

Abstract

# Machine Learning Strategies for Drug Discovery in AML: Focus on RUNX1 Bioactivity<sup>†</sup>

Deepesh Kumar Verma

ExcelR Solutions, Bangalore 560068, Karnataka, India; deepeshvashu@gmail.com

<sup>†</sup> Presented at the 4th International Electronic Conference on Cancers, 6–8 March 2024; Available online: <https://sciforum.net/event/IECC2024>.

**Keywords:** acute myeloid leukemia (AML); blood cancer; RUNX1; machine learning; mutations; computational drug discovery; bioactivity; molecular descriptors; PubChem fingerprints

Acute myeloid leukemia (AML) is an aggressive blood cancer where immature stem cells in the bone marrow multiply rapidly, disrupting blood cell production and leading to infections, anemia, and bleeding. This devastating disease claims around 85,000 lives annually and is projected to double by 2040, highlighting its critical importance for research and improved treatment strategies. The RUNX1 transcription factor, a critical gene for hematopoiesis, is highly prevalent in AML and linked to poor patient outcomes. Mutations disrupt RUNX1's function, essentially acting as a "bad switch" that promotes aggressive leukemia growth and significantly reduces survival chances. Targeting this master regulator holds promise for developing novel therapies to improve patient outcomes in AML.

In the current study, we utilized a computational drug discovery approach, involving bioactivity data retrieval for Human RUNX1 "CHEMBL2093862" from the ChEMBL database, where RUNX1 is the target protein. We performed chemical space analysis using Lipinski descriptors to identify whether the compounds have the properties of ideal drugs or not. We calculated molecular descriptors, specifically PubChem fingerprints, to identify the unique structure of the compounds. We applied machine learning algorithms, like Random Forest, Linear Regression, Decision Tree, and XGBoost, to create a model with the ability to classify whether the compounds are active or inactive. This study uses a user-friendly bioactivity prediction app using Streamlit so that researchers can check for the bioactivity and potency of drugs in real time for the targeting of RUNX1 in AML. This study introduces a comprehensive plan for drug development targeting RUNX1, offering potential interventions for AML mediated by RUNX1.

**Supplementary Materials:** The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/proceedings2024100012/s1>, Conference Poster: Machine Learning Strategies for Drug Discovery in AML: Focus on RUNX1 Bioactivity.

**Funding:** This research received no external funding.

**Institutional Review Board Statement:** Not applicable.

**Informed Consent Statement:** Not applicable.

**Data Availability Statement:** Data sharing is not applicable to this abstract.

**Conflicts of Interest:** The authors declare no conflict of interest.

**Disclaimer/Publisher's Note:** The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.



**Citation:** Verma, D.K. Machine Learning Strategies for Drug Discovery in AML: Focus on RUNX1 Bioactivity. *Proceedings* **2024**, *100*, 12. <https://doi.org/10.3390/proceedings2024100012>

Academic Editor: Ulrich Pfeffer

Published: 27 March 2024



**Copyright:** © 2024 by the author. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).