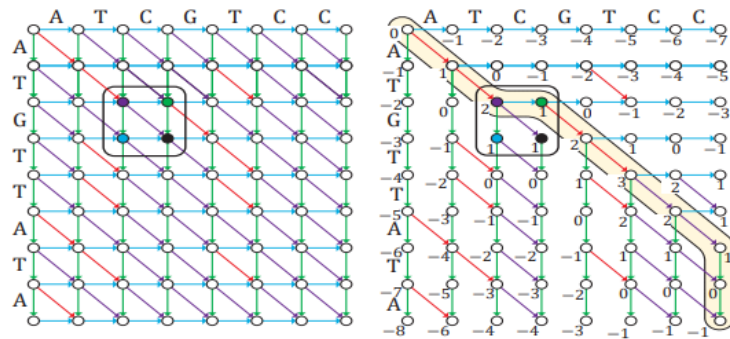


## Accelerating DNA sequencing algorithm in mMPU

Smith-Waterman (SW) is a dynamic programming algorithm used for aligning two sequences against each other (considering Insertions, deletions, and mismatches). This alignment is needed for aligning a 'read' against the 'reference genome', which is a stage in the pipeline of DNA sequencing.

DNA sequencing algorithms require a huge amount of data. Moving this data out of the memory and to the processing units requires a lot of time and power. Thus, to improve performance and power consumption we propose to implement these algorithm inside the memory in what is called a Processing-In-Memory (PIM) Architecture.

In this project, SW is chosen to be implemented inside the memristor Memory Processing Unit (mMPU). It is a unit where data can be stored and processed in the same place.



### Schedule

- Study Smith-Waterman algorithm for Read Alignment
- Learn knowledge about memristors, memristors' in crossbars, and mMPU (memristore memory processing unit)
- implement SW using memristors in the mMPU,
- Simulate the memristive devices based cellular network with real memristive device behavior.

**Prerequisites:** Matlab/Python/Virtuoso,

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