SLAS Technology 28 (2023) 98–100

Contents lists available at ScienceDirect

SLAS Technology

journal homepage: www.elsevier.com/locate/slast

From the Literature

Life sciences discovery and technology highlights

Advances in biotechnology

An introduction to spatial transcriptomics for biomedical research. For many years, cells were examined at genome-scale, in hope to achieve comprehensive understanding of the molecular details of how mechanisms are employed. Such understanding may spur potential developments to tackle a plethora of conditions like cancers and metabolic disorders. Thus, driving efforts to delve into transcriptomics, in particularly, single-cell transcriptomics or more commonly referred to as single-cell RNA-seq (scRNA-seq). Despite the enduring success of scRNA-seq, this method is greatly hindered by the need to recover intact and viable cells from the tissue, in which limits many cell types from study and abolishes spatial context that could otherwise provide information on cell identity and function. Therefore, there is great motivation in conducting transcriptomics on intact tissue. This will help to improve understanding on the spatial positioning of cells, relative to its neighbour and non-cellular structures. Through studying intact tissue, spatial information can be preserved and thus, such methods have been referred to as spatial transcriptomics. In this review, applicability of this technology is discussed, with insights on possible technical implications that may influence the study. Moreover, the authors provided guidance on relevant methodologies to unravel the huge data that comes out of spatial transcriptomics, hoping to give aid to those seeking to employ this technology in their research (Williams, C.G., Lee, H.J., Asatsuma, T. et al. An introduction to spatial transcriptomics for biomedical research. Genome Med 14, 68 (2022). https://doi.org/10.1186/s13073-022-01075-1).

Rapid biosensor development using plant hormone receptors as reprogrammable scaffolds. Due to the numerous advantages that biosensors bring about, it has garnered more attention to contribute into the research and development of this technology. Biosensors are devices that combine a biological component with a physical or chemical transducer to detect a specific analyte. The biological component will selectively interact with the target analyte, while the transducer converts this binding event into a measurable signal. Biosensors can be utilized in many applications, including medical diagnosis, food safety testing, drug detection and environmental monitoring. Some of the most common biosensors today are glucose detectors and home pregnancy tests. However, there is always a need to produce new biosensors for various purposes. Moreover, designing a sensitive, specific, and portable biosensor continues to be huge hurdle in biotechnology. In hope to overcome this challenge, the authors developed an approach to enable rapid engineering of biosensors using PYR1 (Pyrabactin Resistance 1). This component is a plant abscisic acid (ABA) receptor that comes with a malleable ligand-binding pocket and requires ligand-induced heterodimerization, in which supports the building of sense-response functions. Furthermore, in this article, the authors demonstrated the capability of this approach as a scaffold to conduct rapid development of new biosensors for a wide range of sense-response applications. (Beltrán, J., Steiner, P.J., Bedewitz, M. et al. Rapid biosensor development using plant hormone receptors as reprogrammable scaffolds. Nat Biotechnol 40, 1855–1861 (2022). https://doi.org/10.1038/s41587-022-01364-5)

High-throughput total RNA sequencing in single cells using VASA-seq. In an attempt to unravel the molecular details involved in biological events, single-cell RNA sequencing (scRNA-seq) is employed. This technology has aided in transforming the understanding of complex biological events over the last decade. In general, scRNA-seq investigates the sequence information within each cell and provides high resolution of cellular differences that is useful in uncovering the mechanisms involved. Since the development of scRNA-seq, multiple applications have found its way to incorporate this technology to achieve its goal. For instance, revealing the transcriptional differences of a cellular population leads to identification of cellular subpopulations, such as the malignant cells of a tumour mass. In scRNA-seq, harvested cells are first lysed, then enriched with poly[T]-primers, before subjected the product to be converted into complementary DNA (cDNA). As such, this compromises the detection of many long non-coding, short non-coding and non-polyadenylated protein-coding transcripts. Therefore, this hinders the analysis on alternative splicing, alternative promoter usage and differential expression of non-coding RNAs. In this article, the authors developed 'vast transcriptome analysis of single cells by dA-tailing' (VASA-seq) to overcome these challenges. VASA-seq enables the detection of total transcriptome in single cell by fragmenting and tailing all RNA molecules of lysed cells. Moreover, the authors employed VASA-seq to provide comprehensive analysis of mammalian post-implantation development, highlighting its sensitivity to discover novel biological information. (Salmen, F., De Jonghe, J., Kaminski, T.S. et al. High-throughput total RNA sequencing in single cells using VASA-seq. Nat Biotechnol 40, 1780–1793 (2022). https://doi.org/10.1038/s41587-022-01361-8).

Artificial intelligence in science

A machine-learning based objective measure for ALS disease severity. Amyotrophic Lateral Sclerosis (ALS) is a neurodegenerative disease that affects nerve cells in the brain and spinal cord, specifically the motor neurons that control voluntary muscle movement. As the disease progresses, these motor neurons gradually degenerate and die, leading to a loss of muscle control and eventual paralysis. This progressive motor neuron disease is usually focal initially, then spreads from the onset site in both upper and lower motor neuron compartments. This can affect a person's ability to move, speak, swallow, and breathe. Assessment

https://doi.org/10.1016/j.slast.2023.02.005

of ALS often relies on subjective evaluation of overall functionality of the patient, particularly through qualitative evaluation of various aspects. The current tool utilized for monitoring ALS disease severity is a questionnaire-based, revised ALS Functional Rating Scale (ALSFRS-R). However, such subjective measures of disease severity have proved to be challenging in unravelling disease diagnosis, prognosis, and in identification of effective therapeutics. With that in mind, the authors aim to develop objective methods to measure ALS disease severity. In this article, they built a machine learning (ML) based objective measure, based on voice samples and accelerometer measurements from a four-year longitudinal dataset. Overall, the authors demonstrated the potential value of such objective measurement method to study ALS, where ML can be applied to such measurement methods to objectively predict ALS disease severity, and to monitor and reveal progression of disease (Vieira, F.G., Venugopalan, S., Premasiri, A.S. et al. A machine-learning based objective measure for ALS disease severity. NPJ Digi. Med 5, 45 (2022). https://doi.org/10.1038/s41746-022-00588-8).

Machine learning and artificial intelligence in pharmaceutical research and development. Artificial Intelligence (AI) refers to the ability of machines to perform tasks that would typically require human intelligence, such as recognizing speech, making decisions, and solving problems. On the other hand, machine learning (ML) is a subfield of artificial intelligence that involves training algorithms to automatically learn and improve from experience without being explicitly programmed. In other words, it involves developing computer programs that can learn and improve over time by analysing large amounts of data and identifying patterns or relationships in the data. In recent years, both artificial intelligence and machine learning have flourished tremendously, driven by the revolutionary development in computational technology. This advancement has revolutionised the ability to collect and process large volumes of data. With the rise of this technology, it has been appealing to industries that require greater efficiency, especially due to the technology's automated nature, predictive capabilities. In this review article, the authors discussed about the status of AI/ML in drug development and described on new areas where the potential of such utilization can arise from, in hope to bring balanced perspective on the optimal use of AI/ML in pharmaceutical research and development. (Kolluri S, Lin J, Liu R, Zhang Y, Zhang W. Machine Learning and Artificial Intelligence in Pharmaceutical Research and Development: a Review. AAPS J 2022 Jan 4;24(1):19. doi: https://doi.org/10.1208/s12248-021-00644-3.)

Single-sequence protein structure prediction using a language model and deep learning. Proteins are complex molecules that is made up of one or more long chains or amino acid residues. Proteins are vital parts of organisms and are involved in several processes within the cells. The activity of the proteins is largely dependent on its structure and more often than not, it is a major challenge in biophysics of practical and theoretical importance when it comes to 3D protein structure prediction. One of the major hurdles in this aspect is due to the combinatorial explosion of possible conformations that a protein can adopt, in which there are many possible ways that a protein can conform into. Despite the development of superior computational systems (e.g. AlphaFold2) in recent years, much work remains to be done to improve prediction methods. Herein the article, the authors described an end-to-end differentiable system, RGN2. This system employs a protein language model to predict protein structure from single protein sequences. In this context, the protein language model of interest aims to capture the latent information in a string of amino acids that implicitly specifies protein structure. Moreover, the authors then delve deeper to implement and train this model. They managed to demonstrate the practical and theoretical strengths of protein language models relative to multiple sequence alignments in structure prediction. (Chowdhury, R., Bouatta, N., Biswas, S. et al. Single-sequence protein structure prediction using a language model and deep learning. Nat Biotechnol 40, 1617–1623 (2022). https://doi.org/10.1038/s41587-022-01432-w)

Advances in nanotechnology

Application of nanomaterials against SARS-CoV-2: An emphasis on their usefulness against emerging variants of concern. Pandemics and outbreaks have been part of human history for thousands of years, in which has caused significant impacts on human societies, resulting in widespread illness, death and economic disruption. One of the most recent outbreaks is caused by a novel coronavirus, SARS-CoV-2, where it was revealed to be phylogenetically associated with SARS viruses. This virus has brought chaos to several countries for the past few years and has challenged every available treatment method. To overcome this disease, several vaccines were developed to control the outbreaks such as live-attenuated vaccines, inactivated virus, recombinant protein, and DNA and RNA vaccines. Unfortunately, controlling of outbreaks *via* vaccination has proved to be difficult due to the rapidly evolving characteristic of the viral strains, in which variants of concern arise from time to time. To tackle the challenges faced in managing this disease, nanotechnology is investigated for its potential in overcoming the limitations faced by existing therapies and strategies used against it. In this review, the authors described the possibility of utilizing nanomaterials in these areas, where they explore the efforts of nanomaterials, in hope to unravel its potential in tackling against the current and emerging future variants of concern. (Iqbal R, Khan S, Ali HM, Khan M, Wahab S and Khan T (2022) Application of nanomaterials against SARS-CoV-2: An emphasis on their usefulness against emerging variants of concern. Front Nanotechnol 4:1060756. doi: 10.3389/fnano.2022.1060756)

Nanomaterials in the future biotextile industry: A new cosmovision to obtain smart biotextiles. Humans first started to wear clothes to protect themselves from the elements. Early humans used animal hides and furs to make clothes, and later developed the ability to weave fabric from plant fibers such as cotton, linen, and silk. However, the non-sustainable characteristic of the textile industry urges for the innovative transformation of this industry, by adopting cutting-edge biotechnological approaches. In this context, biofabrication is explored to resolve the sustainability issue faced in the textile industry. It combines principles of engineering and life sciences to create functional biological structures or devices using biologically derived or biomimetic materials. Moreover, it involves the use of advanced techniques such as 3D printing and microfabrication. In this regard, the authors delve deeper into the field of nanotechnology, in hope to unravel its potential in alleviating the shortcomings faced by some of the novel biomaterials. The authors wanted to present the cosmovision of biotextiles, by capitulating on the potential benefits provided by nanomaterials, in which may revolutionize the textile industry. In this article, one may be intrigued by the perspective portrayed, bringing upon new thoughts and ideas into the future of the textile industry. (Fuentes KM, Gómez M, Rebolledo H, Figueroa JM, Zamora P and Naranjo-Briceño L (2022) Nanomaterials in the future biotextile industry: A new cosmovision to obtain smart biotextiles. Front Nanotechnol 4:1056498. doi: 10.3389/fnano.2022.1056498)

The potential impact of nanomedicine on COVID-19-induced thrombosis. COVID-19 is an infectious respiratory illness caused by a newly discovered coronavirus called SARS-CoV-2. It first emerged in December 2019 and has since spread to become a global pandemic. It spreads primarily through respiratory droplets of an infected person and can also be transmitted through contact with contaminated surfaces. This disease has potential in causing a hypercoagulable state in some patients, whereby it was demonstrated in some studies that COVID-19 infection may lead to a higher risk of blood clots, including deep vein thrombosis (DVT), pulmonary embolism (PE), and stroke. One possible mechanism on this phenomenon is that COVID-19 can inflict an inflammatory response in the body, resulting in the activation of the blood clotting system. On the other hand, another common theory postulates that COVID-19 may damage the cells lining blood vessels, leading to the formation of blood clots. In this regard, thrombolytics are often administered to counteract this COVID-19-induced event. However, this treatment method comes with its own set of disadvantages, in which limits their use in

this context. Therefore, to alleviate this situation, the authors wanted to delve into the field of nanomedicine. Through this review article, they are hoping to highlight some of the most promising nanocarrier systems and design strategies that may be adapted for nanomedicine development, to aid in the fight against COVID-19. (Russell, P., Esser, L., Hagemeyer, C.E. et al. The potential impact of nanomedicine on COVID-19-induced thrombosis. Nat. Nanotechnol. 18, 11–22 (2023). https://doi.org/10.1038/s41565-022-01270-6)a.

Jamien Lim
Dyson, Singapore, Republic of Singapore

Tal Murthy
TDK Electronics Inc. New Hampshire, USA

E-mail addresses: jamienlim90@gmail.com (J. Lim), tal.murthy@gmail.com (T. Murthy)