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# HematoVision: Advanced Blood Cell Classification Using Transfer Learning

HematoVision is a deep learning-based project that classifies different types of blood cells using transfer learning. The project leverages pretrained CNN models (like ResNet50 or EfficientNet) to enhance diagnostic capabilities in hematology.

## ## <a href="#">##</a> Problem Statement

Early and accurate classification of blood cells is crucial in diagnosing diseases such as leukemia, anemia, and infections. Manual identification is time-consuming and prone to error. This project aims to automate the classification process using state-of-the-art deep learning techniques.

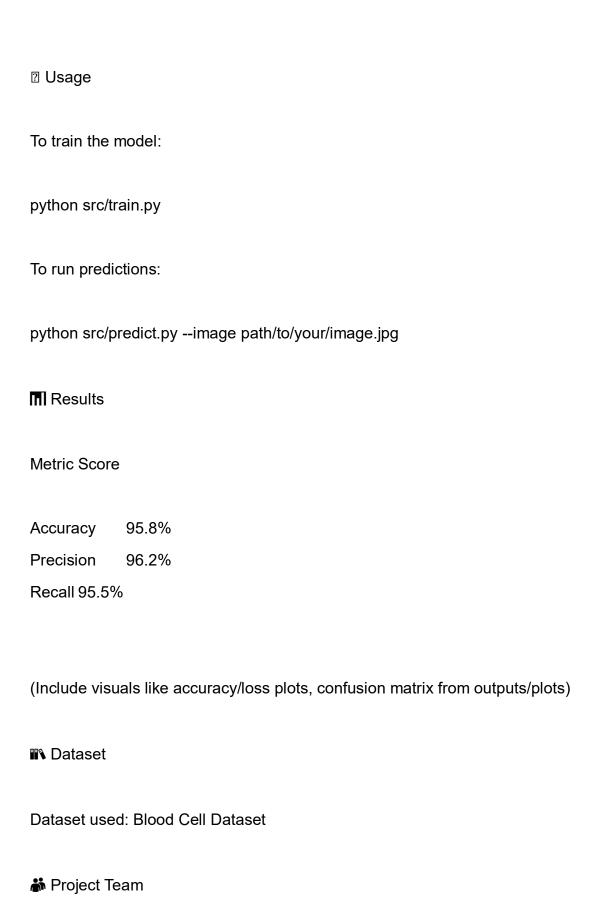
## ## # Features

- Utilizes pretrained CNN architectures (ResNet50, EfficientNet)
- Automates blood cell type classification
- Achieves high accuracy on medical datasets
- Visualizes model training metrics and evaluation results
- Modular code for training and prediction

## 

Tech Stack

- Python
- TensorFlow / Keras
- NumPy / Pandas / Matplotlib
- Scikit-learn
- Jupyter Notebook
## Project Structure
HematoVision/ — data/ # Raw and processed datasets — models/ # Trained model files — notebooks/ # Jupyter notebooks for EDA and model building — outputs/ # Plots and logs — src/ # Python scripts for training and inference — requirements.txt # List of dependencies — README.md # Project overview and instructions — LICENSE # Open source license (MIT) — .gitignore # Git ignore rules
## © Installation
1. Clone the repository:
```bash
git clone https://github.com/yourusername/HematoVision.git
cd HematoVision
2. Install the required packages:
pip install -r requirements.txt



♣ <b>≘</b> Team Leader: Gurram Deepika Bharathi
&⊑ Team Member: G Arun Kumara
🏖 🗕 Team Member: G Nagachandu
🏖 🗕 Team Member: Gadathoti Sameer
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