



Editorial

A Yet Another AI Journal?

Dmitrij Frishman

Department of Bioinformatics, TUM School of Life Sciences, Technical University of Munich, 85354 Freising, Germany; dmitrij.frishman@gmail.com

How To Cite: Frishman, D. A Yet Another AI Journal? *LifeAI* 2025, 1(1), 1.

1. The AI Revolution in Life Sciences: A New Era Begins

Artificial intelligence (AI) is everywhere, seamlessly integrating into our daily lives, from voice assistants like Siri and Alexa to recommendation algorithms on Netflix and YouTube. In recent years AI has also been making significant strides in the life sciences, with applications spanning drug discovery, genomics, structural biology, and clinical medicine. Some of the most notable recent applications include:

- DeepMind's AlphaFold [1] and Meta's ESMFold [2] have revolutionized protein structure prediction and facilitated structural studies across multiple biological domains.
- AI-Based protein engineering methods are enabling the design of *de novo* proteins with tailored functions [3].
- AI models, such as those developed by Insilico Medicine [4], are generating novel molecular structures tailored for specific protein targets.
- Transformers are revolutionizing single-cell genomics and proteomics by improving data integration, spatial analysis, and cell-type classification [5].
- Protein language models enable accurate genome-wide disease variant effect prediction [6].
- AI-powered algorithms for clinical decision support are transforming modern medicine by enhancing diagnostic accuracy, optimizing treatment strategies, and improving patient outcomes [7].

The proliferation of AI in life sciences has been accelerated by powerful software libraries such as Keras (keras.io), TensorFlow (www.tensorflow.org), and PyTorch (pytorch.org), which have lowered technical barriers and democratized access to deep learning applications in biology and medicine.

2. Bridging the Divide: A Journal for AI-Driven Biology

AI is thus no longer a futuristic concept in life sciences—it is a driving force shaping our understanding of biology at an unprecedented scale. However, as AI-driven research in biology expands rapidly, a crucial gap has emerged: existing journals are either too broad, covering all aspects of AI, or too specialized, limiting their focus to isolated subfields of life sciences. Most AI journals prioritize algorithmic innovations, often neglecting biological context and experimental validation. Conversely, life science journals incorporating AI contributions frequently lack sufficient depth in machine learning methodology. *LifeAI* is designed to bridge this gap by serving as a dedicated venue for research at the intersection of AI and the life sciences, ensuring rigorous evaluation of both computational methods and their biological implications.

3. LifeAI: More than a Journal, a Community

LifeAI is not merely about AI—it is about life. It is committed to uniting computational breakthroughs with tangible biological insights. Beyond publishing cutting-edge research, *LifeAI* aspires to serve as a hub for the rapidly growing AI-in-life-sciences community by:

- Providing open-access publishing to ensure broad dissemination of knowledge
- Encouraging interdisciplinary collaborations, fostering special issues that bring together AI researchers, biologists, and clinicians



- Promoting reproducibility by emphasizing rigorous benchmarking and mandating access to code and data
- Building partnerships with AI and life science conferences

So, is *LifeAI* just another AI journal? We hope to establish it as the premier venue where AI meets biology with purpose. Join us in shaping the future of AI-driven life sciences.

Conflicts of Interest

The author declares no conflict of interest.

References

1. Jumper, J.; Evans, R.; Pritzel, A.; et al. Highly accurate protein structure prediction with AlphaFold. *Nature* **2021**, *596*, 583–589.
2. Lin, Z.; Akin, H.; Rao, R.; et al. Evolutionary-scale prediction of atomic-level protein structure with a language model. *Science* **2023**, *379*, 1123–1130.
3. Watson, J.L.; Juergens, D.; Bennett, N.R.; et al. De novo design of protein structure and function with RFdiffusion. *Nature* **2023**, *620*, 1089–1100.
4. Ivanenkov, Y.A.; Polykovskiy, D.; Bezrukov, D.; et al. Chemistry42: An AI-Driven Platform for Molecular Design and Optimization. *J. Chem. Inf. Model.* **2023**, *63*, 695–701.
5. Szalata, A.; Hrovatin, K.; Becker, S.; et al. Transformers in single-cell omics: A review and new perspectives. *Nat. Methods* **2024**, *21*, 1430–1443.
6. Brandes, N.; Goldman, G.; Wang, C.H.; et al. Genome-wide prediction of disease variant effects with a deep protein language model. *Nat. Genet.* **2023**, *55*, 1512–1522.
7. Rajpurkar, P.; Chen, E.; Banerjee, O.; et al. AI in health and medicine. *Nat. Med.* **2022**, *28*, 31–38.