Editorial

Biofilms are colonies of microorganisms, usually growing on solid-liquid interfaces, consisting of cells and a matrix of extracellular polymeric substances (EPS). Such colonies are often elaborately structured and highly dynamic, expanding through cell division and recruitment of cells from outside, and contracting via individual cells or flocs (groups of cells and biofilm matrix) detachment from the biofilm surface. Even amongst simplest single species bacterial biofilms, the behaviour (phenotype) of individual cells is highly heterogenous across the biofilm due to microenvironment variation (e.g. nutrient concentration, pH) and cell-cell signalling (quorum sensing); consequently, many researchers consider biofilms as more akin to multi-cellular organisms rather than a colony of autonomous individual cells.

The impact of biofilms to humanity is considerable. Whilst biofilms in the gut are essential for the effective digestion of food and, according to recent studies, important for our mental wellbeing, they are also a major clinical issue in wound infections, implanted materials, dental decay and for any individuals who are in some way immuno-compromised. The 3D structure of biofilms provides a diffusive barrier against antibiotics, the situation being further exacerbated by the continuing rise in antimicrobial resistant (AMR) strains due to the decline in new antibiotic drugs and the mismanaged administration of existing ones. In an industrial setting, biofilms are, for example, exploited for sewage processing, water purifying and oil recovery/degradation. However, the biofilms' propensity to grow in warm, moist environments has detrimental consequences in many industrial processes, for example, leading to clogging and corrosion of pipes and contamination in food processing.

In the early years, mathematical modelling of biofilm was almost exclusively a research program undertaken by engineers, published in environmental, chemical and bioengineering journals (Chaudhury & Beg, 1998, Wanner *et al.*, 2006). A main ingredient of these studies were steady state semi-linear diffusion-reaction models in one spatial dimension, perpendicular to the substratum on which the biofilm forms (Rittmann & McCarty, 1980). A quasi-standard for the dynamical description of biofilm processes is the celebrated one-dimensional Wanner-Gujer model (Wanner & Gujer, 1986), a hyperbolic, nonlocal free-boundary value problem for particulate fractions of the biomass, coupled with diffusion-reaction equations for dissolved components, typically explored in computational simulations.

By the late 1990s and early 2000s, mathematicians (and physicists, and biologists) were attracted to the field and papers began to appear in mathematical biology and more general applied mathematics journals, at about the same time as biofilm modelling in the engineering literature expanded to include multi-dimensional effects (van Loosdrecht *et al.*, 2002, Picioreanu *et al.*, 2004). Simultaneously, minisymposia on topics of biofilm modelling became regular occurrences at the major international mathematical biology conferences, such as the meetings of the Society for Mathematical Biology, the European Society of

Mathematical and Theoretical Biology, and the SIAM Life Science group. Today, while the number of mathematical biologists working in the field is still very small compared to other areas such as infectious disease modelling, cancer modelling and theoretical ecology, the area has established itself as a subfield of Mathematical Biology, as is also evidenced by several review articles that were published in recent years, each with its own focus (Klapper & Dockery, 2010, Frunzo *et al.*, 2018, Wang & Zhang, 2010). When mathematicians entered biofilm modelling first, their focus was on models describing biofilm structure and on continuum mechanical properties of biofilms. This scope, meanwhile has been considerably extended, partly motivated by advancements in experimental techniques (e.g. DNA analysis, confocal microscopy) providing much deeper understanding of biofilm activities on a number of scales. Biofilm modelling nowadays combines approaches from finite and infinite dimensional dynamical systems, partial differential equations, asymptotic analysis, fluid and continuum mechanics, numerical analysis and scientific computing, and more recently stochastic analysis. The shear breadth of approaches was beautifully demonstrated from the 40 or so contributions at the recent "Workshop on Mathematics for Complex Microbial System" held at the Fields Institute, Toronto, Canada in May 2018. This special issue of the European Journal of Applied Mathematics provides a representative snapshot of the research currently being undertaken in biofilm modelling.

The papers in this special issue can be broadly separated into three subsets based on the length scale of interest. One subset of papers, is concerned with macro- or reactor scale systems, in which biological activity is due to biofilms, but without explicit spatial resolution of the colony scale processes. Explored in these papers are co-existence of floating and aggregated bacterial cells in a chemostat (Rapaport, 2018), the dynamics of pathogen contamination in drinking water distribution networks (Marzooq *et al.*, 2018) and the effect of diffusion limitation and heterogeneity formation induced by microbial colonies embedded in matrices of materials (Aristotelous *et al.*, 2018). A second group examines biofilms on a mesoscale, i.e. the actual length scale of biofilm colonies, including the numerical handling of degenerate parabolic spatially structured population model of multispecies biofilms with cross-diffusion effects (Ghasemi *et al.*, 2018) and the likelihood of biofilms fragments colonising elsewhere in a shear flow (Kightely *et al.*, 2018). The third group lies between the lengthscales of the first two groups. These include the combining of chemostat approaches with that of Wanner & Gujer to analyse invasion of cells into biofilms in an an idealisation of moving bed biofilm reactors (D'Acunto *et al.*, 2018), an upscaling approach to modelling biofilms, suspended bacteria and substrate removal in porous media reactors (Gaebler & Eberl, 2018) and a statistical physics approach to investigate how the assumptions on the microscale effect mesoscale mechanical properties of biofilm aggregates (Stotsky *et al.*, 2018). These papers are a small demonstration of the diversity of problems and mathematics arising from biofilms, and with their continuing concern in industry and in the age of AMR, they will continue to provide new challenges and opportunities to mathematicians for many years to come.

From co-editors of the special edition: Hermann Eberl and John Ward.

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