PUMA

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Extremely simplified MRF introduction

- Generate a dictionary of possible Magnetic Resonance signals
  - Consider points in the space of tissue parameters, for example t1 and t2 relaxation times
  - One dictionary entry for each point
- For each dictionary entry, calculate the expected MR signal

- After acquiring one MR image, compare each pixel with all entries in the dictionary.
  - The comparison is performed as a scalar product between the data and each dictionary entry
  - The dictionary entry with the highest scalar product is used as estimate of the tissue parameter

- Result: a quantitative estimate of tissue parameters in each point.

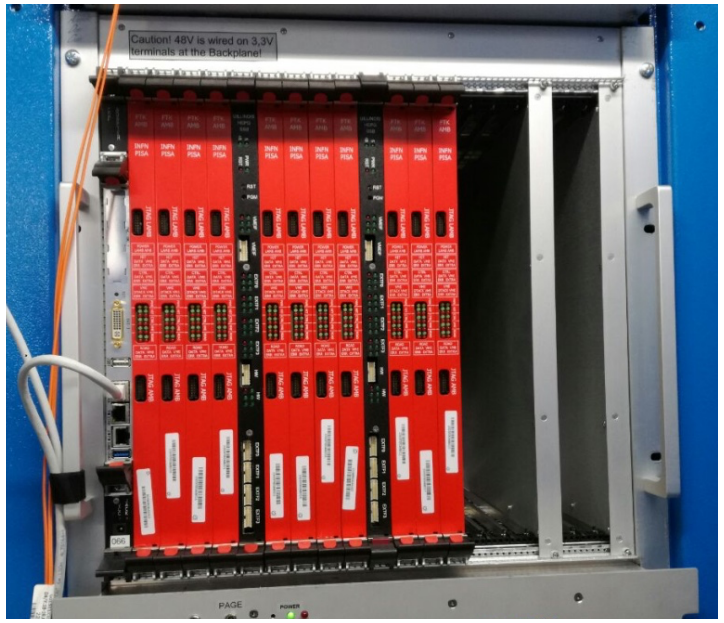
Goals for PUMA

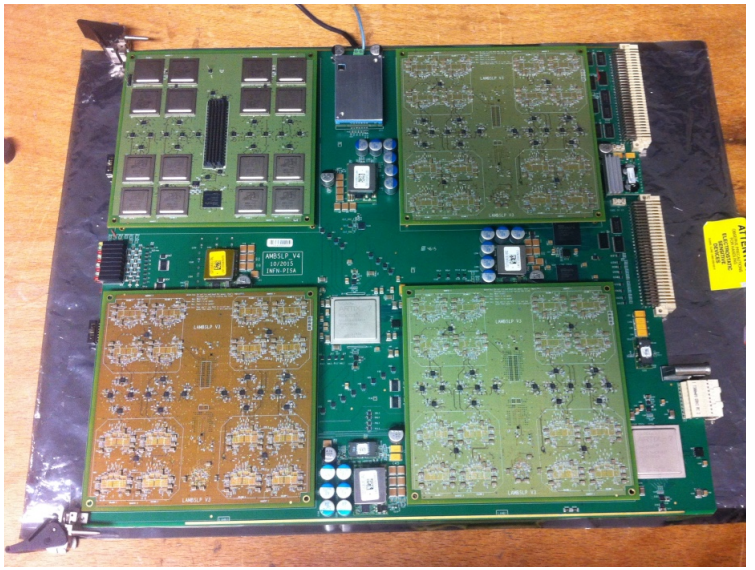
- The main goal of the PUMA project is to provide a speed up of MRF processing using the Associative Memory

- For MRF applications, we estimate potential processing time reduction of a factor ~400 for the FTK AM, ~5000 for the HTT one compared to state of the art.

Associative Memory for MRF

- Use the Associative Memory (AM) to compare the acquired pixels with the dictionary entries
- The idea is to convert dictionary entries in AM patterns in advance
- For each MR image, compare the MR signal from each pixel with all AM patterns in parallel
  - Typical execution time with current HW 3 microseconds per pixel
- The matched pattern(s) of each pixel provide pointer(s) to the original dictionary entries
- Second step: refine the tissues parameter estimate





Potential performance gains

	Number of patterns	Intel® Xeon® processor E5-2600 v4 (48 cpu)	NVIDIA Tesla K80 GPU	PUMA expectations (estimated)
1. MR Relaxation times only	250 000 (each 10 complex singles)	615 s	340 s	~0.5s
2. Adding fat fraction estimations	3 186 414 (each 30 complex singles)	6.5 hours	3 hours	~2s
3. Adding two blood perfusion parameters	3 e8 (each 30 complex singles)	27 days (estimated)	14 days (estimated)	~150s
4. Adding diffusion tensor estimations	1.56 e10 (each 10 complex singles)	3.5 years (estimated)	1.5 years (estimated)	~1h

This assumes the use of AM09

Table 1 Benchmark values (time per each exam) for reconstructing 3D MR Fingerprinting on a brain using a 128x128x128 image matrix, with: 1) The current dictionary, used in on going clinical trials. 2) A recently demonstrated technique, including useful diagnostic information on the local fat fraction, which is difficult to use in clinical trials due to long matching times. 3) A technique currently difficult to demonstrate due to long matching times, including blood perfusion. 4) A model including the whole water diffusion tensor, currently intractable.

PUMA goal from the proposal

- The most important goal of the project is the reconstruction of some MRI images with this setup and evaluate the timing performances and the diagnosis accuracy to be compared with the state of the art. This would make the FTK AM ready for usage for MRI imaging.

Work Packages

- WP1: Detailed Simulation of the full MRF algorithm to check the HW. Leader Buonincontri, FSM; INFN and Elios collaborate. This WP includes the study of the MRF dictionary to be downloaded in the HW.
- WP2: HW commissioning. Leader Annovi, INFN, EMC and FSM collaborate. The technology and the AM ASIC that is the most innovative device have been proposed for the first time by INFN Pisa, designed and produced by INFN and LPNHE for two HEP experiments [2], [3]. INFN Pisa is the most expert of this technology today. This WP includes the AM bank production/optimization.
- WP3: MRF algorithm acceleration. Leader Rossi, Elios; INFN, EMC and FSM collaborate. This work package includes: (a) the software to connect the algorithm executed in the CPU with the pattern matching executed in the HW; (b)the eventually needed FW adaptations.
- WP4: Measurement and evaluation of timing and accuracy performances. Leader Buonincontri, FSM?; INFN, Elios, EMC, GEHC participate.

Deliverables

D.1.1 MRF Dictionary definition and its organization in the AM bank (for pattern matching) ready. M3

Available for MR relaxation times only. See Orlando's talk

D.1.2 Full simulation of MRF algorithm ready. M5

First step (AM) done for MR relaxation times only. See Orlando's talk

To be completed with more sophisticated banks, and with a second processing step.

D2.1 VME crate (HW) and AMboard ready for tests. M5

Ready from FTK

D3.1 Software and FW needed to download data and recover results to/from VME crate, ready for tests. M5

Initial version of SW and FW ready. Need to convert files from Orlando into formats for the HW test.

D4.1 Results of a group of MRI reconstructed with new technology; evaluation and comparison with state of the art. M11

Ready to start with pattern banks for MR relaxation time.

Need further offline studies to increase parameters, e.g. add fat fraction estimations

Need offline studies for the refinement after AM output, to complete image processing,

D4.2 Dissemination, Exploitation plan. M12

Milestones

Milestone 1: HW, SF and FW ready for tests. M5

ok

Milestone 2: ~5 MRI images processed with MRF algorithm accelerated by the VME crate. M10

Next step: test with HW & consider more complex processing

Milestone 3: decision between (a) continuation with the VME HW; (b) production of a more friendly setup; M12

Rather than decision, evaluate pros and cons of both options