

**Thorough scrutinization of radiomic features
makes it possible to convert complicated
radiomic models into comprehensible
parsimonious signatures**

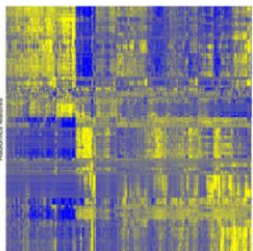


21/01/2021

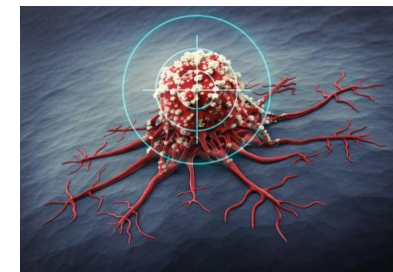
Contexte

Très difficile d'interpréter des signatures radiomiques avec plusieurs dizaines/centaines de variables !

Signature
radiomique



Interprétation
biologique



Efforts supplémentaires pour le déchiffrement des signatures :

- compréhension des mécanismes
- transformation en biomarqueurs robustes et plus simples


Données publiques : décrypter une signature comportant 43 index radiomiques issus des images TEP pré-traitement pour distinguer les sous-types de cancer pulmonaire

European Journal of Nuclear Medicine and Molecular Imaging (2018) 45:1649–1660
<https://doi.org/10.1007/s00259-018-3987-2>

ORIGINAL ARTICLE



Ability of FDG PET and CT radiomics features to differentiate between primary and metastatic lung lesions

Margarita Kirienko¹ • Luca Cozzi^{1,2} • Alexia Rossi^{1,3} • Emanuele Voulaz⁴ • Lidija Antunovic⁵ • Antonella Fogliata² • Arturo Chiti^{1,5} • Martina Sollini¹ 


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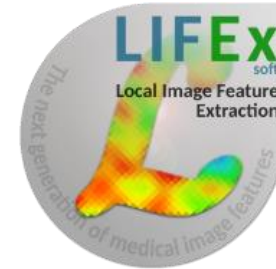
Margarita Kirienko¹ • Luca Cozzi^{1,2} • Alexia Rossi^{1,3} • Emanuele Voulaz⁴ • Lidija Antunovic⁵ • Antonella Fogliata² • Arturo Chiti^{1,5} • Martina Sollini¹ 



Matériel & Méthodes

- Cohorte de 372 patients avec un cancer pulmonaire non à petites cellules (NSCLC)
- Images TEP au 18F-FDG pré-traitement
- Segmentation tumorale : seuil = 40%SUVmax + fermeture si nécessaire
- 43 index radiomiques calculés avec LIFEx et fournis par les auteurs

	A	B	C	D	E	F	G	H
	Ability of FDG PET and CT radiomics features to differentiate between primary and metastatic lung lesions							
1								
2	Patient_ID	Type	SUVmin	SUVmean	SUVstd	SUVmax	SUVpeak_sphere	Volume_mL
3	Adk 001	adk	7.010085	11.251889	2.695772	17.441681	13.958117	4.140553
4	Adk 002	adk	7.569045	11.412258	2.942112	18.844810	13.622371	2.800962
5	Adk 003	adk	7.640660	11.906543	2.782868	18.805794	0.000000	1.875427
6	Adk 004	adk	5.263036	8.190163	1.944405	13.107503	11.320787	12.206050
7	Adk 005	adk	5.158333	7.462656	1.877833	12.621318	8.589192	2.338195
8	Adk 006	adk	8.461947	13.118494	2.897497	20.875221	16.537750	7.375457
9	Adk 008	adk	7.926716	10.976498	2.582120	19.731722	0.000000	2.143345
10	Adk 009	adk	4.525605	7.038227	1.833990	11.289939	9.179366	4.935884
11	Adk 011	adk	5.135100	8.102908	1.949239	12.830703	10.411253	5.017376
12	Adk 012	adk	4.253967	6.142152	1.449317	10.603572	8.464988	8.793816
13	Adk 013	adk	4.329852	6.401899	1.350178	10.820948	9.015270	31.911644
14	Adk 014	adk	7.209742	10.876075	2.672258	17.994123	14.152692	4.676390
15	Adk 015	adk	2.089751	3.131971	0.876107	5.187099	0.000000	3.630995
16	Adk 016	adk	6.933538	10.426388	2.376176	17.333845	15.332006	30.872042
17	Adk 017	adk	5.534906	8.519845	2.164740	13.788886	10.611314	3.896991
18	Adk 018	adk	6.956689	10.053874	2.265749	17.387516	12.802896	14.638073

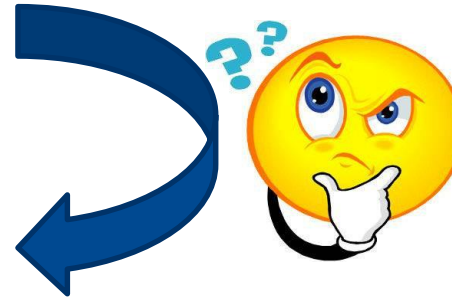


- Construction de la signature radiomique :
 - ✓ Set d'apprentissage : 2/3
 - ✓ Set de validation : 1/3**x 100 fois**

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- Analyse Discriminante Linéaire (LDA) :
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- Signature parcimoniseuse avec 2 à 4 index
- Evaluation des performances : Index de Youden = $Se + Sp - 1$ (sur le set de validation !)

x 100 fois



Résultats

- Analyse histologique :
 - ✓ Adénocarcinome : 169 patients
 - ✓ Epidermoïde ou « autre » : 203 patients

Résultats

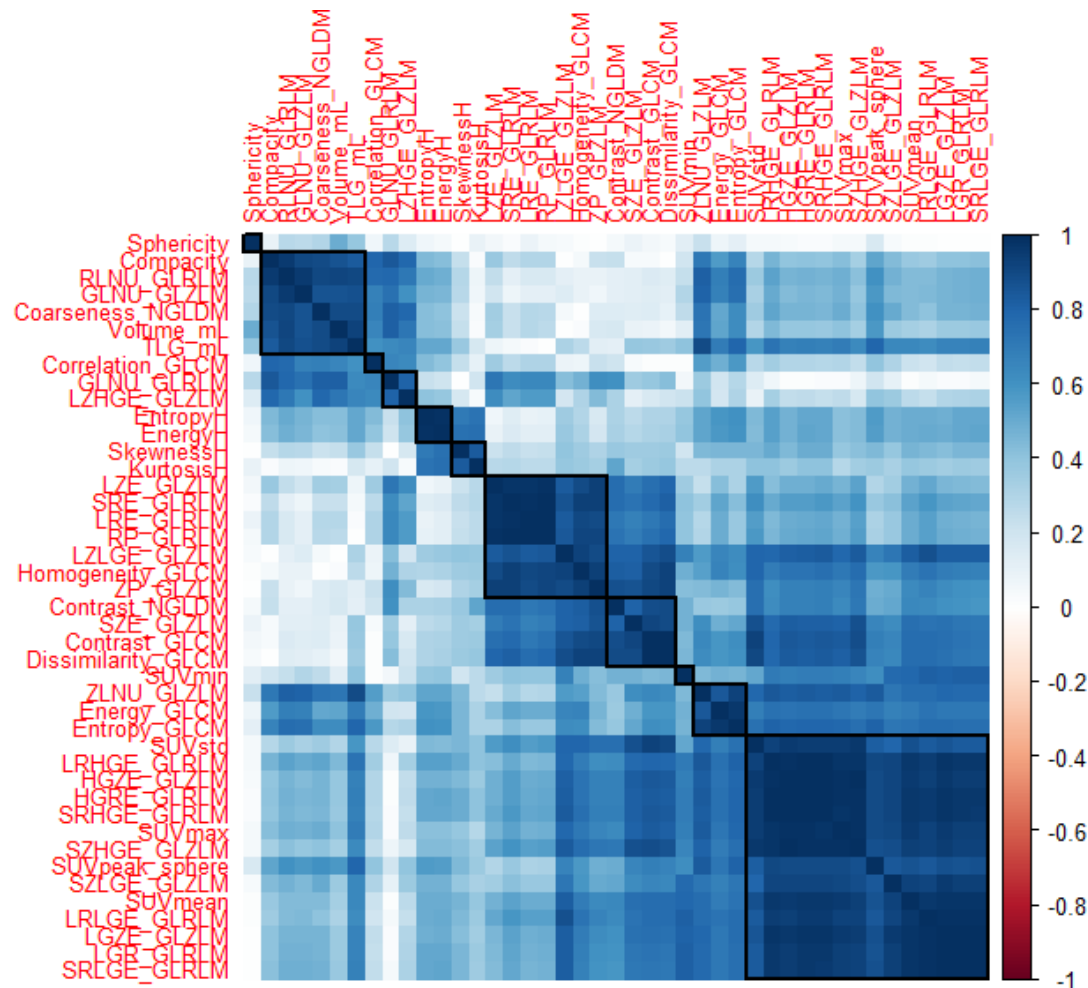
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- [Kirienko et al. EJNMMI 2018] :

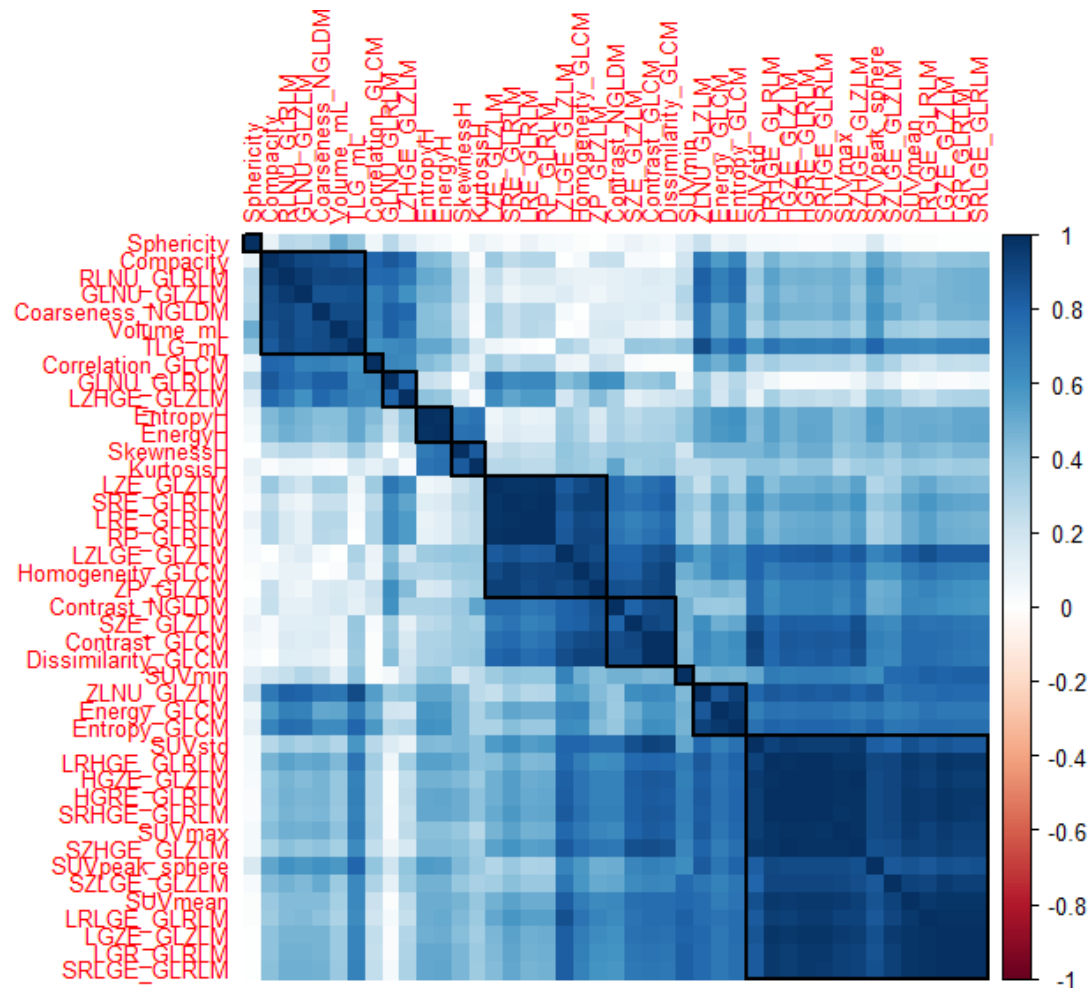
PET ($n = 378^b$)

	No. of patients in group	Adc vs. Sqc or Other				
		AUC	Cut-off	Sensitivity (%)	Specificity (%)	Accuracy (%)
Training	278	0.90 ± 0.10	V1 0.46 ± 0.07 ;	86.0 ± 0.3	74.9 ± 2.4	80.0 ± 1.7
Validation	100	0.80 ± 0.04	V2 -0.20 ± 0.01	78.9 ± 6.1	67.9 ± 6.1	72.7 ± 3.8

Youden = 0.47

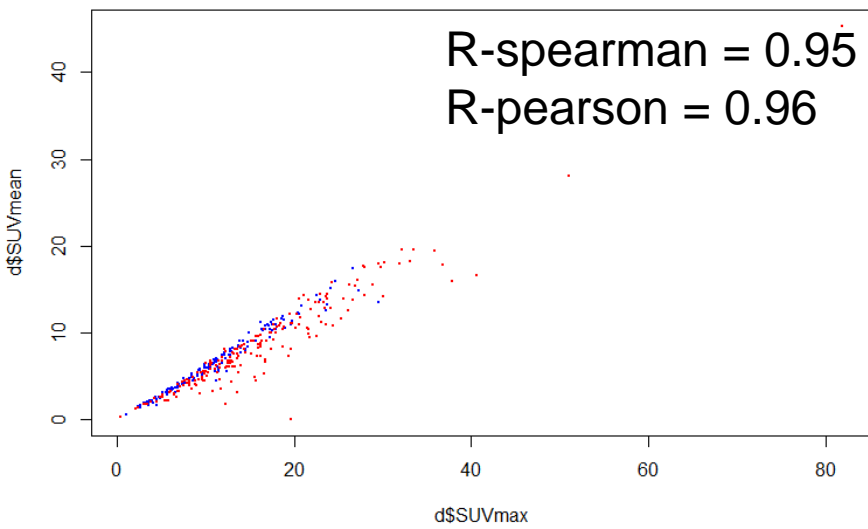
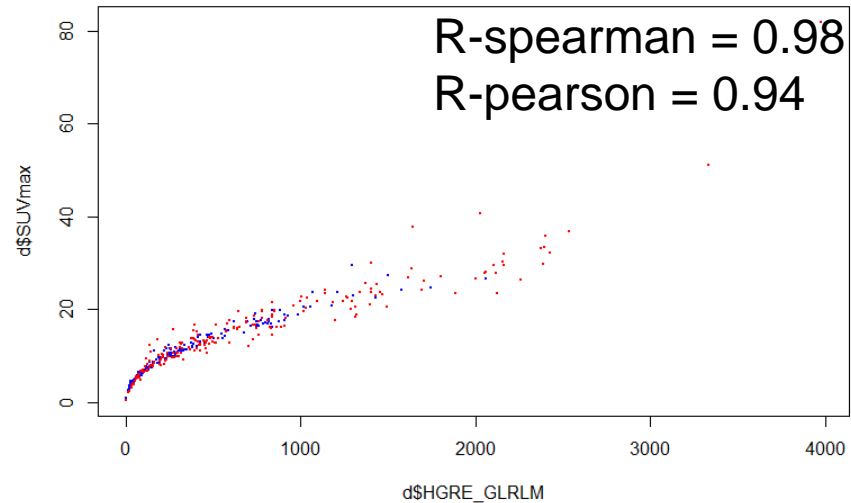
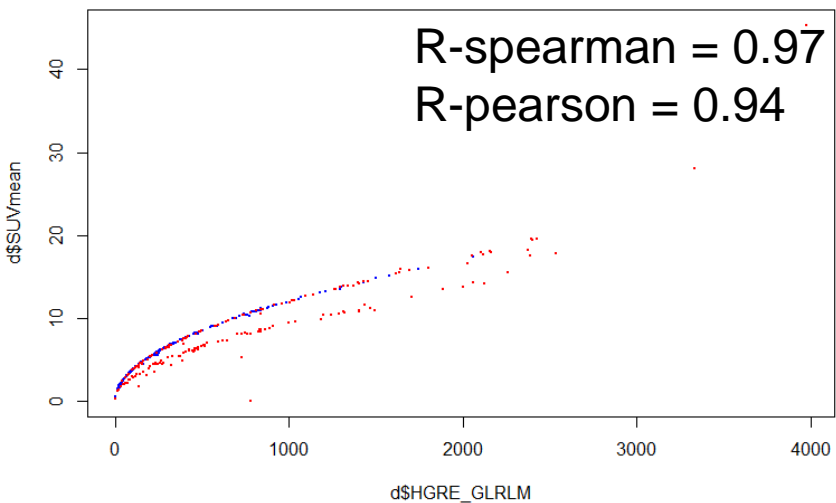
	Sensitivity	Specificity	Youden Index
LDA(all features) → 43 features	77%	67%	0.45±0.07
LDA(backward feature selection) → 38±2 features	78%	67%	0.45±0.07
LDA(forward feature selection) → 1.2±0.4 features	64%	64%	0.28±0.09





LDA(SUVmean ; SUVmax ; HGRE)
→ Youden=0.49

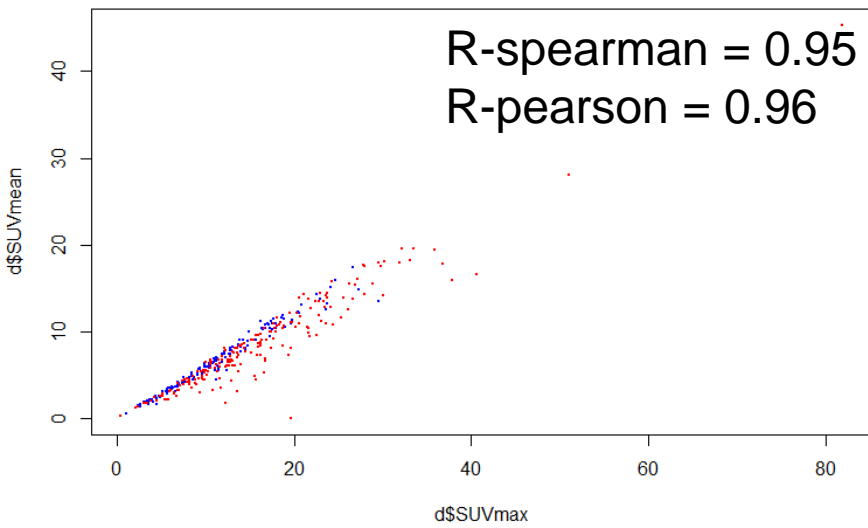
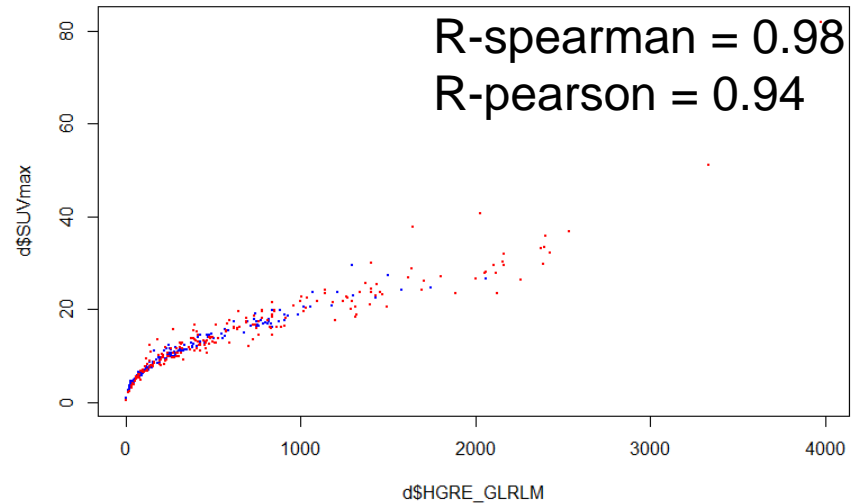
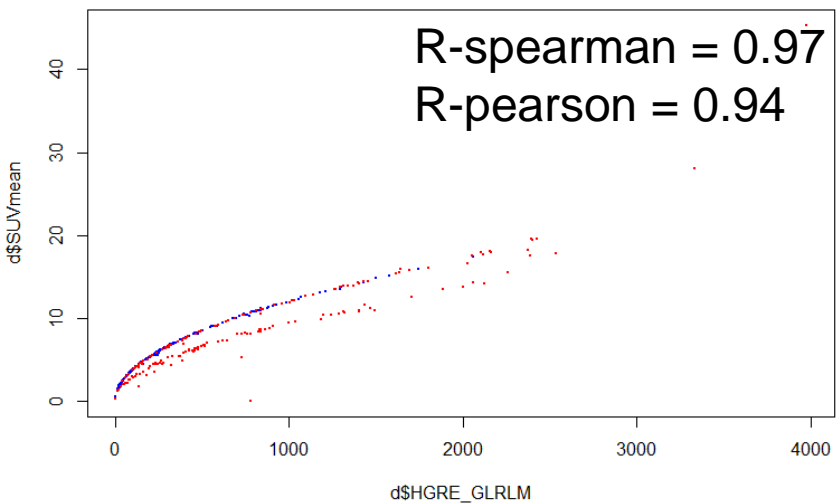
Résultats



HGRE : *High Gray-level Run Emphasis*

Bleu = adk
Rouge = sq

Résultats



HGRE : *High Gray-level Run Emphasis*

Influence de la machine TEP ?
Influence du Volume de la lésion ?

Bleu = adk
Rouge = squ

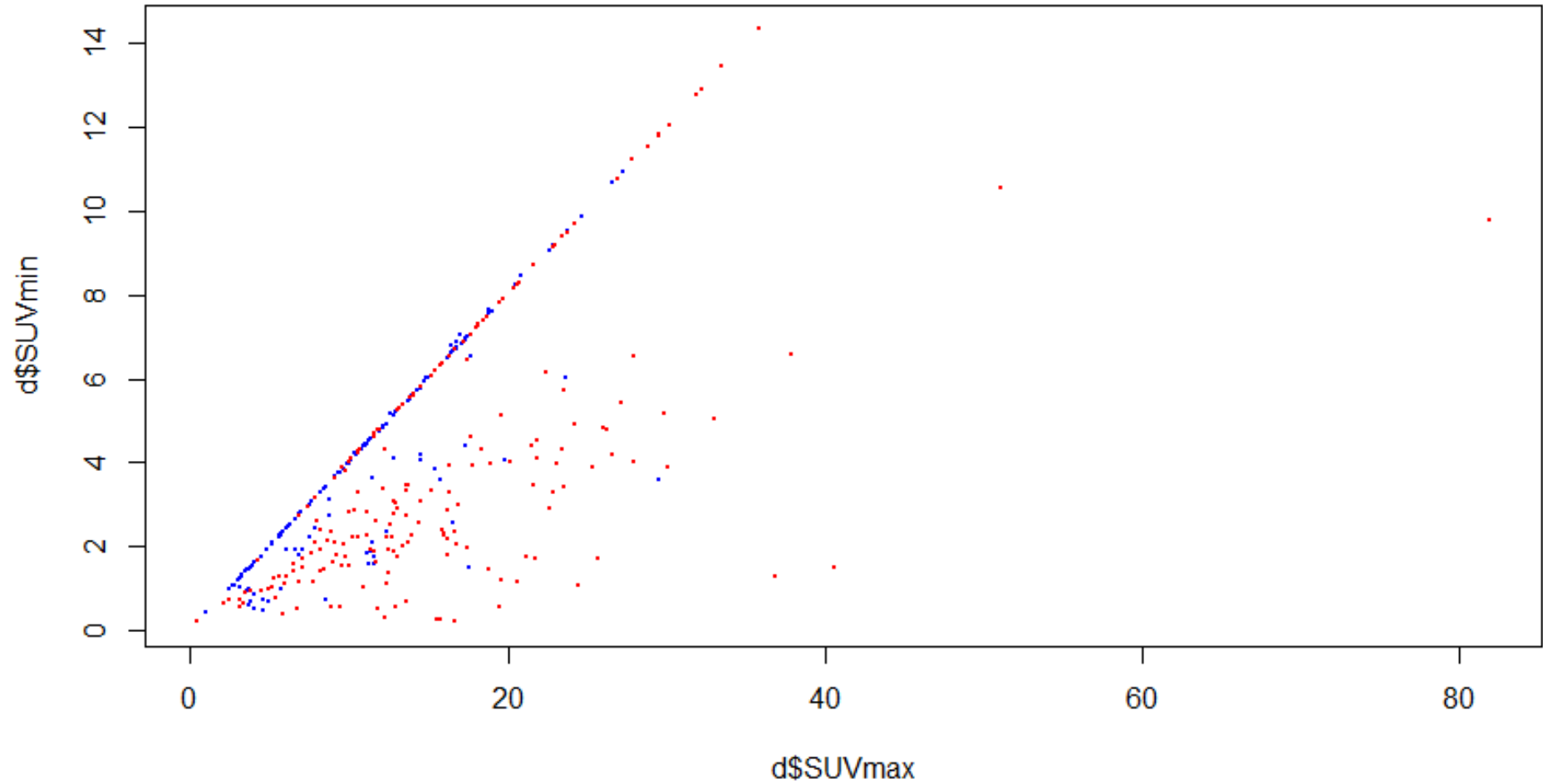


Résultats

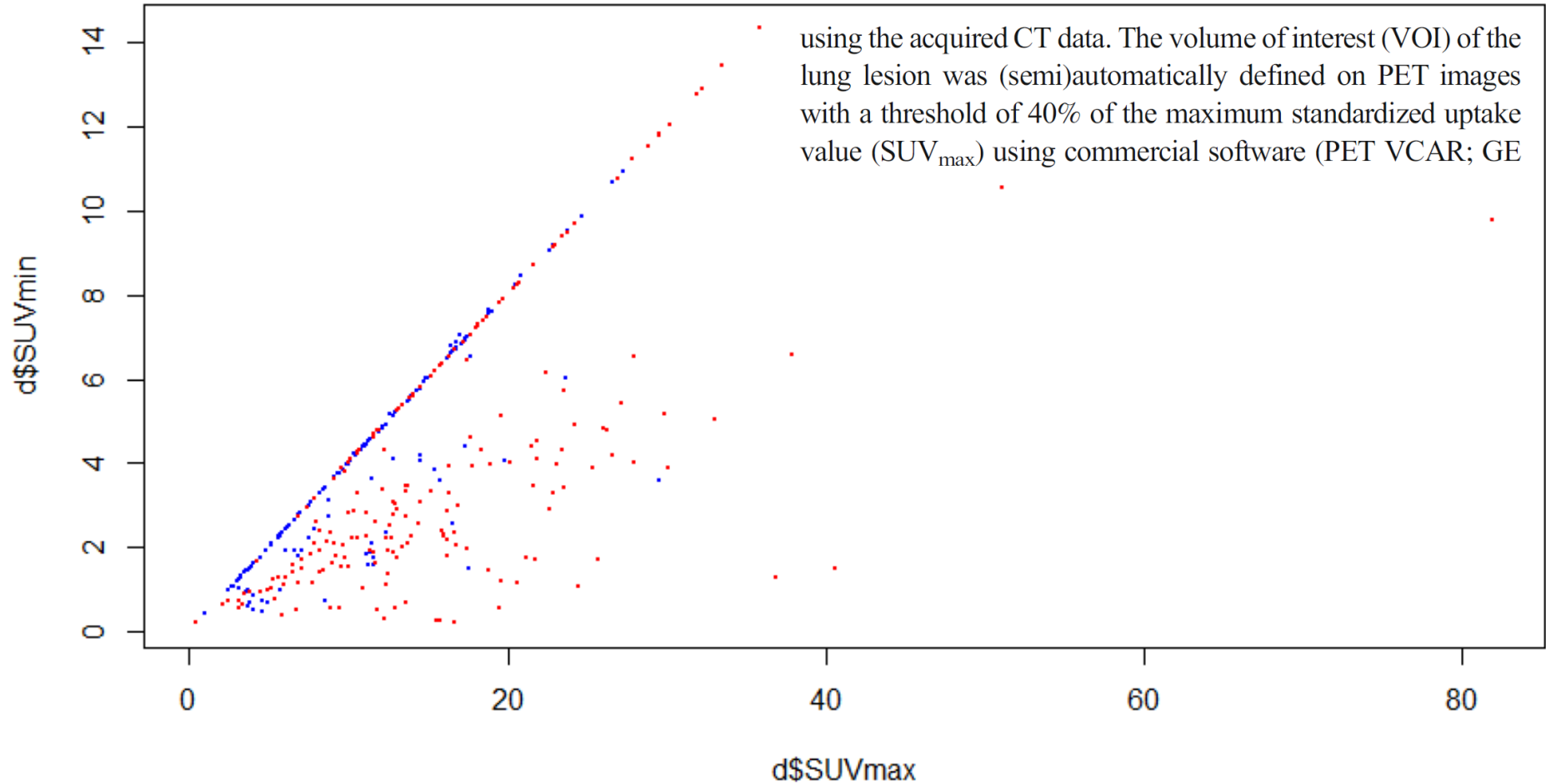
Cherche la
relation
mathématique et
tu trouveras



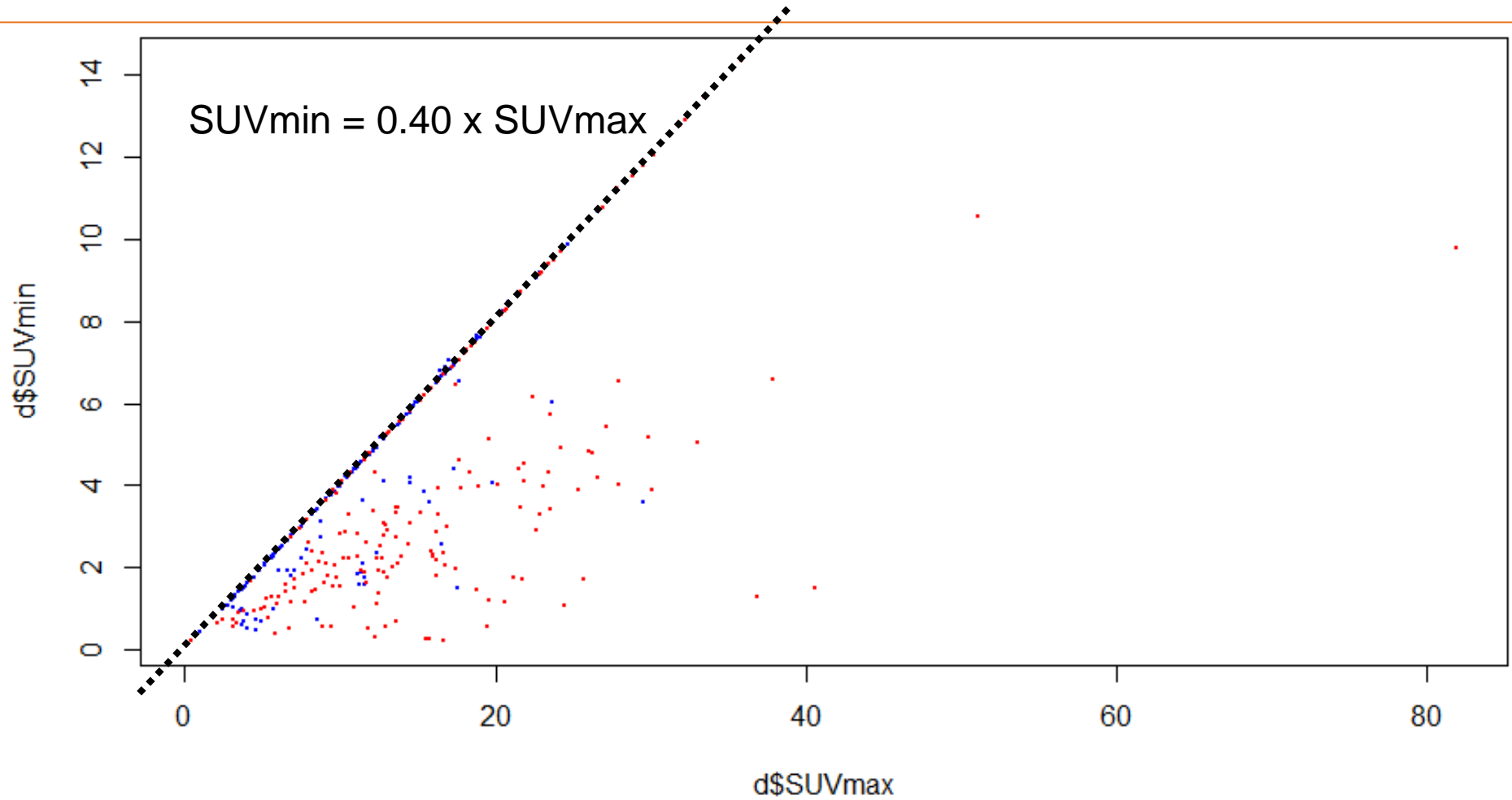
Résultats : SUVmin vs SUVmax



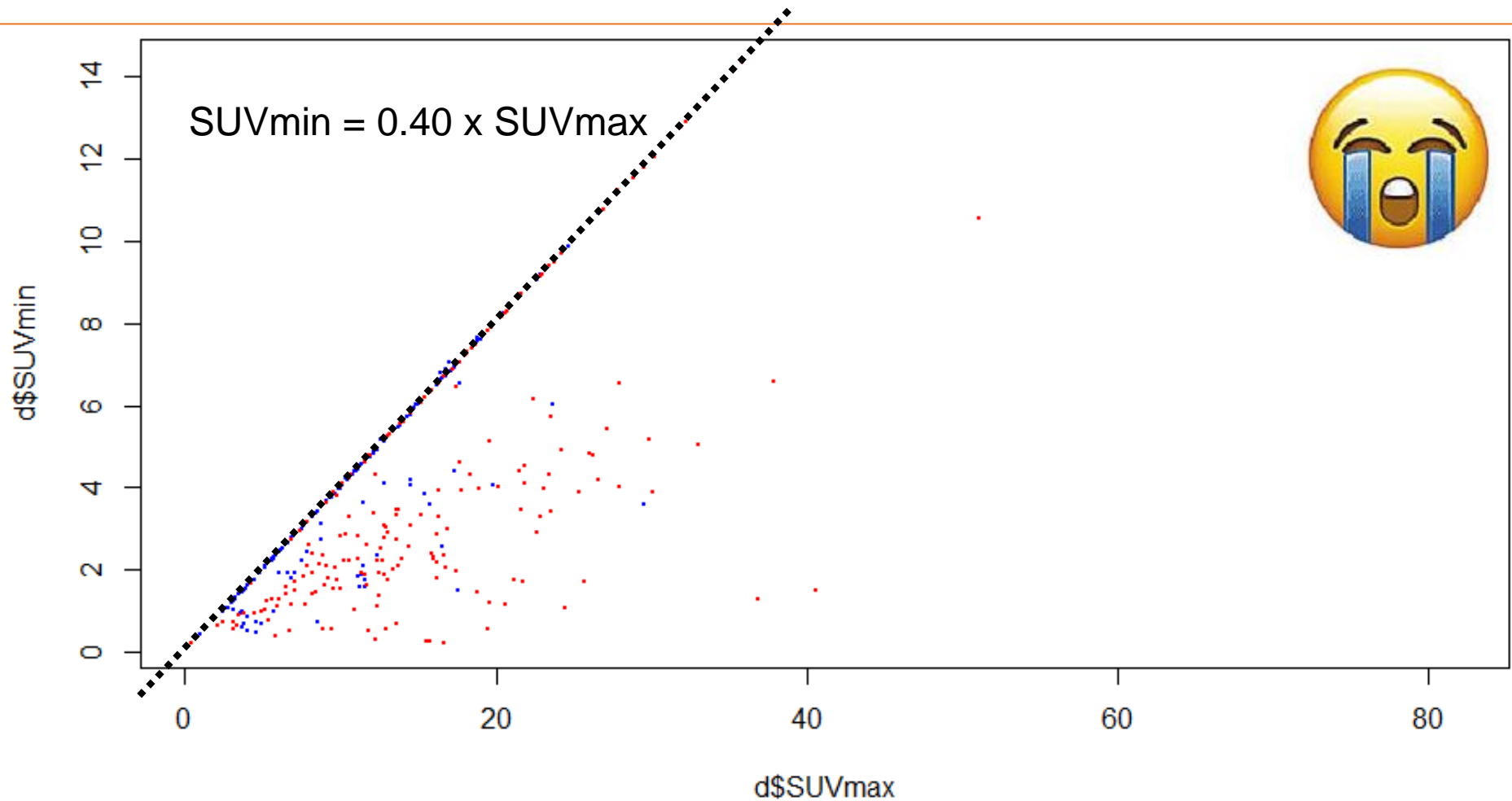
Résultats : SUVmin vs SUVmax



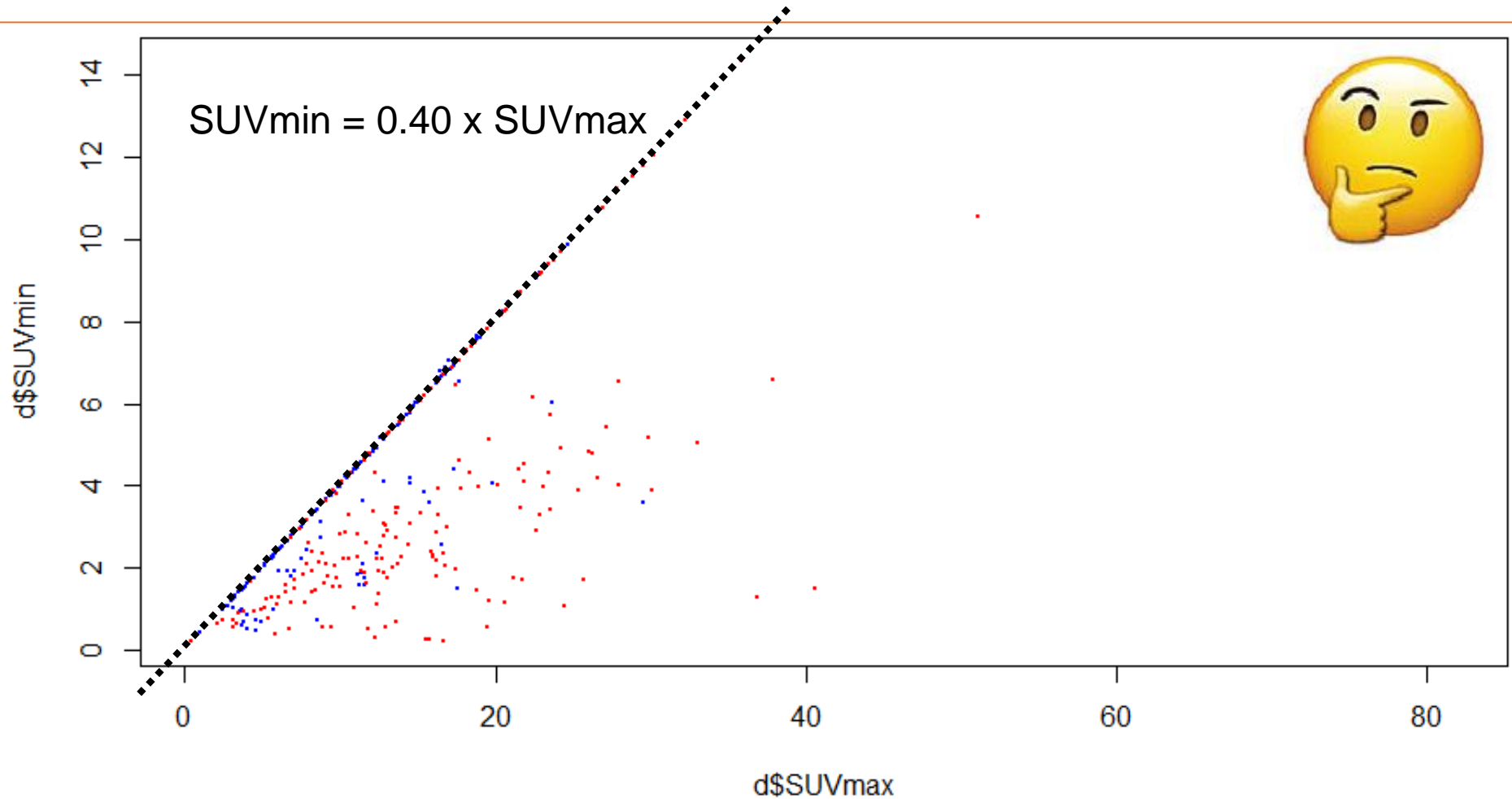
Résultats : SUVmin vs SUVmax



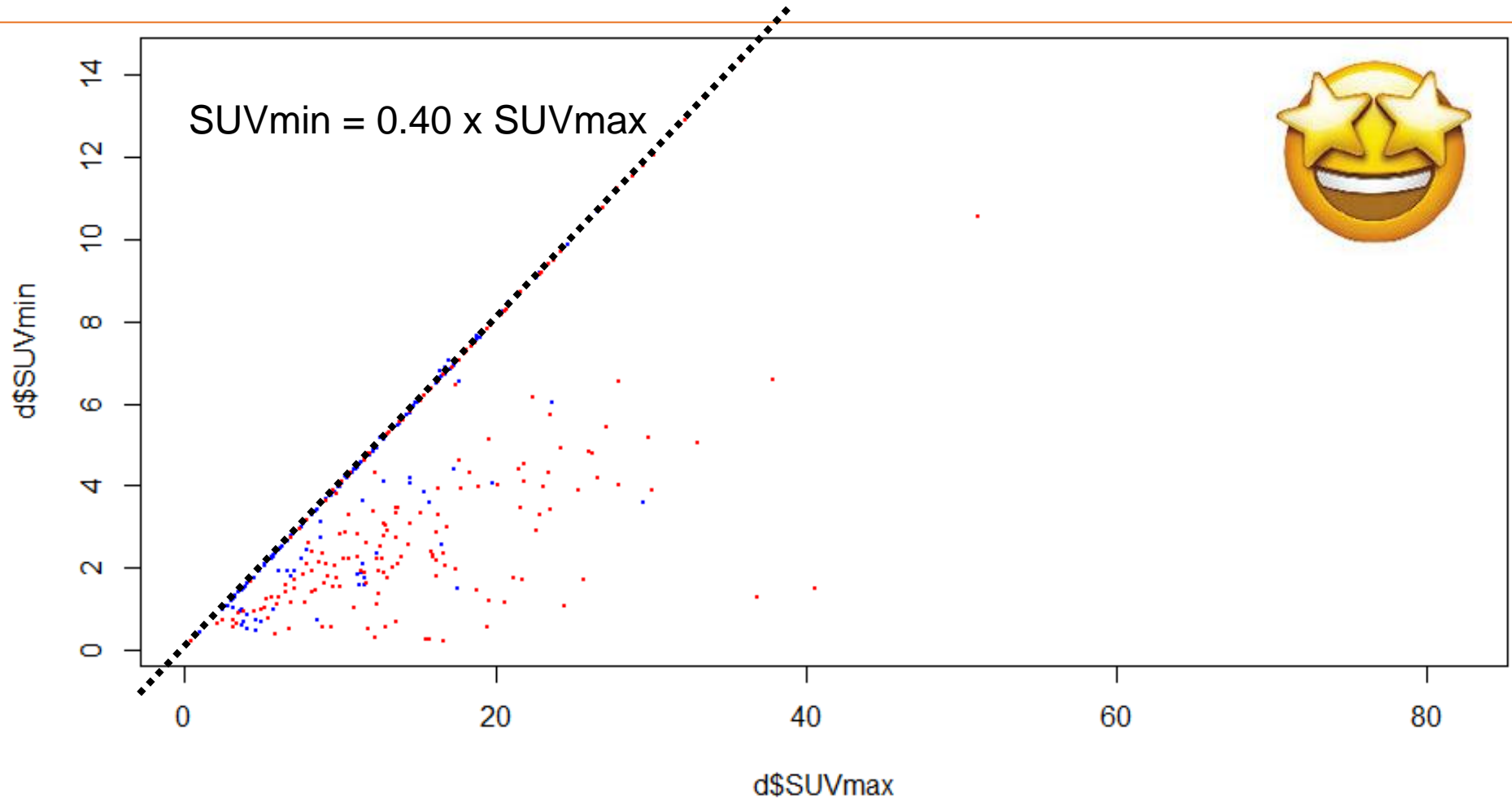
Résultats : SUVmin vs SUVmax



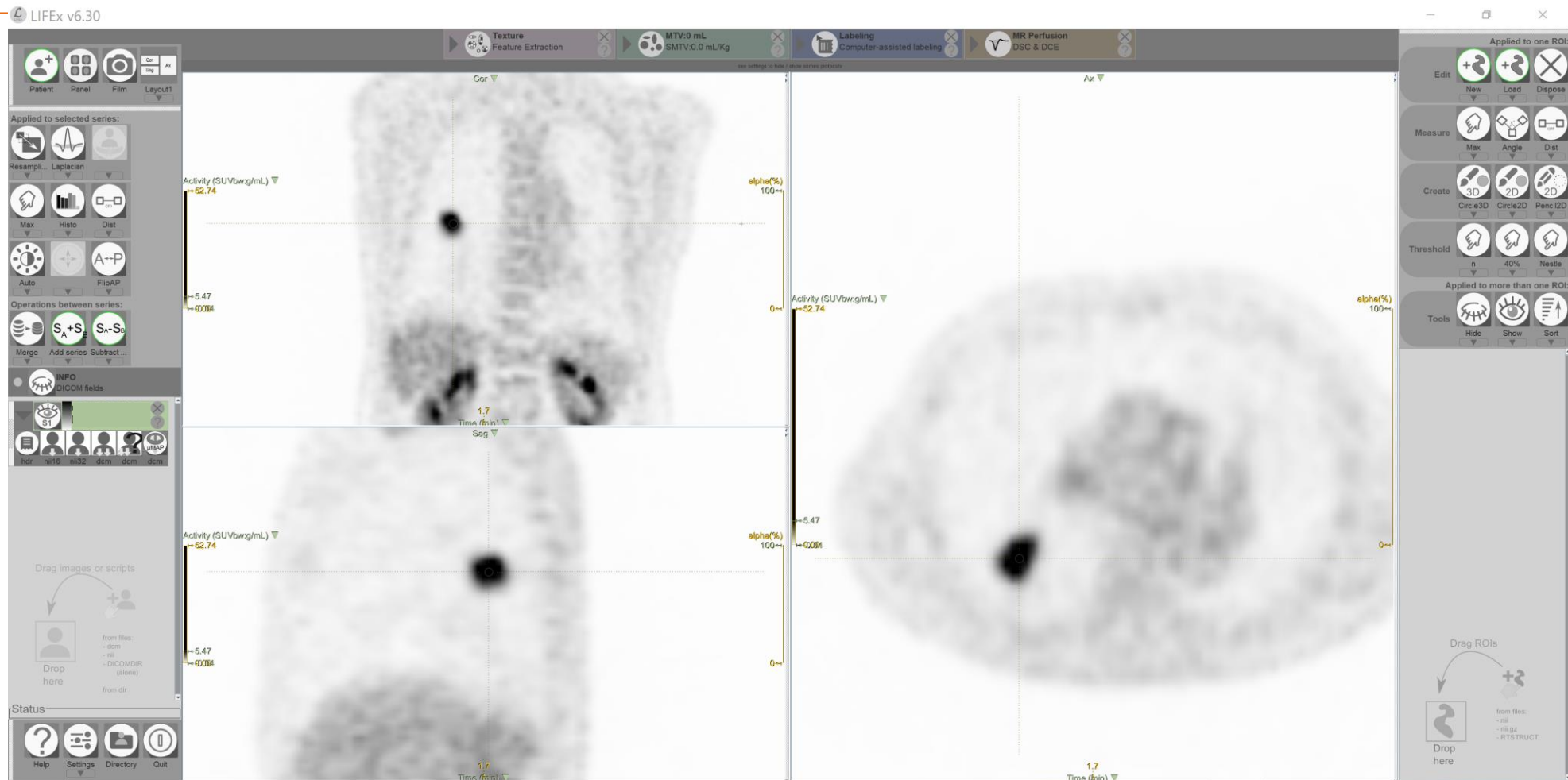
Résultats : SUVmin vs SUVmax



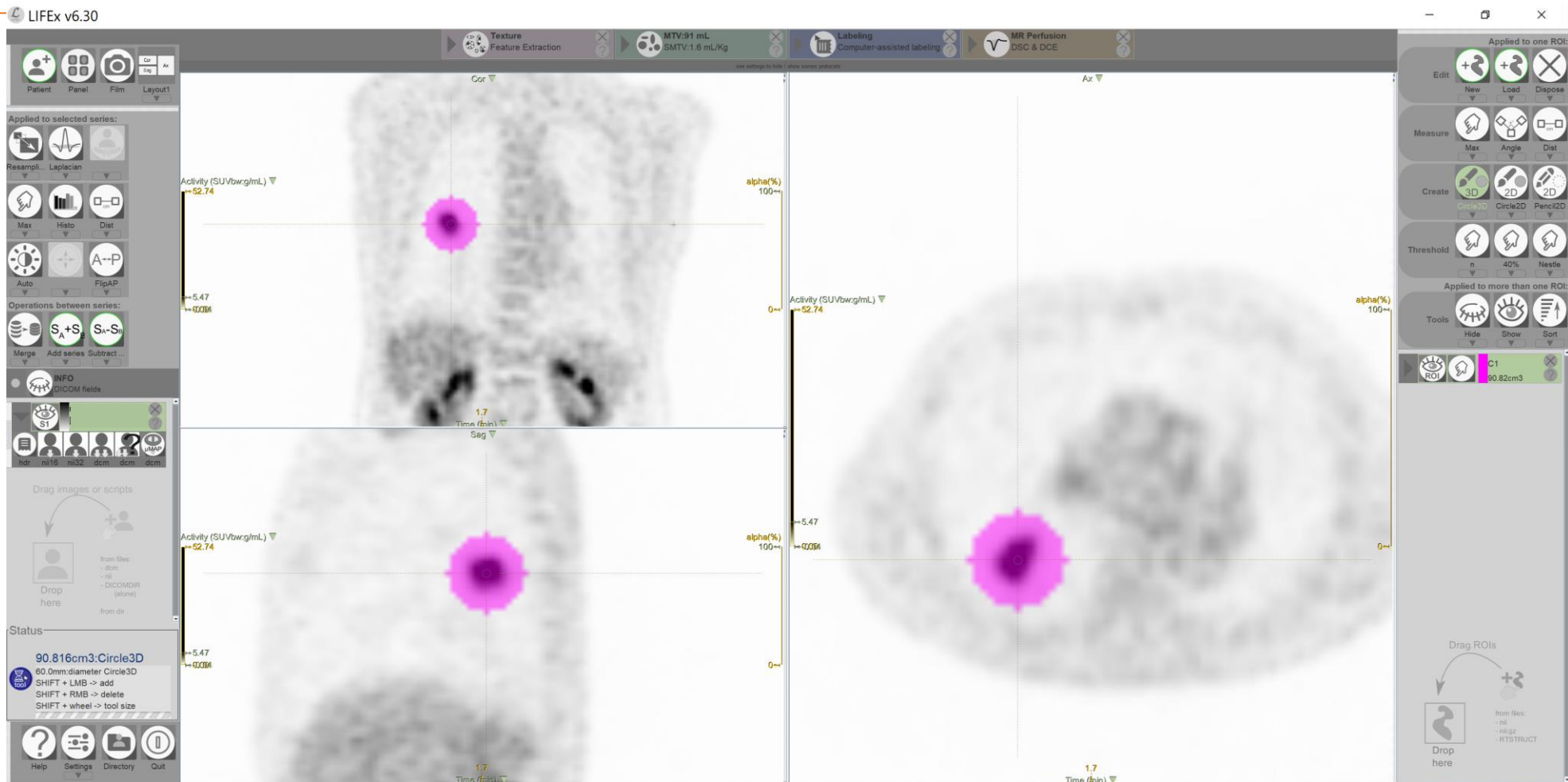
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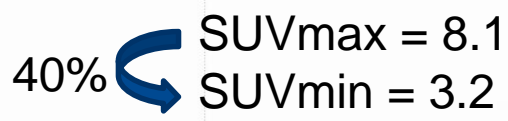


Patient #1



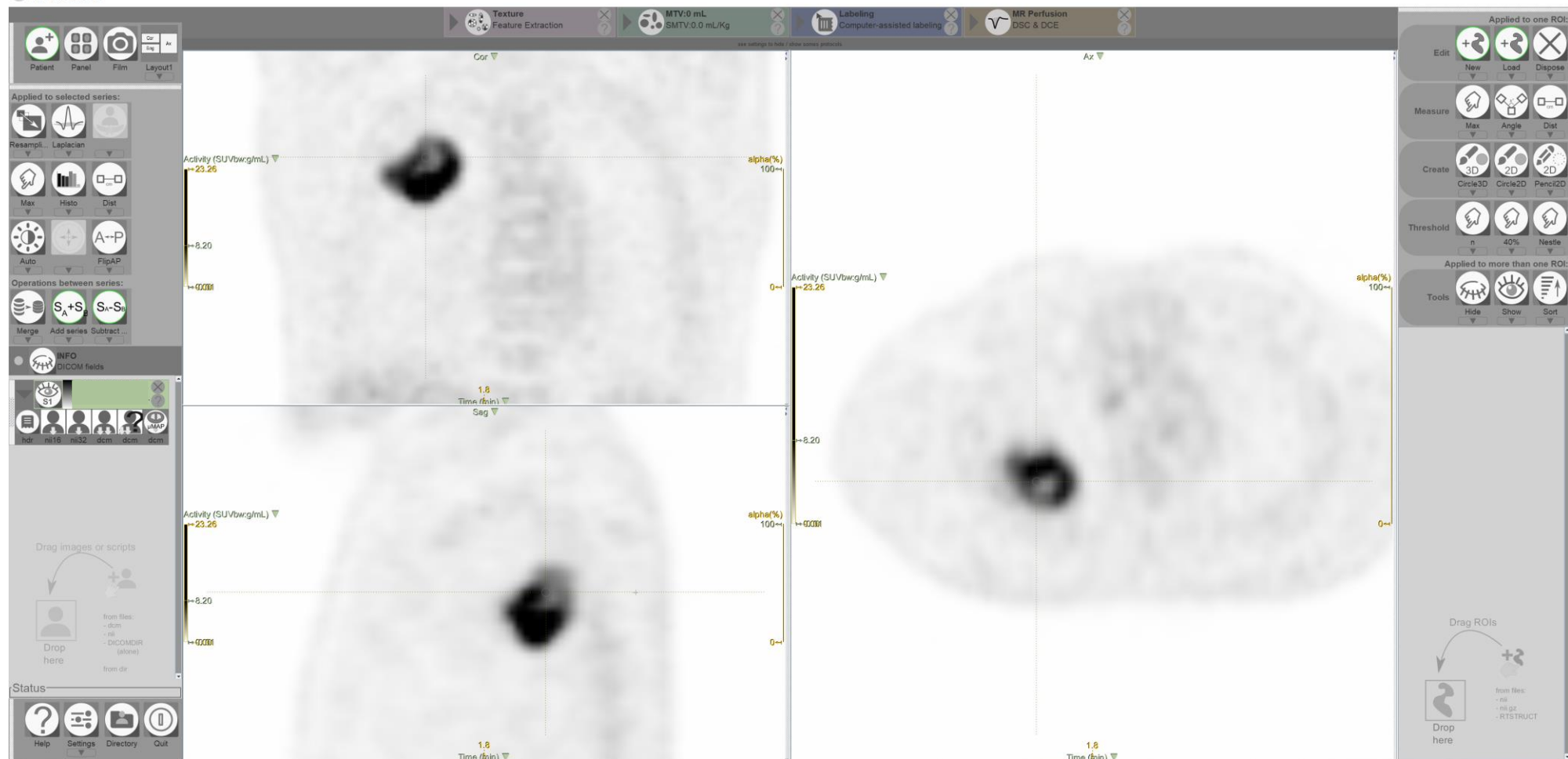
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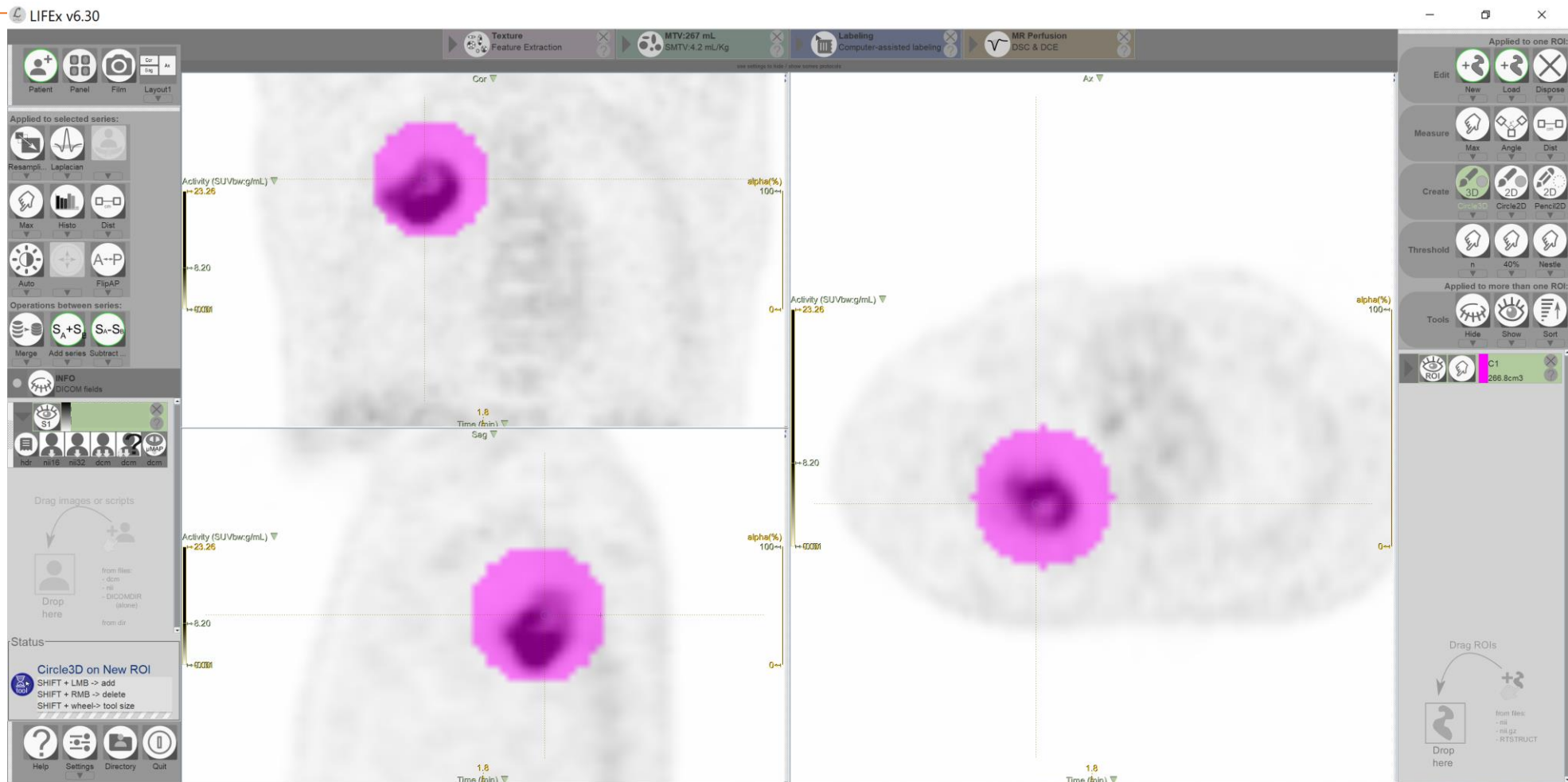
 LIFEx v6.30

Patient #2

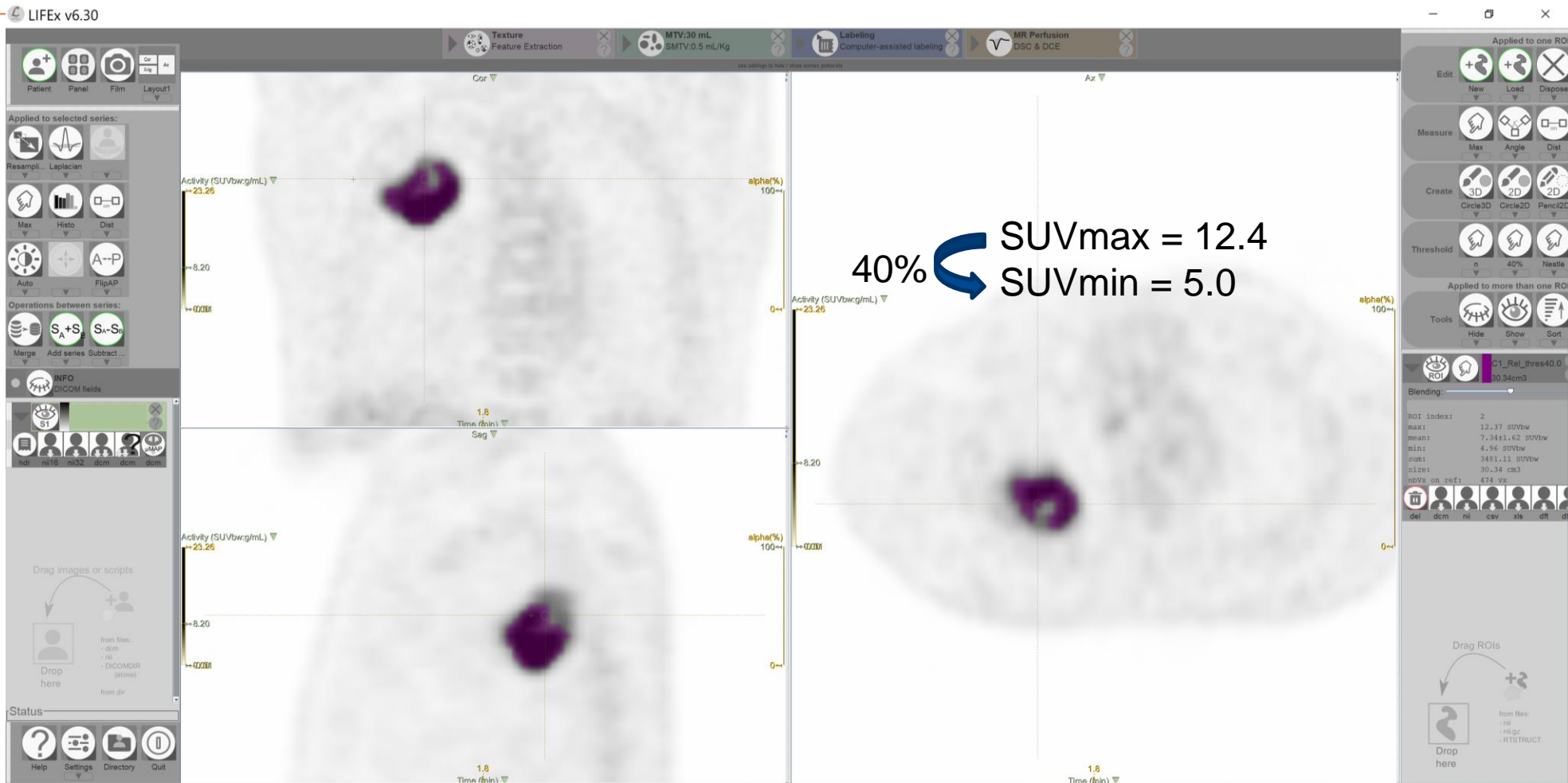
LIFEx v6.30



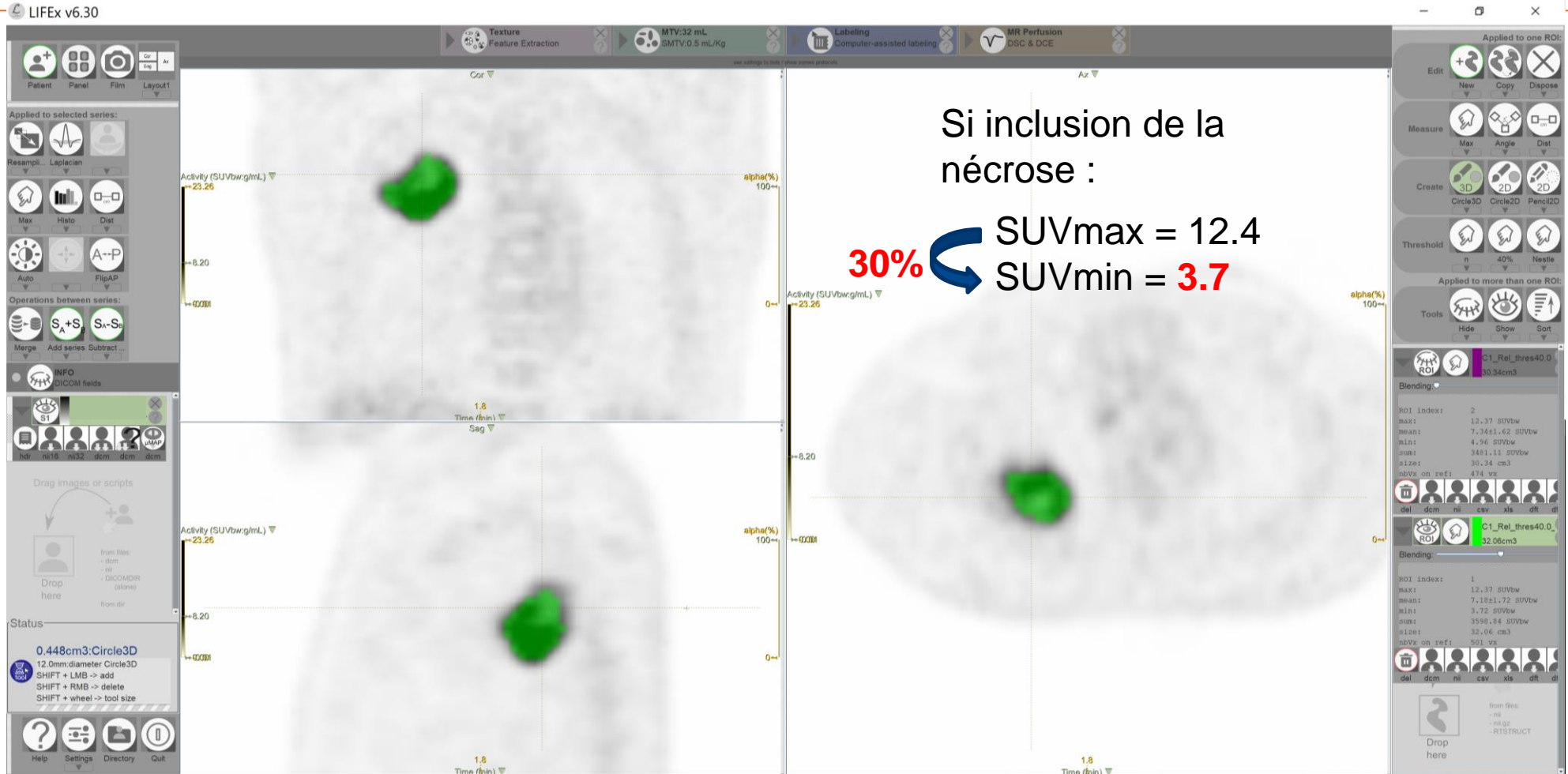
Patient #2



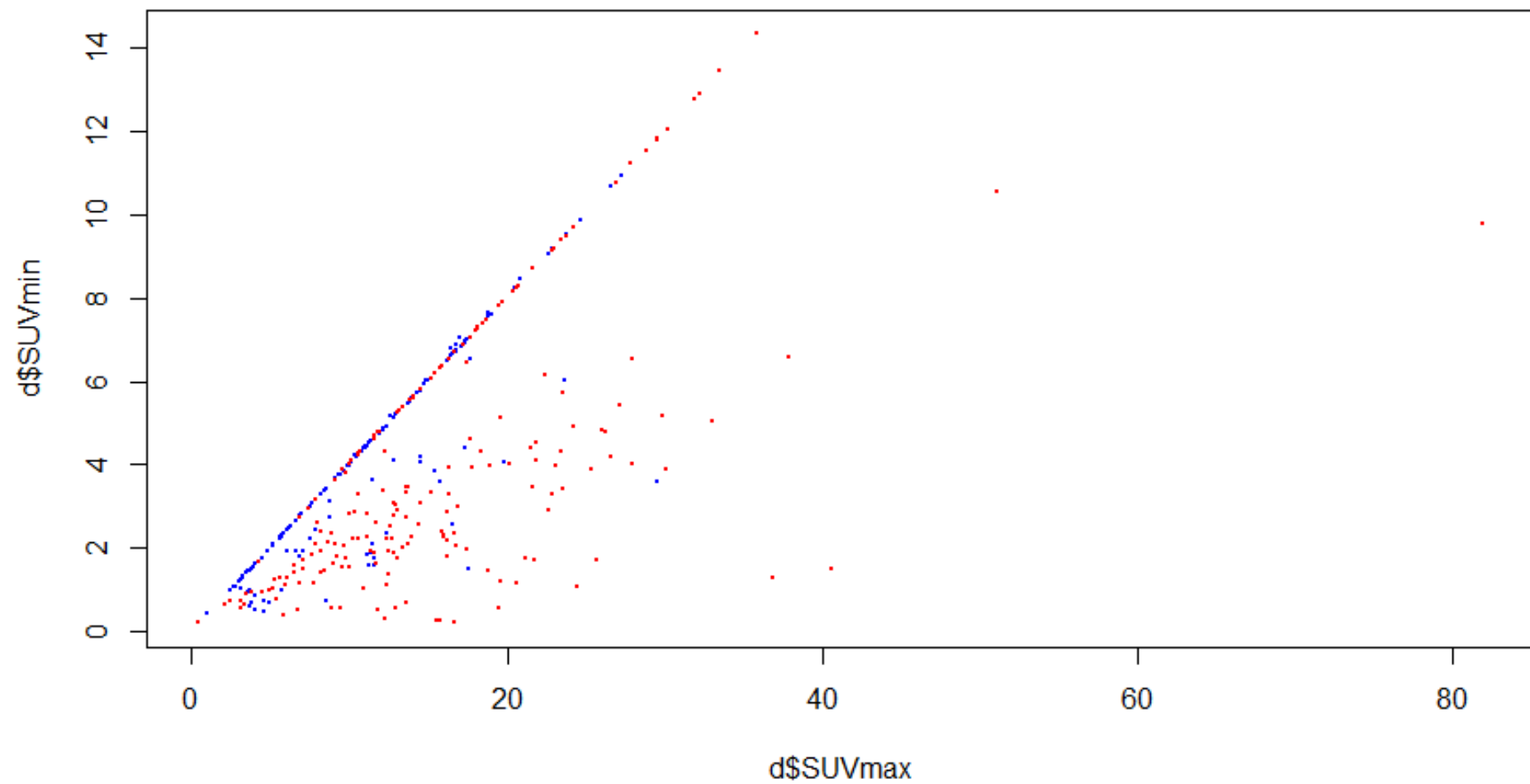
Patient #2



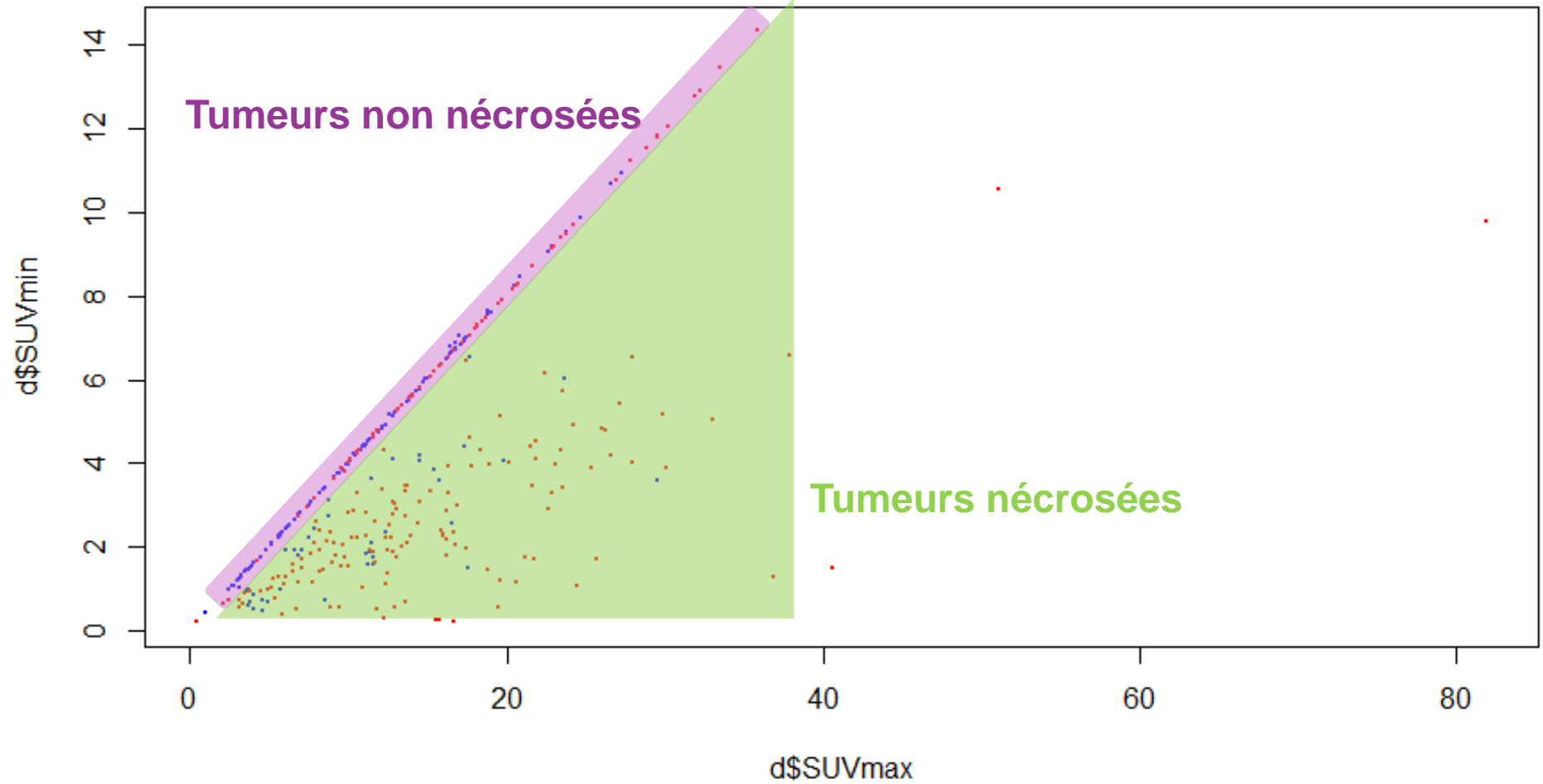
Patient #2



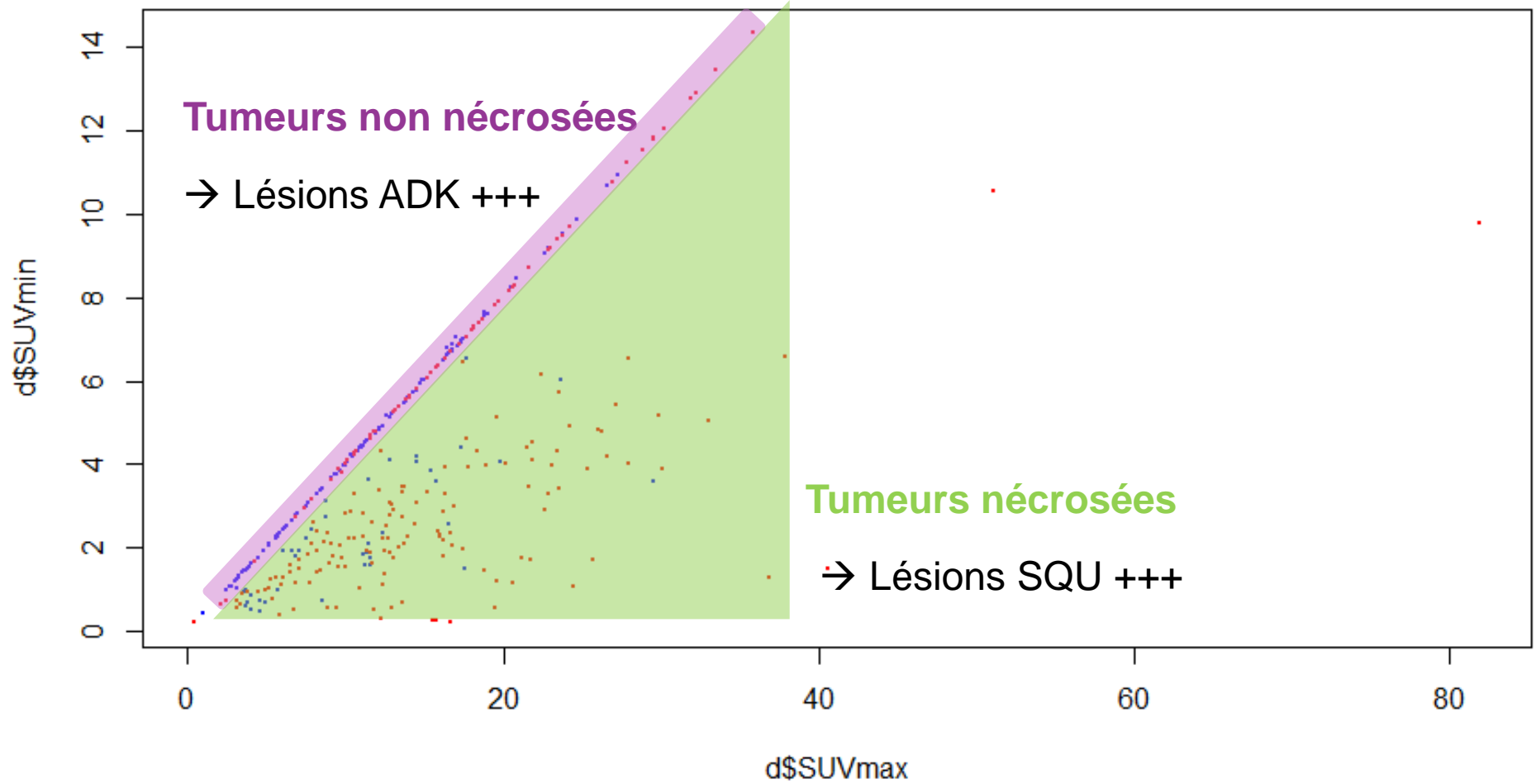
Résultats



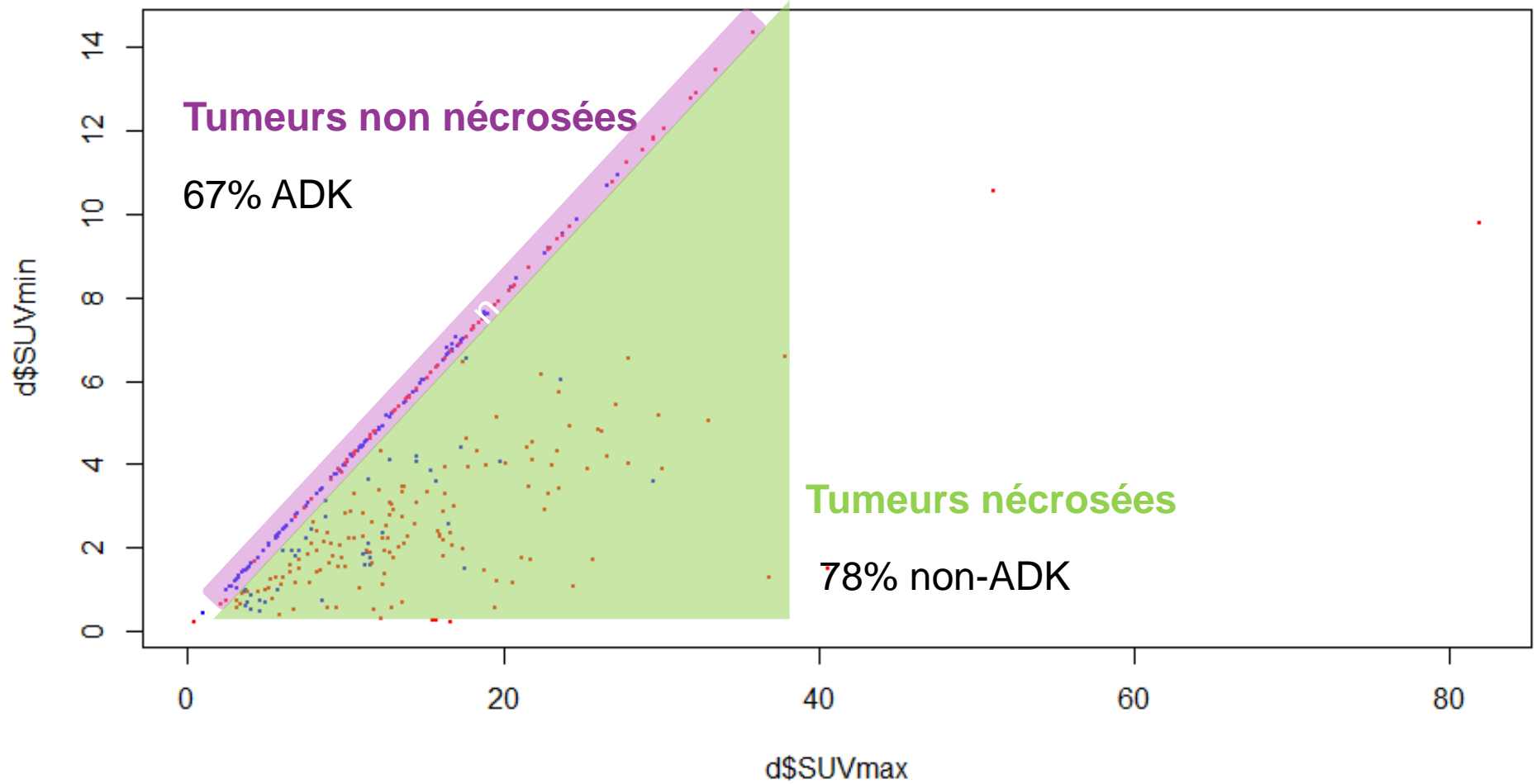
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LDA(SUVmin)	3%	94%	-0.02±0.05
LDA(SUVmax)	55%	69%	0.24±0.07
LDA(SUVmin ; SUVmax)	82%	61%	0.44±0.07
LDA(SUVmin/SUVmax)	79%	67%	0.46±0.06
LDA(SUVmin/SUVmax ; SUVmax)	80%	71%	0.50±0.06

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LDA(SUVmin/SUVmax)	79%	67%	0.46±0.06
LDA(SUVmin/SUVmax ; SUVmax)	80%	71%	0.50±0.06
RF(all features) → 43 features	69%	73%	0.41±0.06
RF(recursive feature elimination)	68%	72%	0.40±0.08
RF(SUVmin ; SUVmax)	67%	75%	0.42±0.07
RF(SUVmin/SUVmax ; SUVmax)	70%	76%	0.46±0.07

Conclusion

- Intérêt de partager des données pour permettre une ré-analyse par d'autres équipes
- Principale caractéristique pour distinguer les lésions en sous-type ici : présence d'une nécrose
→ quantifiable grâce à une signature à 2 index : SUVmin et SUVmax
- Meilleures performances avec 2 index (Youden=0.50) par rapport à 43 index (Youden=0.45)