Readable and efficient HEP data analysis with bamboo using python, PyROOT, cling, and RDataFrame

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Personal experience: need for speed makes analysis code messy (hard to find bugs), inflexible, or both

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(Definition of not see the wood for the trees from the Cambridge Advanced Learner's Dictionary & Thesaurus © Cambridge University Press)



image credit: Claudio Caputo

there are many ideas to address this problem — this is only one attempt, based on what seemed promising for my use-case

RDataFrame: ROOT's declarative data analysis approach





E. Guiraud, "RDataFrame", ROOT users' workshop 2018

18

from this talk, see also today's CERN EP Software Seminar

Pieter David (UCLouvain)

Readable and efficient HEP data analysis with bamboo

Cling (C++ interpreter / JIT compiler) and PyROOT

- The ROOT interpreter is based on <u>Clang/LLVM</u>: correctly handles almost any valid modern C++ code (templates, lambda functions...)
- PyROOT exposes almost all of ROOT's functionality in python (and that of any C++ you add)
- Experimental PyROOT is bringing python callables to RDataFrame (and much more)
- Current bamboo compromise: pass expressions to RDataFrame as strings (generated with python)







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- Every analysis derives from a base class, such that e.g. splitting in batch jobs, and plotting code can be reused

Example: plot a dimuon invariant mass distribution. The momenta are in the branches Muon_pt[nMuon], Muon_eta[nMuon], Muon_phi[nMuon], and Muon_mass[nMuon] (and there may be more than two muons in the event)

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```
using ROOT::Math::VectorUtil::InvariantMass;
using LorentzVector =
    ROOT::Math::LorentzVector<ROOT::Math::PtEtaPhiM4D<float>>;
df.Define("Dimuon_mass",
    [] (const auto& pt, const auto& eta, const auto& phi, const auto& m) {
        return InvariantMass(LorentzVector(pt[0], eta[0], phi[0], m[0]),
                                LorentzVector(pt[1], eta[1], phi[1], m[1]));
        }, {"Muon_pt", "Muon_eta", "Muon_phi", "Muon_mass"}
    ).Histo1D(..., "Dimuon_mass", ...);
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        }, {"Muon_pt", "Muon_eta", "Muon_phi", "Muon_mass"}
    ).Histo1D(..., "Dimuon_mass", ...);
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Alternative, using the JIT compiler instead of a lambda function

```
df.Define("Dimuon_mass_v2",
    "InvariantMass("
        "LorentzVector(Muon_pt[0], Muon_eta[0], Muon_phi[0], Muon_mass[0]),"
        "LorentzVector(Muon_pt[1], Muon_eta[1], Muon_phi[1], Muon_mass[1]))"
    ).Histo1D(..., "Dimuon_mass_v2", ...);
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- For jets: need to take different branches for systematic variations
- In practice: need to compose, e.g. invariant mass of the two highest- p_T b-tagged jets that are not within $\Delta R < 0.3$ from any selected muon

bamboo equivalent:

```
from bamboo import treefunctions as op
Plot.make1D(...,
    op.invariant_mass(t.Muon[0].p4, t.Muon[1].p4), ...)
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```
Solution to #3:
```

```
cleanedBJets = op.select(t.Jet, lambda j : op.AND(
    op.NOT(op.rng_any(muons, lambda mu : op.deltaR(mu.p4, j.p4) < 0.3)),
    j.bTag > 0.6))
Plot.make1D(...,
```

op.invariant_mass(cleanedBJets[0].p4, cleanedBJets[1].p4), ...)

Not the fairest comparison — just to show how this can make code simpler

Implementation: expressions and proxies

Expressions

- are composed of simple python objects, e.g. t.Muon[0].pt (Muon_pt[0]) becomes GetItem(GetArrayLeaf("Muon_pt"),0)
- can be converted to a string for RDataFrame/JIT
- are considered immutable as soon as they are fully constructed and passed around (but a fresh clone can be modified by the owner)

Proxies

- Wrap an expression
- Emulate the value type of expression's result (through python operator overloading and other magic methods)
- float-like, integer-like, object-like, and a few list-like classes — but no complete type system (yet), so limited checks at construction

Currently each of these interfaces has about 25 implementations – the user should only need the decorated tree and the bamboo.treefunctions module

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- Groups of non-array branches: "group proxy" in between: t.HLT.MuXX, t.pdf.x1
- Groups of array branches: container proxy, and a proxy for the elements: t.Muon[0].IDLoose
- Can also add references and arbitrary functions: t.Jet[0].Mu1.pt, t.Muon[0].p4.E()



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- Can also add references and arbitrary functions: t.Jet[0].Mu1.pt,t.Muon[0].p4.E()
- Needs to be adapted to recognize different tree formats, but for *flat trees* (most common) this is fairly straightforward (examples are from CMS NanoAOD, one other format is implemented)



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Current solution (bamboo.plots):

- Selection class, with each instance (optionally) holding a set of selection requirements (cuts) and weight factors
- Selections are defined by adding cuts or weights to a more inclusive selection (starting point: all events in the input, unit weight)
- Plot instances are defined by a Selection, variable(s), binning(s), and layout options

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- RDataFrame nodes are created when Selection and Plot objects are constructed

Selections and plots: an example

```
def definePlots(self, t, noSel, sample=None, sampleCfg=None):
  from bamboo.plots import Plot, EquidistantBinning
  from bamboo import treefunctions as op
  plots = []
  muons = op.select(t.Muon, lambda mu : mu.pt > 20.)
  twoMuSel = noSel.refine("dimu", cut=(op.rng_len(muons) > 1))
  plots.append(Plot.make1D("dimu_M",
    op.invariant_mass(muons[0].p4, muons[1].p4), twoMuSel,
    EquidistantBinning(100, 20., 120.), title="Dimuon invariant mass"))
  jets = op.select(t.Jet, lambda j : j.pt > 20.)
  plots.append(Plot.make1D("dimu_nAllJets", op.rng_len(jets), twoMuSel,
    EquidistantBinning(10, 0., 10.), title="Number of jets (uncleaned)"))
  cleanedJets = op.select(jets, lambda j : op.NOT(
    op.rng_any(muons, lambda mu : op.deltaR(mu.p4, j.p4) < 0.3)))
  plots.append(Plot.make1D("dimu_nJets", op.rng_len(jets), twoMuSel,
    EquidistantBinning(10, 0., 10.), title="Number of jets (cleaned)"))
  twoMuTwoJetSel = twoMuSel.refine("dimudijet",
    cut=(op.rng_len(cleanedJets) > 1))
  plots.append(Plot.make1D("dimudijet_leadJetPT", cleanedJets[0].pt,
    twoMuTwoJetSel, EquidistantBinning(50,0.,250.),title="Leading jet PT"))
  return plots
 Pieter David (UCLouvain)
                       Readable and efficient HEP data analysis with bamboo
                                                                  PyHEP 2019
```

Implementation: interface to RDataFrame and Cling

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- When converting an expensive expression to a C++ string, values are defined on-demand by attaching Define nodes (and functions declared with the interpreter as needed; global scope, so can be reused everywhere)
- Much of this needs fast searches through expression trees for dependencies etc., which is achieved by caching the value-based hash of every expression (possible because they are immutable)



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With different options one can:

• interactively explore the decorated tree (in an IPython prompt)

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- enable "implicit multi-threading"

Written in python, and tried to keep things loosely coupled (interfaces), so many things are straightforward to customise and extend:

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- There is a hook to specify additional command-line arguments from the analysis module
- The sample definition (YAML) is open-ended, the base class only looks at the attributes it needs (e.g. input files, to do the job splitting), and the plotting library at a few more (normalisation for MC, grouping and ordering, colors...)

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Implementation: the backend code scans cuts, weights, and variables for marked nodes, and defines the additional RDataFrame nodes as needed (alternative weights are cheap, but anything used in cuts may change the events passing a filter, so need to branch off, and duplicate subsequent defines)

Quite some bookkeeping, but fully generic (changes to analysis code are minimal), and the code for this is localised in a handful of places

Future developments and links

- Development status: beta; usable, but moving from a narrow proof-of-concept to actual research, so some interfaces may still change
- Performance: memory usage increases to about 5GB for 5000 histograms (more than expected, under investigation), CPU time acceptable for now $(\mathcal{O}(1\min)$ for defining plots compiled code speed for the event loop)
- Being used or evaluated for three CMS analyses early adopter feedback has been extremely valuable; many thanks, especially to Khawla Jaffel (UCLouvain) and Sébastien Wertz (Universität Zürich)
- Technical requirements: python3.6+, a recent ROOT (6.14/06, 6.16/00 or 6.18/04), and a few python packages (typical installation: with pip in a virtualenv). plotIt (a ROOT-based C++ tool) is used for turning histograms into pdf/png stack plots
- The code is public in this repository, and there is <u>HTML documentation</u>

Conclusion

- RDataFrame is a very powerful tool (especially when paired with Cling for piece-by-piece compilation)
- For actual analysis use: still a lot of bookkeeping to do, especially for flat trees (e.g. indices)
- bamboo is an attempt to bridge this gap, such that the user code is little more than a compact description of the analysis
- Hopefully some (not too) creative uses of python, and interesting ideas
- Started from a simple problem and idea, ended up writing a more general tool... usable, but much room for improvement and additionss

Thanks for your attention, I am looking forward to hearing your thoughts/suggestions/criticism and exchange ideas

Additional material

Installation

Suggested way to get a recent ROOT release: from the <u>LCG software distribution</u> on CVMFS

Installation (to be improved):

```
source /cvmfs/sft.cern.ch/lcg/views/LCG_95apython3/x86_64-centos7-gcc8-opt/setup.sh
python -m venv myvenv
source myvenv/bin/activate
git clone -o upstream git+https://gitlab.cern.ch/cp3-cms/bamboo.git
cd bamboo/ext
./getjetclasses.sh ## copy some source files from CMSSW
cd -
pip install ./bamboo
```

plotIt (for pdf/png output):

```
git clone -o upstream https://github.com/cp3-llbb/plotIt.git
cd plotIt/external
./build-external.sh
cd ..
B00ST_R00T=$CMAKE_PREFIX_PATH make -j4
cd ..
cp plotIt/plotIt myvenv/bin
```

Upload to pip/condaforge is planned

(the bamboo name is taken, so probably bamboo-hep)

CP3SlurmUtils on test.pypi.org, will be uploaded to production PyPI soon

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