Classification of Human Leukemias

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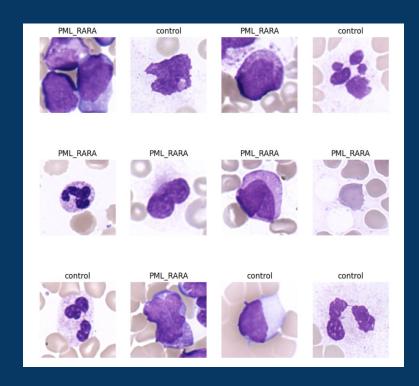
Cancer Image Archive

Blood Cell Images from Normal and Leukemia patients

4 Classes of Leukemia:

- 1. **Normal** (20,305 images)
- 2. Leukemia with PML::RARA fusion (11,584 images)
- 3. Leukemia with NPM1 mutation (17,710 images)
- 4. Leukemia with CBFB::MYH11 fusion (17,212 images)
- 5. Leukemia with RUNX1::RUNX1T1 fusion (14,403 images)

Normal (control) vs PML::RARA Leukemia



Input

Conv2D (64) Batch Normalization (64) Max Pooling (64)

Conv2D (64) Batch Normalization (64) Max Pooling (64)

Conv2D (128)
Batch Normalization (128)
Max Pooling (128)

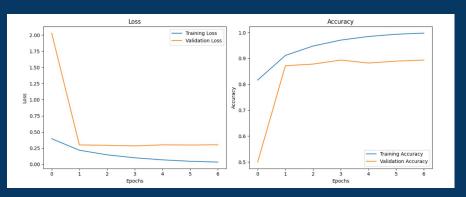
Flatten

Dense layer (128)

Dense layer (1)

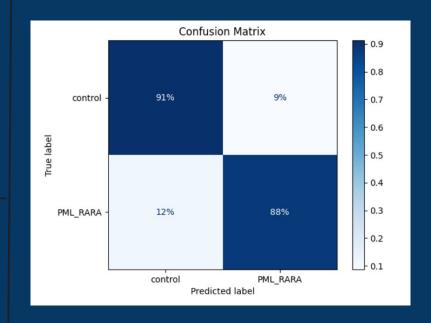
Output

Normal (control) vs PML::RARA Leukemia

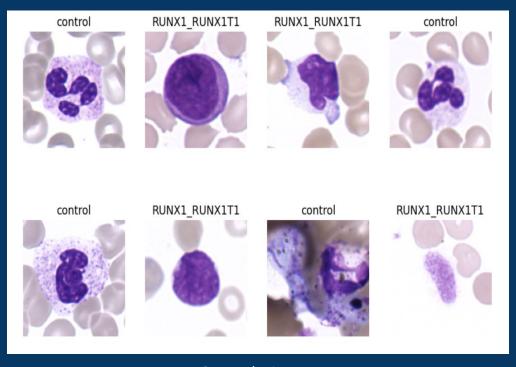


Training Loss (Post hyperparameter tuning)

Predictions	Precision	Recall	f1-Score	Support
Control	0.88	0.91	0.9	800
PML_RARA	0.91	0.88	0.9	800
Accuracy			0.9	1600
Macro Avg	0.9	0.9	0.9	1600
Weighted Avg	0.9	0.9	0.9	1600

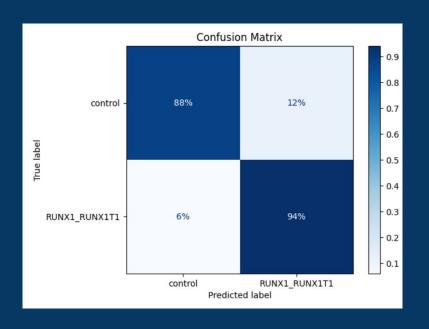


Normal (control) vs Leukemia with RUNX1 fusion

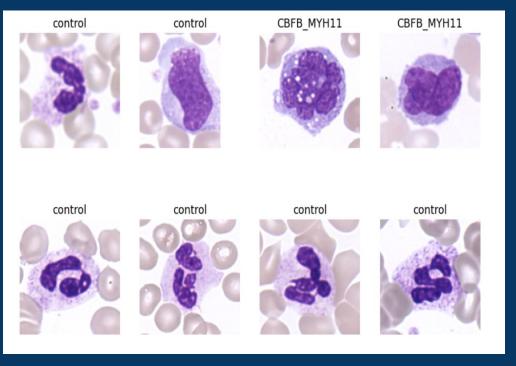


Normal (control) vs Leukemia with RUNX1 fusion

Predictions	Precision	Recall	f1-Score	Support
Control	0.94	0.88	0.91	800
RUNX1_RUNX1T1	0.89	0.94	0.91	800
Accuracy			0.91	1600
Macro Avg	0.91	0.91	0.91	1600
Weighted Avg	0.91	0.91	0.91	1600

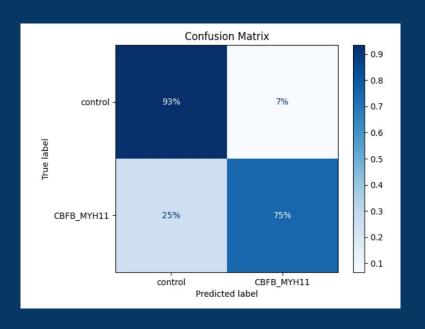


Normal (control) vs Leukemia with CBFB-MYH11 fusion

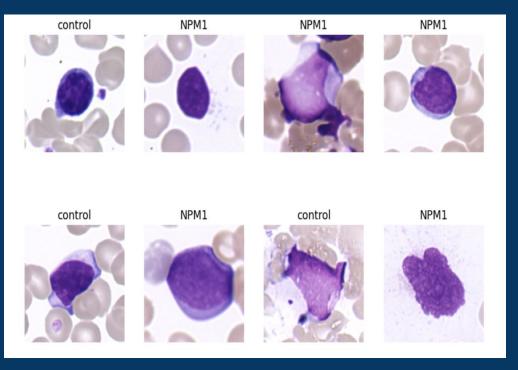


Normal (control) vs Leukemia with CBFB-MYH11 fusion

Predictions	Precision	Recall	f1-Score	Support
Control	0.79	0.93	0.86	800
CBFB-MYH11	0.92	0.75	0.83	800
Accuracy			0.84	1600
Macro Avg	0.85	0.84	0.84	1600
Weighted Avg	0.85	0.84	0.84	1600

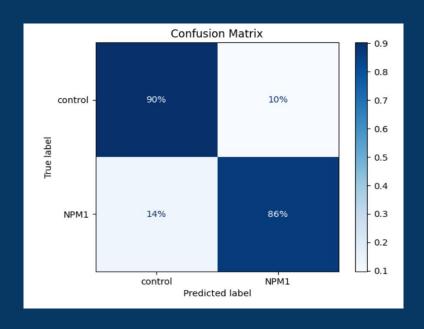


Normal (control) vs Leukemia with NPM1 Mutation



Normal (control) vs Leukemia with NPM1 Mutation

Predictions	Precision	Recall	f1-Score	Support
Control	0.87	0.90	0.89	800
NPM1	0.90	0.86	0.88	800
Accuracy			0.88	1600
Macro Avg	0.88	0.88	0.88	1600
Weighted Avg	0.88	0.88	0.88	1600



Conclusion

- All 4 Leukemia classifications showed F1 score ~0.9.
- Use only ~5000 images to train (due to hardware limitations)
- Leukemia patients sample may contain normal white blood cells.
 - May in part explain misclassification?
 - Datasets needs to be curated?
- Models presented here may be used as a base model to train other Leukemias using Transfer Learning