

High pathological grade **prediction** in **prostate cancer** patients undergoing 18F-PSMA PET/CT using **matRadiomics**

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Research activity: **Personalized medicine for the diagnosis and prognosis of oncological and neurodegenerative diseases: Radiomics and Artificial Intelligence to support clinical decision-making**



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1

Aim

Radiomics models based on Prostatic Specific Membrane antigen (**[18F]-PSMA**) positron emission tomography (PET) images for the **prediction** of high pathological grade (**Gleason score > 7**)

2

Our approach

Classical radiomics pipeline

Image acquisition



Dataset: 86 or more



matRadiomics

3

Expected Results

Build a model able to predict high risk prostate tumor

Show the **potentiality** of **radiomics biomarkers**

matRadiomics as a comprehensive tool for radiomics analysis

Devices

PET/CT

Siemens Horizon
Biograph

GE Discovery 690



Dataset

| GS Score | Siemens | GE |
|----------|---------|----|
| 6 | 22 | 13 |
| 7 | 14 | 14 |
| 8-10 | 17 | 6 |
| tot | 53 | 33 |

86 patients or more,
Only cancer staging

matRadiomics is a freeware that allows the user to carry out the **whole radiomics** framework:

- 1 import medical images
- 2 segmentation
- 3 feature extraction
- 4 feature selection
- 5 model building
- 6 prediction.

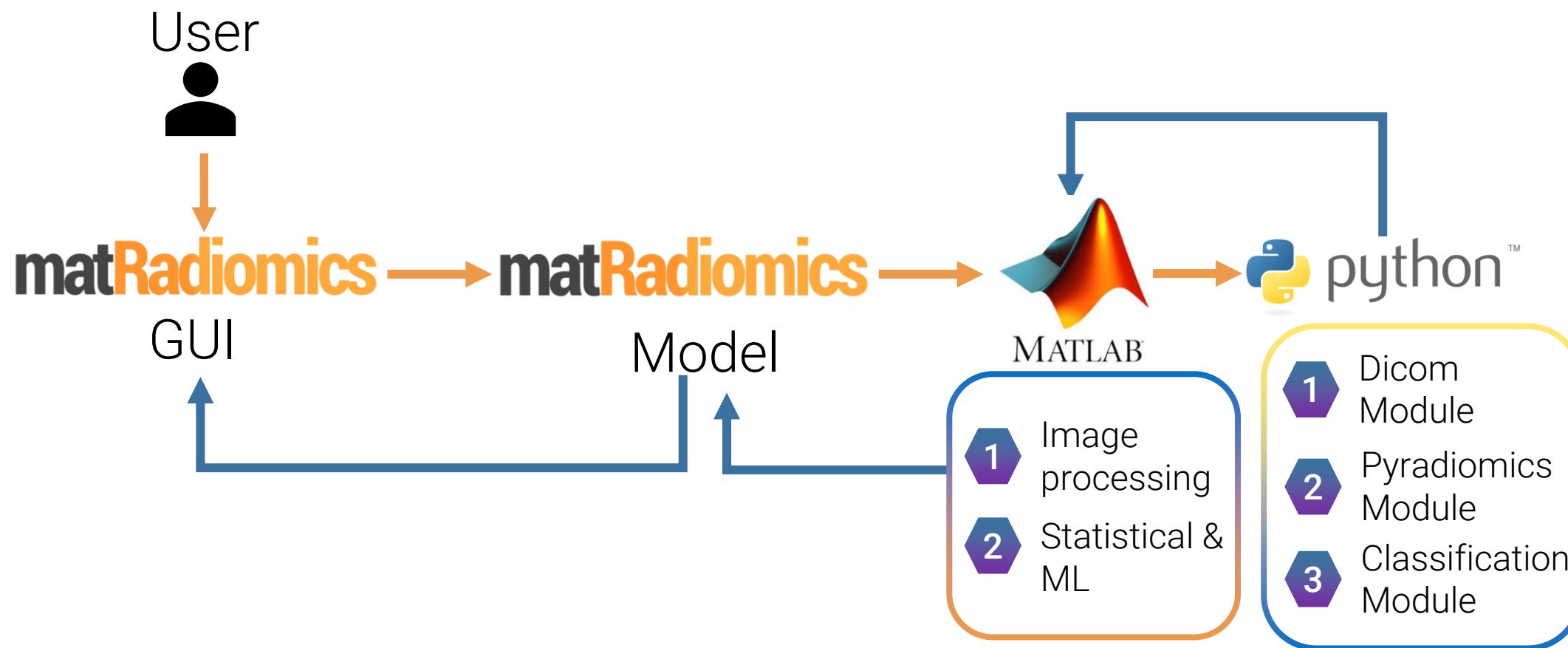
matRadiomics

A complete radiomics freeware



Journal of Imaging

<https://doi.org/10.3390/jimaging8080221>



Our approach through matRadiomics: Import Medical Images

1

Supported Image format:

DICOM, CT, PET, MRI,
DBT

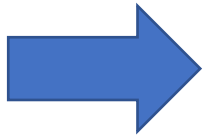
2

Visualize: Slices, Scroll mouse wheel

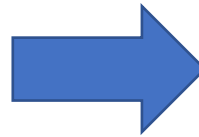
3

Contrast Adjustment

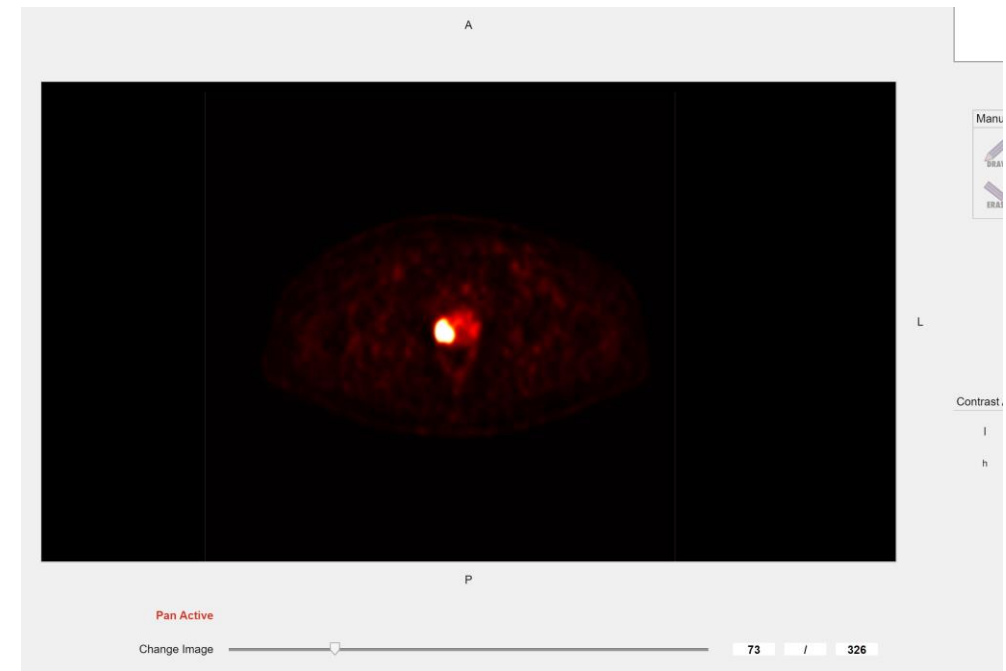
Dataset



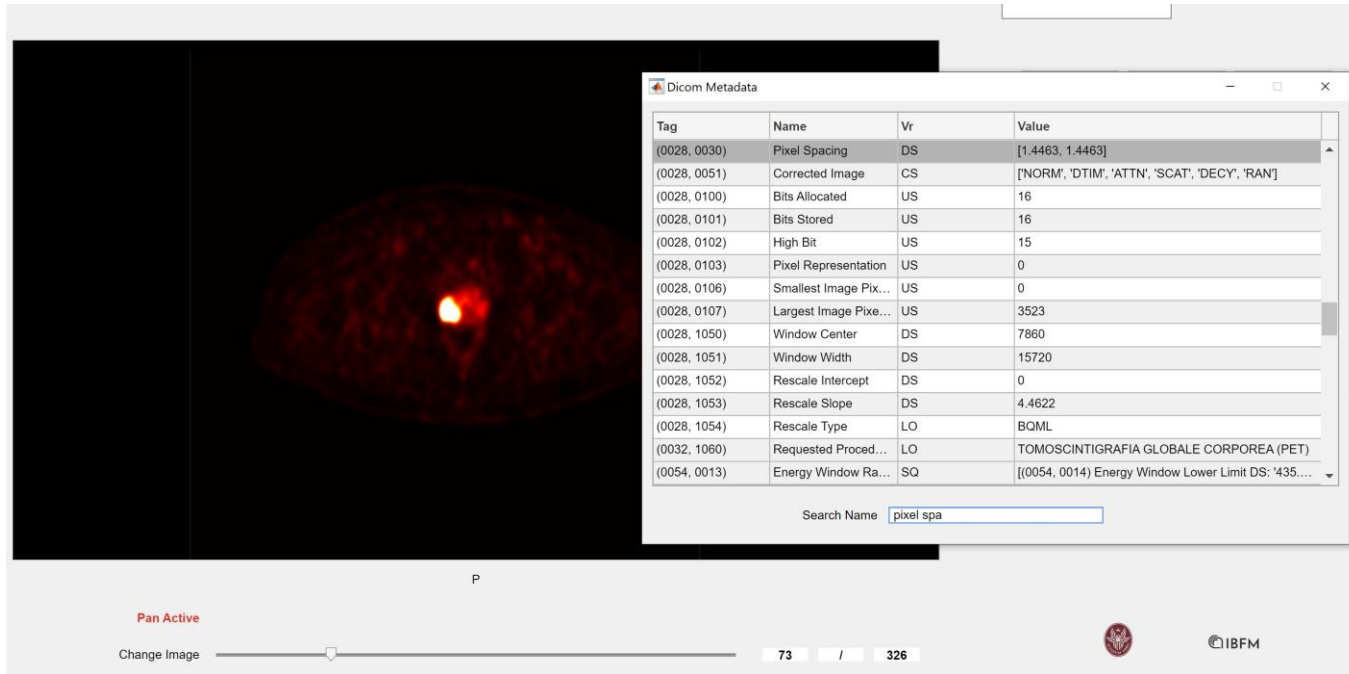
matRadiomics



ex.
ANON37910

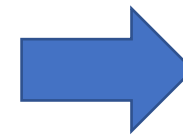


Visualize DICOM attributes: Patient Position, Pixel Spacing, etc...



The screenshot displays a medical imaging application. On the left, a PET scan image is shown with a bright, localized area of high intensity (red/yellow) against a dark background. A 'Pan Active' status indicator is visible below the image. On the right, a 'Dicom Metadata' window is open, displaying a table of DICOM attributes. The table has four columns: Tag, Name, Vr, and Value. The 'Pixel Spacing' attribute (Tag: 0028, 0030) is highlighted. Below the table, there is a search bar with the text 'pixel spa' entered. At the bottom of the application window, there is a 'Change Image' button and a progress bar showing '73 / 326'.

| Tag | Name | Vr | Value |
|--------------|-----------------------|----|--|
| (0028, 0030) | Pixel Spacing | DS | [1.4463, 1.4463] |
| (0028, 0051) | Corrected Image | CS | ['NORM', 'DTIM', 'ATTN', 'SCAT', 'DECY', 'RAN'] |
| (0028, 0100) | Bits Allocated | US | 16 |
| (0028, 0101) | Bits Stored | US | 16 |
| (0028, 0102) | High Bit | US | 15 |
| (0028, 0103) | Pixel Representation | US | 0 |
| (0028, 0106) | Smallest Image Pix... | US | 0 |
| (0028, 0107) | Largest Image Pixe... | US | 3523 |
| (0028, 1050) | Window Center | DS | 7860 |
| (0028, 1051) | Window Width | DS | 15720 |
| (0028, 1052) | Rescale Intercept | DS | 0 |
| (0028, 1053) | Rescale Slope | DS | 4.4622 |
| (0028, 1054) | Rescale Type | LO | BQML |
| (0032, 1060) | Requested Proced... | LO | TOMOSCINTIGRAFIA GLOBALE CORPOREA (PET) |
| (0054, 0013) | Energy Window Ra... | SQ | [(0054, 0014) Energy Window Lower Limit DS: '435.... |



Check for homogeneity of attributes such as pixel spacing, slice thickness, kvp

Our approach through matRadiomics: Segmentation

1

Segmentation algorithms:

manual, thresholding, active contours,
Automatic (?)

Identify the best
segmentation method

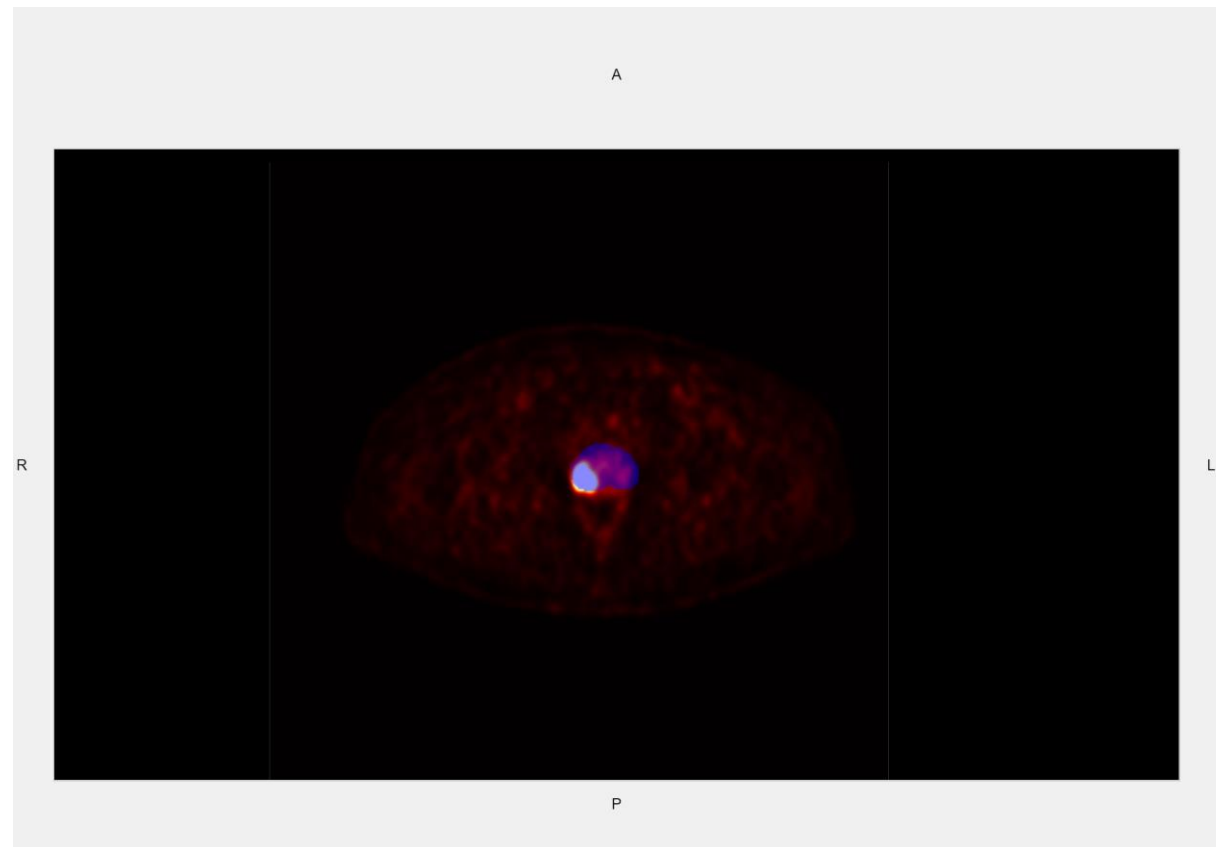
2

Import segmentations:

Dicom and DicomRT

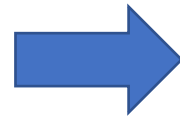
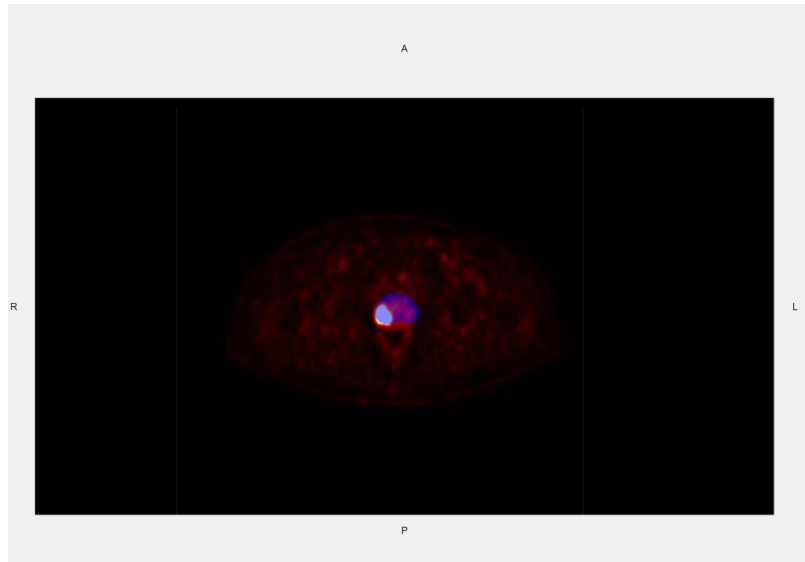
3

Change mask opacity and colour
And switch between segmentations



Our approach through matRadiomics: Feature Extraction

Image and mask



Feature Extractor:
Pyradiomics
integrated in
matRadiomics



UI for Feature Extraction (matRadiomics) showing a list of features and a table of extracted features.

Features List:

- All features enabled
- firstorder
- shape
- glcm
- glrlm
- glszm
- glcm
- nglcm

Feature Extraction Parameters:

- Resampling: 1, 1, 1
- Pixel Spacing: 1
- Interpolator: None
- Pad Distance: 5

Feature Extraction Results Table:

| patient | original_shape_Elongation | original_shape_Flatness | original_shape_LeastAxisLength | original_shape_MajorAxisLength | original_shape_Volume |
|-----------|---------------------------|-------------------------|--------------------------------|--------------------------------|-----------------------|
| ANON37910 | 0.3402 | 0.1719 | 17.7436 | 103.1960 | |

Study Name: s.kjsssoisosois

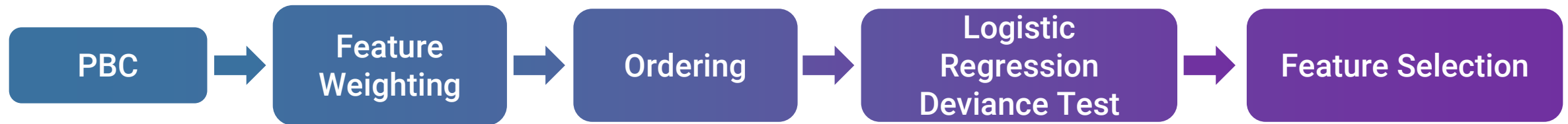
Save Study

Extract Features For classification

| patient | original_shape_Elongation | original_shape_Flatness | original_shape_LeastAxisLength | original_shape_MajorAxisLength | original_shape_Volume |
|-----------|---------------------------|-------------------------|--------------------------------|--------------------------------|-----------------------|
| ANON37910 | 0.3402 | 0.1719 | 17.7436 | 103.1960 | |
| ANON37910 | 0.3402 | 0.1719 | 17.7436 | 103.1960 | |
| ANON37910 | 0.3402 | 0.1719 | 17.7436 | 103.1960 | |
| ANON37910 | 0.3402 | 0.1719 | 17.7436 | 103.1960 | |

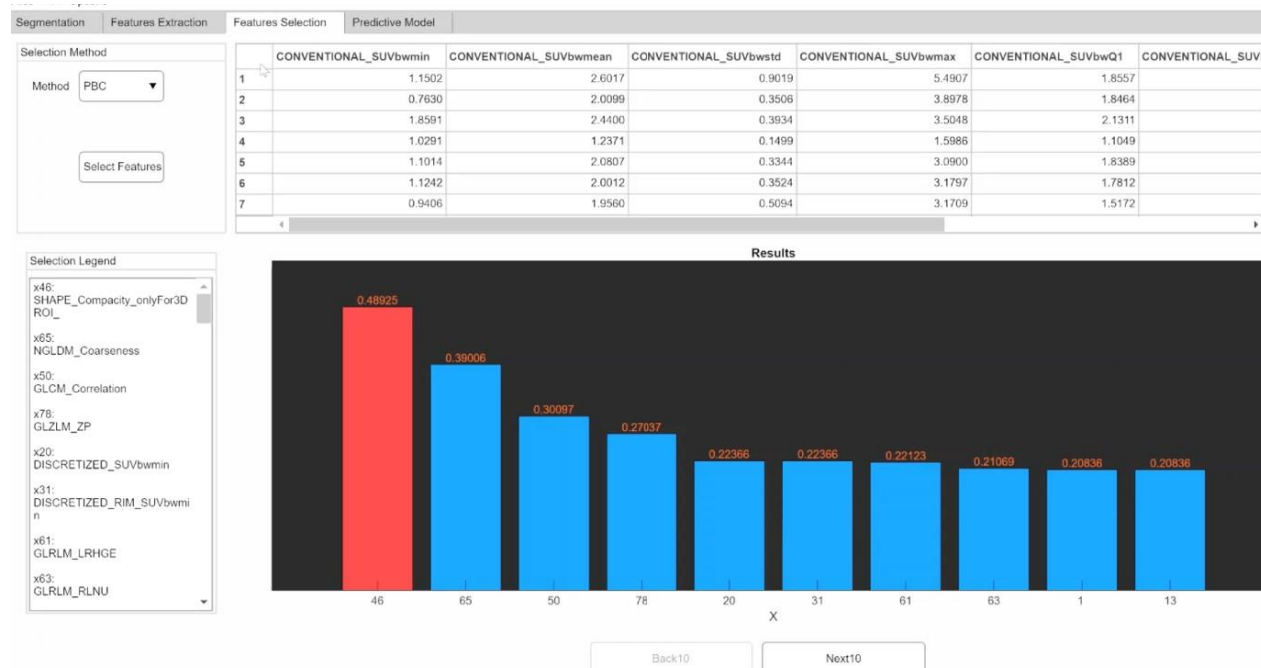
Our approach through matRadiomics: Feature Selection

Feature Selection: Hybrid descriptive-inferential method, LASSO, Relieff



Built iteratively
P-value check
each cycle

Selected
features



Our approach through matRadiomics: Machine Learning

1

Classifiers:

LDA, KNN, SVM

2

K-Fold Cross validation:

Stratified, non stratified

3

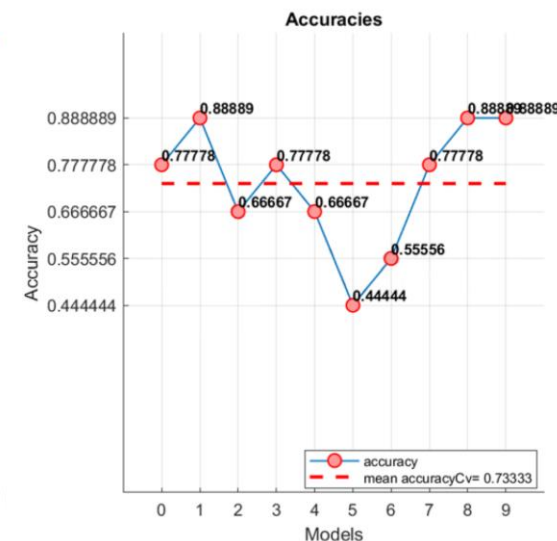
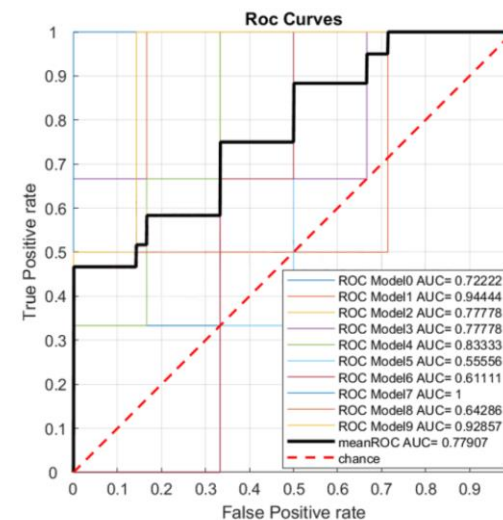
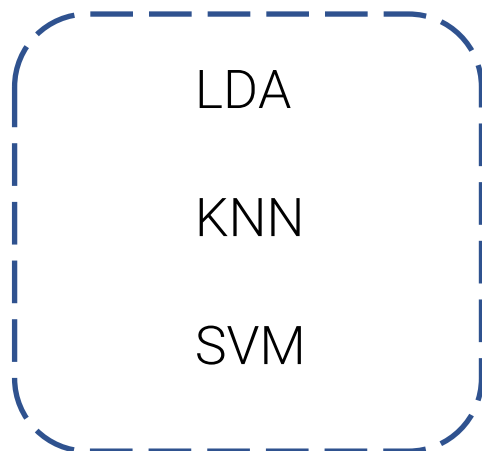
Model Saving

4

Performance Metrics:

accuracy, roc,
confusion
matrix

Selected
features



Cross
Validated

Our approach through matRadiomics: Metadata, Import a Study

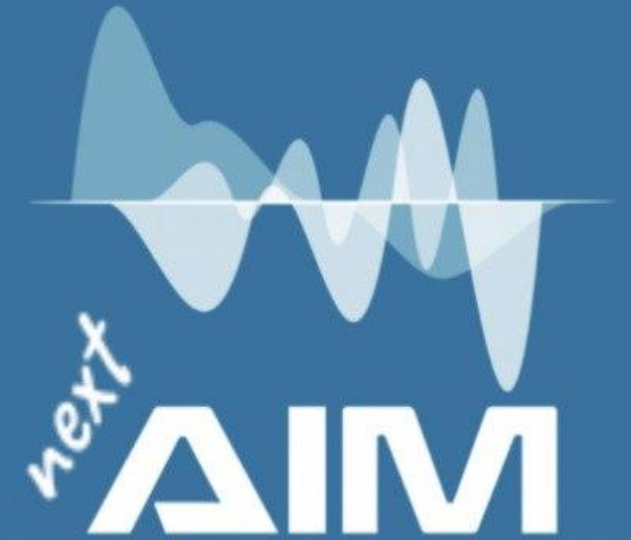
Feature Extraction

```
"matRadiomicsName": "matRadiomicsLight",
"matRadiomicsVersion": "1.0",
"studyName": "journal_of_imaging2",
"fileType": "Dicom",
"modality": "CT",
"segmentationMethod": "imported",
"extractionInfo": {
  "extractor": "Pyradiomics_v3.0.1",
  "imageType": "Original",
  "enabledFeatures": "All Features Enabled",
  "enableNormalize": "False",
  "normalizeScale": 1,
  "removeOutliers": 1,
  "interpolator": "None",
  "xSpacing": 1,
  "ySpacing": 1,
  "zSpacing": 1,
  "padDistance": 5,
  "enablePreCrop": "False",
  "resegmentMode": "None",
  "lowResegmentRange": 0,
  "upResegmentRange": 0,
  "enableResegmentShape": "False",
  "minROIDim": 2,
  "enableMinROIsize": "None",
  "minROIsize": 1,
  "enableGeometryTolerance": "None",
  "geometryTolerance": 0,
  "enableCorrectMask": "False",
  "discretizationMode": "Bin Count",
  "discretizationValue": 64,
  "enableForce2D": "False",
  "dimensionForce2D": 0,
  "dAlgo": "None",
  "gldm_a": 0,
  "voxelArrayShift": 0,
  "enableSymmetricalGLCM": "True"
```

Feature Selection and ML

```
},
"selectionInfo": {
  "selectedFeatureName": [
    "original_shape_Flatness",
    "original_gldm_DependenceNonUniformityNormalized"
  ],
  "method": "relieff"
},
"harmonizationInfo": {
  "harmonization": "false",
  "adjustment": "parametric",
  "batchName": []
},
"modelInfo": {
  "classifier": "LDA",
  "validationType": "K-fold Stratified Cross Validation",
  "validationkFold": 10,
  "saved": "False"
}
```

Import a Study



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UNIVERSITÀ DI ROMA

