6<sup>th</sup> international workshop on PET in Lymphoma

## Problems in MTV measurements in lymphoma

Irène Buvat and Christophe Nioche with patient data from Michel Meignan

Imagerie Moléculaire In Vivo (IMIV) CEA – Service Hospitalier Frédéric Joliot Orsay, France <u>irene.buvat@u-psud.fr</u>

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### Outline

- MTV measurement: current status
- How to go beyond the current limitations
  - make MTV calculation easier
  - use a cooperation approach
- Conclusion

### Existing MTV delineation methods

- Many methods:
  - Using a fixed SUV threshold (eg, voxels with SUV>2.5 is tumor)
  - Using a relative SUV threshold (eg, voxels with SUV>41% SUV<sub>max</sub> is tumor)
  - Using a threshold relative to the liver activity (eg, SUV >  $1.25 \text{ SUV}_{max_{liver}}$ )
  - Using an adaptive threshold accounting for  ${\rm SUV}_{\rm max}$  and  $\mbox{ surrounding activity (eg, Nestle method^1)}$
  - Using a fitting method accounting for SUV<sub>max</sub>, surrounding activity and spatial resolution of the imaging system (Tylski method<sup>2</sup>)
  - Using a threshold adjusted iteratively as a function of the tumor-to-background activity, requiring a calibration curve (Daisne method<sup>3</sup>)
  - Using a threshold adjusted iteratively as a function of the mean SUV in the tumor region, requiring a calibration curve (Black method<sup>4</sup>)

- and many others ...

<sup>1</sup>Nestle et al J Nucl Med 2005 <sup>2</sup>Tylski et al J Nucl Med 2010 <sup>3</sup>Daisne et al Radiother Oncol 2003 <sup>4</sup>Black et al Int J Radiat Oncol Biol Phys 2004

#### Performance of these methods

• All have merits and weaknesses, eg:





Meignan et al EJNMMI 2014

• Fortunately, all of them provide correlated results



but with substantial differences : Bland Altman plots



**Peripheral T** cell lymphoma

- No method is always the most accurate: performance vary as a function of the activity distribution, noise, spatial resolution, contrast
- In a given setting, each method has some specific bias.
   A specific cut-off should ideally be used to distinguish between groups



Table 1. Studies on the Prognostic Value of MTV in Lymphoma									
Tumor Volume Parameters									
Study	Type of Lymphoma	Patients (No.)	Median SUV	Threshold (%)	Median MTV (cm <sup>3</sup> )	Range (cm <sup>3</sup> )*	Predictors of PFS	Determination of MTV Cutoff	
Kanoun et al <sup>15</sup>	HL	59	NR	41	117	4-1,611	MTV 225 cm <sup>3</sup> ields 4-year PFS 85% v 42%	ROC analysis†, no validation sample	
Sasanelli et al <sup>17</sup>	DLBCL	114	NR	41	313	4-2,650	MT( 550 cm <sup>3</sup> ) ields 3-year PFS 77% <i>v</i> 60%	ROC analysis, no validation sample	
Adams et al <sup>11</sup>	DLBCL	73	22.0	40	272	6-2,454	Neither MTV nor TLG predicted outcome	N/A	
Mikhaeel et al <sup>16</sup>	DLBCL	147	27.2	41	595	2-7,360	MTV 396 cm <sup>3</sup> yields 5-year PFS 92% v 42% Best predictive model combines MTV with i-PET Deauville score	ROC analysis, no validation sample	
Cottereau et al <sup>26</sup>	DLBCL	81	18	41	320	IQR: 106-668	MTV 300 cm <sup>3</sup> vields 5-year PFS 75% v 42%	ROC analysis, no validation sample	
Schöder et al <sup>18</sup>	DLBCL	65	23.4	Various‡	226	9-3,453	MTV did not predict	N/A	
Ceriani et al <sup>12</sup>	PMBL	103	18.8	25	406	NR	MTV 703 cm <sup>3</sup> yields 5-year PFS 97% v 60% TLG 5,814 yields 5-year PFS 99% v 64%	ROC analysis, no validation sample	
Cottereau et al <sup>13</sup>	PTCL	108	14	41	224	3-3,824	MTV 230 cm <sup>3</sup> vields 2-year PFS 71% v 26%	ROC analysis, no validation sample	
Meignan et al <sup>19</sup>	FL 1-3a	185	10.0	41	297	IQR: 135-567	MTV 510 cm <sup>3</sup> ields 2-year PFS 87% <i>v</i> 58%	X-tile analysis	

Schöder et al JCO 2016

These results regarding MTV are consistent with previously reported results regarding SUV to assess tumor response

#### **Metastatic colorectal cancer**

Interim PET @ day 14 of treatment Targeting a 95% sensitivity for detecting responding lesions

Index	Cut-off	Sensitivity	Specificity
$\Delta \text{SUV}_{\text{max}}$	-14%	95%	53%
$\Delta \text{SUV}_{\text{mean40\%}}$	-22%	95%	64%
$\Delta \text{SUV}_{\text{max}}$	-15%	80%	53%
$\Delta \text{SUV}_{40\%}$	-15%	95%	53%

Buvat et al EJNMMI 2012

#### Current limitations in MTV measurements in lymphomas

- There is no such thing as THE accurate method for MTV estimate
- TMTV measurement is tedious: tumors should first be roughly delineated
- Choice of the "optimal" threshold unclear for prospective studies
- Results are good but far from perfect, eg:

AUC ~ 0.68 to 0.71 for PFS prediction in peripheral T cell lymphomas<sup>1</sup> AUC ~ 0.60 to 0.62 for OS prediction in peripheral T cell lymphomas<sup>1</sup> AUC ~ 0.62 for PFS prediction in follicular lymphomas<sup>2</sup>

- Standardization of PET image quality is on-going and useful but:
  - scanners are evolving faster than standardization
  - what about "old" cohorts?

Is MTV calculation worth the effort? How can we move forward?

<sup>1</sup> Cottereau et al J Nucl Med 2016 <sup>2</sup> Meignan et al JCO 2016

#### How can we go beyond? First track

Make the TMTV calculation **easy**, traceable, reproducible, so that a large number of centres can gain experience with this metrics and more results can be obtained

This involves:

1) Simplifying the initial delineation of regions

2) Having several MTV delineation methods available

3) Allowing for user interaction as no method is perfect and medical expertise is required

4) Making a software widely available

5) Providing user assistance

#### Texture analysis: is it worth it and where are we?

- In lymphoma, still to be investigated closely<sup>1</sup>, but worth dedicated studies see posters
- Textural metrics calculated from PET images start being understood:
  - How they correlate to conventional metrics<sup>2,3</sup>
  - How robust they are<sup>2,4</sup>
  - How they should be calculated<sup>5,6</sup>
  - How they relate to visual assessment of activity distribution heterogeneity<sup>7</sup>

- How they relate to the spatial organisation of cells as seen on pathological slides<sup>8</sup>

<sup>1</sup>Lartizien et al IEEE J Biomed. Health Inform 2014
<sup>2</sup>Orlhac et al J Nucl Med 2014
<sup>3</sup>Hatt et al J Nucl Med 2015
<sup>4</sup>Yan et al J Nucl Med 2015
<sup>5</sup>Orlhac et al Plos One 2015
<sup>6</sup>Leijenaar et al Sci Rep 2015
<sup>7</sup>Orlhac et al J Nucl Med 2016b (in press)
<sup>8</sup>Orlhac et al J Nucl Med 2016a