Is bioinformatics a suitable workload for the Cell?

- **Application Characteristics**
  - 8 vectorized cores allow for data level and thread level parallelism found in bioinformatics codes.
  - Regular access to data works well with the explicit data-movement of the SPUs.

- **Programming Choices:**
  - IBM SDK has SPU timing tool which is very effective.
  - Rapidmind does not support char, short and double datatypes on Cell.

- **Coding**
  - Small time consuming kernels with pre-existing vectorized code
  - Local store is insufficient to work for average-sized sequences and the working set.

- **Hardware/ISA issues:**
  - Saturated arithmetic instructions not supported
    - \textit{Vec_adds/subs (2 – 5 -> 0) is not supported natively.}
  - Overflow detection is not well supported.