Improving the Performance of a CUDA algorithm

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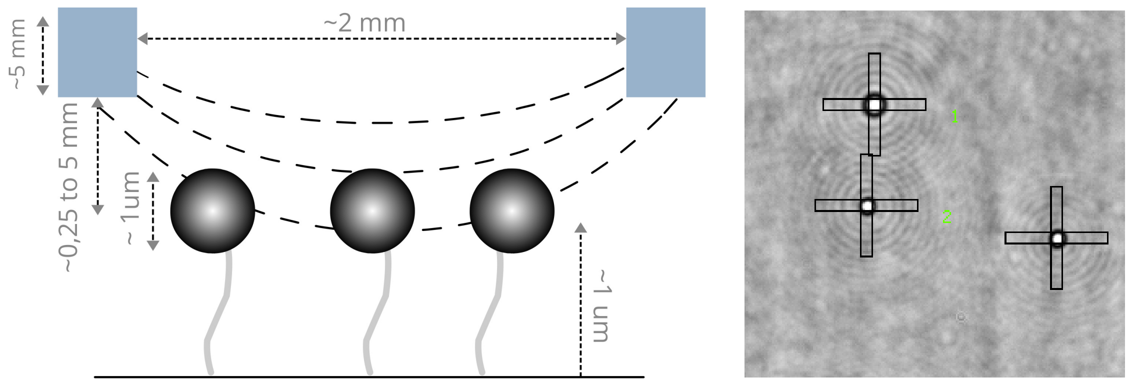
In this project, we propose to optimize an existing CUDA code, which is currenlty used for tracking micron-sized particles at high frequencies [**Level: M1/2 (with background in Mathematics and Informatics). Good knowledge of C++ and CUDA is mandatory**]

Magnetic Tweezers (MT) is a single-molecule technique that relies on the tracking of micron-sized particles (to which single bio-molecules are attached). Using advanced algorithms, fast camera (with allows to average signals) and powerful sources (to reduce shot noise), it is possible to track those particles (in all 3 directions) with an accuracy that is much below one nanometer (e.g. ∼ 1/1000 of a pixel) in a bandwidth of a few tens of Hz. Because these length and time scales are typical of that of enzymatic reactions, MT attracts a considerable attention in biophysics.
The software we are using (Labview + CUDA, X64) allows to track 20,000+ beads par second. Still, we believe it could be signicantly improved using (i) an optimize choice of parameters (grid, blocks) for specific functions and (ii) a better memory management.
To do so, we are looking for a motivated student with a good knowledge of CUDA.



[Here, a single molecule is attached on one end to a glass surface and at the other end to a magnetic bead. A magnetic field (produced by a pair of permanent magnets) attracts the bead (the force acting on the bead depends on the distance between the bead and the magnets). Using a slightly coherent source of light (that generates diffraction rings around the beads), the x, y and z positions of the beads can be determined with sub-nanometer accuracy. Subsequently, the force acting on the bead is measured from the variance of the x and y positions. The magnetic field is homogeneous over large distances (mm, parallel to the glass slide) and varies slowly with the distance (perpendicular to the glass). Therefore, multiple beads (up to hundreds of beads) can be studied in parallel at a constant force. While force versus extension curves can be measured, MT are best suited to study molecular motors (at a constant force) or enzymes that have a topological effect on DNA]