New Developments In Analysis

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Outline

- New features
  - HDF5
  - Merging ntuples
- Other developments & Plans

g4tools @ Wollongong

diff –u « since last workshop »

G.Barrand, CNRS/IN2P3/LAL

Main ideas

- g4tools is an automatic extraction of some code found in the softinex/inlib and namespaced “g4tools” for an embedding in Geant4.
- Pure header code. Highly portable (including iOS and Android). Easily embeddable (no “config.h” or specific build tool in the way).
- Strongly OO. No implicit management.
- Thread safe (no writable statics).
- See http://softinex.lal.in2p3.fr

What's new : HDF5

- Code to write histos and ntuples by using the HDF5 library.
- (Then a relationship to an external package).
- HDF5 : a library dedicated to do binary IO for scientific data. See https://www.hdfgroup.org/HDF5 for the technicalities.
- See https://www.hdfgroup.org for the sociology and also the "A few of our users" for existing applications.

HDF5 : directories

- API and functionalities are here to do what we want. No blocking point for the moment.
- In particular we use the named “H5Group” to organize data in file in “directories” in a way similar to what is done with ROOT/IO.
- (In HDF5, whilst you know what is a H5File, a H5Group and a H5Dataset, you know the essential).

HDF5 : histos

- The data for one histo are put in one named group and there is one named “H5Dataset” per “field” (bin_Sw, bin_Sw2, etc..).
- This permits to keep a “data schema” comprehensible without having at hand the writing (g4tools/hdf5/h2file) code. In particular the “h5ls” program, coming with the library, permits to scan easily a file.
- (For generic data as an histo, it looks more interesting to store in this way than having a “H5Compound” storing an histo in one blind “BLOB” in the file).

HDF5 : ntuples

- Similar API than for the ROOT/IO driver.
- An ntuple handles columns which are paged.
- An ntuple is attached to a named H5Group which contains one group per column. Each column group maintains a H5Dataset, and a page of data (a buffer in memory) is appended/written to the dataset when full.
- The logic here is similar to the basket logic of ROOT/IO.

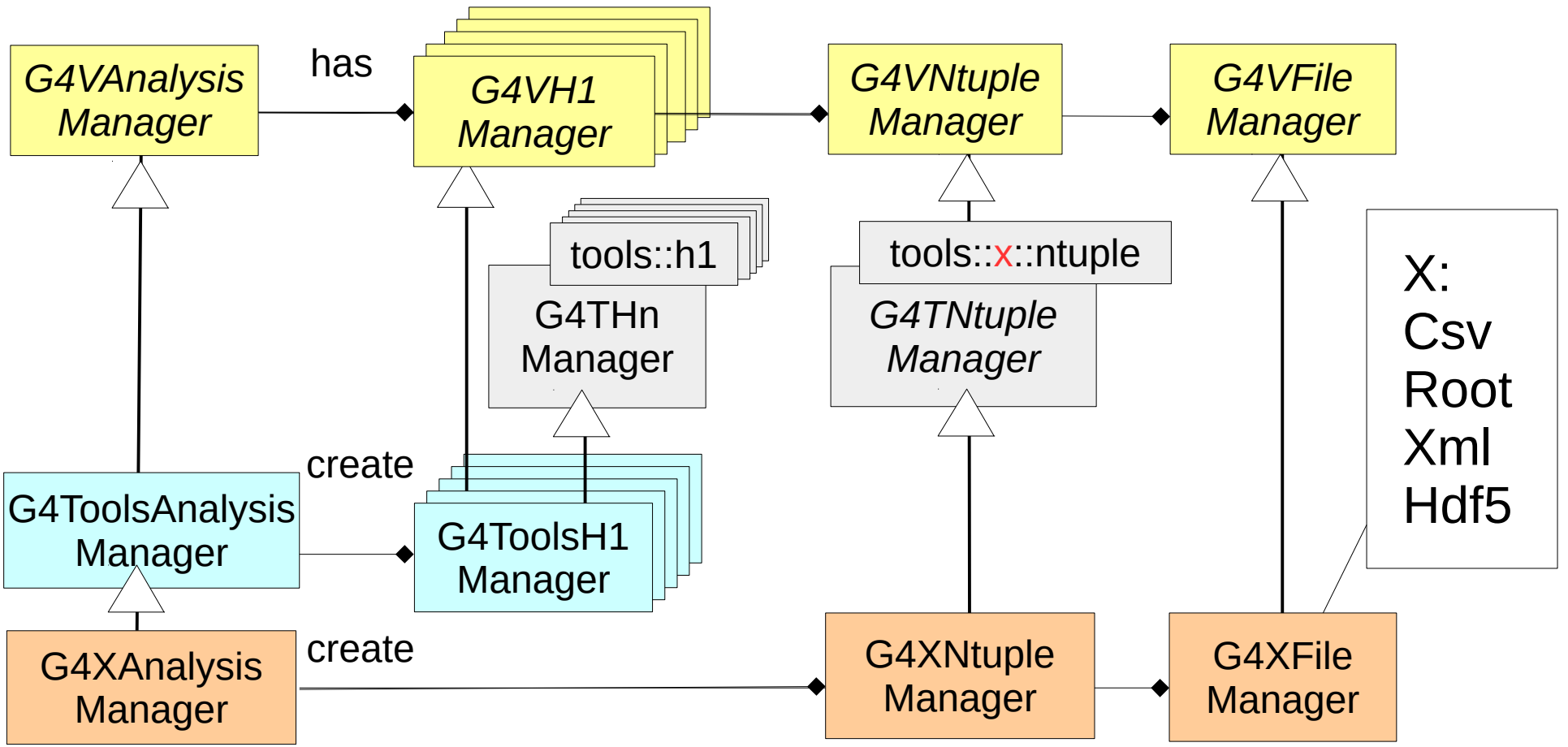
HDF5 : ntuples (2)

- We can handle columns of basic types and string and vector of basic types and string.
- There is also compression (done with zlib).
- Performances are similar to CERN-ROOT (if using same page/basket size). (Sure, the logic is the same and we are dominated, in both cases, by the speed of the file system).
- We provide an example (cern_root_hdf5_ntuple.cpp) to read an ntuple from a g4tools/hdf5 file, project on an TH1D and plot in a TCanvas.

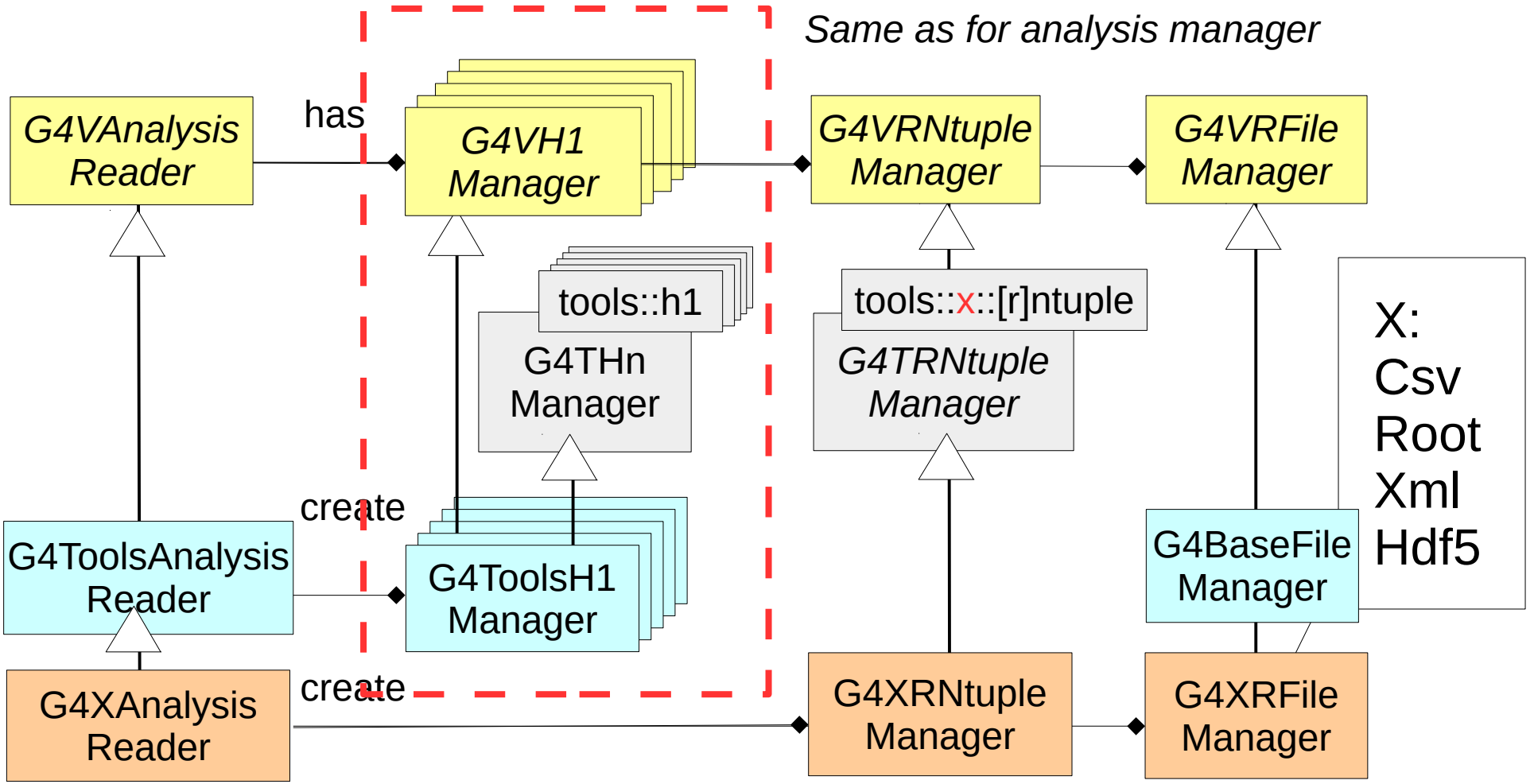
Design Improvements
(in analysis category)

- Templates were introduced where suitable to avoid code duplications in Geant4 10.2:
  - They concerned only analysis classes internals and did not affect the API seen by the users
  - Added G4ToolsAnalysisManager class – common handling all histograms/profiles
- New in Geant4 10.4:
  - Consolidated the ntuple manager templates,
  - Templated classes also in the reader classes

Analysis Manager Design



Analysis Reader Design



New for HDF5

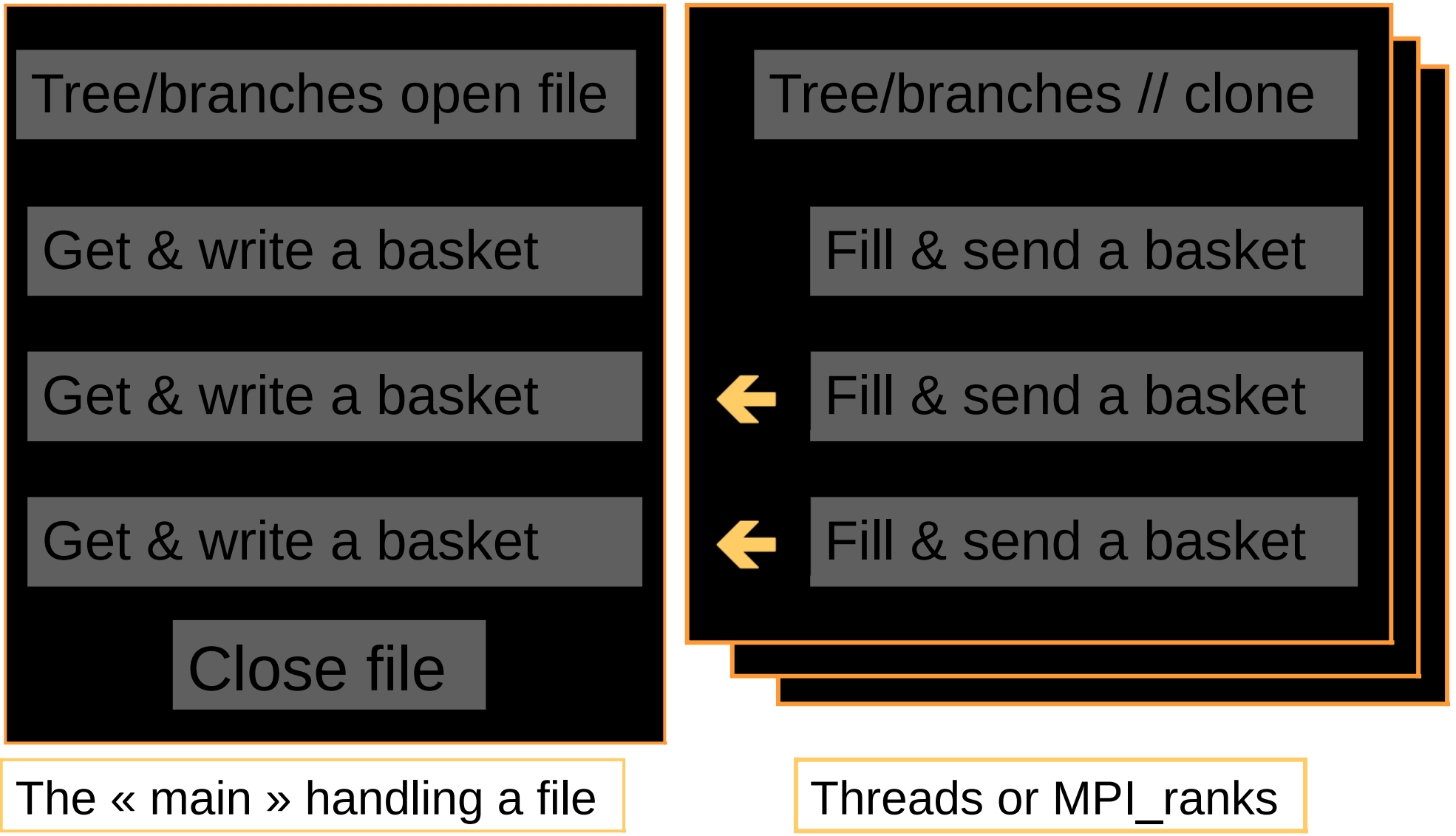
- New **analysis/hdf5** sub-category including:
  - Classes for analysis manager:
    - G4Hdf5AnalysisManger, G4Hdf5NtupleManager, G4Hdf5FileManager
  - Classes for analysis reader:
    - G4Hdf5AnalysisReader, G4Hdf5RNtupleManager, G4Hdf5RFileManager
- Extended **G4VAnalysisReader::Read**[Hn][Pn][Ntuple] functions with an optional `directoryName` argument
- Added **test03/testHdf5** in geant4/tests
- Added **GEANT4_USE_HDF5** build option in Geant4 CMake configuration files

Merging Ntuples

- Requirement from A. Dotti in 2016: number of output ntuple files will become an issue when running on supercomputers with O(1000) workers in MPI & MT mode
- Introduced in Geant4 10.3
- Merging ntuples can be activated with Root output via the new G4RootAnalysisManager function:

```
void SetNtupleMerging(G4bool mergeNtuples,
        G4int nofReducedNtupleFiles = 0,
        unsigned int basketSize = fgkDefaultBasketSize);
```

- Users can choose to merge all ntuples in a single file or in a given number of files
- The implementation was presented in detail in the last collaboration meeting


Tree/branches open file
Get & write a basket
Get & write a basket
Get & write a basket
Close file
Tree/branches // clone
Fill & send a basket
Fill & send a basket
Fill & send a basket
The « main » handling a file
Threads or MPI_ranks

Merging Ntuples in MPI

- Merging in MPI planned for this year release
- Will require adapting the operation mode of G4MPI:
  - Actually all ranks, including the master rank do event processing
  - In difference from the other merged data, which are merged to the master rank at the end of event processing, **the ntuples are merged during event processing** by sending baskets to master rank.
  - We need to define a dedicated rank which will be receiving the ntuple data from the worker ranks (like what we do with threads) and which will not run event processing.
  - To be further discussed with Andrea and Koichi

Bug Fixes

- Restored clean-up of Root empty files in MT mode (which was lost with previous updates)
- Fixed problem of removing non-empty ntuple files in user application where ntuples are created after open file. (This mode is used in dna examples, eg. dnaphysics.)
- Added **GetP[1,2]Id(const G4String&**) functions to the G4AnaysisManager public interface (problem report #1949.)
- Corrected handling of open file failure (problem report #1957.)

Plans

- Problem in merging ntuples via column-wise ntuple paging (reported in hypernews) – to be addressed in 10.4
- Features requested by users
  - Handling more files by analysis manager – still to be considered
- Continue addressing new requests from users

HDF5 : //

- It works in multi-threads, with one file per thread, with an HDF5 lib built for multi-threads.
- We have to look if we can do the same logic that we have now for the ROOT/IO format to have only one file for multiple threads and/or MPI workers.
- Passing histos should be ok. For an ntuple we have to look if we can pass “pages” from one slave to a master handling a single file.
- But HDF5 has some “parallel” logic, then perhaps all is already here. To be looked.

HDF5 : H5Fclose

- For the moment I am very happy with HDF5.
- (And beside my Mac and Linux, I can read a file on my Windows-10, Android and iOS devices).
- The “data schemas” in file is keep simple so that it should be easy to read histos and ntuples from other contexts without the g4tools/hdf5 readers (from python ? from some web tool ?).
- It gives ideas : storing G4 geometries with HDF5 ?