

Annotated Bibliography

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References

- [1] Seonwoo Min, Byunghan Lee, and Sungroh Yoon. Deep learning in bioinformatics. *Briefings in Bioinformatics*, 18(5):851–869, 2017. Accessed: January 29, 2026.

This review paper surveys the application of deep learning methods to major bioinformatics challenges arising from large-scale biomedical data. The authors categorize existing research by both application domain, including omics analysis, biomedical imaging, and signal processing, and by neural network architecture, such as deep neural networks, convolutional neural networks, and recurrent neural networks. Representative studies are summarized to illustrate how deep learning models extract meaningful patterns from complex biological data. The source is credible and authoritative, as it is published in the peer-reviewed journal *Briefings in Bioinformatics* and written by established researchers in machine learning and bioinformatics. As a review article, it synthesizes a broad range of prior work and provides a balanced discussion of both successes and limitations. This paper is relevant to research interests in applying machine learning to biological data, offering a structured overview of current approaches and highlighting key challenges and future research directions in the field.

- [2] Vidal Rene, Zhihui Zhu, and Benjamin D. Haeffele. Optimization landscape of neural networks. In Philipp Grohs and Gitta Kutyniok, editors, *Mathematical Aspects of Deep Learning*, pages 200–228. Cambridge University Press, 2022.

Many tasks in machine learning involve solving a convex optimization problem which significantly facilitates the analysis of properties of the resulting algorithms, such as their optimality, robustness, and generalization. An important challenge in training neural networks occurs when the associated optimization problem is non-convex; this complicates the analysis because global optima can be difficult to characterize and the optimization landscape can also include spurious local minima and saddle points. As a consequence, different algorithms might attract different weights depending on initialization, parameter tuning, etc. Despite this challenge, in practice existing algorithms routinely converge

to good solutions, which suggests that the landscape might be simpler than expected, at least for certain classes of networks.

- [3] Peter W. Shor. Polynomial-time algorithms for prime factorization and discrete logarithms on a quantum computer. *SIAM Journal on Computing*, 26(5):1484–1509, 1997.

The Church-Turing thesis says that a digital computer is a universal computational device; that is, it is able to simulate any physically realizable computational device. It has generally been believed that this simulation can be made efficient so that it entails at most a polynomial increase in computation time. This may not be true if quantum mechanics is taken into consideration. A quantum computer is a hypothetical machine based on quantum mechanics. We explain quantum computing, and give an algorithm for prime factorization on a quantum computer that runs asymptotically much faster than the best known algorithm on a digital computer. It is not clear whether it will ever be possible to build large-scale quantum computers. One of the main difficulties is in manipulating coherent quantum states without introducing errors or losing coherence. We discuss quantum error-correcting codes and fault-tolerant quantum computing, which can guarantee highly reliable quantum computation, given only moderately reliable quantum computing hardware.