**Running the OpenCL version of PaSWAS**

The application is executed through the *run* script which is located in the *paswas\_opencl\_final* folder.  
This script is executed as follows:

./run <Sequence file> <Target file> <Total #sequences> <Total #targets> <Scoring> <Minimum score> <Partitioner> <Threshold>

The parameters are elaborated briefly:

* Sequence file: location of the sequence file.
* Target file: location of the target file.
* Total #sequences: number of sequences in the sequence file.
* Total #targets: number of sequences in the target file.
* Scoring: Scorings matrix to use (DNA\_RNA, BLOSUM62 or BASIC)
* Minimum score: alignments will be outputted with at least a score higher than Minimum score (float).
* Partitioner: type of partitioner to use (no\_partitioner, partitioner\_alg\_threshold or partitioner\_alg\_threshold2).
* Threshold: Tuning parameter for partitioning the sequence and target file. A higher value for this parameter allows for a coarser partitioning.

Examples:

Using one of the datasets prepared on the GitHub we can invoke the script as follows:

./run Ig454.fa isotypes.fa 55295 7 DNA\_RNA 350.0 no\_partitioner x

When we do not apply any partitioning (no\_partitioner) the threshold parameter does not have any effect and can be omitted.

If we do apply a partitioning scheme (either partitioner\_alg\_threshold or partitioner\_alg\_threshold2), the OpenCL version of PaSWAS is executed as follows:

./run Ig454.fa isotypes.fa 55295 7 DNA\_RNA 350.0 partitioner\_alg\_threshold 1.0