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Processing-in-Memory to speed up NGS analysis

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All current computing platforms are designed following the von Neumann architecture principles, originated in the 1940s, that separate computing units from memory. Processing-in-memory (PIM) consist of processing capabilities tightly coupled with the main memory. Contrary to bringing all data into a centralized processor, which is far away from the data storage, in-memory computing process the data directly where it resides, suppressing most data movement, and, thereby greatly improving the performance of massive data application by orders of magnitude.

NGS data analysis completely falls in these application domains where PIM can strongly accelerate the main time-consuming software in genomic and metagenomic areas. More specifically, mapping algorithms, intensive sequence comparison algorithms or bank searching, for example, can highly benefit of the parallel nature of the PIM concept.

New memory components based on PIM principles have been developed by the UPMEM company, a young startup created in 2015. The company has designed an innovative DRAM Processing Unit (DPU), a RISC processor integrated directly in the memory chip, on the DRAM die. An UPMEM PIM server counts no less than 2560 DPUs for 160 GB of PIM memory and 256 GB of legacy memory.

First experiments on the UPMEM PIM server have demonstrated that an average speed-up of X20 can generally be obtained on various time-consuming tasks of NGS pipelines.

The talk will detail the concept of Processing-in-Memory, which category of NGS algorithms can benefit of the PIM architecture, the way they can be parallelized on such structure, and what are the expected gains compared to a standard multicore platform.