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AI-Guided Molecular Design Using Deep Reinforcement Learning for Drug Discovery

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Poster description

Drug discovery remains a long, expensive, and resource-intensive process, with many candidate compounds failing during the early stages of development. A major challenge is the efficient identification of chemically valid and pharmacologically relevant molecules within a vast chemical space, especially for cancer-targeted and disease-relevant therapeutic applications. To address this challenge, this work presents an artificial intelligence framework for de novo molecular design using deep reinforcement learning, specifically a Deep Q-Network (DQN) model, as published in our 2025 conference paper [1]. The framework uses molecular descriptors derived from the ZINC dataset, allowing the agent to iteratively explore chemical space through sequential decision-making. By enlarging the action space, the model improves its ability to generate novel molecular structures while optimizing drug-likeness properties. The resulting compounds exhibit favorable physicochemical characteristics, including balanced LogP values, suitable molecular weight, and acceptable hydrogen-bonding profiles. Importantly, the framework achieves 100% chemical validity for the generated molecules. Compared with existing methods, the proposed approach delivers competitive performance while retaining a simpler and more interpretable architecture. These contributions also align with broader applications of artificial intelligence and reinforcement learning in biomedical and health sciences, including oncology, disease detection, and treatment optimization [2]–[4].

References

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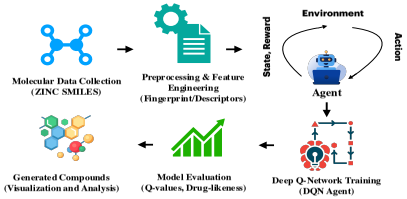
Introduction

- Drug discovery is slow, high-risk, and expensive often taking 10+ years and billions of dollars per approved drug.
- The Design–Make–Test–Analyze (DMTA) cycle remains a major bottleneck, even with progress in genomics, molecular biology, and computation [1].
- While high-throughput screening can find leads, it is often too costly to scale broadly.
- Virtual screening and docking help prioritize candidates early, but they still struggle to explore the vast chemical space efficiently, leaving many viable structures unexplored [2].
- Reinforcement learning (RL) reframes molecular design as a sequential decision-making task, enabling both property-driven optimization and exploration of novel chemotypes beyond conventional search strategies [3].

Methods

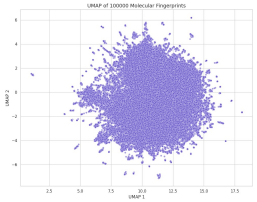
- Used a Deep Q-Network (DQN) for de novo molecular generation.
- Trained on molecular descriptors derived from the ZINC dataset.
- Expanded the action space to encourage broader exploration and improve the chance of generating drug-like candidates.



End-to-End DQN Workflow for Molecular Generation

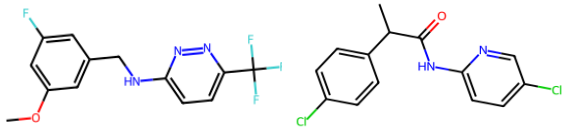
Results

- Generated molecules demonstrated favorable physicochemical profiles (e.g., balanced LogP, appropriate molecular weight, and hydrogen-bonding characteristics).
- Achieved 100% chemical validity across generated compounds.
- Compared with prior generative baselines (e.g., ReLeaSE, GCPN, MolDQN), the proposed DQN framework achieved competitive performance while maintaining a simpler architecture [3].



UMAP visualization of molecular fingerprints

Two drug-like molecules generated by the DQN model



Compound 1	Compound 2
MW: 301	MW: 295
LogP: 3.26	LogP: 4.13
HBD/HBA: 1 / 4	HBD/HBA: 1 / 2
Best Q-value: 22.34	Best Q-value: 0.292

Conclusions

- DQN-based de novo design complements traditional screening by reducing early-stage time and cost.
- Achieves high chemical validity with a simple, lightweight architecture, comparable to prior DRL methods.
- Improves chemical space exploration and generates drug-like candidates.
- Generated molecules align with cancer target relevant scaffolds.

Future work

- Add richer reward terms (e.g., solubility, metabolic stability, formulation constraints).
- Use LLMs to expand dataset diversity and scale.
- Sharing our findings with medical experts and pharmacists will support clinical relevance.
- Conducting real-world evaluations will help validate the effectiveness and reliability of the DQN models in clinical and pharmaceutical settings.

References

[1] R. M. Plenge, T. M. Scolnick, and D. Altshuler, “Validating therapeutic targets through human genetics,” Nat. Rev. Drug Discov., 2013.
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