

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
 - ***Vec_adds/subs (2 – 5 -> 0) is not supported natively.***
- Overflow detection is not well supported.