

CONFERENCE REPORT

Biomathematics in Africa: an emerging activity

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The old colonial borders of Africa to a large extent remain barriers between scientific cooperation. The only way to overcome them is by consistent effort to find partners and projects, and conferences in Africa for Africans are in my view vital to support that. It is true that conferences, for the most part, are neither funders nor publishers. However, they have no equivalent as a provider of opportunities to form scientific acquaintances.

Networks of scientists have several layers of intimacy: the team that communicate daily, challenging you, frustrating you, gradually building the project with countless small and large tasks; the old friends and colleagues, who sweated through exams with you, sat through interminable meetings with you, who know the people you know; the promising youngsters, perhaps still completing their theses ... as well as other, less easily characterized components.

How does one build this network? I'd say by luck and effort. The point of conferences is to increase the chances that you get lucky: you meet the friends of your colleagues and the colleagues of your friends, you approach speakers after their talks, maybe you simply bump into someone on the hotel terrace. A conference multiplies those opportunities.

It is very early days to speak of the biomathematics community in Africa, but we are getting there. We have formed the African Society for Biomathematics (ASB)

(<http://euromedbiomath.free.fr/asb/>), and we do manage the occasional meeting. The papers that follow were first presented at one such—a small meeting, yet we managed to welcome speakers from six African countries: Botswana, Morocco, Senegal, South Africa, Tanzania and Uganda. The ASB was formed in January 2008 at a meeting in Marrakech, with over 150 participants from more than 40 African countries, and the University of Cape Town will host the inaugural ASB conference in 26–30 January 2009.

Enough PR. It is the science that matters, after all. The articles that follow show a wide range, from quite abstract to extremely practical, from small to large scales, using a wide variety of tools. They show that biomathematics in Africa is active, interesting and valuable.

But are they accessible to a non-mathematician? Well, yes and no. In order to follow the detail, you have to learn the maths. But, and this is sometimes overlooked, you do not need the mathematical detail to grasp the overall import. If it is relevant, it will influence you at least a little bit, and if it is important to your own work, you will study the detail—perhaps leaning on a helpful expert. This is no different from how one would look at any work in a field outside one's own expertise.

Yet mathematics is indeed somewhat different. Firstly, it has to be admitted that, quite often, papers in mathematics make it quite hard to see the big picture. Mathematics has a unique ability to appear self-contained, in that one can seem to state all the axioms and completely prove all the theorems in the paper itself. We

have tried to ensure that the papers here give at least some indication of their import in a wider context. Secondly, it can be difficult to distinguish detail from relevance in mathematics, and indeed to a mathematician they are not necessarily different. In what follows, I summarize how I see the importance and context of each paper.

Banasiak emphasizes a fundamentally new insight: chaos can occur in linear systems, but to do so they must be of infinite dimension (page 173). There is a simple and biologically relevant case: DNA sequences—which in principle can be arbitrarily long, hence the need for a space of infinitely many dimensions. By implication, even a linear model of evolution may have chaotic dynamics.

Models, although meant to be far simpler than reality, may nevertheless be very complex. It is therefore useful to have tools to simplify them. One fruitful approach that achieves this is to separate the system into slow and fast processes. Dao Duc *et al.* use this to obtain interesting results for the classical predator–prey context as extended to two patches (page 180). In particular, they show that density-dependent prey migration increases the equilibrium densities of both predator and prey.

Edwards and Plagányi provide a very good example of the crucial role that modelling should play in the management of renewable resources (page 185). There is a very tasty mollusc known to us as perlemoen and to the world's buyers of shellfish as abalone. Because of its rarity and taste, it commands a high price. It is also easy to poach, as it can be taken at night from small boats near the shore. Since poaching is illegal, its extent cannot be directly measured. Edwards and Plagányi show that a judicious combination of simple mathematical modelling, Bayesian statistics and computation can yield informative estimates from very small data sets.

Continued on page 191

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Biomathematics in Africa (continued from page 172)

The paper by Lett and Mirabet reviews the state of the art in the modelling of motion in animal groups (page 192). The currently dominant approach is simply to simulate a very large number of individuals, and the focus of the research is the model of individual motion. Of particular interest is the effect of nearby individuals. The authors show that very realistic group motions emerge from very simple individual rules.

The paper by Welte illustrates the extreme difficulties presented by the various time scales in the HIV/AIDS pandemic (page 199). Treatment depends on time since infection, and planning depends on a reasonably good understanding of how many people have been 'recently infected'. The author shows that using both RNA and antibody test results allows reliable estimates, but then points out that this is not practical in the foreseeable future in

South Africa. Mathematically, the difficulty is due to the extremely short 'window period' (interval between infection and its detectability) of these highly sensitive tests. Paradoxically, a less sensitive test with a longer window period is needed for estimating the population size of 'recently infected' patients. Of course, the more sensitive tests are still necessary, as they are best for individual treatment.

Age is important in biology, as it is perhaps impolite to remind some of our readers. The simplest approach is to consider a small number of age classes, as in the classical Leslie matrix. Moussaoui *et al.* extend this to space by considering two patches, and obtain a useful, if crude, characterization of ecotoxicity: that if one patch is sufficiently polluted, the population will go extinct in both (page 203).

Perrier and Laurie describe a technique for spatial data analysis (page 209). Multi-

fractals have been of interest in a number of environmental sciences for some years, and the Rényi dimensions $D(q)$ are frequently used in describing them. What Perrier and Laurie provide is a simple way to estimate Rényi dimensions directly from density data.

Ouifki *et al.* is another contribution to the slowly emerging understanding of the HIV/AIDS pandemic and its management (page 216). Presumably because time scales are broadly similar, there is strong coupling of the various population dynamics: the virus within a host, the virus among the host population, and the host population itself. In this complex setting, careful modelling may well be crucial to humanity's eventual mastery of the disease; Ouifki and his colleagues explore the within-host dynamics of a simple model under a variety of treatment options. □