From the Literature

Life sciences discovery and technology highlights

Advances in biotechnology

**Killing tumor-associated bacteria with a liposomal antibiotic generates neoantigens that induce anti-tumor immune responses**

Tumor microbiota refers to the diverse community of microorganisms, including bacteria, viruses, fungi, and other microbes, that exist within and around tumor cells in cancerous tissues. Traditionally, the human body was believed to be mostly sterile, however in recent studies, it has revealed the presence of various microorganisms in different organs and tissues, including cancerous tumors. The study of tumor microbiota and its role in cancer development and progression is a relatively new and rapidly evolving field of research. The strength of this field lies in its innovative methodology and the promising implications it holds for cancer patients. By focusing on the intricate relationship between tumors and its community of microorganism, the researchers have identified a unique pathway to enhance the body’s natural defenses against cancer. However, it is crucial to acknowledge that while this research is immensely promising, it is likely in the early stages of development. Further studies, including preclinical and clinical trials, will be necessary to validate the findings and assess the long-term safety and efficacy of this approach in human patients. Additionally, exploring potential resistance mechanisms that tumors might develop against this treatment will be vital to ensuring its sustained effectiveness. In this article, the authors presented a groundbreaking approach in the field of cancer immunotherapy. The study explores a novel strategy by employing liposomal antibiotics to target bacteria associated with tumors, resulting in the production of neoantigens that trigger robust anti-tumor immune responses. This research represents a significant advancement, offering new avenues for cancer treatment and potentially reshaping the future of immunotherapeutic interventions. (Wang, M., Rousseau, B., Qiu, K. et al. Killing tumor-associated bacteria with a liposomal antibiotic generates neoantigens that induce anti-tumor immune responses. Nat Biotechnol (2023). https://doi.org/10.1038/s41587–023–01957–8)

**Direct measurement of engineered cancer mutations and their transcriptional phenotypes in single cells**

Genome sequencing studies involve decoding the complete DNA sequence of an organism to identify genetic variations. In the context of cancer, genome sequencing studies aim to understand the genetic alterations that drive tumorigenesis. Cancer is caused by genetic mutations that accumulate in specific genes, leading to uncontrolled cell growth and the formation of tumors. By sequencing the entire genome of cancer cells, researchers can identify these mutations and gain insights into the genetic basis of cancer. However, deciphering the phenotypic consequences of mutations remains a challenge due to the complexity of genomic data, the need for functional validation, tumor heterogeneity, and the integration of multi-omics information. Overcoming these challenges is essential for translating genomic insights into effective cancer therapies and personalized medicine approaches. In this paper, the authors developed a system that delves into the intricacies of cancer mutations at the single-cell level, offering a profound understanding of how engineered mutations impact transcriptional phenotypes. By quantifying engineered cancer mutations and their transcriptional consequences within individual cells, the study bridges the gap between genomic alterations and their functional outcomes, unveiling a level of complexity previously unseen. Moreover, it also provides unprecedented insights into the heterogeneity of cancer mutations. (Kim, H.S., Grimes, S.M., Chen, T. et al. Direct measurement of engineered cancer mutations and their transcriptional phenotypes in single cells. Nat Biotechnol (2023). https://doi.org/10.1038/s41587–023–01949–8)

**Integration of spatial and single-cell data across modalities with weakly linked features**

In an era where technology continues to produce vast amounts of data from diverse sources, integrating this information is essential for understanding the complexities of life, unraveling disease mechanisms, and developing innovative therapies. Cross-modal integration, in the context of biological research, refers to the process of combining and analyzing data from different experimental techniques or modalities. These techniques can include genomics, transcriptomics, proteomics, metabolomics, imaging, and more. The integration of data from these diverse sources allows researchers to gain a more comprehensive and nuanced understanding of biological systems. Moreover, the synergy created by combining different types of data enhances the depth and breadth of our knowledge, propelling the field of biology into new realms of understanding and innovation. In this paper, the authors described a method that opens a gateway to a new frontier of biological discovery, through the use of all information in each modality to obtain high-quality integration, in conjunction with its acknowledgement and accommodation of weakly linked features. This achievement represents a critical step towards holistic biological insights. (Chen, S., Zhu, B., Huang, S. et al. Integration of spatial and single-cell data across modalities with weakly linked features. Nat Biotechnol (2023). https://doi.org/10.1038/s41587–023–01935–0)
Artificial intelligence in science

Simplifying complex antibody engineering using machine learning

Antibody engineering refers to the process of designing and modifying antibodies to enhance their specificity, affinity, stability, and therapeutic properties. Antibodies play a crucial role in recognizing and neutralizing pathogens, such as bacteria and viruses. In the context of biotechnology and medicine, engineered antibodies are used as therapeutic agents to treat various diseases, including cancer, autoimmune disorders, and infectious diseases. Despite the numerous benefits this technology brings about, multiple challenges await to be addressed. These challenges require a multidisciplinary approach involving bioinformatics, structural biology, immunology, and engineering. With the advances in technology, many are hoping that these developments are instrumental in overcoming these hurdles and driving the field of antibody engineering forward. In this review article, the authors discussed on the integration of machine learning techniques to simplify the intricacies of antibody engineering has ushered in a new era, redefining the landscape of biotechnology and pharmaceutical development. By harnessing the power of machine learning, researchers can analyze massive datasets, identify patterns, and predict optimal antibody designs with unprecedented speed and accuracy. As machine learning continues to evolve and researchers refine these techniques, the possibilities for biomedical research are boundless. (Makowski, Emily K., Hsin-Ting Chen, and Peter M. Tessier. “Simplifying Complex Antibody Engineering Using Machine Learning.” Cell Systems 14, no. 8 (August 16, 2023): 667–75. https://doi.org/10.1016/j.cels.2023.04.009.)

Machine learning for cross-scale microscopy of viruses

Viruses are small infectious agents that can only replicate inside the living cells of other organisms. They consist of genetic material (either DNA or RNA) enclosed in a protein coat called a capsid. They are considered obligate intracellular parasites, relying on host cells to replicate and propagate. Deep understanding of viruses is crucial for developing effective treatments and preventive measures. Even though significant progress has been made in virology, the complexity, diversity, and rapid evolution of viruses present ongoing challenges. In this review article, the authors discussed on a transformative stride in the field of virology, where cutting-edge technology meets the power of artificial intelligence. The integration of machine learning techniques with microscopy, a fusion that holds immense promise for virological research. Viruses, often too small to be directly imaged by traditional light microscopes, have long eluded detailed scrutiny. This cross-scale microscopy approach allows for the visualization of viral structures with unprecedented clarity, enabling scientists to delve deep into the realms of viral morphology, assembly, and interaction with host cells. This technological advancement enables us to move one step closer to unlocking the secrets of these tiny entities that wield enormous influence over human health. (Petkidis, Anthony, Vardan Andriasyan, and Urs F. Greber. “Machine Learning for Cross-Scale Microscopy of Viruses.” Cell Reports Methods 3, no. 9 (September 25, 2023). https://doi.org/10.1016/j.crmeth.2023.100557.)

Application of machine learning algorithms to predict lymph node metastasis in gastric neuroendocrine neoplasms

Neuroendocrine neoplasms, also known as neuroendocrine tumors, are a group of rare tumors that originate from neuroendocrine cells. Neuroendocrine neoplasms can be diagnosed and classified through various tests, in which affects the therapeutic decision-making process. As technology advances, artificial intelligence has shown tremendous potential in revolutionizing the field of oncology by assisting in various aspects. By harnessing machine learning algorithms, the authors have successfully transformed this process into a highly accurate and efficient predictive tool. The ability to analyze vast datasets, identify intricate patterns, and discern subtle correlations allows for a level of predictive accuracy, and offer clinicians valuable insights to make informed decisions regarding patient care. Accurate prediction of lymph node metastasis is paramount in determining the stage of cancer and guiding treatment strategies, potentially leading to improved survival rates for patients. As machine learning continues to evolve, studies like these pave the way for a new era in oncology, offering hope to patients and setting new standards of excellence in cancer care. (Liu, Lu, Wen Liu, Zhenyu Jia, Yao Li, Hongyu Wu, Shuting Qu, Jinzhou Zhu, Xiaolin Liu, and Chunfang Xu. “Application of Machine Learning Algorithms to Predict Lymph Node Metastasis in Gastric Neuroendocrine Neoplasms.” Heliyon 9, no. 10 (October 1, 2023). https://doi.org/10.1016/j.heliyon.2023.e020928.)

Advances in nanotechnology

Tumor microenvironment-responsive DNA-based nanomedicine triggers innate sensing for enhanced immunotherapy

In the ever-evolving landscape of cancer therapy, the integration of nanotechnology and immunotherapy stands as a beacon of hope. This integration represents a transformative approach to cancer therapy, offering hope to patients through targeted, personalized, and efficient treatments, while continually pushing the boundaries of scientific understanding and innovation. In this article, the authors explore the innovative approach of leveraging tumor microenvironment-responsive DNA-based nanomedicine to augment immunotherapeutic strategies. By ingeniously designing DNA-based nanomedicine that responds dynamically to the tumor microenvironment, the authors managed to capitalize on the unique physiological characteristics of the tumor milieu, thereby enhancing the precision and efficacy of immunotherapeutic interventions. The concept of tumor microenvironment-responsive DNA-based nanomedicine has the potential to revolutionize cancer treatment paradigms, paving the way for a future where cancer may no longer be an insurmountable foe. (Li, J., Han, X., Gao, S. et al. Tumor microenvironment-responsive DNA-based nanomedicine triggers innate sensing for enhanced immunotherapy. J Nanobiotechnol 21, 382 (2023). https://doi.org/10.1186/s12951–023–0132–6)

Advancing sustainable agriculture: a critical review of smart and eco-friendly nanomaterial applications

Nanotechnology involves the manipulation of matter at the nanoscale, where one nanometer is one billionth of a meter. Nanotechnology allows scientists to engineer and manipulate materials, creating nanoparticles and nanomaterials with specific characteristics. This technology holds enormous potential in the field of agriculture, where by enhancing precision, improving efficiency, and mitigating environmental impact, nanotechnology contributes significantly to sustainable and productive farming practices. In this article, the authors discussed about the integration of smart and environmentally responsible nanomaterials in agricultural practices. The integration of nanotechnology, when approached conscientiously, has the potential to revolutionize agricultural practices, ensuring food security while minimizing environmental degradation. Moreover, by challenging existing paradigms and offering a roadmap for responsible innovation, this article not only informs the scientific community but also fosters a deeper understanding of the intricate relationship between nanotechnology and sustainable agriculture. This will in turn guide the agricultural sector toward a future where innovation and environmental consciousness harmoniously coexist. (Balusamy, S.R., Joshi, A.S., Perumalsamy, H. et al. Advancing sustainable agriculture: a critical review of smart and eco-friendly nanomaterial applications. J Nanobiotechnol 21, 372 (2023). https://doi.org/10.1186/s12951–023–02135–3)
Macrophage targeted iron oxide nanodecoys augment innate immunological and drug killings for more effective mycobacterium tuberculosis clearance

Tuberculosis is a potentially serious infectious disease caused by the bacterium Mycobacterium tuberculosis. It primarily affects the lungs but can also affect other parts of the body, such as the brain, kidneys, or spine. Tuberculosis spreads through the air when an infected person coughs, sneezes, or talks, releasing tiny droplets containing the bacteria into the air. Till date, Tuberculosis remains a major global health problem, with millions of new cases reported each year. This problem is further exacerbated by the challenges faced in treating Tuberculosis. In this article, the authors explore the strategic use of macrophage-targeted iron oxide nanodecoys to bolster the innate immune response and enhance drug efficacy, ultimately leading to more effective clearance of the tuberculosis-causing pathogen. The integration of nanodecoys targeting specific immune cells highlights the potential for personalized medicine, where tailored nanotechnological interventions could augment the body’s natural defenses against a variety of diseases. Furthermore, this study serves as a blueprint for similar approaches in tackling other intracellular pathogens, paving the way for innovative therapies in the fields of infectious diseases and immunology. (Shen, L., Liao, K., Yang, E. et al. Macrophage targeted iron oxide nanodecoys augment innate immunological and drug killings for more effective Mycobacterium Tuberculosis clearance. J Nanobiotechnol 21, 369 (2023). https://doi.org/10.1186/s12951-023-02103-x)

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