**Project Prerequisites for HematoVision**

**🔧 Technical Prerequisites**

| **Area** | **Requirements** |
| --- | --- |
| **Programming Language** | **Python 3.7+** |
| **Libraries/Frameworks** | **TensorFlow or PyTorch, NumPy, Pandas, Matplotlib, Scikit-learn** |
| **Image Processing** | **OpenCV, PIL** |
| **Environment** | **Jupyter Notebook / Google Colab / VS Code** |
| **Hardware** | **GPU support (local or via cloud like Google Colab, Kaggle, AWS, etc.) for faster model training** |

🧠 **Knowledge Prerequisites**

| **Area** | **Understanding Needed** |
| --- | --- |
| **Python Programming** | Functions, classes, file I/O, libraries |
| **Deep Learning Basics** | CNNs, activation functions, loss functions, backpropagation |
| **Transfer Learning** | Fine-tuning pre-trained models like ResNet, EfficientNet, etc. |
| **Image Classification** | Preprocessing, data augmentation, evaluation metrics |
| **Model Evaluation** | Accuracy, Precision, Recall, F1-score, Confusion Matrix |

📦 **Software/Tools Required**

| **Tool** | **Purpose** |
| --- | --- |
| **Anaconda / Python Environment** | Managing Python packages |
| **Jupyter Notebook / Colab** | Interactive coding and visualization |
| **TensorBoard / Matplotlib / Seaborn** | Visualizing training and evaluation metrics |
| **Git** | Version control |
| **Google Colab / Kaggle / Local GPU** | Training large models with better hardware |
| **📁 Dataset Requirements**   * **Images of blood cells, properly annotated by type (eosinophil, lymphocyte, monocyte, neutrophil).** * **Dataset format: Should be organized into folders or labelled CSV file.** * **dataset/**   **├── eosinophils/**  **├── lymphocytes/**  **├── monocytes/**  **└── neutrophils/** | |  |