# Supplementary Material

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**Figure S1.** Example of minimal Python code executing the radiomics experiment.

**Table S2.** Additional evaluation for the prostate MRI datasets for differentiation between clinically significant and clinically non-significant prostate cancer.

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| --- | --- | --- | --- | --- |
| **Dataset** | **AUC** | **F1** | **Sensitivity** | **Specificity** |
| 5-fold CV | test | test | test | test |
| Prostate masks: |  |  |  |  |  |
|  PROSTATEx | 0.73 ± 0.08 | 0.70 [0.33-0.97] | 0.68 [0.47-0.84] | 0.65 [0.41-0.86] | 0.75 [0.54-0.94] |
|  UCLA | 0.48 ± 0.07 | 0.40 [0.29-0.50] | 0.13 [0.05-0.23] | 0.07 [0.02-0.13] | 1.0 [1.0-1.0] |
|  PROSTATEx→UCLA\* |  | 0.70 [0.61-0.78 | 0.77 [0.70-0.83] | 0.68 [0.60-0.76] | 0.69 [0.55-0.84] |
|  UCLA→PROSTATEx |  | 0.48 [0.14-0.81] | 0.66 [0.40-0.87] | 0.57 [0.31-0.83] | 0.66 [0.2-1.0] |
| Lesion masks: |  |  |  |  |  |
|  PROSTATEx  | 0.67 ± 0.09 | 0.51 [0.23-0.79] | 0.56 [0.27-0.78] | 0.43 [0.18-0.71] | 0.84 [0.5-1.0] |
|  UCLA | 0.56 ± 0.05 | 0.58 [0.46-0.70] | 0.58 [0.46-0.70] | 0.51 [0.40-0.62] | 0.70 [0.55-0.86] |
|  PROSTATEx→UCLA |  | 0.55 [0.44-0.66] | 0.78 [0.71-0.85] | 0.83 [0.75-0.91] | 0.33 [0.18-0.48] |
|  UCLA→PROSTATEx |  | 0.37 [0.08-0.70] | 0.77 [0.58-0.92] | 0.86 [0.64-1.0] | 0.17 [0.0-0.56] |

\*Arrow denotes external validation of the model trained on PROSTATEx dataset in the Prostate-UCLA dataset

**Appendix S3.** Details on final pipeline configuration for each task.

For each of the eight datasets evaluated, parameters including optional feature selection, ML classifier and its parameters, were tuned in 5-fold cross-validation. The final configurations are described below:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Dataset** | **Lipo** | **Desmoid** | **Liver** | **GIST** | **CRLM** |
| Feature selection  | Boruta | Boruta | Boruta | RFE | RFE |
| ML classifier | Random Forest | LogReg | LogReg | LogReg | LogReg |
| ML classifier parameters | n\_estimators: 882,max\_depth: 2,max\_features: sqrt,min\_samples\_leaf: 6,min\_samples\_spllits: 3,bootstrap: False | penalty: L1,C:9.44 | penalty: L2,C: 0.027 | penalty: L1,C: 6.97 | penalty: L2, C: 0.007 |
| **Dataset** | **Melanoma** | **PROSTATEx (prostate masks)** | **UCLA (prostate masks)** | **PROSTATEx (lesion masks)** | **UCLA (lesion masks)** |
| Feature selection  | RFE | RFE | RFE | RFE | RFE |
| ML classifier | SVM | XGBoost | SVM | LogReg | LogReg |
| ML classifier parameters | kernel: rbf,C: 0.03,gamma: 0.17,degree: 1.0 | lambda: 3.8,alpha: 1.4,colsample\_bytree: 0.2,subsample: 0.95,booster: gbtree,max\_depth: 5min\_child\_weight: 8,eta: 3.71,gamma: 0.0002,grow\_policy: depthwise | kernel: linear,C: 0.05,gamma: 0.11,degree: 1.0 | penalty: L2,C: 0.79 | penalty: L2,C: 0.02 |
|  |  |  |  |  |  |

\*RFE – recursive feature elimination, LogReg – logistic regression, SVM – Support Vector Machine