio-temporal modeling



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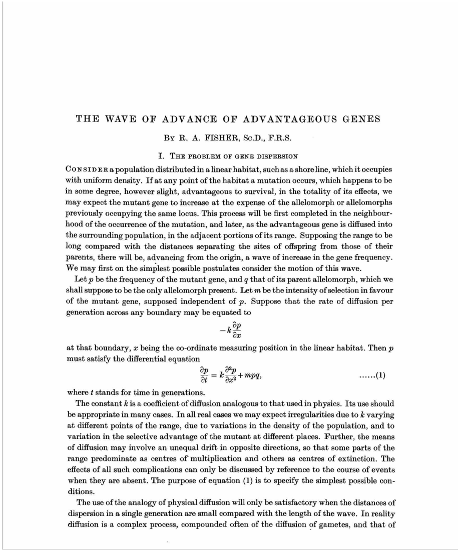


THE WAVE OF ADVANCE OF ADVANTAGEOUS GENES

By R. A. FISHER, Sc.D., F.R.S.

I. The problem of gene dispersion

Consider a population distributed in a linear habitat, such as a shore line, which it occupies with uniform density. If at any point of the habitat a mutation occurs, which happens to be in some degree, however slight, advantageous to survival, in the totality of its effects, we may expect the mutant gene to increase at the expense of the allelomorph or allelomorphs previously occupying the same locus. This process will be first completed in the neighbourhood of the occurrence of the mutation, and later, as the advantageous gene is diffused into the surrounding population, in the adjacent portions of its range. Supposing the range to be long compared with the distances separating the sites of offspring from those of their parents, there will be, advancing from the origin, a wave of increase in the gene frequency. We may first on the simplest possible postulates consider the motion of this wave.

Let p be the frequency of the mutant gene, and q that of its parent allelomorph, which we shall suppose to be the only allelomorph present. Let m be the intensity of selection in favour of the mutant gene, supposed independent of p. Suppose that the rate of diffusion per generation across any boundary may be equated to

$$-k\frac{\partial p}{\partial x}$$

at that boundary, x being the co-ordinate measuring position in the linear habitat. Then p must satisfy the differential equation

$$\frac{\partial p}{\partial t} = k\frac{\partial^2 p}{\partial x^2} + mpq, \qquad \text{......(1)}$$

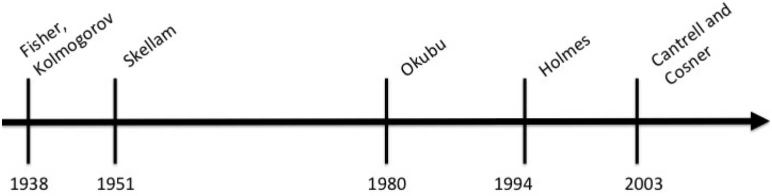
where t stands for time in generations.

The constant k is a coefficient of diffusion analogous to that used in physics. Its use should be appropriate in many cases. In all real cases we may expect irregularities due to k varying at different points of the range, due to variations in the density of the population, and to variation in the selective advantage of the mutant at different places. Further, the means of diffusion may involve an unequal drift in opposite directions, so that some parts of the range predominate as centres of multiplication and others as centres of extinction. The effects of all such complications can only be discussed by reference to the course of events when they are absent. The purpose of equation (1) is to specify the simplest possible conditions.

The use of the analogy of physical diffusion will only be satisfactory when the distances of dispersion in a single generation are small compared with the length of the wave. In reality diffusion is a complex process, compounded often of the diffusion of gametes, and that of

<Fisher photo>

Deterministic dynamic spatio-temporal modeling



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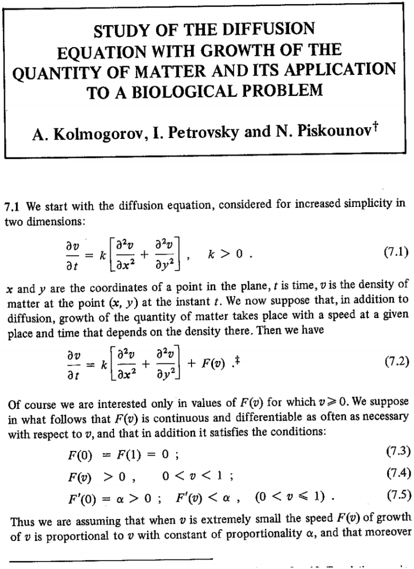

STUDY OF THE DIFFUSION EQUATION WITH GROWTH OF THE QUANTITY OF MATTER AND ITS APPLICATION TO A BIOLOGICAL PROBLEM

A. Kolmogorov, I. Petrovsky and N. Piskounov[†]

7.1 We start with the diffusion equation, considered for increased simplicity in two dimensions:

$$\frac{\partial v}{\partial t} = k\left[\frac{\partial^2 v}{\partial x^2} + \frac{\partial^2 v}{\partial y^2}\right], \quad k > 0\ . \tag{7.1}$$

x and y are the coordinates of a point in the plane, t is time, v is the density of matter at the point (x, y) at the instant t. We now suppose that, in addition to diffusion, growth of the quantity of matter takes place with a speed at a given place and time that depends on the density there. Then we have

$$\frac{\partial v}{\partial t} = k\left[\frac{\partial^2 v}{\partial x^2} + \frac{\partial^2 v}{\partial y^2}\right] + F(v)\ .^{\ddagger} \tag{7.2}$$

Of course we are interested only in values of $F(v)$ for which $v \geqslant 0$. We suppose in what follows that $F(v)$ is continuous and differentiable as often as necessary with respect to v, and that in addition it satisfies the conditions:

$$F(0) = F(1) = 0\ ; \tag{7.3}$$

$$F(v) > 0\ , \qquad 0 < v < 1\ ; \tag{7.4}$$

$$F'(0) = \alpha > 0\ ; \quad F'(v) < \alpha\ , \quad (0 < v \leqslant 1)\ . \tag{7.5}$$

Thus we are assuming that when v is extremely small the speed $F(v)$ of growth of v is proportional to v with constant of proportionality α, and that moreover

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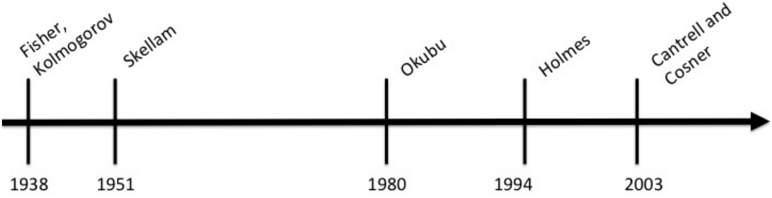
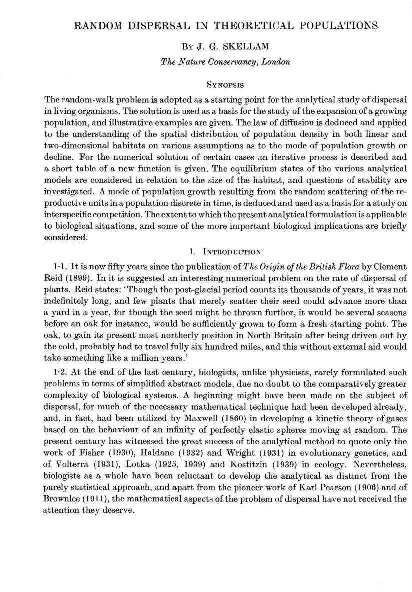
<Kolmogorov photo>

Deterministic dynamic spatio-temporal modeling



Deterministic dynamic spatio-temporal modeling



RANDOM DISPERSAL IN THEORETICAL POPULATIONS

By J. G. SKELLAM

The Nature Conservancy, London

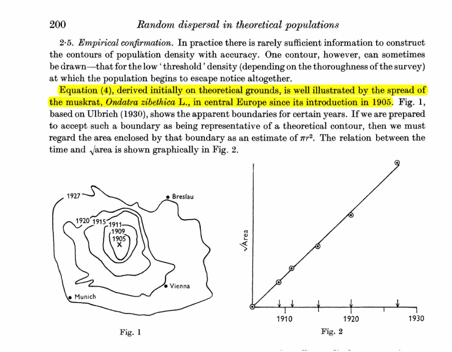
Synopsis

The random-walk problem is adopted as a starting point for the analytical study of dispersal in living organisms. The solution is used as a basis for the study of the expansion of a growing population, and illustrative examples are given. The law of diffusion is deduced and applied to the understanding of the spatial distribution of population density in both linear and two-dimensional habitats on various assumptions as to the mode of population growth or decline. For the numerical solution of certain cases an iterative process is described and a short table of a new function is given. The equilibrium states of the various analytical models are considered in relation to the size of the habitat, and questions of stability are investigated. A mode of population growth resulting from the random scattering of the reproductive units in a population discrete in time, is deduced and used as a basis for a study on interspecific competition. The extent to which the present analytical formulation is applicable to biological situations, and some of the more important biological implications are briefly considered.

1. Introduction

1·1. It is now fifty years since the publication of *The Origin of the British Flora* by Clement Reid (1899). In it is suggested an interesting numerical problem on the rate of dispersal of plants. Reid states: 'Though the post-glacial period counts its thousands of years, it was not indefinitely long, and few plants that merely scatter their seed could advance more than a yard in a year, for though the seed might be thrown further, it would be several seasons before an oak for instance, would be sufficiently grown to form a fresh starting point. The oak, to gain its present most northerly position in North Britain after being driven out by the cold, probably had to travel fully six hundred miles, and this without external aid would take something like a million years.'

1·2. At the end of the last century, biologists, unlike physicists, rarely formulated such problems in terms of simplified abstract models, due no doubt to the comparatively greater complexity of biological systems. A beginning might have been made on the subject of dispersal, for much of the necessary mathematical technique had been developed already, and, in fact, had been utilized by Maxwell (1860) in developing a kinetic theory of gases based on the behaviour of an infinity of perfectly elastic spheres moving at random. The present century has witnessed the great success of the analytical method to quote only the work of Fisher (1930), Haldane (1932) and Wright (1931) in evolutionary genetics, and of Volterra (1931), Lotka (1925, 1939) and Kostitzin (1939) in ecology. Nevertheless, biologists as a whole have been reluctant to develop the analytical as distinct from the purely statistical approach, and apart from the pioneer work of Karl Pearson (1906) and of Brownlee (1911), the mathematical aspects of the problem of dispersal have not received the attention they deserve.



200 *Random dispersal in theoretical populations*

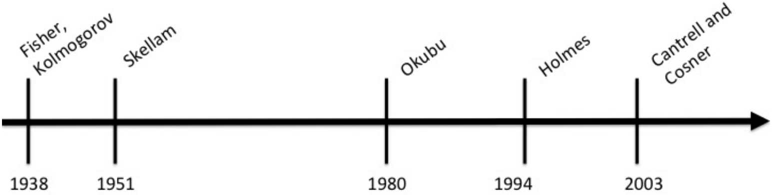
2·5. *Empirical confirmation.* In practice there is rarely sufficient information to construct the contours of population density with accuracy. One contour, however, can sometimes be drawn—that for the low 'threshold' density (depending on the thoroughness of the survey) at which the population begins to escape notice altogether.

Equation (4), derived initially on theoretical grounds, is well illustrated by the spread of the muskrat, *Ondatra zibethica* L., in central Europe since its introduction in 1905. Fig. 1, based on Ulbrich (1930), shows the apparent boundaries for certain years. If we are prepared to accept such a boundary as being representative of a theoretical contour, then we must regard the area enclosed by that boundary as an estimate of πr^2. The relation between the time and $\sqrt{\text{area}}$ is shown graphically in Fig. 2.

Fig. 1

Fig. 2

Deterministic dynamic spatio-temporal modeling



Statistical implementation

How do we incorporate deterministic PDEs in a statistical framework?

- Assume process can be observed (potentially with error)
- Assume PDE is scientifically motivated, but not exact
- Seek to estimate model parameters, given the data

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- Seek to estimate model parameters, given the data

Or alternatively:

- Uncertainty in data
- Uncertainty in spatio-temporal process
- Uncertainty in parameters
- [data, process, parameters]

Hierarchical Modeling

Hierarchical modeling

Joint uncertainty: $[\mathbf{y}, \mathbf{u}, \boldsymbol{\theta}]$

We can factor joint distribution into a product of conditional distributions:[1]

$$[\mathbf{y}, \mathbf{u}, \boldsymbol{\theta}] = [\mathbf{y}|\mathbf{u}, \boldsymbol{\theta}][\mathbf{u}|\boldsymbol{\theta}][\boldsymbol{\theta}]$$

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[1] Berliner (1996), Hierarchical Bayesian time series models *in* Maximum entropy and Bayesian methods

Hierarchical modeling

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$$[\mathbf{y}, \mathbf{u}, \boldsymbol{\theta}] = [\mathbf{y}|\mathbf{u}, \boldsymbol{\theta}][\mathbf{u}|\boldsymbol{\theta}][\boldsymbol{\theta}]$$

- Data model: $[\mathbf{y}|\mathbf{u}, \boldsymbol{\theta}]$
- Process model: $[\mathbf{u}|\boldsymbol{\theta}]$
- Parameter model: $[\boldsymbol{\theta}]$

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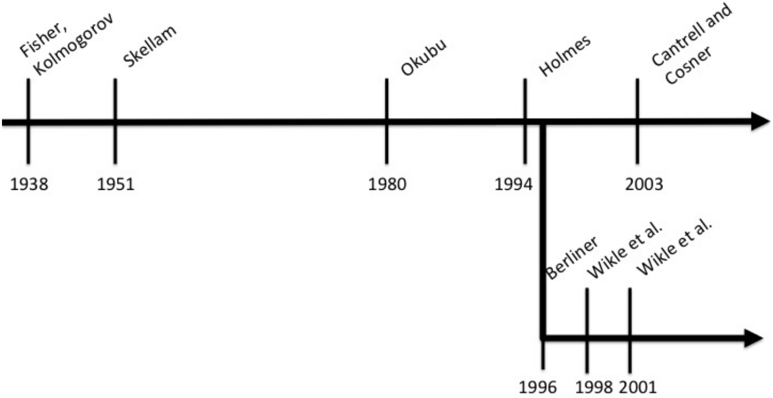
Hierarchical modeling

- $[\mathbf{y}|\mathbf{u},\boldsymbol{\theta}]$: Uncertainty in the observations
    - Error in counts
    - Experience of observers
    - Detection probability

- $[\mathbf{u}|\boldsymbol{\theta}]$: Uncertainty and complexity in spatio-temporal process
    - diffusion and growth
    - species interactions
    - important environmental covariates

- $[\boldsymbol{\theta}]$: Uncertainty in parameters
    - Random variation in parameters

Dynamic spatio-temporal *statistical* modeling



Descriptive vs. dynamic: *revisited*

Two approaches for modeling spatio-temporal processes:

- Descriptive (aka *marginal*, *phenomenological*)
- Dynamic (aka *conditional*, *mechanistic*)

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[1] Hefley et al. (2017), Ecology 98:632–646

Descriptive vs. dynamic: *revisited*

Two approaches for modeling spatio-temporal processes:

- Descriptive (aka *marginal*, *phenomenological*)
- Dynamic (aka *conditional*, *mechanistic*)

Data models:[1]

- Descriptive: $[\mathbf{y}|\boldsymbol{\theta}_m]$
  - Difficult to derive realistic covariance matrices

- Dynamic: $[\mathbf{y}|\mathbf{u}, \boldsymbol{\theta}_c]$
  - All of the complicated spatio-temporal structure can come from the conditional mean, simplifying conditional dependence

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Hierarchical DSTM

Data Model: $y(\mathbf{s}_i, t) \sim [y(\mathbf{s}_i, t) | u(\mathbf{s}_i, t), \phi],$

Process Models:

$$\begin{aligned} \frac{\partial u(\mathbf{s}_i, t)}{\partial t} &= \left(\frac{\partial^2}{\partial s_1^2} + \frac{\partial^2}{\partial s_2^2} \right) [\delta(\mathbf{s}, t) u(\mathbf{s}, t)] + \gamma(\mathbf{s}_i) u(\mathbf{s}_i, t), \\ u(\mathbf{s}_i, 1) &= f(\zeta_i), \\ \delta(\mathbf{s}, t) &= g(\mathbf{X}_t \boldsymbol{\beta}), \\ \gamma(\mathbf{s}_i, t) &= h(\mathbf{W}_t \boldsymbol{\alpha}), \end{aligned}$$

Parameter Model: $\boldsymbol{\theta} \sim [\phi, \boldsymbol{\alpha}, \boldsymbol{\beta}, \boldsymbol{\zeta}]$

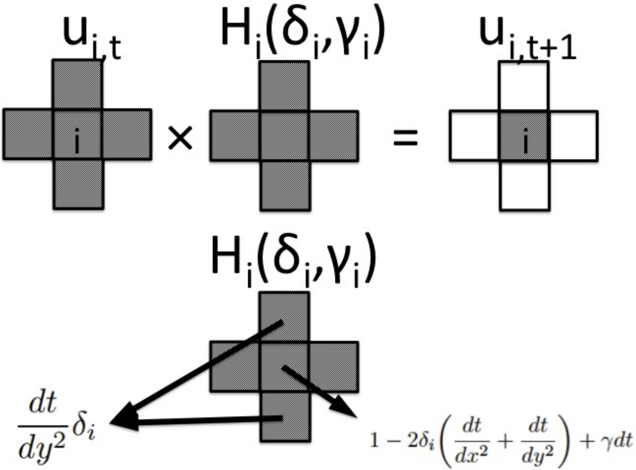
Computational implementation

Simple finite-difference discretization and Markov assumption implies the vector difference equation

$$\mathbf{u}_t = \mathbf{H}\mathbf{u}_{t-\Delta t} + \mathbf{H}^{(\mathrm{b})}\mathbf{u}^{(\mathrm{b})}_{t-\Delta t}$$

where $\mathbf{u}_t \approx u(\mathbf{s}, t)$

Finite differencing



Hierarchical DSTM

Data Model: $y_{i,t} \sim [y_{i,t} | u_{i,t}, \phi]$,

$$\textbf{Process Models: } \begin{aligned} \mathbf{u}_t &= \mathbf{H}\mathbf{u}_{t-\Delta t}, \\ \mathbf{u}_1 &= f(\zeta), \\ \boldsymbol{\delta}_t &= g(\mathbf{X}_t \boldsymbol{\beta}), \\ \boldsymbol{\gamma}_t &= h(\mathbf{W}_t \boldsymbol{\alpha}), \end{aligned}$$

Parameter Model: $\boldsymbol{\theta} \sim [\phi, \boldsymbol{\alpha}, \boldsymbol{\beta}, \zeta]$

Applications of DSTM statistical models

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[1] Hooten and Wikle (2008), Environmental and Ecological Statistics 15:59–70

Applications of DSTM statistical models

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[1] Hooten et al. (2010), Spatial and Spatio-temporal Epidemiology 1:177–185