

Radiomics for outcome modeling: state-of-the-art and challenges

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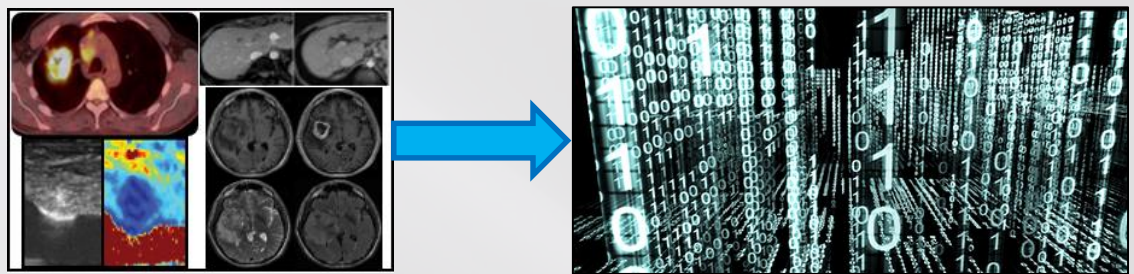
LaTIM, UMR INSERM-UBO 1101, Brest

Orsay, 23 Mars 2018

Introduction

Radiomics: definition

- ❑ Radiomics is the high-throughput extraction of quantitative features from medical images¹
- ❑ The approach considers « pictures » as « minable » data²



- ❑ Radiomics aims at building models that are predictive of some patient outcome (e.g. survival, response to therapy...) or characteristic (tumor type, phenotype, genotype...)



1. Lambin, *et al.* Radiomics: extracting more information from medical images using advanced feature analysis. *Eur J Cancer* 2012
2. Gillies, *et al.* Radiomics: Images Are More than Pictures, They Are Data. *Radiology* 2016

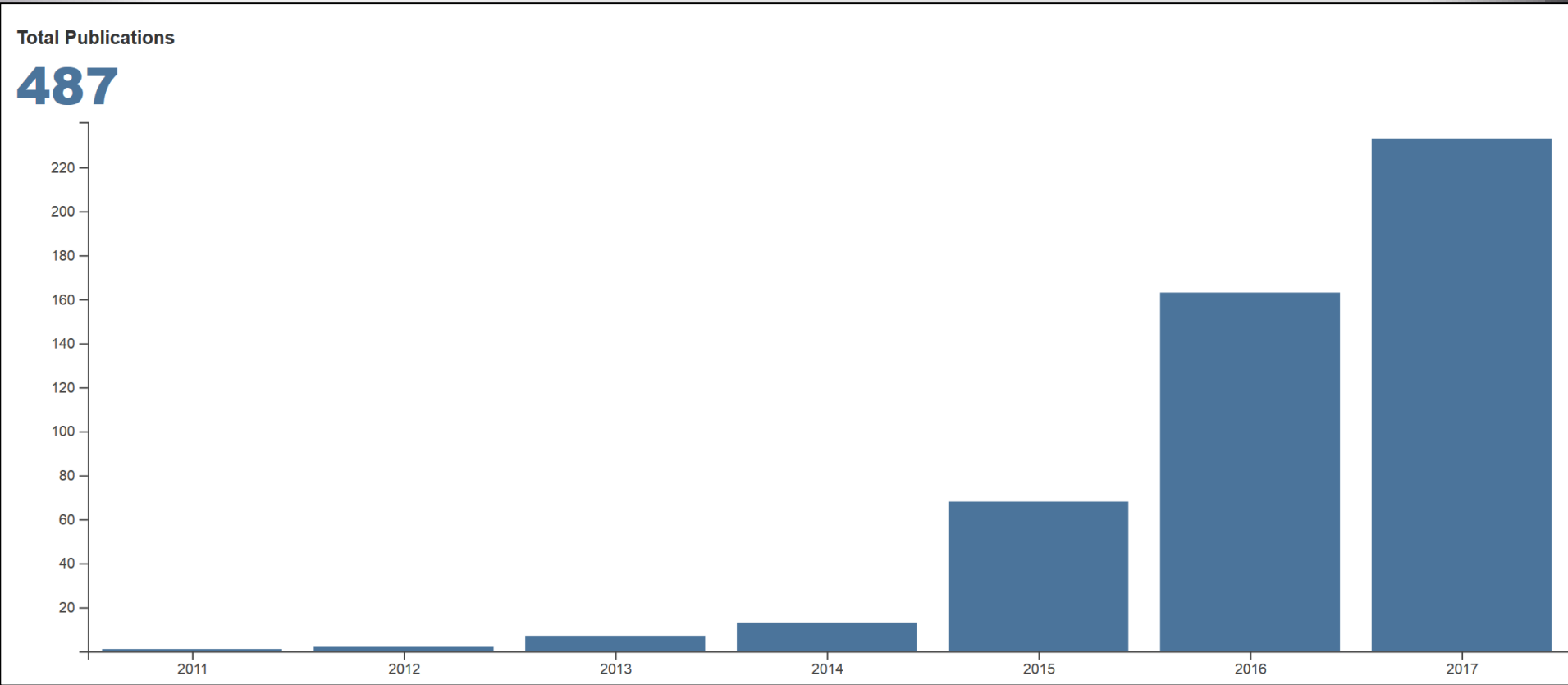


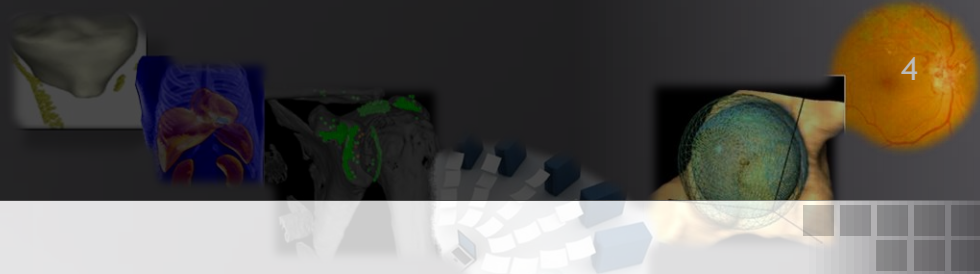
Introduction

Radiomics: exponential growth



Radiomics: ~500 publications





The terms “radiomics” and “radiogenomics” were first employed in 2010 to describe how imaging features can reflect gene expression:

NIH-PA Author Manuscript

...because of motion (17). This diffusion images are typically collected at only a single diffusion weighting. Although quantitative values of diffusion are not derived, the data are nonetheless very amenable to pixelwise analysis of heterogeneity.

Anatomic Imaging and gene expression patterns: **Radiomics**

Referring again to figure 1, the physiology and anatomy of organs and tumors is driven by gene expression patterns which are a product of cellular genetics interfacing with the microenvironment. Over the last few years, it has become clear that distinct sub-regions of tumors, identifiable by MR imaging, have distinct gene expression patterns (31, 42–44). This indicates that underlying molecular biology can affect the “anatomy”. Recently, there have been attempts to determine if quantitative analysis of the anatomy can be used to infer an underlying molecular gene expression pattern. This involves “radiomics” which is the extraction of quantitative features from radiographic images. Relating these to gene expression patterns using sophisticated bioinformatic approaches is sometimes termed

Clin Radiol. Author manuscript; available in PMC 2014 May 04.

Gillies et al.

Page 5

“radiogenomics”. The central hypothesis of cancer radiomics is that tumor imaging features

Gillies, *et al.* The biology underlying molecular imaging in oncology: from genome to anatomy and back again. *Clin Radiol* 2010

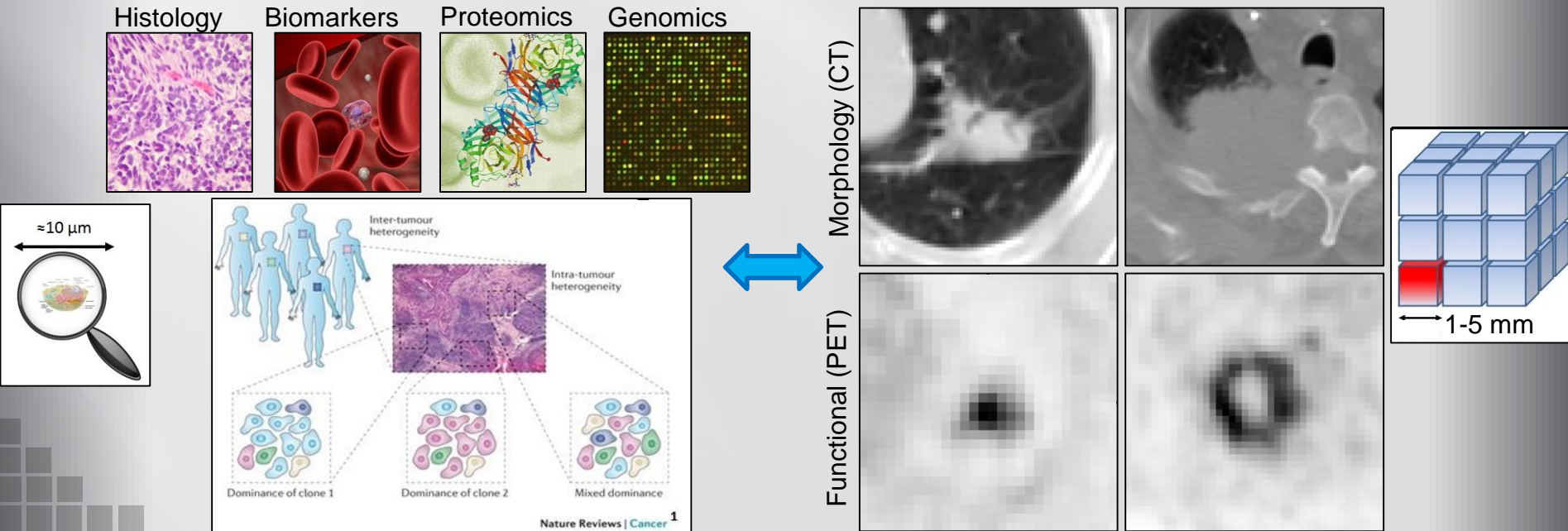


- The term radiomics has become popular since 2012
- Textural features (a large chunk of radiomics features) exist since the 70's and have been used in medical imaging since the 90's [1-3]
- Numerous publications before 2012 (quantification) could be categorized as « radiomics studies »
- Some « new » elements of radiomics:
 - Larger number of features (>hundreds) / « high-throughput »
 - Relying on machine learning (selection/classifier)
 - Link with biology (including genetics)

1. Schad, *et al.* MR tissue characterization of intracranial tumors by means of texture analysis. *Magn Reson Imaging* 1993
2. Mir, *et al.* Texture analysis of CT-images for early detection of liver malignancy. *Biomed Sci Instrum.* 1995
3. El Naqa, *et al.* Exploring feature-based approaches in PET images for predicting cancer treatment outcomes. *Pattern Recognit.* 2009

Macroscopic/microscopic heterogeneity

- Tumours are heterogeneous entities [1]
 - Genetic, cellular, tissular
 - Hypothesis:** characteristics in images (macro scale) reflect at least partly characteristics in smaller scales (including genetic) [2]

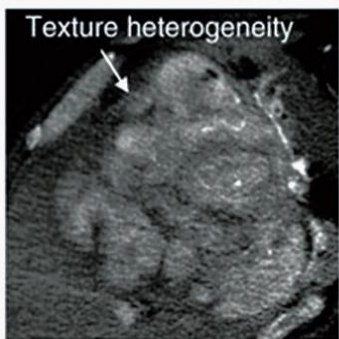
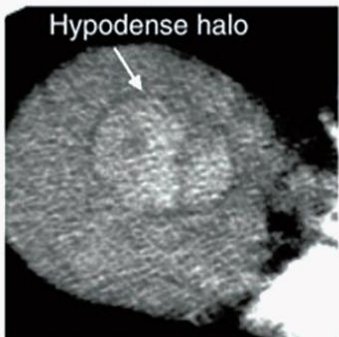
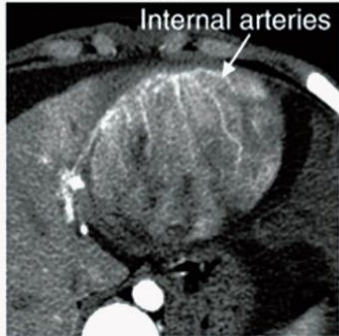
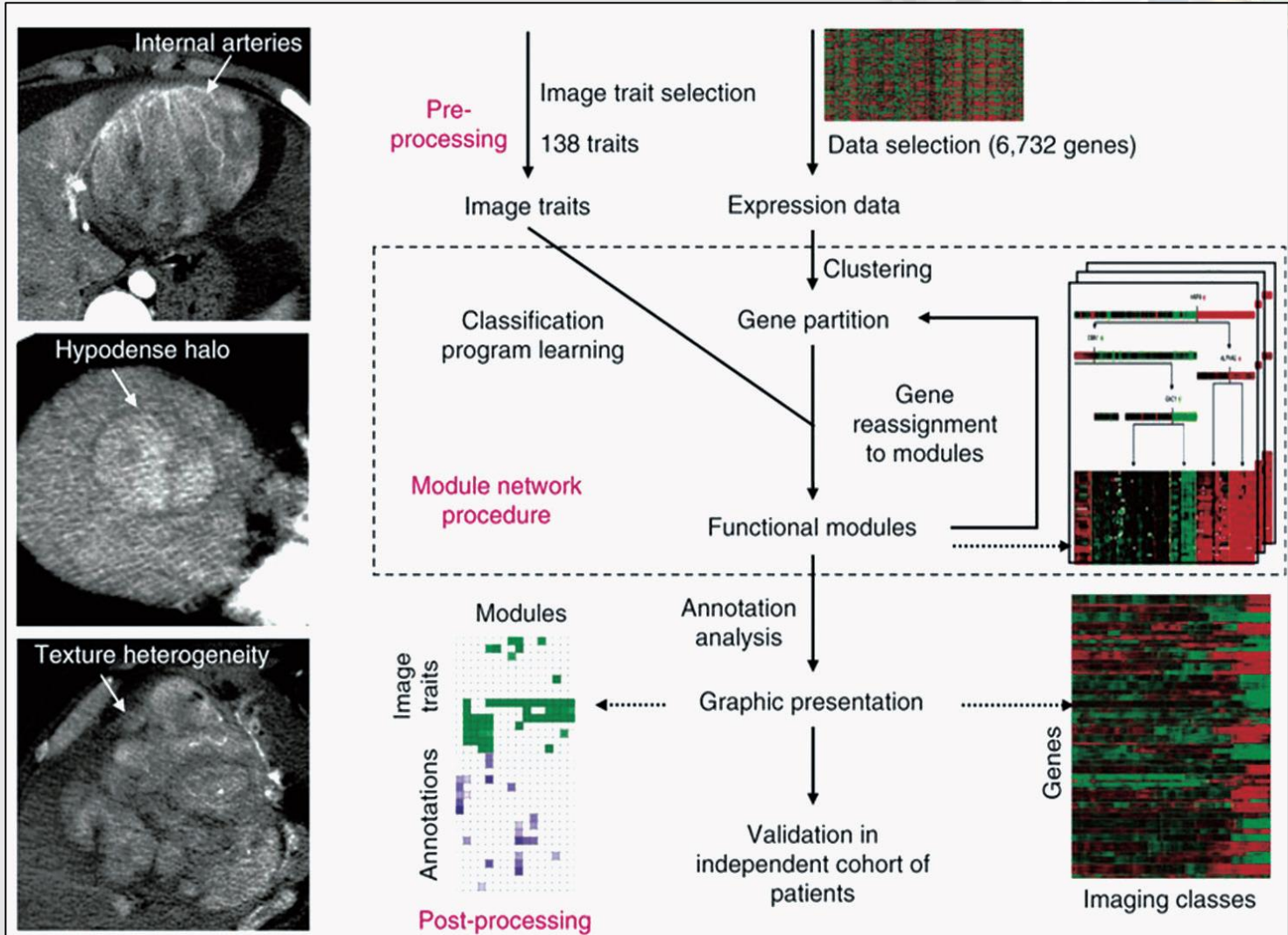


1. Gerlinger, *et al.* Intratumor heterogeneity and branched evolution revealed by multiregion sequencing. *N Engl J Med.* 2012

2. Segal, *et al.* Decoding global gene expression programs in liver cancer by noninvasive imaging. *Nat Biotechnol.* 2007

Introduction

Early works (example)

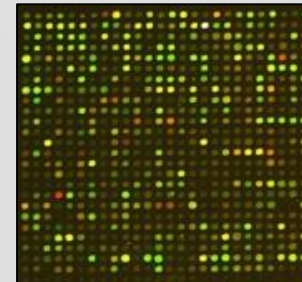
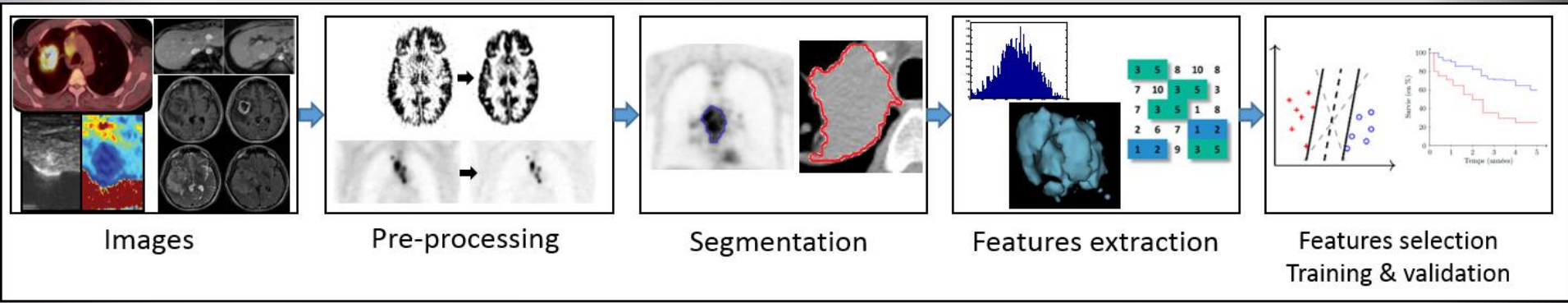


Radiomics

Standard workflow



Clinical data



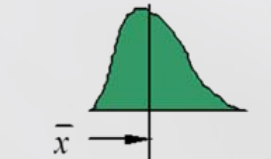
Genomics (and other -omics)



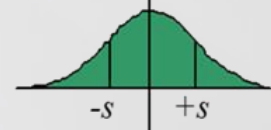
« Usual » radiomics:

- Intensity-based (e.g. histogram)
- Shape descriptors (e.g. sphericity)
- Texture analysis 2nd or higher order (e.g. GLCM)

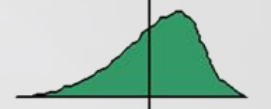
First Moment:
mean - measure of location



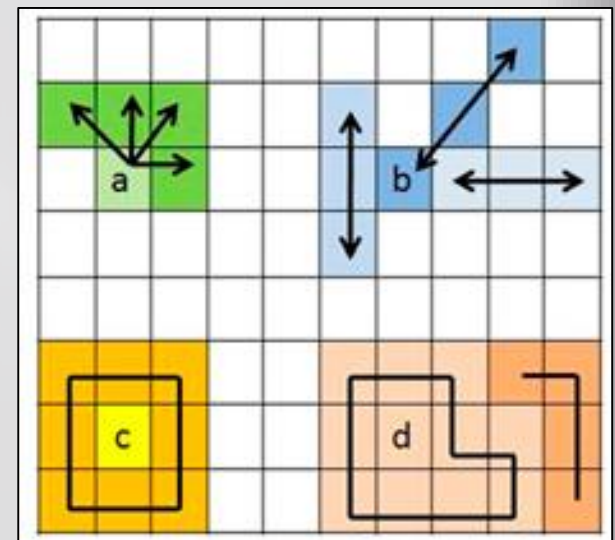
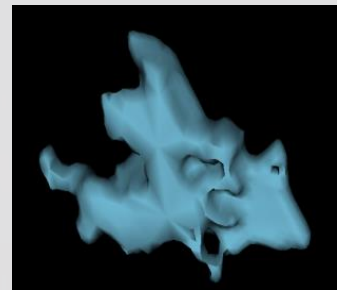
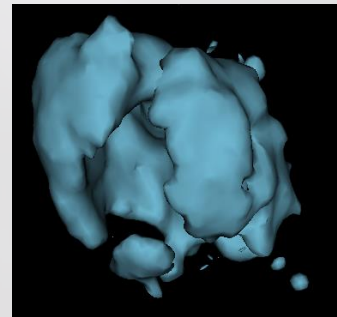
Second Moment:
Standard deviation - measure of spread



Third Moment:
skewness - measure of symmetry

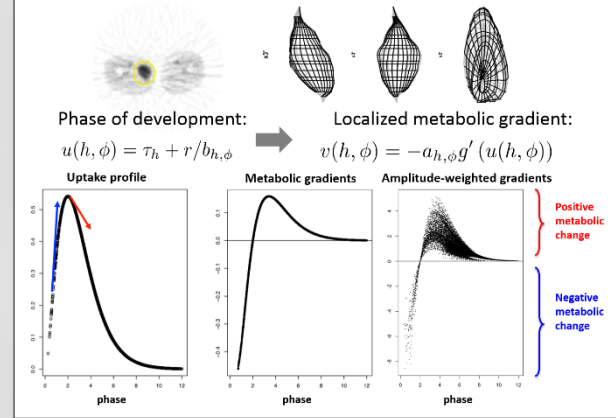
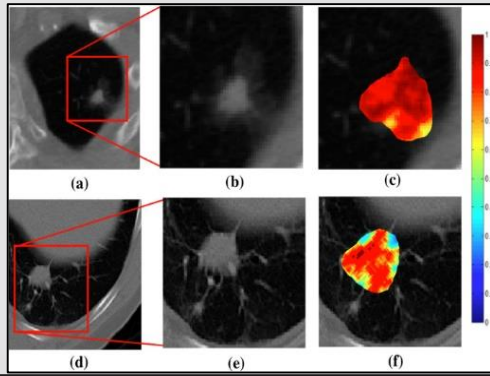
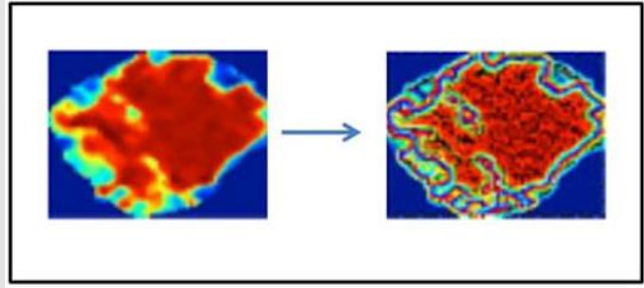
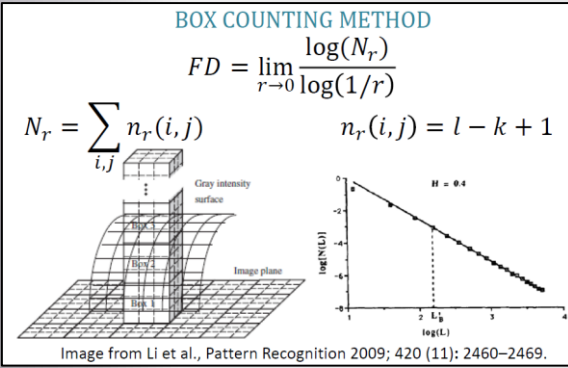


Fourth Moment:
kurtosis - measure of peakedness



Less frequently used / more recent:

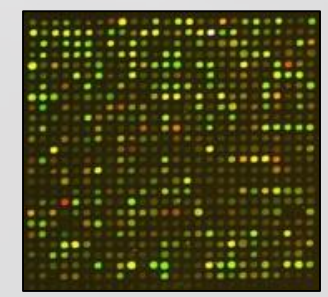
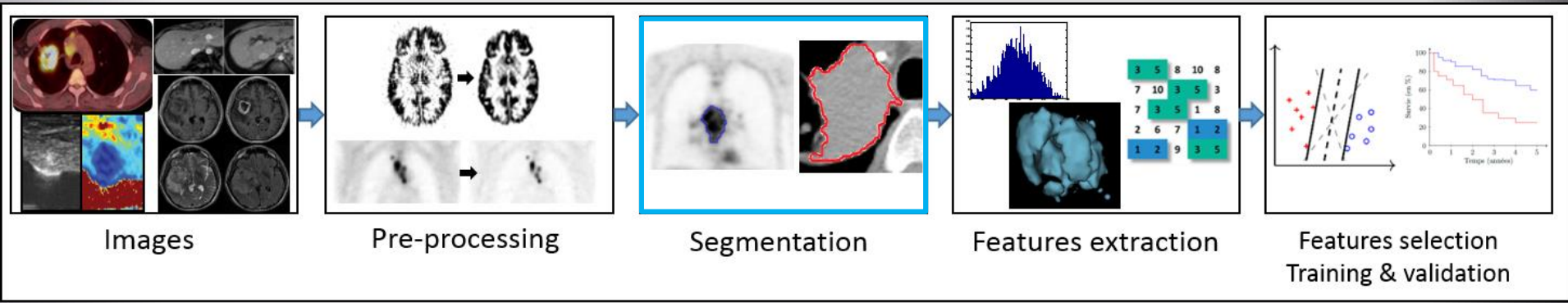
- Fractal analysis¹
- Filter-based (e.g. Law's, Riesz² ...)
- Others (metabolic gradient³, CoLIAGE⁴ ...)



1. Michallek, et al. Fractal analysis in radiological and nuclear medicine perfusion imaging: a systematic review. *Eur Radiol.* 2014
2. Cifujeda, et al. A 3-D Riesz-Covariance Texture Model for Prediction of Nodule Recurrence in Lung CT. *IEEE Trans Med Imaging.* 2016
3. Wolsztynski, et al. Localized metabolic gradient as an independent prognostic variable from FDG-PET in sarcoma. *SNMMI.* 2017
4. Prasanna, et al. Co-occurrence of Local Anisotropic Gradient Orientations (CoLIAGE): A new radiomics descriptor. *Sci Rep.* 2016



Clinical data

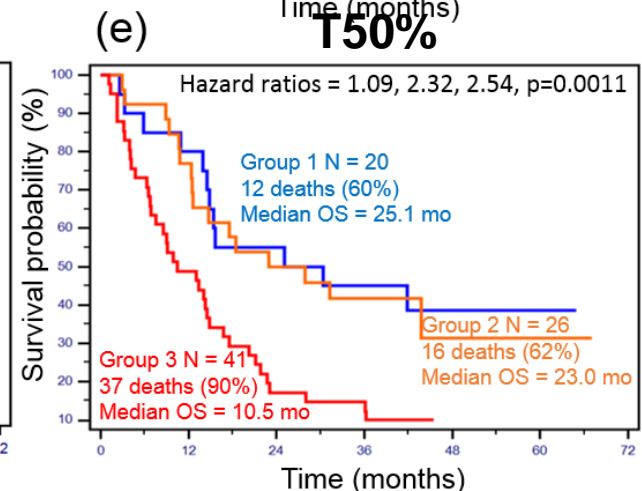
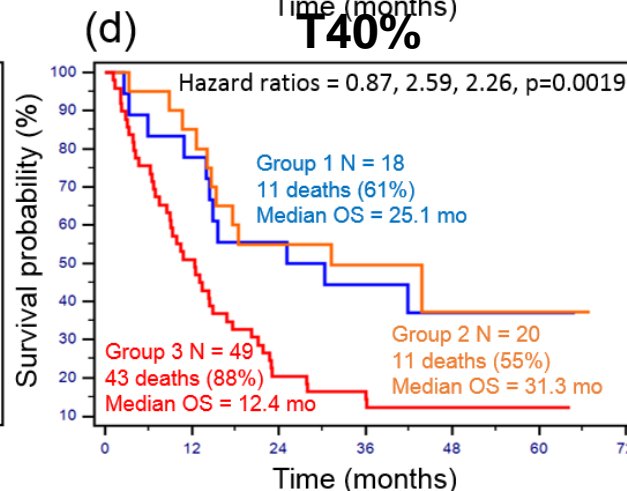
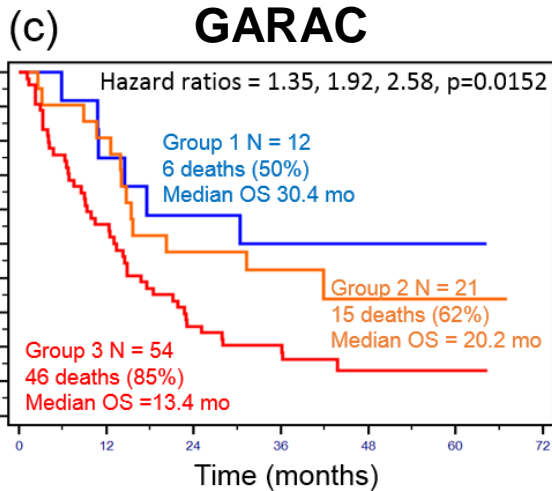
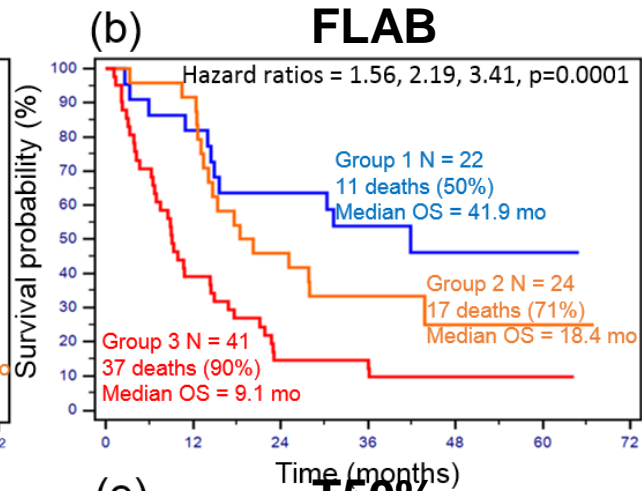
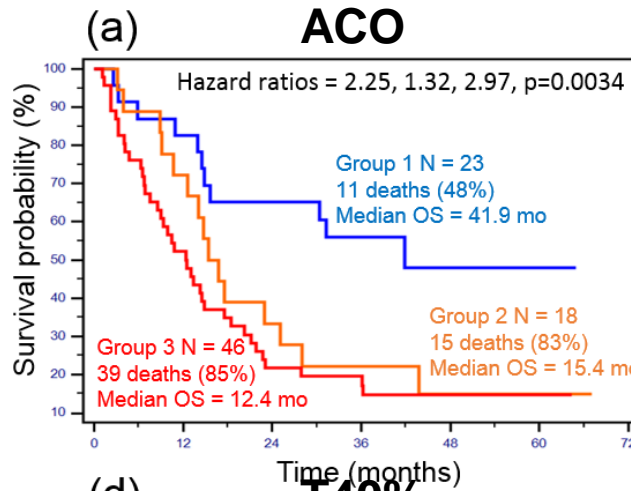


Genomics (and other -omics)



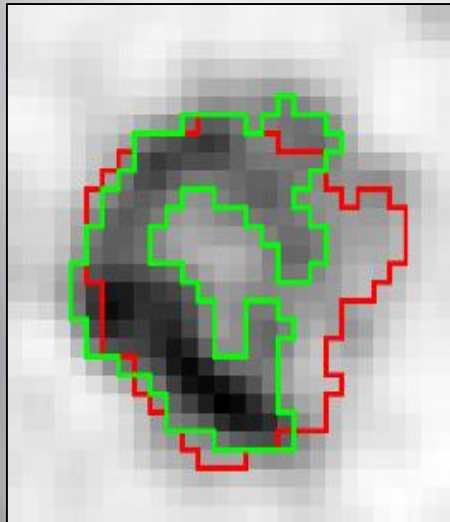
Segmentation step: how critical for radiomics?

87 NSCLC patients
(stage II-III)

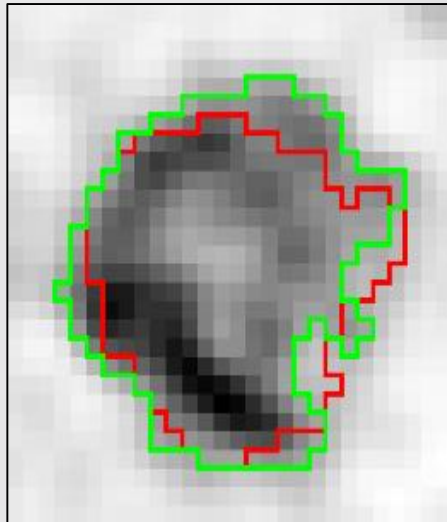




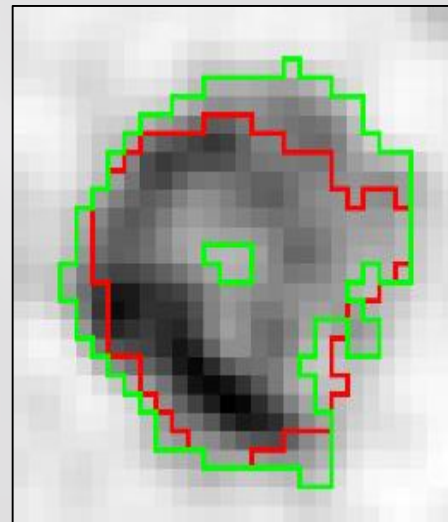
- Segmentation step: how critical for radiomics?
 - Potential solutions:
 - Use ensemble / consensus methods (e.g. STAPLE)¹



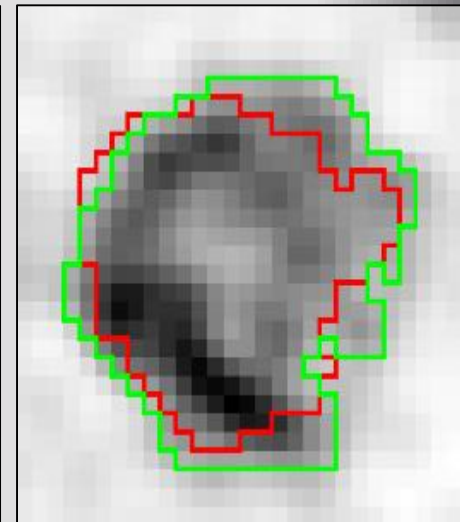
T40



FLAB



CNN



STAPLE
consensus



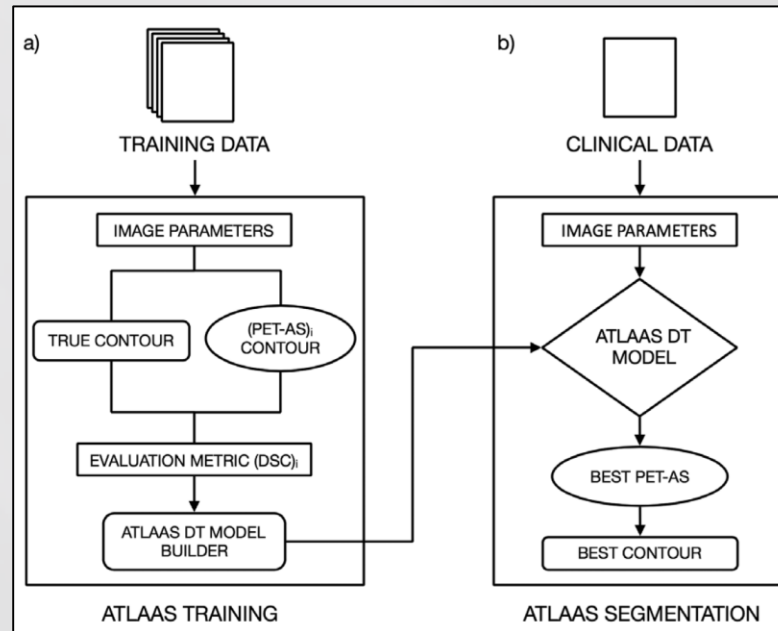
1. Hatt, *et al.* The first MICCAI challenge on PET tumor segmentation. *Med Image Anal.* 2018
2. Berthon, *et al.* ATLAAS: an automatic decision tree-based learning algorithm for advanced image segmentation in positron emission tomography. *Phys Med Biol* 2016



Segmentation step: how critical for radiomics?

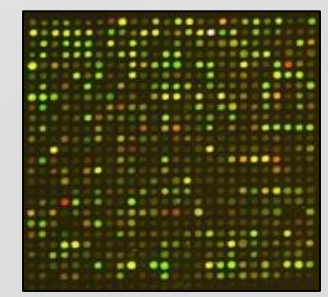
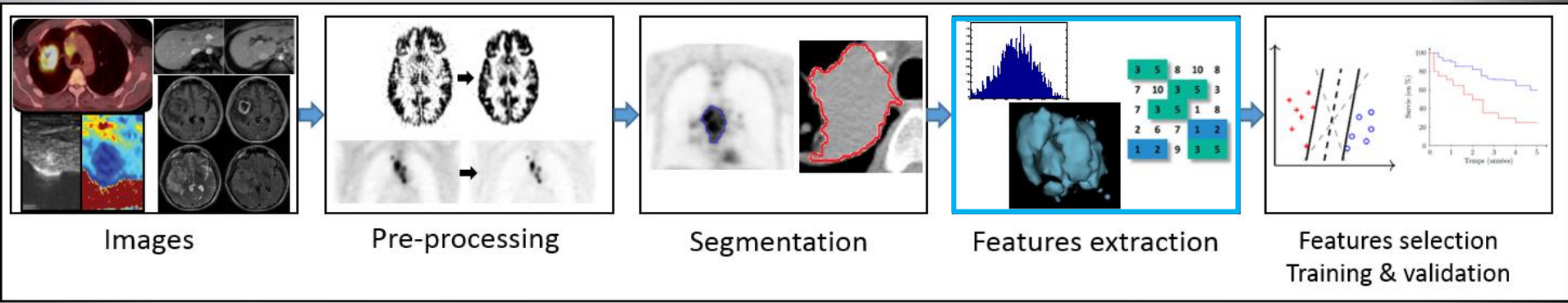
- Potential solutions:

- Use ensemble / consensus methods (e.g. STAPLE)¹
- Use machine learning models that select the best method for a given configuration (e.g. ATLAAS)²





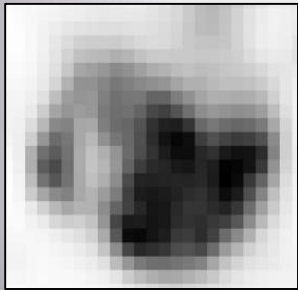
Clinical data



Genomics (and other -omics)

- Workflow complexity

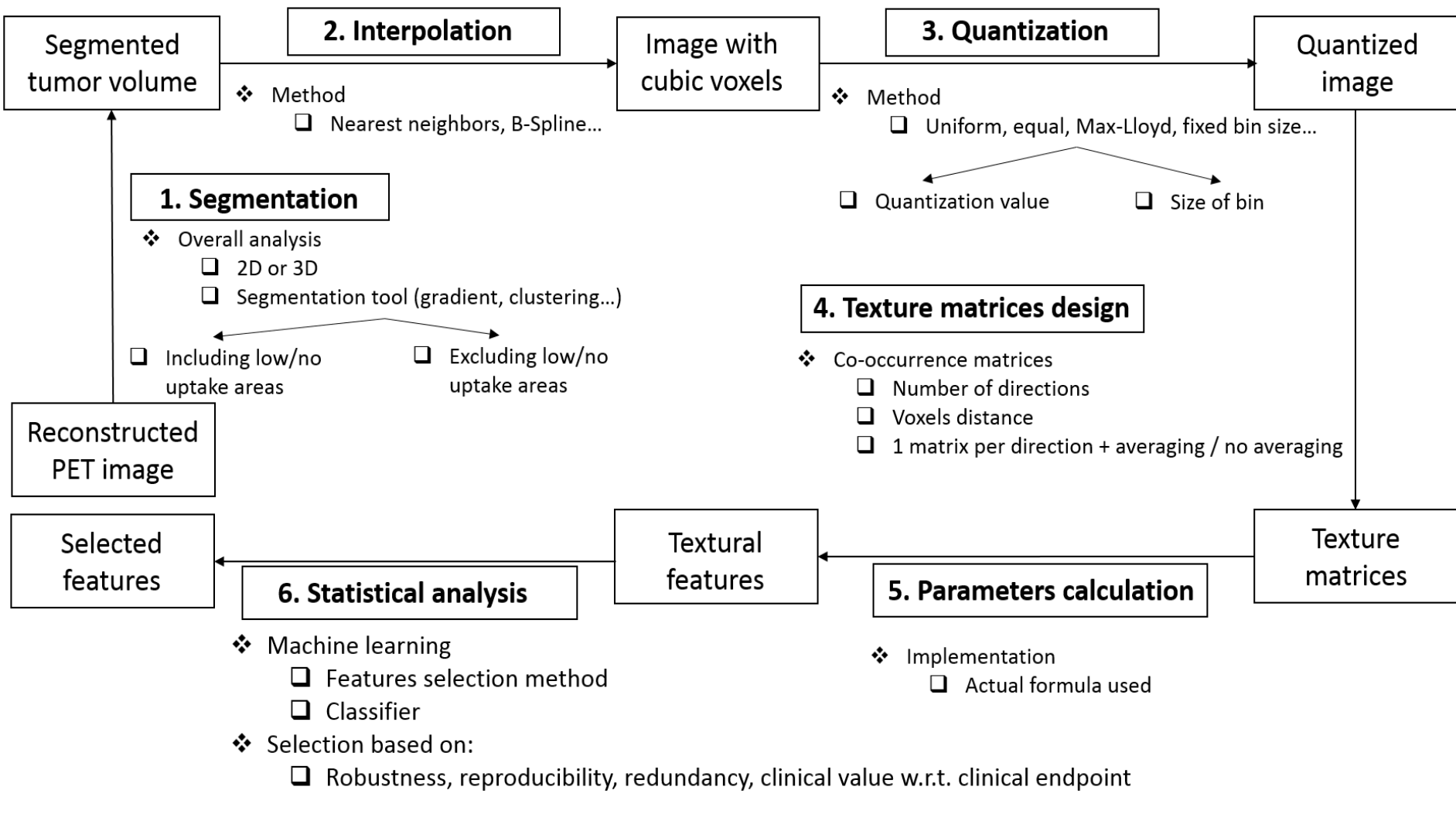
PET image

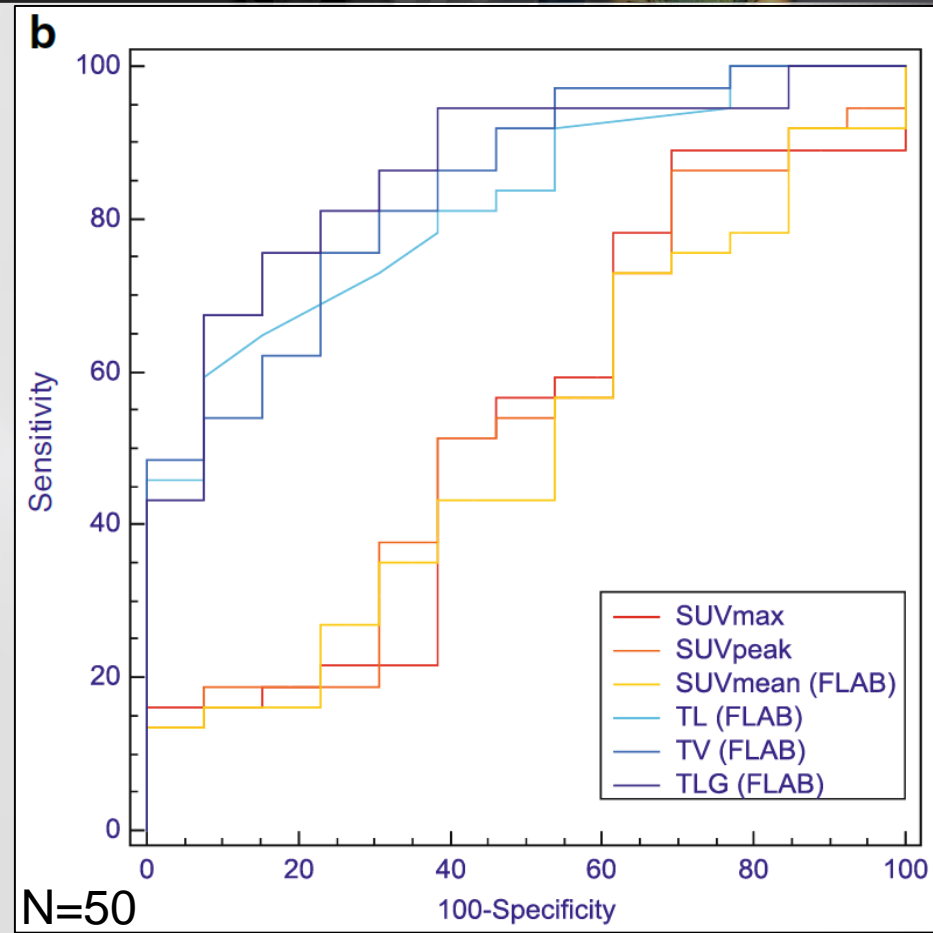
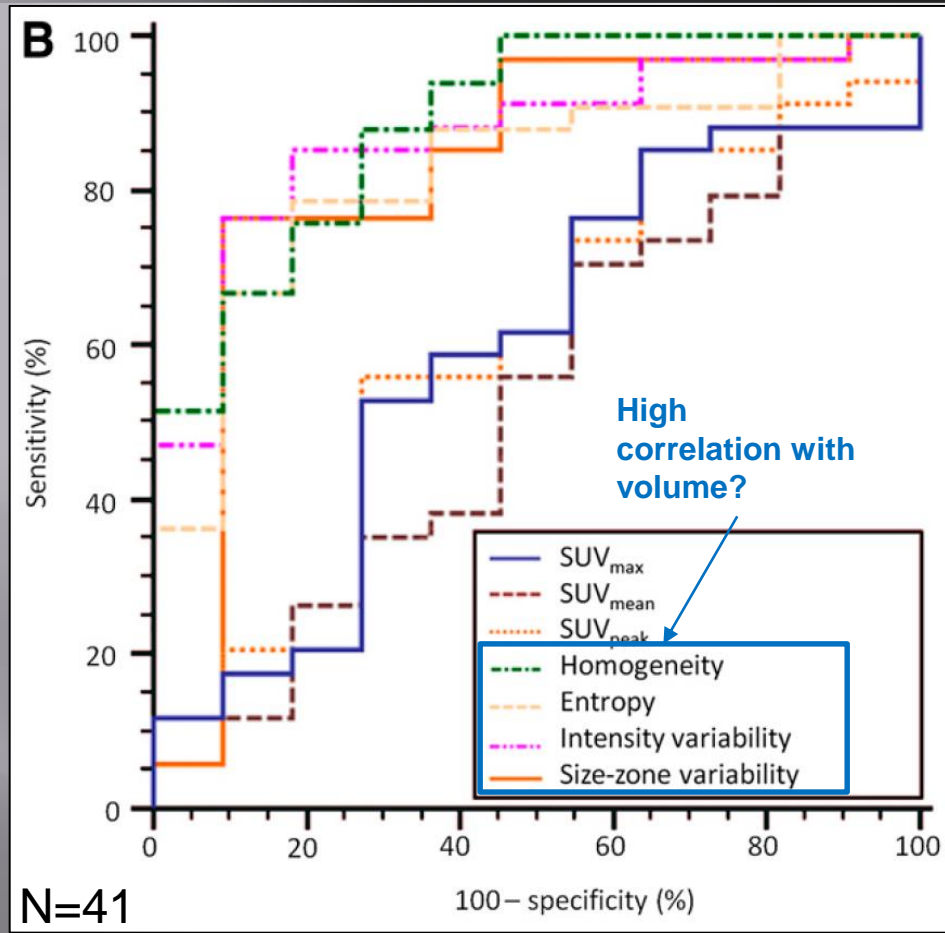


« Let's compute some textural features! »

Useful
quantification of
heterogeneity







FDG PET, esophageal cancer patients

Tixier, *et al.* Intratumor heterogeneity characterized by textural features on baseline ¹⁸F-FDG PET images predicts response to concomitant radiochemotherapy in esophageal cancer. *J Nucl Med* 2011

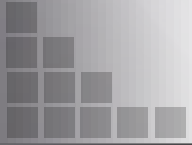
Hatt, *et al.* Baseline ¹⁸F-FDG PET image-derived parameters for therapy response prediction in oesophageal cancer. *Eur J Nucl Med Mol Imaging* 2011

Table 2 Correlations (Pearson coefficients) between parameters derived from FLAB delineations on noncorrected PET images. Significant correlation are shown in bold

Parameter	SUV _{mean}	MATV	Entropy	Homogeneity	Dissimilarity	Intensity variability	Size-zone variability	Zone percentage	High intensity emphasis	Area under the curve of the cumulative histogram
SUV _{mean}	1.00	0.20	0.30	-0.10	-0.02	0.08	0.09	-0.40	0.40	-0.50
MATV	1.00	1.00	0.82	0.69	-0.77	0.97	-0.16	-0.70	-0.22	0.07
Entropy			1.00	0.60	-0.80	0.77	-0.25	-0.90	-0.08	-0.07
Homogeneity				1.00	-0.93	0.80	-0.36	-0.42	-0.67	0.59
Dissimilarity					1.00	-0.83	0.41	0.60	0.58	-0.45
Intensity variability						1.00	-0.25	-0.62	-0.41	0.28
Size-zone variability							1.00	0.24	0.43	-0.32
Zone percentage								1.00	-0.18	0.32
High intensity emphasis									1.00	-0.97
Area under the curve of the cumulative histogram										1.00



Parameter	FT42%	AT	FLAB	FLAB PVC
SUV _{mean}	0.66	0.65	0.64	0.60
MATV	0.84	0.87	0.89	0.87
Entropy	0.84	0.86	0.88	0.85
Homogeneity	0.74 ^a	0.82	0.86 ^a	0.87
Dissimilarity	0.74 ^a	0.81	0.85 ^a	0.88
Intensity variability	0.85	0.87	0.90	0.88
Size-zone variability	0.66	0.70	0.72	0.86
Zone percentage	0.74	0.78	0.81	0.82
High intensity emphasis	0.59	0.65	0.65 ^a	0.83 ^a
Area under the curve of the cumulative histogram	0.56	0.60	0.60 ^a	0.77 ^a



CONCLUSION

Each PET-imaged tumor is a single sampling of all radioactivities that are physically and biologically permissible for that particular scanner–tumor combination. Because image heterogeneity statistics accrue manifestations of possibilities, it is the very nature of these statistics to reflect small sample sizes. Thus, inclusion of small tumor volumes necessarily biases tracer uptake heterogeneity studies toward statistically significant differences even when no difference in uptake exists. We have argued that this bias is lessened if all ROIs included in comparative heterogeneity analyses are above a minimum number of voxels. We have described a technique for computing this number that, when applied to our specific ^{18}F -FDG PET image data, yields a minimum comparison volume of 45 cm^3 .

Brooks, *et al.* The effect of small tumor volumes on studies of intratumoral heterogeneity of tracer uptake. *J Nucl Med* 2014

Example Heterogeneity Statistic

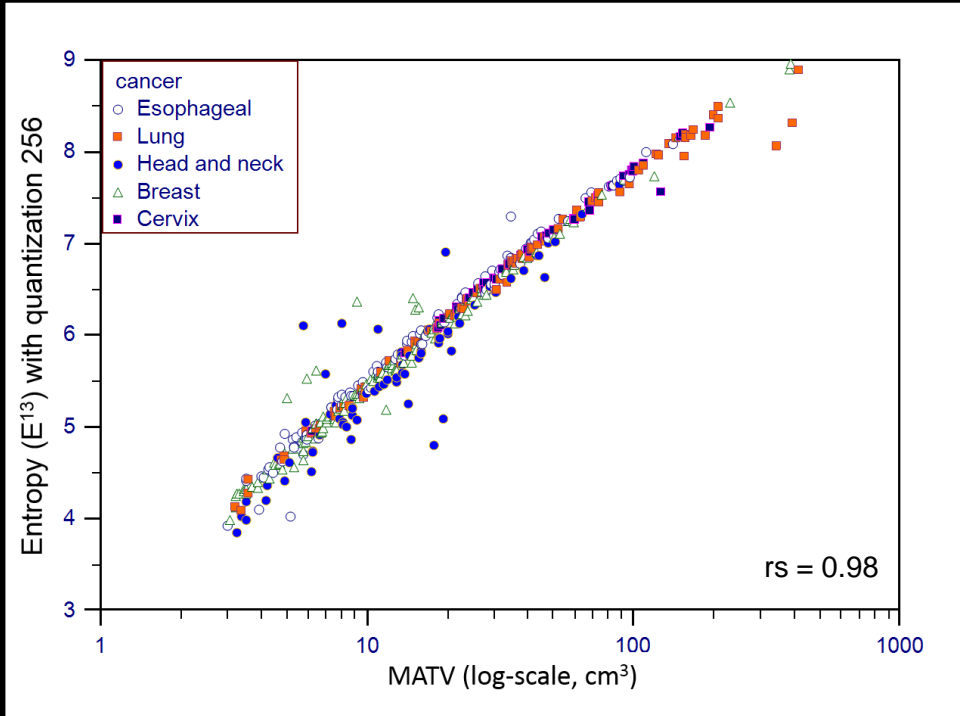
We computed the local information entropy of a 2-dimensional image as described by Haralick et al. (13). In brief, the cooccurrence matrix describes the probability p that a pixel of a shade i occurs next to a pixel of shade j . This matrix can be computed for various directions, pixel separations, and bit depths. We computed the horizontal and vertical cooccurrence matrices for the nearest pixel neighbors of 8-bit gray-scale images. From each of these matrices, the local entropy

$$h = - \sum_{j=103}^{255} \sum_{i=103}^{255} p(i,j) \ln p(i,j) \quad \text{Eq. 1}$$

was computed for each direction and then root-mean-square-averaged to obtain a single local entropy value. The limits on the summations reflect the 40% clinical threshold within the 8-bit (0–255) color scale.

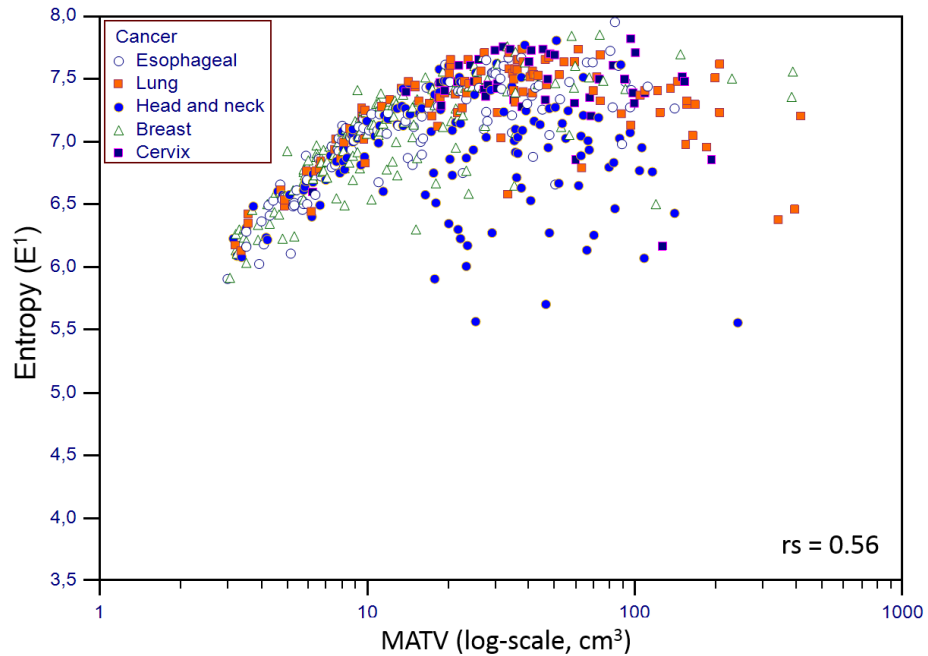
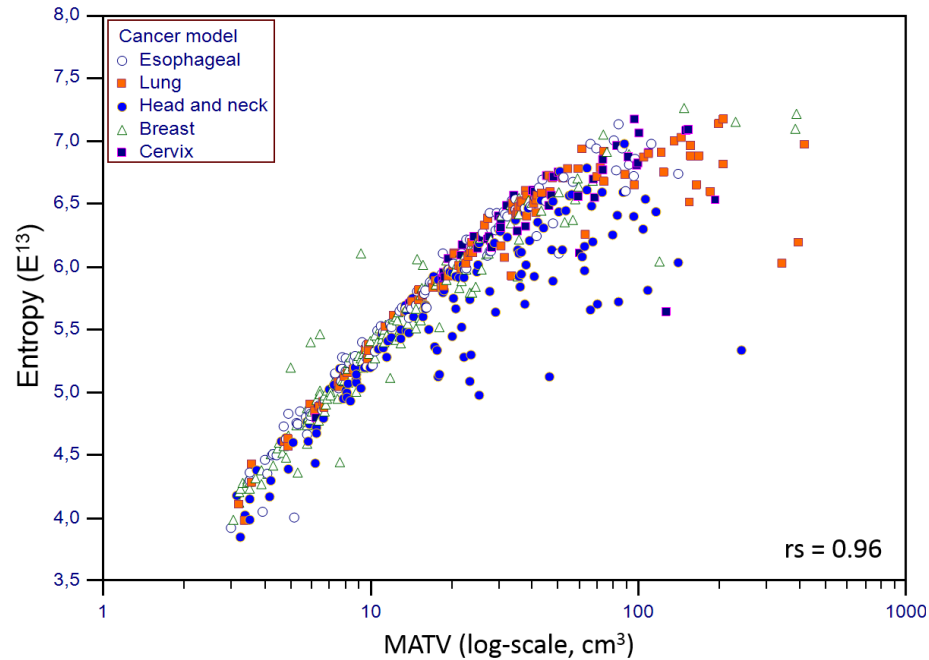
- A single texture: entropy_{GLCM}
- Calculated following one single workflow:
 - Linear discretization into 152 bins
 - 2 GLCM matrices for 2 directions (vertical+horizontal) followed by averaging

256 → 64 grey-levels

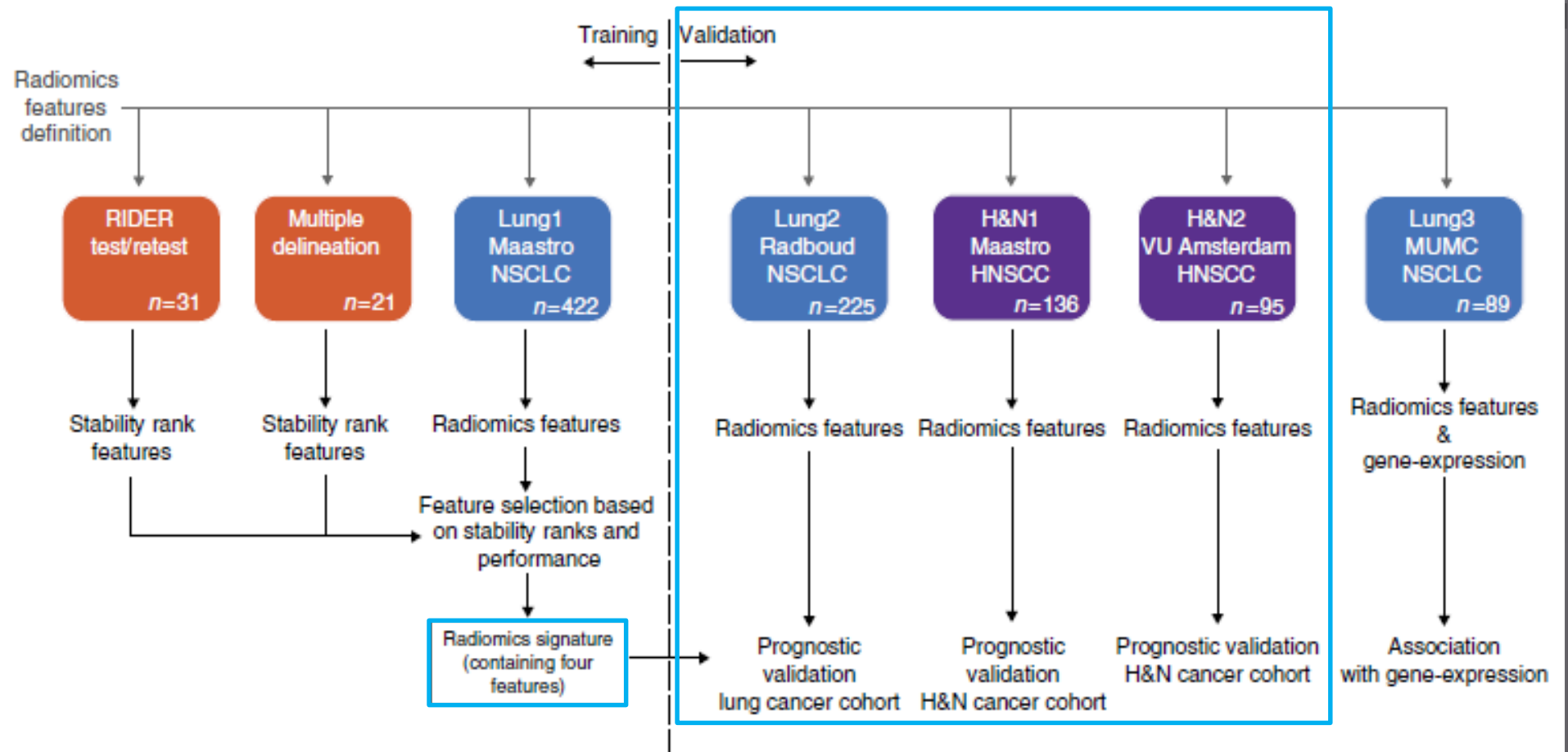


256 → 64 grey-levels

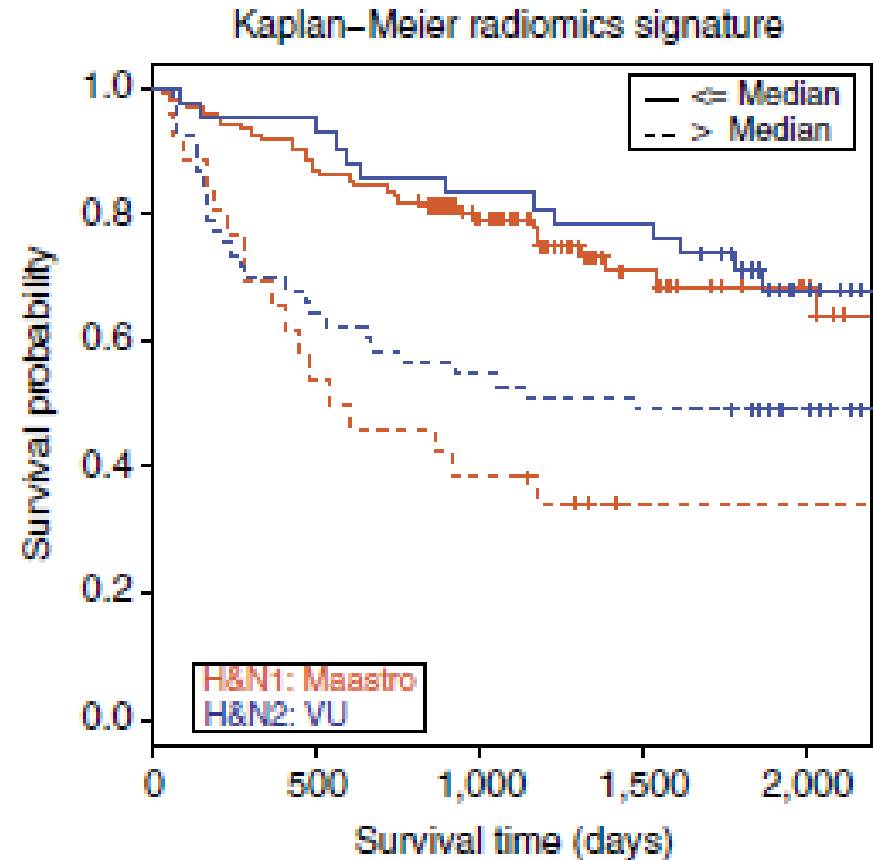
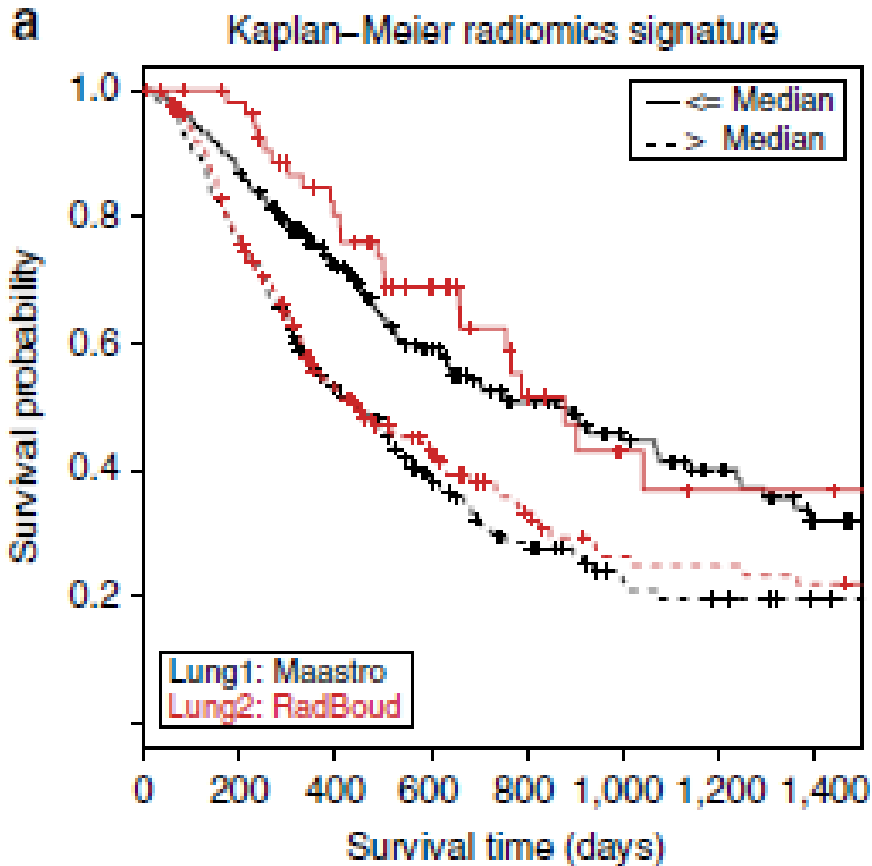
13 GLCMs followed by averaging
→ 1 GLCM (13 directions)



Hatt, *et al.* ^{18}F -FDG PET uptake characterization through texture analysis: investigating the complementary nature of heterogeneity and functional tumor volume in a multi-cancer site patient cohort. *J Nucl Med* 2015



Intensity	Shape	Textural	Textural (wavelet)
Energy	Compactness	Grey-level non-uniformity	GLNU in HLH subband



Intensity	Shape	Textural	Textural (wavelet)
Energy	Compactness	Grey-level non-uniformity	GLNU in HLH subband

“(...) shown for the first time the translational capability of radiomics in two cancer types (...) radiomics quantifies a general prognostic cancer phenotype that likely can broadly be applied to other cancer types”



Supplemental table (C-index)				TNM-	Volume-
Dataset	TNM	Volume	Radiomics	Radiomics	Radiomics
Lung2	0.60	0.63	<u>0.65</u>	0.64	<u>0.65</u>
H&N1	0.69	0.68	<u>0.69</u>	0.70	<u>0.69</u>
H&N2	0.66	0.65	<u>0.69</u>	0.69	<u>0.68</u>

Spearman rank correlation with volume (N=300 H&N cancer patients):
 PET: energy: 0.73, compactness: 0.98, GLNU: 0.99, GLNU_HLH: 0.89
 CT: energy: 0.71, compactness: 0.94, GLNU: 0.98, GLNU_HLH: 0.95

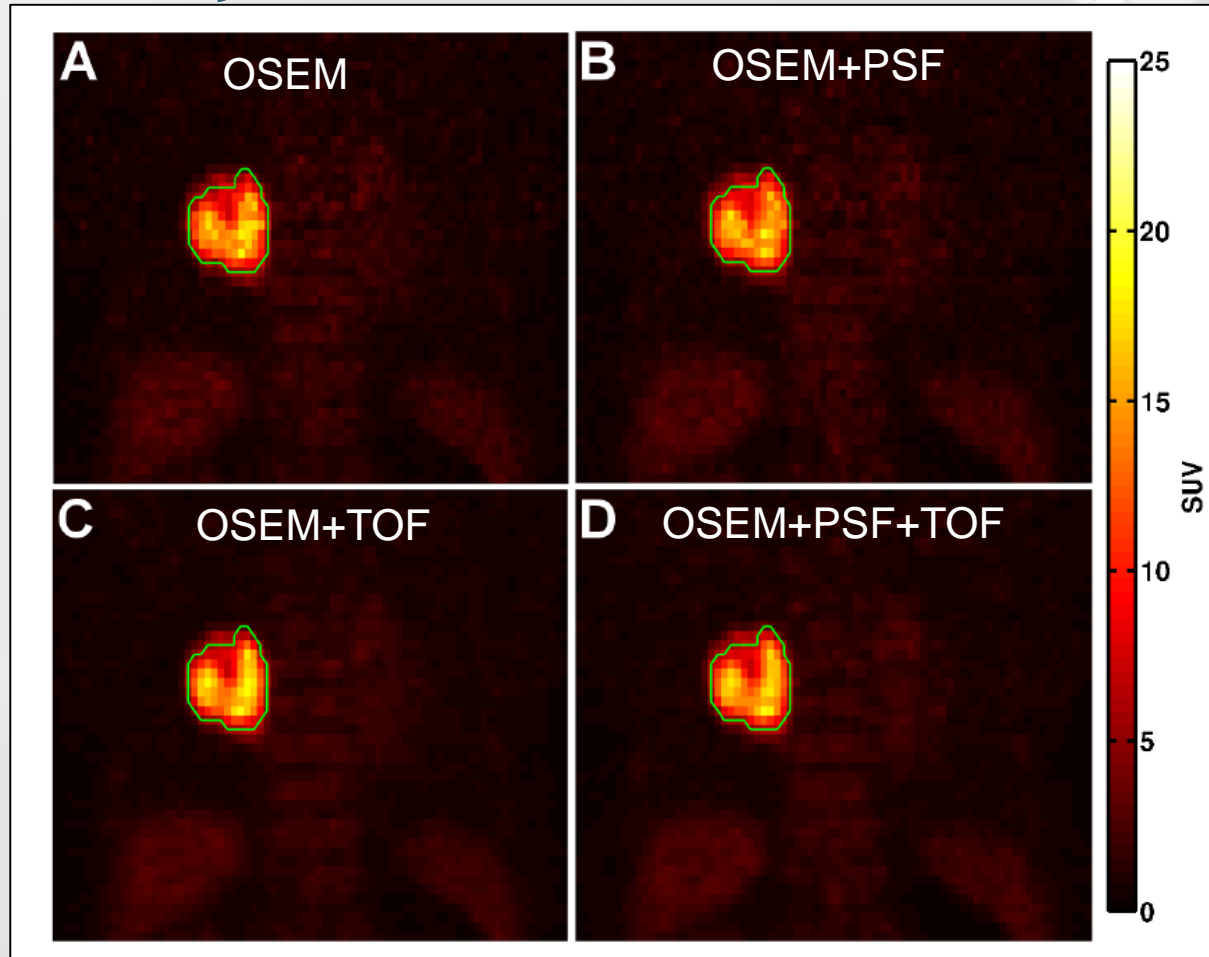
Dependency on reconstruction: PET

Image #	Acq. Mode	Grid-Size	Recon. Alg	Iter. number	Post-filter width (mm)	Legend
1	2D	128×128	OSEM	2	3	2D-128-OSEM2-3mm
2	2D	128×128	OSEM	2	5	2D-128-OSEM2-5mm
3	2D	128×128	OSEM	4	5	2D-128-OSEM4-5mm
4	2D	256×256	OSEM	2	3	2D-256-OSEM2-3mm
5	2D	256×256	OSEM	2	5	2D-256-OSEM2-5mm
6	3D	128×128	ITER	2	3	3D-128-ITER2-3mm
7	3D	128×128	ITER	2	6	3D-128-ITER2-6mm
8	3D	128×128	ITER	4	6	3D-128-ITER4-6mm
9	3D	256×256	ITER	2	3	3D-256-ITER2-3mm
10	3D	256×256	ITER	2	6	3D-256-ITER2-6mm

Acq. Mode = acquisition mode; Recon. Alg = reconstruction algorithm; Iter = iteration.



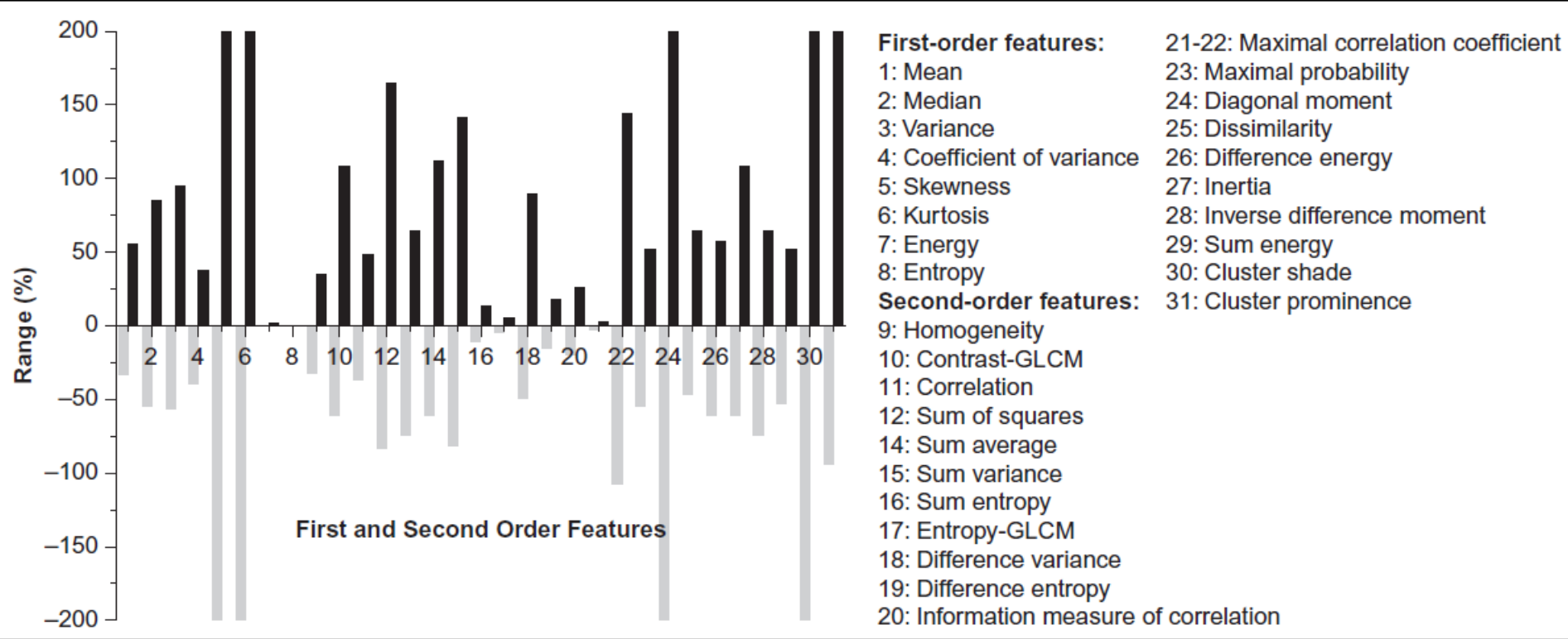
Dependency on reconstruction: PET



Gavalis, *et al.* Variability of textural features in FDG PET images due to different acquisition modes and reconstruction parameters. *Acta Oncol.* 2010

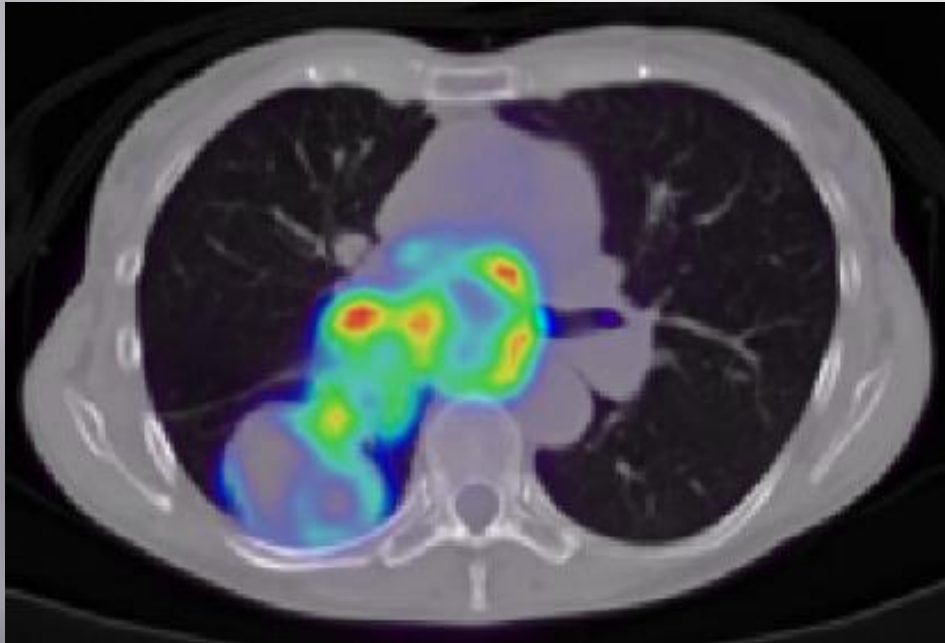
Yan, *et al.* Impact of Image Reconstruction Settings on Texture Features in 18F-FDG PET. *J Nucl Med* 2015

Dependency on reconstruction: PET

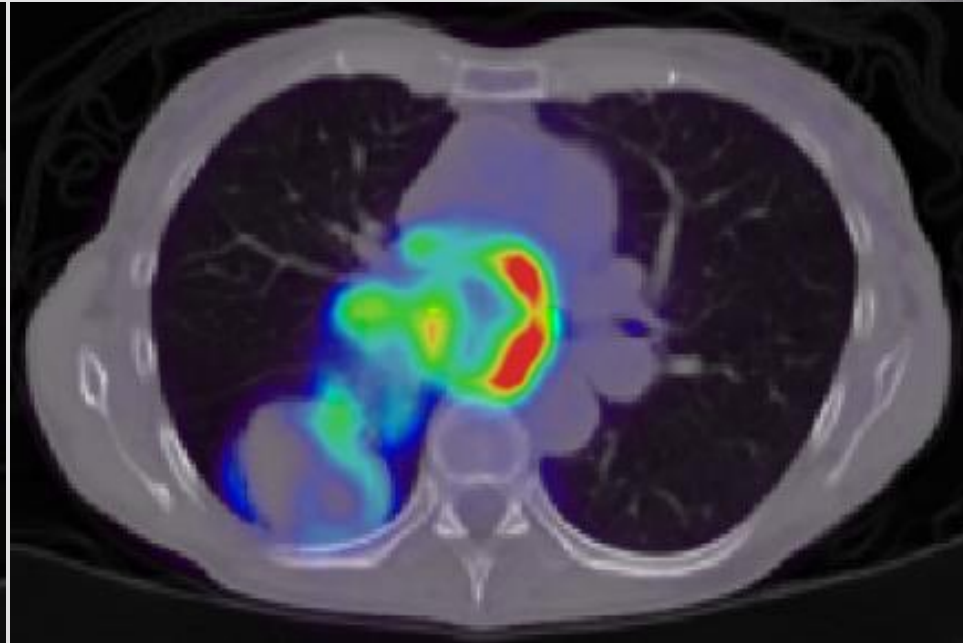


Multicentric data !

➤ Test-retest



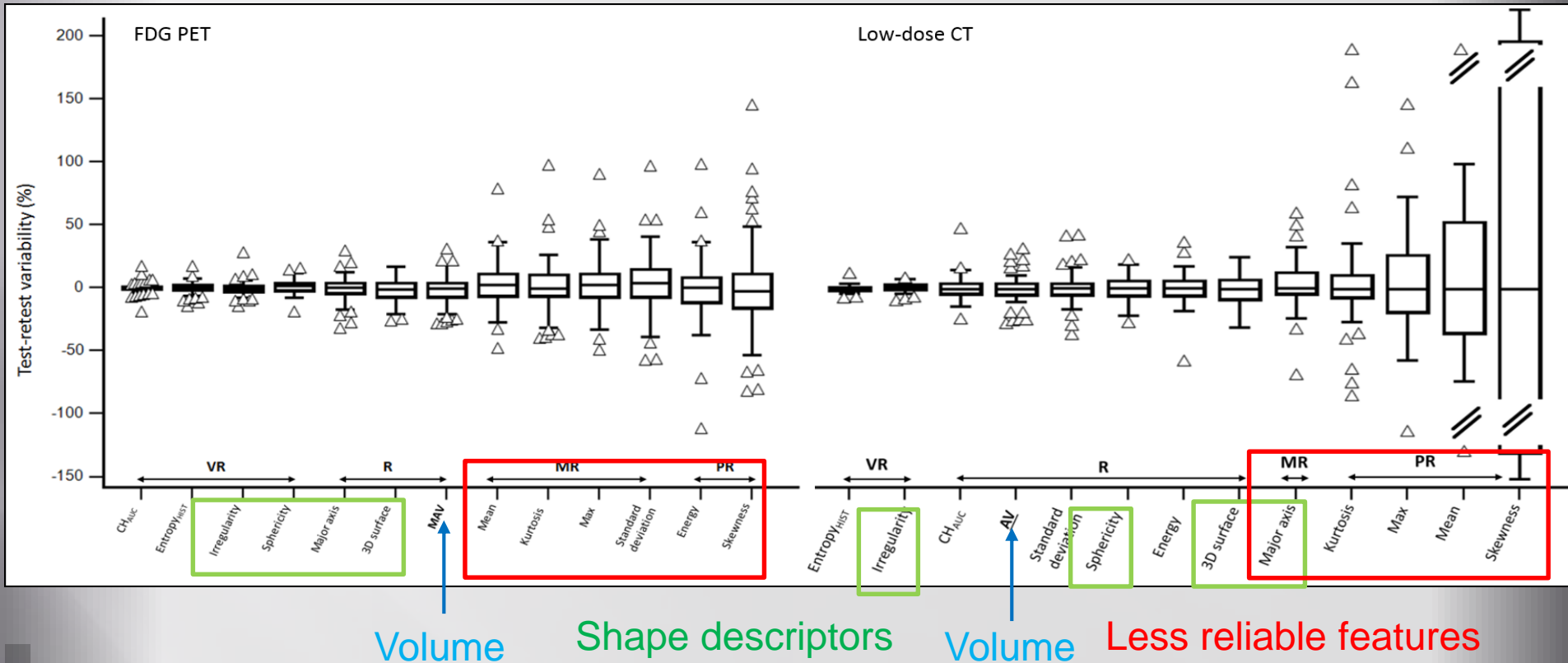
Test PET/CT



Re-test PET/CT



Test-retest



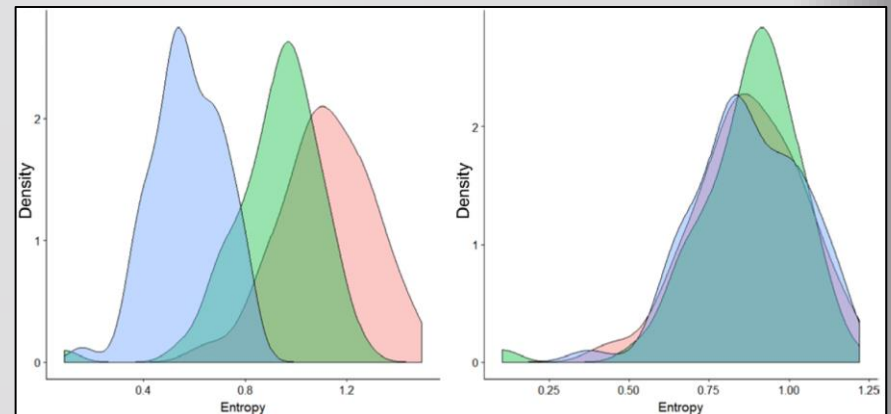
Tixier, *et al.* Reproducibility of tumor uptake heterogeneity characterization through textural feature analysis in 18F-FDG PET. *J Nucl Med.* 2012

Desseroit, *et al.* Reliability of PET/CT shape and heterogeneity features in functional and morphological components of Non-Small Cell Lung Cancer tumors: a repeatability analysis in a prospective multi-center cohort. *J Nucl Med* 2016

- Identify a compromise between:
 - Non reliable features (small pattern changes lead to large variability of the feature values)
 - and
 - Perfectly « robust » features (always give the same value, unable to capture patterns or changes)

- Solutions for multi-centric data:

- Use robust features only¹
- Pre-process images²
- Post-process features³



1. Upadhaya, *et al.* Prognosis classification in glioblastoma multiforme using multimodal MRI derived heterogeneity textural features: impact of pre-processing choices. *SPIE Medical Imaging* 2016

2. Vallières, *et al.* A radiomics model from joint FDG-PET and MRI texture features for the prediction of lung metastases in soft-tissue sarcomas of the extremities. *Phys Med Biol.* 2018

3. Orlhac, *et al.* A post-reconstruction harmonization method for multicenter radiomic studies in PET. *J Nucl Med.* 2018

- ◉ Lack of standardisation and reproducibility of results
 - Different definitions / nomenclature
 - Missing implementation details
 - Different implementations / software (black boxes)

This results in:

- Sometimes confusing literature
- Meta-analysis impossible (e.g. entropy in paper 1 may not be the same entropy as in paper 2 !)
- Difficult or even impossible to reproduce / confirm the results

◉ Nomenclature

Textural Parameters of Tumor Heterogeneity in ^{18}F -FDG PET/CT for Therapy Response Assessment and Prognosis in Patients with Locally Advanced Rectal Cancer

Ralph A. Bundschuh¹⁻³, Julia Dinges¹, Larissa Neumann¹, Martin Seyfried¹, Norbert Zsótér⁴, Laszló Papp⁴, Robert Rosenberg⁵, Karen Becker⁶, Sabrina T. Astner⁷, Martin Henninger⁸, Ken Herrmann², Sibylle I. Ziegler¹, Markus Schwaiger¹, and Markus Essler^{1,3}

¹Nuklearmedizinische Klinik und Poliklinik, Klinikum rechts der Isar der Technischen Universität München, Munich, Germany; ²Klinik und Poliklinik für Nuklearmedizin, Universitätsklinikum Würzburg, Wuerzburg, Germany; ³Klinik und Poliklinik für Nuklearmedizin, Universitätsklinikum Bonn, Bonn, Germany; ⁴Mediso Medical Imaging Systems Ltd., Budapest, Hungary; ⁵Chirurgische Klinik, Kantonsspital Baden, Baden, Switzerland; ⁶Institut für Pathologie, Klinikum rechts der Isar der Technischen Universität München, Munich, Germany; ⁷Klinik und Poliklinik für Radioonkologie und Strahlentherapie, Klinikum rechts der Isar der Technischen Universität München, Munich, Germany; and ⁸Institut für Röntgendiagnostik, Klinikum rechts der Isar der Technischen Universität München, Munich, Germany

➤ Nomenclature

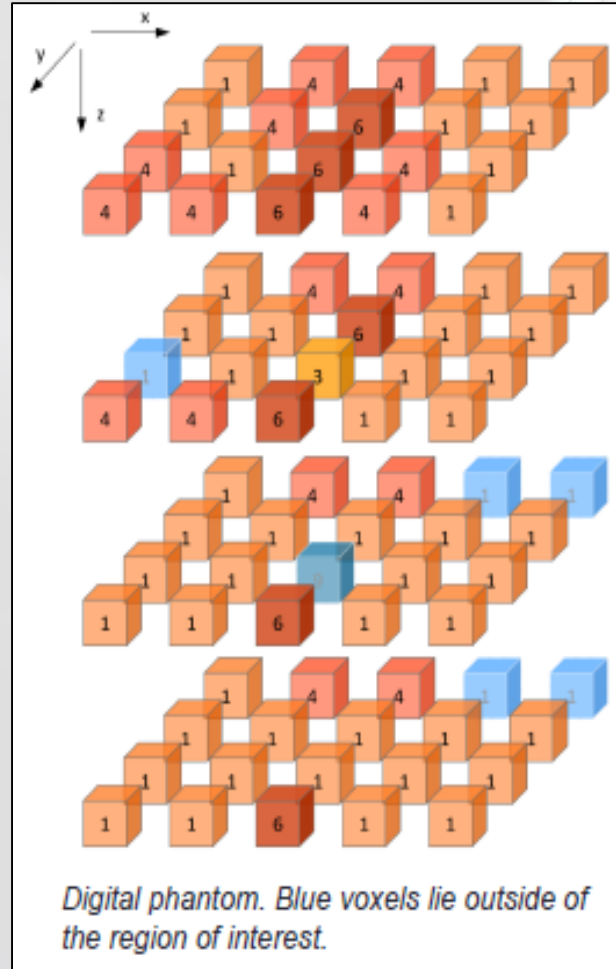
Parameter	AUC	95% confidence interval
SUV _{max}	0.52	0.32–0.71
<u>Skewness</u>	0.55	0.33–0.75
<u>Kurtosis</u>	0.61	0.39–0.81
SUV _{mean}	0.68	0.48–0.85
Diameter	0.68	0.48–0.85
<u>COV</u>	0.73	0.53–0.88
Volume	0.75	0.55–0.90
TLG	0.79	0.59–0.92

1st order features ≠ textural features !

Bundschuh, *et al.* Textural Parameters of Tumor Heterogeneity in ¹⁸F-FDG PET/CT for Therapy Response Assessment and Prognosis in Patients with Locally Advanced Rectal Cancer. *J Nucl Med.* 2014

Imaging biomarkers standardisation initiative

- 06/2016-02/2018
- 20 research groups, 8 countries:
 - USA
 - Germany
 - The Netherlands
 - France
 - Canada
 - United Kingdom
 - Italy
 - Switzerland

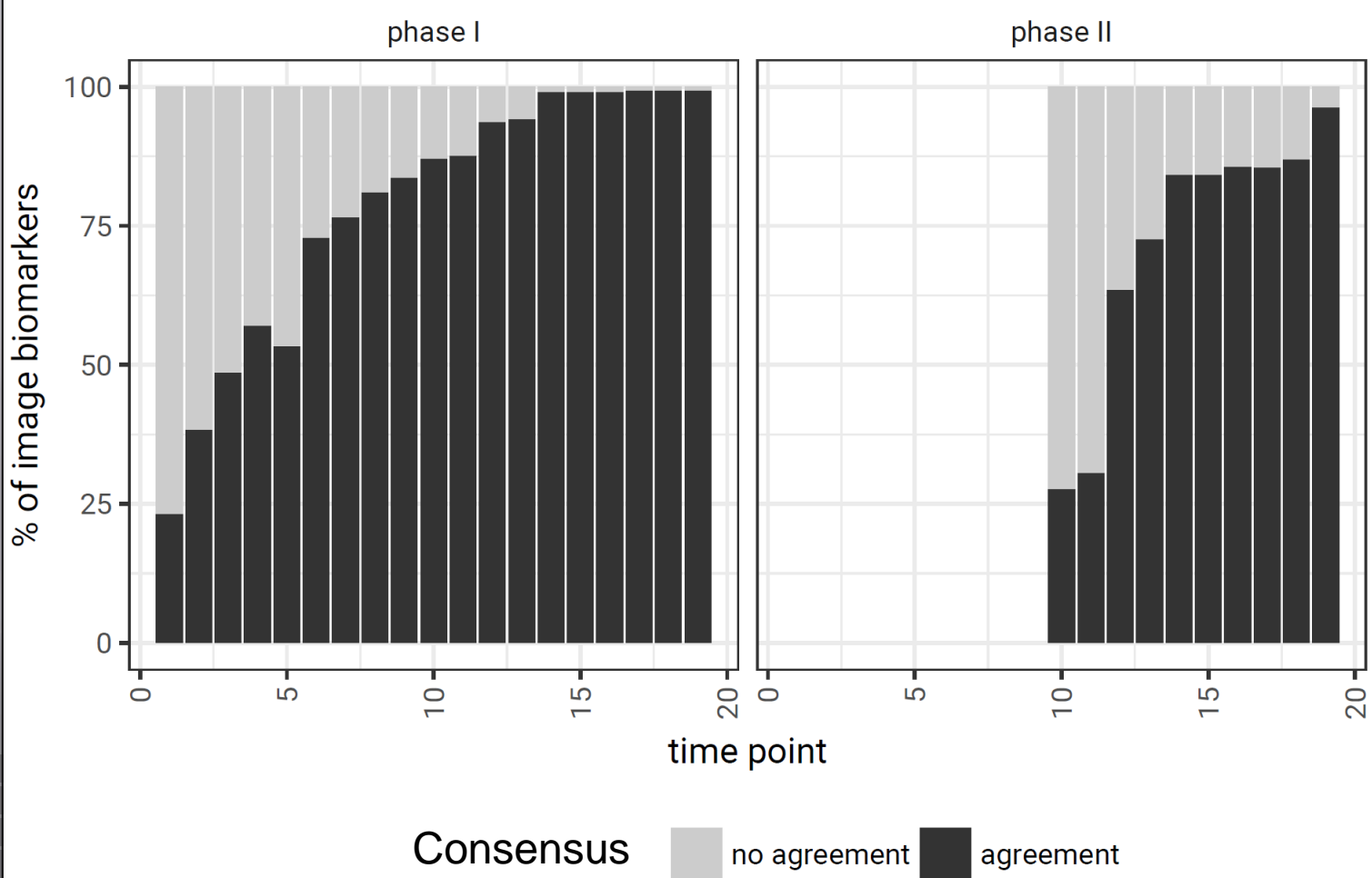


Participants

- Study leader: Alex Zwanenburg
- Cardiff University
Philip Whybra, Emiliano Spezi
- Dana Farber Cancer Institute and Brigham and Women's Hospital, Harvard University
Andriy Fedorov, Hugo Aerts
- Gemelli ART, Università Cattolica del Sacro Cuore
Jacopo Lenkovicz, Luca Boldrini, Nicola Dinapoli, Vincenzo Valentini
- German Cancer Research Center (DKFZ)
Michael Götz, Nils Gählerl, Fabian Isensee, Klaus H. Maier-Hein
- INSERM Brest, University of Brest
Marie-Charlotte Desseroit, Taman Upadhaya, Mathieu Hatt
- Leiden University Medical Center
Floris H.P. van Velden
- MAASTRO clinic, Maastricht University
Ralph T.H. Leijenaar, Philippe Lambin
- McGill University
Martin Vallières, Issam El Naqa
- Memorial Sloan Kettering Cancer Center
Aditya Apte
- Moffitt Cancer Center
Mahmoud A. Abdalah, Robert Gillies
- OncoRay – National Center for Radiation Research in Oncology and NCT Dresden
Alex Zwanenburg, Stefan Leger, Esther Troost, Christian Richter, Steffen Löck
- The Netherlands Cancer Institute (NKI)
Joost van Griethuysen, Cuong Viet Dinh, Ulrike van der Heide
- Universitätsklinikum Tübingen, Eberhard Karls University Tübingen
Jairo Socarras Fernandez, Daniela Thorwarth
- University Hospital Zürich, University of Zürich
Martha Bogowicz, Stephanie Tanadini-Lang, Matthias Guckenberger
- University of Bergen
Are Losnegård
- University of California, San Francisco
Olivier Morin
- University of Groningen, University Medical Center Groningen
Lisanne V. van Dijk, Jörn Beukinga, Nanna M. Sijtsma, Roel J.H.M. Steenbakkers, Ronald Boellaard



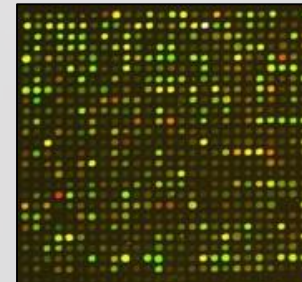
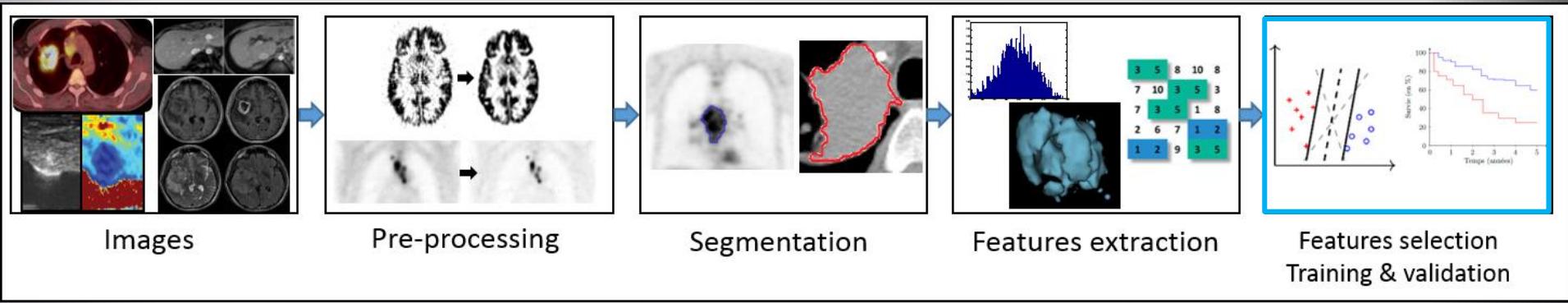
Imaging biomarkers standardisation initiative



- Participants**
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Clinical data



Genomics (and other -omics)

Inappropriate statistical analysis

Table 1. Statistical characteristics of the selected studies divided in three categories: A) Studies with multiple hypotheses testing only, B) studies employing both multiple hypothesis testing and the optimum cut-off approach and C) studies with multiple hypothesis testing, with or without the optimum cut-off approach, but with validation analysis.

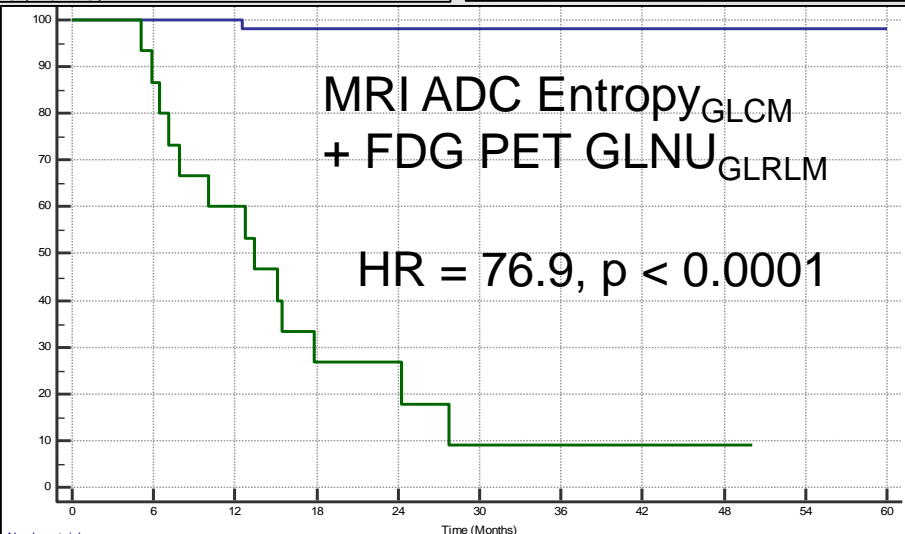
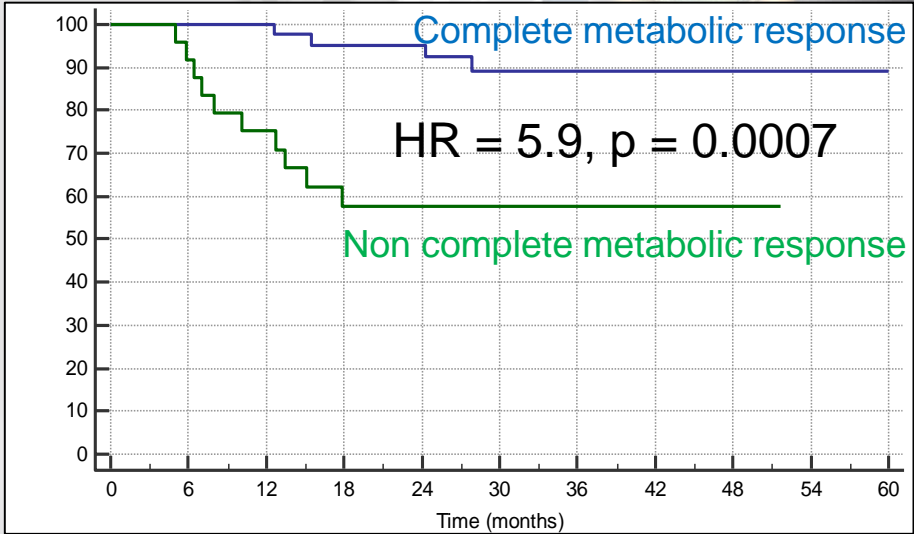
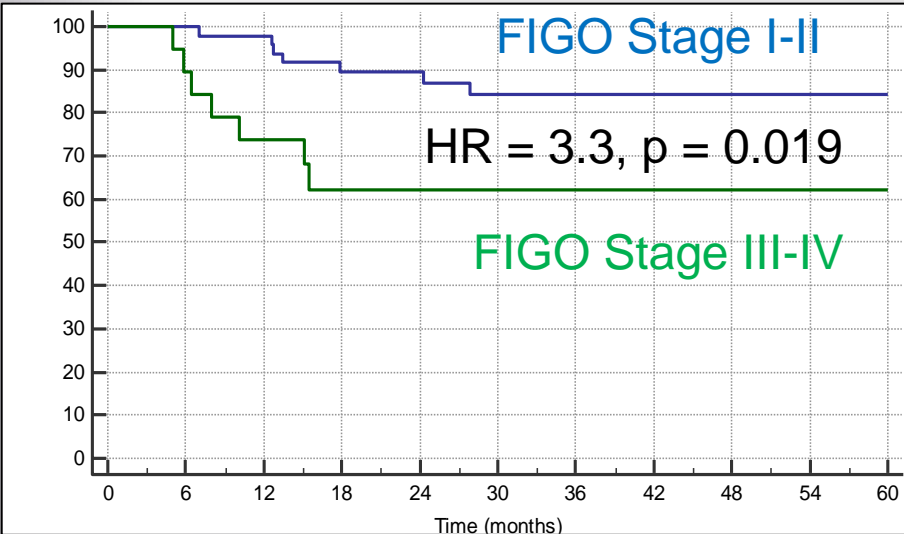
Category	Study	Multivariate analysis included volume	Optimum cut-off	Type I error adjustment	Validation dataset	cross correlation reported	Sample size	Hypotheses tested
A	Willaime [19]	Not applicable	No/Mean	No	No	Yes	12	68
	El Naqa [31]	NI*	Not clear	No	No	No	14/9	19
	Tixier [33]	NI	Not clear	No	No	Yes	41	54
	Yip [41]	No	No/Median	Yes [#]	No	No	36	90
B	Miles [30]	No	Yes	No	No	No	48	10
	Goh [32]	No	Yes	No	No	No	39	24
	Cook [29]	No	Yes	No	No	Yes	53	30
	Ganeshan [28]	No	Yes	No	No	Yes	21	15
	Ganeshan [34]	No	Yes	No	No	No	54	8
	Ng [36]	No	Yes	No	No	Yes	55	25
	Zhang [40]	Yes	Yes	No	No	No	72	40
C	Cheng [39]	Yes	Yes	No	No	Yes	70	59 [†]
	Vaidya [35]	Yes	No	No	LOOCV [†]	No	27	102
	Win [37]	No	Yes	No	Yes	No	66	12
	Ravanelli [38]	No	No/Median	No	LOOCV	No	53	16

* No information provided

[#]For multiple hypotheses tested

[†]Leave one out cross validation

[‡] Number is a conservative approximation due to the difficulty establishing the exact number of hypotheses tested



Cervical cancer
Chemoradiotherapy
Loco-regional control

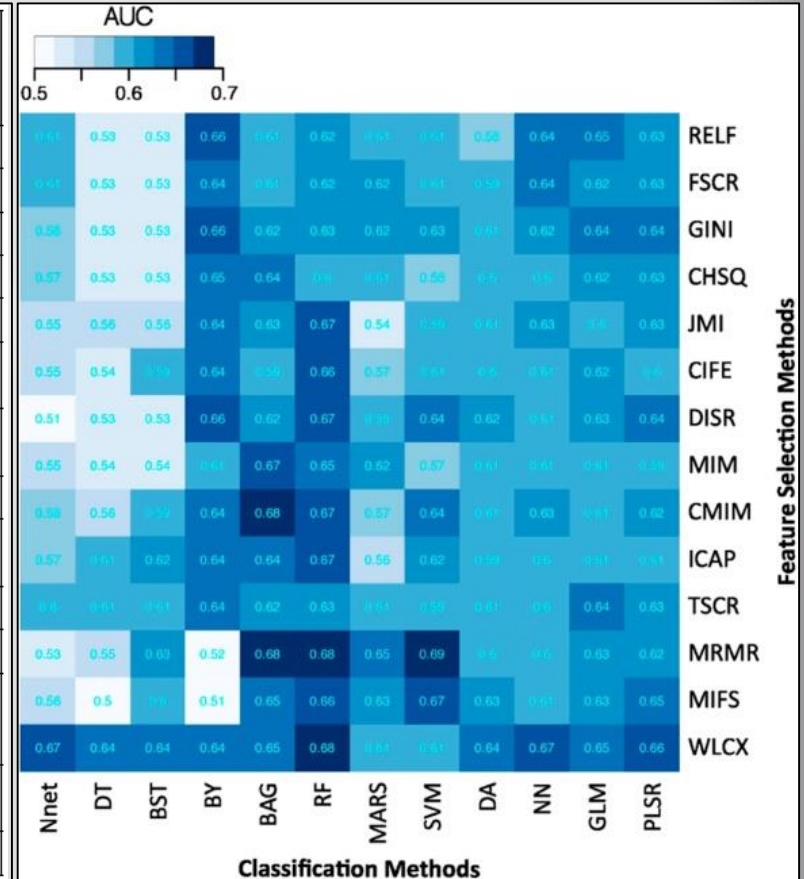
Radiomics

Challenges and issues: how to use machine learning?

Machine learning

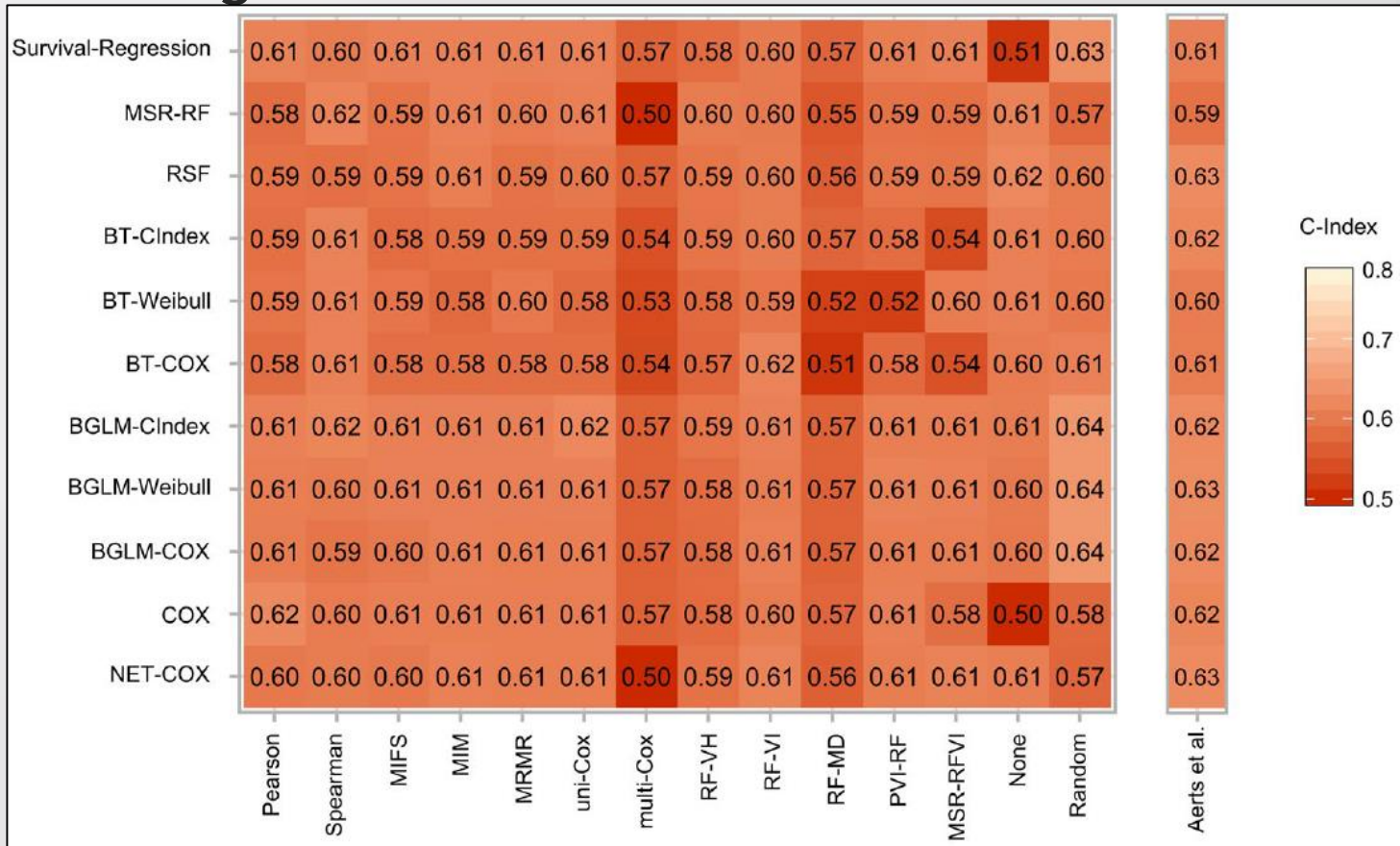
- Choosing a classifier/feature selection method?

Classification method acronym	Classification method name	Feature Selection method acronym	Feature selection method name
Nnet	Neural network	RELF	Relief
DT	Decision Tree	FSCR	Fisher score
BST	Boosting	GINI	Gini index
BY	Bayesian	CHSQ	Chi-square score
BAG	Bagging	JMI	Joint mutual information
RF	Random Forset	CIFE	Conditional infomax feature extraction
MARS	Multi adaptive regression splines	DISR	Double input symmetric relevance
SVM	Support vector machines	MIM	Mutual information maximization
DA	Discriminant analysis	CMIM	Conditional mutual information maximization
NN	Neirest neighbour	ICAP	Interaction capping
GLM	Generalized linear models	TSCR	T-test score
PLSR	Partial least squares and principal componenet regression	MRMR	Minimum redundancy maximum relevance
—	—	MIFS	Mutual information feature selection
—	—	WLCX	Wilcoxon



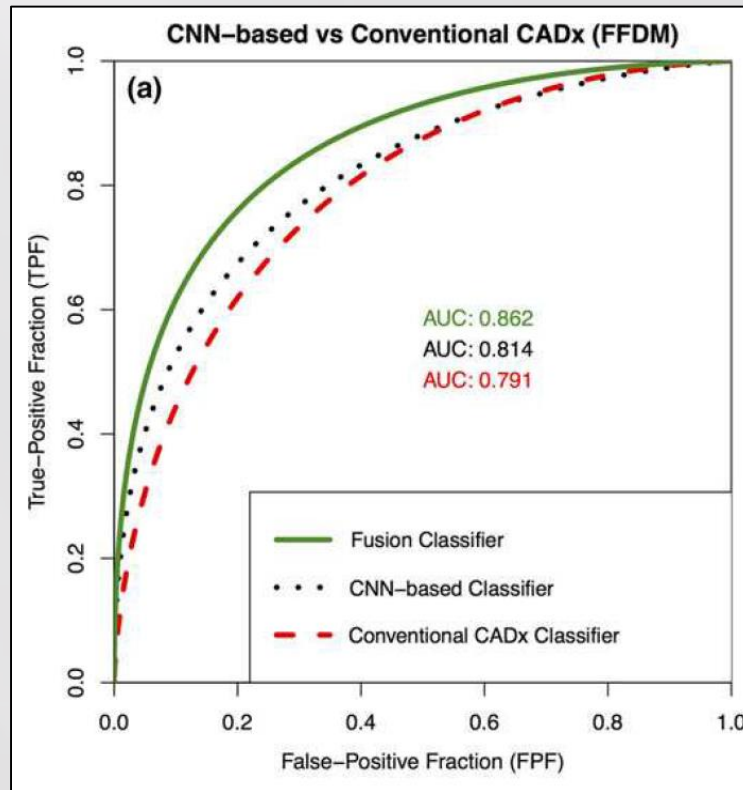
Machine learning

- Choosing a classifier/feature selection method?



Machine learning

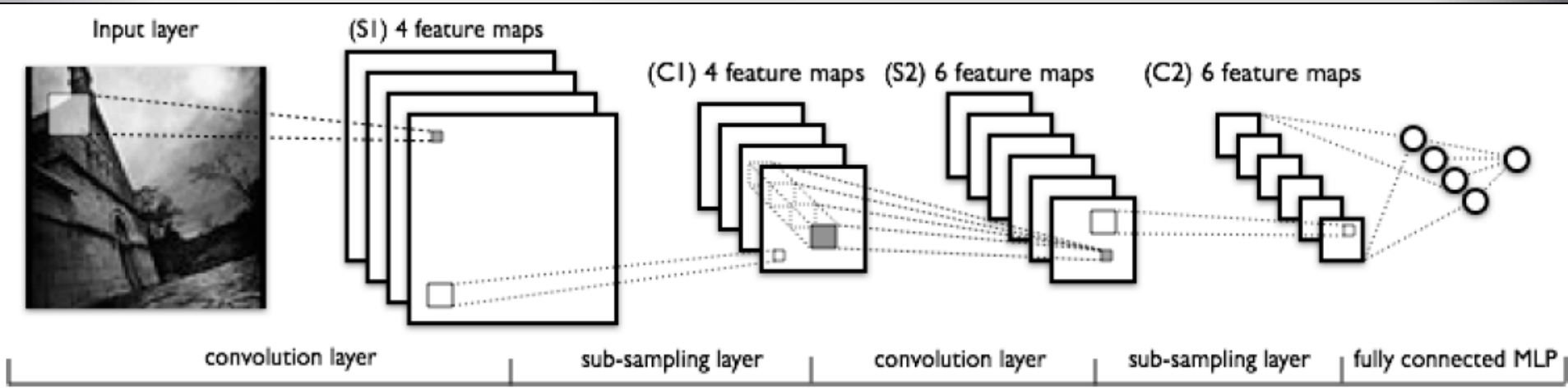
- Choosing a classifier/feature selection method?
 - Potential solution: ensemble methods



Antropova, *et al.* A deep feature fusion methodology for breast cancer diagnosis demonstrated on three imaging modality datasets. *Med Phys* 2017

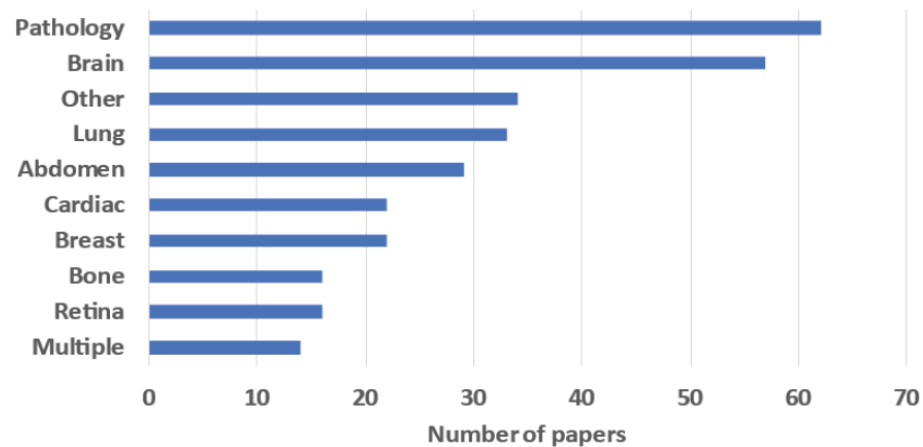
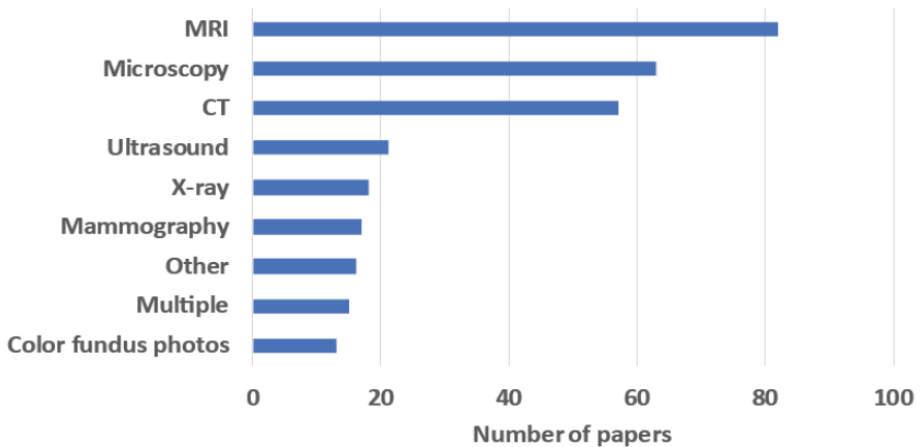
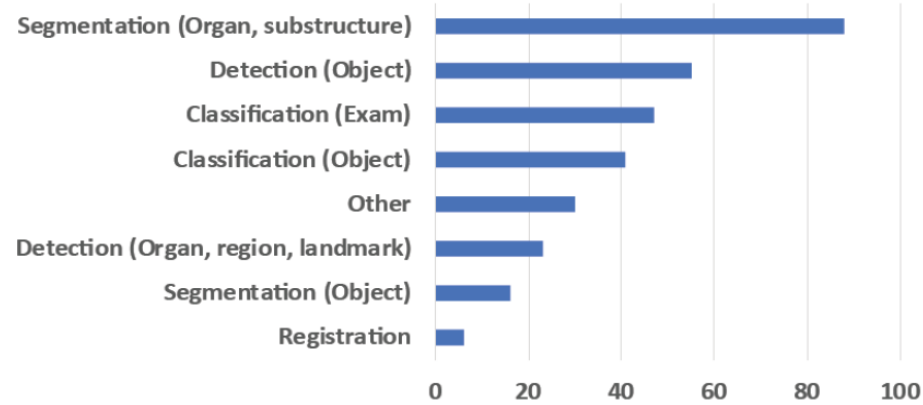
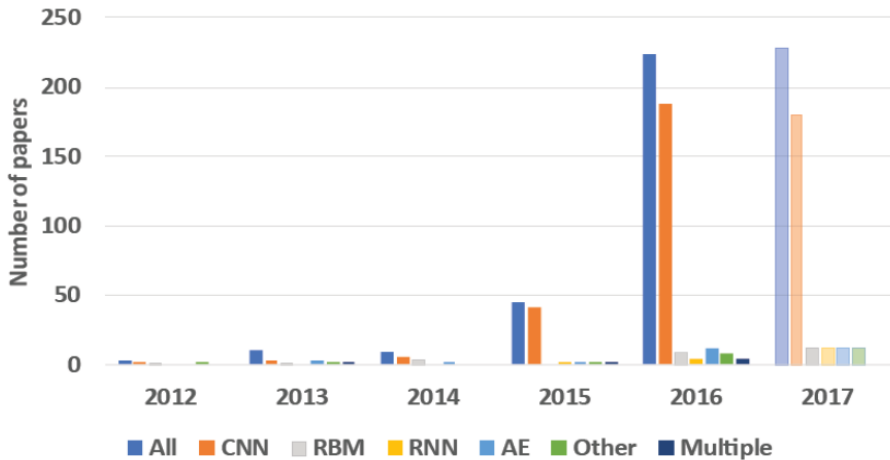
Deep learning

- Convolutional Neural Networks (CNN)



- Limitations (*a priori*)
 - Need (very) large datasets for efficient training
 - Black boxes that do not generate knowledge

Deep learning in medical imaging

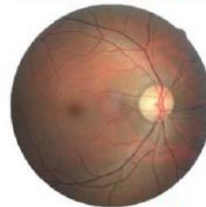
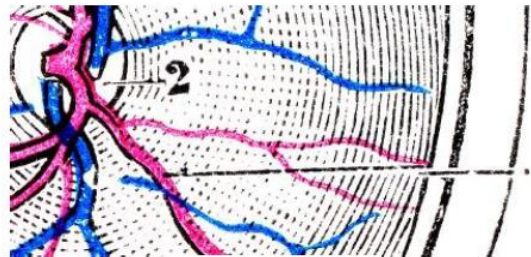
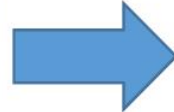


- Deep learning limitations?
 - Need for large datasets
 - Data augmentation
 - Transfer learning / fine-tuning



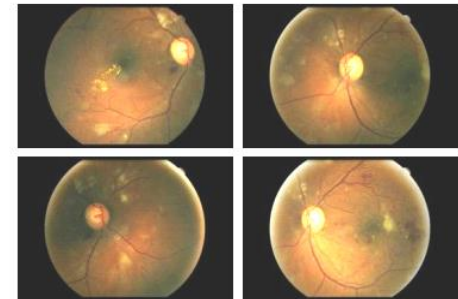
IMAGENET

(1.2 M images)



kaggle

(88,702 images)



OPHDIAT

(25,702 *groups* of images,
107,798 *images*)

• Deep learning limitations?

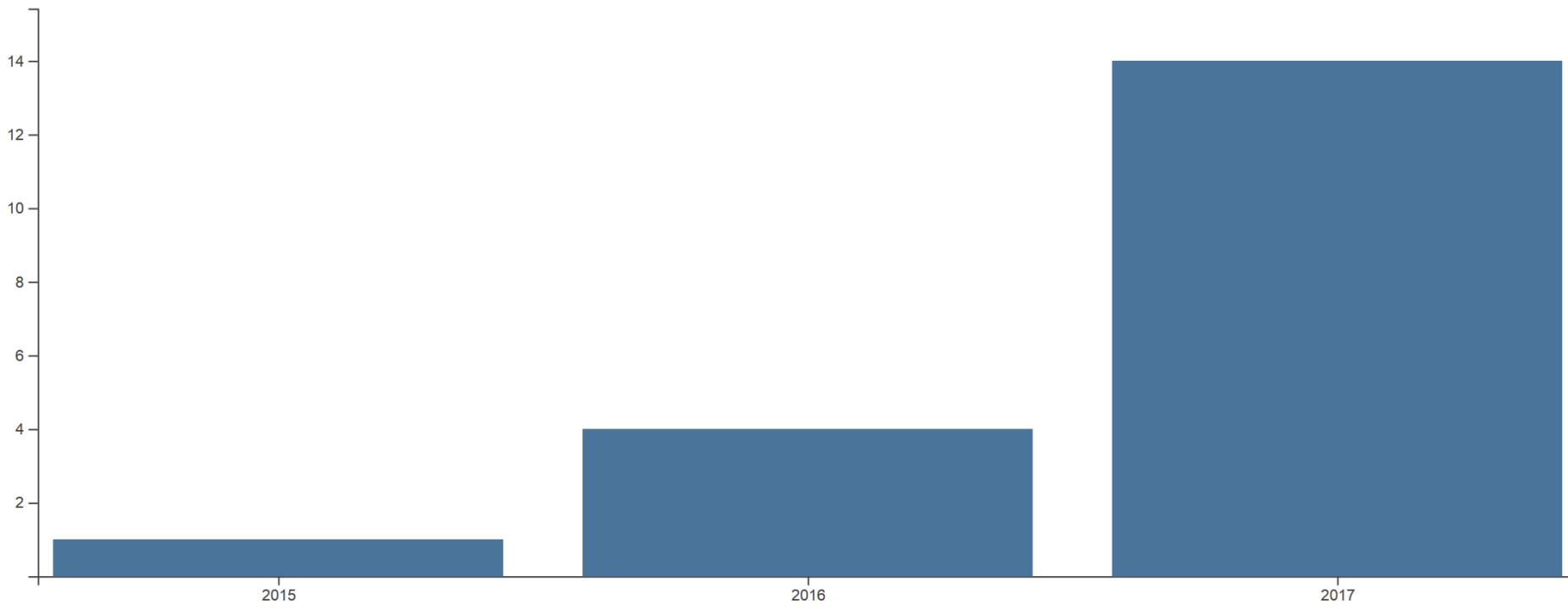
- Need for large datasets
 - Data augmentation
 - Transfer learning / fine-tuning

- Black boxes / knowledge generation
 - Networks visualization
 - Back propagation to exploit networks

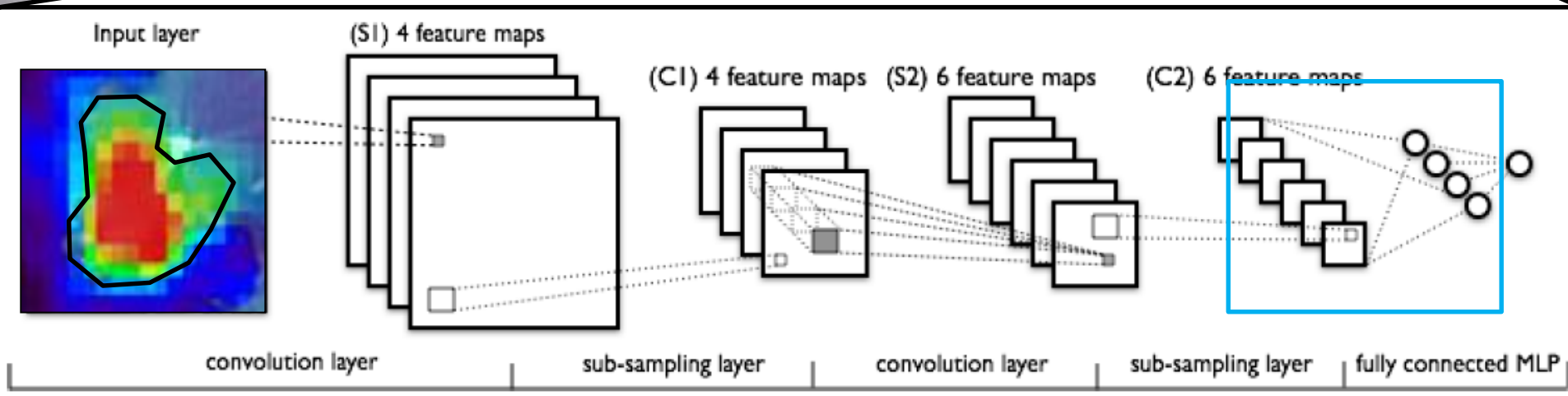
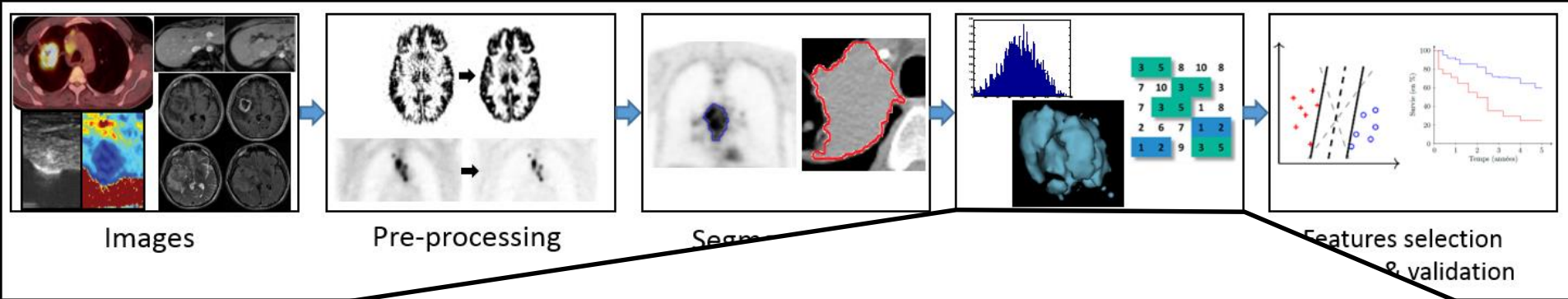
Deep learning / CNN + radiomics

Total Publications

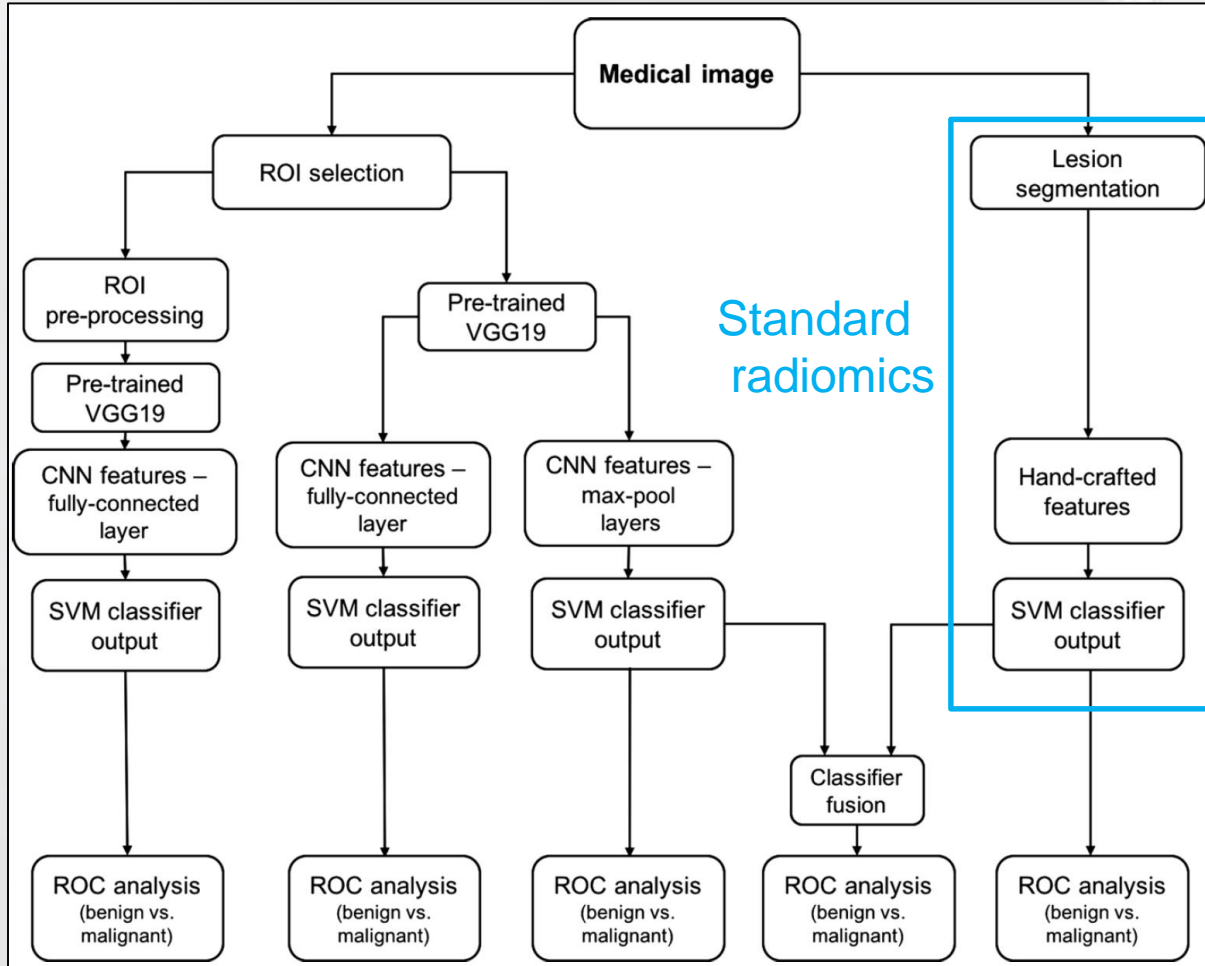
19



Deep learning / CNN + radiomics



Deep learning / CNN + radiomics



Antropova, *et al.* A deep feature fusion methodology for breast cancer diagnosis demonstrated on three imaging modality datasets. *Med Phys* 2017

Radiomics

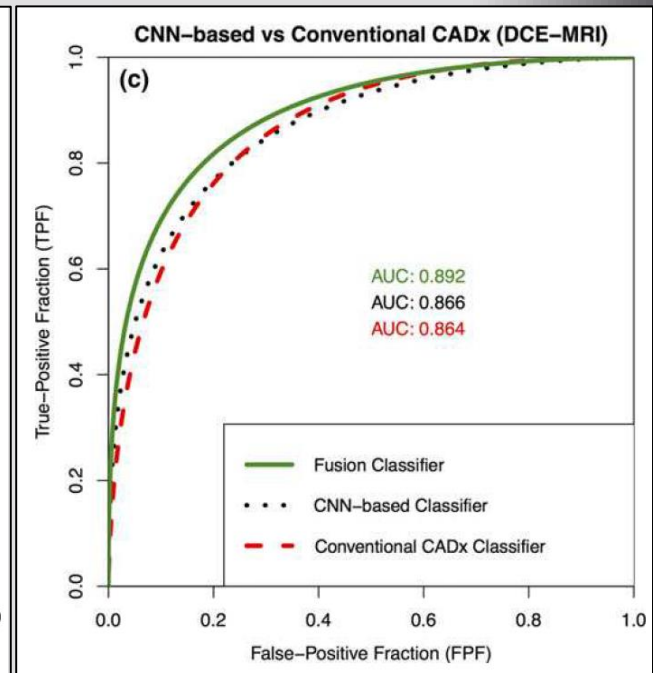
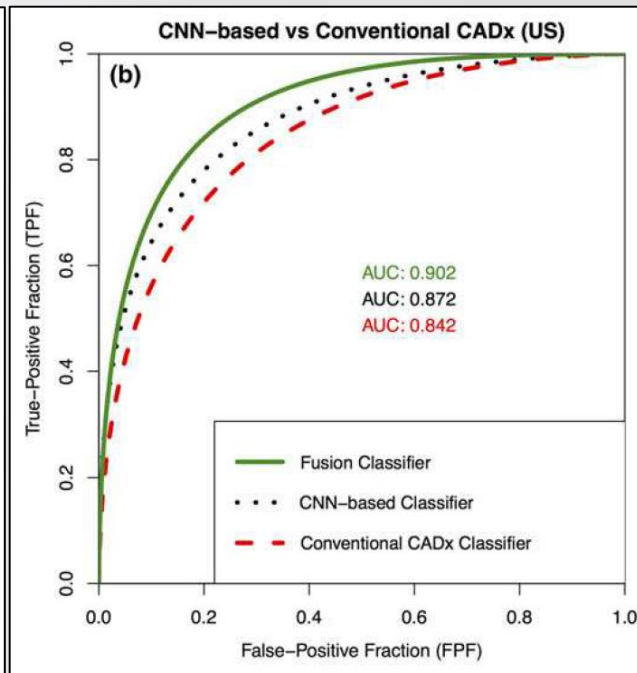
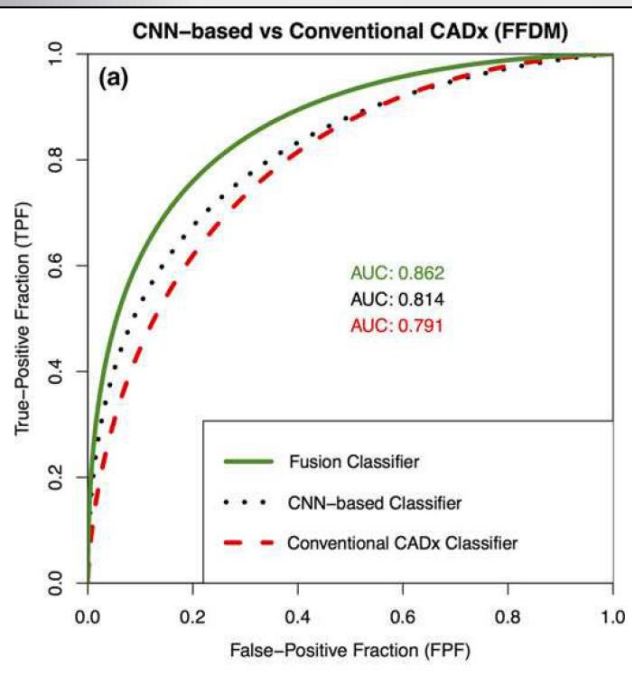
Perspectives: potential of deep learning?

Deep learning / CNN + radiomics

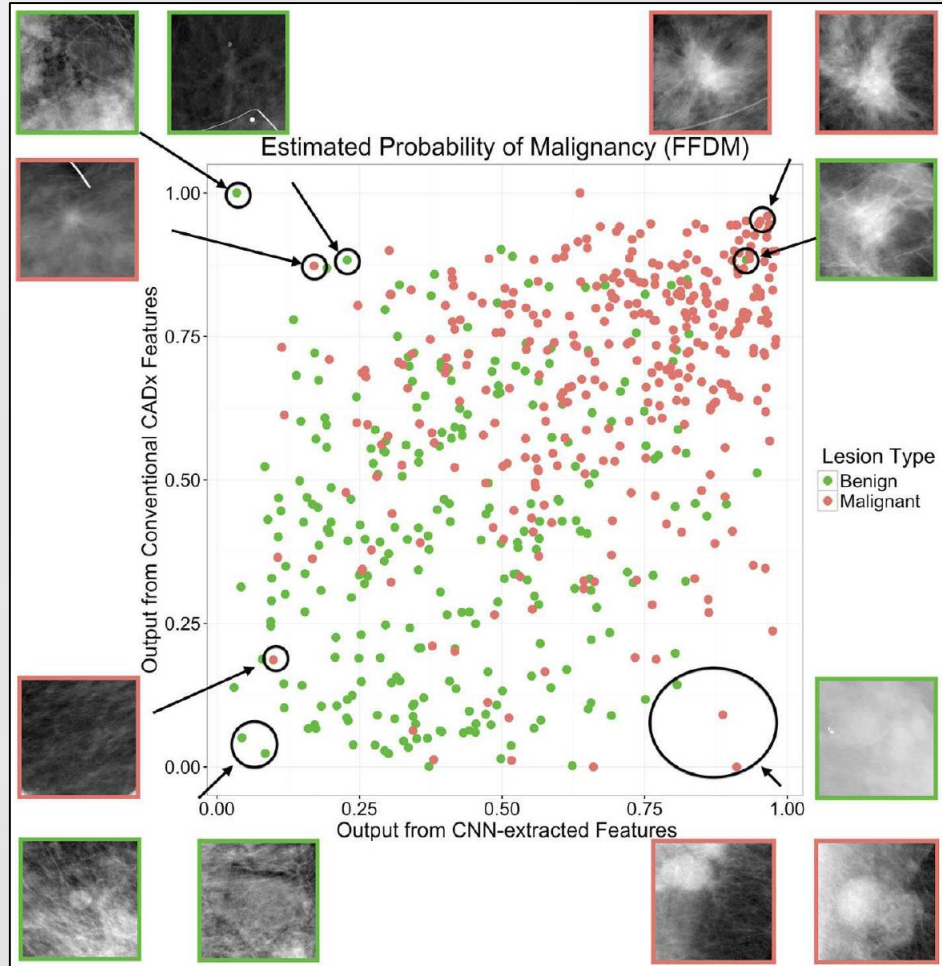
Full field digital mamography (FFDM)
N=245

Ultrasound (US)
N=1125

DCE-MRI
N=690

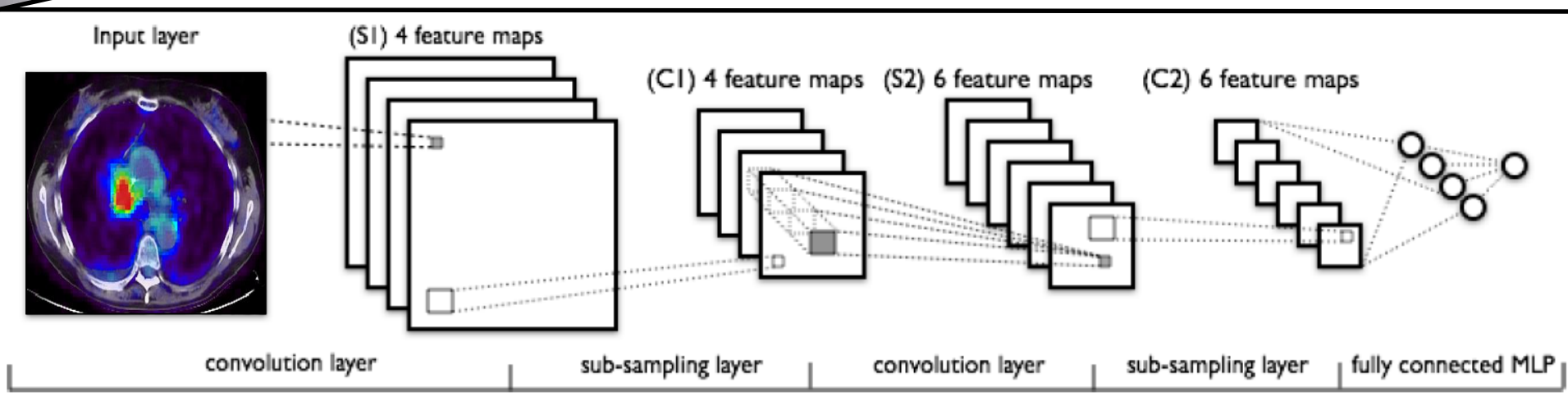
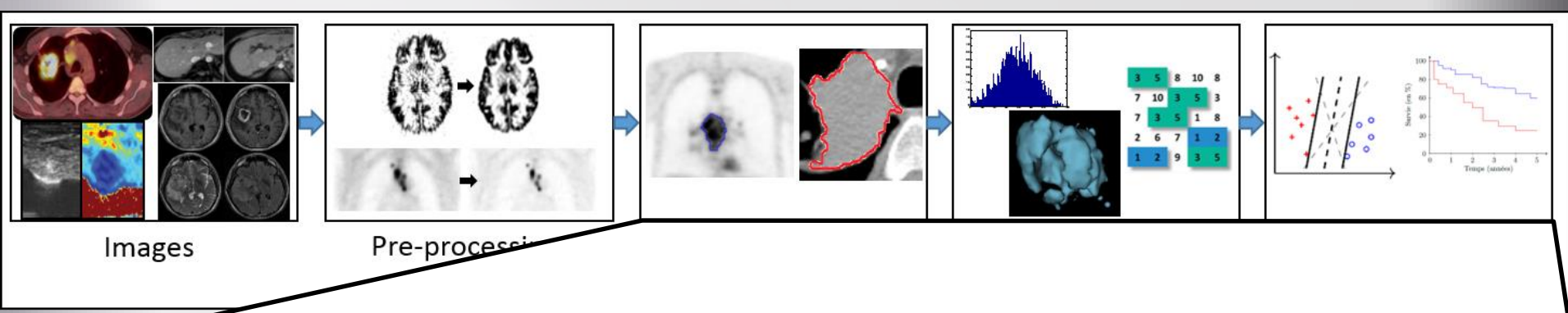


Deep learning / CNN + radiomics



Antropova, *et al.* A deep feature fusion methodology for breast cancer diagnosis demonstrated on three imaging modality datasets. *Med Phys* 2017

Deep learning / CNN + radiomics

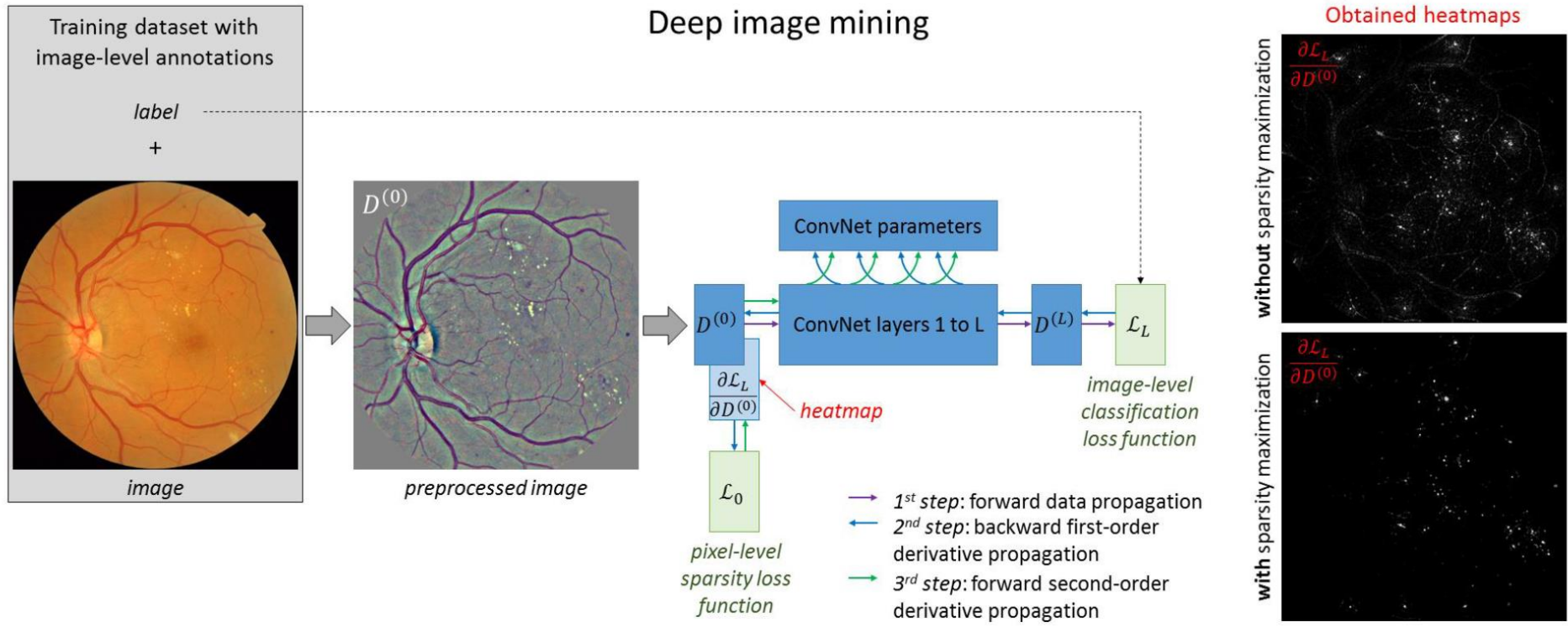


- Deep learning / CNN + radiomics

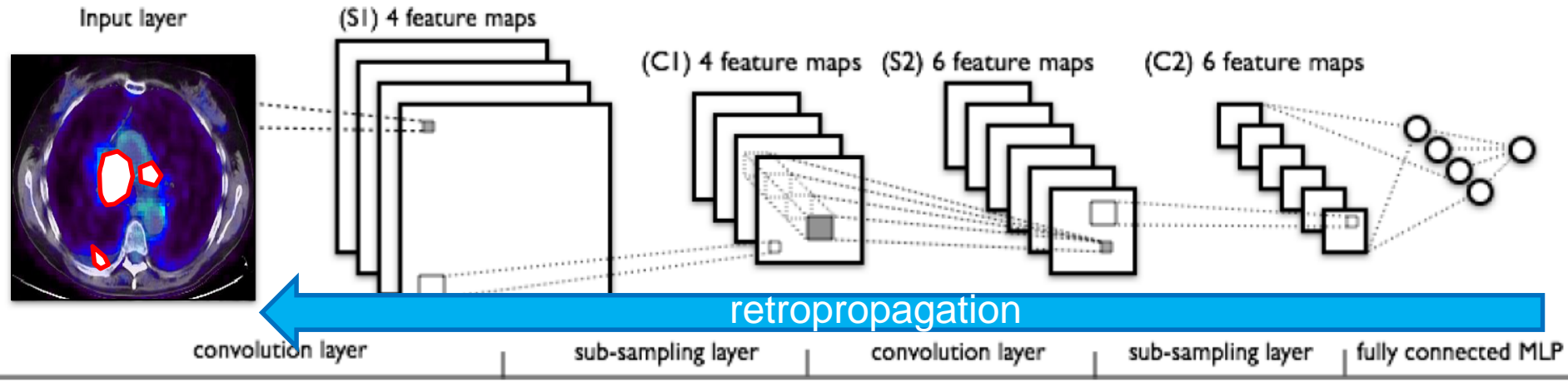


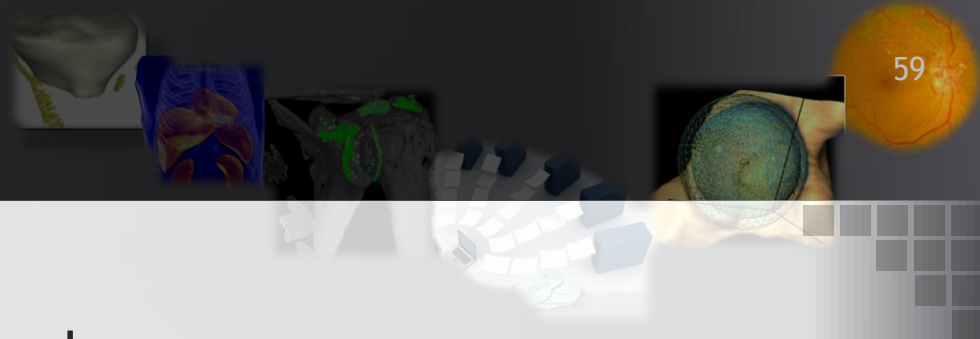
Samek, et al. Evaluating the Visualization of What a Deep Neural Network Has Learned. *IEEE Trans Neural Networks and Learning Systems*. 2017

- Deep learning / CNN + radiomics
 - « Endpoint-guided » segmentation



- Deep learning / CNN + radiomics
 - « Endpoint-guided » segmentation





- **Radiomics**
 - Dynamic field of research
 - Numerous challenges and methodological issues
 - Lack of standardization (workflow, features)
 - Difficult statistical validation

- **Potential solutions, perspectives**
 - Larger, prospective, multicentric studies
 - Use robust machine learning methods (deep learning?)
 - Standardization of radiomics (ongoing)
 - Responsible research (share methods & data)





Thanks for your attention

60

