UNIVERSITY
OF TRENTO - Italy
Information Engineering
and Computer Science Department

TIME-SERIES SIMILARITY QUERY ANSWERING USING iSAX ON MAP REDUCE

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Ermias Andargie Walelgne

Advisor:

Prof. Themis Palpanas

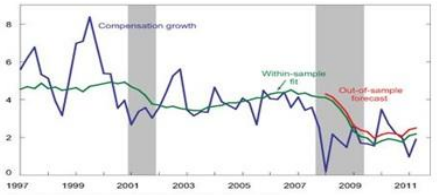
Time Series Data

- An organized discrete sequence of n real number values.

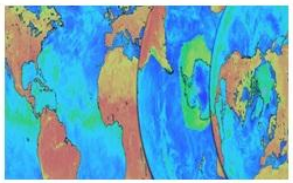
$$T = (t_1, \ldots, t_n), t_i \in R$$

- A contiguous recorded result of a certain phenomena, a measurement or, an observation collected at constant time interval.
- Applicable in various areas:

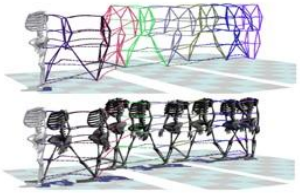
Finance and Economic



Hydrology



Motion detector



Anomaly Detection

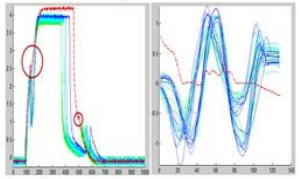
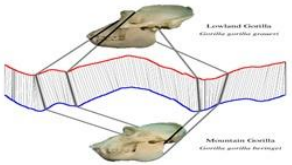
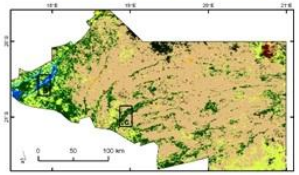


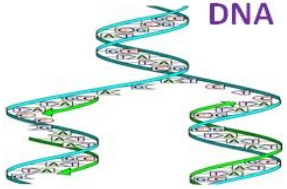
Image Processing



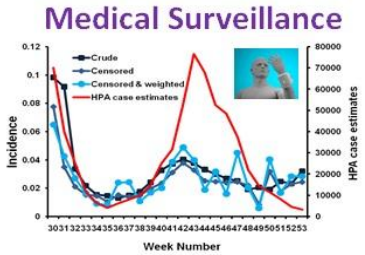
Remote sensor



DNA

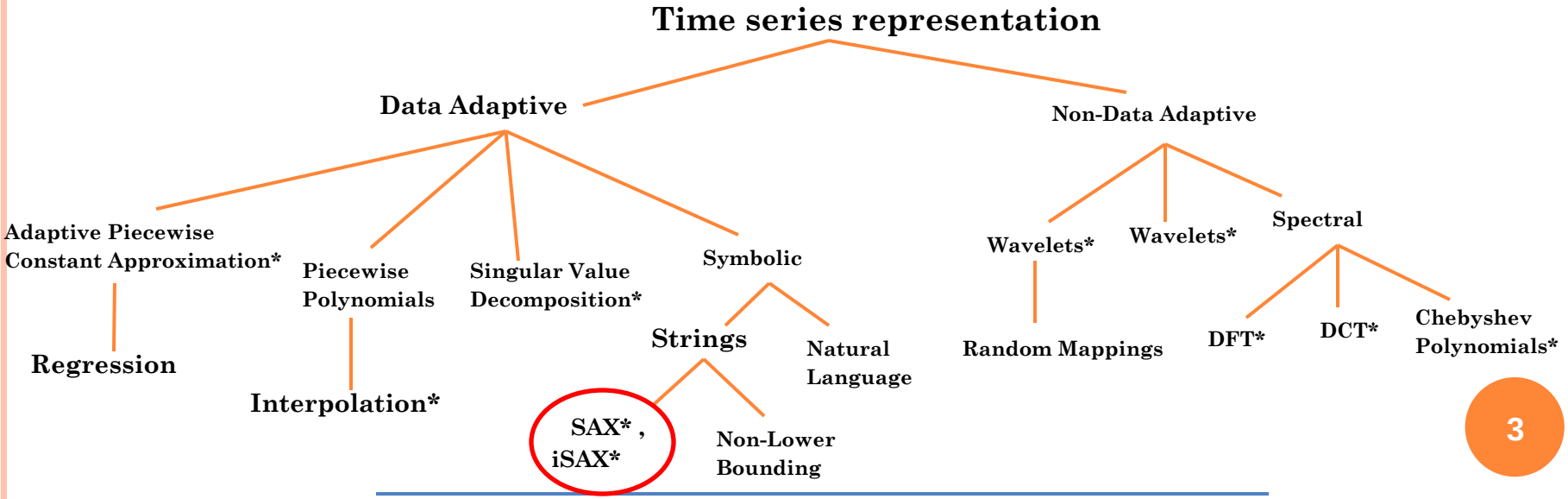


Medical Surveillance



Time series data representation and indexing

- Since time series data is high dimensional
- Processing the 'raw' time series requires:
  - High computation time and large memory space
- Dimensionality reduction and indexing methods



Motivation

- Indexing is a key for processing time series, but query answering even with an index can be slow
- iSAX and its extension iSAX 2.0 indexes really massive dataset
- MapReduce is a software framework for processing large dataset

Question:

- How we can answer iSAX based quires faster in distributive environment using MapReduce

Problem statement

- iSAX exact search is an expensive search - required an intensive computation and I/O cost
- Query answering takes more time as index size increases

Objective :

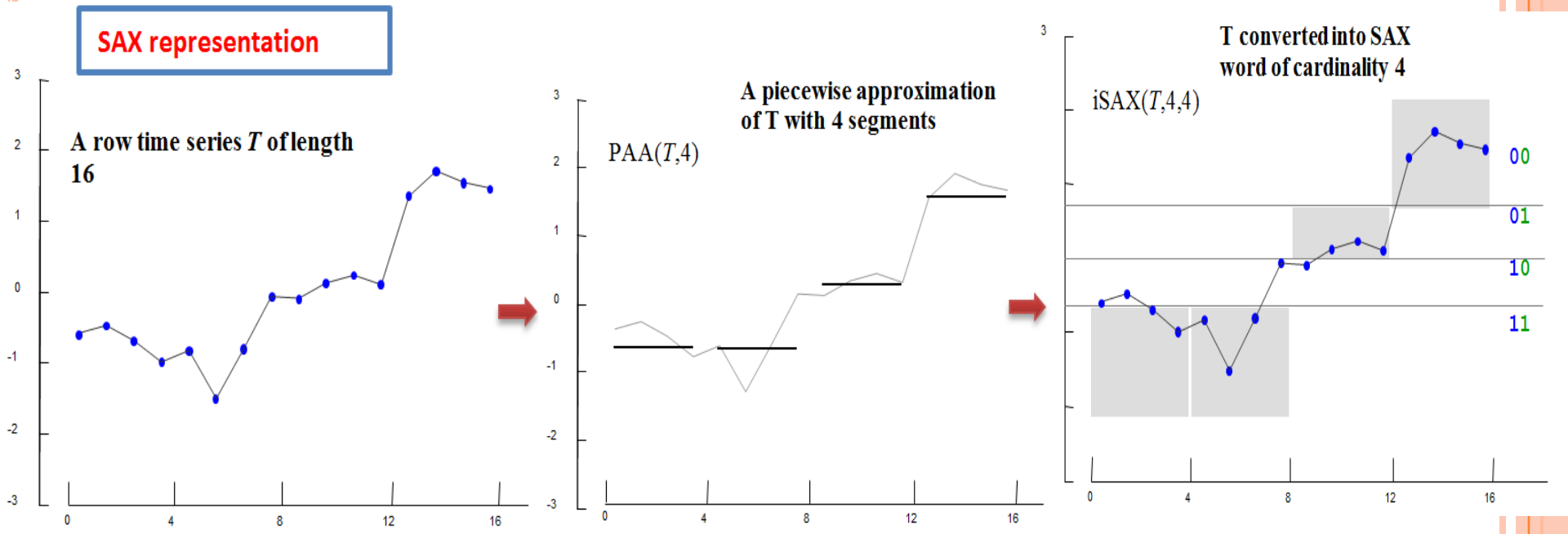
- Implement iSAX exact search in MapReduce
- Improve lower bound distance calculation method
- Analysis the execution time of simple, MapReduce, and KNN search
  - Using synthetic and real dataset
- Optimizing MapReduce query answering using other frameworks such as Memcached.

PRESENTATION OUTLINE

- Time series representation and indexing method
  - iSAX
- Introduction to MapReduce
- Implementation and methods
  - MapRedExactSearch
  - MaxCardMapRedExactSearch
  - K-Nearest Neighbor Search
- Experimental Results
- Summary and future directions
- Questions

SAX: Symbolic Aggregate approXimation

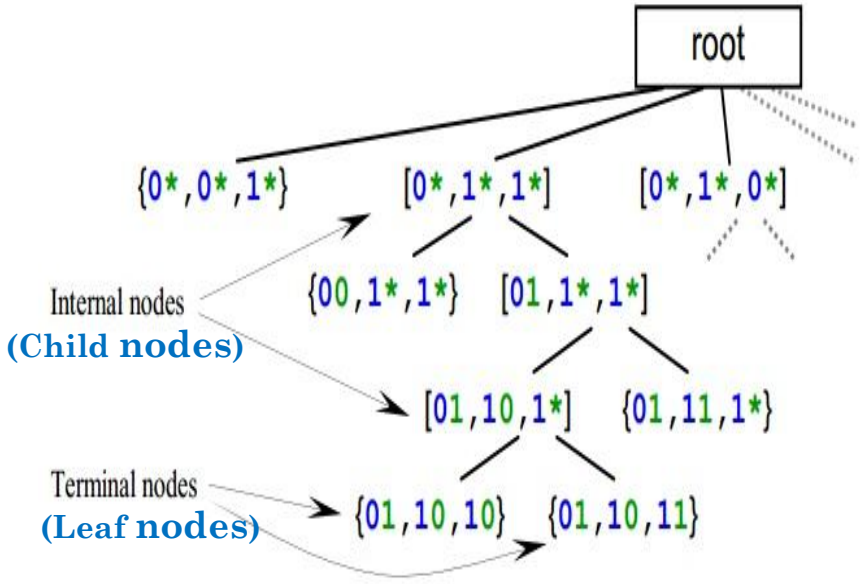
- Represent a time series T of length n into w segments

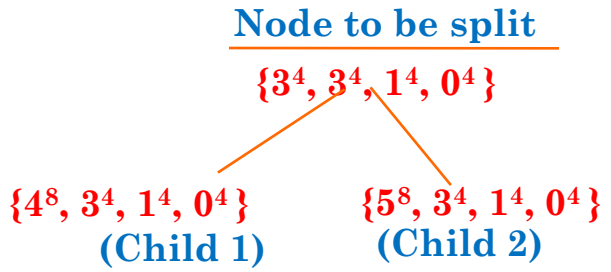


- iSAX word : $T^4 = iSAX(T, 4, 4) = \{11,11,01,00\} = \{3^4, 3^4, 1^4, 0^4\}$
- Comparing two iSAX words of different cardinality
- Comparing different cardinalities within a single word

iSAX indexing

- Hierarchical tree structure.
- **Leaf node** points to index file on the disk.
  - Example: iSAX word $\{7^8, 5^8, 3^8, 1^8\}$ can be mapped to 7.8_5.8_3.8_1.8.txt
- **Terminal nodes:** created when the number of time series in a leaf node exceeds leaf size

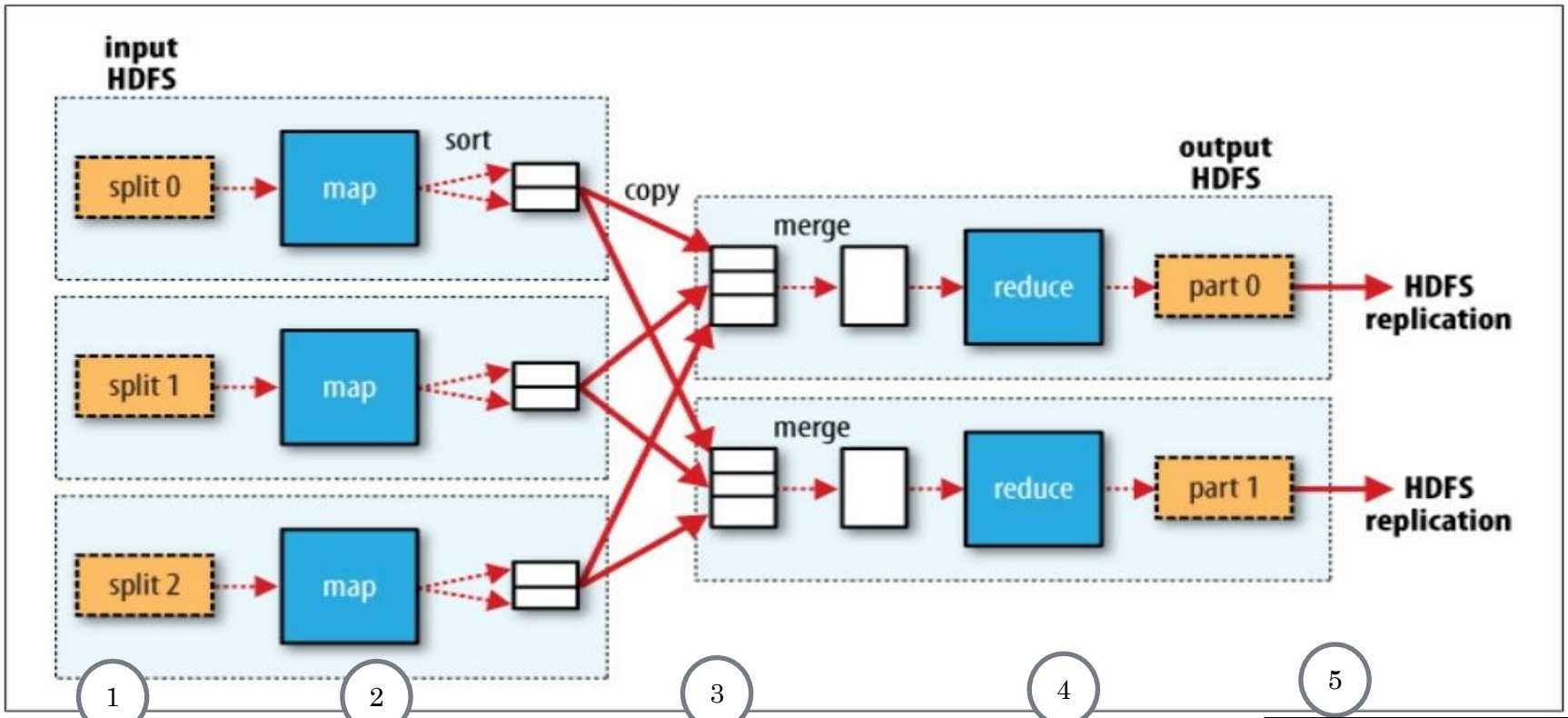




For given (c = cardinality, w = word length) => c^w different iSAX words.

Leaf size (threshold): maximum time series a word (leaf node) can hold

MapReduce



1. Read input file and split it up across separate Map node
2. Map function runs and produce output for each map
3. Intermediate key-value pairs, which then input to Reducer
4. Reduce function generates an output for each Reduce node
5. Reads and aggregates the outputs from each node.

Exact search using MapReduce

- **Begin**: before starting the map tasks
  - Combined input file using CombineFileInputFormat
  - Each combined file is processed by different map task.
- **Mapper**:
  - Read all the time series from the combined file
  - Compute the minimum distance for each time series

Before Reducer

- Grouped Mapper output based on filename
- Ordered based on the distance.

- **Reducer:** processes each group separately.
  - Output the minimum from each group.
- **Result**:
  - Minimum distance of of all entries from the query.

EXACT SEARCH USING MAXIMUM CARDINALITY

- Lower bound distance:
  - Symbolic distance $\leq$ actual distance
  - Used to prune the search space
  - Computed using the highest cardinality (8 bit)
- Used two separate Sequence files in HDFS
  1. Leaf Node with iSAX representation of each time series
  2. Leaf Node with raw time series

K - nearest neighbor search (KNN)

First MapRed Job output

KNNMapRedJob1

Outputs **k** closest entries from the query for each index file

KNNMapRedJob2

- **Mapper**:
  - Reads the records outputted by the first job
  - Changes the key of all the records to the same key

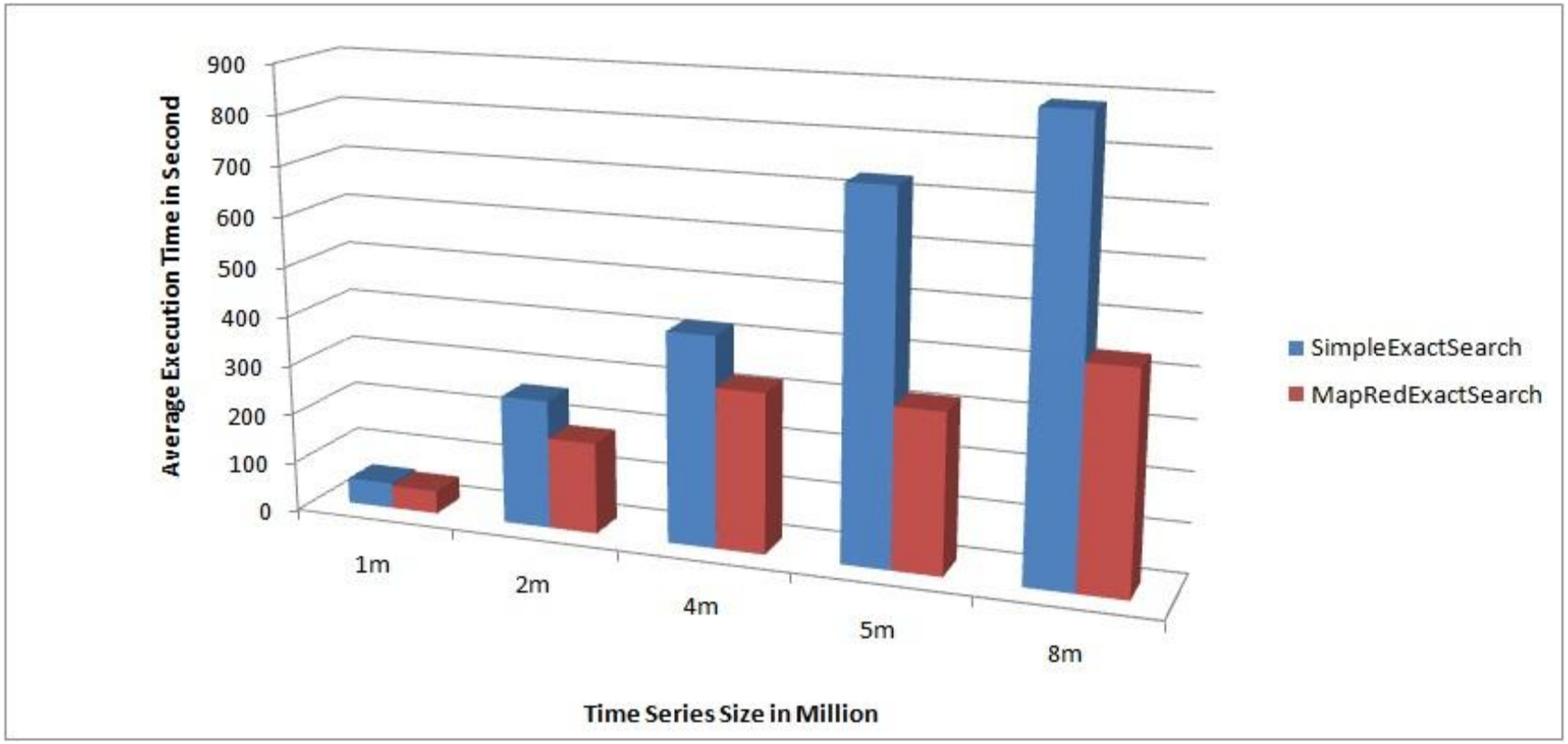
Before Reducer: Group all the out put together
Ordered according to the distance.

- **Reducer**:
  - Output the k first records.
- **Finally**:
  - Update the existing closest neighbor's list with k smallest distance

Experimental setup

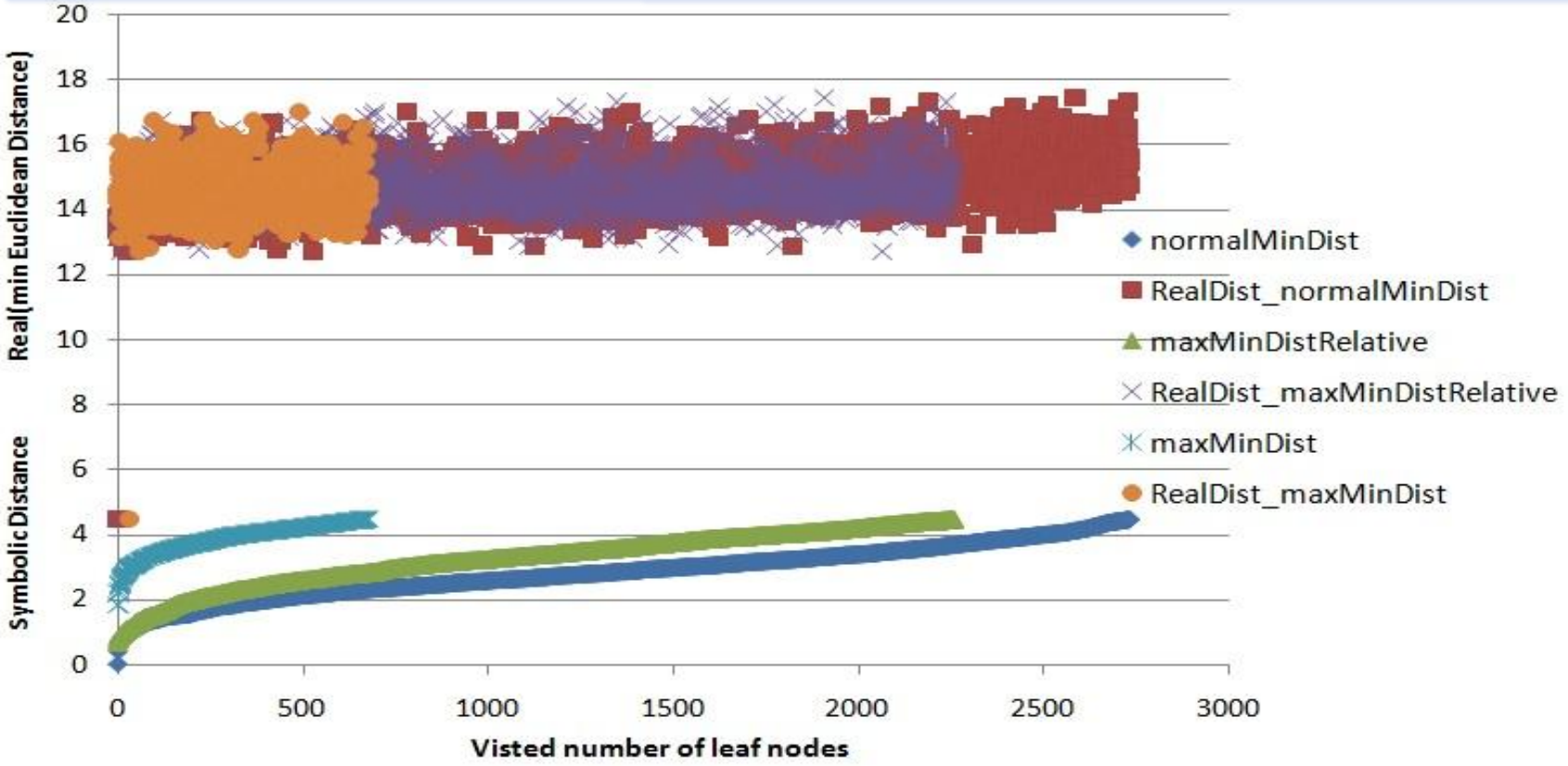
- Experiments are conducted on single node pseudo distributed mode
- Configured:
  - On Intel 64 bit Core i5-2430M CPU @ 2.4GHz
  - Memory size 4GB and Ubuntu 12.04 LTS
  - Hadoop version 1.0.3
  - Java as Programming language
- Data sets:
  - Randomly generated with length 128,
    - Base cardinality=2, Word length=8, leaf size = 100,1000,&10000
    - Time series size1, 2, 4, 5 and 8 million
  - Homo.sapiens.NCBI36 42 DNA chromosome 5 and 11
- Results are averages over 5 runs for each query
- Average execution time measured in seconds

MapRedExactSearch compared to simple exact search



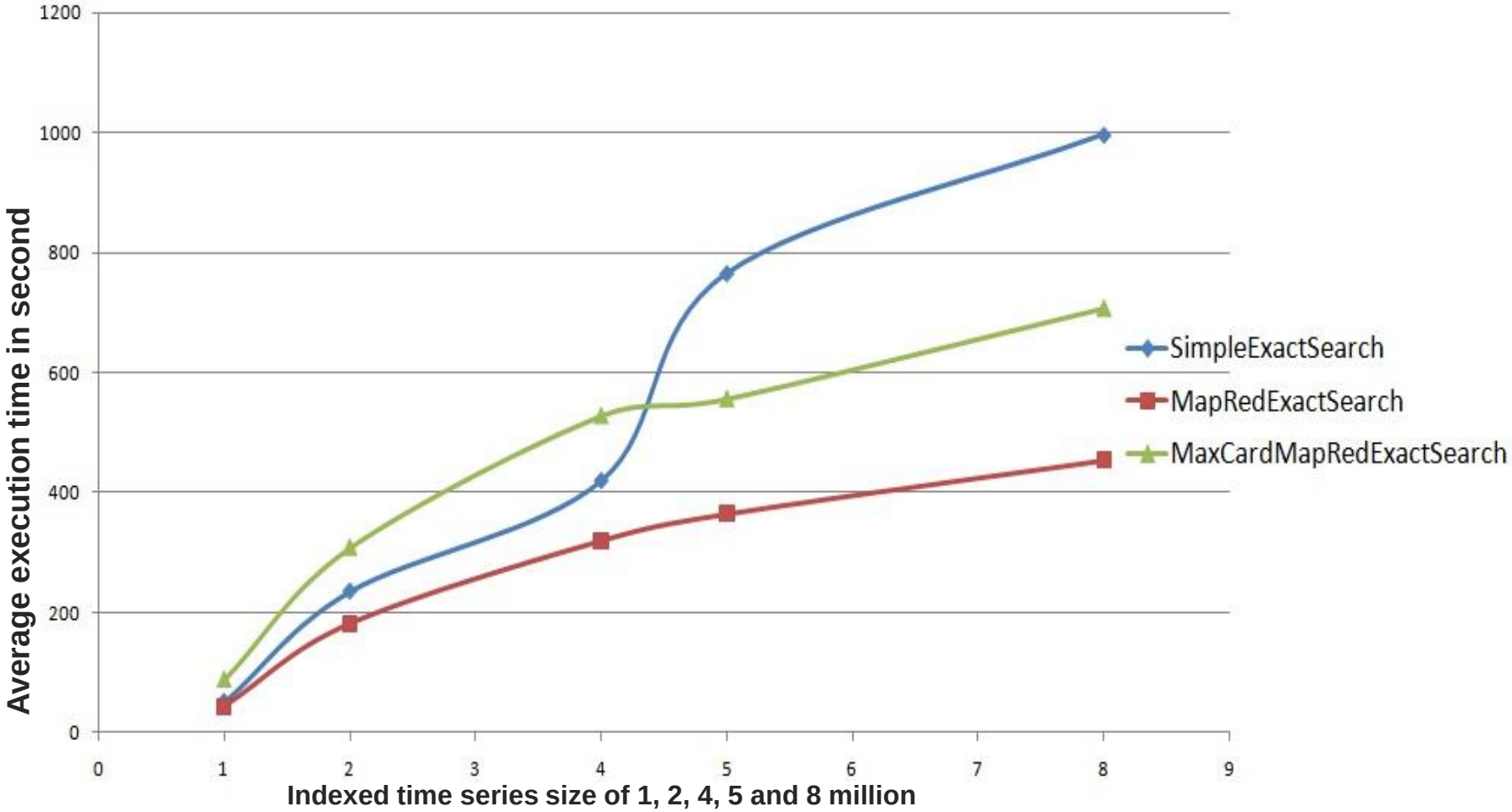
- Figure: Different average execution time of Simple and MapReduce implementation for indexed size 1m, 2m, 4m, 5m and 8m time series leaf size=10000

Maximum cardinality and lower bound



- Bound is calculated using
  - **Maximum Cardinality=256**
  - **Maximum Cardinality selected local to each leaf node**, and
  - **Symbolic representation of the leaf node**

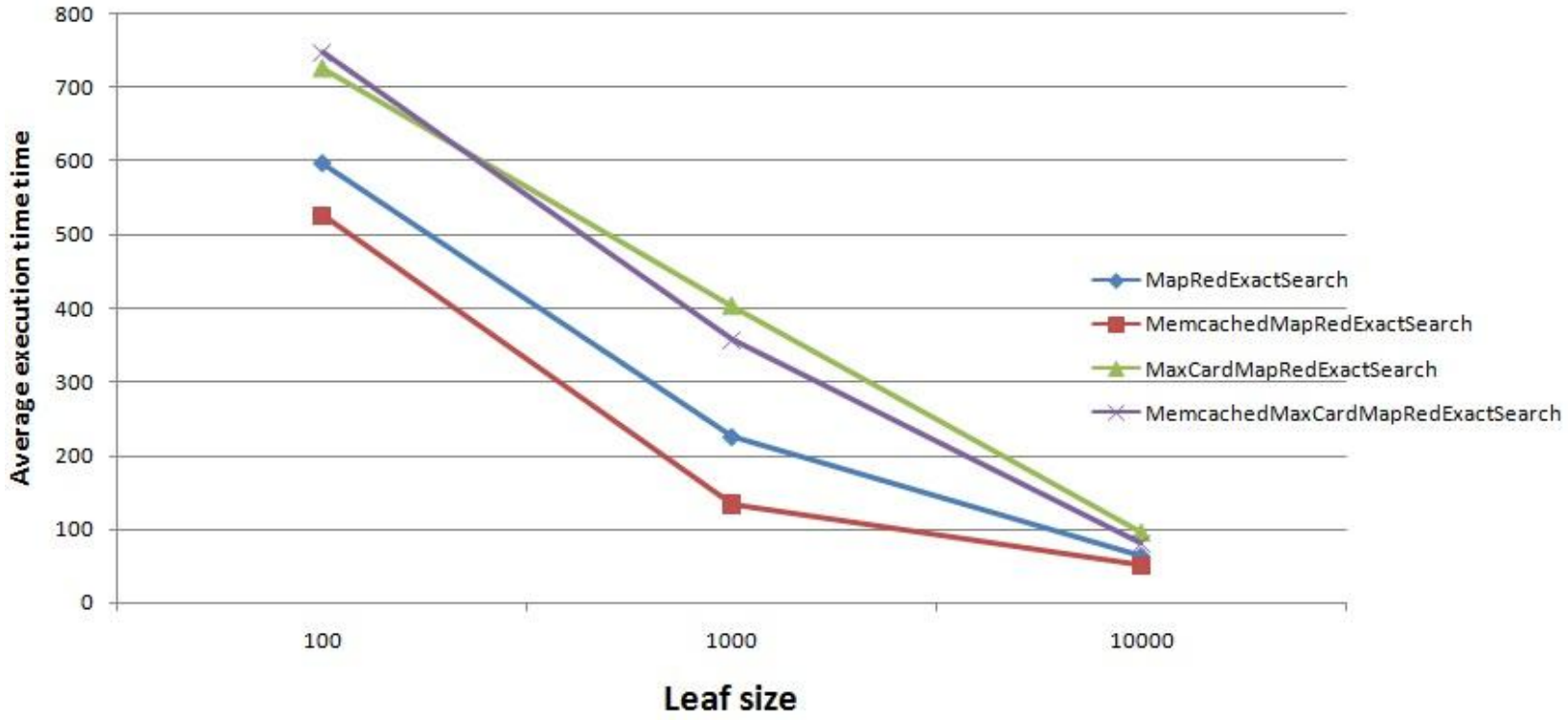
Simple ,MapRedExactSearch, and MaxCardMapRedExactSearch



- Average execution time of searching queries in seconds tested for
  - **Simple search**,
  - **MapReduce with out using Maximum cardinality** and
  - **MapReduce using Maximum cardinality**

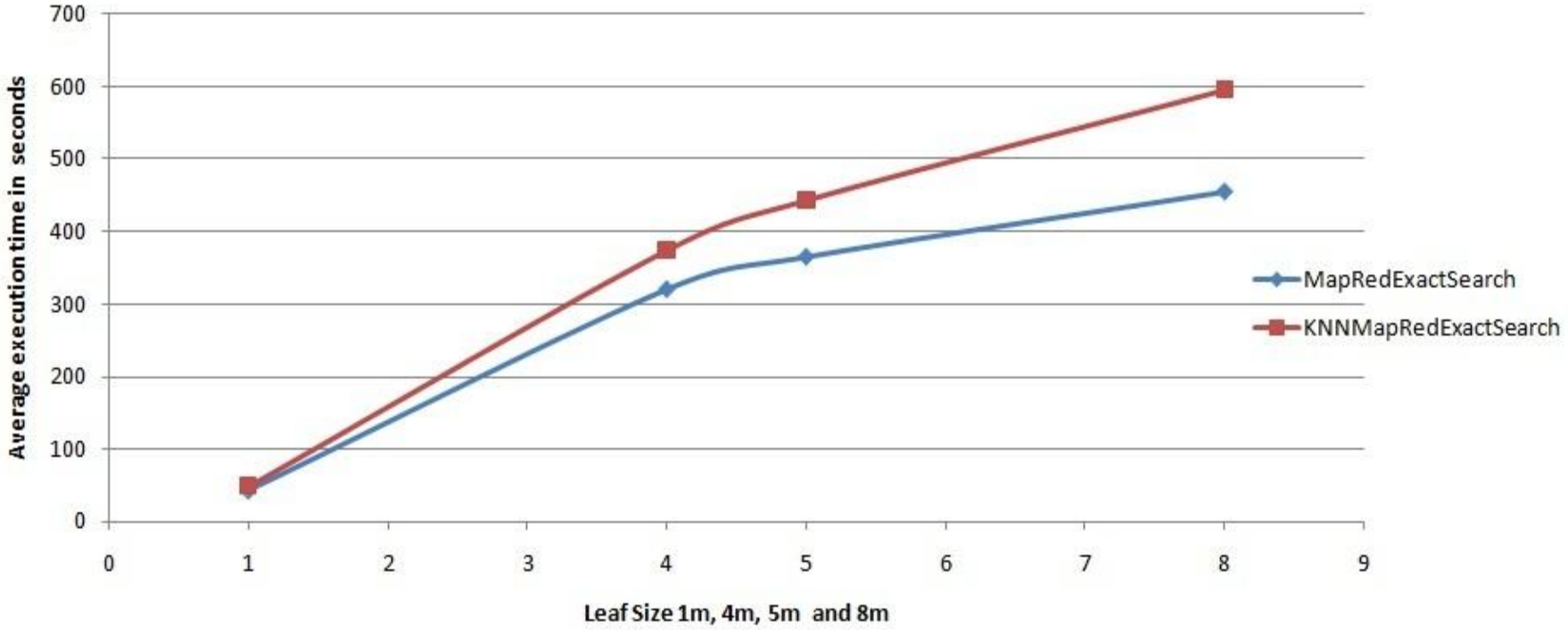
Substituting the Reducer with Memcached option

- **Memcached** : distributed memory-based object catching system
- Often used to hold small objects in RAM for fast possessing



- Average execution time of 1million time series under leaf size 100,1000 and 10000 using **memcached**

K –Nearest Neighbor compared with MapRedExactSearch



- Average execution time of K-NN and MapRedExactSearch for time series size 1,4,5 and 8 million, where **k=4**

Genome data

- Each genome data converted into time series and indexed with base cardinality =2, word length=8, time series length=128, leaf size =10000
- Generated 5 different queries by randomly changing two DNA symbols of the sequence

Avg. execution time	SimpleExactSearch	MapRedExactSearch
Query set 1	463.681	385.319
Query set 2	319.005	254.102

Summary

- On this thesis:
  - MapReduce to answer iSAX time series query with small average execution time than simple search
  - Highest cardinality for computing lower bound minimize the number of leafs visited
    - Has computation cost
  - MapReduce implementation using highest cardinality get advantage over simple search for large dataset
  - MapRedExactSearch algorithm has very fast execution time than the other approaches
  - Applicable for K-Nearest Neighbor search

Future directions

- Running all algorithms using real cluster of multiple nodes.
- More research on memcached implementation
- Carful consideration of MapReduce job configuration is crucial.
  - Example: On the split size and number of Reducers
- Supporting with other distributive frameworks such as ActiveMQ

Thank you!

Any Questions ?