Complementarity of PET texture features with respect to the information provided by metabolic volume, uptake-standardized value and total lesion glycolysis: effect of resampling method.

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AIM: To study the complementarity of texture features (TF) and conventional indexes information for two resampling methods in TF computation.

INTRODUCTION

- An increasing interest is focusing on **metabolic heterogeneity characterization** by PET image features (IF) for its use in **prognosis** and **monitoring** of radiotherapy treatment response for lung cancer patients.

Which **resampling method** for texture features computation maximize the **complemental information that PET-TF** could provide **with respect to the conventional indexes** (maximum Standard Uptake Value SUV_{max}, metabolic volume **V** and total lesion glycolysis **TLG)** ?

MATERIALS & METHODS

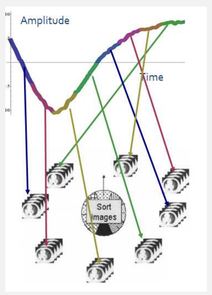
31 (36 lesions) lung cancer patients

- 73 ± 8 y
- 311 ± 60 MBq FDG
- **Tumor localization**: 43% low - 13% middle - 42% upper lobe
- **Respiratory Motion Amplitude**: average 7 ± 5 mm & maximum 23 mm.

4D- PET/CT acquisition

Philips System GEMINI TF TOF (64)

- PET and CT acquisitions **synchronized to the breathing cycle.**
  - Pressure sensor belt: *Mayo Clinic Respiratory Feedback System*
- Data processing results in 10 **phases.**



- 15 min (PET) and 33 s (CT)
- BLOB-OSEM-TOF
  - 2 iterations & 33 subsets
- Image voxel volumes
  - CT: 1.17x1.17x3 mm^3
  - PET: 4x4x4 mm^3

Tumor segmentation

- **PET volume ($VOI_{40\%}$):** contouring lesions by a fixed threshold of 40% of the lesion maximum intensity. Its feasibility for texture features computation has been previously proved with heterogeneous phantoms [1].

Resampling method (SUV discretization)

– **RN**. Tumor intensities were resampled with a constant number of bins (eq. 1) with N=16, 32 and 64 [2].

$$RN_k = N.\frac{SUV_k - SUV_{min}}{SUV_{max} - SUV_{min}} \quad (1)$$

$$RW_k = \frac{SUV_k}{W} - |min[\frac{SUV_{1...Z}}{W}] + 1 \quad (2)$$

– **RW**: the width of the resampling bin (SUV resolution) was constant along the lesions (eq. 2) with W=0.05, 0.1 and 0.5 [3].

Analysis

PET Image features: For TF calculation, the 3D version of the gray-level co-occurrence matrix (GLCM), gray level run length matrix (GLRLM) and neighborhood gray tone difference matrix (NGTDM) were computed.

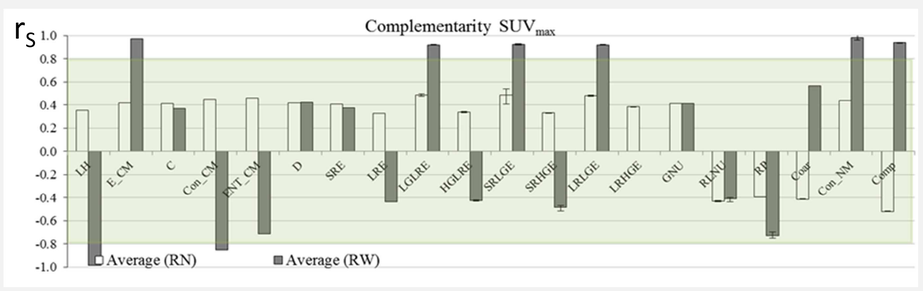
GLCM	Local Homogeneity (**LH**), Correlation (C_{CM}), Contrast (Con_{CM}), Energy (E_{CM}), Entropy (Ent_{CM}), and Dissimilarity(D)
GLRLM	Short Run Emphasis (**SRE**), Long Run Emphasis (**LRE**), Low Gray-Level Run Emphasis (**LGRE**), High Gray-Level Run Emphasis (**HGRE**) , Short Run Low Gray-Level Emphasis (**SRLGE**), Short Run High Gray-Level Emphasis (**SRHGE**), Long Run Low Gray-Level Emphasis (**LRLGE**), Long Run High Gray-Level Emphasis (**LRHGE**) Gray-Level Non-uniformity (**GNU**), Run Length Non-uniformity (**RLNU**) and Run Percentage (**RP**)
NGTDM	Coarseness (**Coar**), Contrast (Con_{NM}), Complexity (**Comp**) and Texture Strength (**TS**)

Spearman´s correlation (p<0.05): We considered **TF with added value** the ones that did not show strong correlation with any of the 3 conventional indexes: p>0.05 or (p<0.05, r<0.8) for all indexes.

RESULTS

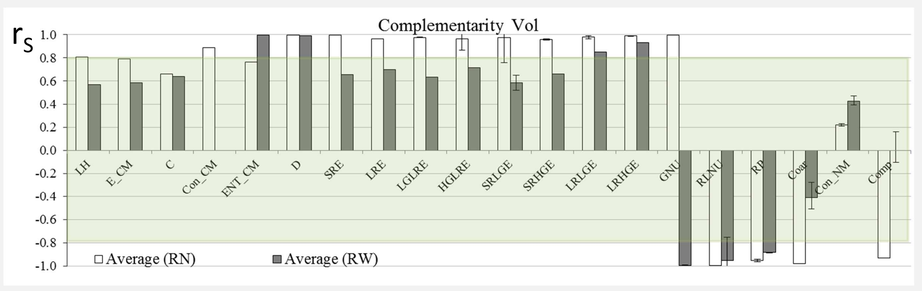
– **PET TF** were **averaged over the 10 time frames of 4D-PET** (normal distributed). We studied the correlations of **TF** with respect to the **metabolic volume (Vol), maximum uptake-standardized value (SUV_{max}) and total lesion glycolysis:**

➢ Spearman´s correlation coefficients (r_s) showed that TF complementarity with respect to conventional indexes was dependent on the resampling method.



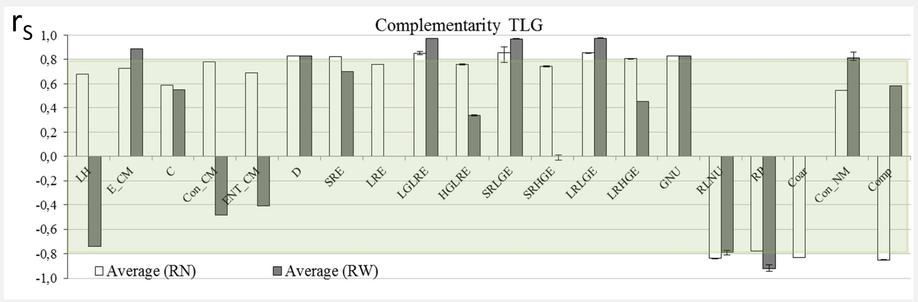
➢ For RW stronger correlations with SUV_{max} were found:

0/20 TF for RN and 8/20 for RW



➢ TF with RN were more correlated with volume:

16/20 TF for RN and 7/20 TF for RW



10/20 TF for RN and 8/20 for RW

RW gave rise to the largest number of TF with added value

RN (16)	RN (32)	RN (64)	RW (0.05)	RW (0.1)	RW (0.5)
4	4	4	5	7	6
Con_CM	Con_CM	Con_CM	Con_CM	Con_CM	Con_CM
C	C	C	Con_NM	Con_NM	Con_NM
D	D	D	LGRE	LGRE	LGRE
Comp	Comp	Comp	SRLGE	SRLGE	SRLGE
			LRLGE	LRLGE	GNU
				D	D
				LRE	

CONCLUSIONS

✓ From the results, **RW with a SUV resolution of 0.1 should be recommended** as the resampled method to use in PET-TF computation **for tumor heterogeneity quantification**

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