Spotting L3 Slice in CT Scans using Deep Convolutional Network and Transfer Learning

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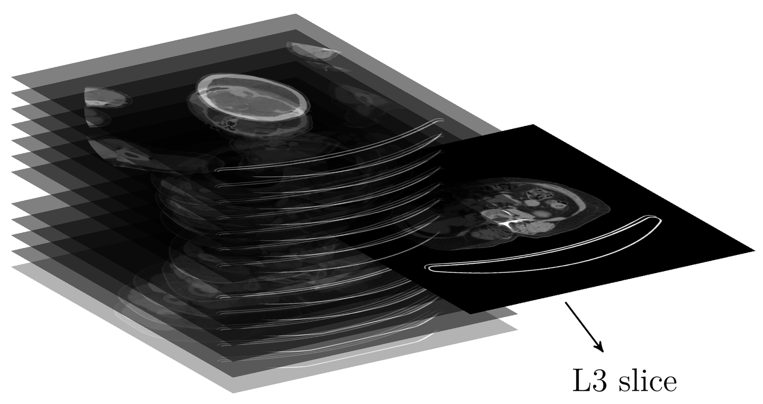
① Context & Problem Description

Data



- Collaboration with Henri-Becquerel center, Rouen.
- L3CT1: a dataset composed of 642 computerized tomography (CT) scans provided by Henri-Becquerel center. A scan is a stack of 2D images.
- Provided annotation: the position of the 3rd lumber vertebra.

Task

⇒ Locate the L3 slice.
- Input: a new CT scan.
- Output: position of the L3 slice.

Difficulties

- Inter-patients variability.
- Visual similarity of the L3 slice.
- The need to use the context to localize the L3 slice.

Proposed Solution

⇒ Use machine learning (regression): Deep convolutional networks.

Machine Learning Issues

- Few training samples.
  ⇒ use transfer learning.
- High dimension of the input data (3D CT scan).
  ⇒ use frontal Maximum Intensity Projection (MIP) (pre-processing).
- Variability of the hight of the input data.
  ⇒ use sliding window + maximum correlation (post-processing).

② Proposed Pipeline

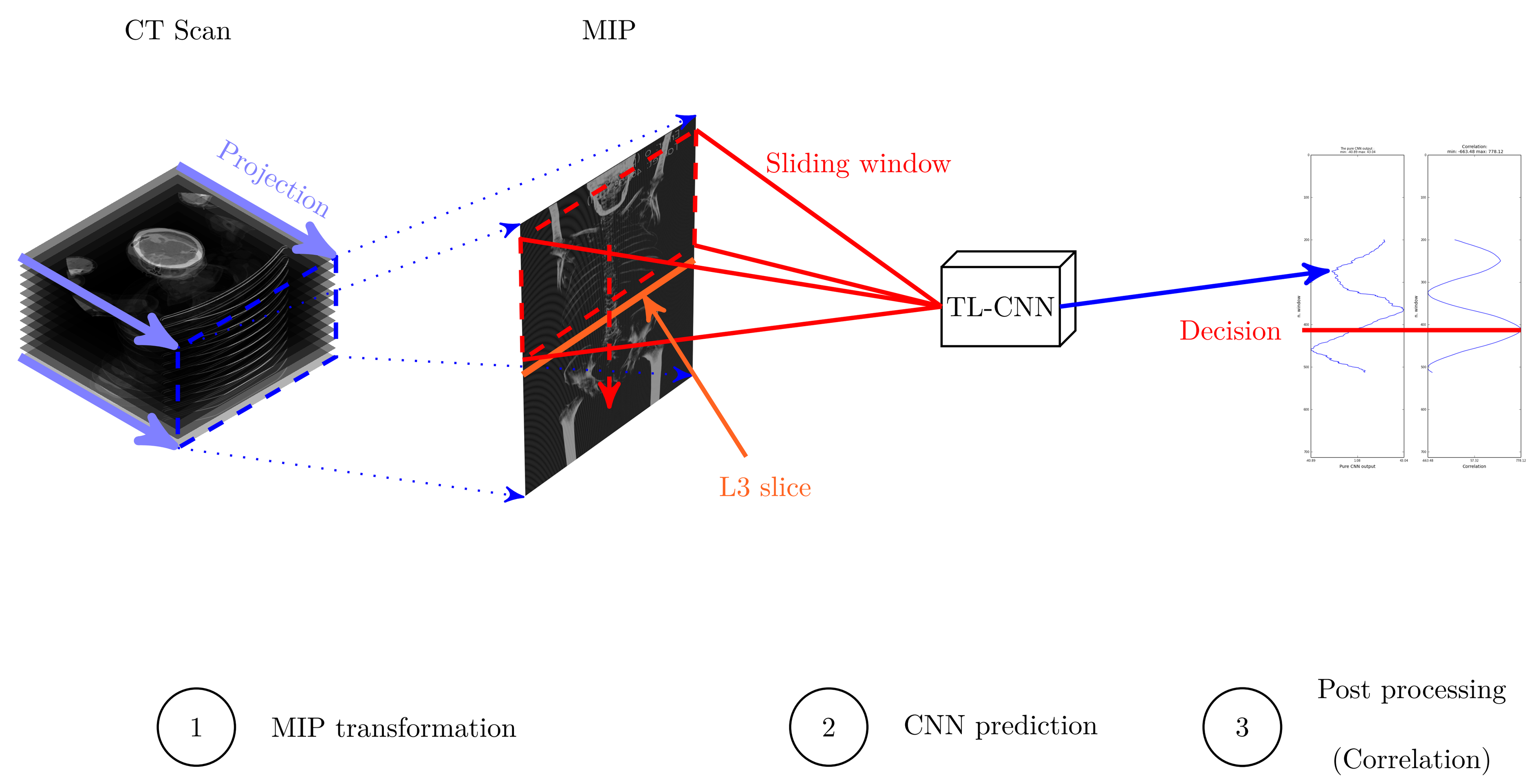


Figure 1 : System overview describing the three important stages of our approach : MIP transformation, TL-CNN prediction, and post processing.

CNN: Convolutional Neural Network. TL: Transfer Learning. MIP: Maximum Intensity Projection.

③ Training

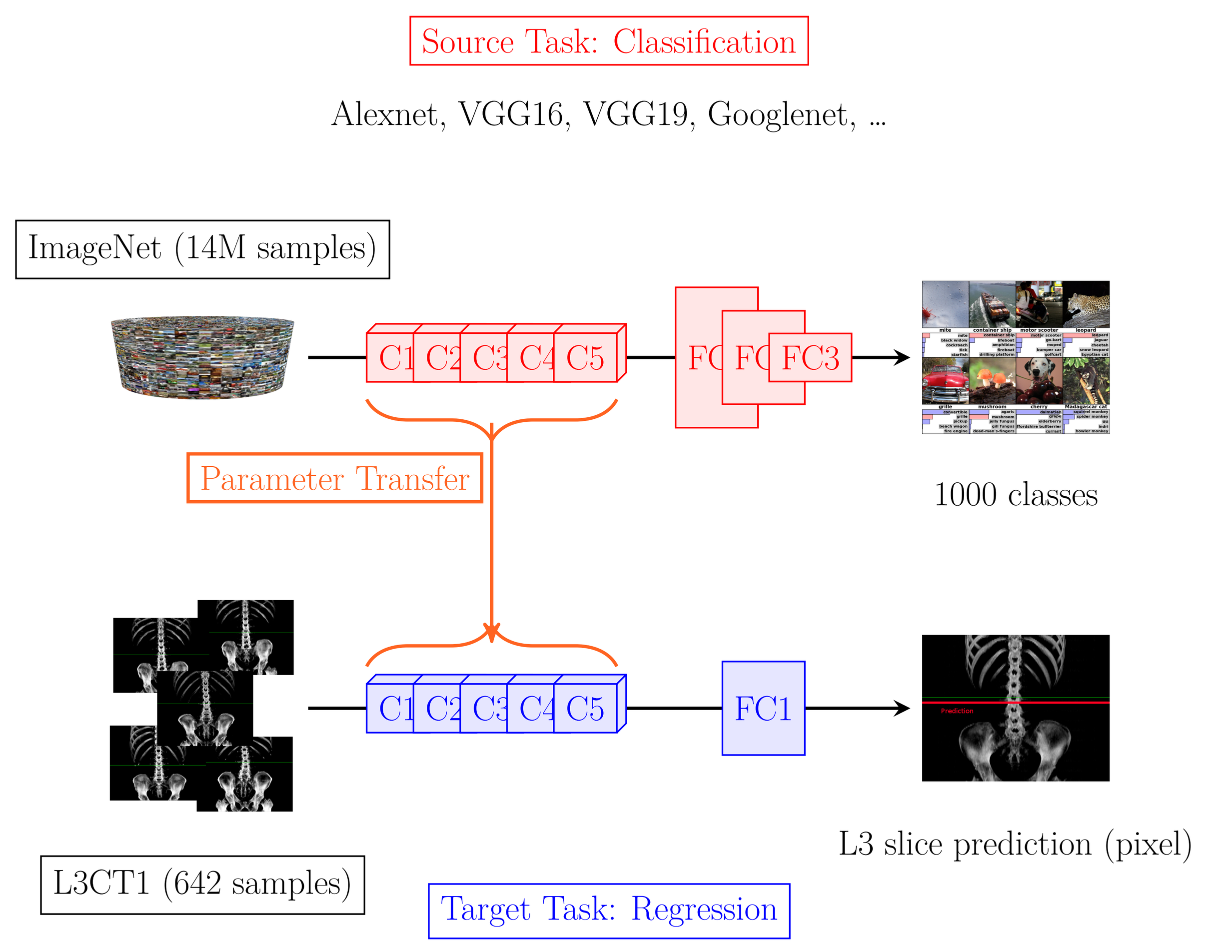


Figure 2 : System training using transfer learning. Layers C_i are Convolutionnal layers, while FC_i denote Full Connected layers. Convolution parameters of previously learned ImageNet classifier are used as initial values of corresponding L3 regressor layers to overcome the lack of CT training examples.

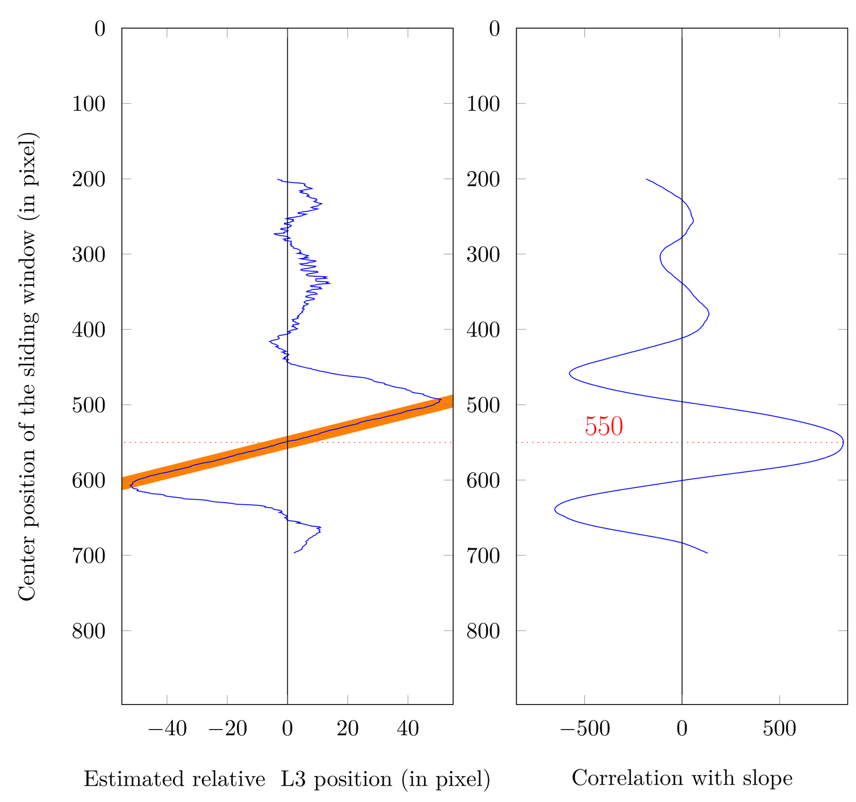


Figure 3 : Post-processing using correlation. [left]: CNN output sequence obtained for H = 400 and a = 50 on a test CT scan. The sequence contains the typical straight line of slope −1 centered on the L3 (the theoretical line is plotted in orange), surrounded by random values. [right]: correlation between the CNN output sequence and the theoretical slope. We retain the maximum of correlation as an estimation of the L3 position.

④ Results

	RF500	CNN4	Alexnet	VGG16	VGG19	Googlenet
fold 0	7.31 ± 6.52	2.85 ± 2.37	2.21 ± 2.11	2.06 ± 4.39	1.89 ± 1.77	1.81 ± 1.74
fold 1	11.07 ± 11.42	3.12 ± 2.90	2.44 ± 2.41	1.78 ± 2.09	1.96 ± 2.10	3.84 ± 12.86
fold 2	13.10 ± 13.90	3.12 ± 3.20	2.47 ± 2.38	1.54 ± 1.54	1.65 ± 1.73	2.62 ± 2.52
fold 3	12.03 ± 14.34	2.98 ± 2.38	2.42 ± 2.23	1.96 ± 1.62	1.76 ± 1.75	2.22 ± 1.79
fold 4	8.99 ± 7.83	1.87 ± 1.58	2.69 ± 2.41	1.74 ± 1.96	1.90 ± 1.83	2.20 ± 2.20
Average	10.50 ± 10.80	2.78 ± 2.48	2.45 ± 2.42	$\mathbf{1.82 \pm 2.32}$	1.83 ± 1.83	2.54 ± 4.22

Table 1 : Cross-validation. Error expressed in slice over all the folds using different models: RF500 (random forest with 500 random trees), CNN4 (homemade model), and Alexnet/VGG16/VGG19/GoogleNet (pre-trained models).

Errors (slices) / operator	CNN4	VGG16	Ragiologist #1	Radiologist #2	Radiologist #3
Review at time t_1	2.37 ± 2.30	1.70 ± 1.65	0.81 ± 0.97	0.72 ± 1.51	0.51 ± 0.62
Review at time t_2	2.53 ± 2.27	1.58 ± 1.83	0.77 ± 0.68	0.95 ± 1.61	0.86 ± 1.30

Table 2 : New evaluation set: 43 CT scans annotated (at two different times t_1, t_2) by the same reference radiologist who annotated the 642 CT scans. Three radiologists were asked to locate the L3 slice. The table shows the comparison of the performance of both the automatic systems and three radiologists. The L3 annotations given by the reference radiologist (and the the three other radiologists) vary between the two reviewing periods.

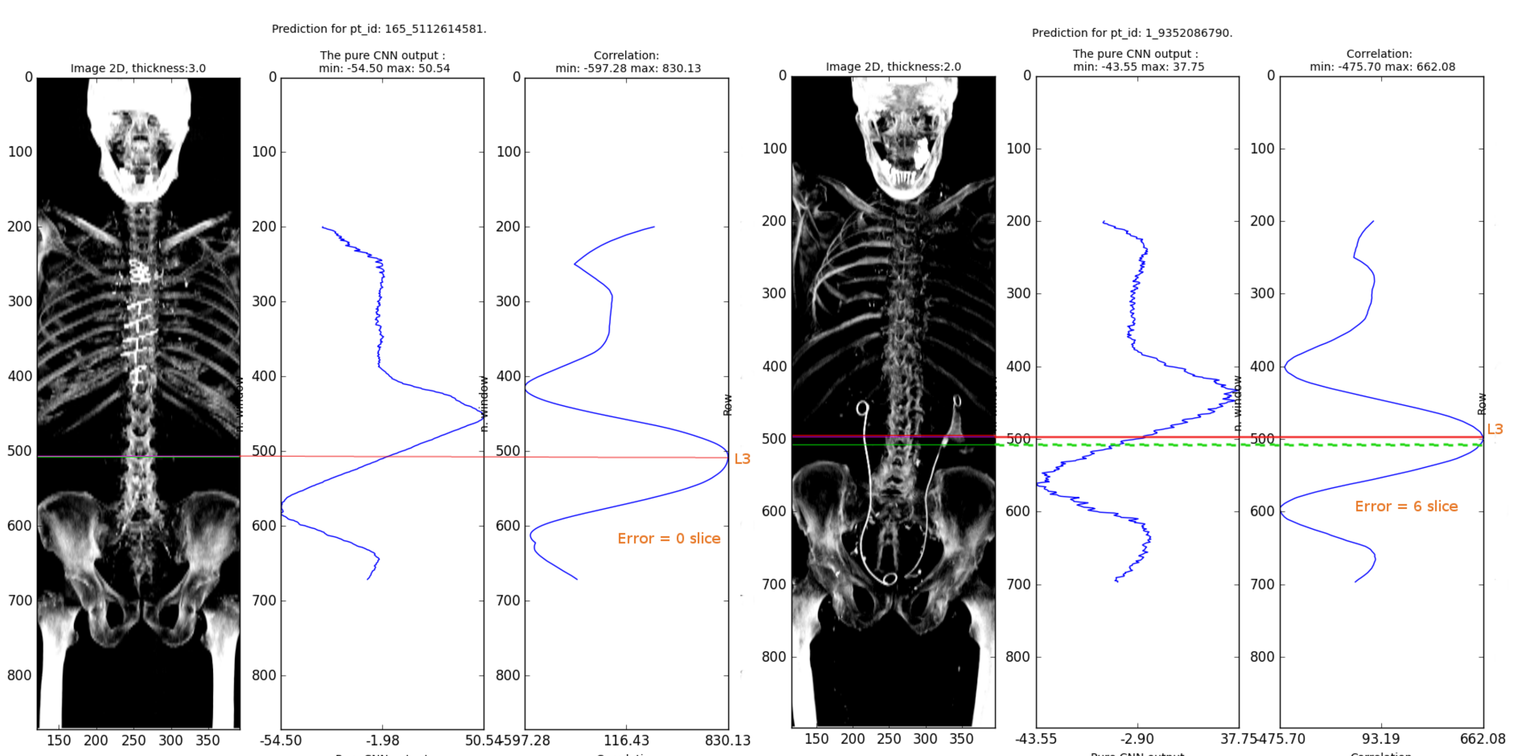


Figure 4 : Examples of predictions on test sets. [Left]: Localization error: 0 slice.. [Right]: Localization error: 6 slice..

Valorization: This work has been integrated in the software of the project "BodyComp.AI" who won one of the 2017 French Innovative Unicancer Prize. This software has been diffused to the European centers for cancer.

Rouen, 2018. ✦ Henri-Becquerel center, Rouen. "Deep In France" ANR-16- CE23-0006. soufiane.belharbi@insa-rouen.fr.