



## **Model Optimization and Tuning Phase Template**

Date	25 July 2024
Team ID	SWUID20240034367
Project Title	Anemia-Sense-Leveraging-Machine- Learning-For-Precise-Anemia- Recognitions-using-python
Maximum Marks	10 Marks

## **Hyperparameter Tuning Documentation (8 Marks):**

Model	Tuned Hyperparameters
1. Decision Tree (DT)	<ul> <li>Criterion: The criterion was tuned to 'entropy' instead of the default 'gini' to enhance information gain at each split, leading to a more refined tree.</li> <li>Max Depth: The maximum depth was carefully adjusted to 10 to prevent the tree from becoming overly complex, which could lead to overfitting.</li> <li>Min Samples Split: Set to 5 to ensure that each split in the tree was supported by a sufficient number of samples, preventing unnecessary splits.</li> <li>Min Samples Leaf: Tuned to 2, ensuring that each leaf node had enough samples to represent a valid prediction, thereby reducing overfitting.</li> </ul>
2. Random Forest (RF)	Number of Estimators: Increased to 200 trees to improve the robustness of the model through ensemble learning, allowing for better generalization.





	• Max Features: Set to 'sqrt' to limit the number of features considered
	for each split,
	balancing the model's accuracy and training time.
	Bootstrap: Enabled to allow sampling with replacement, enhancing
	the diversity of the individual trees in the forest and reducing variance.
3. Logistic	• Penalty: The penalty parameter was set to 'l2' (Ridge) to introduce
Regression (LR)	regularization and prevent the model from overfitting to the training data.
	• Solver: The 'liblinear' solver was chosen for its efficiency with smaller
	datasets and binary classification tasks.
	• C (Inverse Regularization Strength): Tuned to 1.0 to balance the trade-off
	between regularization and model complexity, ensuring the model could
	capture the essential patterns without overfitting.





## **Final Model Selection Justification (2 Marks):**

Final Model	Reasoning
	After extensive hyperparameter tuning and model evaluation, the
	Random Forest (RF) was selected as the final model for anemia
	detection.
	• Performance: The Random Forest outperformed other models in
	terms of accuracy, precision, recall, and F1 score, making it the
	most reliable model for detecting anemia in the dataset. Its
	ensemble nature allowed it to effectively capture the complex
	relationships between the features and the target variable.
	• Robustness: The model's ability to generalize well across
	different subsets of the data was demonstrated through cross-
	validation, with consistently high performance metrics. This
	robustness was further enhanced by the model's inherent ability to
Random forest	mitigate overfitting through the use of multiple trees.
	• Interpretability: Although more complex than Logistic
	Regression, the Random Forest still provided a level of
	interpretability by allowing us to analyze feature importance,
	offering insights into which clinical factors were most indicative of
	anemia.
	Computational Efficiency: Despite its complexity, the Random
	Forest model was computationally efficient and well-suited for
	deployment, making it a practical choice for real-time anemia
	detection in a clinical setting.