

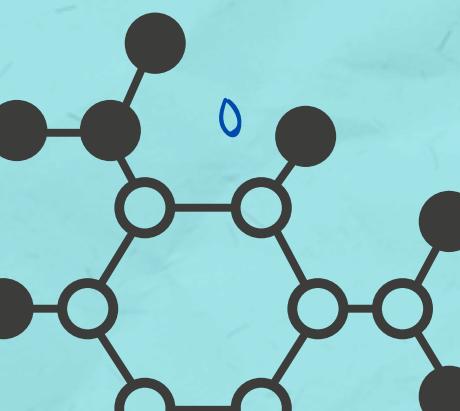
Unmasking Childhood ALL: Understanding Acute Lymphoblastic Leukemia in the Young

Team

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2022044
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[Project Link](#)



PROBLEM STATEMENT

This project aims to investigate the genetic mechanisms and environmental influences contributing to **ALL**, focusing on understanding why this cancer disproportionately affects children. Further, investigate how **ALL** manifests across different ethnicities and explore potential reasons for observed differences. Also, make a simple classification-based model for **ALL**.

PROGRESS AND WORKFLOW



Analysis of ALL
and seeing how
it varies in
various age
groups



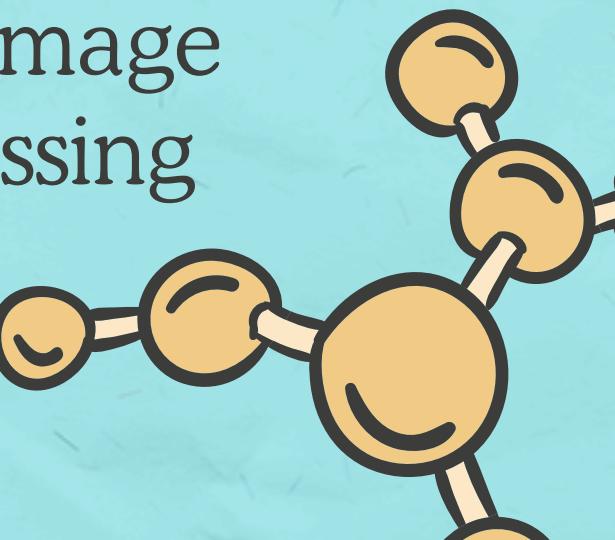
Understanding
the factors
affecting ALL



Ethnicity Analysis
of ALL



Classification
Model
Development
using image
processing



INITIAL ANALYSIS

Mutations in many different genes can be found in ALL cells, but larger changes in one or more chromosomes are also common. Even though these changes involve larger pieces of DNA

Translocations are the most common type of chromosome change that can lead to leukemia.

The most common translocation in **ALL in adults** is known as the **Philadelphia chromosome**, which is a swap of DNA between chromosomes 9 and 22, abbreviated as t(9;22). Many other, less common translocations, can occur as well, including those between chromosomes 4 and 11, t(4;11), or 8 and 14, t(8;14)

[Source](#)



INITIAL ANALYSIS



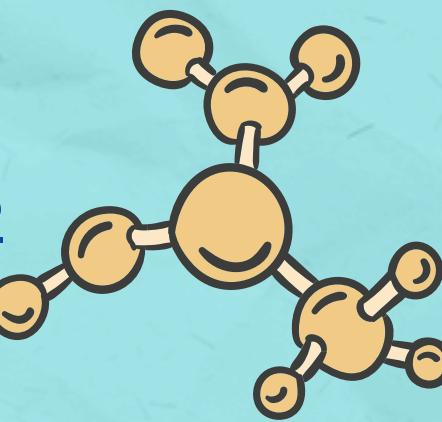
Other chromosome changes, such as **deletions** (the loss of part of a chromosome) and **inversions** (the rearrangement of the DNA within part of a chromosome), are also sometimes found in ALL cells,

Usually, DNA mutations related to ALL are acquired during the person's lifetime rather than being inherited. They may result from outside causes like exposure to **radiation** or cancer-causing chemicals.

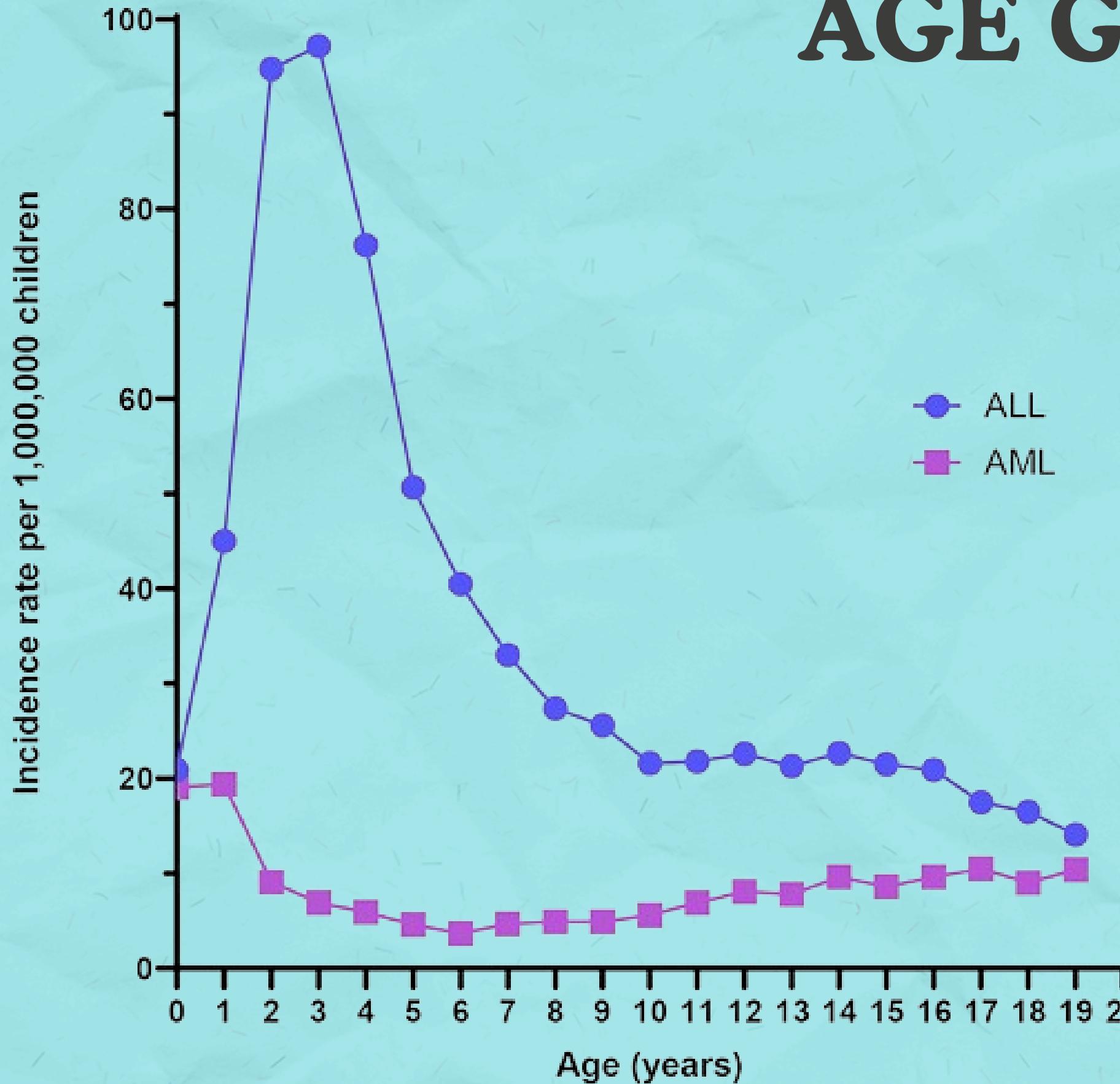


Many of these gene changes are random events that sometimes happen inside a cell without having an outside cause. These changes can build up as we age, which might help explain why **ALL** in adults gets **more common** as people get **older**.

[Source](#)



VARIATION OF ‘ALL’ IN VARIOUS AGE GROUPS



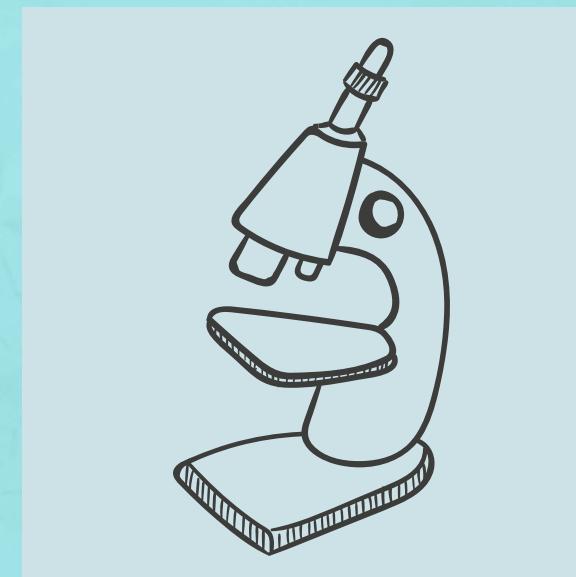
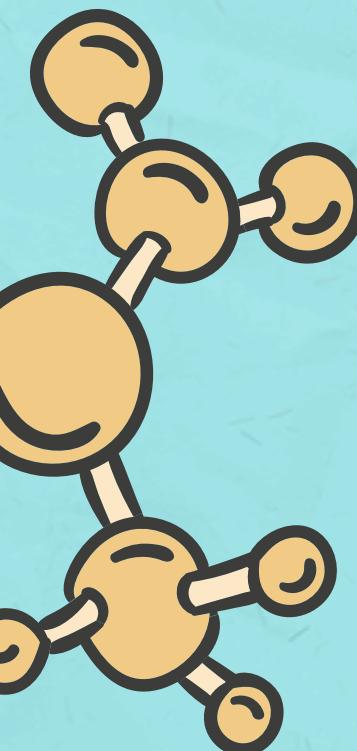
0-5 age group
children have the
highest risk of ALL

And of all ALL cases
65% of them occur in
the **0-34** age groups

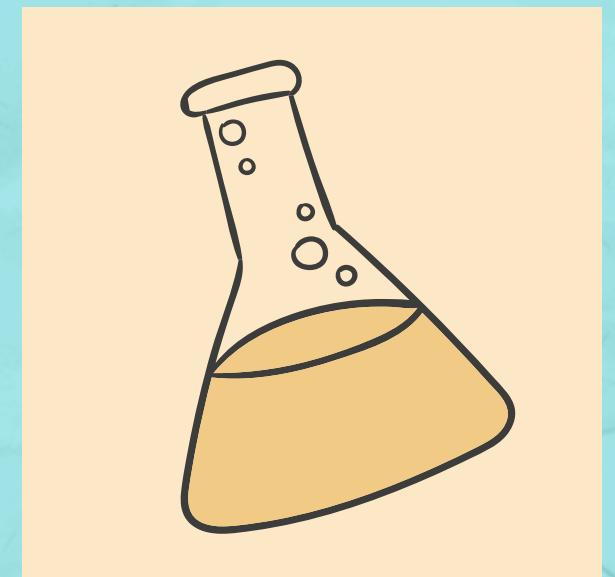
Source

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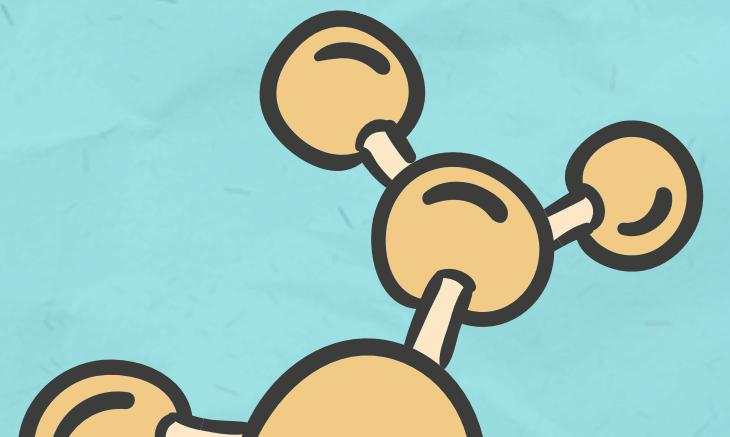
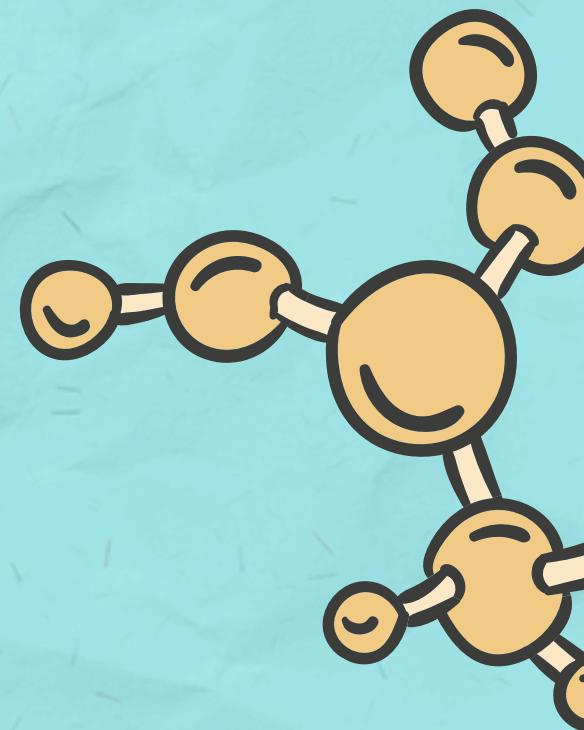
FACTORS WHICH ARE INVOLVED IN ALL IN CHILDREN



Genetic factors such as
Down Syndrome, SNP's
etc



Environmental factors
such as use of pesticides,
smoking, Radiations etc



How leukemia is linked with Down Syndrome

Children with **Down syndrome** have a significantly **higher risk** of developing certain types of leukemia including **ALL** and **AML**.

Down syndrome caused by an extra **chromosome 21**, disrupts cell growth and division, increasing leukemia risk.

The **HMGN1** gene on chromosome 21 overexpresses in individuals with Down syndrome, altering **chromatin** structure and **gene expression**, including the activation of leukemia-associated genes like **CRLF2**.

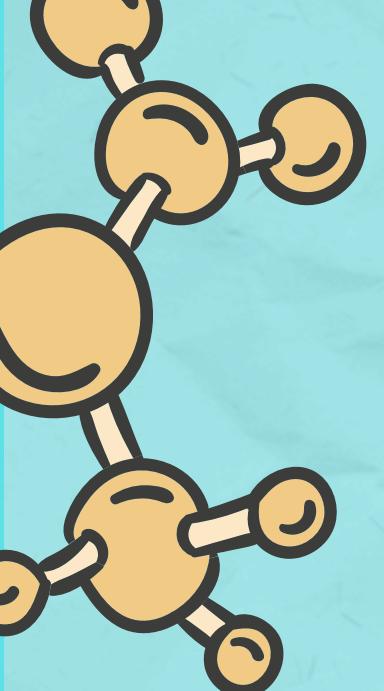
This leads to abnormal cell cycle regulation and proliferation of immature leukemia cells, raising leukemia incidence in these individuals.

[**Source**](#)

Other genetic factors

TEL-AML1 Fusion Gene: This is the most common genetic abnormality in childhood ALL. The fusion of the TEL gene on chromosome 12 and the AML1 gene on chromosome 21 leads to the abnormal behavior of blood cells, increasing the risk of leukemia.

Hyperdiploidy: Many cases of ALL in children involve cells with more than the normal number of chromosomes. This "hyperdiploidy" is associated with a higher rate of cell division and growth, which can contribute to leukemia development.



ENVIRONMENTAL FACTORS

01

Ionizing
Radiation

03

Pesticides

02

Chemicals +
Hydrocarbons

04

Alcohol, Drug
and Cigarettes





Ionizing Radiation



There was an increase in childhood leukemia in children whose **fathers had diagnostic X-rays**.

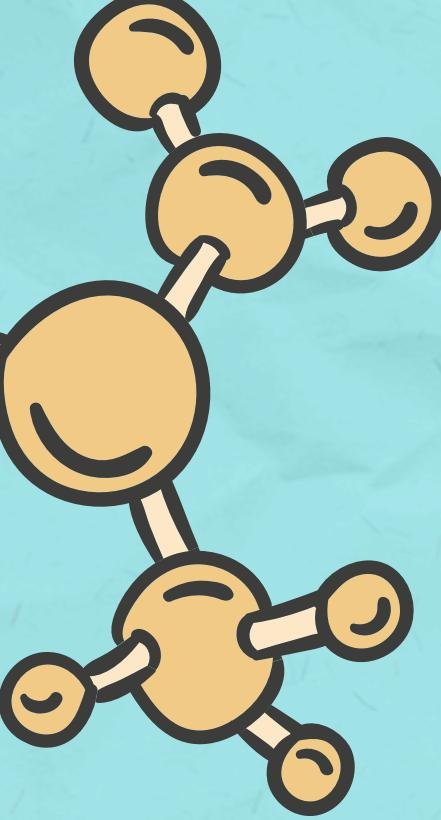
This was statistically significant for men who had had **two or more X-rays** in the **lower abdomen** region.

However, the preconception exposure of X-rays to the mother did not appear to have a significantly higher risk of childhood leukemia



X-ray exposure to children, it was found that the risk for children to develop **pre-B cell ALL** increases when exposed to **three or more X-rays in children older than five years old**. Post-birth X-rays have shown some, but not significant, increase in childhood leukemia risk

[**Source**](#)



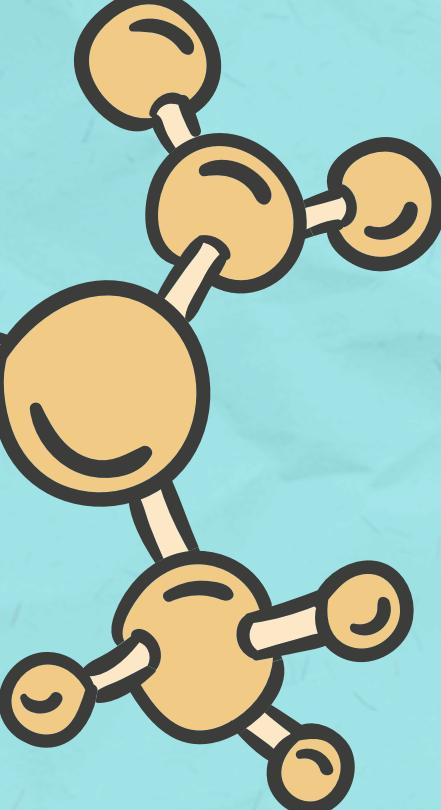
Hydrocarbons



There is a statistically significant increase in **ALL** levels when there was prenatal exposure to newly **painted homes and artwork with solvents.**

Various studies investigated the link between parental occupations and childhood leukemia. Occupations with **exposure to paints and pigments** displayed the highest correlation with leukemia development.

Paternal hydrocarbon exposure seems to be related to an increase in both AML and ALL in **children less than 1 years old.**



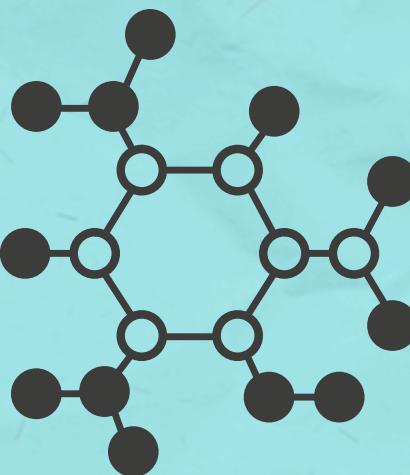
Alcohol, Drug and Cigarettes



Maternal consumption of **alcohol** during **pregnancy** showed an increased risk for AML during childhood and showed a significant impact on ALL too.

The medical use of **marijuana** during the **pre-pregnancy** and during the **gestation** is correlated to childhood **AML** and **ALL**.



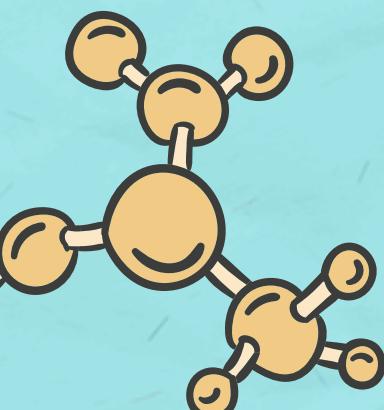


Pesticides

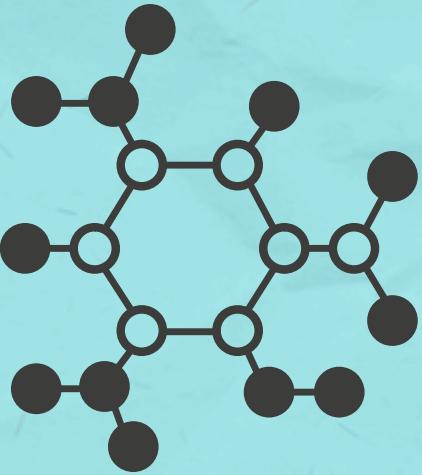


The study indicates that **indoor pesticide use** during **pregnancy** significantly **increases** the risk of childhood **ALL**, especially when combined with specific genetic susceptibilities (**CYP1A1m1** and **CYP1A1m2** polymorphisms).

This suggests both a critical exposure period and a gene-environment interaction that heightens leukemia risks, highlighting the importance of cautious pesticide use around vulnerable populations.



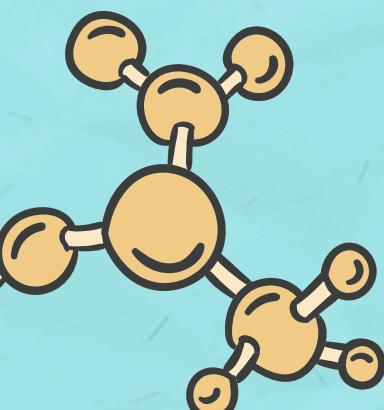
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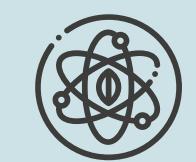
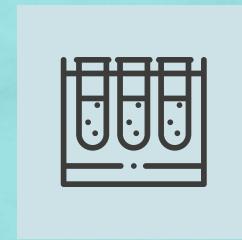
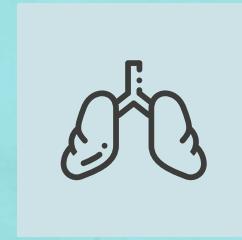
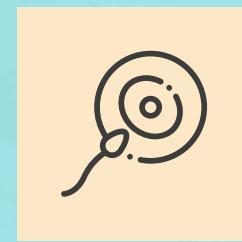
Ethnicity



The **highest risk of ALL was observed for children with a combination of Hispanic ethnicity and White race** compared to non-Hispanic Whites. The lowest risk was observed for non-Hispanic Blacks. Associations for total childhood leukemia were similar to ALL.



FACTORS



- **Genetic Variations:** Certain high-risk genetic variations in genes like **ARID5B**, **GATA3**, **PIP4K2A**, and **ERG** have been found to be more common in Hispanic children. These variations are associated with an increased chance of developing ALL. The gene ERG, in particular, has been identified as having inherited genetic variations that contribute significantly to ALL risk primarily in Hispanic children
-
- **Ancestry-Linked Risk:** Hispanics' Indigenous American ancestry is linked to a higher risk of acute lymphoblastic leukemia (ALL) due to specific gene variants like IKZF1 gene in which they found variation in 3 SNPs. These variants increase leukemia susceptibility, highlighting the intricate link between genetic heritage and disease risk.

[Source1](#)

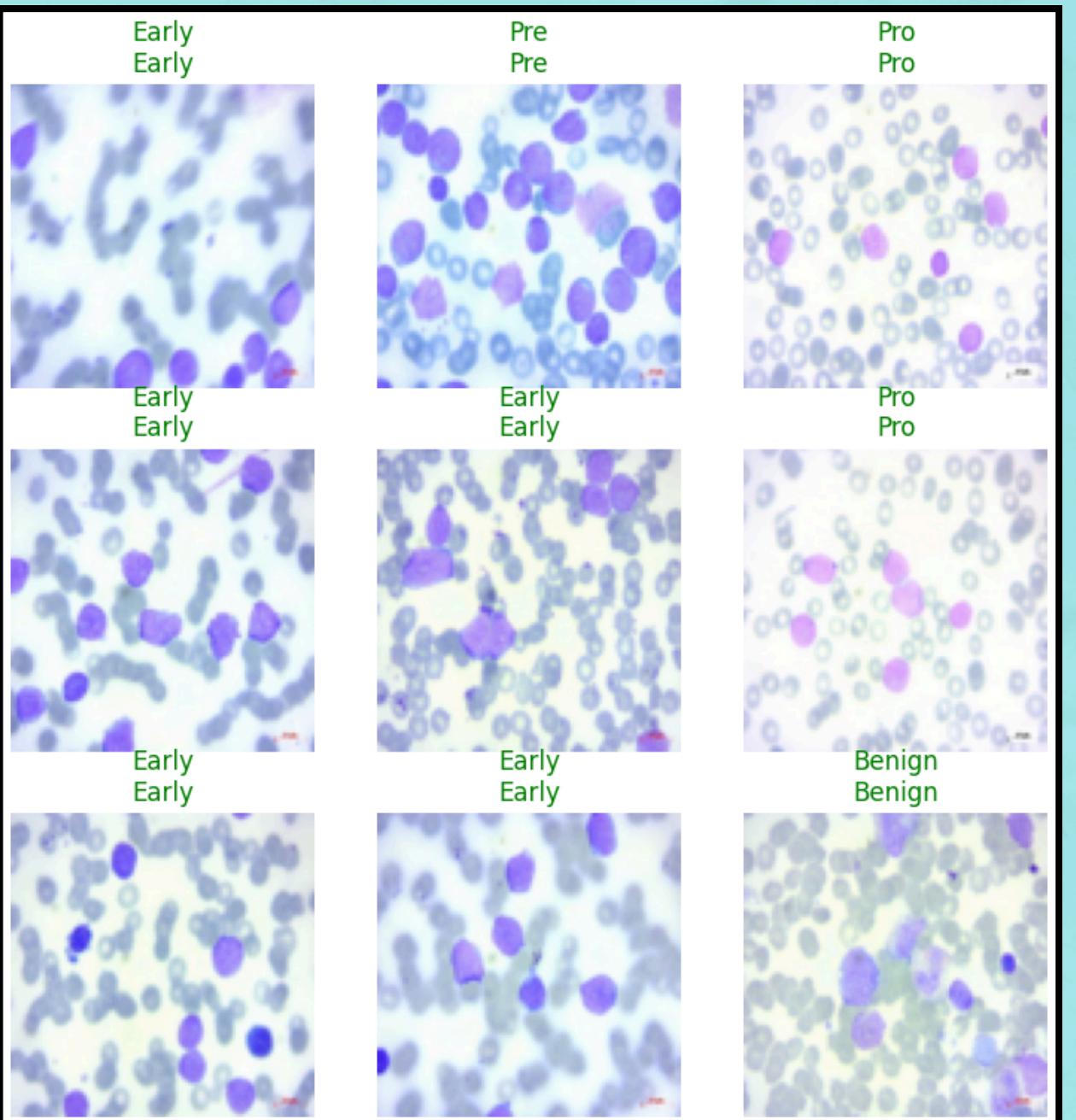
[Source2](#)

Classification Model

Dataset Citation -Mehrad Aria, Mustafa Ghaderzadeh, Davood Bashash, Hassan Abolghasemi, Farkhondeh Asadi, and Azamossadat Hosseini,

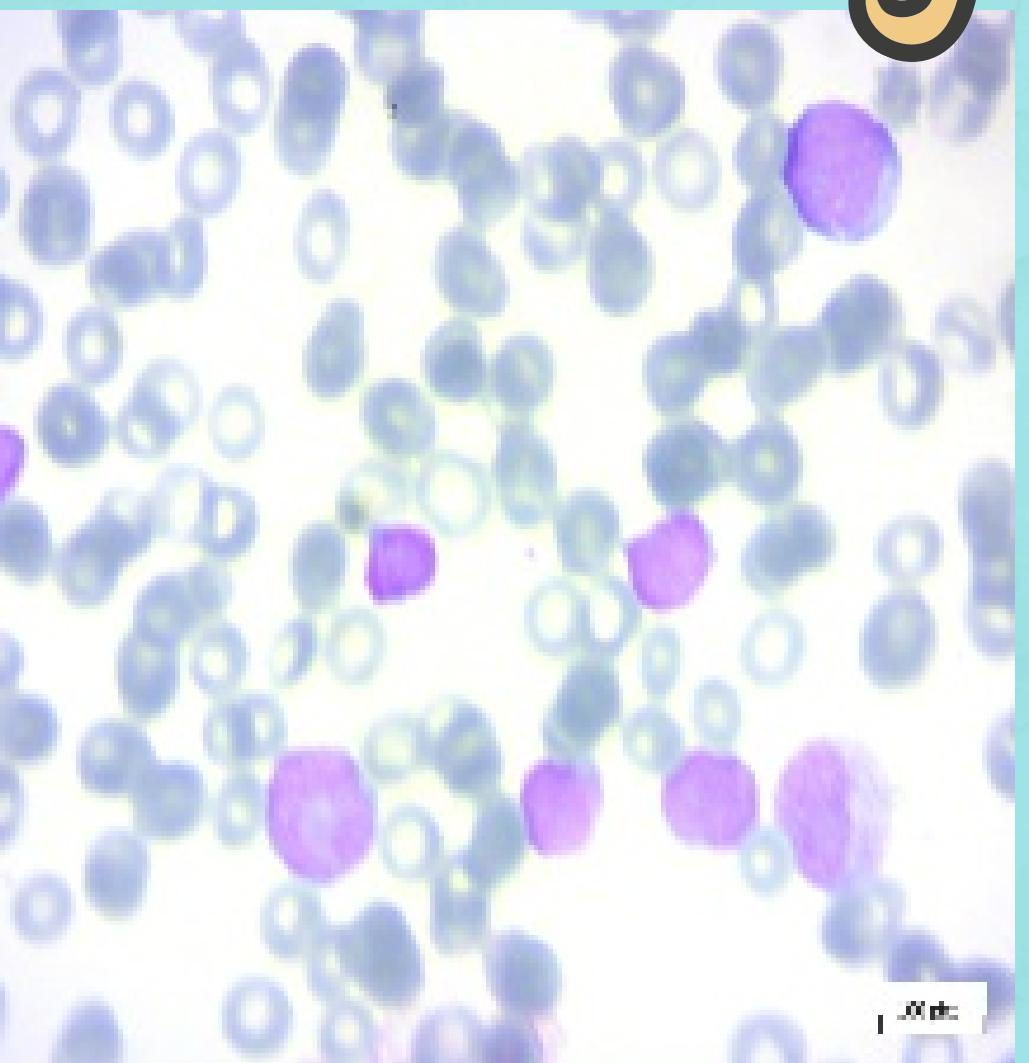
[Dataset Link](#)

[Research Paper](#)



ABOUT OUR DATASET

This dataset is divided into two classes: **benign** and malignant. The former comprises hematogones; the latter is the ALL group with three subtypes of malignant lymphoblasts: **Early Pre-B, Pre-B, and Pro-B** ALL. All the images were taken using a Zeiss camera in a microscope with 100x magnification and saved as JPG files



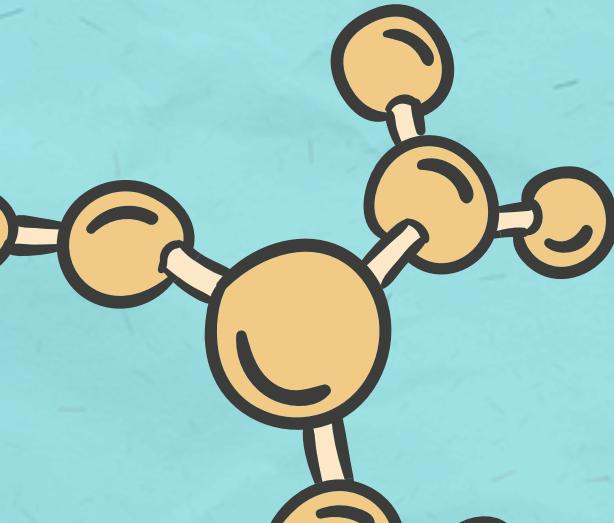
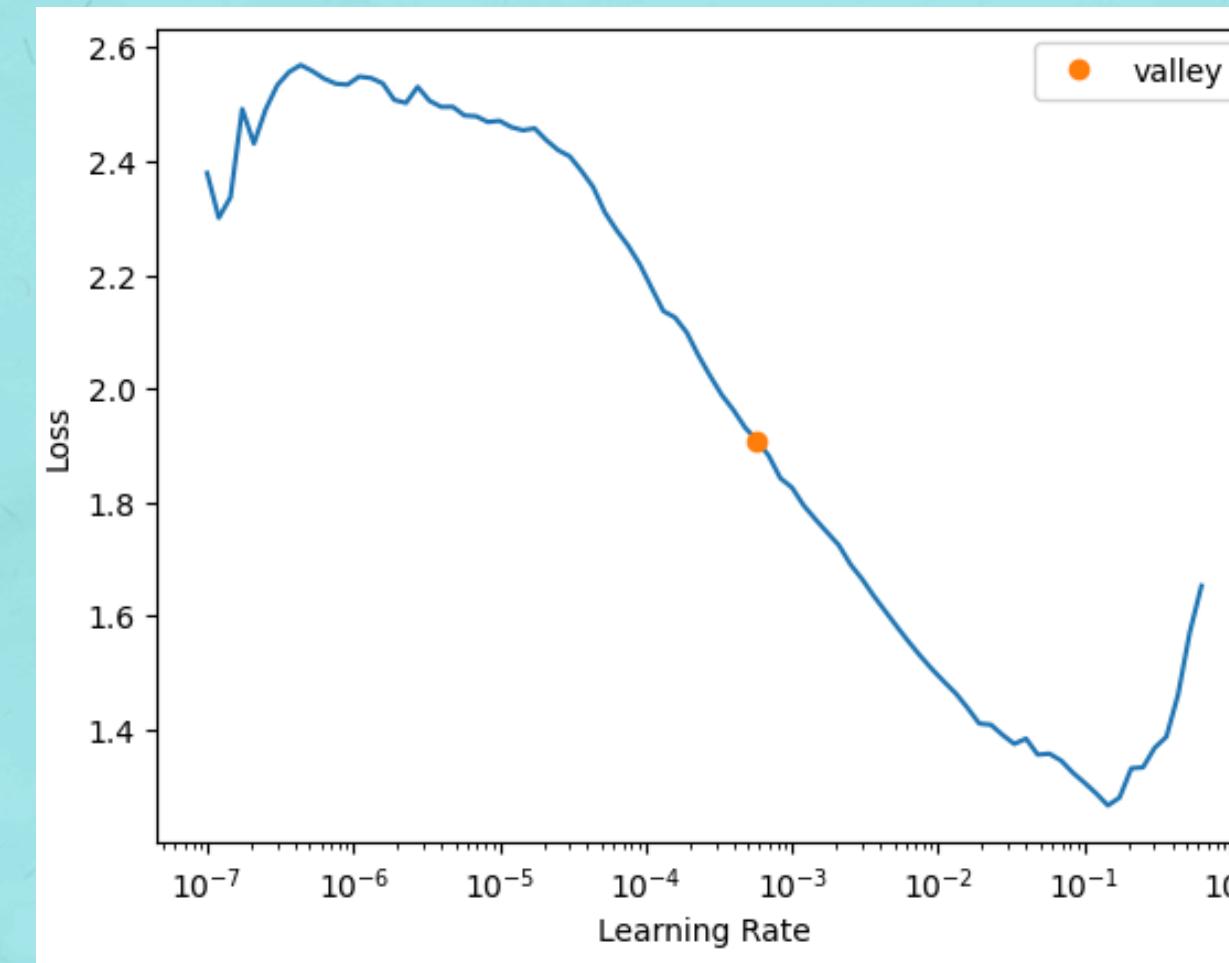
Model

ABOUT OUR MODEL

The model we used to help us was **ResNet-18 (as a learner)**

ResNet-18 is a convolutional neural network architecture, part of the ResNet.

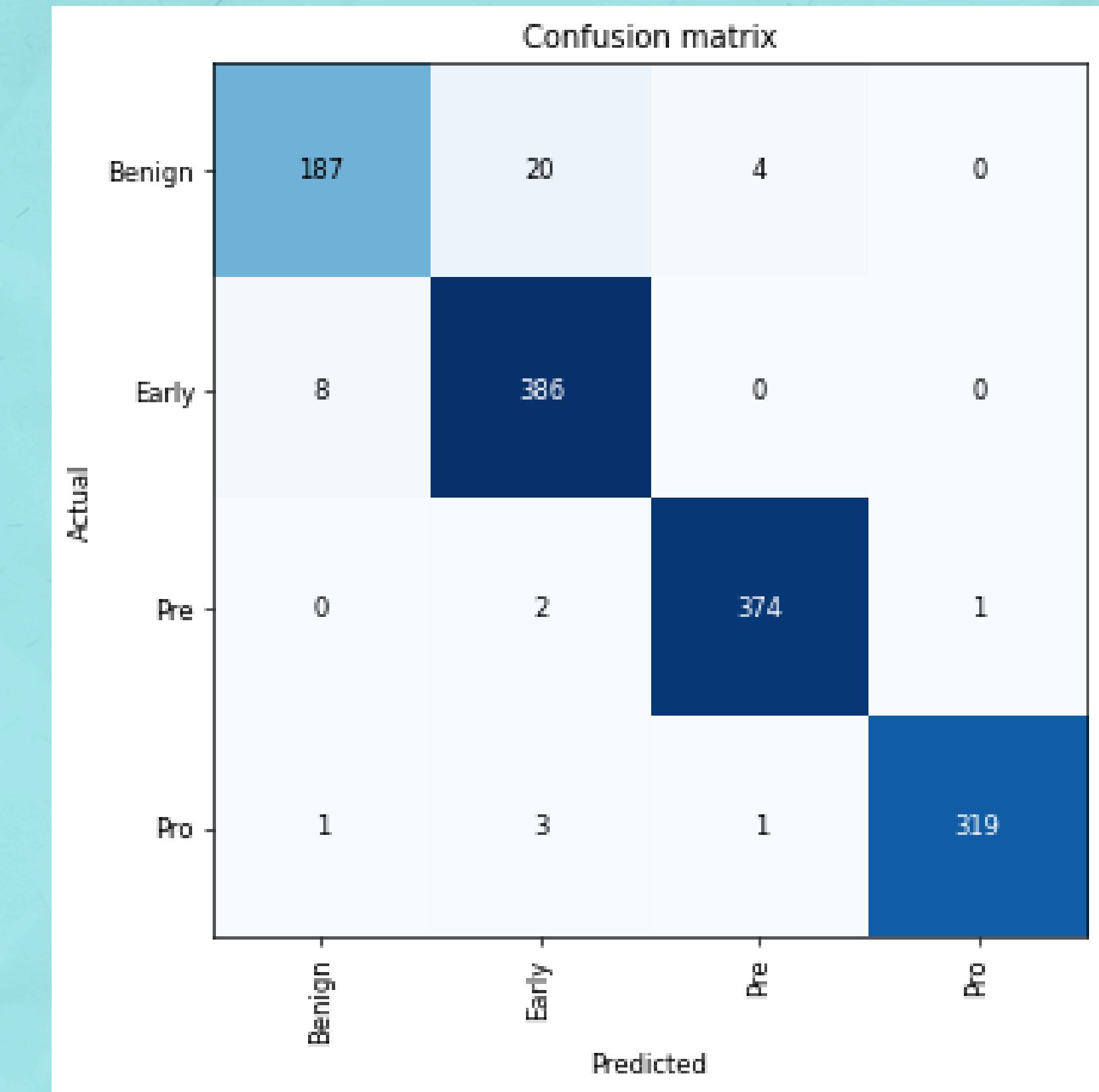
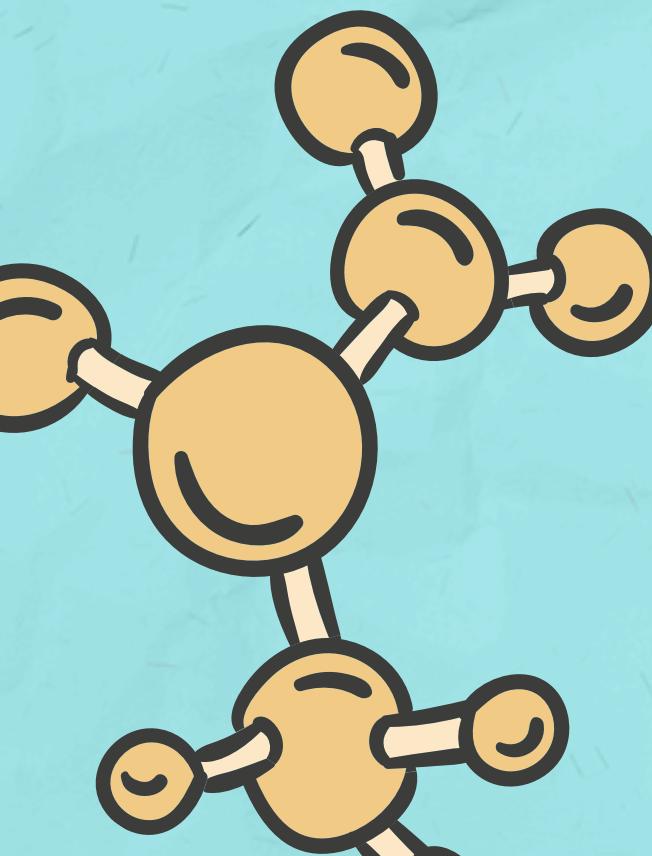
Reaching an **accuracy** of about **~96%**



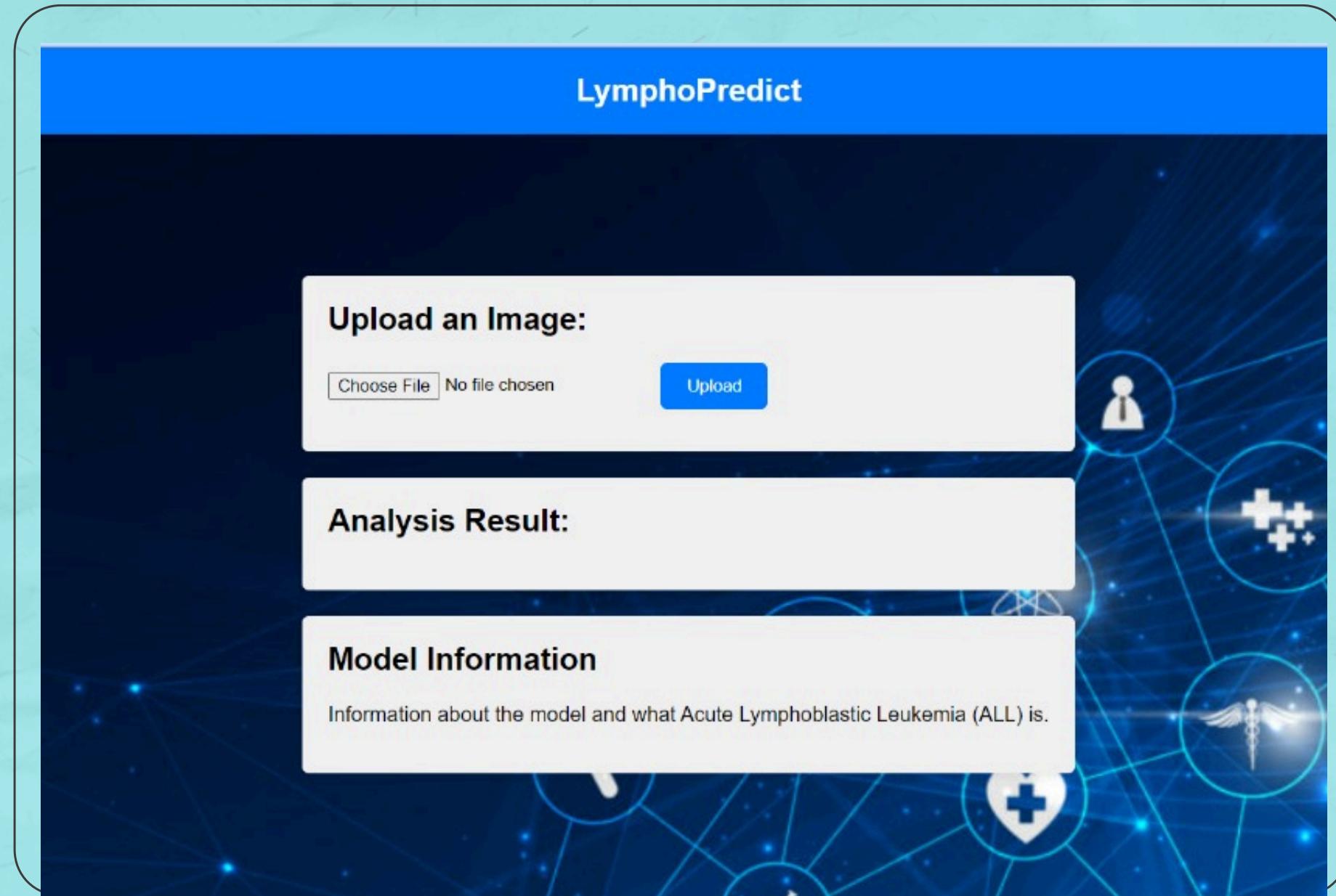
Model

Confusion matrix of our model

Showing a good amount of accuracy
in prediction on our validation set,
which was made using a random 60-
40 split (60->training,40->validation)



Future Scope of our Web Page for Model



We started building a platform that was linked to our model so that we could upload images of blood smears on it and get the classification from our model

And we would like to continue building the platform.

Contributions

Agraney Tripathi

Model + research on
ALL diagnosis by
blood smears

Sarthak Sharma

Model + research on
ALL diagnosis by
blood smears

Shrutiya Chawla

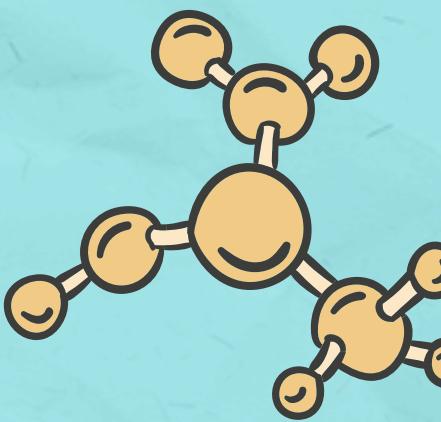
Research on
Age, race factors

Vansh Yadav

Research on
Environmental
Factors affecting ALL

Yashovardhan Singhal

Research on Genetic
factors causing ALL in
Children



THANK YOU

