

Advanced quantification in oncology PET

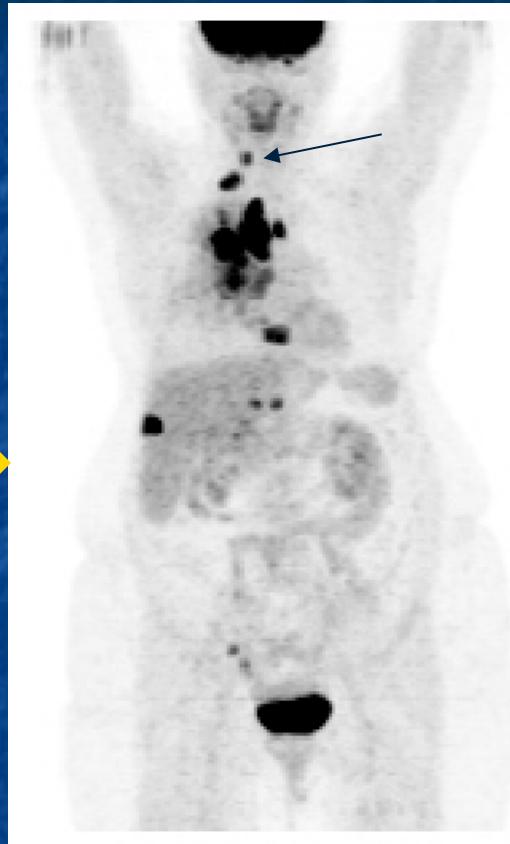
Irène Buvat

IMNC – UMR 8165 CNRS – Paris 11 University
Orsay, France

buvat@imnc.in2p3.fr

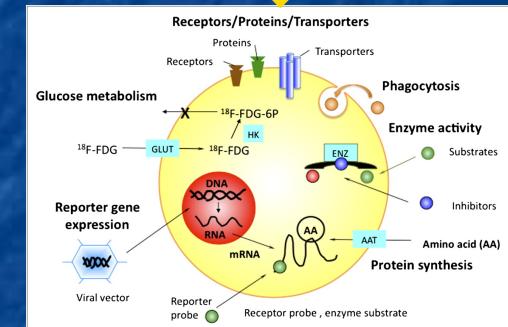
<http://www.guillemet.org/irene>

Two steps



Radiotracer
concentration (kBq/
mL)

Static imaging
Dynamic imaging



- Glucose metabolism
- Metabolically active tumor volume
- etc...

Quantification issues in oncology PET

- Tumor segmentation
- Identification of indices that best characterize the tumor in a specific context
- Interpretation of tumor changes during therapy
- Understanding the relationship between macroscopic parameters (from PET images) and microscopic tumor features

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Current quantification in oncology PET



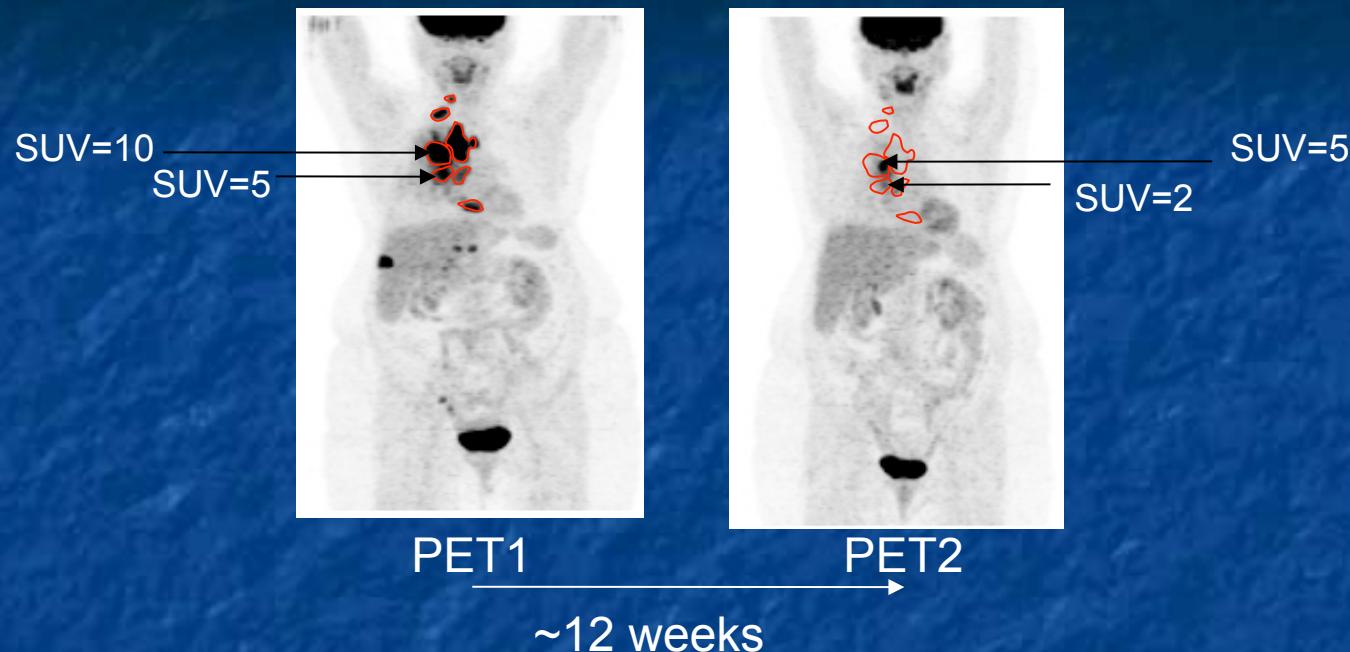
Tracer uptake (kBq/mL)

SUV (Standardized Uptake Value)

$$\text{SUV} = \frac{\text{Tracer uptake}}{\text{Injected activity / patient weight}}$$

SUV ~ metabolic activity of tumor cells

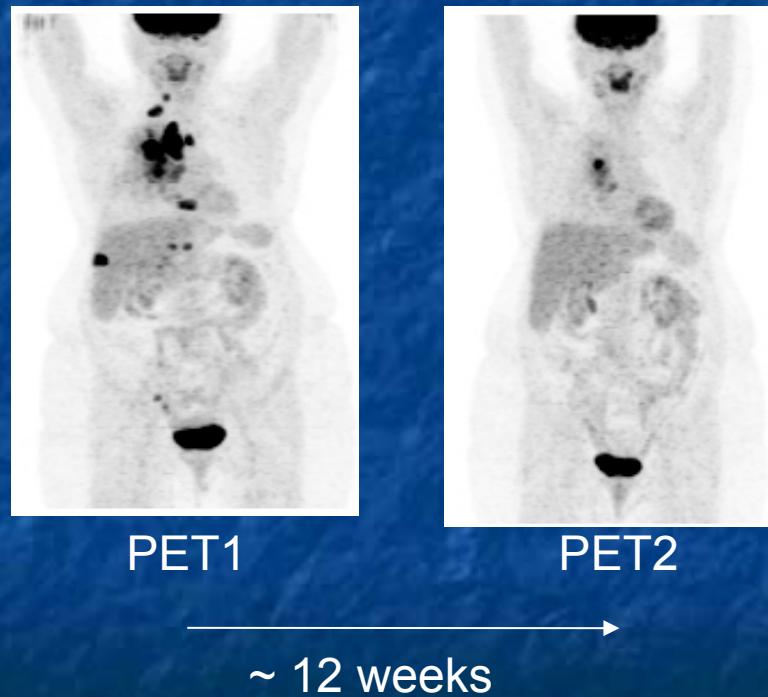
Comparing 2 PET scans : current approach



- Need to identify and possibly delineate the tumors
- Each tumor = 1 single SUV
- Change compared to an empirical threshold (provided in recommendations such as EORTC, PERCIST)
- Tedious when there are many tumor sites

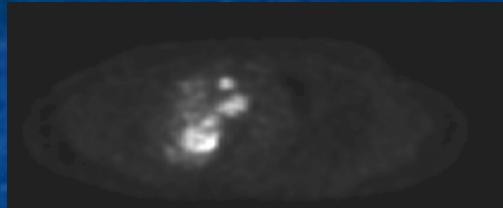
A novel parametric imaging approach

Goal : Get an objective **voxel-based** comparison of 2 PET/CT scans

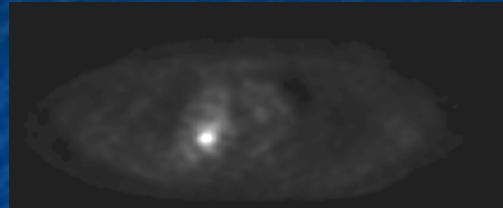


Main steps

1. PET image registration based on the CT associated with the PET scans

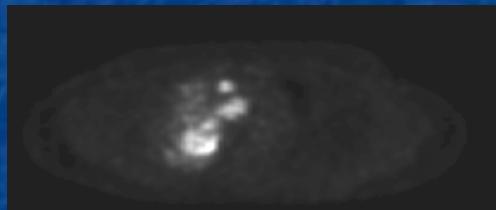


PET1



PET2

2. Voxel-based subtraction of the 2 image volumes



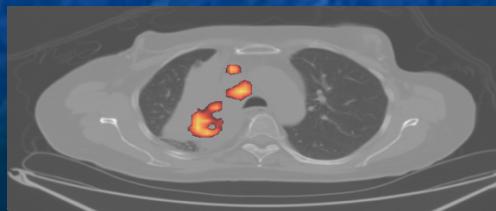
PET1

$$- T_{21} \left\{ \begin{array}{c} \text{PET2} \\ \end{array} \right\} =$$



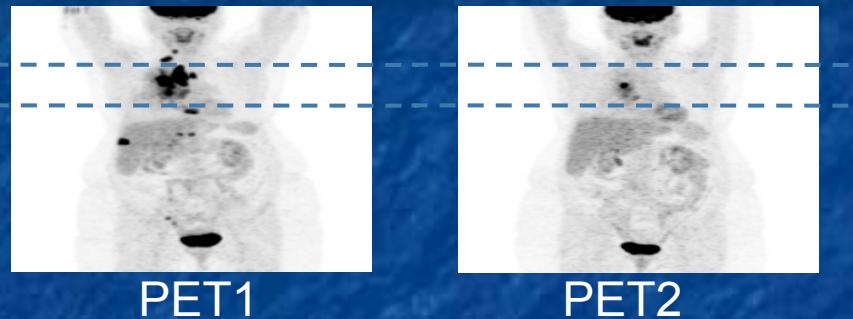
PET1-PET2'

3. Identification of voxels in which SUV significantly changed between the 2 scans using a biparametric analysis



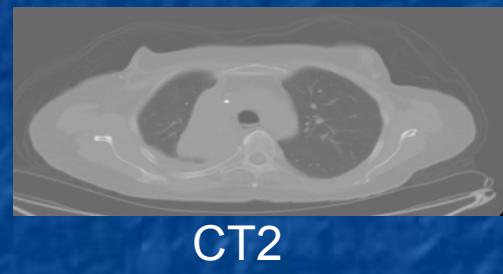
Step 1

VOI selection



CT1 CT2

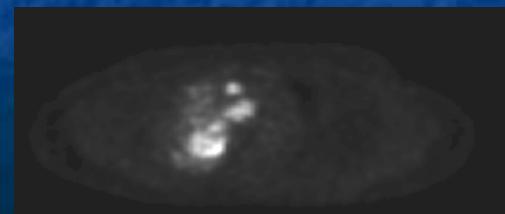
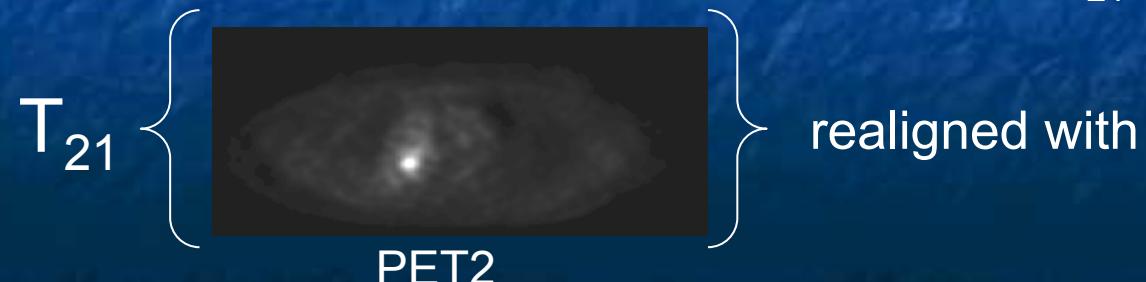
Identification of the transformation needed to realign the 2 CT



T_{21}
rigid transform using
Block Matching

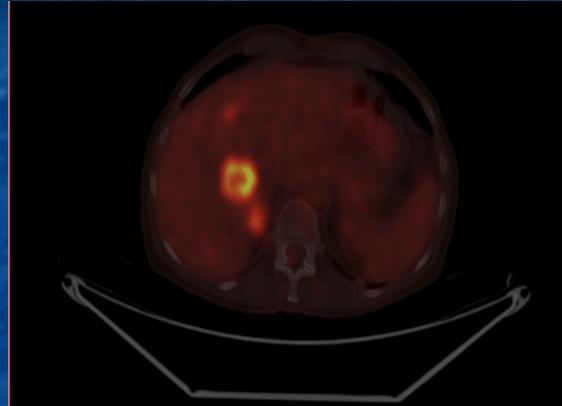


Registration of the PET volumes using the T_{21} transformation

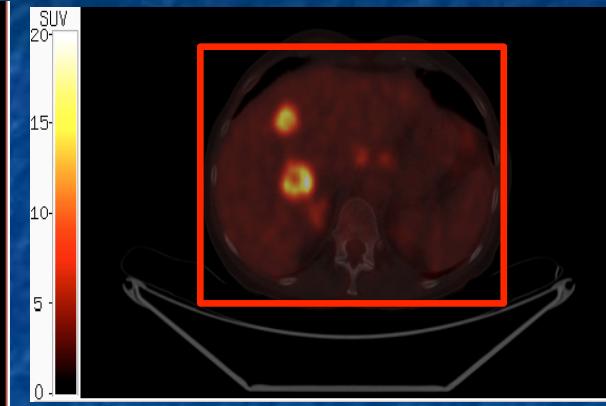


Step 2

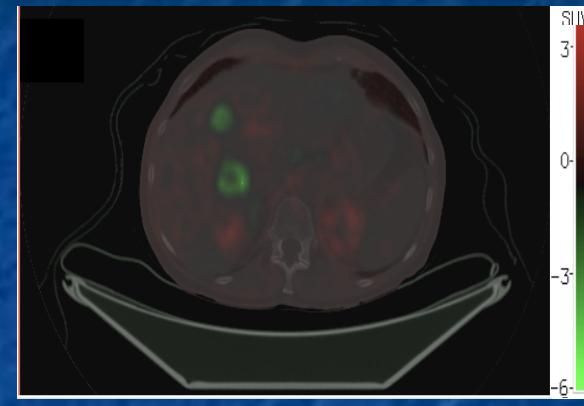
Subtraction of the 2 realigned PET scans



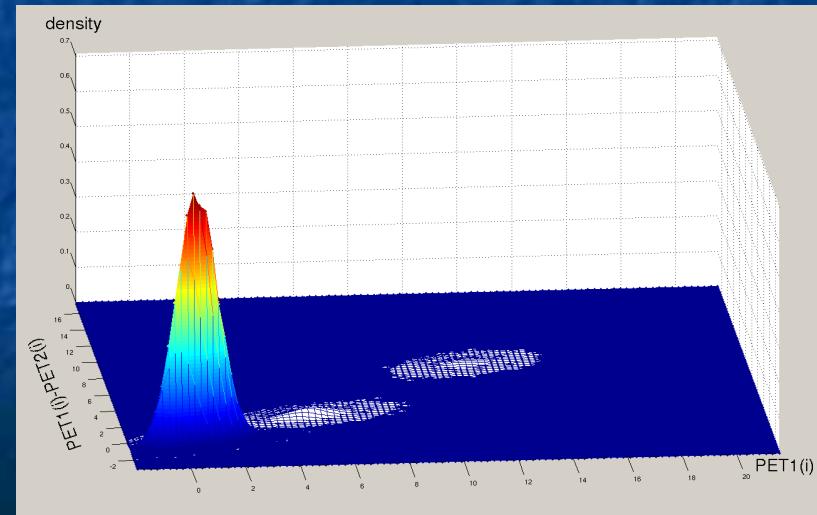
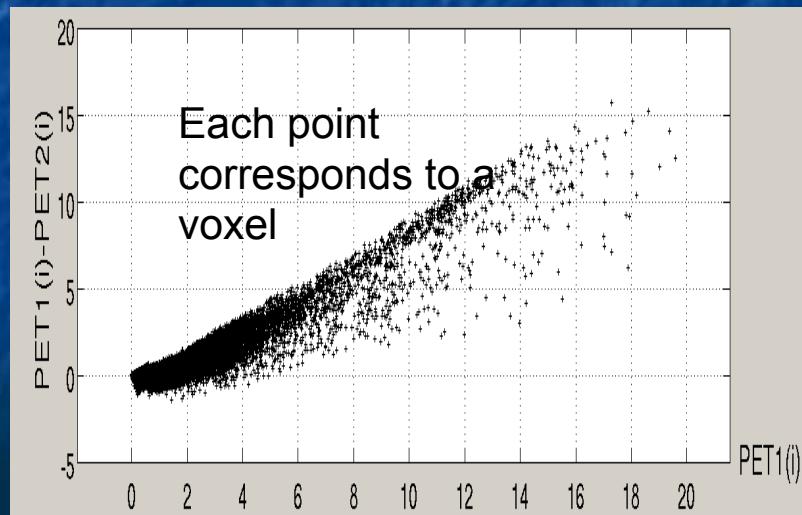
$$T_{21}\{\text{PET2/CT2}\}$$



$$- \quad \text{PET1/CT1}$$

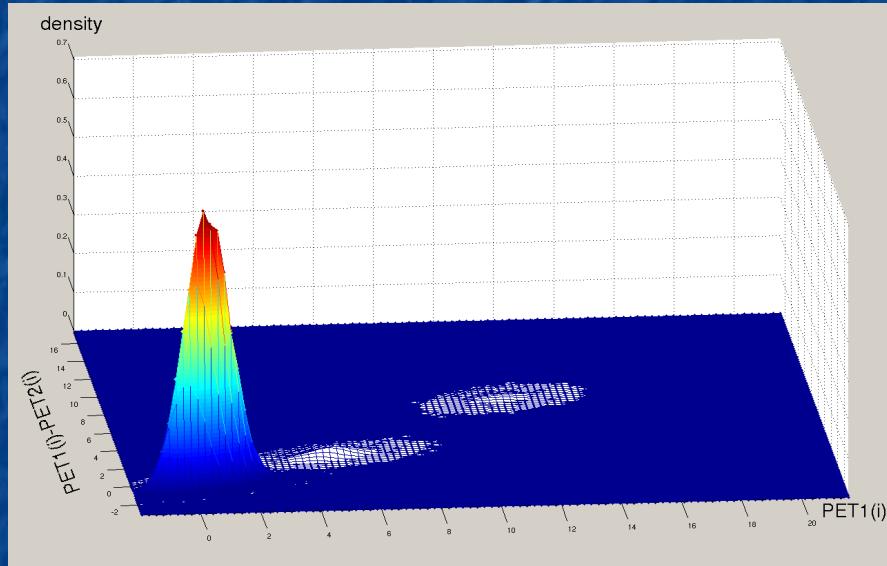


$$= T_{21}\{\text{PET2}\} - \text{PET1/CT1}$$



Step 3

Identification of the significant tumor changes in the 2D-space by solving a Gaussian mixture model



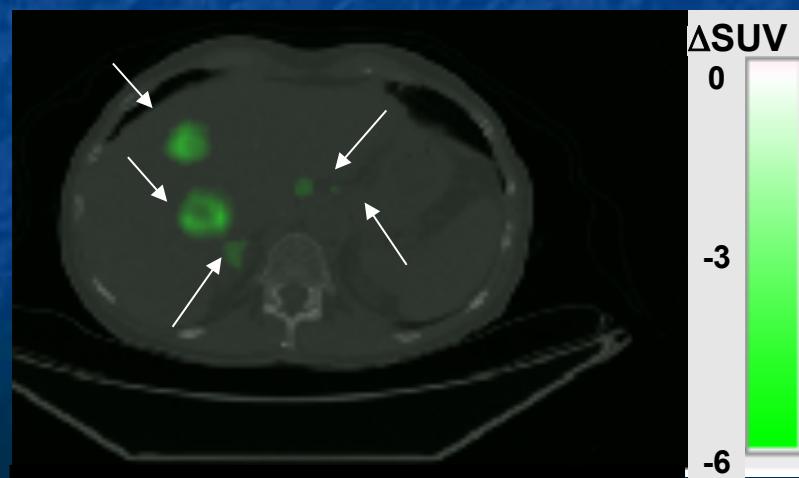
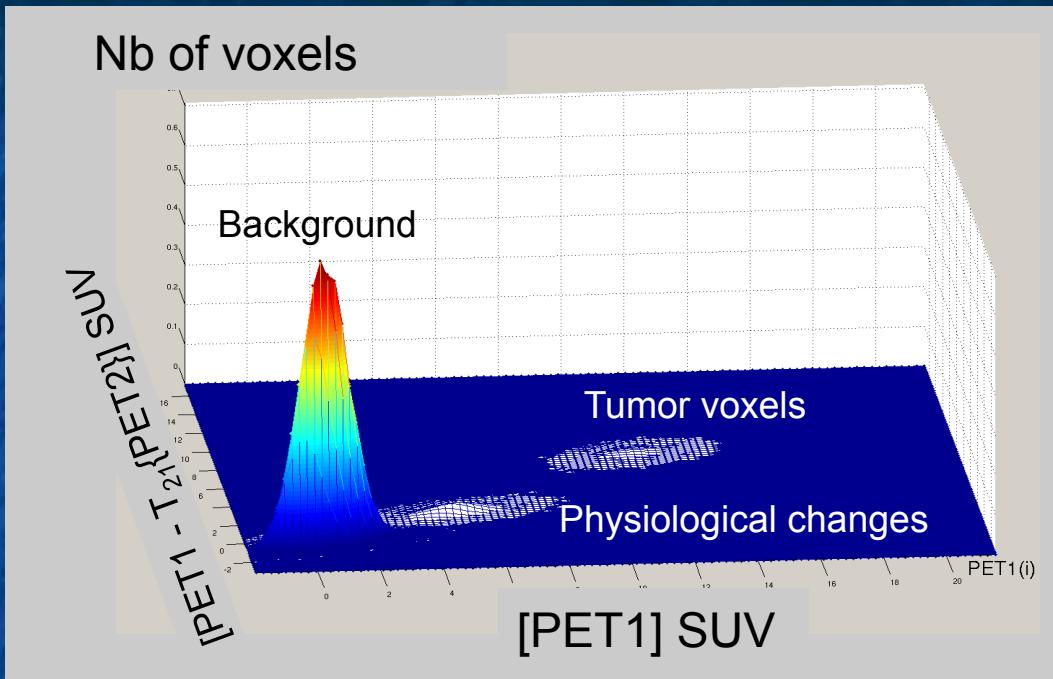
$$x_i \begin{bmatrix} \text{PET1}(i)-\text{PET2}(i) \\ \text{PET1}(i) \end{bmatrix}$$

$$f(x_i|\theta) = \sum_{k=1}^K p_k \phi(x_i|\mu_k, \Sigma_k)$$

↑
mixture parameters

θ : vector of parameters ($p_1, \dots, p_K, \mu_1, \dots, \mu_K, \Sigma_1, \dots, \Sigma_K$)

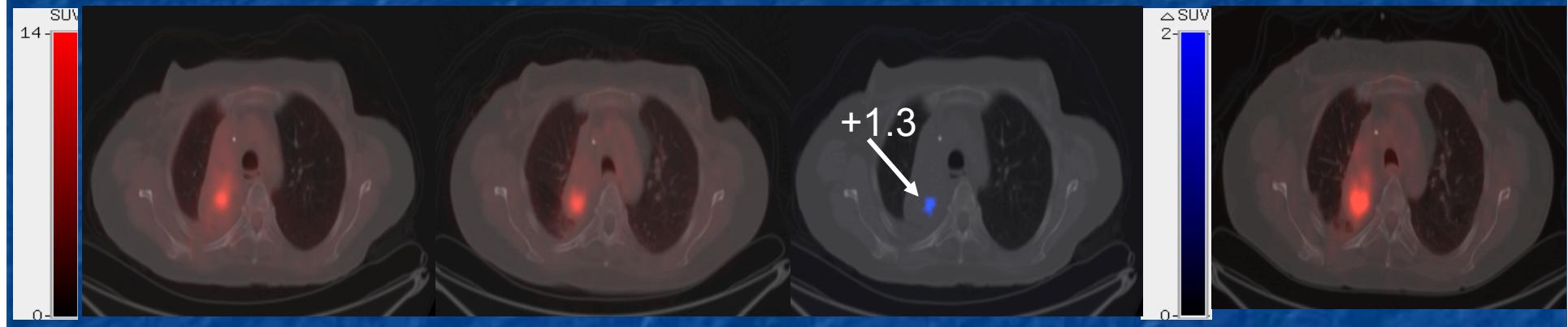
Step 3: results



Parametric image
 ΔV : volume with a significant change
 ΔSUV : change magnitude

Example

Identification of small tumor changes (lung cancer)

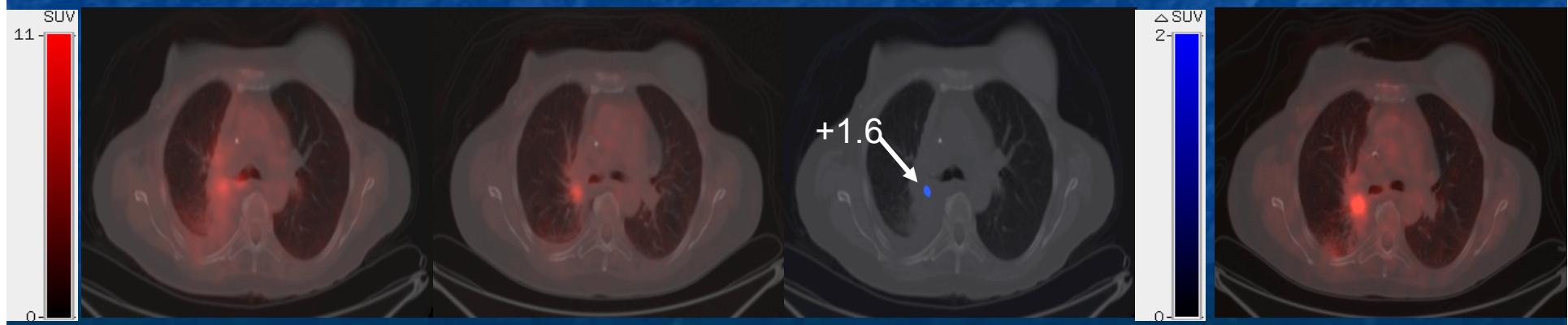


PET1

T₂₁{PET2}

T₂₁{PET2} - PET1
after solving the GMM

PET3



PET1

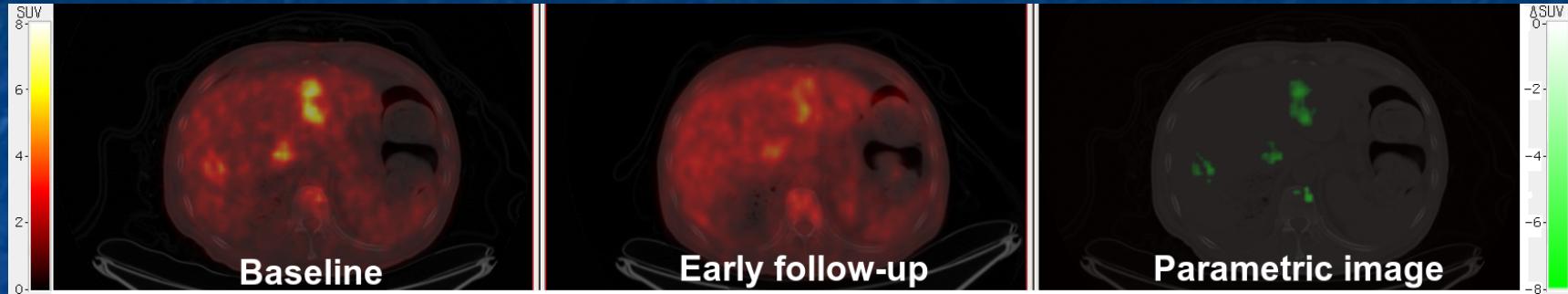
T₂₁{PET2}

T₂₁{PET2} - PET1
after solving the GMM

PET3

Clinical validation : 28 patients with metastatic colorectal cancer

78 tumors with 2 PET/CT (baseline and 14 days after starting treatment)



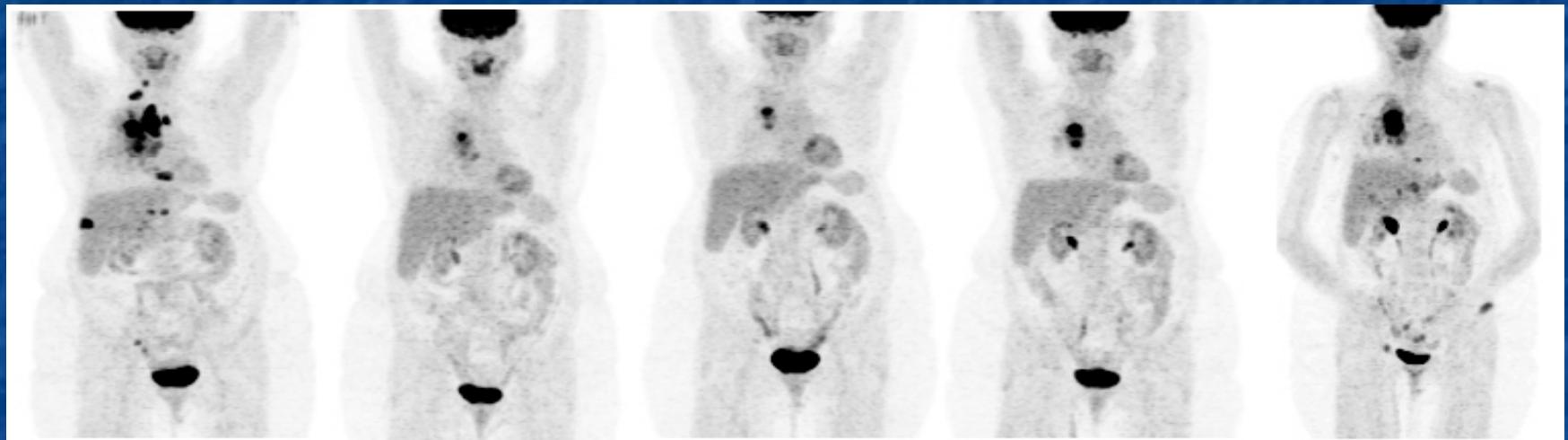
	NPV	PPV	Sensitivity*	Specificity
EORTC	91%	38%	85%	52%
PI	100%	43%	100%	53%

* for detecting lesions

- All tumors identified as progressive tumors at D14 were confirmed as such 6 to 8 weeks after based on CT (RECIST criteria)
- Among the 14 tumors identified as progressive tumors by RECIST criteria, 12 were identified as such at D14 using PI while only 2 were identified using EORTC criteria (SUVmax)

Comparing more than 2 PET/CT scans

Longitudinal study



0

12

23

35

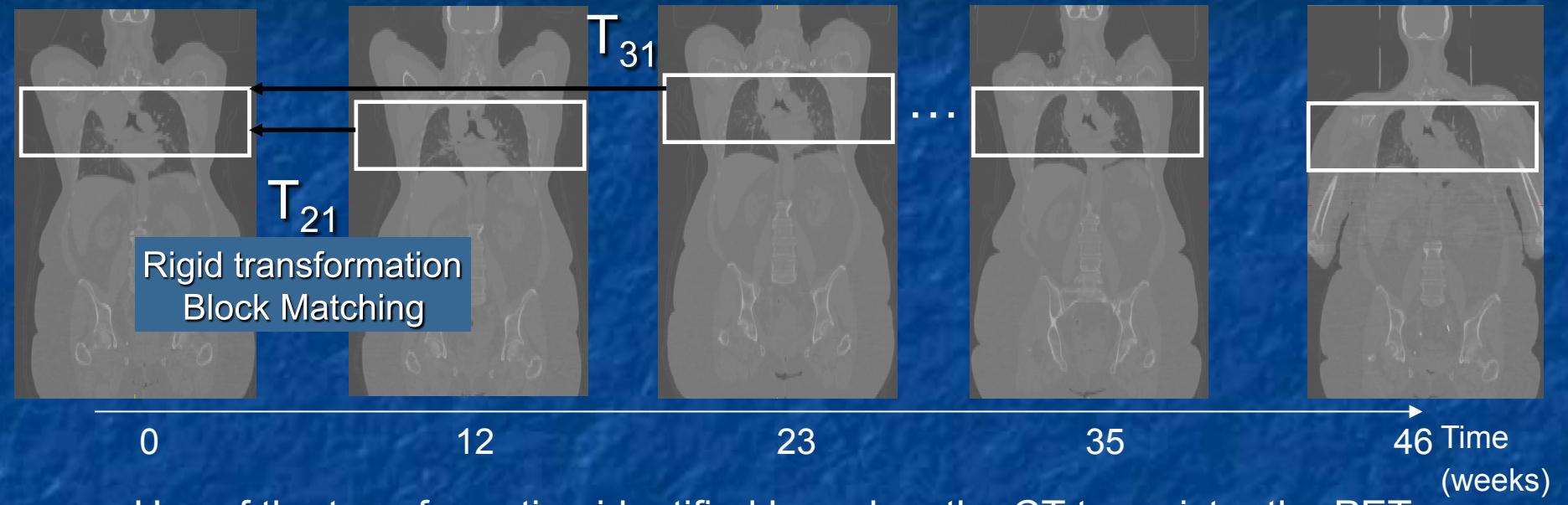
46

time (weeks)

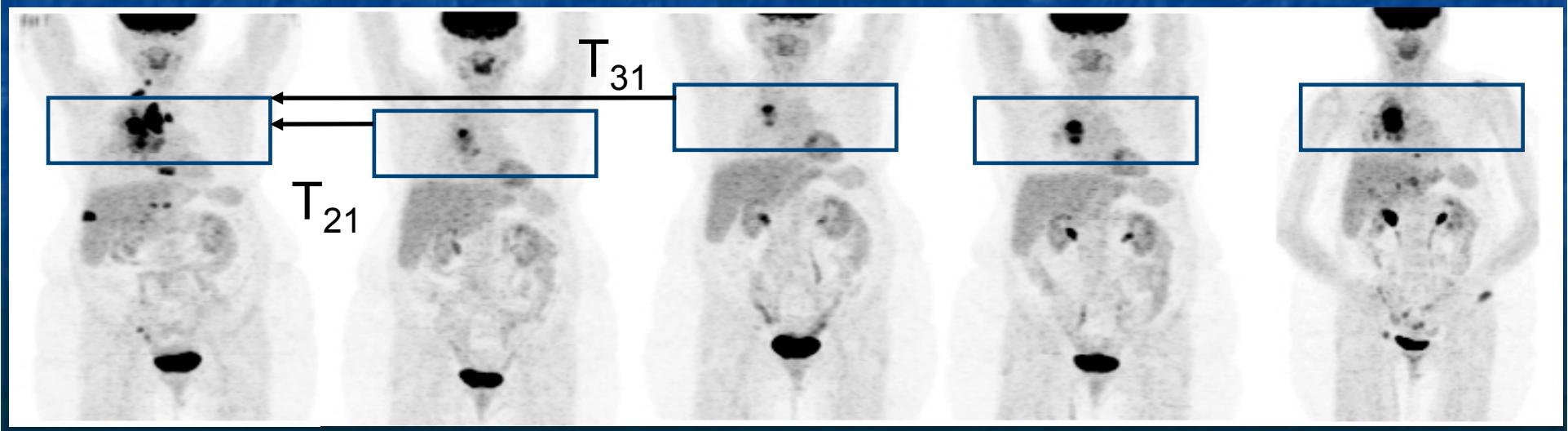
Problem : characterize the tumor changes
No method, each scan is usually compared
only to the previous one

A parametric imaging solution

First step: PET image registration based on the associated CT



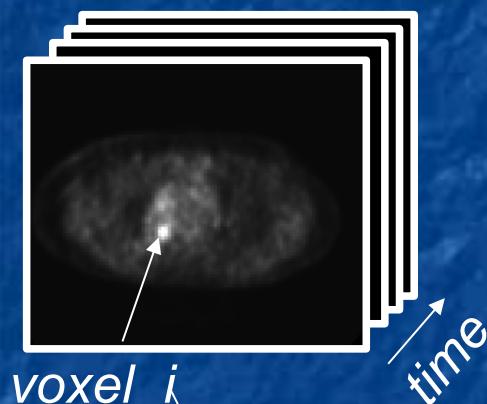
Use of the transformation identified based on the CT to register the PET scans



Model : a factor analysis model

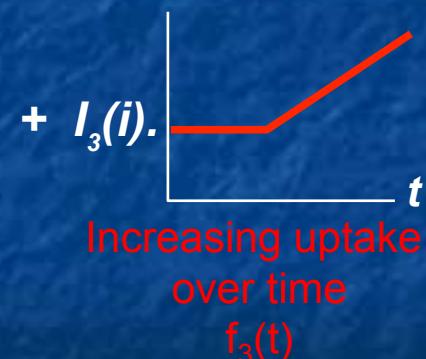
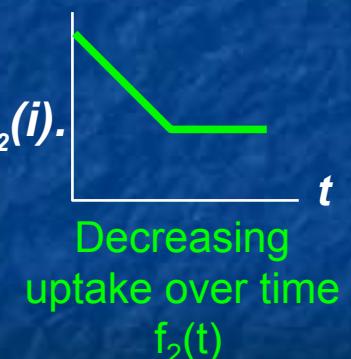
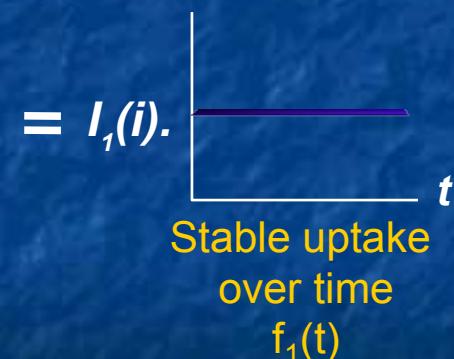
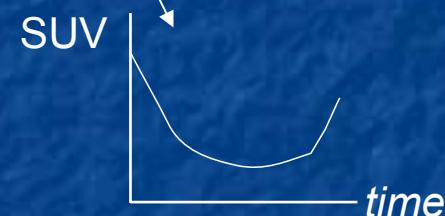
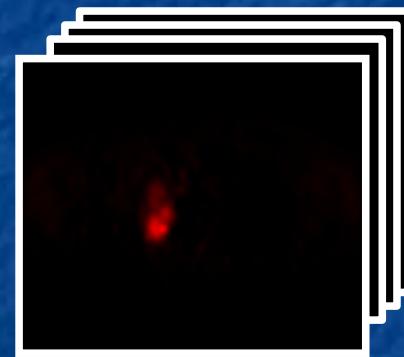
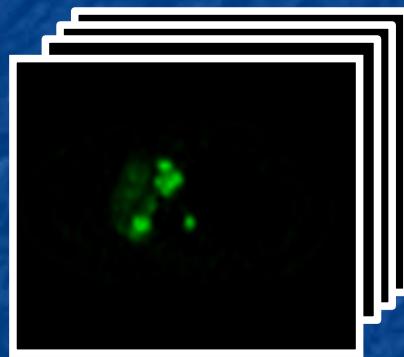
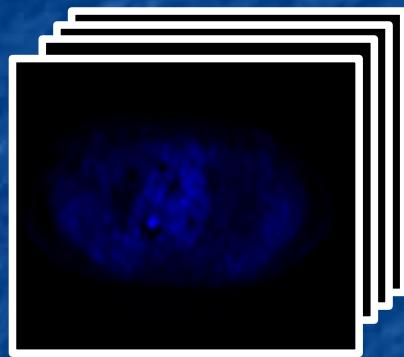
$$\text{SUV } (i, t) = \sum_{k=1}^K l_k(i) \cdot f_k(t) + \varepsilon_k(t)$$

SUV units



voxel *i*

time



Solving the model

$$SUV(i, t) = \sum_{k=1}^K I_k(i) \cdot f_k(t) + \varepsilon_k(t)$$

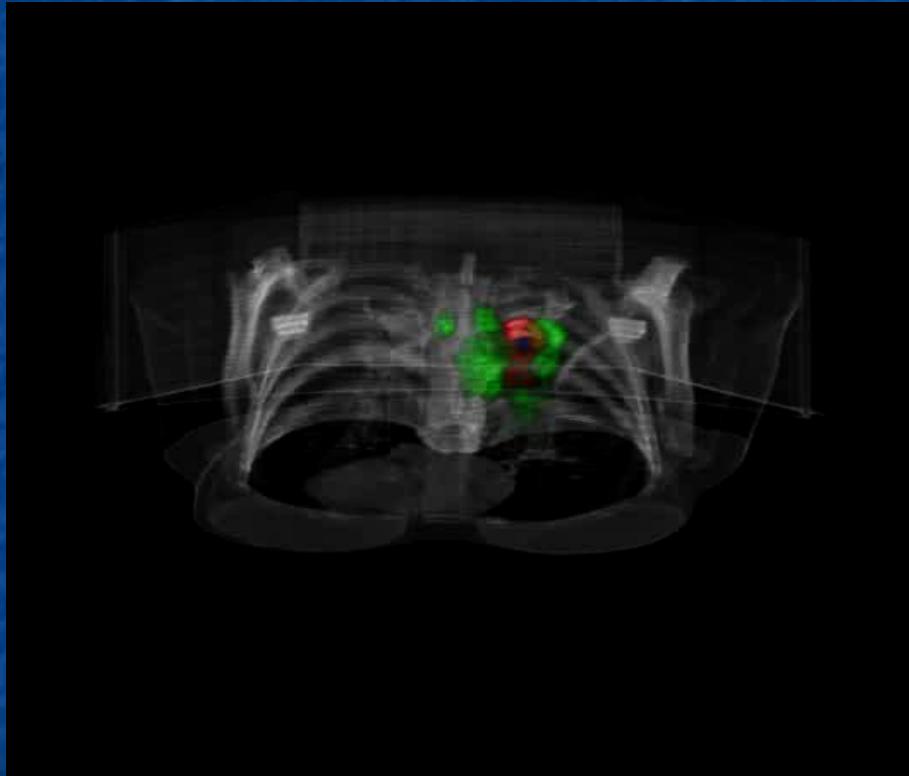
Priors :

- Non-negative $I_k(i)$ coefficients
- Non-negative $f_k(t)$ values
- In each voxel, the variance of the voxel value is roughly proportional to the mean

Iterative identification of $I_k(i)$ et $f_k(t)$ (Buvat et al Phys Med Biol 1998) using a Correspondence Analysis followed by an oblique rotation of the orthogonal eigenvectors

Sample results

Lung cancer patient with 5 PET/CT scans

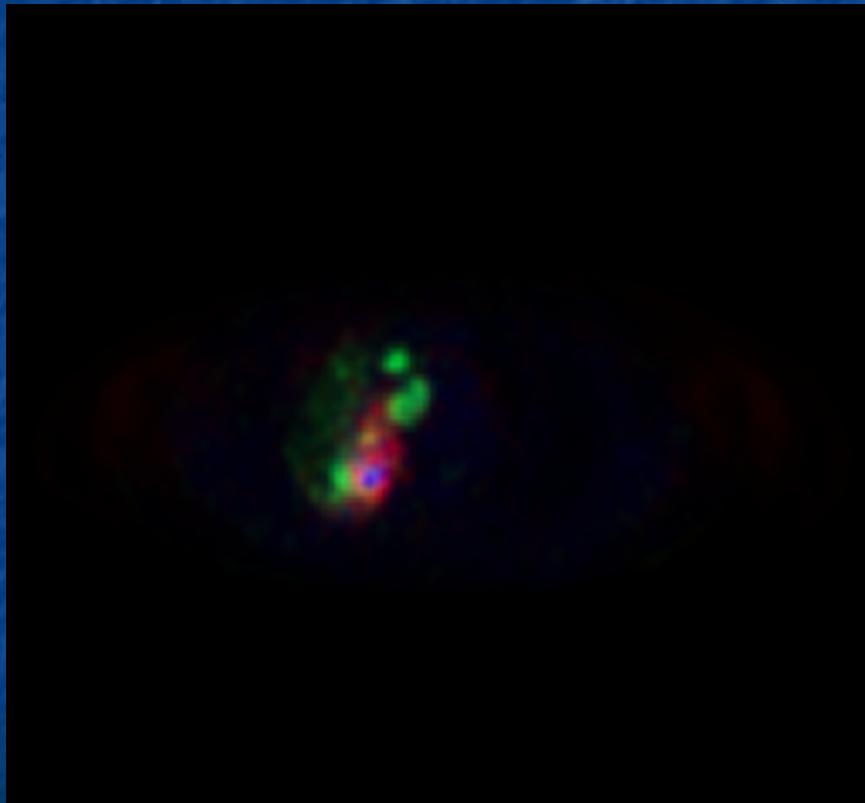


Normalized SUV



Why is such an approach useful?

Heterogeneous tumor responses can be easily identified

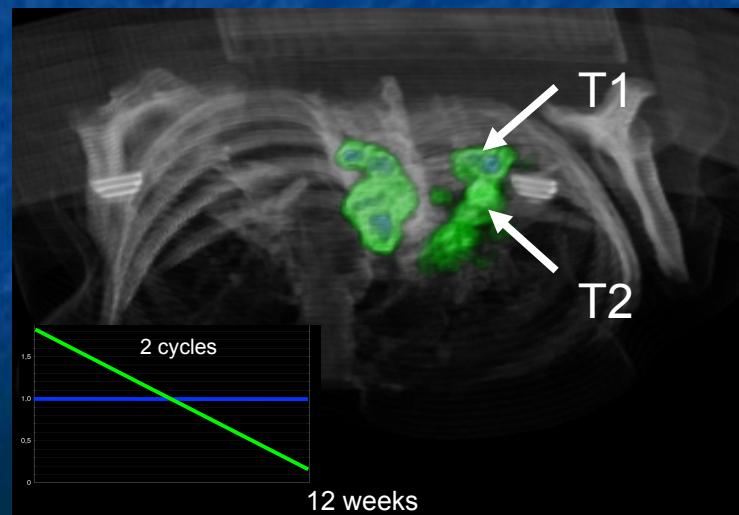
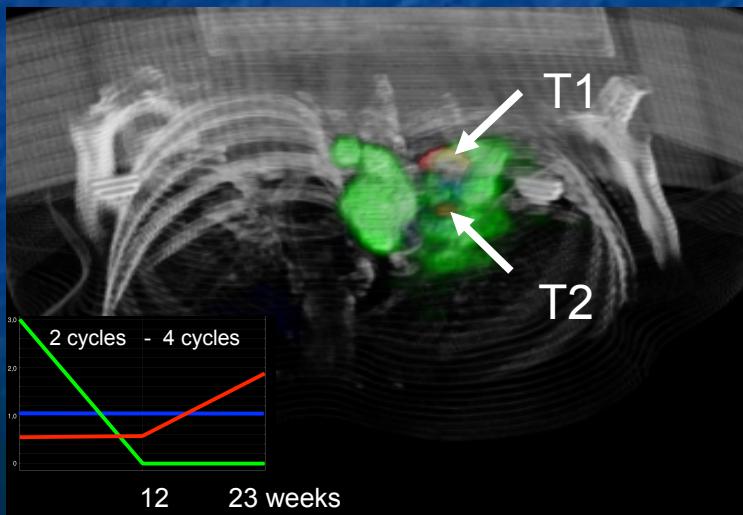
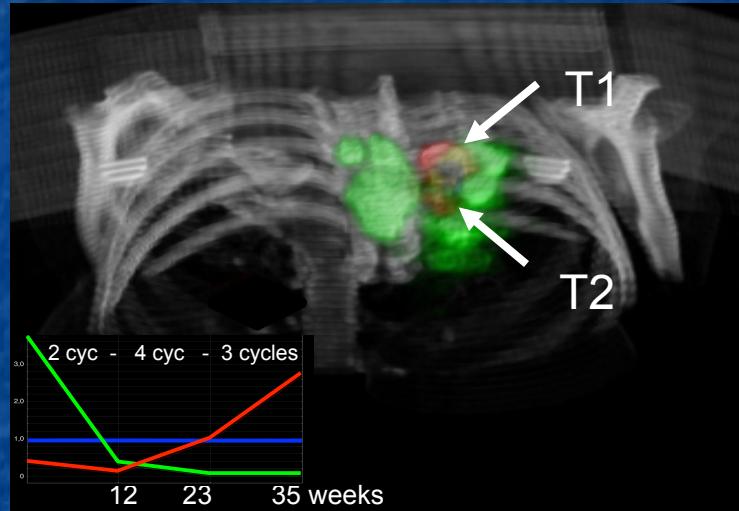
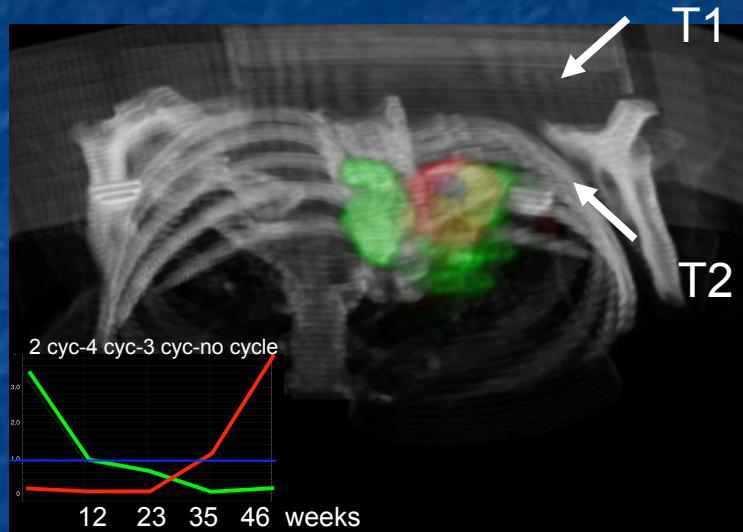


Normalized SUV

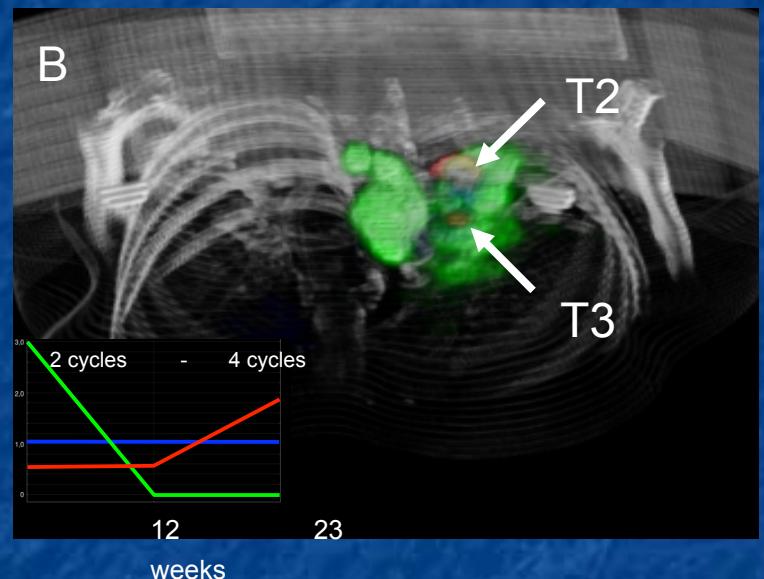
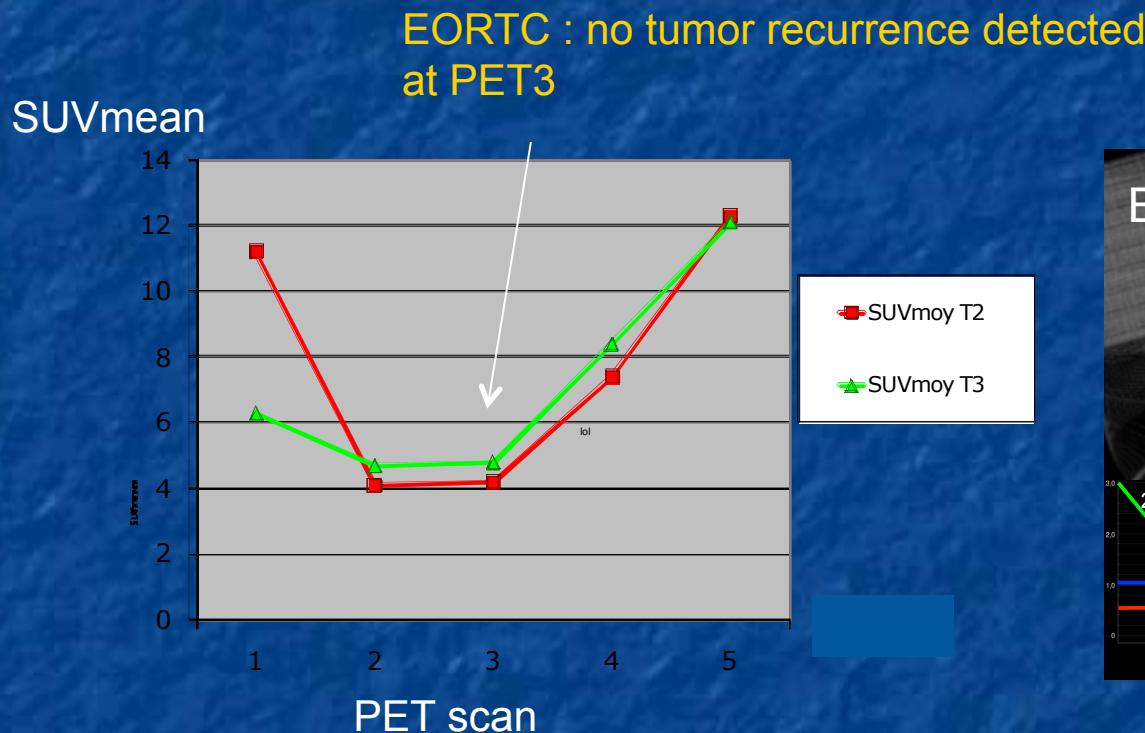


weeks

Sample results: early detection of tumor recurrence (1)



Sample results: early detection of tumor recurrence (2)



PI : tumor recurrence detected at PET3

Discussion / conclusion

- No need to precisely delineate the tumors
- Makes it possible to detect small changes in metabolic activity
- Summarizes changes between two or more scans in a single image
- Shows heterogeneous tumor response within a tumor or between tumors

Thanks to

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