Final Report

Mengdi Lin (ml3567)

BTree Index HowTos

To Compile To An Exectuable

```
# set your PAGE_SIZE in BTreePage.h
BTREE_SIZE=<PAGE_SIZE in BTreepPage.h>
make -j 2
```

This should generate an executable with `test_<#>` where # corresponds to the page size

To Build A BTreeIndex With The Executable

```
./test_<#> -build <path_to_idx> <path_to_index> &> log
```

To Perform Equality-Probe On Key With The Executable

```
#if we want to probe on a single key
./test_<#> -probe_key <key> <index_file_path> <binary_data_file_path>

#if we want to probe on a file of keys (file format must be the same as idx format)
./test_<#> -probe_file <data_file_path> <index_file_path> <binary_data_file_path>
```

To Perform Range-Probe On Key With the Executable

```
#if we are searching for all keys x such that: x >= key
./test_<#> -range_probe_key_gt <key> <index_file_path> <binary_data_file_path>

#if we are searching for all keys x such that: key >= x
./test_<#> -range_probe_key_lt <key> <index_file_path> <binary_data_file_path>

#if we are searching for all keys x such that: start_key <= x <= end_key
./test_<#> -range_probe_key_endpts <start_key> <end_key> <index_file_path> <binary_da
ta_file_path>
```

BTreeIndex API Functions

To Build Index

```
BTreeIndex btree;
//dataIdxFilePath is a string representing the path of data idx file
vector<DataEntry> entries = btree.parse_idx_file(dataIdxFilePath);
//build the tree in memory
btree.build_tree(entries);
//flush it to index file. indexFilePath is a string representing the path to index fi
le
btree.flush(indexFilePath);
```

To Perform Equality Probe On A Key

```
BTreeIndex btree;
//key is uint64_t
//index_fd and data_bin_fd are file descriptors of index file and data.bin file
//result is a pair where the first item is a boolean indicating
// whether key is found in index. second item is the rid of key, if key is found
auto result = btree.probe(key,index_fd, data_bin_fd);
```

To Perform Range Probe On A Key

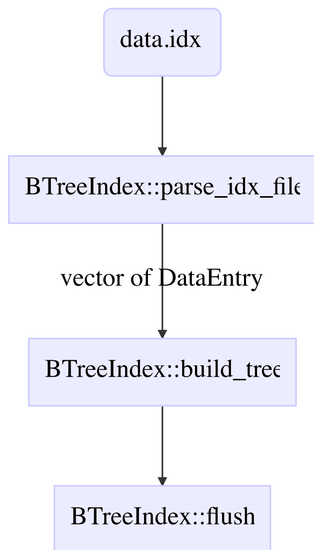
```
//if we are searching for all keys x such that: x >= key
//key is uint64_t
//index_fd and data_bin_fd are file descriptors of index file and data.bin file
//bin_file_size is the file size of data_bin_fd
auto result = btree.range_probe_gt(key, index_fd, data_bin_fd, bin_file_size);

//if we are searching for all keys x such that: key >= x
auto result = btree.range_probe_lt(key, index_fd, data_bin_fd);

//if we are searching for all keys x such that: start_key <= x <= end_key
auto result = btree.range_probe_endpts(start_key, end_key, index_fd, data_bin_fd, bin
_file_size);
```

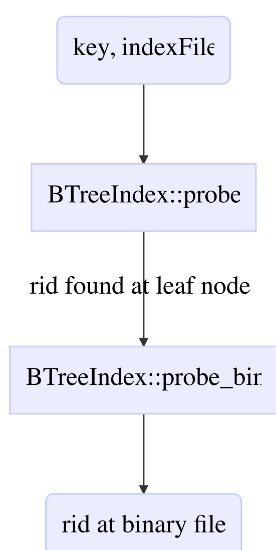
BTreeIndex Architecture

BTree Build Process



`BTreeIndex` takes an `idx file`, passes it to `BTreeIndex::parse_idx_file` which parses the file and returns a `vector<DataEntry>`. `BTreeIndex::build_tree` takes the vector and builds a tree in memory. `BTreeIndex::flush` flushes the tree onto a file.

BTree Probe Process



`BTreeIndex` takes `key`

and `indexFile` file descriptor for an equality probe and passes them to `BTreeIndex::probe` which does a probe on the Btree and returns the `rid` found at the leaf node that corresponds to the `key`. Then, it calls `BTreeIndex::probe_bin` with `rid` as parameter to probe `data.bin` file to find the actual offset of the key in `data.bin`. Range probes follow similar design as equality probe.

BTreeIndex Experiments

Background

2 sets of experiments were performed with 2 data sets in /dev/shm/genome/probes (both 0/ and 1/). Btree indicies were built from the 2 data sets (0/ and 1/) in /dev/shm/genome/probes and probed using random min hashes provided in /dev/shm/genome/probes. Codes for building and probing for btree indices are built with -O4 optimization turned on.

Size of Btree Index

running on data in /dev/shm/genome/probes/0

page size	btree index size
1024	43.0 MB
128	54.43 MB
2048	42.33 MB
256	47.41 MB
4096	42.0 MB
512	44.4 MB

running on data in /dev/shm/genome/probes/1

page size	btree index size
1024	44.12 MB
128	55.83 MB
2048	43.43 MB
256	48.64 MB
4096	43.09 MB
512	45.55 MB

BTree Index Build Time

This is the total time the bulkloading algorithm takes to create a btree index. Note that not all entries in data.idx are in the leaf nodes of the btree index. Instead, btree index only stores keys whose rids are every 4K apart in its leaf. Thus, btree index size is significantly smaller than hash index.

running on data in /dev/shm/genome/probes/0

page size	build time (microseconds)
1024	288276.0
128	674109.0
2048	262092.0
256	454288.0
4096	248702.0
512	346141.0

running on data in /dev/shm/genome/probes/1

page size	build time (microseconds)
1024	294377.0
128	739542.0
2048	291138.0
256	463576.0
4096	261638.0
512	355268.0

Performance of Btree Index Probe On Single Key

To measure the performance of a equality probe on a single key, I ran 581223607 random probes using the probe file provided in /dev/shm/genome/probes/0 and then took the average of the total time the index had taken to perform 581223607 random probes.

running on data in /dev/shm/genome/probes/0

page size	number of probes	avg microsecond per probe	successful probe	unsuccessful probe
1024	581223607	10	581018721	204886
128	581223607	13	581018721	204886
2048	581223607	10	581018721	204886
256	581223607	11	581018721	204886
4096	581223607	9	581018721	204886
512	581223607	10	581018721	204886

running on data in /dev/shm/genome/probes/1

page size	number of probes	avg microsecond per probe	successful probe	unsuccessful probe
1024	581223607	12	521002767	60220840
128	581223607	16	521002767	60220840
2048	581223607	11	521002767	60220840
256	581223607	12	521002767	60220840
4096	581223607	11	521002767	60220840
512	581223607	13	521002767	60220840

For a btree index, the larger the page size, the faster the probe since a large page size also indicates a shorter tree (fewer traversals to get to the leaf level). I noticed that btree indices take slightly longer when probing on the second data set which have a significantly higher number of unsuccessful probes. This can be explained by the implementation of the probe. For a btree probe, after it has reached the child node, the probe algorithm has to open data.bin and does a linear scan from a specific offset, looking for the key. If the key is not in data.bin, then the algorithm will keep reading until it has read 4096B. On the other hand, if the key is in data.bin, the algorithm will most likely terminate early before it finishes reading 4096B.

Performance of BTree Index Range Probe

To measure the performance of range probe, I generated an input file with 10000 rows using `generate_range_sample_for_test` in `test.cpp`. Within each row, there is a start key, an end key, and the number of keys inbetween start and end keys (which is 1000). start keys are in random order (obtained from /dev/shm/genome/probes/0/probes.idx). When I ran the experiment, I probed on start and end keys until the end of input file.

running on data in /dev/shm/genome/probes/0

page size	number of probes	result size (number of keys, rids)	avg microsecond per probe
1024	10000	1000	64
128	10000	1000	70
2048	10000	1000	67
256	10000	1000	68
4096	10000	1000	67
512	10000	1000	69

running on data in /dev/shm/genome/probes/1

page size	number of probes	result size (number of keys, rids)	avg microsecond per probe
1024	10000	1000	64
128	10000	1000	72
2048	10000	1000	72
256	10000	1000	73
4096	10000	1000	70
512	10000	1000	71

HashIndex HowTos

To Compile To An Exectuable

```
# set your PAGE_SIZE in Page.h
HASH_SIZE=<PAGE_SIZE in Page.h>
make -j 2
```

This should generate an executable with `hash_test_<#>` where # corresponds to the page size

To Build A Hash Index With The Executable

```
./hash_test_<#> -build <path_to_idx> <path_to_index> <load_capacity> &> log
```

To Perform Equality-Probe On Key With The Executable

```
#if we want to probe on a single key
./test_<#> -probe_key <key> <path_to_index> <load_capacity> &> log

#if we want to probe on a file of keys (file format must be the same as idx format)
./test_<#> -probe_file <path_to_idx> <path_to_index> <load_capacity> &> log
```

HashIndex API Functions

To Build Index

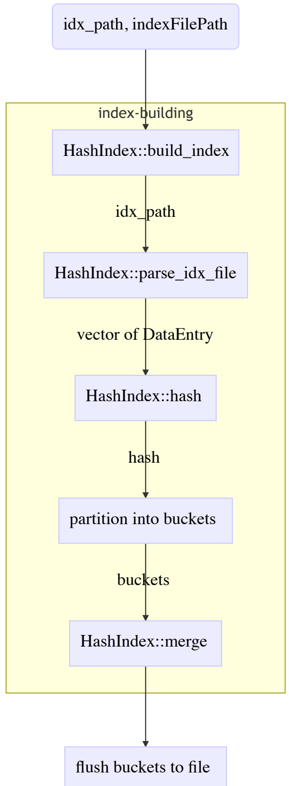
```
//load_capacity is a float in the range of (0,1]
HashIndex index(load_capacity);
//dataFilePath is the idx file path
//indexFileName is the path to output index file
index.build_index(dataFilePath, indexFileName);
```

To Perform Equality Probe On A Key

```
//load_capacity is a float in the range of (0,1]
HashIndex index(load_capacity);
//index_fd is the file descriptor of index file
pair<bool,uint64_t> t_result = index.search(key, index_fd);
```

HashIndex Architecture

Hash Index Build Process

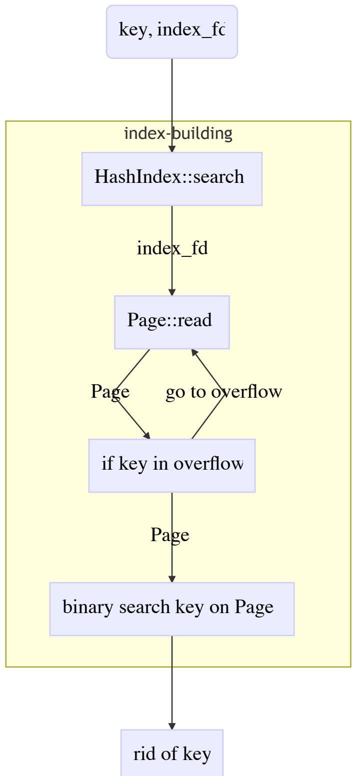


`HashIndex` takes `idx_path` and `indexFilePath`, and passes them to `HashIndex::build_index`.

`build_index` has 5 steps.

```
1. Parses idx file into a vector of DataEntry
2. hash each key in DataEntry to number corresponding to a bucket
3. partition keys based on their hash into a bucket
4. merge empty primary buckets with overflow pages
5. flush
```

Hash Index Probe Process



`HashIndex` takes `key` and `index_fd`, and passes them to `HashIndex::search`. `search` has 3 steps.

```
1. read page from current offset in index
2. if search key is larger than the largest key in current page, go to overflow page.
 Else, perform a binary search on the current page to get key.
3. return rid
```

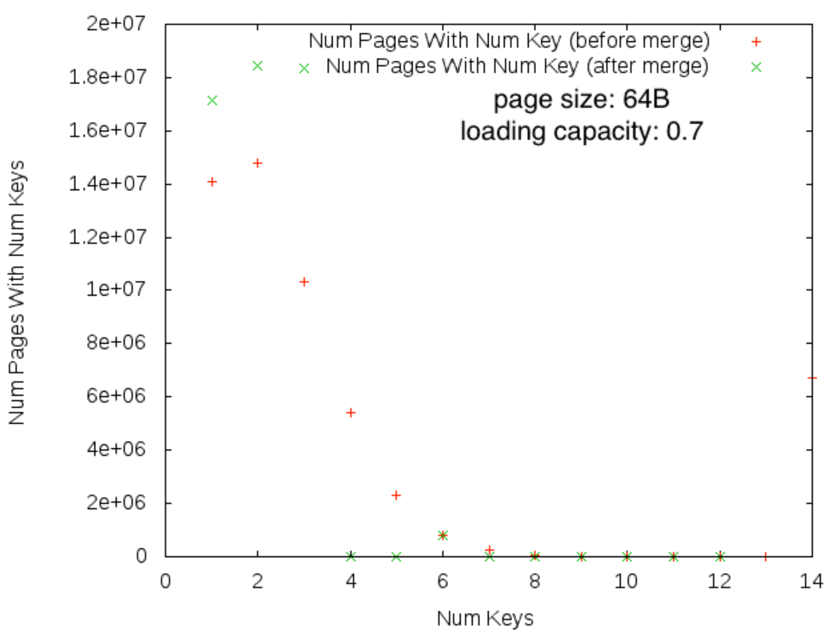
HashIndex Experiments

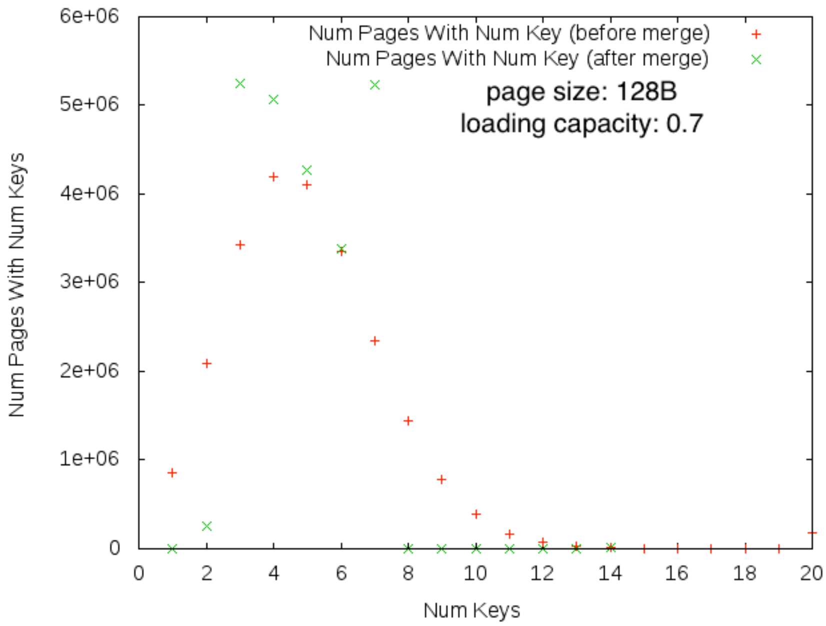
Background

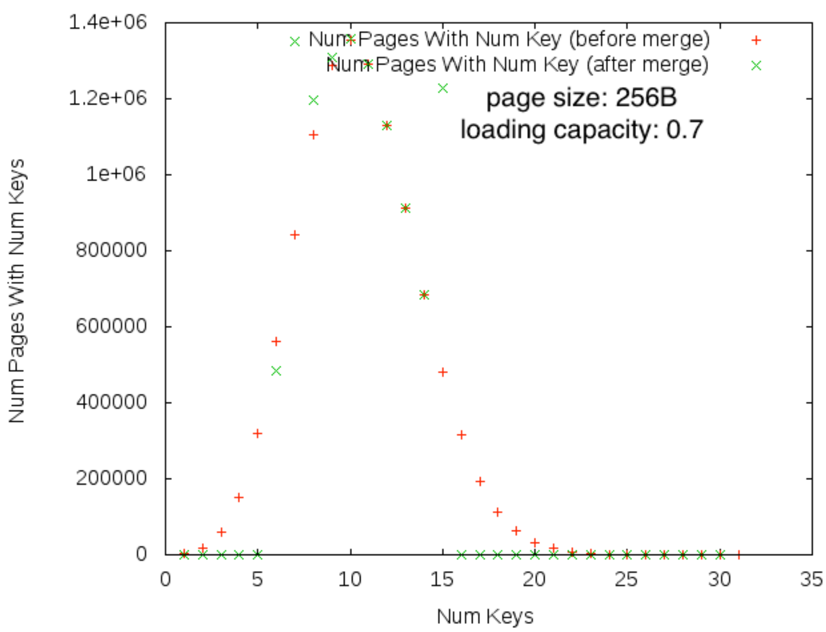
3 sets of experiments were performed with 3 data sets in /dev/shm/genome/probes. Hash indicies were built from the 3 data sets in /dev/shm/genome/probes and probed using random min hashes provided in /dev/shm/genome/probes. Codes for building and probing for btree indices are built with -O4 optimization turned on. All experiments are ran on Ingatan.

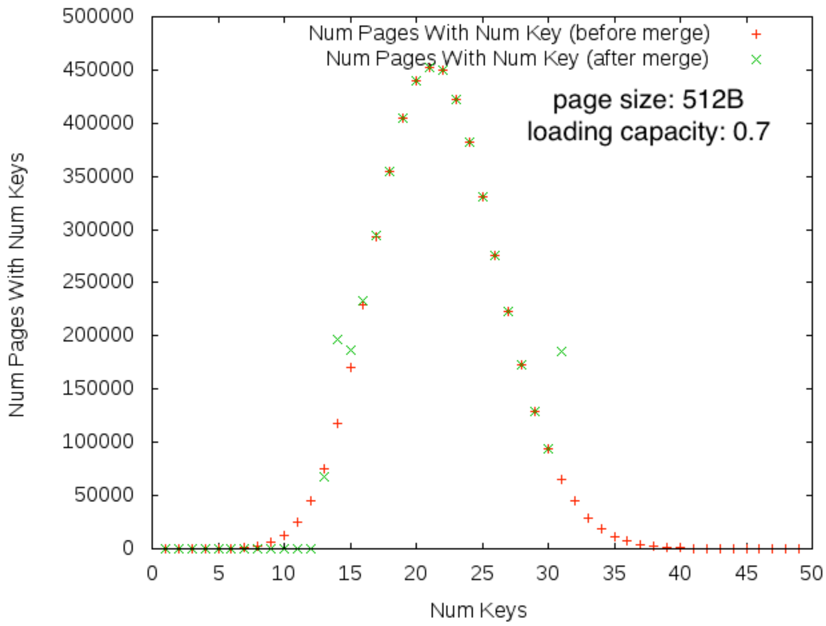
Hash Distribution Plots For Data In /dev/shm/genome/probes/0

Graphs below represent the distribution of keys per page in a hash index with a specific page size and load capacity. The distributions of hashed keys exhibit a normal curve, centering around `(PAGE_SIZE/16B)*load_capacity` (number of entries per page if entries are evenly distributed). The red curve is the distribution before `merge` algorithm tries to find empty hash buckets to merge with overflow pages. The green curve is the distribution after `merge` algorithm has been applied and empty primary buckets have been merged with overflow pages. `merge` algorithm does nothing for page sizes >= 1024B. For smaller page sizes, `merge` algorithm has collapsed the two ends of the distribution such that the ends are flatter and more points are concentrated around the median.

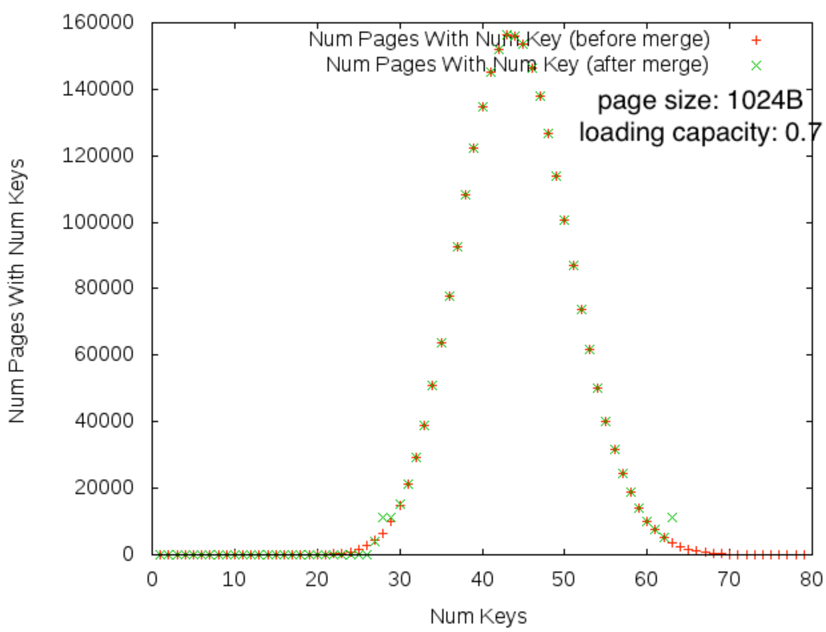



Num Pages With Num Key (before merge)
Num Pages With Num Key (after merge)
page size: 128B
loading capacity: 0.7
Num Pages With Num Keys
Num Keys
6e+06
5e+06
4e+06
3e+06
2e+06
1e+06
0
0
2
4
6
8
10
12
14
16
18
20

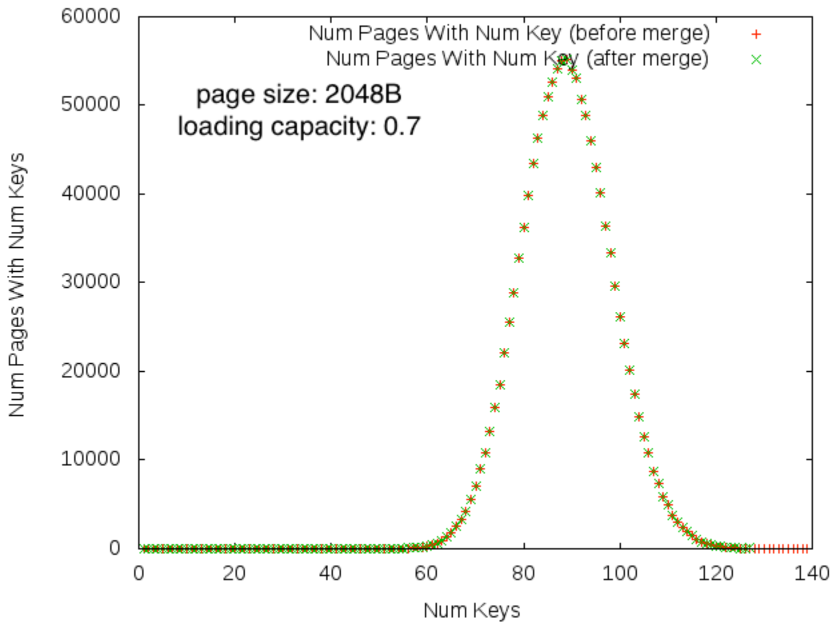

Num Pages With Num Key (before merge)
Num Pages With Num Key (after merge)
page size: 256B
loading capacity: 0.7
Num Pages With Num Keys
Num Keys
1.4e+06
1.2e+06
1e+06
800000
600000
400000
200000
0
0
5
10
15
20
25
30
35

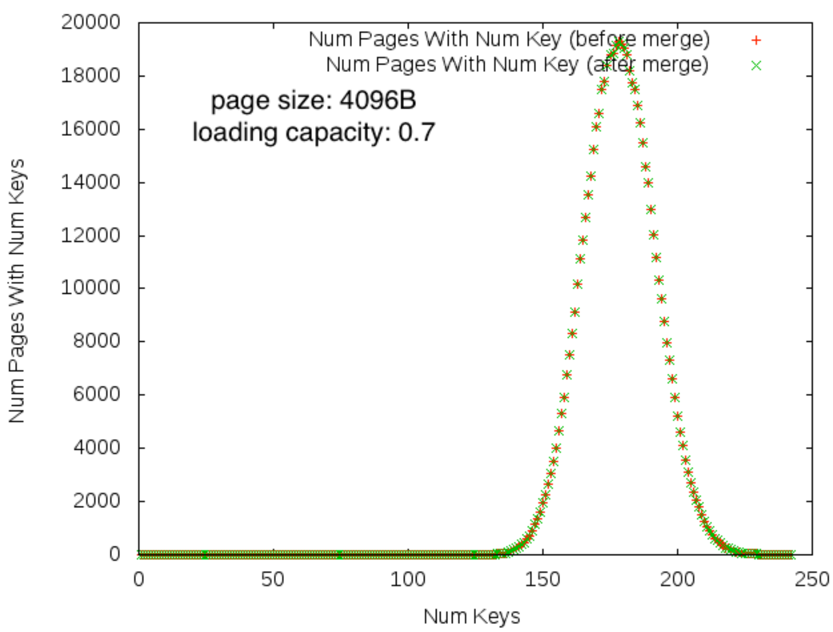


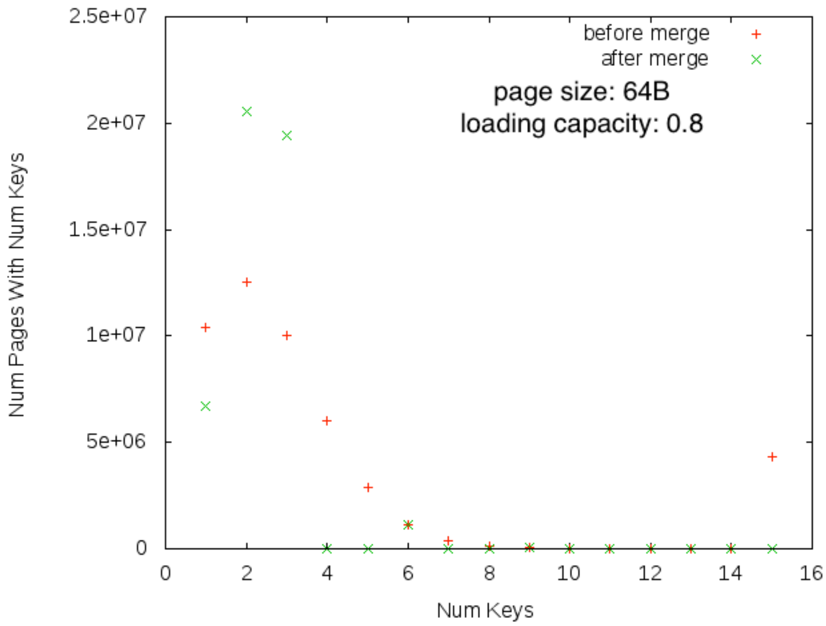
Num Pages With Num Key (before merge)
Num Pages With Num Key (after merge)
page size: 512B
loading capacity: 0.7
Num Pages With Num Keys
Num Keys



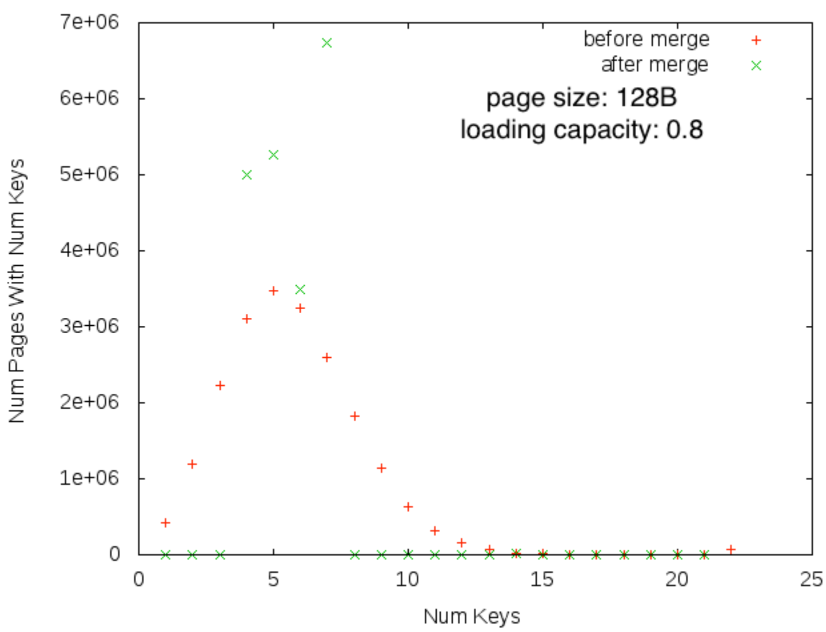
Num Pages With Num Key (before merge)
Num Pages With Num Key (after merge)
page size: 1024B
loading capacity: 0.7
Num Pages With Num Keys
Num Keys


Num Pages With Num Key (before merge)
Num Pages With Num Key (after merge)
page size: 2048B
loading capacity: 0.7
Num Pages With Num Keys
Num Keys
0
10000
20000
30000
40000
50000
60000
0
20
40
60
80
100
120
140

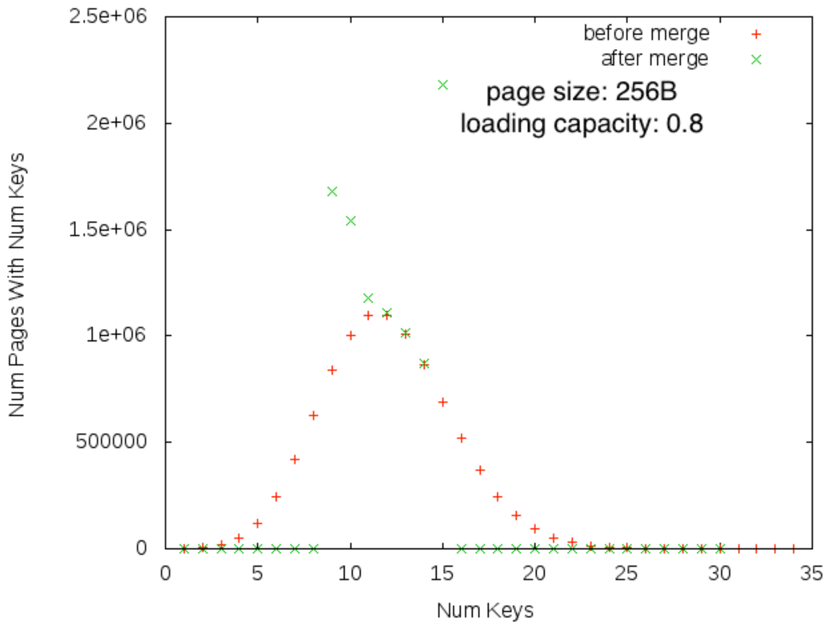

Num Pages With Num Key (before merge)
Num Pages With Num Key (after merge)
page size: 4096B
loading capacity: 0.7
Num Pages With Num Keys
Num Keys
0
2000
4000
6000
8000
10000
12000
14000
16000
18000
20000
0
50
100
150
200
250

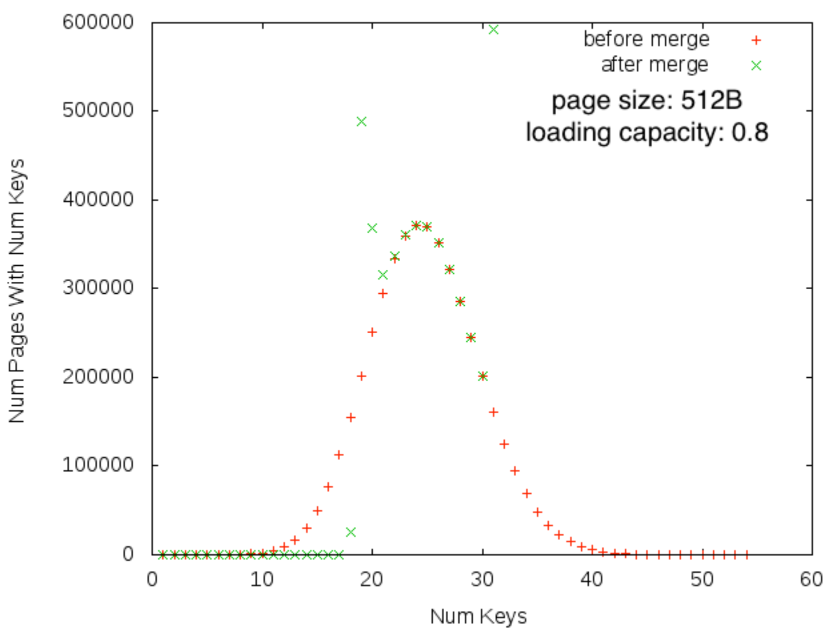


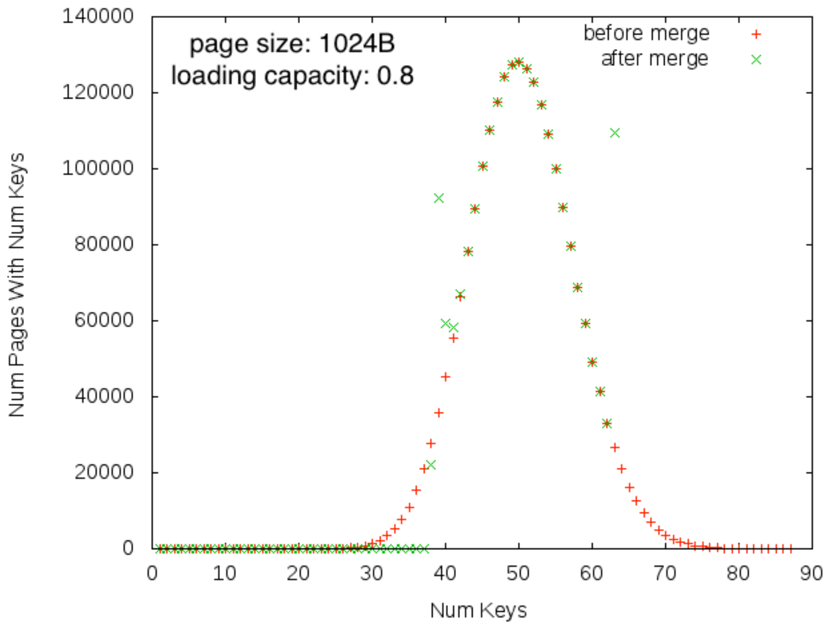
before merge
after merge
page size: 64B
loading capacity: 0.8
Num Pages With Num Keys
Num Keys

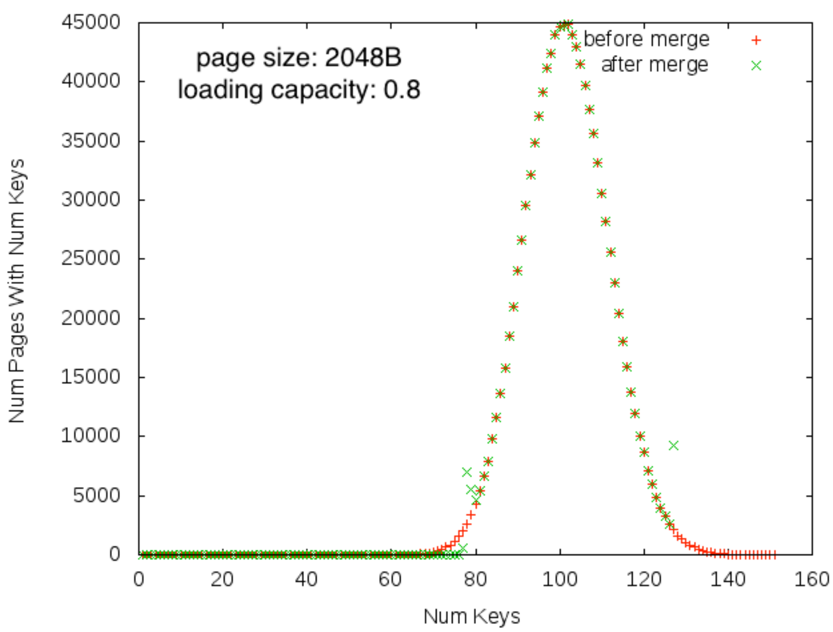


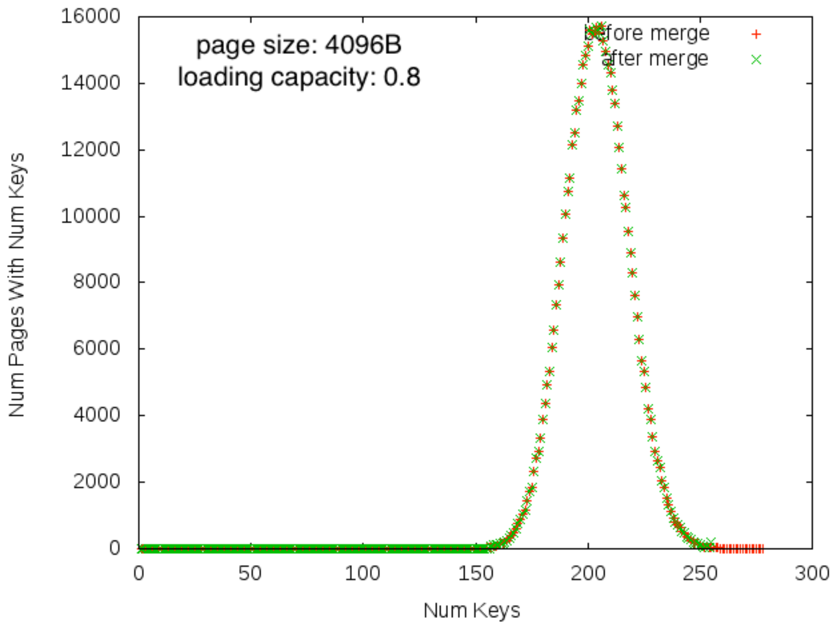
before merge
after merge
page size: 128B
loading capacity: 0.8
Num Pages With Num Keys
Num Keys


before merge
after merge
page size: 256B
loading capacity: 0.8
Num Pages With Num Keys
Num Keys
2.5e+06
2e+06
1.5e+06
1e+06
500000
0
5
10
15
20
25
30
35


before merge
after merge
page size: 512B
loading capacity: 0.8
Num Pages With Num Keys
Num Keys
600000
500000
400000
300000
200000
100000
0
10
20
30
40
50
60


page size: 1024B
loading capacity: 0.8
before merge
after merge
Num Pages With Num Keys
Num Keys
0
20000
40000
60000
80000
100000
120000
140000
0
10
20
30
40
50
60
70
80
90


page size: 2048B
loading capacity: 0.8
before merge
after merge
Num Pages With Num Keys
Num Keys
0
5000
10000
15000
20000
25000
30000
35000
40000
45000
0
20
40
60
80
100
120
140
160



Codes For Generating Graphs

```
python clean_log.py <build log> <before merge log> <after merge log>
gnuplot
>set term png
>set output "64_80.png"
>set xlabel "Num Keys"
>set ylabel "Num Pages With Num Keys"
>plot "64_80_before_merge" using 1:2 title "before merge", "64_80_after_merge" using
1:2 title "after merge"
>plot "4096_80_before_merge" using 1:2 title "Num Pages With Num Key (before merge)",
 "4096_70_hash_after_merge" using 1:2 title "Num Pages With Num Key (after merge)"
```

Size of Hash Index

In general, the larger the page size and the higher the load capacity, the smaller the index size. The smallest index comes from index with page size 4096B and 100% load capacity. Increasing the page size reduces the size of the index more significantly for page sizes <= 1048B whereas for indices with page size > 1048B, increasing the page size only reduces the index size with a small amount.

running on data in /dev/shm/genome/probes/0

page size (bytes)	load capacity	file size
1024	100	1.75 GB

1024	70	2.49 GB
1024	80	2.17 GB
1024	90	1.93 GB
128	100	2.0 GB
128	70	2.8 GB
128	80	2.45 GB
128	90	2.19 GB
2048	100	1.74 GB
2048	70	2.47 GB
2048	80	2.16 GB
2048	90	1.92 GB
256	100	1.86 GB
256	70	2.61 GB
256	80	2.28 GB
256	90	2.03 GB
4096	100	1.73 GB
4096	70	2.46 GB
4096	80	2.15 GB
4096	90	1.91 GB
512	100	1.79 GB
512	70	2.53 GB
512	80	2.21 GB
512	90	1.96 GB
64	100	2.48 GB
64	70	3.33 GB

64	80	2.96 GB
64	90	2.69 GB

running on data in /dev/shm/genome/probes/1

page size (bytes)	load capacity	file size
1024	100	1.79 GB
1024	70	2.55 GB
1024	80	2.23 GB
1024	90	1.98 GB
128	100	2.05 GB
128	70	2.87 GB
128	80	2.51 GB
128	90	2.24 GB
256	100	1.9 GB
256	70	2.67 GB
256	80	2.34 GB
256	90	2.08 GB
512	100	1.83 GB
512	70	2.59 GB
512	80	2.26 GB
512	90	2.01 GB
64	100	2.54 GB
64	70	3.41 GB
64	80	3.03 GB
64	90	2.75 GB

running on data in /dev/shm/genome/probes/2

page size (bytes)	load capacity	file size
1024	100	1.8 GB
1024	70	2.55 GB
1024	80	2.23 GB
1024	90	1.98 GB
128	100	2.05 GB
128	70	2.87 GB
128	80	2.51 GB
128	90	2.24 GB
256	100	1.9 GB
256	70	2.67 GB
256	80	2.34 GB
256	90	2.08 GB
512	100	1.83 GB
512	70	2.59 GB
512	80	2.26 GB
512	90	2.01 GB

Hash Index Build Time

Large page size and high load capacity correlates with a shorter index build time. Building a hash index is moderately faster than building a btree index as seen from the build times of both hash and btree indices.

running on data in /dev/shm/genome/probes/0

page size	load capacity	build time (ms)
1024	100	171389.135136
1024	70	223710.145579

1024	80	168161.630477
1024	90	166776.003406
128	100	234563.707079
128	70	289828.123695
128	80	236725.524979
128	90	235922.372648
2048	100	167470.062586
2048	70	202760.919218
2048	80	176125.10483
2048	90	162039.708698
256	100	200483.511471
256	70	221573.838233
256	80	207636.302969
256	90	203757.940441
4096	100	160234.395502
4096	70	164579.079287
4096	80	158014.133829
4096	90	160892.606469
512	100	181270.80125
512	70	191675.995715
512	80	179316.751932
512	90	180707.174209
64	70	347764.071148
64	80	315848.490653

64	90	322349.01136

running on data in /dev/shm/genome/probes/1

page size	load capacity	build time (ms)
1024	100	169212.891371
1024	70	170016.062537
1024	80	162829.003763
1024	90	177309.245472
128	100	222264.495195
128	70	247171.878918
128	80	232301.465799
128	90	238997.341209
256	100	192225.984272
256	70	202073.177647
256	80	208734.958637
256	90	207179.320846
512	100	179182.509888
512	70	188705.391672
512	80	178942.686694
512	90	183014.701338
64	100	308592.543915
64	70	251495.116857
64	80	249108.102207
64	90	267156.510625

running on data in /dev/shm/genome/probes/2

page size	load capacity	build time (ms)
1024	100	166695.284624
1024	70	171969.419878
1024	80	171068.201793
1024	90	165339.598203
128	100	217734.888551
128	70	224562.107108
128	80	216592.967218
128	90	213045.054758
256	100	201341.027593
256	70	194945.271324
256	80	214449.548223
256	90	191886.920873
512	100	178424.062664
512	70	182022.679635
512	80	180544.243822
512	90	174793.360486

Performance of Hash Index Probe

For the first data set `/0/`, hash index with page size of 512B and load capacity of 70 yields the fastest average probe time. hash index with page size of 256B and load capacity of 90 yields the second fastest average probe time. Hash index with page size of 512B and load capacity of 100 yields the third fastest average probe time.

For the second data set `/1/`, hash index with page size of 512B and load capacity of 70 yields the fastest average probe time. Hash index with page size of 1024B and load capacity of 70 yields the second fastest average probe time. Hash index with page size of 512B and load capacity of 80 yields the third fastest average probe time.

For the third data set `/2/`, hash index with page size of 128B and load capacity of 70 yields the fastest average probe time. Hash index with page size of 256B and load capacity of 100 yields the second fastest average probe time. Hash index with page size of 256B and load capacity of 80 yields the third fastest average probe time.

Overall, page sizes larger than 1048B and page sizes smaller than 128B do not perform as well as pages that are within [128B, 1048B]. There is no one page size that performs consistently the best across probes on three data sets. However, hash index with page size of 512B and load capacity of 70 performs above average in comparison to other hash indices. Even though the second data set have a significantly higher number of unsuccessful probes (probing on key not found in index), there is no significantly change in the speed of probe. Thus, hash indices perform equally well for a successful and an unsuccessful probe.

running on data in /dev/shm/genome/probes/0

page size	load capacity	total probes	average probe time (ns)	total probe time (s)	num of successful probe	num of unsuccessful probe
1024	100	581223607	1857	1079.49	581018721	204886
1024	70	581223607	1316	765.09	581018721	204886
1024	80	581223607	2113	1228.44	581018721	204886
1024	90	581223607	1908	110.92	581018721	204886
128	70	581223607	1527	888.065	581018721	204886
128	80	581223607	1535	892.44	581018721	204886
128	90	581223607	1623	943.55	581018721	204886
2048	100	581223607	2564	1490.75	581018721	204886
2048	70	581223607	2361	1372.65	581018721	204886
2048	80	581223607	2398	1394.05	581018721	204886
2048	90	581223607	2026	1177.88	581018721	204886
256	100	581223607	1643	955.32	581018721	204886

256	70	581223607	1622	942.89	581018721	204886
256	80	581223607	1403	815.49	581018721	204886
256	90	581223607	1187	690.28	581018721	204886
4096	100	581223607	1763	1025.03	581018721	204886
4096	70	581223607	2551	1482.82	581018721	204886
4096	80	581223607	2969	1726.14	581018721	204886
4096	90	581223607	2876	1671.77	581018721	204886
512	100	581223607	1270	738.58	581018721	204886
512	70	581223607	1184	688.63	581018721	204886
512	80	581223607	1532	890.55	581018721	204886
512	90	581223607	1904	110.68	581018721	204886
64	100	581223607	1678	975.50	581018721	204886
64	70	581223607	1458	847.86	581018721	204886
64	80	581223607	1334	775.88	581018721	204886
64	90	581223607	1615	938.93	581018721	204886

running on data in /dev/shm/genome/probes/1

page size	load capacity	total probes	average probe time (ns)	total probe time (s)	num of successful probe	num of unsuccessful probe
1024	100	581223607	1970	1145.42	521002767	60220840
1024	70	581223607	1285	746.95	521002767	60220840
1024	80	581223607	1939	1127.19	521002767	60220840
1024	90	581223607	1954	1135.75	521002767	60220840
128	100	581223607	1599	929.91	521002767	60220840
128	70	581223607	1479	859.97	521002767	60220840
128	80	581223607	1574	915.05	521002767	60220840
128	90	581223607	1562	908.21	521002767	60220840
256	100	581223607	1679	976.35	521002767	60220840
256	90	581223607	1464	851.38	521002767	60220840
512	100	581223607	1445	840.24	521002767	60220840
512	70	581223607	1199	697.16	521002767	60220840
512	80	581223607	1303	757.69	521002767	60220840
512	90	581223607	1855	1078.25	521002767	60220840
64	100	581223607	1327	771.85	521002767	60220840
64	70	581223607	1634	950.28	521002767	60220840
64	80	581223607	1375	799.31	521002767	60220840
64	90	581223607	1568	911.64	521002767	60220840

running on data in /dev/shm/genome/probes/2

page size	load capacity	total probes	average probe time (ns)	total probe time (s)	num of successful probe	num of unsuccessful probe
1024	100	581223607	2250	1308.24	581078110	145497
1024	70	581223607	2068	1202.24	581078110	145497
1024	80	581223607	2165	1258.79	581078110	145497
1024	90	581223607	2043	1187.81	581078110	145497
128	100	581223607	1584	921.09	581078110	145497
128	70	581223607	1065	619.51	581078110	145497
128	80	581223607	1529	888.95	581078110	145497
128	90	581223607	1639	953.08	581078110	145497
256	100	581223607	1124	653.62	581078110	145497
256	70	581223607	1473	856.30	581078110	145497
256	80	581223607	1246	724.42	581078110	145497
256	90	581223607	1502	873.53	581078110	145497
512	100	581223607	1878	1091.65	581078110	145497
512	70	581223607	1924	1118.85	581078110	145497
512	80	581223607	2047	1190.21	581078110	145497
512	90	581223607	1929	1121.36	581078110	145497

Ingatan Stats

- Processor model name: Intel(R) Xeon(R) CPU E5-4620 0 @ 2.20GHz
- Architecture: x86_64
- CPU(s): 64
- L1d cache: 32K
- L1i cache: 32K
- L2 cache: 256K

- L3 cache: 16384K
- MemTotal: 528359424 kB

Conclusion

Btree indices (~4MB), on average, are 500 times smaller than hash indices (~2GB) because not all entries in data.idx are in the leaf nodes of the btree index. Instead, btree index only stores keys whose rids are every 4K apart in its leaf. On the other hand, hash indices must store all (key, rid) pairs provided in data.idx file. On the other hand, a btree index probe (~10ms) is 10 times slower than a hash index probe (~1ms). Probing a key that is not in the index is shown to be slower when doing a btree probe, whereas the existence of key in the index does not impact the probe speed in the hash index.