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Editorial

Rigorous Analysis of Microbes and Infectious Diseases Using an Expanding Range of Robust *In Silico* Technologies

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In 1965, Gordon Moore, co-founder of Intel, described an observation that "the number of transistors in an integrated circuit doubles every two years, while the cost of the chip remains relatively low" [1]. This observation, which came to be known as Moore's Law, turns out to be correct in the last 60 years, and has provided guidance to the research and development strategies of the semiconductor industry, leading to an exponential expansion in the computer science-related industries, including hardware and software development, networking, and so on and so forth. All these technological progress became the driving forces behind the remarkable success in machine learning, artificial intelligence, bioinformatics, big data analysis, etc., which is best exemplified by the recent awards of the Nobel Prize of Physics 2024 to John J. Hopfield and Geoffrey E. Hinton "for foundational discoveries and inventions that enable machine learning with artificial neural networks" (https://www.nobelprize.org/prizes/physics/2024/summary, accessed on 17 December 2024), and the Nobel Prize of Chemistry 2024 to David Baker "for computational protein design" and Demis Hassabis and John Jumper "for protein structure prediction" (https://www.nobelprize.org/prizes/chemistry/2024/summary, accessed on 17 December 2024). The use of in silico technologies in various fields of life science, such as genome sequencing, assembly and annotation, structure prediction and novel drug discovery, epigenomic profiling, mathematical and epidemiological modelling, and clinical trial simulations, has been phenomenal in the last few decades. More recently, following breakthroughs in machine learning and artificial intelligence, these technologies have been applied to image recognition in a number of fields in clinical and laboratory medicine, some of the most prominent ones being dermatology for clinical diagnosis of skin lesions, radiology for analysis of radiographic, ultrasonographic and computer tomographic images, and histopathology for distinguishing various pathological conditions [2,3].

Parallel to the advancement of "dry-lab" experiments is the marked decrease in complexity in performing "wet-lab" experiments. First, there has been a significant increase in the use of commercial kits in the last few decades. Thirty years ago, to expand a plasmid with a cloned DNA fragment for downstream characterization, the researcher had to follow the traditional method that used a Cesium chloride gradient to separate the DNA from other molecules, which would take almost a week to finish [4]. With the development of commercial kits for this purpose, it takes only two hours to prepare 4 mg of high copy number plasmid DNA from a half-liter *Escherichia coli* culture. Another common example is DNA sequencing. A few decades ago, sequencing a fragment of DNA using the Sanger method involved incorporation of chain-terminating ^{32}P-labelled dideoxynucleotides into the elongating DNA which is the target of the experiment, running of a 40-cm long polyacrylamide gel, developing and fixing X-ray films, and analyzing the results base-by-base manually with a light box [5]. By the end of the last century, the development of fluorescent labels, commercially available sequencing kits and capillary array electrophoresis have made DNA sequencing experiments much easier to carry out. Second, the development of high-throughput and robotic machines to perform "wet-lab" experiments has contributed to a further reduction of the need for manual work. Some notable examples include second-generation and third-generation sequencing platforms, as well as robotic systems for chemical screening and drug discovery, large-scale DNA and RNA extraction, cell culture automation, liquid chromatography and mass spectrometry, high-throughput protein purification and structural analysis. Third, in addition to the advancement in commercial kits and robotic systems, there has been an expansion of highly specialized laboratories that generate their revenue by conducting selected

"wet-lab" experiments for researchers. Some typical services provided by such laboratories include gene cloning, protein expression and purification, monoclonal antibody production, next-generation sequencing, CRISPR-Cas9 gene editing, drug design and synthesis, and virus packaging such as lentivirus and adenovirus. Scientists could now outsource a number of steps of an experiment that involve intensive technical support to these commercial laboratories, allowing researchers to spend their time on other priorities. All these changes in the "wet-lab" ecology have made the work of researchers much more efficient, and at the same time have generated a tremendous amount of data for downstream in silico analysis.

Microbes, though cannot be seen by the naked eye, are of paramount importance as they could cause devastating impacts to the modern society. The chilling scenes of burning corpses and the severe difficulties in coping with international travel bans, compulsory quarantine, mandatory face shielding, social lockdown, etc. as a result of the COVID-19 pandemic are still haunting memories to most people across the world. This fatal infection has claimed more than seven million human lives and led to massive economic loss, for example, the world's collective gross domestic product has fallen by 3.4% in 2020. Post-COVID-19, the global importance of research in microbes for pandemic preparedness cannot be understated. The increased ease of performing "wet-lab" experiments and advances in various fronts of computer-based analysis have shifted the paradigm in the study of microbes and infectious diseases. In silico analytical methods, such as bioinformatics, big data analysis, and artificial intelligence, have become more and more robust, and are often one of the crucial techniques used in a scientific paper. In fact, we have entered a new computer-based era for the study of microbiology and infectious diseases, which has resulted in breakthrough studies on microbiome, genomics, transcriptomics, proteomics, metabolomics, next-generation sequencing-based laboratory diagnosis, artificial intelligence-based methods for identification of microbes and diagnosis of infectious diseases, etc. In view of such a fundamental change, we are excited to introduce a new scientific journal *eMicrobe*, which emphasizes on the rigorous use of such an expanding range of robust in silico technologies for the study of microbes and infectious diseases.

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Conflicts of Interest

The author declares no conflict of interest.

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