15440 - Fall 2017

Project 4

Rubrics

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1 MapReduce K-Means (Points: 50%)

- K-Means using MapReduce for 2D data points (25%)
- K-Means using MapReduce for DNA strands (25%)

Details (these are same for DNA and 2D data points versions):

- The code compiles and runs correctly (1%)
- Create map and reduce classes, extend MapReduceBase and implement Mapper and Reducer (1%)
- Configuring jobs correctly including setting the mapper and reducer classes, the input and output formats, the file input and output formats, launching a job, and looping over for new rounds (3%)
- Read the value of centroids at each mapper (3%)
- Create the map function with correct input and output key-value pairs (i.e., correct input and output formats) (3%)
- Apply K-Means at the mapper (2%)
- Create the reduce function with correct input and output key-value pairs (i.e., correct input and output formats) (3%)
- Compute new means at the reducer (3%)
- Write the value of centroids at each reducer (3%)
- Outputting final results and aborting cleanly (3%)

Rubric continues on the next page

2 Write-up (Points: 45%)

- Performance comparison between sequential, MPI, and MapReduce with a fixed dataset size (10%)
- Development effort comparison between sequential, MPI and MapReduce (2%)
- MapReduce scalability w.r.t 1, 2, and, 4 map slots (10%)
- MapReduce scalability w.r.t 32MB, 64MB, and 128MB block sizes (10%)
- MapReduce scalability w.r.t 1, 2, 3 VMs (10%)
- Performance trade-offs between MPI and MapReduce (2%)
- Thoughts on the applicability of K-Means to MapReduce (2%)
- Recommendations regarding the usage of MapReduce for algorithms similar to K-Means (2%)
- Paper structure, level of writing, and language (2%)

3 Code Style (Points: 5%)

• Method Comments, Block comments, Readability, Dead code, Code Design (5%)