Optimized workflow for analyses with multiple RDataFrames

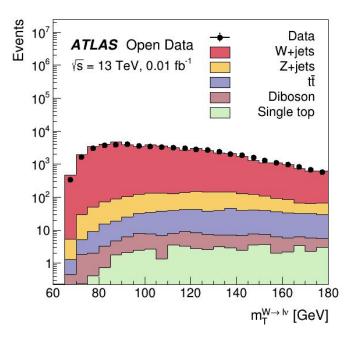
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ROOT Data Analysis Framework https://root.cern

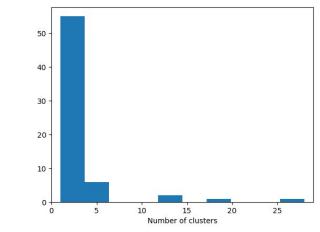
The example analysis

- All (realistic) analyses have to use multiple RDFs
- At least one RDF per process
- Typically each process is described with multiple datasets (W+1jet, W+2jet, ...)
- This example:
- 4.8 GB in total
 - Compressed size
 - About 10% of the total dataset size
 - 2.3 GB read (measured with <u>TTreePerfStats</u>)
- 65 files (4 data + 61 simulation)
- 25 M events in total with 81 columns each
- Data + 5 simulated processes
- Setup requires 65 RDFs because each dataset requires different event weights





The core of the analysis



- Run very similar computation graphs for all dataset, but no TChain is possible (differences between data/MC, different weights per MC sample, ...)
- Event loops are multi threaded (on very few TTree clusters), but RDFs run sequential
 → Results in an inefficient CPU usage!

ROOT.EnableImplicitMT(12)

```
histos = {} # histograms
df = {...} # 65 RDFs
for s in samples:
    histos[s] = df[s].Filter(...)\
        .Define(...)\
        .Histo1D(...)
```

```
# Trigger the event loops
for s in samples: h[s].Draw()
```

How could we improve the workflow?

```
ROOT.EnableImplicitMT(12)
```

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# Trigger the event loops
for s in samples: h[s].Draw()
```

- Using TChains?
 Often not possible due to small differences in the computation graphs
 →Tree or file based Define and Filter nodes?
- Setup of the computation graphs is declarative, in principle as we want the user to use RDF
- Can we parallelize the sequential execution of multiple RDFs?

Run RDFs in parallel!

void RLoopManager::Run()

```
- CleanUpNodes();
```

+

```
R__LOCKGUARD(gInterpreterMutex);
```

```
CleanUpNodes();
```

```
fNRuns++;
```

```
fNRuns++;
```



Hacked in thread safety for a proof of concept to enable running multiple RDataFrames in parallel!

Trigger the event loops, in parallel!

```
ROOT.EnableImplicitMT(12)
```

```
histos = {} # histograms
df = {...} # 65 RDFs
for s in samples:
    histos[s] = df[s].Filter(...)\
        .Define(...)\
        .Histo1D(...)
```

```
# Trigger the event loops, all in parallel!
ROOT.gInterpreter.ProcessLine('std::vector<ROOT::RDF::RResultPtr<TH1D>> ptrs;')
for s in samples: ROOT.ptrs.push_back(histos[s])
```

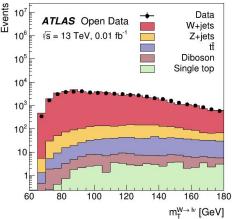
```
R0OT.gInterpreter.ProcessLine('''
R0OT::TThreadExecutor pool;
pool.Map([](R0OT::RDF::RResultPtr<TH1D> ptr) { *ptr; }, ptrs);
''')
```

All RDFs share the same thread pool!

Is it worth it?

- Multi threading on 12 (physical?) cores (running on almost empty machine with 24/48 physical/logical cores)
- Read data from storage server with SSDs and 20 GBit connection
- Sequential execution of RDFs
 - 90s wall time
 - 300s CPU time
 - 330% CPU usage
 - 1.3 GB max resident size



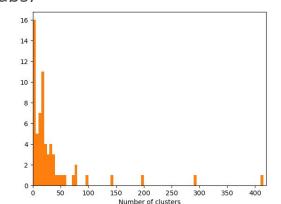


- Parallel execution of RDFs
 - 36s wall time
 - 310s CPU time
 - 870% CPU usage

- \rightarrow 90/36 = 2.5x faster runtime!
- \rightarrow slightly increased, due to higher contention?
- → 870/330 = **2.5x higher CPU usage!**
- 2 GB max resident size \rightarrow concurrent event loops?

Does it matter with big data?

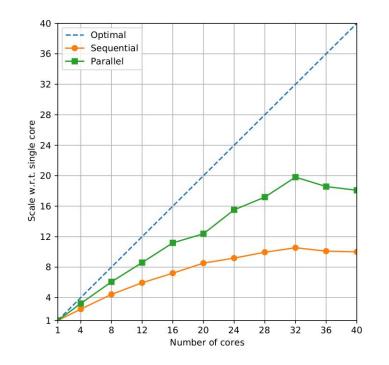
- Let's try again with the full dataset of 66 GB (see plot on the bottom for # of clusters)
- In realistic settings, files with <12 clusters are still common!
- Issue amplifies when using more cores (machines with >48 cores are already typical for larger university groups)
- Scaling up to 100 cores in a realistic analysis?
 In practise, easily blocked by this!



- Sequential execution of RDFs (MT=12)
 - 470s wall time
 - 4500s CPU time
 - 970% CPU usage
 - 2.1 GB max resident size
- Parallel execution of RDFs (MT=12)
 - 380s wall time→1.2x faster!
 - 4300s CPU time
 - 1140% CPU usage→**1.2x higher!**
 - 3.2 GB max resident size
- Sequential execution of RDFs (MT=24)
 - 203s wall time
 - 3200s CPU time
 - 1610% CPU usage
 - 3.6 GB max resident size
- Parallel execution of RDFs (MT=24)
 - 127s wall time→1.6x faster!
 - 2800s CPU time
 - 2210% CPU usage→1.4x higher!
 - 6.1 GB max resident size

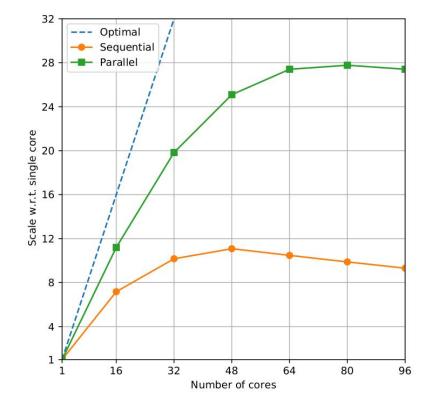
Scaling is back!

- Full dataset with 66 GB
 - Compressed size
 - 23.8 GB read (measured with TTreePerfStats)
- Machine with 64/128 physical/logical cores
- Data read from storage server with SSDs and 20 GBit connection
 - iperf: 5.2 GBit/s to the storage server
 - rsync: ~220MB/s (copy to local SSD)
- Limited for >32 cores again by number of clusters?
- Limited by network/IO?
 - With 32 cores:
 23.8 GB / 105 s = 230 MB/s = 1.8 Gbit/s
 - Beyond capabilities of HDDs
 - Beyond capabilities of most network connections
 - Saturates the connection to the storage server?



Scaling is back, reloaded!

- cgroups limited my share to 32 cores!
- Moved the dataset to a local SSD with NVMe interface
- With 64 cores: 23.8 GB / 75 s = **325 MB/s**
- Scaling saturates at
 - 28x with parallel RDFs
 - 11x with sequential RDFs



Proposal: Reference benchmark suite

- Set up a benchmark suite which scaling we know in optimal conditions
- Most important: Simple to run and to reproduce
- Allows to "calibrate" results on new systems and can identify bottlenecks, which are not related to our software
- Make it part of rootbench?

Final thoughts

• Multiprocessing + RDF

- Works!
- But suffers heavily with imbalanced datasets because you have to wait for the slowest process (see Massimilliano's and Vincenzo's studies!)

• Multithreading + RDF

- Allows to use all your resources efficiently
- Speeds up complex analyses and restores scaling using many cores
- Important for efficient usage of N cores batch jobs (without manual file splitting to tackle the imbalance)
- Can we make it work with Python's <u>ThreadPoolExecutor</u>?
- Alternative solution: Tree/file based Define and Filter transformations
 - Solves the same issue with a different programming model
 - Less problems with implicit dependencies between RDFs
 - Goes well with the implicit parallelism model in ROOT
 - You can think of other solutions?
 - What is the strategy for PyRDF, naturally using many cores/nodes?