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Integrating Genomic and Clinical Parameters to Predict Outcomes in Pediatric Acute Lymphoblastic Leukemia

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INTRODUCTION

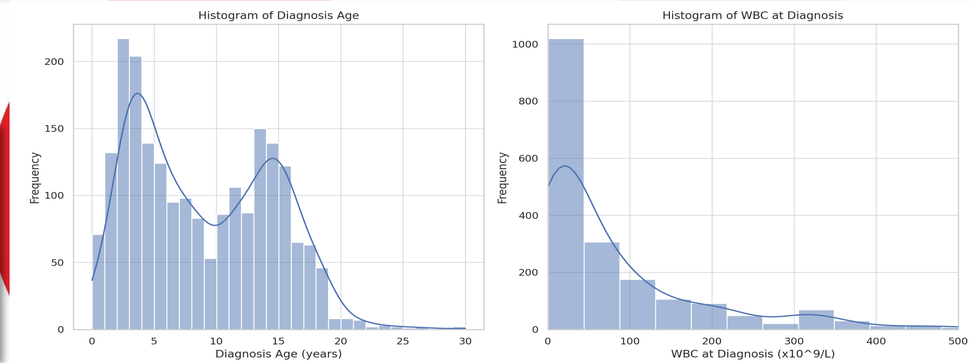
Acute lymphoblastic leukemia (ALL) is the most common childhood cancer, characterized by heterogeneous genetic features that influence disease progression and treatment response. The integration of genomic data with traditional clinical parameters holds promise for advancing personalized medicine in ALL.

AIM

To evaluate the predictive power of combined genomic and clinical data in forecasting treatment outcomes and survival rates among pediatric ALL patients.

METHOD

- This retrospective study utilized genomic and clinical data from three major pediatric ALL cohorts, incorporating over 2,000 patient samples. Key clinical parameters included diagnosis age, white blood cell (WBC) count at diagnosis, and overall survival. Genomic data encompassed mutation counts, cytogenetic abnormalities, and gene expression profiles from CBIOPORTAL.
- The analysis was performed using a comprehensive bioinformatics pipeline, integrating data imputation methods for missing values, exploratory data analysis for feature selection, and predictive modeling to assess patient outcomes.
- The study aimed to identify significant predictors of treatment response and survival, developing a predictive model with high accuracy and generalizability for clinical use in pediatric ALL.



RESULTS

Preliminary analyses revealed key genomic features, such as specific mutations and gene expression patterns, that correlated significantly with treatment outcomes. Integrating these genomic markers with clinical parameters (e.g., WBC count, diagnosis age) improved the prediction accuracy of treatment response and survival, compared to using clinical data alone. The final predictive model demonstrated an AUC-ROC of 0.85 for treatment response and a concordance index of 0.8 for survival prediction.

CONCLUSIONS

The integration of genomic and clinical data provides a more accurate and nuanced approach to predicting treatment outcomes in pediatric ALL. This study underscores the potential of precision medicine in enhancing prognostic models and personalizing treatment strategies. Future research should focus on validating these findings in prospective cohorts and exploring the mechanistic underpinnings of identified genomic markers.

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