

g – 2's Analysis Computing

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g – 2 / SCD Workshop - 03/02/22

Introduction

- Aim: sketch out what we use for our analysis processes
- There are many different analyzers, each with their own workflow – I won't capture all that detail
- I will try and give a representative picture of what roughly happens
- We have separate analysis programs for magnetic field and “fast” detectors that see $\mu^+ \rightarrow e^+$ decays
 - Focus on e^+ data as this is more relevant for computing resources

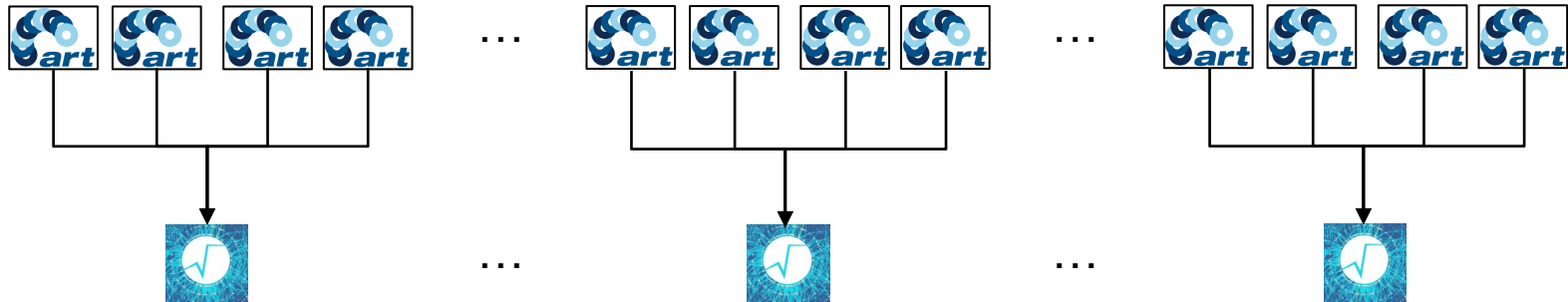
A Typical e^+ Analysis Workflow

- Start with **art files** from production:



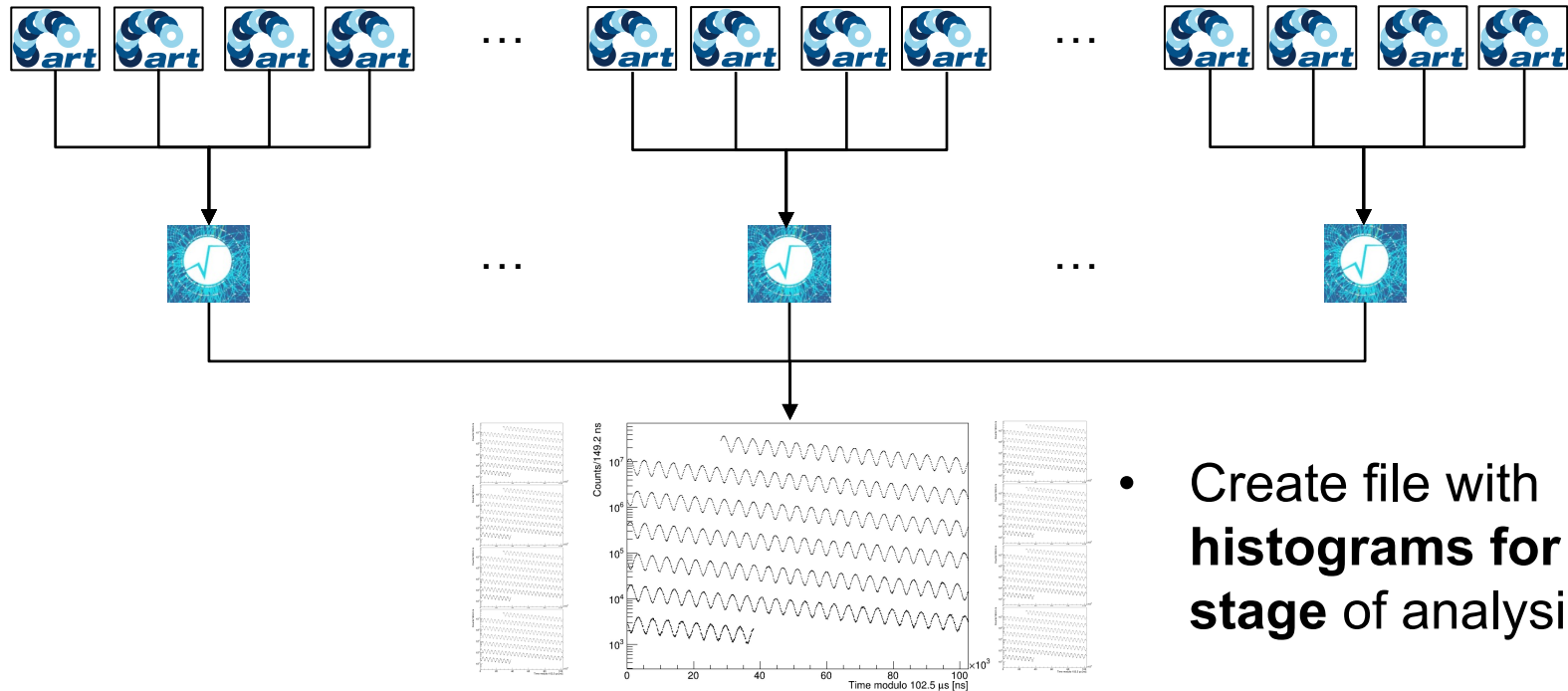
- Usually **process 1 “dataset” at a time**, defined by running conditions
 - Vary in size, but typically might have **35k files & 70 TB**
 - Slimmed production files can reduce this to 10 - 20% in size
 - Add >1 datasets together at end, but need to check consistency first
- Whole process is **repeated many times**:
 - Run-2/3 analysis: **~20 datasets**.
 - Run-4/5: **2 – 3 times as much data**
 - Will need to run multiple times for some systematic scans

A Typical e^+ Analysis Workflow



- `art::analyzers` used to create **histograms or trees** in ROOT files
- Usually **perform simple operations** like histogram filling, time-randomization, searching for nearby calo hits for pile-up estimation etc.
 - Some analyzers find it **hard to maintain high CPU efficiency** due to **large fraction of i/o** compared to computation
- Hard to keep **under 2 GB** memory target:
 - Basic unit is 5000 time bins x 200 energy bins x 24 calorimeters
 - Some analyzers do get under 2 GB, others ask for more slots
- Typically takes a few hours (< 12h) to run jobs + recovery

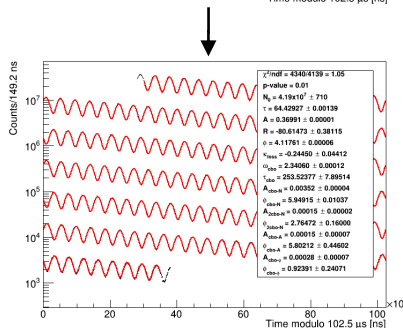
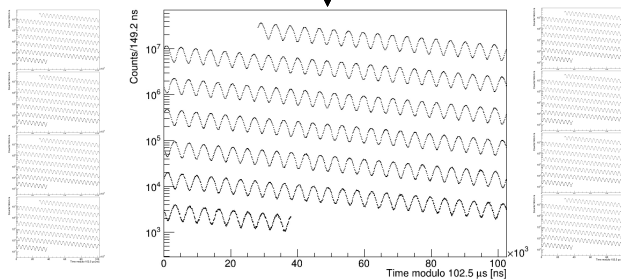
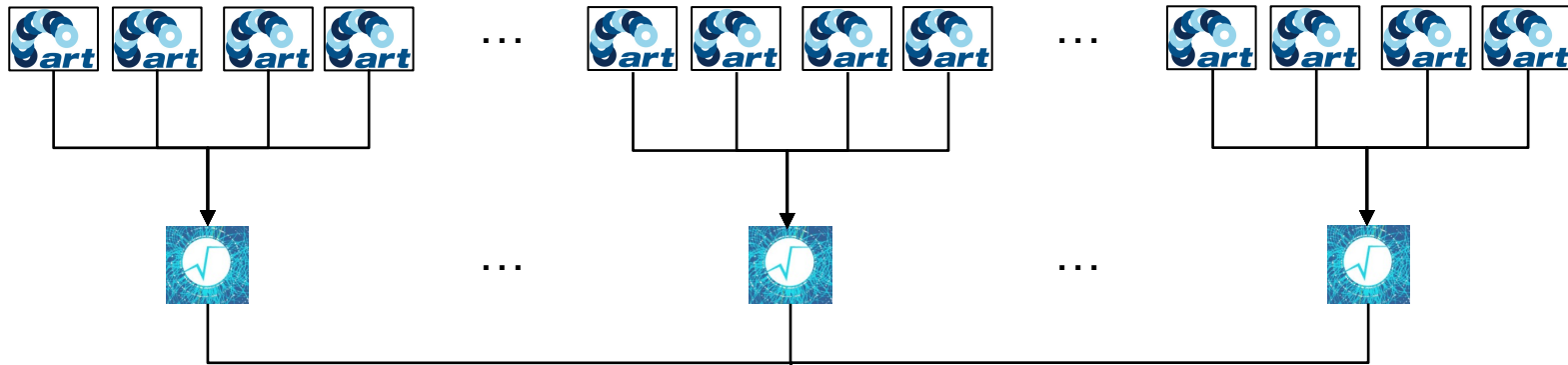
A Typical e^+ Analysis Workflow



- **Histogram Input:** hadding many files (usually run locally – takes ~1 – 2 h)
- **Tree Input:** Fill histograms (grid or local – slower but with more flexibility)

- Create file with **histograms for final stage of analysis**

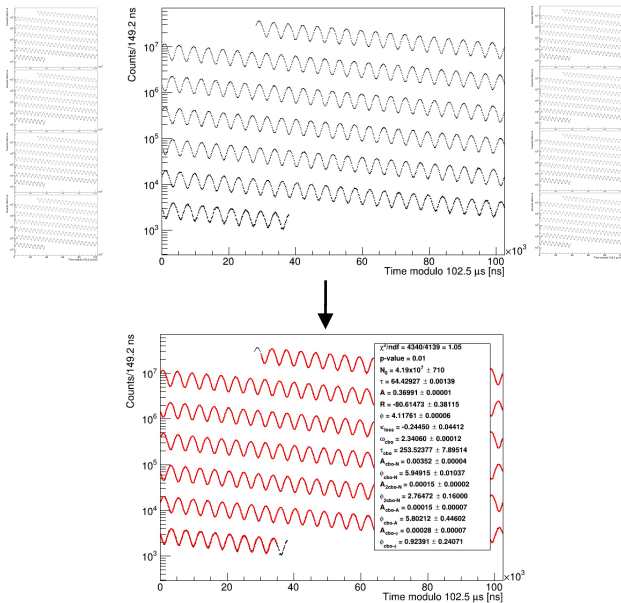
A Typical e^+ Analysis Workflow



- **Fit preparation:** subtract pile-up, weight data, collapse TH2s to TH1s...

- **Do the fit:** extract parameters of interest

Fitting & Analysis Frameworks



- We placed **high value on independent analyses** to ensure robustness
- Means **every analyzer** has their **own code base** – I'd guess we have ~15 at one time
- Most use **C++ and ROOT**.
- Few use **python**: both with & without ROOT

- Some code is in **main redmine repositories**, and some is **separate**
- At least one uses **fhicl** for configuration settings.
- **Magnetic field** analysis has separate DAQ and workflow.
 - Smaller scale: production takes a few days and then analysis proceeds on single server

Default User Interface

- **4 x virtual machines** (gm2gpvm01,02,03,04)
 - 4 single-core CPUs, 12G RAM, minimal local storage
- **Worked well for early stages** of analysis: mostly development, smaller datasets, fewer users...
- Each machine is **easily overloaded** (single users kill machine by mistake) & **building is very slow**
- Doesn't match well to a lot of our current needs:
 - **Fitting can be slow** (~1-2 m per fit) but is parallelizable: 4 separate machines with 4 cores doesn't make that easy
 - **Large trees as input** don't work well (network speed can be slow)
 - Similarly for **hadding** large numbers of histograms
- Needed something to **fill gap** between the grid and virtual machines

Other User Interfaces

- Several groups have bought own machines that are supported by SCD:

gm2cornellsrv1

32 CPU
250G RAM
300 TB HDD

gm2fnalsrv1

48 CPU; 1 GPU
192G RAM
7 TB SSD

g2field-server

4 CPU; 1 GPU
32G RAM
50 T HDD; 14 T SSD

**gm2ucl, gm2liv,
gm2ita...**

~40 CPUs,
3 – 30 TB HDD

- Typically used for
 - **Parallelization**: fitting, toy MC, building
 - **Filling trees** into histograms
 - Memory intensive tasks (histogramming, 6D acceptance studies)
 - GPU for ML training or frequency extraction (field)
- This **model works fine** for us now but there are some issues:
 - **Not a universal resource** for all collaborators – some are running on personal machines or on clusters at their institutes
 - GPUs are generally underutilized