Analysis Workflows at ATLAS

... and current bottlenecks

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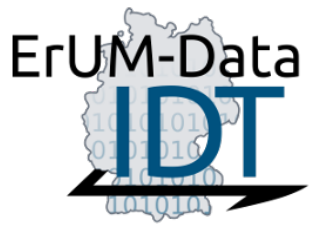
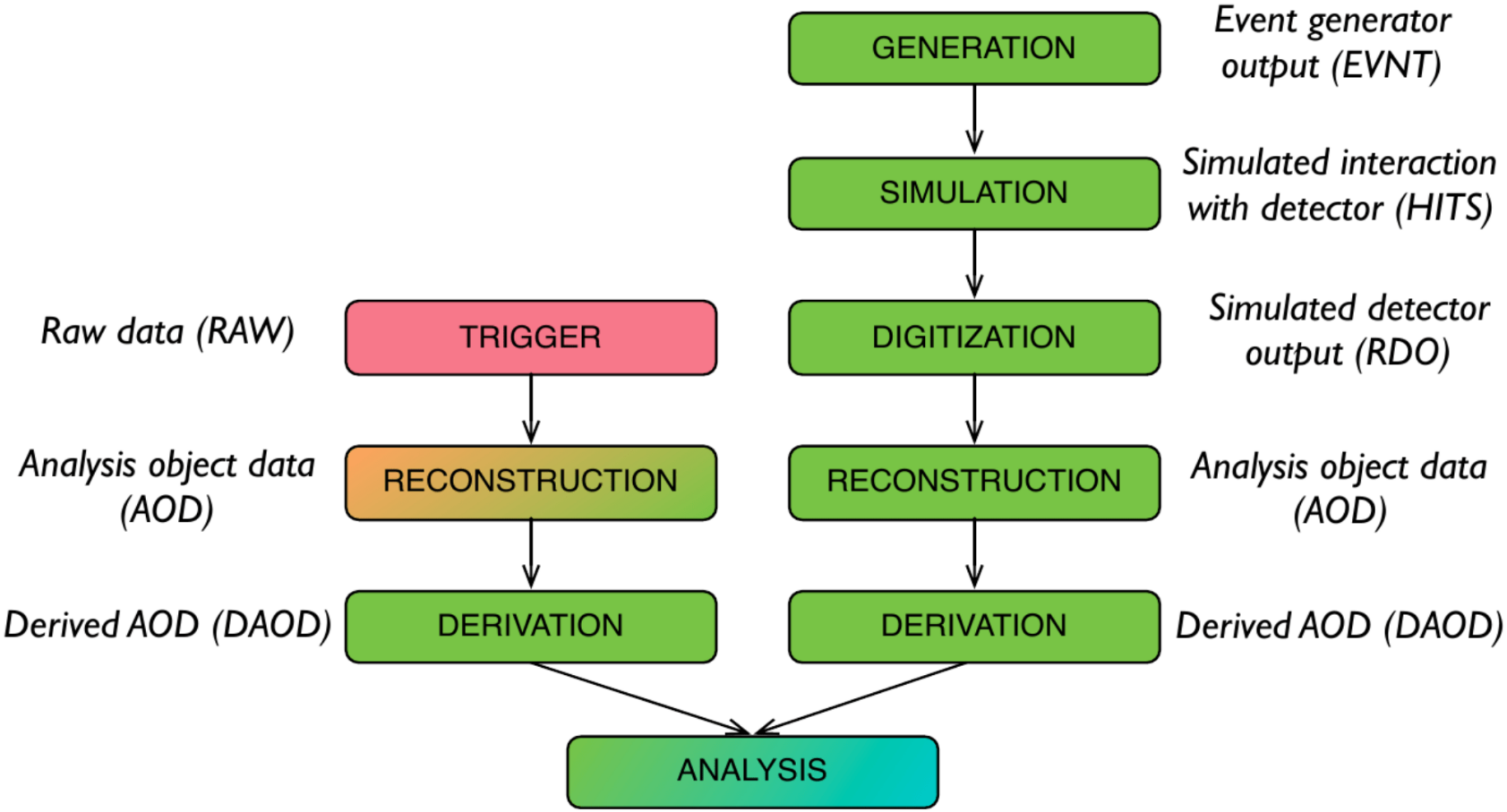


Outline

Overview based on personal (and people in our group) experience and on what was reported in a joint DOMA/HSF analysis meeting

- Current analysis workflows at ATLAS
- Workflow changes planned for the future
- Bottlenecks, turn-around times
- The role of new technologies/methods

Workflow at ATLAS



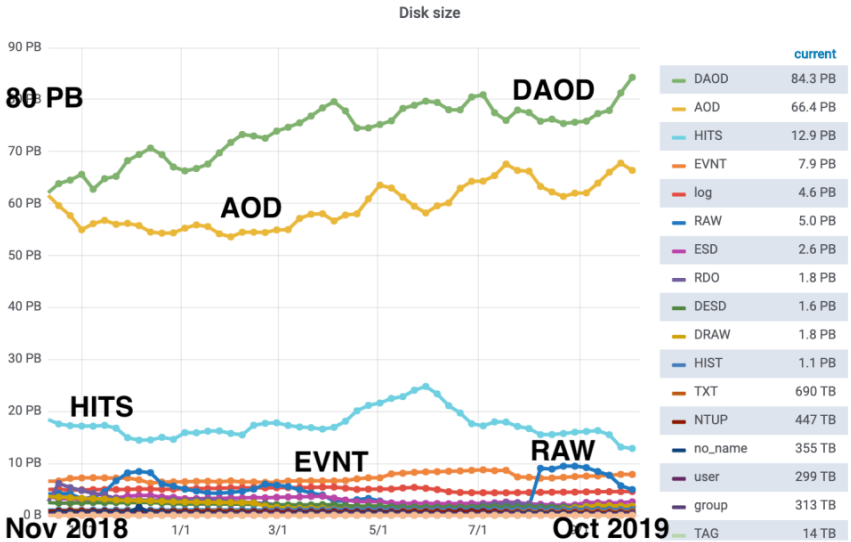
The analysis step

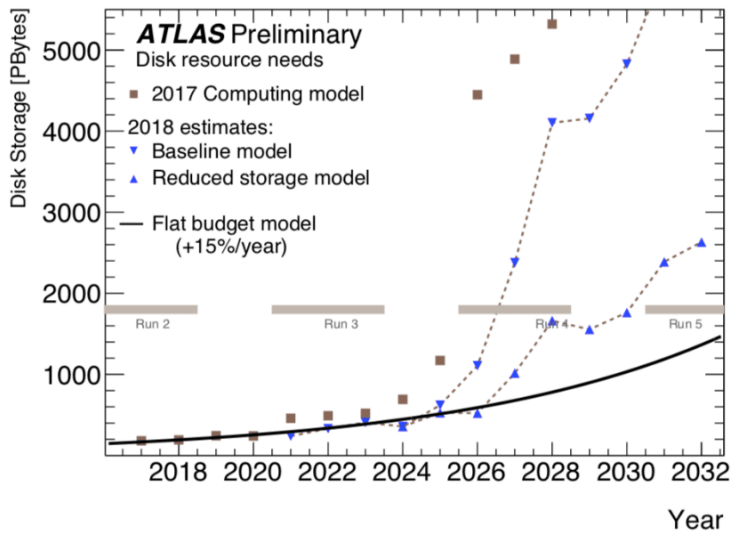
The last step typically consists of

- (optionally) producing yet another intermediate format
- (most of the time) producing a small ntuple from the intermediate format or directly from DAOD
- making plots/histograms and statistical analysis from the small ntuple or the intermediate format
- ntuples produced using custom code (that makes use of central tools from the performance groups)

The problem: too much disk space

80 different DAOD formats take up too much space





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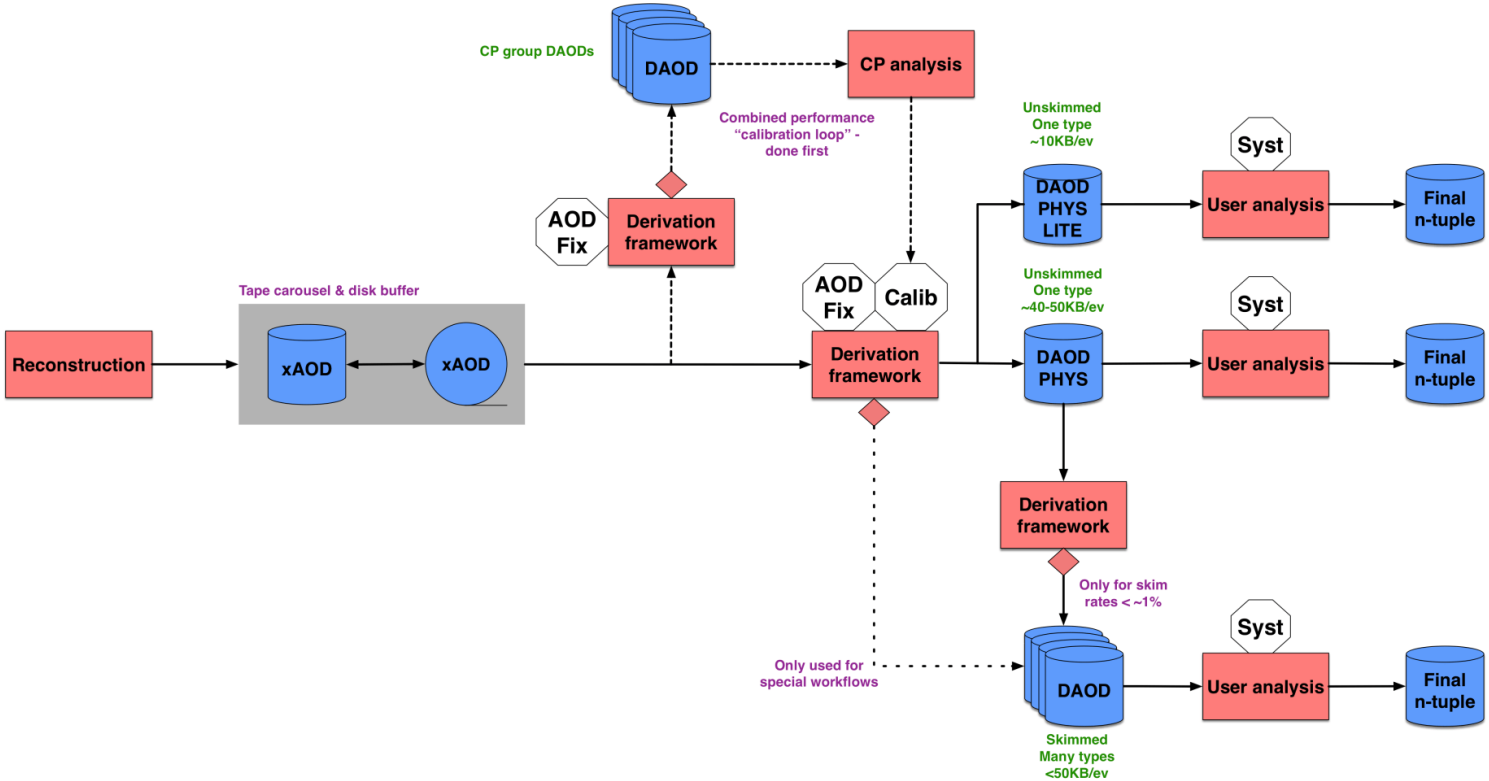
Plans for the future



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- replace DAODs by one small format (DAOD_PHYS, $\approx$ 50kB/evt)
- add another even smaller format with calibrations applied, simpler storage model potentially readable via columnar data analysis (DAOD_PHYSLITE, $\approx$ 10kB/evt)
- allows reduced storage and potential for better centralized workflows

Data sizes

Example: SUSY 1L analysis
(thanks to Eric Schanet for providing the numbers)

- Input DAOD files: total size $\approx$ 180 TiB, in 250k files, 6e9 events (background, signal, data)
- Ntuple output size: $\approx$ 100-150 GB either with or without systematics (systematics ntuples only written with minimal information needed for statistical analysis)
  $\rightarrow$ nominal ntuples sometimes skimmed further for quick plotting/studies

Turnaround times

Time for producing new ntuples from DAOD:

- Without systematics: few days
- With systematics: few weeks, worst case months (when also dealing with problems on the grid)

$\rightarrow$ rerunning over DAOD is a significant bottleneck!
$\rightarrow$ at least with systematics, processing is CPU limited ($\approx$ Hz speeds)
$\rightarrow$ needed when recommendations (calibration, systematics) change
$\rightarrow$ additional difficulty: all analysis run this at the same time (before important conferences)

In contrast: Analysis on final ntuple typically fast/negligible turnaround times (sometimes larger turnaround times for final statistical analysis)

See more examples from ATLAS and CMS from the DOMA-ACCESS/HSF-DAWG meeting

New technologies

What we might do more in the future:

- Interactive/In-memory analysis e.g with python tools in jupyter notebooks
  $\rightarrow$ alternative to ROOT TTree::Draw ntuple analysis
- Analysis on computing clusters via spark/dask, RDataFrame?
  $\rightarrow$ replace batch jobs?
  $\rightarrow$ needs to be easy to use, reliable (does anybody use PROOF?)
- Have services (like ServiceX) where events can be dynamically requested (potentially with some on-the-fly transformations)?
  $\rightarrow$ replace producing new ntuples for specific studies?
  $\rightarrow$ pre-calibrated datasets (ATLAS DAOD_PHYSLITE and CMS nanoAOD go in this direction) might offer wider possibilities

Summary and Discussion

- Current analysis workflow based on creating ROOT ntuples from central DAODs
  $\rightarrow$ some analysis introduce another step for more flexibility
  $\rightarrow$ in all cases rerunning on large DAODs is the major bottleneck!
- Ntuple analysis (on local machine) typically fast
  $\rightarrow$ if not, can often reduce ntuple size for specific studies
  $\rightarrow$ will stay an important workflow, maybe more interactive/in-memory analysis
- Concerning new technologies, we should ask the following questions:
  - Where can they provide new, useful possibilities for analysis?
  - Where can they help to circumvent the bottleneck of running a huge number of grid jobs?
- Having central datasets with CPU intense steps pre-done is crucial! (But keep in mind exotic signatures e.g. long-lived searches)