

Utilisation des paramètres RIM calculés dans LIFEx

Intérêt sur un cas d'usage issu de IRM-omics

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Développement d'une signature radiomique et clinique pour différentes tâches (T) de classification:

- ***T1 : Prédire le sous type histologique (ADK/CE) des tumeurs***
- ***T2 : Prédire la survie (1 an) dans le cancer du poumon***

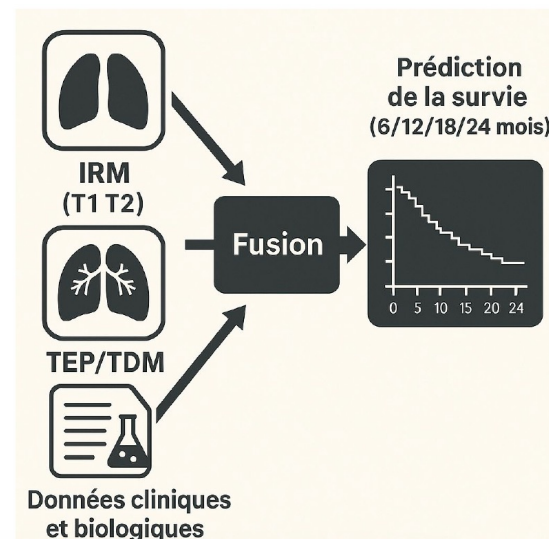
- Utilisation des données de l'étude **IRMOmics** (Pr. PY Brillet, Hôpital Avicenne)

- Analyse combinée :

 **IRM (T1 & T2)**

 **(TEP/TDM)**

 **Données cliniques et biologiques**





Données utilisées dans l'étude

3

Imagerie multimodale (par patient)

- IRM T1
- IRM T2
- ROIs segmentés sur la tumeur entière, extraits pour chaque modalité

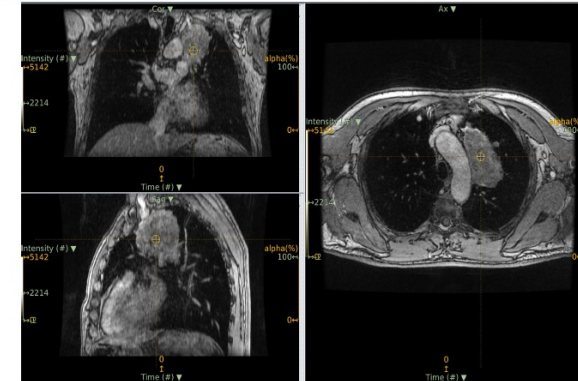


Figure 1 – Images IRM T1 thoracique

Données cliniques, biologiques et sémantiques

- Données patient : Sexe, âge, IMC, statut tabagique / cannabis
- Survie : étiquette binaire à 6 mois
- Histologie : Type histologique, statut PD-L1
- Métastases cérébrales : à l'inclusion & au suivi
- Caractéristiques tumorales sémantiques



Extraction des index radiomiques

4

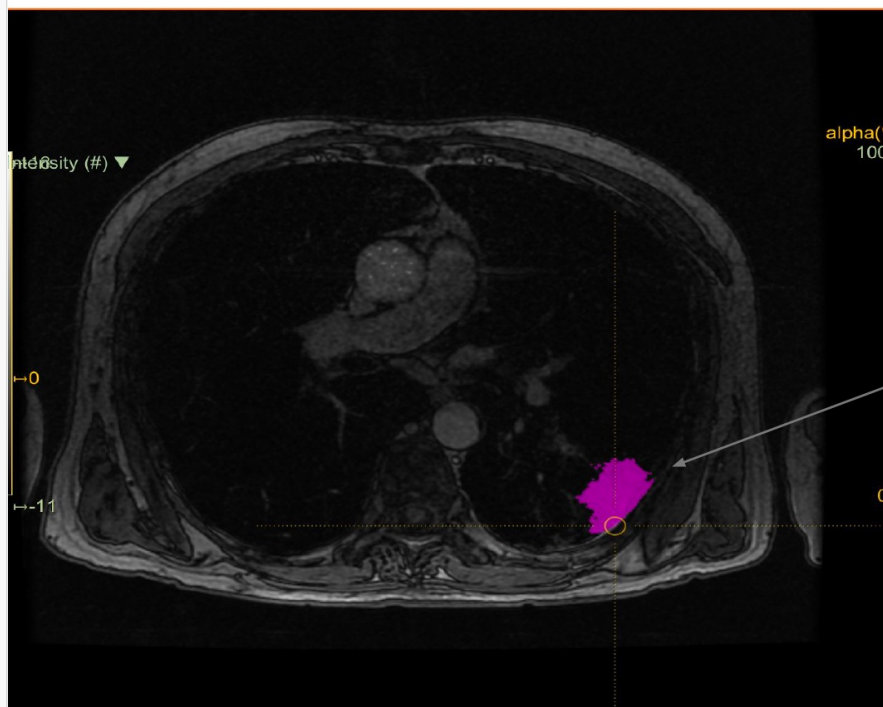
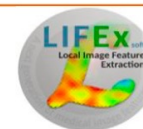


Image IRM T1 en coupe axiale montrant la tumeur pulmonaire (en violet)



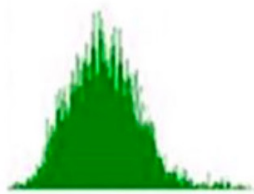
Extraction pour les 2 modalités d'imagerie T1 et T2 de la tumeur

Tumor shape



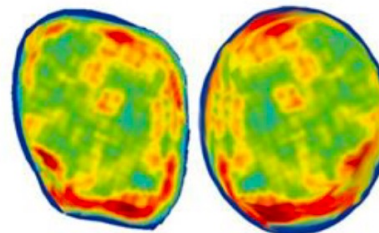
n = 35

Tumor intensity



n = 68

Tumor texture



n = 57



LIFEx.Patient0.Series0.Operation0 = Texture, true, false, false, 1, 3D, Absolute, 0, 256, -25, 25

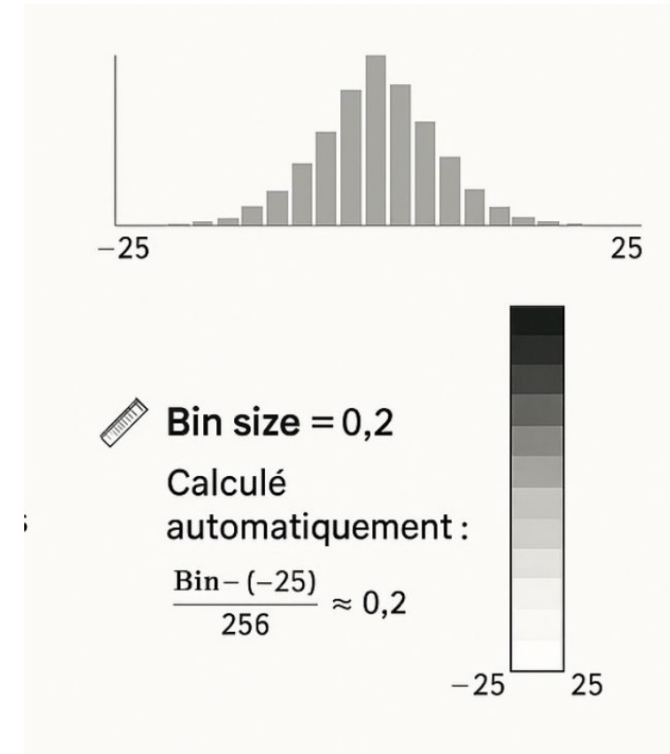
🎯 Pourquoi ces valeurs ?

1 2 3 4 256 niveaux de gris (bins)

- Recommandé par **IBSI**
- Permet une **discrétisation fine** des intensités
- Utilisé dans l'étude de **Lacroix et al.** pour extraire les textures

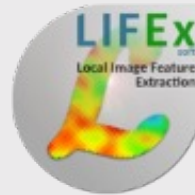
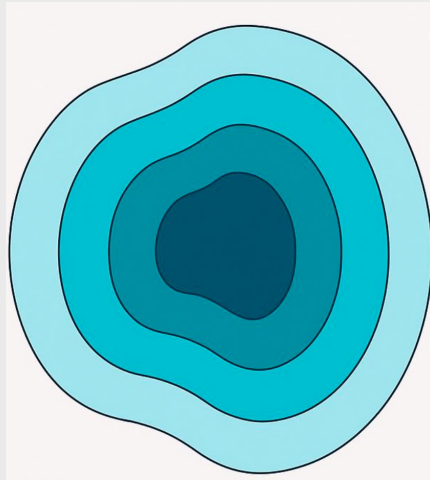
🟡 Fenêtre d'intensité [-25 ; +25]

- Les images sont **normalisées** ($\mu = 0, \sigma \approx 1$)
- Cette fenêtre permet de **couvrir tous les voxels utiles**, même ceux avec des valeurs extrêmes



Envelope is the radial successive layer of voxels from the outside of the region to the inside

n envelopes
depending on
tumor size and
shape

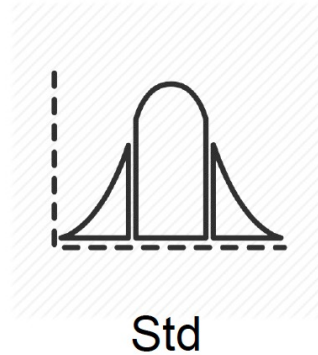


RIM-IntensityMean(IBSI:No)[Intensity]

INTENSITY-BASED-RIM_RIM-IntensityMean(IBSI:No)[Intensity]	
-10.72637334677178 -10.069121494612283 -9.58164804286677 -9.393802998646024 -9.343537354563779 -9.395119802034813 -9.425471629157212 -9.5014348873823	
-10.602832806509065 -10.007833220212387 -9.731446176486829 -9.53336005242821 -9.328495854221721 -9.143274868713029 -9.003039056613476 -8.906770587748	
-8.53561798228847 -8.59339256547013 -8.315801684106324 -7.087373040443242 -6.426251024813266 -6.491671442985536 -6.49112590154012 NaN	
-6.40075195226592 -6.374154343509203 -6.260708574311654 -6.197478113698747 -6.2080925630063435 -6.368467092514038 NaN	

7 indices INTENSITY-BASED / 7 indices HISTOGRAM-BASED from the n envelopes

- _RIM-IntensityMin(IBSI:No)[Intensity] : Minimum voxel value inside each E_i
- _RIM-IntensityMean(IBSI:No)[Intensity] : Mean voxel value inside each E_i
- _RIM-IntensityStd(IBSI:No)[Intensity] : Standard deviation of voxel values inside each E_i
- _RIM-IntensityMax(IBSI:No)[Intensity] : Maximum voxel inside each E_i
- _RIM-CountingVoxels(IBSI:No)[vx] : Volume in voxel unit of all voxels inside each E_i
- _RIM-ApproximateVolume(IBSI:No)[mL] : Volume in milliliter unit of all voxels inside each E_i
- _RIM-IntensitySum(IBSI:No)[Intensity] : Sum of voxel values inside each E_i

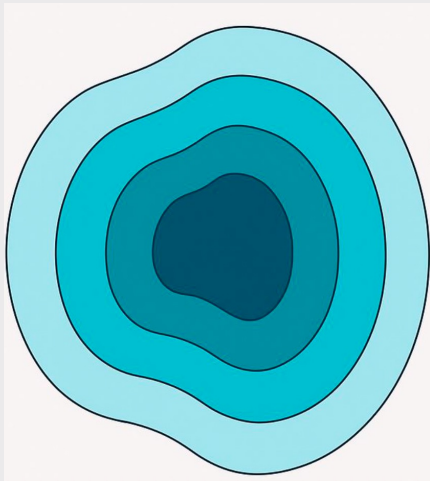


Mean

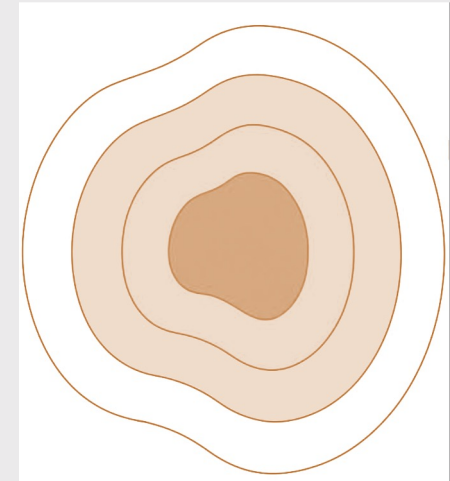
➔ INTENSITY BASED RIM sum: ➔

- INTENSITY BASED RIM
sum_mean
- INTENSITY BASED RIM
sum_std
- INTENSITY BASED RIM
sum_min
- INTENSITY BASED RIM
sum_max

n envelopes E_i
depending on
tumor size and
shape
 $i=1,...,n$



n-1 envelopes G_j :
differences entre
les valeurs sur les
envelopes E_j et E_{j-1}
 $j=1,..., n-1$



7 indices INTENSITY-BASED_GRADIENT from the n-1 envelopes G_i

7 indices HISTOGRAM-BASED_GRADIENT

Difference between two successive layers of

Minimum voxel values : `_RIM-IntensityGradientMin(IBSI:No)[Intensity]`

Mean voxel values : `_RIM-IntensityGradientMean(IBSI:No)[Intensity]`

Standard deviation of voxel values : `_RIM-IntensityGradientStd(IBSI:No)[Intensity]`

Maximum voxel values : `_RIM-IntensityGradientMax(IBSI:No)[Intensity]`

Volumes in voxel unit of voxels : `_RIM-CountingVoxelsGradient (IBSI:No)[vx]`

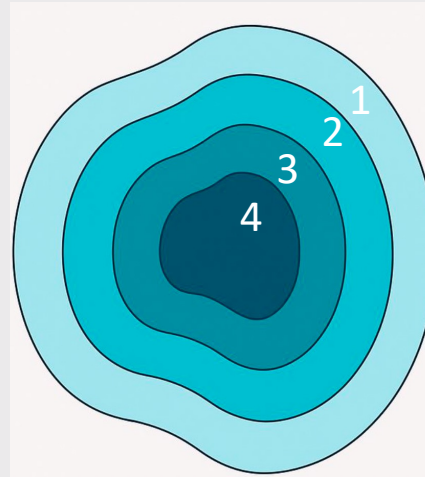
Volume in milliliter unit of all voxels : `_RIM-ApproximateVolumeGradient (IBSI:No)[mL]`

Sum of voxel values : `_RIM-IntensitySumGradient (IBSI:No)[Intensity]` :



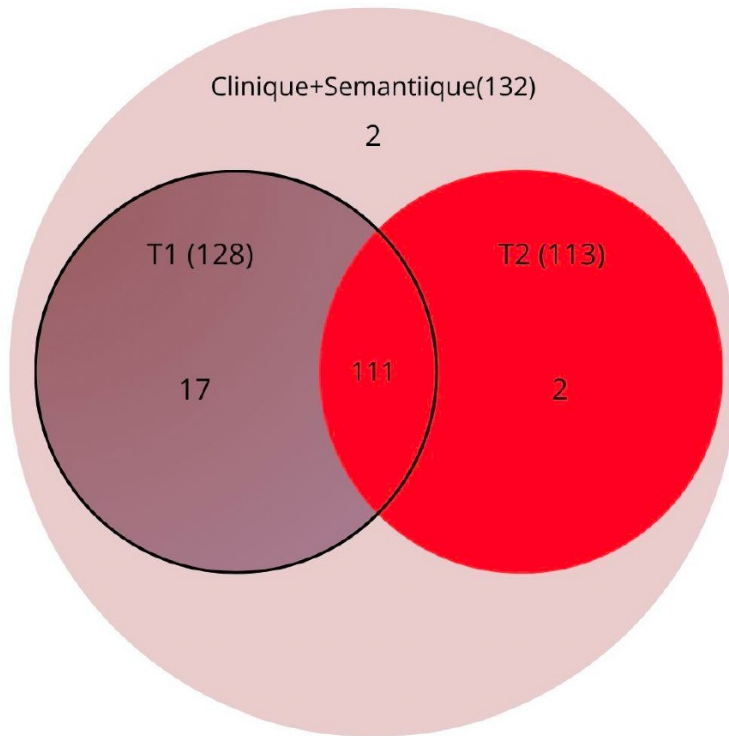
Number of zones of linked voxels which share a specific discretised grey level value and possess the same distance to ROI edge [\[Thibault2014\]](#).

GLSZM + distance map

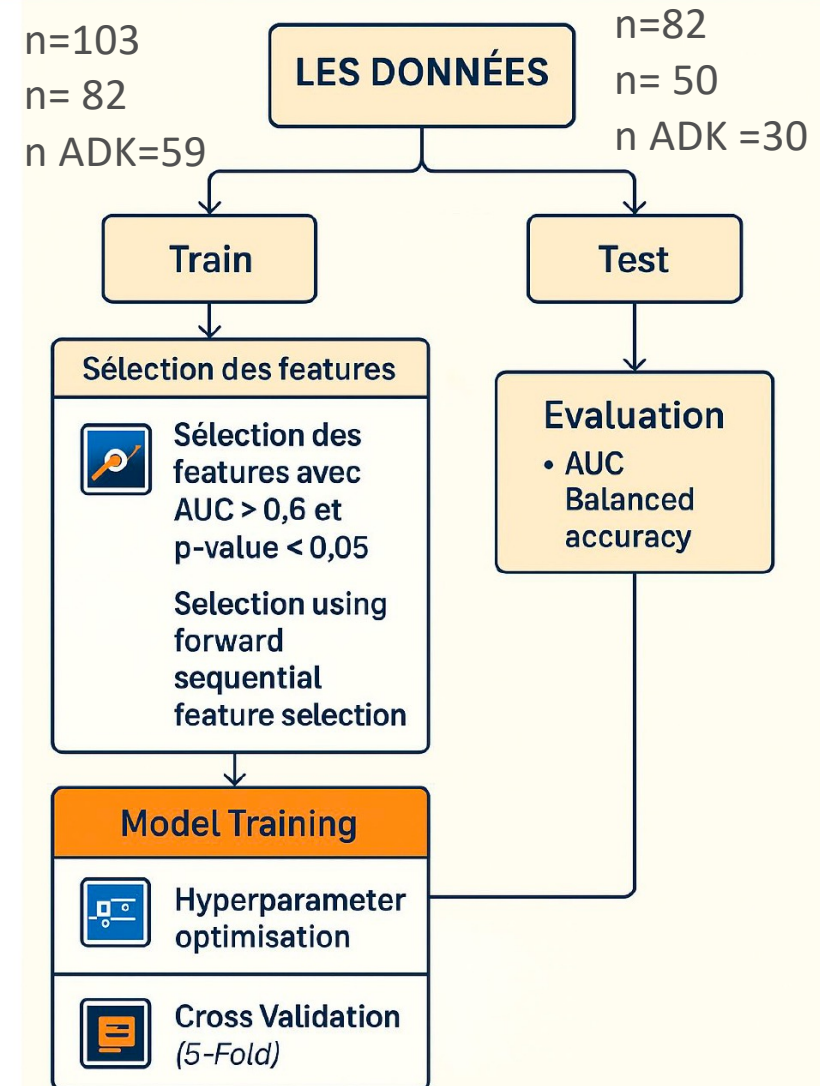


Pyradiomics : GLDM

Tâche de ADK VS CE



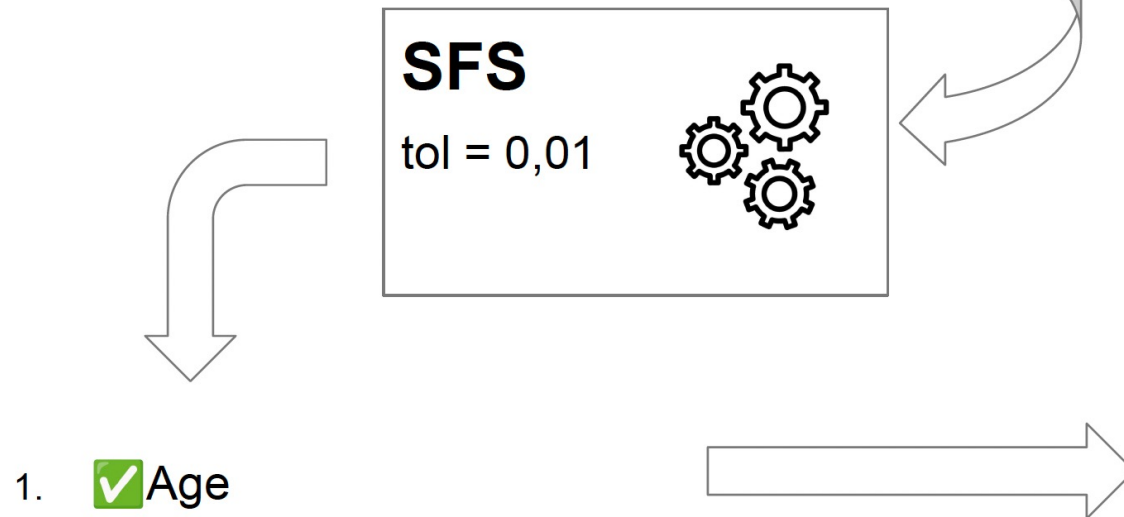
Number of class CE : 43
Number of class ADK : 89



Model clinique :

Selected features using AUC >0,6 and pvalue<0,05:

1. Age
2. Tabagisme_cannabis



Validation Set:

AUC: 0.629

Accuracy: 0.585

Precision: 0.821

Recall(Sensitivity): 0.542

F1-score: 0.653

Specificity: 0.696

Balanced Accuracy: 0.619

Number of Samples: 82

Test:

AUC : 0.6617

Accuracy : 0.6400

Precision : 0.6875

Recall (Sensitivity): 0.7333

F1 Score : 0.7097

Specificity : 0.5000

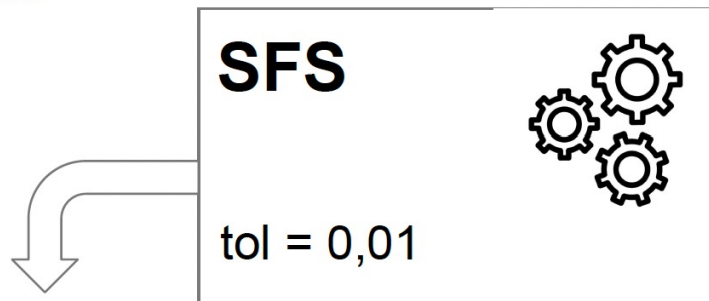
Balanced Accuracy : 0.6167

Samples : 50

Model T1 :

Selected features using AUC >0,6 and pvalue<0,05:

1. MORPHOLOGICAL_RadiusRoiNorm-MaxIntensityCoor-RoiCentroidCoor-Dist(IBSI:No)[]_T1_cube
2. INTENSITY-HISTOGRAM_RootMeanSquare(IBSI:No)[Intensity]_T1_cube
3. GLCM_Correlation(IBSI:NI2N)_T1_cube
4. GLSZM_ZoneSizeNonUniformity(IBSI:4JP3)_T1_cube



1. MORPHOLOGICAL_RadiusRoiNorm-MaxIntensityCoor-RoiCentroidCoor-Dist(IBSI:No)[]_T1_cube
2. GLCM_Correlation(IBSI:NI2N)_T1_cube

Validation Set:

AUC: 0.649

Accuracy: 0.613

Precision: 0.814

Recall: 0.603

F1-score: 0.693

Specificity: 0.636

Balanced Accuracy: 0.620

Number of Samples: 80

Test:

AUC : 0.5517

Accuracy : 0.5208

Precision : 0.6364

Recall (Sensitivity): 0.4828

F1 Score : 0.5490

Specificity : 0.5789

Balanced Accuracy : 0.5309

Samples : 48

ADK VS CE (Gradient)

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<https://docs.google.com/document/d/1HODpUyRnwsIq9zRRxFQS9hHu9ZwQ2gGy0BD53IC5IVU/edit?tab=t.0>

Clinique: Age

Semantique: Contingent_Hypersignal_T2

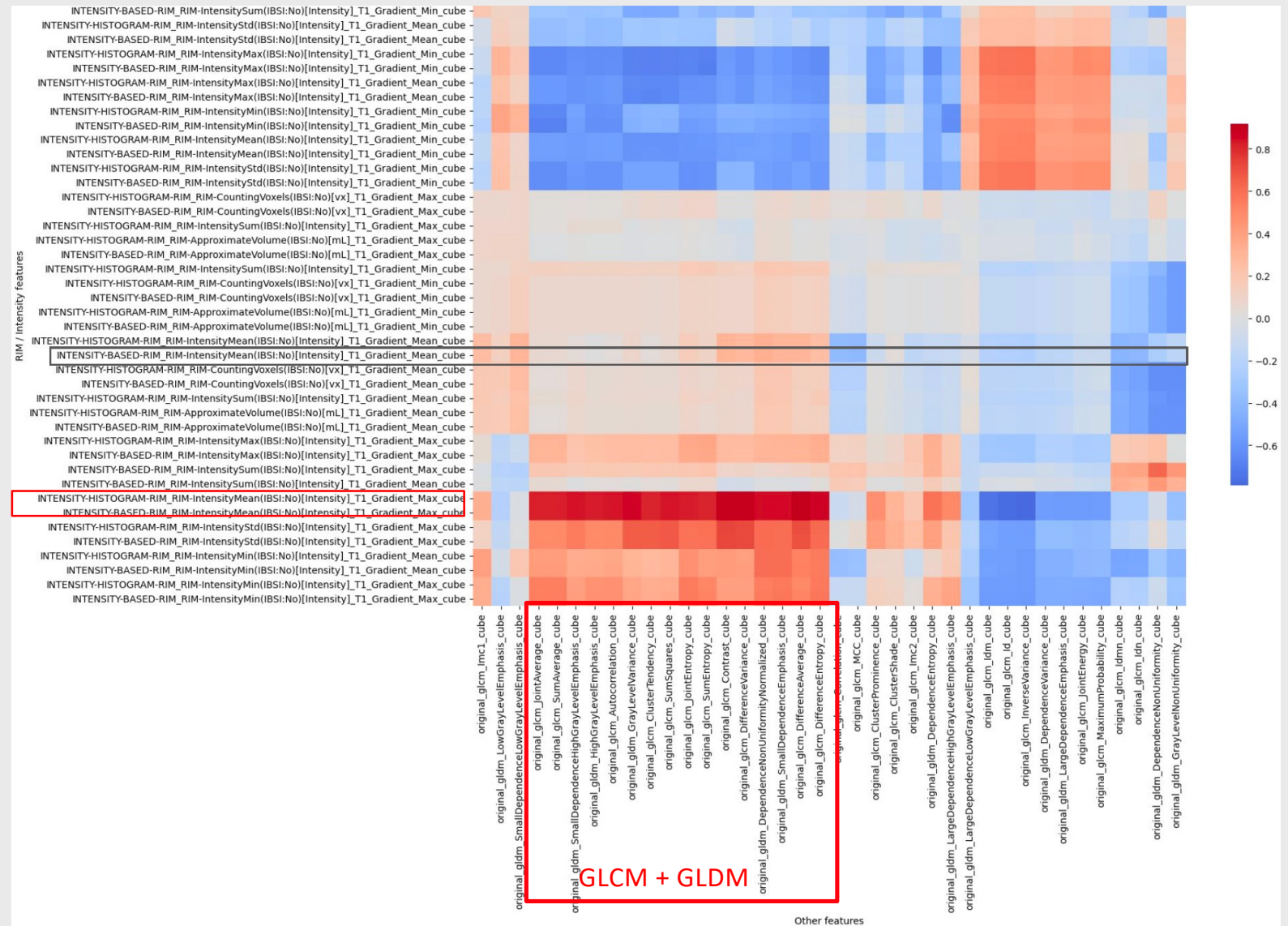
T1:

1-INTENSITY-BASED-RIM_RIM-IntensityMean(IBSI:No)[Intensity]_T1_Gradient_Mean_cube

T2: 1-INTENSITY-BASED-RIM_RIM-IntensitySum(IBSI:No)[Intensity]_max_22,
2-INTENSITY-BASED-RIM_RIM-IntensityStd(IBSI:No)[Intensity]_Gradient_Max_22'

Images T1

ADK/CE



1^{er} modèle (sans RIM- gradient)

Validation set

Test set

Clinique

AUC : 0.629

Bal Acc : 0.619

0.612

T1

AUC : 0.649

Bal Acc : 0.620

0.531

Clinique +T1

AUC : **0.694**

Bal Acc : **0.665**

0.651

1^{er} modèle (sans RIM- gradient)

Validation set

Test set

Clinique

AUC : 0.629

Bal Acc : 0.619

0.612

T1

AUC : 0.649

Bal Acc : 0.620

0.531

Clinique +T1

AUC : **0.694**

Bal Acc : **0.665**

0.651

2^{ème} modèle (avec RIM- gradient)

Validation set

Test set

Clinique

AUC : 0.629

Bal Acc : 0.619

0.617

T1

AUC : 0.628

Bal Acc : 0.611

0.617

Clinique +T1

AUC : **0.673**

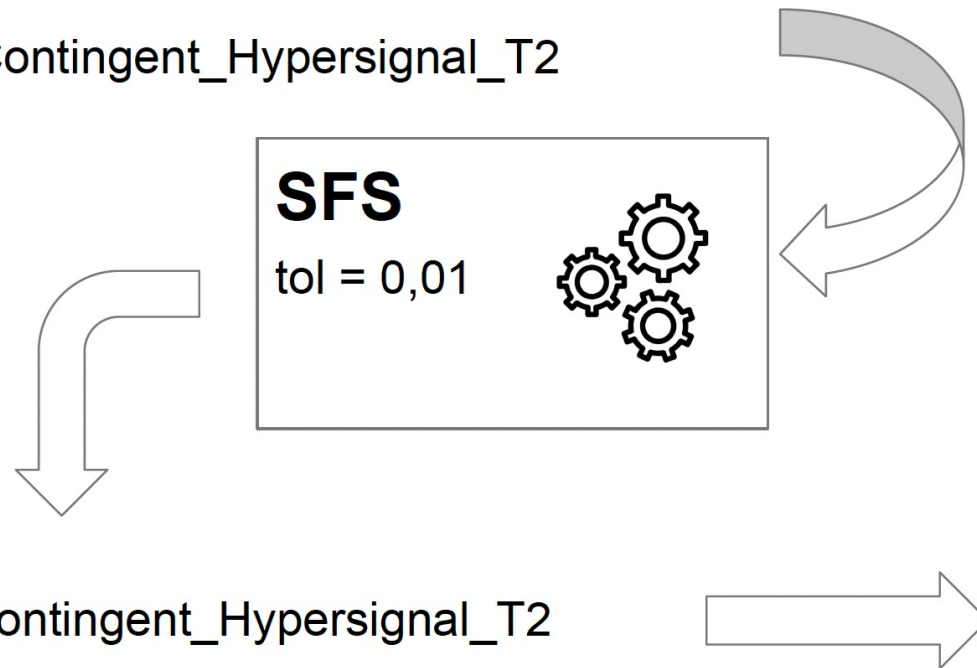
Bal Acc : **0.683**

0.667

Model semantique :

Selected features using AUC >0,6 and pvalue<0,05:

1. Contingent Hyporehaussé_T1
2. Contingent_Hypersignal_T2



Validation Set:

AUC: 0.745

Accuracy: 0.732

Precision: 0.930

Recall: 0.678

F1-score: 0.784

Specificity: 0.870

Balanced Accuracy: 0.774

Number of Samples: 82

Test:

AUC : 0.5875

Accuracy : 0.5400

Precision : 0.6667

Recall (Sensitivity): 0.4667

F1 Score : 0.5490

Specificity : 0.6500

Balanced Accuracy : 0.5583

Samples : 50

Model T2 :

Selected features using AUC >0,6 and pvalue<0,05:

1. MORPHOLOGICAL_Volume(IBSI:RNU0)[cm3]_22
2. original_gldm_GrayLevelNonUniformity_22
3. GLCM_Correlation(IBSI:NI2N)_22
4. INTENSITY-BASED-RIM_RIM-IntensityMax(IBSI:No)[Intensity]_mean_22
5. INTENSITY-BASED-RIM_RIM-IntensitySum(IBSI:No)[Intensity]_max_22

SFS



tol = 0,01

1. MORPHOLOGICAL_Volume(IBSI:RNU0)[cm3]_22
2. GLCM_Correlation(IBSI:NI2N)_22
3. INTENSITY-BASED-RIM_RIM-IntensityMax(IBSI:No)[Intensity]_mean_22

Validation Set:

AUC: 0.650

Accuracy: 0.677

Precision: 0.816

Recall: 0.689

F1-score: 0.747

Specificity: 0.650

Balanced Accuracy: 0.669

Number of Samples: 65

Test:

AUC : 0.5244

Accuracy : 0.5319

Precision : 0.6071

Recall (Sensitivity): 0.6071

F1 Score : 0.6071

Specificity : 0.4211

Balanced Accuracy : 0.5141

Samples : 47

Résultats

Deep Learning

T1:

TEST (patient-level; threshold=0.5)

Mean— AUC 0.694 | BalAcc 0.639 | Acc 0.681 | Np 47 |

T2:

TEST (patient-level; threshold=0.5)

Mean— AUC 0.589 | BalAcc 0.579 | Acc 0.652 | Np 46 |

Rappel radiomique

Test set

T1

Bal Acc : 0.617

Clinique +T1

AUC : **0.673**

Bal Acc : **0.683**

0.667