**Model Comparisons: All Key Metrics**

| **Metric** | **nrounds=100, threshold=0.47** | **nrounds=100, threshold=0.65** | **nrounds=200, threshold=0.45** | **nrounds=200, threshold=0.65** |
| --- | --- | --- | --- | --- |
| **True Positives (TP)** | 118 | 75 | 118 | 75 |
| **False Positives (FP)** | 164 | 40 | 164 | 40 |
| **False Negatives (FN)** | 9 | 52 | 9 | 52 |
| **True Negatives (TN)** | 427 | 551 | 427 | 551 |
| **Accuracy** | 75.91% | **87.19%** | 75.91% | **87.19%** |
| **Sensitivity** | **92.91%** | 59.06% | **92.91%** | 59.06% |
| **Specificity** | 72.25% | **93.23%** | 72.25% | **93.23%** |
| **Precision (PPV)** | 41.84% | **65.22%** | 41.84% | **65.22%** |
| **Negative Predictive Value (NPV)** | 97.94% | 91.38% | 97.94% | 91.38% |
| **Balanced Accuracy** | 82.58% | 76.14% | 82.58% | 76.14% |
| **Kappa** | 0.4406 | **0.543** | 0.4406 | **0.543** |

| **Metric** | **nrounds = 100** | **nrounds = 200** | **nrounds = 300** |
| --- | --- | --- | --- |
| **Best max\_depth** | 6 | 9 | 9 |
| **Best eta** | 0.01 | 0.01 | 0.01 |
| **Best gamma** | 5 | 5 | 5 |
| **colsample\_bytree** | 0.6 | 0.6 | 0.6 |
| **min\_child\_weight** | 1 | 1 | 1 |
| **subsample** | 0.6 | 0.6 | 0.6 |
| **Accuracy** | 79.02% | 64.34% | 66.43% |
| **Sensitivity (Recall)** | 66.67% | 87.50% | 83.33% |
| **Specificity** | 81.51% | 59.66% | 63.03% |
| **Precision (PPV)** | 42.11% | 30.43% | 31.25% |
| **Negative Predictive Value (NPV)** | 92.38% | 95.95% | 94.94% |
| **Balanced Accuracy** | 74.09% | 73.58% | 73.18% |
| **Kappa** | 0.3908 | 0.2698 | 0.2784 |
| **True Positives (TP)** | 16 | 21 | 20 |
| **False Positives (FP)** | 22 | 48 | 44 |
| **False Negatives (FN)** | 8 | 3 | 4 |
| **True Negatives (TN)** | 97 | 71 | 75 |

| **File name** | | | **Plot type** | **What it shows** | | **How to interpret** | **Typical use** |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **SV\_importance\_bar.pdf** | | | **Global SHAP importance (bar)** | Features ranked by their mean absolute SHAP value (global influence on the model). Top = most influential. | | Longer bar = greater average impact on predictions. Does not indicate direction (only magnitude). | Identify the most important predictors overall. Useful for feature selection and reporting. |
| **SV\_beeswarm.pdf** | | | **SHAP summary (beeswarm)** | For each feature (y-axis), every point is a sample’s SHAP value (x-axis). Color indicates the feature value (low→blue, high→red). | | Position on x-axis = push toward/away from prediction. Color shows whether high/low feature values cause that push. Dense clouds = common patterns. | See both importance ranking and the direction/magnitude of each feature’s effect. Great for discovering patterns (e.g., high mass → higher risk). |
| **SV\_dependence\_exactMass.pdf** | | | **SHAP dependence (continuous)** | Effect of exactMass on prediction. X-axis = feature value, Y-axis = SHAP value. | | Upward trend = higher values push prediction toward “active”; downward = push toward “inactive.” Spread shows variability due to interactions. | Interpret how a specific continuous feature influences predictions. |
| **SV\_dependence\_top15\_panel.pdf** | | | **Multi-feature dependence panel** | Grid of SHAP dependence plots for the Top-15 most important features. Includes continuous (exactMass) and binary fingerprint bits (Un####). | | For continuous: look for slope/trend; for binary: difference in SHAP between x=0 and x=1 shows impact of “bit on.” | Quick overview of top features’ effects. Use individual high-DPI plots for publication. |
| **Feature** | **Feature type** | **Dependence plot meaning** | | | **Interpretation** | | | |
| **Un8341** | Binary fingerprint | Two vertical bands at x=0 and x=1; higher SHAP for x=1 | | | Presence of this substructure tends to increase predicted activity; absence reduces it. | | | |
| **Un713** | Binary fingerprint | Higher SHAP values for x=1, small spread | | | This bit’s presence moderately raises the probability of being “active.” | | | |
| **Un1534** | Binary fingerprint | Slightly positive SHAP shift for x=1 | | | Presence gives a mild increase in predicted activity. | | | |
| **Un1705** | Binary fingerprint | Clear positive SHAP difference between x=0 and x=1 | | | This substructure is a strong positive predictor of activity. | | | |
| **Un881** | Binary fingerprint | Positive SHAP for x=1, negative/near-zero for x=0 | | | Presence increases predicted risk; absence decreases it. | | | |
| **Un4816** | Binary fingerprint | Positive SHAP shift when present, low variance | | | Consistently pushes predictions toward “active” when present. | | | |
| **Un1200** | Binary fingerprint | Moderate positive SHAP for x=1, narrow spread | | | Reliable but modest increase in risk when present. | | | |
| **Un867** | Binary fingerprint | Higher SHAP for presence; wider spread suggests interactions | | | Presence increases risk, but effect varies depending on other features. | | | |
| **Un511** | Binary fingerprint | Positive SHAP for x=1, stable effect | | | Consistent positive contribution to prediction when present. | | | |
| **Un4394** | Binary fingerprint | Positive SHAP for x=1, small spread | | | Minor but steady increase in activity probability when present. | | | |
| **Un1224** | Binary fingerprint | Moderate SHAP increase for presence | | | Adds moderate positive weight to “active” predictions. | | | |
| **Un8428** | Binary fingerprint | Slight SHAP lift for x=1 | | | Weak positive association with activity. | | | |
| **Un714** | Binary fingerprint | Clear positive SHAP gap between 0 and 1 | | | Stronger positive predictor of “active” class. | | | |
| **Un357** | Binary fingerprint | Moderate positive SHAP effect for x=1 | | | Contributes positively to predictions when present. | | | |
| **exactMass** | Continuous | SHAP trend increases with higher mass | | | Larger molecules tend to be predicted as more likely “active.” | | | |