The "Cumulative" Formulation of (Physiologically) Structured Population Models

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1. STRUCTURED POPULATION MODELS: A CHALLENGE FOR SEMIGROUP THEORY?

The formulation of a physiologically structured population model starts at the individual level (i-level, for short). After the choice of finitely many i-state variables and the feasible i-state space $\Omega \subset \mathbb{R}^n$ one specifies how

- i-state change ('growth')
- probability per unit of time of dying
- probability per unit of time of giving birth
- distribution of i-state of offspring at birth
- influence on the environment ('consumption')

depend on the i-state of the individual concerned and on the state of the environment (see METZ & DIEKMANN, 1986, for a systematic exposition and a wealth of examples).

Lifting the i-model to the population level (p-level, for short) is, at least as long as one restricts attention to the deterministic (i.e. large numbers of individuals) approximation and to formal aspects, a matter of straightforward mathematical book-keeping. If one works with densities, the p-state space is $L_1(\Omega)$ and the Kolmogorov forward equation

takes the form of a first order partial differential equation (pde) with non-local terms or boundary conditions to describe the reproduction. If one chooses the space of measures $M(\Omega)$ as p-state space it is easiest to write down the Kolmogorov backward equation, i.e. the pre-adjoint equation on $C_0(\Omega)$. Again one obtains a first order pde with non-local terms (see METZ & DIEKMANN, 1986, HEIJMANS 1986[a,b], DIEKMANN, to appear).

Thus the models are, completely in line with applied mathematical tradition, formulated in terms of rates and differential equations. The task for mathematicians is now to show that the pde's generate dynamical systems and to analyse how the qualitative and quantitative behaviour of the solution operators depends on the ingredients of the model (see WEBB, 1985, for the special case of age structure).

In order to keep models parameter-scarce, biologists will come up with 'idealizations' of reality which create discontinuities (e.g. individuals start reproducing exactly when their size passes a certain threshold value; size at birth has a fixed value). Such 'idealizations' severely complicate the task of describing the domain of definition of infinitesimal generators in the precise functional analytic sense.

Motivated to some, or even a large, extent by structured population models various linear and semi-linear methods have been developed in recent years to deal with refractory generators, in particular

-   regularization via resolvent (DESCH & SCHAPPACHER 1984)
-   integrated semigroups (ARENDT 1987, KELLERMAN & HIEBER 1989, NEUBRANDER 1988, THIEME 1990[c], ARENDT, NEUBRANDER & SCHLOTTERBECK to appear, LUMER 1990)
-   restriction of maximal operator (GREINER 1987)
-   $\odot$ * calculus (CLÉMENT et al. 1987, 1989, VAN NEERVEN 1992)
-   non-densely defined operators (BÉNILAN, CRANDALL & PAZY 1988, DA PRATO & SINESTRARI 1987, THIEME 1990[b])

All of these methods work well when the i-state space is one dimensional and one restricts to autonomous linear or semilinear problems. For higher dimensional i-state space the best result in published form seems to be in TUCKER & ZIMMERMAN (1988), which is less functional analytic in spirit (and does not cover the case of a fixed birth-size).

It seems legitimate to ask why a general theory is still missing, despite the effort of several people (notably the authors) over a number of years. Are we asking for too much?

Let us concentrate for a moment on the case where the environmental variables are given functions of time (Mathematically speaking: the non-autonomous linear case). While an individual is 'growing', its i-state follows an orbit in Ω. In pde jargon these orbits are the (projected) characteristics. Due to the time-dependence in the 'growth' rates, these orbits change in time. At the p-level we have a density or measure translated along the orbits. The pde presupposes that we have differentiability, in some sense, along the changing orbits.

In the autonomous case the orbits are fixed. The Hille-Yosida theorem tells us that it is possible to unambiguously define a generator which completely characterizes the semigroup. In the non-autonomous case we have an evolutionary system of operators and there is no analogue of the Hille-Yosida theorem for those: it is questionable whether a generating family exists that completely characterizes the evolutionary system. In fact, the example of translating a function along a family of curves, which deform with time, nicely illustrates the difficulties involved.

The great advantage of differential equations as a modelling tool is that we can consider different mechanisms (like 'growth', death and reproduction) separately and then simply add their contributions since, in infinitesimal time intervals, they act independently. Yet there is a technical price (as another manifestation of technical difficulties, notice that birth rates may be undefined on time sets of measure zero, while the numbers, which one obtains by integration, are perfectly well defined). So do we insist on differential equations as the language to formulate the models?

In order to answer this question one has to take stock of alternatives. The aim of this paper is to demonstrate that a very natural and attractive alternative exists (and a very old and familiar one, in fact): integral equations.

2. MODEL INGREDIENTS AT THE i-LEVEL

In this and the next section we consider the situation in which the environmental variables are a given function of time, denoted by E. Even though all objects introduced below depend on E, we shall not express this dependence in our notation. In section 4 we shall describe how nonlinear problems are obtained by feedback through the environment and there we shall employ a more precise (but also more cumbersome) notation.

In this section we list one by one the modelling ingredients related to the various mechanisms of change in i-state or number of individuals. We do so in 'cumulative' terms, as opposed to rates. We first present the ingredients in the form they are needed at the p-level and then discuss how, in certain special situations, these ingredients themselves can be decomposed into more elementary building-blocks.

(i) *i-movement and survival*

$u(t, t_0, y_0)(\omega)$ =   probability that an individual that is in state y_0 at time t_0
                              will still be alive at time t and then have i-state in the
                              (measurable) subset ω of Ω

The interpretation requires that u satisfies the consistency relation

$$u(t + s, t_0, y_0)(\omega) = \int_\Omega u(t + s, t, y)(\omega)u(t, t_0, y_0)(dy) \tag{2.1}$$

which is often called the Chapman-Kolmogorov equation. The survival function $\mathcal{F}$ is defined by

$$\mathcal{F}(t, t_0, y_0) = u(t, t_0, y_0)(\Omega) = \int_\Omega u(t, t_0, y_0)(dy) \tag{2.2}$$

Taking $\omega = \Omega$ in (2.1) we find that the relation

$$\mathcal{F}(t + s, t_0, y_0) = \int_\Omega \mathcal{F}(t + s, t, y)u(t, t_0, y_0)(dy) \tag{2.3}$$

should hold.

In the special case of deterministic growth one postulates the existence of a function $Y(t, t_0, y_0)$, giving the i-state at time t, given that the i-state was y_0 at time t_0 and given survival. One then takes the survival function $\mathcal{F}$ as a second building-block and puts

$$u(t, t_0, y_0) = \delta_{Y(t,t_0,y_0)} \mathcal{F}(t, t_0, y_0) \tag{2.4}$$

where, as usual, δ_y denotes the unit measure concentrated in the point y. Substituting (2.4) into (2.1) we find that Y should have the semigroup property ·

$$Y(t + s, t_0, y_0) = Y(t + s, t, Y(t, t_0, y_0)) \tag{2.5}$$

while $\mathcal{F}$ should satisfy the consistency condition

$$\mathcal{F}(t + s, t_0, y_0) = \mathfrak{R}(t + s, t, Y(t, t_0, y_0)) \, \mathfrak{R}(t, t_0, y_0). \tag{2.6}$$

Most often both Y and $\mathcal{F}$ will be derived from a differential equation, respectively

$$\frac{dY}{dt} = v(Y, E) \quad , \quad Y(t_0, t_0, y_0) = y_0, \tag{2.7}$$

and

$$\frac{d\mathcal{F}}{dt} = -\mu(Y, E)\mathcal{F} \quad , \quad \mathfrak{R}(t_0, t_0, y_0) = 1, \tag{2.8}$$

and then (2.5) and (2.6) will automatically hold. Note that we can write

$$\mathfrak{R}(t, t_0, y_0) = \exp(-\int_{t_0}^{t} \mu(Y(\tau, t_0, y_0), E(\tau))d\tau) \tag{2.9}$$

since (2.7) is decoupled from (2.8). When we start from data, rather than from model equations, $\mathcal{F}$ is the measured quantity and μ is introduced as minus its logarithmic derivative.

(ii) *reproduction*

$\Lambda(t, t_0, y_0)(\omega)$ = expected total number of direct offspring (i.e. children but not grand children, great grand children etc.), with state-at-birth in the (measurable) subset ω of Ω, of an individual having i-state y_0 at time t_0, in the time-interval $[t_0, t]$

Following the terminology of branching processes (JAGERS, 1989, 1991) we shall call Λ the *reproduction kernel*. Note that Λ is unconditional (i.e. we have not conditioned on survival of the individual till time t). Consequently the appropriate additive consistency relation is

$$\Lambda(t + s, t_0, y_0) = \Lambda(t, t_0, y_0) + \int_\Omega \Lambda(t + s, t, y)u(t, t_0, y_0)(dy). \tag{2.10}$$

In the special case of deterministic i-movement (2.10) reduces to

$$\Lambda(t + s, t_0, y_0) = \Lambda(t, t_0, y_0) + \Lambda(t + s, t, Y(t, t_0, y_0))\mathcal{F}(t, t_0, y_0). \tag{2.11}$$

Very often the components

$\lambda(y, e)$ = expected rate at which an individual in i-state y, currently living under environmental conditions e, gives birth

and

$p\,(y,\,e)(\omega)$ = probability that a neonate born from a mother with i-state y under environmental conditions e has itself i-state in the (measurable) subset ω of Ω

are used to define Λ by the formula

$$\Lambda(t,\,t_0,y_0) = \int_{t_0}^{t} \int_{\Omega} p(y,\,E(\tau))\lambda\,(y,\,E(\tau))u(\tau,\,t_0,y_0)(dy)d\tau \qquad (2.12)$$

which in the special case of deterministic i-movement reduces to

$$\Lambda(t,\,t_0,y_0) = \int_{t_0}^{t} p\,(Y(\tau,\,t_0,y_0),\,E(\tau))\lambda(Y\,(\tau,\,t_0,y_0),\,E(\tau))\mathfrak{H}(\tau,\,t_0,y_0)d\tau. \qquad (2.13)$$

In certain pathological cases such a formula does not produce an unambiguous result. For instance, when λ has discontinuities as a function of λ, these have to be crossed transversally by Y, in the sense that the set $\{\tau{:}\lambda(\cdot,\,E(\tau))$ is discontinuous at $Y(\tau,\,t_0,y_0)\}$ has measure zero, in order that the right hand side of (2.13) yields a well-defined number. In a pde formulation, involving the ingredients p, λ, μ and ν (see (2.7), (2.8) and (2.13)), one has to face this difficulty (which is rather hidden in the pde!) when analysing population behaviour. In the present approach, possible pathologies of specific models are dealt with in the phase of modelling i-behaviour, in particular when one concentrates on establishing the relationship between Λ and its constituents. On making, in the next section, the step from the i- to the p-level, we simply assume that Λ is well-defined and has suitable properties. We hope that this digression clarifies the advantage of the 'cumulative' (or renewal equation, see next section) approach as compared to the 'rates' (or pde) approach.

3. BOOK-KEEPING AT THE p-LEVEL

Let the population size and composition at some time t_0 be described by a (Borel) measure m. We shall call this group of individuals the zero'th generation. Let us, for a moment, disregard reproduction. At time $t>t_0$ both the size and composition are changed as a result of i-state change and death. Our description in terms of u at the i-level is immediately lifted to the p-level to yield the *generation development operators* U_0 defined by

$$(U_0\,(t,\,t_0)m)(\omega) = \int_{\Omega} u\,(t,\,t_0,y_0)(\omega)m\,(dy_0) \qquad (3.1)$$

The Chapman-Kolmogorov equation (2.1) guarantees that U_0 is an evolutionary system:

$$U_0(t+s,\,t_0) = U_0(t+s,\,t)U_0(t,\,t_0). \qquad (3.2)$$

Next, let's look at the *direct* offspring of the zero'th generation. The (cumulative) *direct offspring operators* are defined by

$$(K\,(t,\,t_0)m)\,(\omega) = \int_{\Omega} \Lambda\,(t,\,t_0,y_0)(\omega)m\,(dy_0) \qquad (3.3)$$

and they yield the expected cumulative number of direct offspring in the time interval $[t_0,t]$, as distributed with respect to the i-state at birth (whence their name). The consistency condition (2.10) translates into the relation

$$K(t + s, t_0) = K(t, t_0) + K(t + s, t)U_0(t, t_0) \tag{3.4}$$

which is the non-autonomous counterpart of the defining relation for a 'cumulative output family' as introduced in an autonomous setting by DIEKMANN, GYLLENBERG & THIEME (to appear).

So far everything is explicit, i.e. both (3.1) and (3.3) are explicit formulas in terms of the ingredients at the i-level. But now we have to pay attention to offspring of offspring, and so on indefinitely. In other words, we have to iterate the operator family $K(t, t_0)$ with due care for the time structure. As an equivalent alternative for such an infinite sequence expansion we can introduce an abstract Stieltjes renewal equation as follows.

Let the (cumulative) *total offspring operators* $R(t, t_0)$ be the analogues of $K(t, t_0)$ when considering the total clan, i.e. including offspring of offspring of ... . More precisely, $(R(t, t_0)m)(\omega)$ is the expected cumulative number of *all* births, with i-state at birth in the set $\omega \subset \Omega$, in the time interval $[t_0, t]$, given that the population at time t_0 was described by the measure m. Then consistency requires that

$$R(t, t_0) = K(t, t_0) + \int_{t_0}^{t} K(t, \tau)R(d\tau, t_0) \tag{3.5}$$

since any newborn is either the offspring of an individual already present at time t_0 or of an individual born after time t_0. Solving this equation by successive approximations, we obtain the generation expansion alluded to above.

We need a final step to convert i-state at birth to i-state at current time, given the time of birth, while accounting for the possibility of death. Fortunately the operators describing that transformation are already at our disposal, in the form of the U_0-family. We define the *population development operators* U by

$$U(t, t_0) = U_0(t, t_0) + \int_{t_0}^{t} U_0(t, \tau)R(d\tau, t_0) \tag{3.6}$$

which is an explicit expression, once we consider $R(t, t_0)$ as known. So $U(t, t_0)$ tells us how the population size and composition at time t derives from the same information at some earlier time t_0. Hence it should be an evolutionary system, i.e. the algebraic relation

$$U(t + s, t_0) = U(t + s, t)U(t, t_0) \tag{3.7}$$

should hold. The key to a verification of this property is the observation that R should be a cumulative output family for U, i.e.

$$R(t + s, t_0) = R(t, t_0) + R(t + s, t)U(t, t_0). \tag{3.8}$$

Note that (3.8) has exactly the same interpretation as (3.4), the only difference being that now we consider *all* offspring rather than direct offspring only. Relation (3.8) follows from (3.4), the definition (3.6) and the uniqueness of solutions of the renewal equation (3.5).

For completeness we give the expression for U_0 in the special case of deterministic i-state change (see (2.4)):

$$(U_0(t, t_0)m)(\omega) = \int_{\Omega \cap Y(t_0, t, \omega)} \mathcal{F}(t, t_0, y_0)m(dy_0) \tag{3.9}$$

Let us recapitulate the situation. The model ingredients at the i-level introduced in section 2 allow us to define operator families U_0 and K which satisfy the relations (3.2)

and (3.4) or, in words, U_0 is an evolutionary system and K is a corresponding cumulative output family. Only one equation figures in our theory, the renewal equation (3.5), which can be solved by successive approximations. Once we have the solution of (3.5) we can write down an explicit expression, (3.6), for the object that we are after, the evolutionary system U that tells us how p-states at some time are mapped onto p-states at later times.

4. FEEDBACK THROUGH THE ENVIRONMENT

Let us begin by looking at an example. Suppose that substrate concentration S is one of the environmental variables and that substrate is consumed at a per capita rate $\gamma(y, S)$. If substrate dynamics follows the logistic differential equation in the absence of consumers, we add the equation

$$\frac{dS}{dt} = rS(1 - \frac{S}{K}) - \int_\Omega \gamma(y, S)n\,(dy) \tag{4.1}$$

to the description of the system, where n is the measure describing the consumer population and where the time argument is suppressed in the notation. Substituting for n in this equation $U^E(t, t_0)m$, where m is the initial condition at time t_0 and where we now have incorporated the dependence on E by writing a super-index, we are left with a *functional* differential equation for S (recall that E involves S as one of its components), which we have to solve. To verify that one can use a contraction mapping argument amounts to studying the dependence of $\langle \gamma(\cdot, S), U^E(t, t_0)m \rangle$ on the environmental component S, as a given (continuous, say) function on $[t_0, t]$. Here special properties of either $\gamma(\cdot, S)$ or m may contribute to the Lipshitz estimates. The technicalities are somewhat involved and will be dealt with in a future paper.

If all environmental variables are derived from a deterministic dynamical system we have, in general, the ode

$$\frac{dE}{dt} = F(E, L^E(n)) \tag{4.2}$$

where L^E is a continuous linear mapping from the space of measures on Ω into $\mathbf{R}^k$, for some k, with suitable smoothness conditions for both F and $E \mapsto L^E$. Quasi steady state assumptions produce an algebraic equation

$$E = G(E, L^E(n)) \tag{4.3}$$

as an alternative to (4.2).

It may be that only some of the environmental variables are described by an equation of the form (4.2) or (4.3), while others, such as temperature or light intensity, are considered as given (i.e. to be measured or experimentally controlled) functions of time (one does not want to make weather prediction a component of a population dynamics model!). The presence of such variables makes even the resulting non-linear dynamical system non-autonomous. But if such variables are absent, one wants to show that the resulting non-linear dynamical system is autonomous. The key to a proof of this property are the relations

$$\Lambda^{E \cdot \cdot}(t + s, t_0 + s, y_0) = \Lambda^E(t, t_0, y_0) \tag{4.4}$$

and

$$u^{E \cdot \cdot}(t + s, t_0 + s, y_0) = u^E(t, t_0, y_0) \tag{4.5}$$

where

$$E_{-s}(t) := E(t-s) \qquad\qquad (4.6)$$

We intend to elaborate on this topic in the near future.

Finally we remark that in some models the environment is infinite dimensional, rather than finite dimensional as we have assumed in this paper for ease of formulation.

5. CONCLUSIONS

General physiologically structured population models can be mathematically described by a renewal equation and a feedback law. The main advantage of such a formulation is that it avoids the use of unbounded operators (the generating family) for which a precise description of the domain of definition is a technically hard and unpleasant task, if possible at all.

Our plan is to use this formulation as the starting point for a qualitative theory for nonlinear problems, dealing in particular with stability and bifurcation.

We think that even in the linear autonomous case the formulation has advantages. In that case (3.5) reduces to a convolution equation (see DIEKMANN, GYLLENBERG & THIEME, to appear) and Laplace transformation yields information about the asymptotic behaviour. This information is equivalent to a spectral analysis of the generator, but can be obtained without deriving a precise characterization of the domain of definition of the generator. Moreover, quite often a reduction in the 'size' of the problem is obtained, since the support of $A(t, t_0, y_0)$ is usually much smaller than $M(\Omega)$ (e.g., in the case of age, everybody is born with age zero!).

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