Results

Support Vector Machine (SVM) with Linear Kernel

SVM F1: 0.9583333333333333
SVM Precision: 0.9387755102040817
SVM Accuracy: 0.9649122807017544
SVM Sensitivity: 0.9787234042553191
SVM Specificity: 0.9552238805970149
SVM AUC-ROC: 0.9990473166084471
Cross-validation sensitivity for SVM: 0.93 ± 0.04
Cross-validation accuracy for SVM: 0.95 ± 0.02

The SVM model shows strong performance across all metrics, particularly in sensitivity (recall) and AUC-ROC, indicating excellent capability in identifying malignant cases and separating the two classes. The consistency in sensitivity across cross-validation folds (0.93 ± 0.04) suggests the model generalizes well to unseen data, with a relatively low standard deviation indicating stable performance.

Logistic Regression (LR)

LR F1: 0.9574468085106385
LR Precision: 0.9574468085106383
LR Accuracy: 0.9649122807017544
LR Sensitivity: 0.9574468085106383
LR Specificity: 0.9701492537313433
LR AUC-ROC: 0.9968243886948237
Cross-validation sensitivity for LR: 0.92 ± 0.04
Cross-validation accuracy for LR: 0.95 ± 0.02

LR demonstrates similarly high performance, with slightly lower F1 and precision but comparable accuracy and AUC-ROC to the SVM. The specificity is slightly higher than SVM, indicating a marginally better performance in identifying benign cases. The slight drop in cross-validation sensitivity compared to SVM (0.92 ± 0.04) is within a narrow margin, indicating LR also performs reliably across different data subsets.

Random Forest (RF)

RF F1: 0.967741935483871
RF Precision: 0.9782608695652174
RF Accuracy: 0.9736842105263158
RF Sensitivity: 0.9574468085106383
RF Specificity: 0.9850746268656716
RF AUC-ROC: 0.9969831692600826
Cross-validation sensitivity for Random Forest: 0.94 ± 0.05
Cross-validation accuracy for Random Forest: 0.97 ± 0.02

RF shows the best F1 score and the highest precision, indicating a strong balance between recall and precision and a high rate of correctly identifying malignant cases among positive predictions. It also has the highest specificity, suggesting the best performance in correctly identifying benign cases. The RF model achieves the highest cross-validation sensitivity (0.94 ± 0.05), though with a slightly higher standard deviation than SVM and LR, indicating a bit more variability in performance across folds but still excellent sensitivity.

Conclusion

All three models exhibit strong performance, but the Random Forest model demonstrates the highest cross-validation sensitivity (0.94 ± 0.05), making it particularly well-suited for cancer diagnosis where minimizing missed malignancies is crucial. This performance suggests that the RF model is adept at detecting true positive cases. This is a vital attribute in cancer diagnosis, where the cost of missing a malignant case can be life-threatening. Therefore, the Random Forest model offers the most reliable solution for this sensitive application.