

Preface

Cells are individuals. Even microbial cells, which in case of some environmental bacteria present a size down to 0.4 or 0.5 μm , deviate from each other in terms of life cycle, protein composition, and metabolism. This heterogeneity results from distinct intrinsic cell features like age, stage in cell cycle and position of the division plane, gene transfer or loss, mutations, or epigenetic inheritance. Similarly, external parameters influence cellular features due to various micro-environmental inhomogeneities comprising, e.g., the availability of carbon or other sources of energy and of electron acceptors like oxygen and the prevalence of stress conditions like, e.g., mechanical pressure.

All these parameters influence the efficiency of a cell in a biotechnological process. Since every cell contributes to the product yield of, e.g., a fermentation process in industrial biotechnology, dead, inactive or weakly active cells will limit this productivity. Therefore, single cell-related analytical techniques need to be involved in the evaluation and control of such processes. Although many of such technologies are already successfully used in medical sciences, where human cell populations are investigated with a new generation of amazing instruments, this is not true for microorganisms. One reason for this discrepancy is the priority of medical research in terms of funding. A more scientific point is the fact that microbial cells comprise only a thousandth of the volume of a normal blood cell and are therefore much more difficult to observe and to analyse.

In recent years, however, microorganisms have started to come into the focus of many fields as, e.g., chemistry, which were since long thought to have no interest in these ‘un-steerable’ organisms. This is because microorganisms are not only tremendously diverse from a phylogenetic point of view, they also catalyse a wealth of biochemical processes which can be used, e.g., in white biotechnology or in energy producing processes like biogas production. Very often the organisms involved in such applications are still unknown with regard to affiliation and function. Since most of these microorganisms still cannot be cultivated as a pure culture, single cell techniques to follow their performance are of utmost interest and necessity.

Still such techniques are expensive and often difficult to operate. Usually they are used in research laboratories to understand the very basic principles of microbial life. In a few cases, however, people have already tried to obtain information referring to individual microorganisms by using single cell technologies, either relying on sophisticated but also on cheaper equipment, based on chip- and microfluidic devices. Remarkable insights into cell behaviour have already been obtained by using such small-scale and sometimes partly disposable instrumentations.

Population dynamics or subpopulation dynamics in biotechnologically or environmentally relevant processes are responsible for the variability in seemingly homogeneous populations under seemingly homogeneous micro-environmental conditions and result in surprisingly quick intra-population changes within a 'stable' process. Here, not only live/dead states play a crucial role in population development but also the above mentioned intrinsic parameters. For a deeper understanding and forecasting of the behaviour of microbial populations quantitative analysis and mapping into mathematical models will provide the indispensable theoretical foundations. In this context, we can make use of a broad panel of different model concepts. Their usefulness has to be proven by their ability to assign the characteristic features of single cells or of segregated subpopulations to the model variables. These models will ultimately allow to develop, control and enhance microbial performances in bioreactors or in locally confined, natural systems where microorganisms are used for distinct tasks.

All in all, microbial single cell analytics evolved to a large degree within the last 10 years. Nevertheless, these technologies are still on the edge and have the potential to become far more usable and useful for basic research and for application in already well established microbial processes. We hope that this volume intrigues the reader to learn more about microorganism and their complexity but mainly on the techniques which can be used to understand their basic principles of live and survival. Highly resolved information on these small organisms will enable us to quantify their life and to orchestrate their abilities to a successful control and optimisation of bioprocesses.

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