

# Parallel Streaming Decision Tree - Final Report

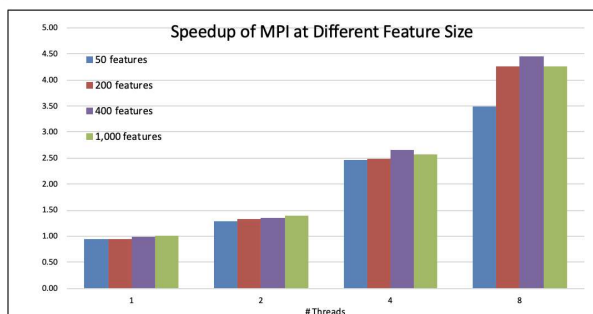
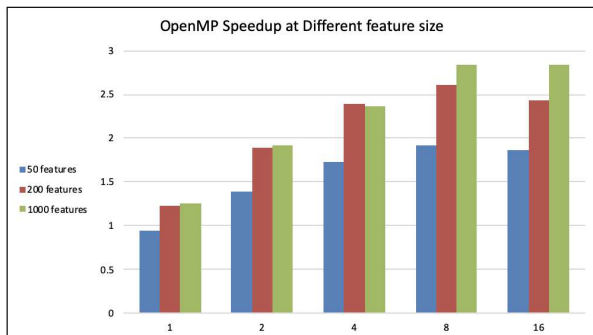
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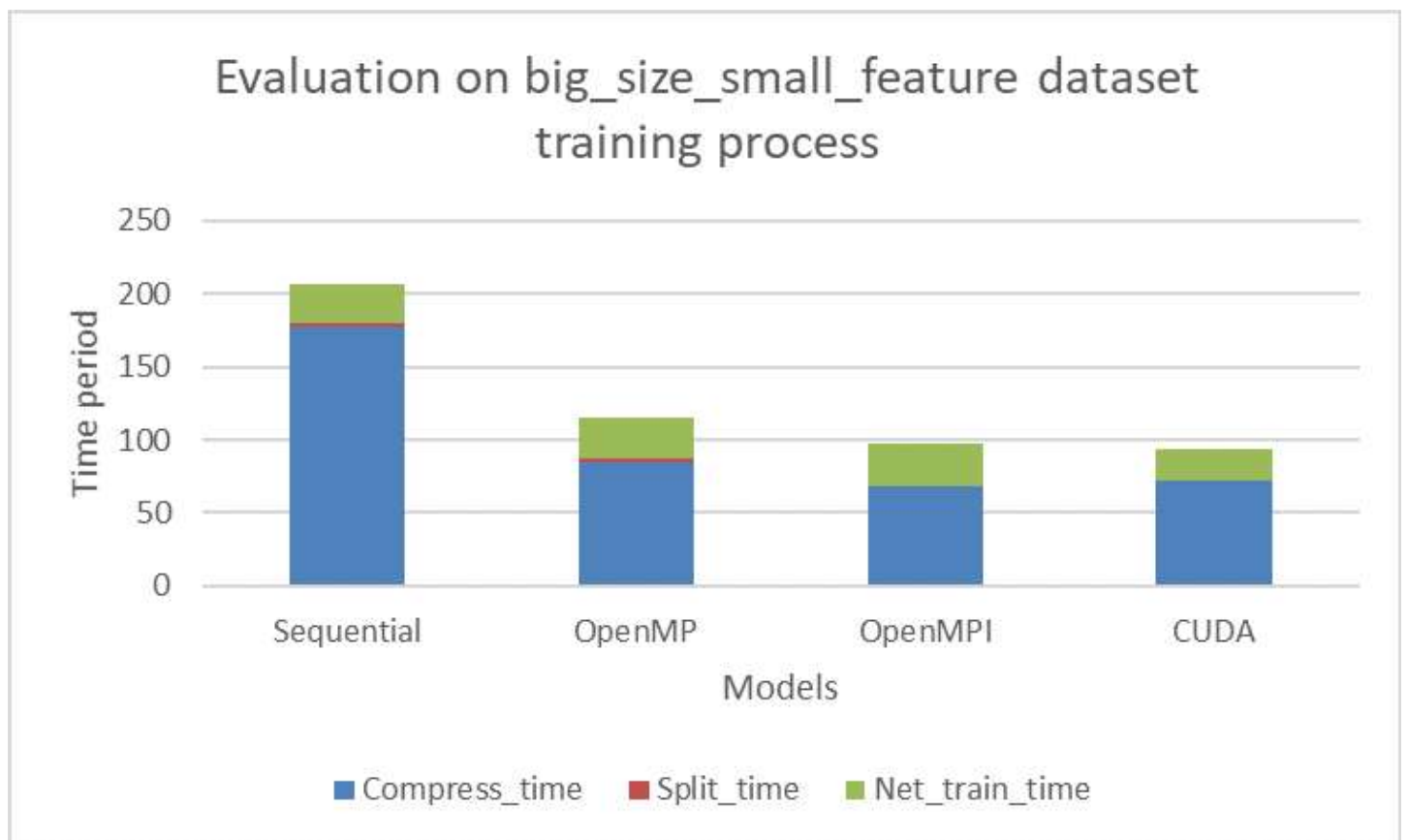
## Summary

We implemented the sequential version, the OpenMP version, the OpenMPI version and the CUDA version for decision tree with histogram and compared the performance of four implementations.

## Takeaways

1. OpenMP scales over feature size, while OpenMPI scales poorly over feature size.
2. OpenMPI could achieve a higher speedup than OpenMPI.
3. On large data size, CUDA could achieve higher speedup than OpenMP and OpenMPI.





## Backgrounds

### Decision Tree

Decision Tree is widely used in Machine learning and it is simple and intuitive.

Traditionally, a decision tree is built in the following way.

```
Function BuildTree(n,A) // n: samples (rows), A: attributes
  If empty(A) or all n(L) are the same
    status = leaf
    class = most common class in n(L)
  else
    status = internal
    a <- bestAttributeSplitPoint(n,A)
    LeftNode = BuildTree(n(a=1), A \ {a}) RightNode = BuildTree(n(a=0), A \ {a})
  end
end
```

However, this approach is expensive in finding the `bestAttributeSplitPoint(n, A)` because it needs to iterate all the data set to find the best split for one feature. So this would lead to a  $O(data * feature)$  complexity. One approach introduced by [A Streaming Parallel Decision Tree Algorithm](#) is to use an approximation algorithm. Firstly, we compress the data into a pre-defined number of bins and then we iterate each bin for one feature, which reduces the complexity to  $O(bins * feature)$ .

```

Call TreeBuilding procedure:
Initialize T to be a single unlabeled node.
foreach batch_data do:
    Reinitialize every leaf in T as unlabeled.
    while there are unlabeled leaves in T:
        Navigate the batch_data to the leaves
        Construct the histogram h(v, i, c) by calling COMPRESS procedure.
        for all unlabeled leaves v in T do:
            if v.should_terminate() or there are no samples reaching v:
                Label v
            else:
                Call find_best_split procedures:
                for all features i do:
                    Merge the h(v, i, 1)..h(v, i, c) and get h(v, i)
                    Determine the candidate splits by calling UNIFORM.
                    Estimate the information gain of each candidate by calling SUM.
                endfor
                Split v with the highest gain.
            endif
        endfor
    endwhile

```

In this approximation algorithm, the computational cost is amortized from one function ( `find_best_split` ) to two functions( `find_best_split` & `compress` ). So our goal is to parallelize these two functions.

## Key Data Structures

### How we store our dataset in vector version

We use the class `Dataset` in `/src/SPDT_general/parser.cpp` to store the dataset. For each data, we use the class `Data` in the same file to store it. The `Data` class contains an int `label` to mark the label of the data, and an `unordered_map` `values` to store the map between feature id and feature values. Some datasets contain sparse features, therefore we are using a map to store all and ignore the other 0's.

The class `Dataset` contains a vector of `Data` , to store all the possible data. It also stores some other dataset parameters, such as the number of features, the number of data.

### How we store our dataset in several serialized arrays for GPU

When we pass the dataset to GPU, the above vector version for dataset storage is not possible here. Therefore, we come up with a new version to store the dataset: several 1-D arrays.

We are storing our dataset into two 1-D arrays. The pointer `label_ptr` points to an array of integers. The pointer `value_ptr` points to an array of floats. Because it's better to pre-alloc place for the whole dataset, we are storing features and values in the dense mode. The size of the `label_ptr` is `num_of_data`. The size of the `value_ptr` is `num_of_data * num_of_features`. If we want to read/write

to the (data\_id, feature\_id), then its label is label\_ptr[data\_id], and its value is value\_ptr[data\_id \* number\_of\_features + feature\_id].

The limitation of serialized arrays dataset is that it's difficult to manage this dataset and provide operations. It's hard to write codes and debug. The memory usage of this version is large. While the memory on GPU is limited, it's difficult for some dataset to run in GPU parallel version.

## **How we serialize histograms**

We are serializing histograms in a huge 1-D array.

For each histogram, we store it into a float array. The first element is the size of the histogram bins. After that, we store the (freq, value) of each element in the histogram. According to these rules, the histogram could be changed into a 1-D array. To malloc the place of all histograms together, for each histogram we initially malloc the place for the max\_bin\_size. We provide some setter and getter functions for histogram related operations.

## **Key Operations**

### **Several operations for histograms**

The operations for histograms are update, sum, merge, uniform, compress. The update function updates a value to a histogram. The sum function calculates the estimated sum distribution for values in a specific range. The merge function merges two histograms. If possible, it would merge the bins in the histogram to fit the max bin size. The uniform function provides possible split values for a histogram. The compress function builds the histogram from a series of data.

## **Algorithm's inputs and outputs**

The input of the algorithm includes the training dataset and the test dataset. It also includes some parameters of the dataset, including the number of data, the number of features, the number of classes and so on.

The output of the algorithm is a decision tree. We could use the decision tree to predict the labels of the test dataset, to verify the correctness of the decision tree.

## **Computationally expensive parts**

### **compress function**

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**Algorithm 6** Compress Data Sets

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**input**  $1/W$  of the training set, where  $W$  is the number of processors

**output** histograms to be transmitted to the master processor

- 1: Initialize an empty histogram  $h(v, i, j)$  for every unlabeled leaf  $v$ , attribute  $i$ , and class  $j$ .
  - 2: **for all** observed training samples  $(\mathbf{x}_k, y_k)$ , where  $\mathbf{x}_k = (\mathbf{x}_k^{(1)}, \dots, \mathbf{x}_k^{(d)})$  **do**
  - 3:   **if** the sample is directed to an unlabeled leaf  $v$  **then**
  - 4:     **for all** attributes  $i$  **do**
  - 5:       Update the histogram  $h(v, i, y_k)$  with the point  $\mathbf{x}_k^{(i)}$ , using the update procedure.
  - 6:     **end for**
  - 7:   **end if**
  - 8: **end for**
- 

## Get gain function

This function calculates the gain of a specific split feature and splits value for the node. It includes many float operations. It also calls functions such as SUM in the histogram.

## Key Challenges

- **Dependency Analysis:** Histogram is a global variable that we need to protect. If we use the shared-memory model, then we need to manually synchronize for the `update` operation to the same  $h(v, i, j)$ . Similarly, in the `find_best_split` operation, a `best_split` is shared and thus needed to be serialized.
- **Memory Latency:** Since the data is disk-residency, the memory latency is large. We have the leverage the temporal locality.

## Approach

There are mainly two functions in the tree building process that are costly. `compress` function and `find_best_split` function. And both of them could be parallelized. To begin with, we introduce our baseline parallel strategy ---- Node Parallel.

## Node Parallel

This parallel method is the most intuitive because there is a natural independent loop in the pseudocode, `for all unlabeled leaves v in T do`. However, this work partitioning strategy suffers from one problem, namely, **imbalanced Workload**: The workload is determined by the number of children of this parent node. However, this is unpredictable. Due to the essential drawback of static assignment of this parallel paradigm, the workload is unbalanced so this strategy is expected to show the worst speedup and bad scalability.

## Feature Parallel

In the `find_best_split` procedure, the `for all features i do` loop could be parallelized. One note is that the best split information should be manually synchronized. One method is to introduce a local variable for each worker and then merge the results afterward. Another method is to use lock-based synchronization to protect the shared variable. After testing, we implemented the first version. Since each thread only needs to send it's the best split feature to the master, the communication cost is  $O(P)$

## Data Parallel

In the `compress` procedure, the `foreach data point (x, y) do` is parallelized. But similarly to the feature parallel version, there is a big challenge. Each data point would update  $h(v, i, y)$ , which means there is a huge contention for the histogram method. To encounter this problem, we reorder the loop in a way that there is no race condition.

Call COMPRESS procedure:

```

    Initialized empty histogram  $h(v, i, j)$  for unlabeled leaf  $v$ , feature  $i$ , class  $j$ 
    #pragma omp parallel for
    foreach unlabeled leaf  $v$  do:
        foreach data point  $(x, y)$  in  $v$  do:
            foreach feature  $i$  do:
                Call UPDATE procedure to update  $h(v, i, y)$ 
            endfor
        endif
    endfor

```

This strategy is used by using the shared-memory model and implement by OpenMP. However, this algorithm would suffer from some trivial work imbalance problem as each leaf contains an unequal number of data points. But this could be mitigated by dynamic scheduling.

We also introduce a message-passing model data-parallel version here. This strategy is essentially streaming and could handle as much as possible. This parallel algorithm is borrowed from [A Streaming Parallel Decision Tree Algorithm](#).

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### Algorithm 6 Compress Data Sets

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**input**  $1/W$  of the training set, where  $W$  is the number of processors

**output** histograms to be transmitted to the master processor

- 1: Initialize an empty histogram  $h(v, i, j)$  for every unlabeled leaf  $v$ , attribute  $i$ , and class  $j$ .
  - 2: **for all** observed training samples  $(\mathbf{x}_k, y_k)$ , where  $\mathbf{x}_k = (\mathbf{x}_k^{(1)}, \dots, \mathbf{x}_k^{(d)})$  **do**
  - 3:     **if** the sample is directed to an unlabeled leaf  $v$  **then**
  - 4:         **for all** attributes  $i$  **do**
  - 5:             Update the histogram  $h(v, i, y_k)$  with the point  $\mathbf{x}_k^{(i)}$ , using the update procedure.
  - 6:         **end for**
  - 7:     **end if**
  - 8: **end for**
-

This algorithm is essentially streaming and needs explicit synchronization. After each work completes their work, all the histogram data would be transferred to the MASTER worker and do the merging process. After merging completes, the result would be broadcasted to other workers. (For more information about merging and some convergence proof, please refer to the paper.) Since each worker would send the histogram to the MASTER, the communication cost is  $O(W \times L \times c \times d)$ , where  $W$  is the number of workers,  $L$  is the number of unlabeled leaves in the current iteration,  $c$  is the number of labels and  $d$  is the number of features. For a summary for this algorithm,

- At most  $N/W$  operations by each processor in the updating phase.
- $O(W \times L \times c \times d)$  communication cost.
- $O(W \times L \times c \times d)$  for merging.

## Data-Feature Parallel

We successfully combined the above two parallel strategies as they should be independent with each other.

## Implementation

### OpenMP & OpenMPI implementations

All the parallel approaches are implemented by OpenMP and also we did a message-passing Data-Feature parallel version on OpenMPI.

### CUDA implementation

Furthermore, we implemented a parallel version on CUDA. The codes could be seen in the `/src/SPDT_CUDA` folder.

We introduced four kernels to provide parallel to CUDA: `histogram_update_kernel`, `calculate_feature_value_kernel`, `calculate_gain_deltas_kernel`, `navigate_sample_kernel`.

`Histogram_update_kernel` is the kernel which updates the histogram with the given (key, value) pair. It is used in the `compress` function. There are two versions of this kernel. The first version is implemented in the data-parallel. The block number is the number of data, the thread number is the number of features. For each thread, it uses the corresponding feature value in the corresponding data to update the histogram. Even though this version could achieve high distribution works, we found out that there is competition for different threads to update the same histogram in the system, causing the wrong result. While the paper [Implementing Streaming Parallel Decision Trees on Graphic Processing Units](#) believes the conflict of updating the same histogram effects little to the correctness, we decide to assign the tasks differently.

We decide to set the block number to be the number of unlabeled leaves, and the thread number to be the number of features. Each thread would go through the dataset and update its histogram according to the data. Therefore, we are parallel over different histograms. Even though there is less parallelism here, our approach is guaranteed to have no data update conflict.

`calculate_feature_value_kernel` is the kernel to calculate the promising split points features and values for the splitting operation for a leaf node. It mainly calls the `CUDA_merge_array_pointers` and `CUDA_uniform_array` functions. It first merges the two possible histograms with the `CUDA_merge_array_pointers` function, then calls the `CUDA_uniform_array` function to uniform the array and come up with possible split points. We set the thread number to be 128, and block number being  $(\text{num\_of\_features} + \text{thread\_num} - 1) / \text{thread\_num}$ . In other words, we are paralleling over different features for the leaf node. The total thread number equals to the number of features. For each thread, we come up with a possible split (feature, value) pairs and store the result to an array.

`calculate_gain_deltas_kernel` calculates the gain and entropy for each promising split point. According to the `calculate_feature_value_kernel` step, for each feature, there is at most `max_bin_size` number of possible split values. Therefore, the block number equals to the feature number, and the thread number equals to the max bin size parameter for histograms.

`navigate_sample_kernel` assigns the data to the leaf nodes. It is parallel over different data points. The thread number is 128. The block number is  $(\text{num\_of\_data} + \text{thread\_num} - 1) / \text{thread\_num}$ . Therefore, the total thread number equals to the number of data. For each thread, it checks the assignment of a data pointer in the dataset. This function is called every time initialize a level of unlabeled leaves of histograms.

We also introduced some helper functions and files to achieve the CUDA implementation. We have re-write other functions in array and pointers. In the CUDA version, data is at most serialized and stored in some 1-D arrays. Moreover, there are no STL vectors allowed in the CUDA kernel codes. Therefore, we have designed specific data structures and algorithms to support the CUDA version.

## Results

### General speed-up figure

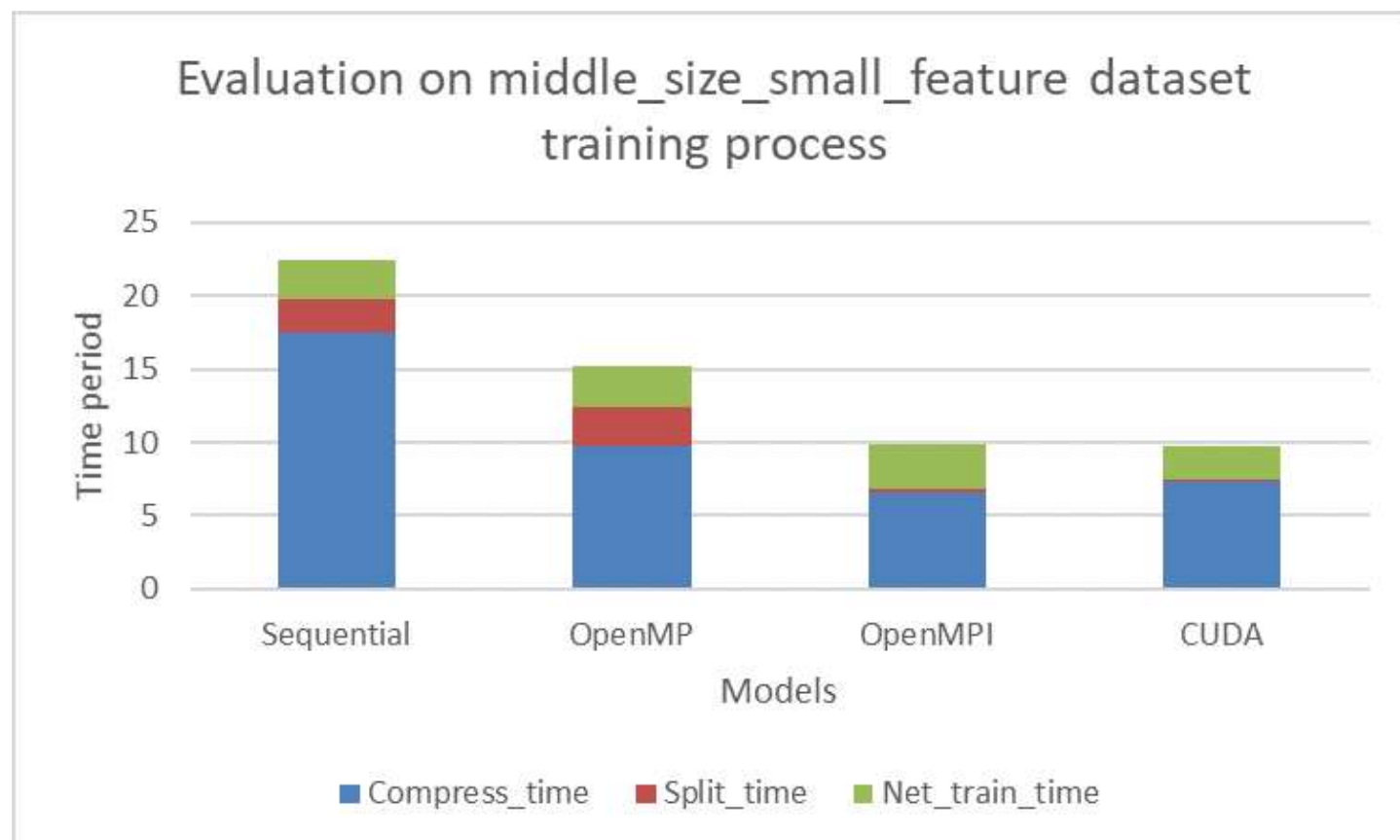
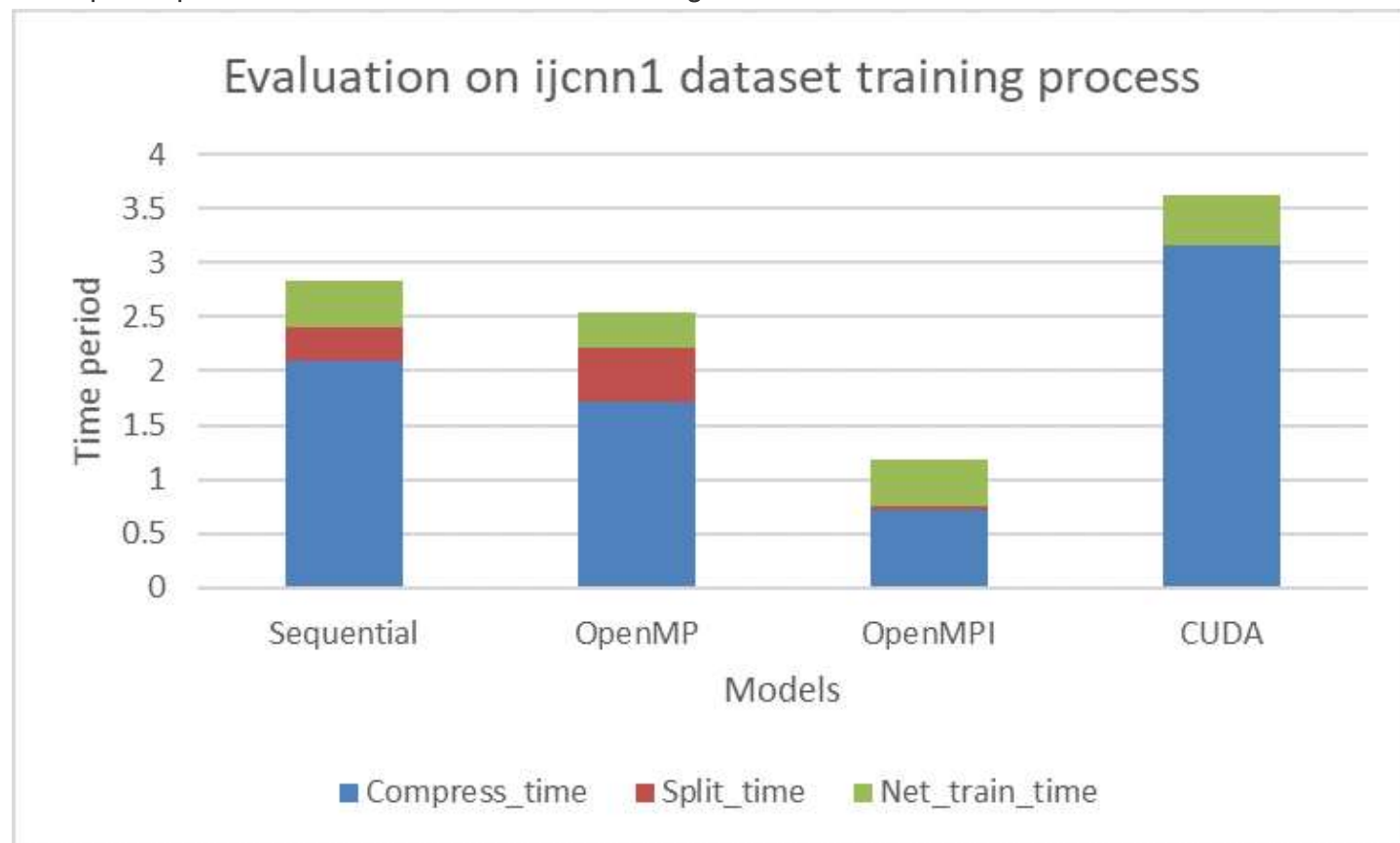
In the general evaluation process, we choose three datasets: `ijcnn1`, `big_size_small_feature`, and `middle_size_small_feature` as samples to evaluate the speedup of them. The dataset `ijcnn1` is taken from [LIBSVM dataset](#) [5]. The feature size is 22. It contains 49990 train data and 91701 test data.

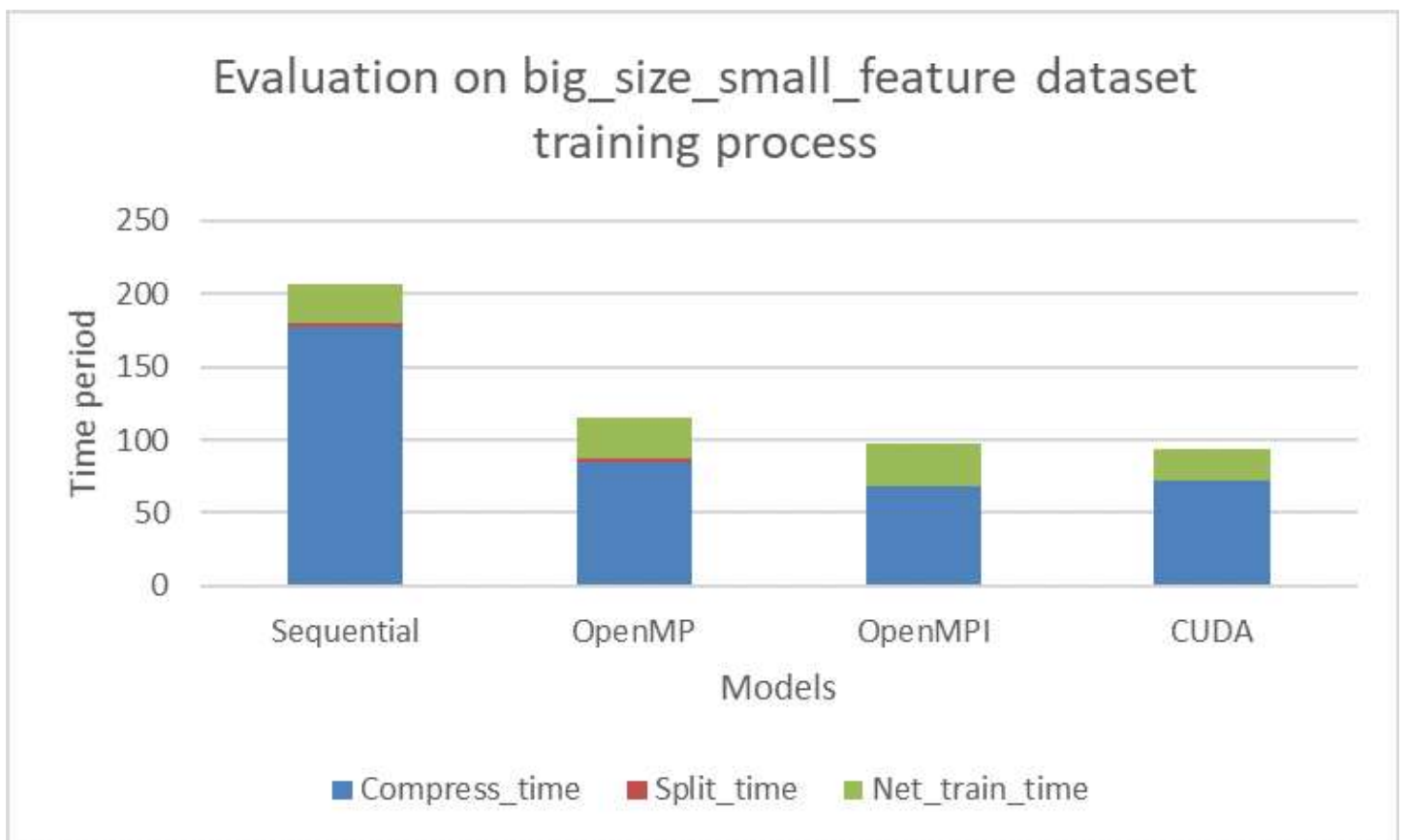
We generated the other two test cases by our scripts. The dataset `big_size_small_feature` contains 1,000,000 train cases and 100,000 test cases. The feature size is 50. The dataset `middle_size_small_feature` contains 100,000 train cases and 10,000 test cases. The feature size is 50. We want to evaluate the scalability of different parallel algorithms, therefore we generate these datasets by ourselves.



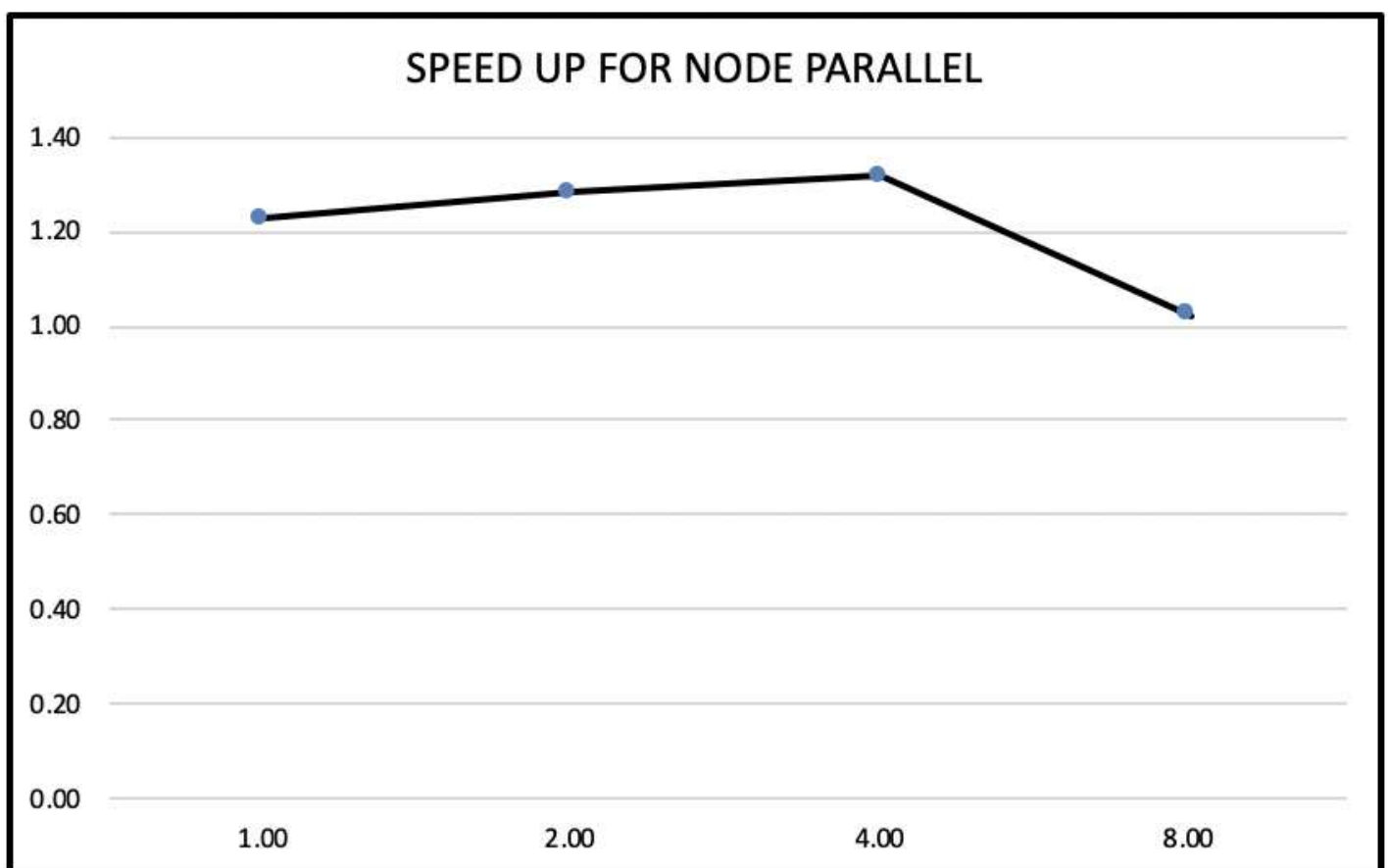
We compared our four approaches: the sequential version, the OpenMP version (thread number = 4), the OpenMPI version (thread number = 4) and the CUDA version. Our baseline is the single-threaded CPU sequential code.

The speedup for four versions could be seen in figures



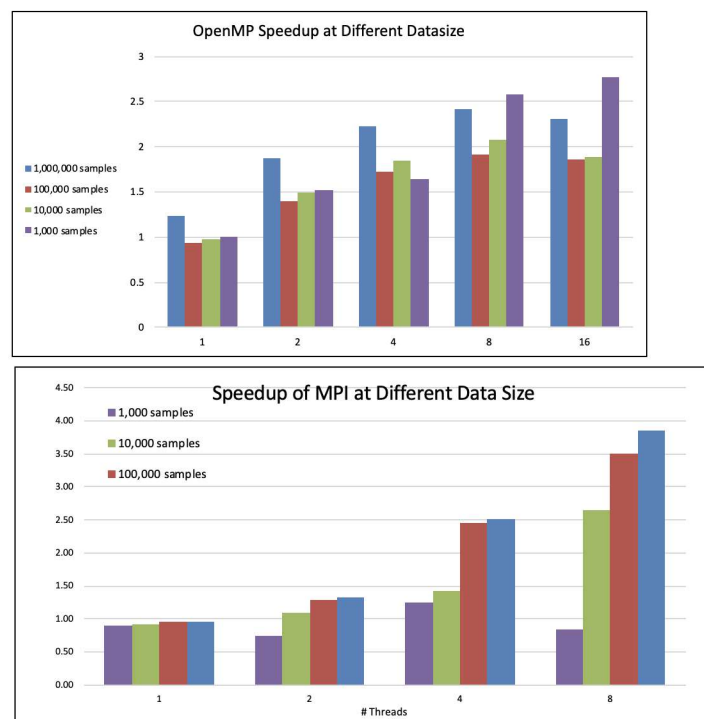


## Node Parallel & Data-Feature Parallel Speedup analysis



As we expected, the node parallel version suffered from a tremendous workload imbalance problem. As we have shown here, the program shows little scalability.

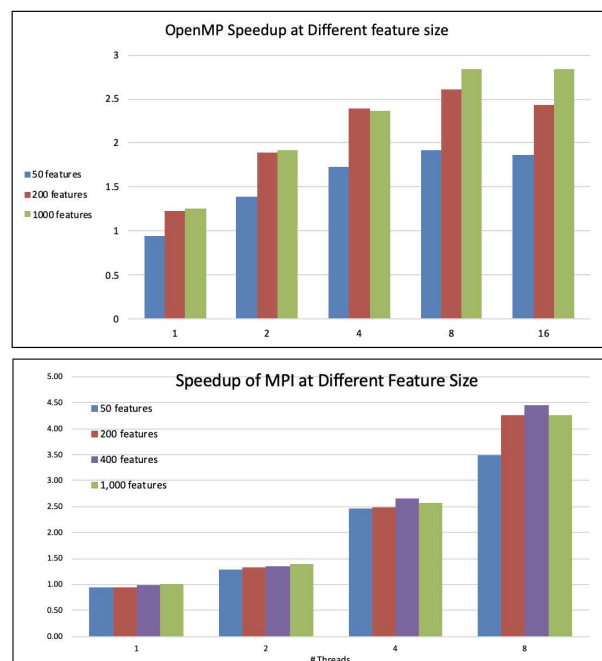
# Data-Feature Parallel Scalability over Data Size



From the above figures, we could see the influence of computation cost and locality. When the sample size is 1000 and we are using 16 threads, we could assume that the data size assigned to each thread is small. Therefore, the data might fit into the cache of the processor. According to the locality, we could achieve a higher speedup for the 1000 samples under 16 and 8 threads in OpenMP implementation. When we talk about the computation cost, we could say that a larger dataset includes more computation cost. Therefore, if we increase the size of the dataset, then we could achieve a higher speedup in OpenMP and OpenMPI versions.

# Data-Feature Parallel Scalability over Feature Size

The data size for the following figure is 100,000.



Shared address model shows better scalability over feature size than message passing. This is because the major computation cost is from `compress` and the workload for each worker for one iteration in `compress` is  $O(\frac{\text{data}}{\text{workers}} * \text{feature})$ . So as feature size increases, the program becomes more computational-intensive.

However, the message passing version shows less scalability as feature size increases from 400 to 1000. This is because that in `compress` function, the master-worker is responsible for merging all the results and thus the computational cost is `ParseError: KaTeX parse error: Expected 'EOF', got '#' at position 3: O(\text{feature} * \text{bin})` and also the communication cost is linearly related to feature size. So even though the increase of feature size leads to higher computational cost, it also increases the non-parallelizable computation in MASTER and communication costs. So the scalability over feature size shows a non-linear relation.

## CUDA Speedup Analysis

From the previous figures we can see, the CUDA version is slower than the sequential version in the `ijcnn1` dataset. When the size of the training dataset began to scale, the CUDA version achieves higher speedup.

When it comes to the largest `big_size_small_feature` dataset, the CUDA version achieves the highest speedup. However, the speedup of CUDA is slightly lower than our expectations. The possible reasons might be as follows.

1. The data transfer time for `cudaMalloc` and `cudaMemcpy`. In the CUDA version, we have to transfer the result between the CUDA device and the host. The data transfer time for the `ijcnn1` dataset is 0.111410 seconds. While the total train time is 3.152414 seconds, the data transfer time occupies 3.53% of the total train time. Therefore, it might lead to slightly poor performance for the CUDA version. The data transfer time for `medium_size_small_feature` dataset is 0.108330 (1.11%) and the data transfer time for `big_size_small_feature` dataset is 0.121970 seconds (0.13%). Therefore, when the dataset began to expand, the influence of data transfer reduces.
2. The inherent operations in the CUDA version. When we change from the sequential version to the CUDA version, we have included other operations to support the CUDA version. For example, in the `calculate_feature_value_kernel` function, we have a new data structure `cuda_feature_value_num` to record the possible split value numbers for each feature. We have to calculate this data structure explicitly. While in the previous versions, there is no need to build this data structure explicitly. The CUDA version creates new calculations.

## References

[1]: Srivastava, Anurag, et al. "Parallel formulations of decision-tree classification algorithms." High Performance Data Mining. Springer, Boston, MA, 1999. 237-261.

- [2]: Ben-Haim, Yael, and Elad Tom-Tov. "A streaming parallel decision tree algorithm." Journal of Machine Learning Research 11.Feb (2010): 849-872.
- [3]: Zhang, Huan, Si Si, and Cho-Jui Hsieh. "GPU-acceleration for Large-scale Tree Boosting." arXiv preprint arXiv:1706.08359 (2017).
- [4]: Jin, Ruoming, and Gagan Agrawal. "Communication and memory efficient parallel decision tree construction." Proceedings of the 2003 SIAM International Conference on Data Mining. Society for Industrial and Applied Mathematics, 2003.
- [5]: Chih-Chung Chang and Chih-Jen Lin, LIBSVM : a library for support vector machines. ACM Transactions on Intelligent Systems and Technology, 2:27:1--27:27, 2011. Software available at <http://www.csie.ntu.edu.tw/~cjlin/libsvm>.

## List of work