



# **Performance of Graph and Biological Analytics on the IBM Cell Broadband Engine Processor**

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# Biological Analytic: SSCA #1

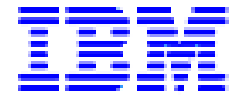


## Background and Intent

- **To develop analytical schemes to identify similarities between sequences of symbols to assist computational biologists**
  - **Optimize for the IBM Cell Broadband Engine Processor**
  - **Find common genes and closely matches between sequences**
- **Five kernels**
- **Methods:**
  - **Local alignment: Water Smith dynamic programming (Kernel 1)**
  - **Searching for similarities (Kernels 2 and 3)**
  - **Global alignment (Kernel 4)**
  - **Multiple alignment: Center Star method (Kernel 5)**
- **Each kernel operates on either the original sequences, the results of the previous kernel, or both**
- **To be entirely integer and character based**



# Graph Analytic: SSCA #2



## Background and Intent

- To develop a scalable synthetic compact application that consists of four kernels requiring irregular access to a large, directed, weight multi-graph
  - Optimize for the IBM Cell Broadband Engine Processor
  - Untimed Scalable Data Generator generates the graph as tuples of vertex pairs and corresponding weights.
- Methods:
  - Cache-friendly adjacency lists (Kernel 1)
  - Parallel scan to classify larger sets of graph (Kernel 2)
  - Parallel BFS (Kernel 3)
  - Dijkstra Single-Source Shortest Path and Betweenness Centrality algorithms(Kernel 4)
- David A. Bader and Kamesh Madduri designed and implemented the first parallel Betweenness Centrality algorithm on symmetric multiprocessors.
- To be entirely integer and character based