IJLAI Transactions on Science and Engineering (ISSN: 3006-3418) 2024, vol. 2, no. 3, pp: 66–71

Exploring Bioinspired AI for Advanced Cell Labeling: Advancements and Applications in Biomedical Research

Mirza Abdul Aleem Baig[1]

Center for Biomedical Engineering
School of Information Science and Technology, University of Science and Technology of China
Anhui, Hefei, P.R. China
baig@mail.ustc.edu.cn

Received September. 14, 2024; Revised and Accepted September. 18, 2024

Abstract. Context: Bioinspired Artificial Intelligence (Bio-AI) has emerged as a transformative tool in biomedical research, addressing challenges in cell labeling essential for understanding cellular behavior and interactions. Traditional cell labeling methods often struggle with accuracy, scalability, and adaptability in complex datasets. Objective: This paper theoretically explores the integration of Bio-AI models into cell labeling process. It aims to assess how these models C encompassing neural networks, swarm intelligence, evolutionary algorithms, and self-organizing maps C can enhance cell identification and classification. Method: The paper examines various Bio-AI models that mimic biological processes such as neural functioning, swarm behavior, and evolutionary dynamics. It also evaluates the application of multimodal AI systems that combine imaging data with molecular and genetic information. In addition, the potential of dynamic cell labeling, inspired by neural plasticity, is discussed. Result: The integration of Bio-AI models has demonstrated significant improvements in accuracy, adaptability, and scalability for cell labeling. Automated labeling systems minimize human error and enhance reproducibility. Recent advancements in multimodal AI systems have shown promise in combining imaging with genetic and molecular data, providing more comprehensive insights into cellular behavior. Dynamic labeling models inspired by neural plasticity offer enhanced tracking of cellular transitions over time. Conclusion: Bio-AI holds transformative potential in biomedical research via enabling real-time, dynamic labeling, essential for tracking cellular changes over time in processes like cancer progression, stem cell differentiation, and immune response. The continued evolution of these AI-driven approaches is expected to accelerate breakthroughs in understanding diseases, tissue engineering, and regenerative medicine.

Keywords: Bioinspired Artificial Intelligence, Biomedical Research, Cell Labeling, Bio-AI Models.

1. Introduction

Cell labeling is a critical technique in modern biomedical research, enabling scientists to track cellular behavior, monitor interactions, and understand cellular dynamics in healthy and diseased tissues. Traditional approaches to cell labeling, such as fluorescent tagging or manual annotation, are labor-intensive, error-prone, and difficult to scale. These methods often rely on subjective human interpretation, which can introduce variability in results, especially in large datasets or complex biological samples [1]. To address these limitations, artificial intelligence has been increasingly employed to automate and enhance the process [2, 3]. In particular, Bio-AI, which draws inspiration from biological systems, offers novel strategies for improving the precision, high-accuracy and high cell labeling effectiveness [4]. These AI-driven approaches can reduce human bias, increase reproducibility, and scale seamlessly to large datasets. In addition, bioinspired algorithms allow for adaptive and dynamic labeling, ensuring that models evolve alongside new data inputs [5]. By leveraging techniques like machine learning and neural networks, Bio-AI has the potential to revolutionize cell labeling, providing more accurate and scalable solutions for advanced biomedical research.

Bio-AI mimics the mechanisms found in nature to solve complex problems. In the context of cell labeling, these algorithms take inspiration from the brains neural networks, the collective behavior of animals, and the processes of evolution and self-organization. By leveraging these biological principles, Bio-AI can address the inherent challenges of cell labeling, such as dealing with high-dimensional data, cellular heterogeneity, and dynamic biological environments. This paper examines the application of Bio-AI for cell labeling, focusing on the latest advancements, benefits, and challenges. Key approaches and models C neural networks, swarm intelligence, evolutionary algorithms, and self-organizing maps C are applied to enhance automated cell labeling accuracy and efficiency. These models not only improve cell tracking and classification but also offer dynamic and adaptable labeling solutions, essential for understanding evolving cellular processes. In addition, this paper explores the integration of multimodal data, combining molecular, genetic, and imaging information, to provide a comprehensive, context-aware approach to labeling.

2. Bioinspired AI Models for Cell Labeling

2.1. Neural Networks Inspired by the Brain

Neural networks, particularly convolutional neural networks (CNNs) and recurrent neural networks (RNNs), are core components of AI systems inspired by the brains architecture and function. These models excel in pattern recognition, making them ideal for processing cellular data [6]. Recent advances in deep learning have led to the development of highly accurate cell labeling systems capable of identifying cells in complex tissues and across multiple imaging modalities [7,8]. For instance, CNNs can be trained to identify subtle differences in cell morphology or fluorescence signals, automating the detection of various cell types in large datasets. W. Yu used CNNs to classify different types of immune cells in tumor microenvironments, significantly improving detection accuracy compared to traditional techniques [9]. RNNs, on the other hand, have shown potential in time-lapse microscopy studies, tracking cell dynamics and labeling cell states over time. P. Madrigal employed RNNs to predict cell division patterns, enabling dynamic labeling in stem cell differentiation experiments [10]. These advancements have made neural network-based models indispensable for large-scale single-cell analysis, where high-throughput and precision are required to capture the complexity of cellular behavior in biomedical research.

Recent research has demonstrated the utility of CNNs in segmenting cells from microscopy images with higher precision compared to traditional image processing techniques [11,12]. CNNs excel in recognizing complex patterns in cellular images, allowing for automated segmentation even in heterogeneous or noisy environments. J.C. Koo used deep CNNs to segment cancerous cells in histopathology images, achieving a higher accuracy rate compared to manual annotations, which are often labor-intensive and subjective [13]. Besides, generative adversarial networks (GANs), a subset of neural networks, have been employed to enhance image resolution, improving the accuracy of downstream cell labeling tasks. E.g., in a study Y. Li used GANs to improve the resolution of fluorescence microscopy images, enabling better identification of subcellular structures [14]. This method allowed researchers to label smaller and more detailed cellular components that were previously challenging to resolve. Such advancements in GANs are particularly valuable in single-cell analysis and tissue imaging, where image quality directly impacts the accuracy of cell identification and classification. GAN-based super-resolution techniques have also shown promise in enhancing live-cell imaging, enabling real-time tracking and labeling of dynamic cell processes at a higher spatial resolution [15].

2.2. Swarm Intelligence for Cell Tracking and Labeling

Swarm intelligence, inspired by the collective behavior of animals such as ants, bees, and birds, has been applied to the problem of cell tracking, labeling and imaging. Algorithms like Particle Swarm Optimization (PSO) and Ant Colony Optimization (ACO) mimic the decentralized, adaptive behavior of these organisms, making them well-suited for tracking cells in dynamic environments, such as time-lapse microscopy studies [16, 17]. These swarm-based approaches leverage the principles of collective intelligence and self-organization, allowing for more robust and flexible cell tracking solutions that adapt to the inherent variability and movement within biological systems. By drawing on natures solutions to complex coordination problems, these algorithms offer innovative strategies for real-time cell monitoring and labeling.

A notable example of swarm-based AI for cell labeling is the use of PSO to identify and label cells in tissue samples, where traditional tracking methods often fail due to the complex and variable movement patterns of cells. PSO algorithms adapt to changing environments and noise in the data, offering a robust method for real-time tracking and labeling. K. Lan applied PSO to enhance cell segmentation and tracking in time-lapse, achieving higher accuracy and reduced errors compared to conventional methods [18]. This example highlight how PSO can effectively manage the inherent variability in cell behavior and environmental noise, leading to more precise and scalable cell labeling solutions in complex biological settings. By leveraging the adaptability and collective intelligence of swarm-based algorithms, researchers can improve the quality and reliability of cell tracking in various biomedical applications.

2.3. Evolutionary Algorithms for Optimization

Inspired by the process of natural selection, evolutionary algorithms (EAs) offer a powerful method for optimizing AI models used in cell labeling. In EAs, solutions evolve over time, with the most effective parameters being selected for the next generation, mimicking the evolutionary process of survival of the fittest. Genetic Algorithms (GAs), one of the most widely used EAs, have been applied to optimize feature selection and classification thresholds in cell labeling tasks. E.g., X. Jiang employed GAs to optimize the parameters of a deep learning model for identifying cancerous cells in histopathology images, leading to significant improvements in classification accuracy [19]. In the same way, N. Erfanian utilized GAs to refine feature extraction methods for single-cell RNA

sequencing data, enhancing the models ability to distinguish between different cell types [20], and, T. I. Mohamed used GAs to optimize a deep learning model for lung cancer detection in CT scans, achieving higher sensitivity and specificity [21]. These algorithms allow researchers to automatically fine-tune AI models, reducing human bias and enhancing the performance of cell identification systems. By evolving solutions through iterative refinement, EAs can address complex challenges in cell labeling, leading to more accurate and efficient models that adapt to varying biological data and conditions. These advancements highlight the effectiveness of EAs in enhancing AI systems for medical imaging, offering more precise and automated solutions for cancer diagnosis and potentially improving patient outcomes through timely and accurate detection.

2.4. Biologically Inspired Self-Organizing Maps (SOMs)

Self-Organizing Maps (SOMs), a type of unsupervised learning model, are inspired by the self-organizing behavior of biological systems [22]. SOMs are particularly effective for organizing and clustering high-dimensional data, making them valuable for identifying different cell types based on multi-dimensional datasets like gene expression profiles or protein activity. SOMs have been successfully used in clustering single-cell RNA sequencing data, facilitating the identification of new cell subtypes in complex tissues. Such as, T. Mori employed SOMs to analyze single-cell sequencing data, uncovering previously unrecognized immune cell subtypes with distinct gene expression patterns and spatial-temporal architectures of cells [23]. By visualizing the relationships between cells in a low-dimensional space, SOMs provide a powerful tool for organizing and labeling cells without the need for predefined categories, enhancing our ability to explore cellular heterogeneity and understand complex biological systems. This approach not only aids in the discovery of new cell types but also improves our understanding of cellular functions and disease mechanisms.

3. Multimodal AI for Advanced Cell Labeling

While Bio-AI approaches have shown great promise in cell labeling, the integration of multimodal data C such as combining imaging with genetic, molecular, and proteomic information C can further enhance their performance. Multimodal AI systems, inspired by the way biological systems process multiple types of information, can incorporate diverse data streams to provide a more comprehensive view of cell characteristics. Such as, integrating imaging data with transcriptomic profiles allows for the simultaneous classification of cells based on both morphological and molecular characteristics, leading to more precise and biologically relevant labeling [24-27]. This integration enables the identification of cell types and states that might not be evident from a single data source alone. Recent research has demonstrated the value of this approach in cancer studies, where tumor heterogeneity poses significant classification challenges. R. Arora studied combined spatial transcriptomics with high-resolution imaging to map out different tumor microenvironments, revealing subpopulations of cancer cells with distinct molecular signatures that predict survival and targeted therapy response [28,29]. Correspondingly, S. Yasar integrated proteomic data with imaging for more accurate tumor classification and prognosis prediction [30]. Such multimodal systems are particularly valuable for understanding complex diseases and developing targeted therapies, offering deeper insights into cellular behavior and disease mechanisms.

Recent advances in multimodal AI have enabled the combination of fluorescence imaging with single-cell RNA sequencing to label cells in tumor microenvironments, leading to new insights into cancer progression and therapeutic resistance [31-33]. By integrating these modalities, researchers can simultaneously capture detailed spatial information and molecular profiles, providing a comprehensive view of the tumors cellular landscape. These multimodal AI systems allow for more precise characterization of the tumor microenvironment, improving our understanding of cancer biology and aiding in the development of targeted and personalized therapeutic strategies. By integrating high-resolution imaging with transcriptomic data, researchers can gain deeper insights into the complex dynamics of cancer and identify potential biomarkers for more effective treatments.

4. Dynamic Cell Labeling with Neural Plasticity Models

Inspired by neural plasticity-the brain's ability to adapt and reorganize itself-AI models that can dynamically adjust their labeling as new data becomes available have recently gained attention. These models are particularly useful in scenarios where cell behavior changes over time, such as in studies of cell differentiation or tissue regeneration. Neural plasticity models can continuously refine cell labels as cells undergo phenotypic changes, allowing researchers to track cellular transitions with higher accuracy. E.g., J. Jiang developed a dynamic neural network model that adjusts cell labels in response to real-time data from live-cell imaging, effectively monitoring the progression of cells through different stages [34]. Correspondingly, L. Yang utilized a neural plasticity-inspired

approach to improve labeling in stem cell differentiation by updating labels as cells transitioned through intermediate states [35]. This dynamic labeling approach mimics the adaptability seen in biological systems, providing a more nuanced understanding of cellular processes in dynamic environments. By incorporating feedback loops and adaptive learning, these models enhance the ability to study and interpret complex cellular behaviors over time, offering valuable insights into tissue regeneration and developmental biology.

5. Challenges and Future Directions

Despite the promising potential of Bio-AI in cell labeling, several challenges remain. One major obstacle is the need for large, high-quality datasets to train AI models. Obtaining sufficient labeled data, especially for rare or difficult-to-categorize cell types, is often laborious and costly. In many cases, the lack of comprehensive datasets hampers the performance of bioinspired algorithms, leading to issues with generalization and accuracy. Likewise, the complexity of biological systems, coupled with the heterogeneity of cell populations, presents a significant challenge for developing universally applicable AI models [36-38]. Cells can vary widely across different tissues, conditions, or disease states, requiring AI systems to be flexible enough to handle diverse data. Addressing these issues may involve combining synthetic data generation, transfer learning, and active learning to train models with fewer annotations while still achieving high accuracy. Furthermore, integrating AI models across various modalities, such as genomic, proteomic, and imaging data, further complicates model development but is critical for achieving more holistic cell classification systems in biomedical research.

Looking ahead, advancements in self-supervised learning and transfer learning could help overcome these challenges by enabling models to learn from smaller, less annotated datasets. Self-supervised learning allows AI to infer patterns and features without extensive labeled data [39], while transfer learning enables models trained on one dataset to be adapted to new, similar tasks with minimal retraining [40]. These approaches are crucial for enhancing Bio-AI's applicability in cell labeling, where high-quality labeled data may be scarce. Besides, as AI techniques continue to evolve, integrating Bio-AI models with emerging technologies like quantum computing and advanced imaging modalities may further enhance their capabilities. Quantum computing, with its ability to process massive datasets simultaneously, could significantly accelerate model training and optimization. Meanwhile, advanced imaging techniques, such as super-resolution microscopy, can provide more detailed cellular images, offering richer data for AI systems to analyze. Together, these innovations could revolutionize AI-driven cell labeling, enabling more accurate, efficient, and scalable solutions for biomedical research.

6. Conclusion

Bio-AI represents a powerful and innovative approach to cell labeling in biomedical research. By mimicking the mechanisms found in nature, such as neural networks, swarm behavior, and evolutionary processes, these algorithms offer new avenues for improving the accuracy, efficiency, and adaptability of cell identification and classification. The adaptability of these AI models allows them to handle complex biological systems and heterogeneity in cell populations, overcoming limitations of traditional labeling methods. As AI models become more sophisticated and capable of integrating multimodal data, such as genetic, molecular, and imaging information C they are poised to revolutionize the field of cellular biology. This integration will enhance our ability to uncover intricate details about cellular behavior, leading to breakthroughs in understanding disease mechanisms, tissue regeneration, and therapeutic development. Additionally, Bio-AI can facilitate real-time, dynamic labeling, essential for tracking cellular changes over time in processes like cancer progression, stem cell differentiation, and immune response, paving the way for more personalized, precise treatments and accelerate breakthroughs in understanding diseases, tissue engineering, and regenerative medicine.

7. Conflict of Interest

The author declares no competing financial interests or personal relationships that could have appeared to influence the work reported in this paper. **Acknowledgments.** None.

References

1. Singh H, Kaur H. A Systematic Survey on Biological Cell Image Segmentation and Cell Counting Techniques in Microscopic Images Using Machine Learning[J]. Wireless Personal Communications, 2024, 137(2): 813-851.

2. Maramraju S, Kowalczewski A, Kaza A, et al. AI-organoid integrated systems for biomedical studies and applications[J]. Bioengineering & Translational Medicine, 2024, 9(2): e10641.
3. S. Yin, H. Li, A. A. Laghari, T. R. Gadekallu, et al. An Anomaly Detection Model Based on Deep Auto-encoder and Capsule Graph Convolution via Sparrow Search Algorithm in 6G Internet-of-Everything[J]. IEEE Internet of Things Journal, 2024. DOI: 10.1109/JIOT.2024.3353337.
4. He C. Deep Learning Approach for Cell Nuclear Pore Detection and Quantification over High Resolution 3D Data[D]. Virginia Tech, 2023.
5. Baig M S, Ahmad A, Pathan R R, et al. Precision Nanomedicine with Bio-Inspired Nanosystems: Recent Trends and Challenges in Mesenchymal Stem Cells Membrane-Coated Bioengineered Nanocarriers in Targeted Nanotherapeutics[J]. Journal of Xenobiotics, 2024, 14(3): 827-872.
6. J. Liu, J. Zhang, S. Yin. Hybrid chaotic system-oriented artificial fish swarm neural network for image encryption. Evolutionary Intelligence, 16, 77-87, 2023. https://doi.org/10.1007/s12065-021-00643-5.
7. Pinto C, Pinto R, Gonalves G. Towards bio-inspired anomaly detection using the cursory dendritic cell algorithm[J]. Algorithms, 2021, 15(1): 1.
8. Schmidgall S, Ziaei R, Achterberg J, et al. Brain-inspired learning in artificial neural networks: a review[J]. APL Machine Learning, 2024, 2(2).
9. S. Yin, H. Li, L. Teng, A. A. Laghari, V. V.a Estrela. Attribute-based Multiparty Searchable encryption model for Privacy Protection of Text Data[J]. Multimedia Tools and Applications, 2023. ttps://doi.org/10.1007/s11042-023-16818-4.
10. Zidane M, Makky A, Bruhns M, et al. A review on deep learning applications in highly multiplexed tissue imaging data analysis[J]. Frontiers in Bioinformatics, 2023, 3: 1159381.
11. Pylvänäinen J W, Gómez-de-Mariscal E, Henriques R, et al. Live-cell imaging in the deep learning era[J]. Current Opinion in Cell Biology, 2023, 85: 102271.
12. Yu W, Liu Y, Zhao Y, et al. Deep learning-based classification of cancer cell in leptomeningeal metastasis on cytomorphologic features of cerebrospinal fluid[J]. Frontiers in Oncology, 2022, 12: 821594.
13. Wang L, Shoulin Y, Alyami H, et al. A novel deep learning-based single shot multibox detector model for object detection in optical remote sensing images[J]. Geoscience Data Journal, vol. 11, no. 3, pp. 237-251, 2024.
14. Yin S, Wang L, Shafiq M, et al. G2Grad-CAMRL: an object detection and interpretation model based on gradient-weighted class activation mapping and reinforcement learning in remote sensing images[J]. IEEE Journal of Selected Topics in Applied Earth Observations and Remote Sensing, 2023, 16: 3583-3598.
15. Madrigal P, Deng S, Feng Y, et al. Epigenetic and transcriptional regulations prime cell fate before division during human pluripotent stem cell differentiation[J]. Nature Communications, 2023, 14(1): 405.
16. Melanthota S K, Gopal D, Chakrabarti S, et al. Deep learning-based image processing in optical microscopy[J]. Biophysical Reviews, 2022, 14(2): 463-481.
17. Aswath A, Alsahaf A, Giepmans B N G, et al. Segmentation in large-scale cellular electron microscopy with deep learning: A literature survey[J]. Medical image analysis, 2023: 102920.
18. Koo J C, Ke Q, Hum Y C, et al. Non-annotated renal histopathological image analysis with deep ensemble learning[J]. Quantitative Imaging in Medicine and Surgery, 2023, 13(9): 5902.
19. Li Y, Zeng G H, Liang Y J, et al. Improving quantitative prediction of protein subcellular locations in fluorescence images through deep generative models[J]. Computers in Biology and Medicine, 2024, 179: 108913.
20. Zargari A. Deep Learning Approaches for Cell Segmentation and Tracking in Time-Lapse Microscopy[D]. University of California, Santa Cruz, 2024.
21. Valdez F. Swarm intelligence: a review of optimization algorithms based on animal behavior[J]. Recent advances of hybrid intelligent systems based on soft computing, 2021: 273-298.
22. Nayak J, Swapnarekha H, Naik B, et al. 25 years of particle swarm optimization: Flourishing voyage of two decades[J]. Archives of Computational Methods in Engineering, 2023, 30(3): 1663-1725.
23. Lan K, Zhou J, Jiang X, et al. Group theoretic particle swarm optimization for multi-level threshold lung cancer image segmentation[J]. Quantitative Imaging in Medicine and Surgery, 2023, 13(3): 1312.
24. S. Yin, H. Li, Y. Sun, M. Ibrar, and L. Teng. Data Visualization Analysis Based on Explainable Artificial Intelligence: A Survey[J]. IJLAI Transactions on Science and Engineering, vol. 2, no. 2, pp. 13-20, 2024.
25. Zhang D, Shafiq M, Wang L, et al. Privacy-preserving remote sensing images recognition based on limited visual cryptography[J]. CAAI Transactions on Intelligence Technology, 2023. https://doi.org/10.1049/cit2.12164.
26. Jiang X, Hu Z, Wang S, et al. Deep learning for medical image-based cancer diagnosis[J]. Cancers, 2023, 15(14): 3608.
27. Erfanian N, Heydari A A, Feriz A M, et al. Deep learning applications in single-cell genomics and transcriptomics data analysis[J]. Biomedicine & Pharmacotherapy, 2023, 165: 115077.
28. Mohamed T I A, Oyelade O N, Ezugwu A E. Automatic detection and classification of lung cancer CT scans based on deep learning and ebola optimization search algorithm[J]. Plos one, 2023, 18(8): e0285796.
29. Shilpa Mehta P, Academics D. An Overview of Network Architectures for Deep Learning: A Comparative Study of Convolutional and Transformer Networks[J]. Neural Networks, 2022, 192.
30. Mori T, Takase T, Lan K C, et al. eSPRESSO: topological clustering of single-cell transcriptomics data to reveal informative genes for spatioCtemporal architectures of cells[J]. BMC bioinformatics, 2023, 24(1): 252.
31. Moffitt J R, Lundberg E, Heyn H. The emerging landscape of spatial profiling technologies[J]. Nature Reviews Genetics, 2022, 23(12): 741-759.
32. Watson E R, Taherian Fard A, Mar J C. Computational methods for single-cell imaging and omics data integration[J]. Frontiers in molecular biosciences, 2022, 8: 768106.

33. Arora R, Cao C, Kumar M, et al. Spatial transcriptomics reveals distinct and conserved tumor core and edge architectures that predict survival and targeted therapy response[J]. Nature Communications, 2023, 14(1): 5029.
34. Yasar S, Yagin F H, Melekoglu R, et al. Integrating proteomics and explainable artificial intelligence: a comprehensive analysis of protein biomarkers for endometrial cancer diagnosis and prognosis[J]. Frontiers in Molecular Biosciences, 2024, 11: 1389325.
35. Yan H, Shi J, Dai Y, et al. Technique integration of single-cell RNA sequencing with spatially resolved transcriptomics in the tumor microenvironment[J]. Cancer Cell International, 2022, 22(1): 155.
36. Xie T, Huang A, Yan H, et al. Artificial intelligence: illuminating the depths of the tumor microenvironment[J]. Journal of Translational Medicine, 2024, 22(1): 799.
37. Jiang J, Zeng Z, Xu J, et al. Long-term, real-time and label-free live cell image processing and analysis based on a combined algorithm of CellPose and watershed segmentation[J]. Heliyon, 2023, 9(10).
38. Yang L, Conley B M, Yoon J, et al. High-content screening and analysis of stem cell-derived neural interfaces using a combinatorial nanotechnology and machine learning approach[J]. Research, 2022.
39. Sapoval N, Aghazadeh A, Nute M G, et al. Current progress and open challenges for applying deep learning across the biosciences[J]. Nature Communications, 2022, 13(1): 1728.
40. Gerace F, Saglietti L, Mannelli S S, et al. Probing transfer learning with a model of synthetic correlated datasets[J]. Machine Learning: Science and Technology, 2022, 3(1): 015030.

Biography

Mirza Abdul Aleem Baig is with the Center for Biomedical Engineering and School of Information Science and Technology, University of Science and Technology of China. Research direction is medical analysis, computer application and AI.