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Using Repetitive Patterns on a Block-Matching Algorithm for Vessel Tracking in 2D and 3D Ultrasound Sequences

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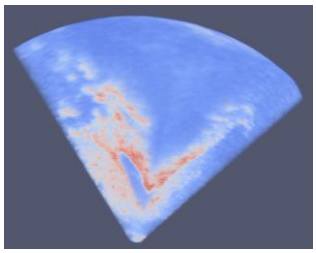
Abstract

Ultrasound imaging is ever more used image guidance during cancer treatments, as it is a high temporal resolution and non-invasive medical imaging solution. One problem is the managing of organ motion during treatment. I propose a robust and real-time solution.

Description of my work

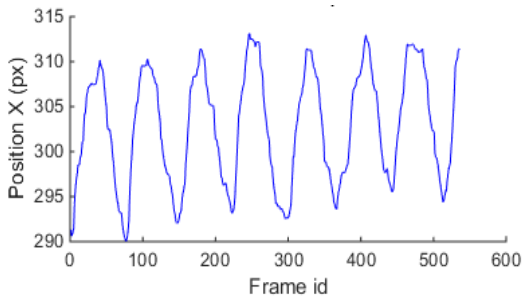
Based on the publications from my supervisor [1], I have implemented a whole pipeline in C++ to track vessels very fast for 2D and 3D images. It includes two parts: a learning-phase uses a registration and builds a Principal Components Analysis space; an application phase computes a Block Matching Algorithm very fast.
Using templates and a cross-compiled library (Insight Toolkit [2]), it is universal and can easily be adapted.

Then, I have fully automatized parameters, improved it, and tested it on around 180 000 images in MICCAI clusters. A article (unpublished) has been written.

Results

More than 4000 lines of code have been written, tested and validated. The mean tracking error is 2,34 mm for 2D and 0,89 mm for 3D, and comparable to the state-of-the-art.
In 2D images, the application phase's duration is less than 10 ms per frame, which is less than the acqusition rate and allows real-time treatments.
Some failure cases are however not well handled.



Conclusion

Results are satisfying and the goals are achieved. The estimation of some parameters could still being improved with a Bayesian framework [3]
Real-time could also be achieved with a parallelized code combined with graphics processing.

Bibliography

[1] De Luca, V. (2013). Liver motion tracking in ultrasound sequences for tumor therapy.
[2] Ibanez, L., Schroeder, W., Ng, L., & Cates, J. (2005). The ITK Software Guide.
[3] Yuan, X., & Shen, X. (2008). Block matching algorithm based on particle swarm optimization for motion estimation