

## **Deep learning for joint super resolution/segmentation: Application to the 3D imaging of the bone structure.**

This work is proposed in team 4 "Tomographic Imaging and Radiotherapy" of the CREATIS laboratory (UMR CNRS 5220, Inserm U1044) of INSA de Lyon and University Lyon I. CREATIS is a research unit specialized in medical imaging and gathering both specialists in signal and image processing, image acquisition as well as medical doctors (180 researchers).

Team 4 is working on tomographic methods for the characterization of bone tissue. This application is motivated by the research on bone fragility disease such as osteoporosis since the risk of fracture is not fully understood and remains difficult to predict. In particular, the team has a long collaboration with the ESRF in Grenoble (European Synchrotron Radiation Facility) in synchrotron micro-tomography imaging. The team has done extensive work on the micro-CT characterization of bone micro architecture and has a high notoriety in this field [1-5]. We are interested in bone imaging at all scales, from the tissue to the patient scale. The investigation of trabecular bone micro-architecture provides relevant information to determine the bone strength. Yet, the spatial resolution of clinical CT scanners is not sufficient to resolve the trabecular structure. High Resolution peripheral Quantitative CT (HR-pQCT) systems have been developed to investigate bone micro-architecture in-vivo at peripheral sites (tibia and radius) on patients.

In previous work, we have investigated super-resolution approaches for improving the quantitative analysis of in-vivo HR-pQCT images of the trabecular bone structure. Since our main goal is the quantification of the binary trabecular bone micro-structure images, we have developed a joint super-resolution/segmentation method. For this purpose, we proposed using a prior based on Total Variation with a convex relaxation (TVbox). The method was implemented using an ADMM algorithm. The validation of the proposed methods was made on experimental micro-CT bone images after simulating the effect of blur, a loss of spatial resolution and degradation by noise (see an illustration in Figure 1) [6-8]. The results showed an improvement of the bone parameters and 3D connectivity with the TVbox method. However the applications of these method is more difficult on experimental HR-pQCT, due to the unknown point spread function, and possibility non-stationary Gaussian noise in such images. To that aim, additional algorithms regarding the estimation of the point spread function and the investigation of additional regularization schemes were developed [9-10].

In the present work, we propose to investigate deep learning approaches to solve this problem, and evaluate it on a clinical image data base.

With the increase of computing resources, the interest of deep learning approaches is booming. In particular, there are an increasing number of applications in medical image analysis. In this work, we aim to use deep learning to solve the joint super resolution/segmentation problem. Based on preliminary tests we believe that such approaches may be very promising to solve our problem, which is so far totally original.

Different schemes will be considered to perform this task based on the knowledge of low and high-resolution images of ex vivo samples. In a first step, the aim will be to optimize the structure and parameters of the networks with respect to the quality of the super resolved images [11,12]. The later will be assessed by comparing the usual quantitative parameters used for the quantification of bone micro architecture, and in particular connectivity parameters. Different schemes will be investigated based on the recent advances on deep learning approaches. In a second step, the method will be evaluated on a large clinical image data base to study if the proposed method allows improving the discrimination of fracture and non-fractured patients.

### **Supervision :**

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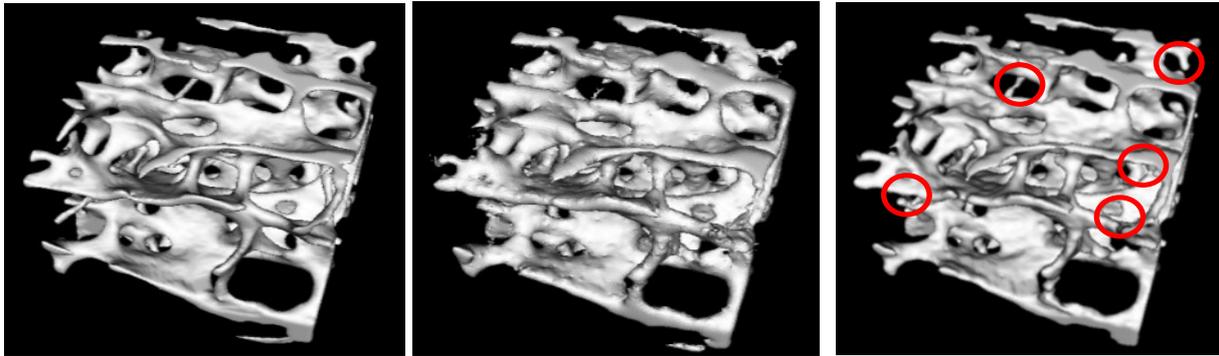


Figure 1 : Left : original 3D bone micro architecture (voxel size at 40 $\mu$ m), middle : degraded image (voxel size 80 $\mu$ m), right : super resolution image (voxel size 40 $\mu$ m) obtained from the TV Box algorithm

#### Publications of the team

1. Salome M., Peyrin F., Cloetens P., Odet C., Laval-Jeantet A.M., Baruchel J., Spanne P., A synchrotron radiation microtomography system for the analysis of trabecular bone samples, *Med. Phys.*, oct. 1999, vol 26, n° 10, p. 2194-2204
2. Nuzzo S., Peyrin F., Cloetens P., Baruchel J., Boivin G., Quantification of the degree of mineralization of bone in three dimension using Synchrotron Radiation Microtomography, *Med Phys*, Nov. 2002, vol 19, n° 11, p. 2672-2681.
3. Peyrin F., Attali D., Chappard C., Benhamou C.L., Local plate/rod descriptors of 3D trabecular bone micro-CT images from medial axis topologic analysis, August 2010, *Med. Phys.* vol 37, n° 8, pp. 4364-4376
4. Dong P, S Hauptert, Gouttenoire PJ, Laugier P, Peyrin F., 3D osteocyte lacunar morphometric properties and distributions in human femoral cortical bone using synchrotron radiation micro-CT images, *Bone*, vol 12,n° 60, pp. 172-185, 2014
5. Zuluaga M, Orkisz M, Pacureanu A, Dong P, Peyrin F., Bone Canalicular Network Segmentation through Geodesic Voting and Image Tessellation in nano-CT Images, *Physics in Medicine and Biology*, vol 59, no. 9, pp. 2155-217
6. Toma A, Sixou B., Peyrin F, Iterative choice of the optimal regularization parameter in TV image restoration, *Inverse Problems and Imaging*, 2015, vol 9, n° 4, pp 1171-1191.
7. Toma A, Sixou B, Denis L., Pialat JB, Peyrin F., Total Variation Based Super-Resolution From A Single Trabecular Bone, *IEEE International Symposium on Biomedical Imaging (ISBI)*, Pékin, China, pp. 1152-1155, April 2014
8. Toma A, Denis L., Sixou B, Pialat JB, Peyrin F., Total Variation Super-Resolution for 3D trabecular bone micro-structure segmentation, *Eusipco 2014*, Lisbonne, Sept 2014, pp. 2220-2224, Aout 2014.
9. Li Y, Toma A, Sixou B, Peyrin F., Super-Resolution/Segmentation of 2D Trabecular Bone Images by a Mumford-Shah Approach and Comparison to Total Variation, *Eusipco 2016*, Bucarest, Proc 4p.
10. Li Y, Sixou B, A. Burghardt Peyrin F., Super-Resolution/Segmentation of 3D Trabecular Bone Images with Total Variation and Nonconvex Cahn-Hilliard Functional, *IEEE ISBI (Int Symposium on Biomedical Imaging)*, Melbourne, Australia, 18-21 April 2017 (4p.), pp. 1193-1196

#### Publications on super resolution and deep learning

11. Dong C, Loy C.C, He K., X.Tang X. , Image super-resolution using deep convolutional networks, 2015, 38(2) 295-307.
12. Ye J.C., Han Y., Cha E., Deep convolutional framelets: a general deep learning framework for inverse problems arXiv preprint arXiv:1707.00372 (2017).

#### Scientific competence:

B.Sixou received a M.Sc degree in Physics from ENS Lyon, France and a Ph.D degree from University of Grenoble, France in 1994 and 1996 respectively. Since 1999, he is assistant Professor in Physics in the National Institute for Applied Science (INSA) in Lyon, France. Since 2011, he focuses his research activity in the Creatis

laboratory specialized on biomedical imaging. His is the author of more than 50 papers in material science and applied mathematics. His current research interests are applied mathematics, inverse problems, phase retrieval, tomography.

Françoise Peyrin received her doctorate degree in Computer Sciences in 1982 from INSA-Lyon, France. Since 1981, she has been a researcher in the CREATIS Laboratory at INSA-Lyon. Her research interests include 3D imaging techniques particularly in x-ray tomography, 3D image analysis and wavelet based methods. The research is particularly applied to bone tissue imaging. She leads a group in the laboratory and is a scientific collaborator at the ESRF, Grenoble, France. She is the author of more than 180 papers in peer reviewed journals and 350 international conferences among which more than 150 in IEEE ICASSP, ICIP or ISBI conferences.

## II-7 Ingénierie biomédicale, Biomedical engineering

The student should have knowledge in signal and image processing, computing and should know matlab and python. He should be interested in the whole imaging chain, from image acquisition to image reconstruction. He or she should have interest in biomedical research and should be ready to collaborate with various multidisciplinary teams.