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A Special Issue Preface on Bacterial Protein Transport and Secretion

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Editorial

This issue of BBA Molecular Cell Research provides an in-depth look of protein flow and secretion in bacteria. Bacterial cells devote a large number of components to ensuring protein targeting to the plasma membrane. These proteins are subsequently either incorporated into the lipid bilayer or released to the opposite side. The ubiquitous and crucial Sec system is used by most proteins for these functions the released Sec-exported proteins can be sorted to Gram-negative cells' periplasm, outer membrane, or extracellular milieu, or Gram-positive bacteria's cell wall or extracellular milieu. In all situations, specialist add-on systems are engaged in these later stage sorting activities, which handle folding, modification, processing, and assembly requirements, as well as stress-protection requirements. Furthermore, evolutionarily unrelated Protein machines that allow exported proteins to penetrate the plasma membrane and cell envelope have been designed [1].

In other circumstances, such trans-cell envelope machineries create extracellular protrusions that act as injection needles, allowing proteins to be transferred directly to neighbouring bacteria or even eukaryotic cells. These inventive and complex secretion solutions are matched by protein-absorption mechanisms. This arsenal of mechanisms ensures that more than 30% of the bacterial proteome ends out beyond the cell. Protein export is required for viability, pathogenicity, symbiosis, and the production of biofilms [2]. We can repurpose the export pathways to create vaccines, heterologous biopharmaceuticals, and industrial enzymes, and then transform them into cancer cell killing devices. Finally, trafficking components are formidable antibiotic discovery targets. This complete collection allows us to marvel at these interesting systems and speculate on the future generation of tools that may open up new avenues of investigation. While the concept of developing mathematical models of signal flow in biological systems is not novel the sources and amount of data for multiscale modelling, as well as many of the computational/mathematical tools accessible, have changed considerably in recent years.

Many of the newer technologies are part of the fast evolving fields of omics genomics, transcriptomics, proteomics, metabolomics and an expanding and quantitative microscopy, which includes gene expression in single cells. The analytical methodologies and software tools developed by computer scientists, mathematicians, and statisticians are critical to our ability to analyse and integrate these new data streams, as well as to design new mathematical models and computational representations of the data. Rather than being associated with any particular. Our talk will centre on the application of computational and mathematical tools to describe system function in the context of endocrine-related cancer biology. For the sake of this review, we define a 'mathematical model' as a dynamic, semi-mechanistic model of dozens of genes and their products created using differential equations and stochastic algorithms [3].

Of course, such dynamical models must be simulated on a digital computer at some point, but we define a 'computational model' as applying machine-learning methods to investigate high-dimensional data containing hundreds or thousands of genes and/or proteins. In order to be clinically helpful, in silico models must be multiscale [4]. Drug action at the molecular level, for example, must be related to clinical effects at the tissue or organism level. Multiscale models incorporate a wide range of data types from various sources, spanning scales ranging from DNA to RNA to protein, metabolites to cells to tissues, tissues to organisms, and even interacting populations. Modelling based solely on genome and/or transcriptome data can be limited because around half of changes discovered in the transcriptome may not be present in the proteome, and an even less percentage of changes discovered in the genome may filter through to the proteome [5].

Conflict of Interest

None.

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