



Pan-Cancer Prognosis Prediction using DeepProg, an Ensemble of Deep-Learning and Machine-Learning Models

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OVERVIEW

DeepProg is a computational platform that uses advanced artificial intelligence to accurately predict cancer patient survival groups using multiple layers of biological data.

- Unites deep-learning and machine-learning models to analyze diverse data types (omics) for robust survival risk stratification.
- Outperforms standard methods, offering superior accuracy for treatment guidance and precision oncology markets.

BACKGROUND

Accurately predicting how a cancer patient will fare is critical for guiding treatment decisions and drug development. Traditionally, this has relied on single data types—like gene expression or DNA methylation—analyzed in isolation. This approach misses deeper biological complexity and struggles with the inherent technical noise of each data type. As a result, prognosis tools often fall short in clinical precision and broad applicability, fueling market demand for more robust, multi-dimensional solutions. Market trends show rapid growth in precision oncology and clinical genomics, with increasing investment in AI-driven solutions and multi-omics integration. Yet, few solutions reliably and directly model survival outcomes across a wide variety of cancers or offer transferable insights between related tumor types.

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INNOVATION

DeepProg uniquely combines deep-learning neural networks and classical machine-learning techniques in an ensemble, allowing it to learn from multiple types of biological data simultaneously (such as RNA expression, methylation, and miRNA). It automatically extracts and combines the most relevant signals connected to patient survival, identifies key risk groups within each cancer type, and builds robust classifiers that can even be cross-applied to predict risks in other, related cancers. Unlike many competitors, DeepProg explicitly uses patient outcome data as a primary target—making its predictions actionable for clinicians and researchers. Its ensemble approach also makes it resilient to data noise, adaptable to variable datasets, and scalable for new types of biological tests, representing a significant leap over both traditional statistical models and other clustering-based multi-omics tools.