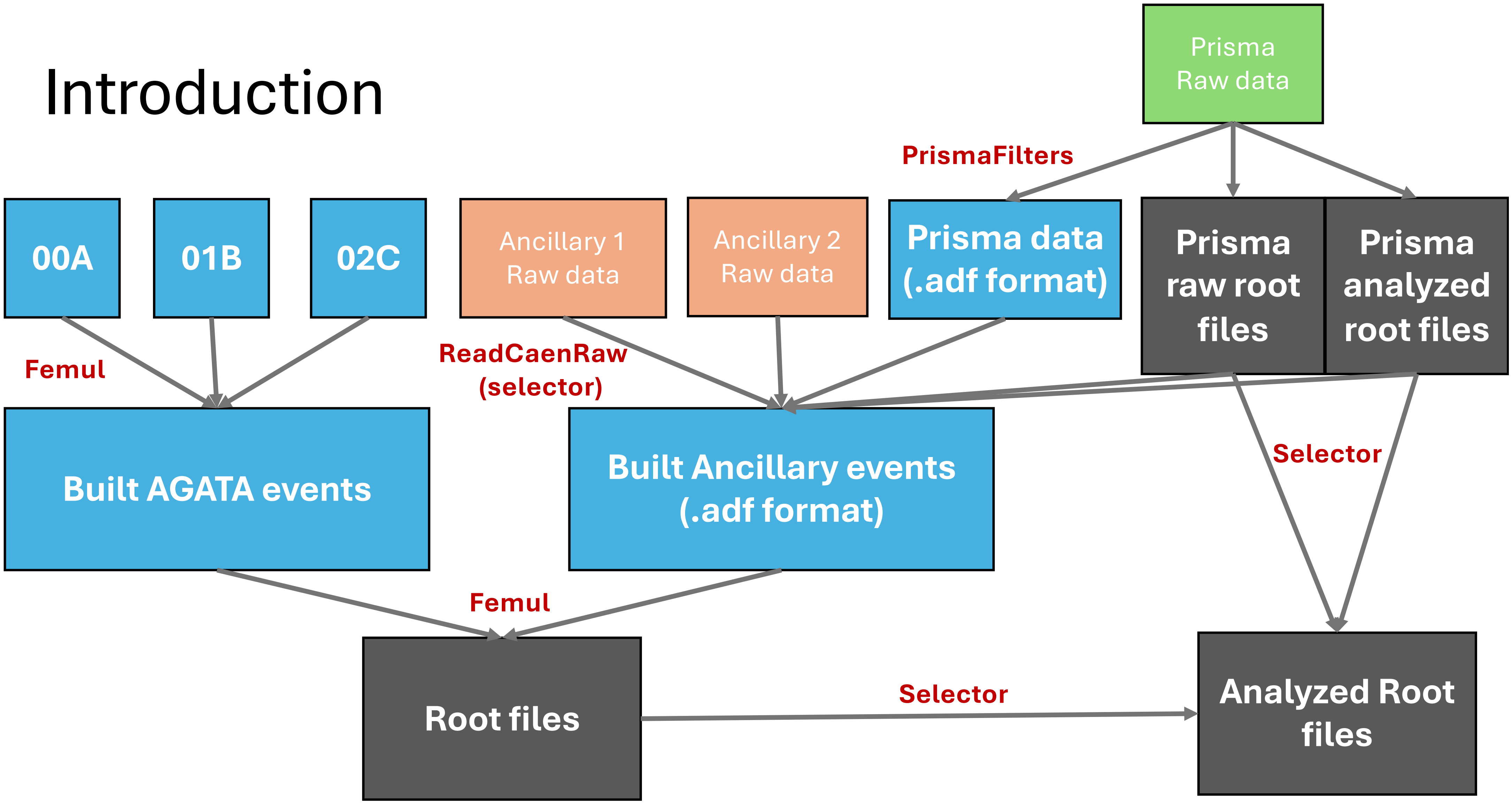
Introduction to ancillary analysis

Daniele Brugnara

Introduction



How is the workshop structured: Wednesday

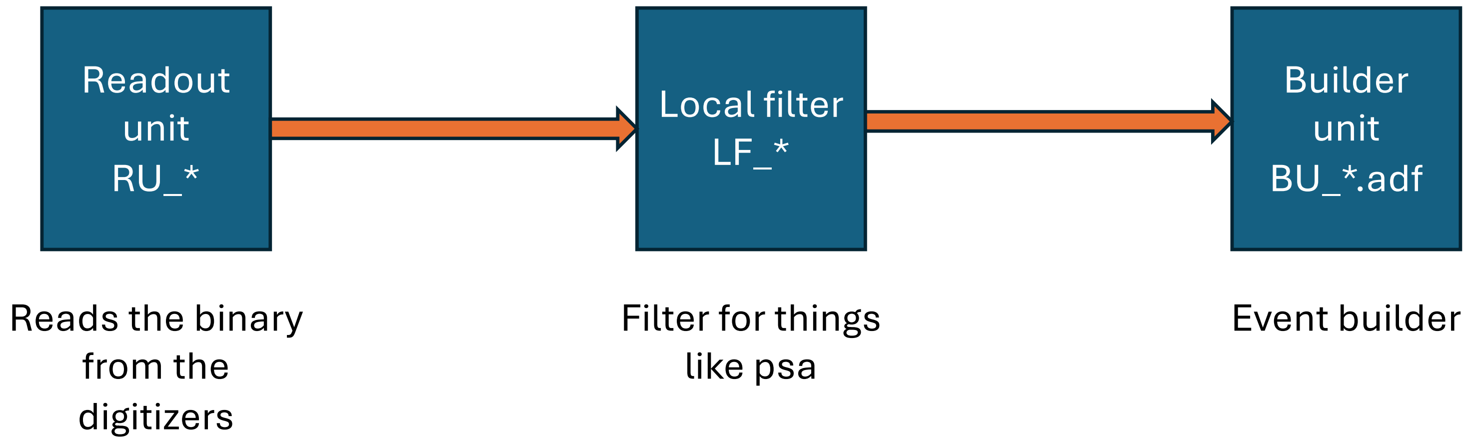
Time	Session	Speaker	Location	Description
09:00 - 10:00	12 - Global data replay	*Jeremie Dudouet*	*RDC-202 - 202, CCIN2P3*	**How to produce the final data from the AGATA side**
10:00 - 10:30	coffee break		*RDC-202 - 202, CCIN2P3*	
10:30 - 12:00	13 - Selector	*Daniele Brugnara*	*RDC-202 - 202, CCIN2P3*	**General info on the selector: what it is and what can you do with it**
12:00 - 13:30	Lunch		*RDC-202 - 202, CCIN2P3*	
13:30 - 15:00	9 - PRISMA: general introduction	*Filippo Angelini*	*RDC-202 - 202, CCIN2P3*	**Detailed description of PRISMA and the data analysis**
13:30 - 15:00	18 - Other ancillaries	*Matus Balogh*	*RDC-202 - 202, CCIN2P3*	**General information on the ancillaries, data format and DAQ**
15:00 - 15:30	coffee break		*RDC-202 - 202, CCIN2P3*	
15:30 - 17:00	10 - PRISMA: steps of the analysis with examples	*Filippo Angelini*	*RDC-202 - 202, CCIN2P3*	**Step-by-step guide on the PRISMA analysis**
15:30 - 17:00	11 - Other ancillaries	*Elia Pilotto*	*RDC-202 - 202, CCIN2P3*	**Information on handling the RAW data of the ancillaries and the optimization procedure**

How is the workshop structured: Thursday

09:00	14 - Hands on session ancillaries	*Daniele Brugnara et al.*	*RDC-202 - 202, CCIN2P3*	09:00 - 10:00	**Read the raw data and build the ancillary events**
10:00	coffee break		*RDC-202 - 202, CCIN2P3*	10:00 - 10:30	
11:00	22 - Hands on session ancillaries	*Daniele Brugn[illegible]l.*	*RDC-202 - 202, CCIN2P3*	10:30 - 12:00	**Produce the root data with a global replay** **Run the selector** / **Prisma analysis I**
12:00 – 13:00	Lunch		*RDC-202 - 202, CCIN2P3*	12:00 - 13:30	
14:00	15 - Hands on session ancillaries	*Daniele Brugnara et al.*	*RDC-202 - 202, CCIN2P3*	13:30 - 15:00	**Try the user selector** / **Prisma analysis II**
15:00	coffee break		*RDC-202 - 202, CCIN2P3*	15:00 - 15:30	
16:00 – 17:00	23 - Hands on session ancillaries	*Daniele Brugnara et al.*	*RDC-202 - 202, CCIN2P3*	15:30 - 17:00	**Optimization and bkg subtraction**

Handling the RAW data

- The DAQ that runs online (xDaq) consists of some actors that handle different tasks.
- Each actor can write data to disk



Handling the RAW data

- It can happen that one of the actors of the daq is overloaded during experiment and stops the data flow
- This can happen for the actor that builds events if there is a sudden increase in rate in one of the channels
- This is usually due to a mistake on the experimental side
- **Nevertheless the data CAN be recovered by reading the output of the readout unit**
- Another reason cold be to change the parameters for the PSA of the ancillaries

Possible issues and how to solve them

<table>
<tr><td>Coincidences stop at some point</td><td>Online building problem</td><td rowspan="2"></td><td rowspan="5">Run ReadCaenRaw and femul</td></tr>
<tr><td>Loss of statistics</td><td>Online building problem</td></tr>
<tr><td>Multiple peaks</td><td>Ancillaries or cores not aligned</td><td>Align with genconf.py or ReadCaenRaw.set</td></tr>
<tr><td>Exponential shape</td><td>The global time offset is wrong</td><td rowspan="2">Find the coincidence peak as explained in Scripts/TimeOffsetPeak</td></tr>
<tr><td>No peak</td><td>There is no global offset</td></tr>
</table>

ReadCaenRaw: how to run and how to configure

- Configuration file-based program
- One needs to set:
  - **Time window**
  - **Digitizer board informazion**
  - **Timestamp offset**
  - **Minimum fold**
- Can also output root files for the selector

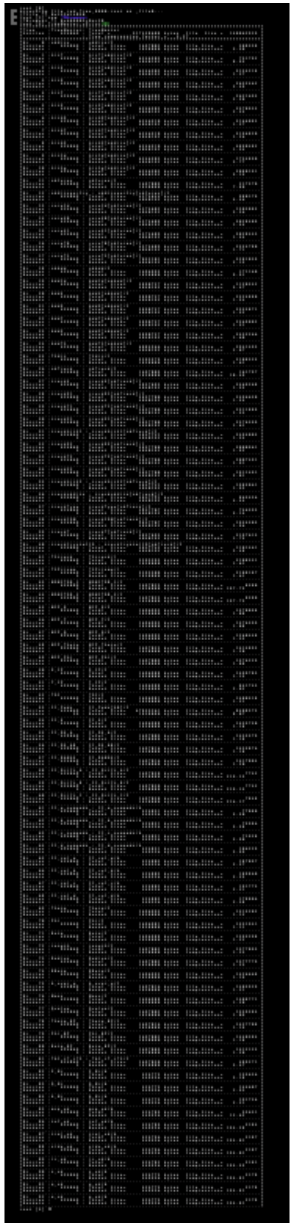
```
daniele@MacBookPro AncMerging % ./ReadCaenRaw
Usage: ./ReadCaenRaw [OPTIONS]

Options:
  --help, -h                       Show this help message and exit
  --root <OutputRootFileName>      Specify the output root file name
  --global-anc-tsoffset <value>    Set the global ancillary timestamp offset (double)
  --nrevts <value>                 Set the number of events to process (integer)
  --prisma <file1> [file2 ...]     Specify one or more input Prisma files
  --input <file1> [file2 ...]      Specify one or more ancillary input files
  --adf <outAdfFileName>           Specify the output ADF file name

Example:
  ./ReadCaenRaw --labrslave --root output.root --global-anc-tsoffset 1.5 --nrevts 100 \
              --dante 5 --prisma prisma1.dat prisma2.dat --input anc1.dat anc2.dat \
              --adf output.adf
```

ReadCaenRaw.set_labrprisma 825 B

```
#window: width of the time window used for the event building (in ns)
window 500

#boardDef:
# arg 1: boardId
# arg 2 :boardVersion(V1725/V1730==1 - VX2740 ==2)
# arg 3 :number of channels
# arg 4: FWVersion (PHA or PSD)
# arg 5: ns per timestamp
# arg 6: ns per sample
# arg 7: data key: 0xFA0201A2 = SPIDER ; LABR = 0xFA0201A5 ; DANTE = 0x
board 1 1 16 PSD 2 2 labr

#minFold:
# arg 1: detector
# arg 2: minFold for this detector
# arg 3: keep only events if coincidence with other board
minfold 1 0

# board   channel   timeOffset
tsoffset 1 0 130
tsoffset 1 1 130
tsoffset 1 2 130
tsoffset 1 3 130
tsoffset 1 4 130
tsoffset 1 5 130
tsoffset 1 6 130
tsoffset 1 7 130
```

The selector project

- **High level analysis based on configuration files**
- The analysis procedure is common to all experiments and there is little benefit of repeating the same steps over and over
- The code was created for the near-line analysis and has since evolved with more refinements with full analysis capabilities
- The user is expected to take a look at the code and check the output data
- The nearline analysis is a great STARTING point and can be recalled with a simple *git clone*



The starting point

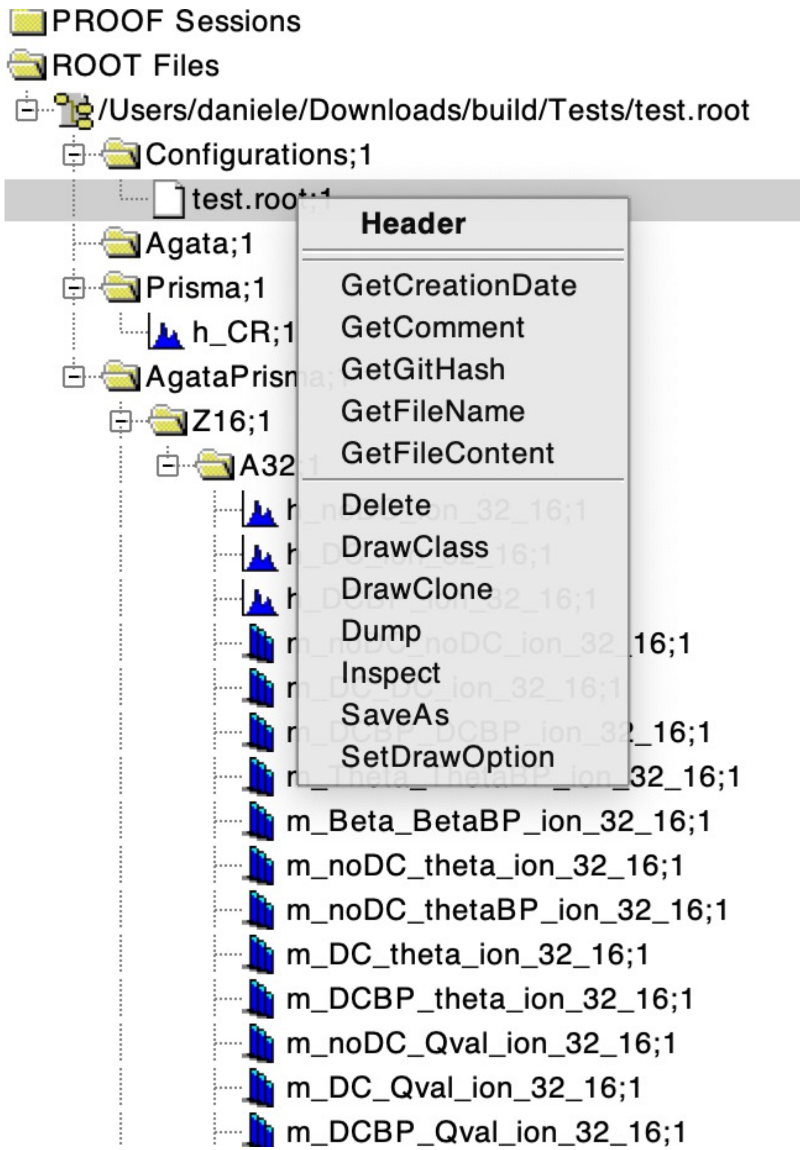
- Femul produces a root file containing MANY leaves
- The selector allows us to have a common code debugged over several experiments
- This also means that sometimes some changes/improvements are made and could break backward compatibility (for instance for the configuration file).
- The README.md file in the root directory, as well as other ones serve as a first documentation
- We try to log on the CHANGELOG.md significant changes in different versions
- Current supported detectors:

  AGATA
  PRISMA
  SPIDER
  EUCLIDES
  DANTE
  $LABR_3$
  SAURON (S1)
  OSCAR
  EXOTIC’s MCPS

Reproducibility

- The output files contain the parameters used to generate it:
  - The entire selector.conf
  - The git hash
  - The date of creation
- This means that the analysis can be reproduced simply by printing the selector.conf used for this specific file and checking out the correct hash
- It is also citable with a DOI:

DOI 10.5281/zenodo.8329198



Structure of the selector.conf

KEYWORD | value(s) | unit of measure | comment

Detectors considered in the analysis

Configuration of the folders, the file patterns, and the TTree names

Configuration of the reaction, multiple ions of interest can be added

Target thickness and rotations, used for energy loss calculaitons. The presence of a degrader before or after the target is also possible.

```
#Configuration file for the selector
#Format: | KEYWORD | value(s) | Unit of measure | Comment |
#Comments are ignored unit of measure # means none
#-----------------------------------------------------------

#-----------------------------------------------------------
DETECTORS_PRESENT
EUCLIDES                        NO      #               Euclides is present YES/NO
PRISMA                  NO      #               Prisma is present YES/NO
DANTE                   NO      #               Dante is present YES/NO
LABR                    NO      #               Labr is present YES/NO
SPIDER                  NO      #               Spider is present YES/NO
AGATA                   NO      #               Agata is present YES/NO
#-----------------------------------------------------------

#-----------------------------------------------------------
REPLAY_CONF
ENABLED_HISTOS                  enabled_histos.conf     #               File name with list of enabled histograms
TREE_NAME                       TreeMaster      #               Input tree name
SUM_FILE_PATTERN                        sum     #               Hadded file pattern
OUT_FILE_PATTERN                        run_    #               Output file pattern
IN_FILE_PATTERN                 Tree_   #               Input file pattern
REPLAY_DIR_PATTERN                      run_    #               Replay directory pattern
IN_SUB_PATH                     /Out/Analysis   #               Input sub path
CONF_PATH                       ./Conf  #               Replay conf folder path
OUT_PATH                        ./Out   #               Output path
IN_PATH                 ./Data  #               Input path
#-----------------------------------------------------------

#-----------------------------------------------------------
REACTION_CONF
REACTION_POSITION                       0.5     #               Position of the reaction in the taget 0->front 0.5->middle, 1->back
ENERGY                  0       MeV             Beam energy
TARGET                  1 1     #               Target ion A Z
BEAM                    1 1     #               Beam ion A Z
ION                     1 1     #               Fragment of interest for binary reaction calculation: A Z (those detected)
#-----------------------------------------------------------

#-----------------------------------------------------------
TARGET_CONF
DEG_DISTANCE                    0       um              Degrader distance in um
DEG_THICKNESS                   0       mg/cm2          Degrader thickness in mg
ROTATIONZ                       0       deg             Target rotation on the Z axis in degrees
ROTATIONX                       0       deg             Target rotation on the X axis in degrees
TILT                    0       deg             Target tilt in degrees; Negative values for clockwise rotations
THICKNESS                       0       mg/cm2          Target thickness-density in mg/cm2 or units alike
DEG_PRESENT                     NO      #               Degrader present YES/NO
DEG_MATERIAL                    none    #               Degrader material
MATERIAL                        none    #               Target material
DEG_POS                 AFTER           Degrader position BEFORE/AFTER
#-----------------------------------------------------------
```

Lookup Tables

- The default LUTs can be found in User/EXP/Template/Conf/LUT/.
- The name of a channel+board combination is important for the analysis
- Generally, they allow to add an energy threshold (low, high), a time offset for alignment, and a N-degree polynomial calibration
- The remaining parameters are detector dependent and include angles or positions in space

LUT_LABR.dat 1.16 KiB

Edit

```
#LaBr Co+Cs
#board (V1730)  channel map     name    thr_lo  thr_hi   theta    phi      TimeOffset      npar_gl p0_ql    p1_q2   npar_qs p0_qs    p1_qs
1       0       0       D0      0       16000   90.422684  124.92098   0       2       -8.590549465 0.5683940043  2     -16.614035 0.584031
1       1       1       D1      0       16000   84.308418  97.489398   0       2       4.994643769  0.441859949    2  10.570262 0.443247
1       2       2       D2      0       16000   90.572804  73.768608   0       2       -4.882700373 0.4567364497   2  -9.782321 0.473778
1       3       3       D3      0       16000   99.968116  51.748253   0       2       -2.68135951  0.4616749283   2  -9.040133 0.473527
1       4       4       D4      0       16000   93.353077  26.901224   0       2       -3.368474921 0.4774816369   2  0.609657 0.481297
1       9       9       D5      0       16000   94.007297  1.3778600   0       2       0            1              2  0        1
1       5       5       D6      0       16000   99.883486  -28.723198  0       2       10.52197059  0.4435828877   2  18.918459 0.444711
1       6       6       D7      0       16000   86.180070  -45.908423  0       2       12.53667474  0.4240481389   2  28.411274 0.421525
1       7       7       D8      0       16000   91.699165  -66.505287  0       2       16.78408614  0.3897415818   2  35.049303 0.387539
1       8       8       D9      0       16000   85.591641  -95.344627  0       2       -12.39452343 0.4289130669  2  -38.673472 0.452371
##########
1       15      15      monitor 0       16000   0                      0       0       2       0          1          2   0          1


```

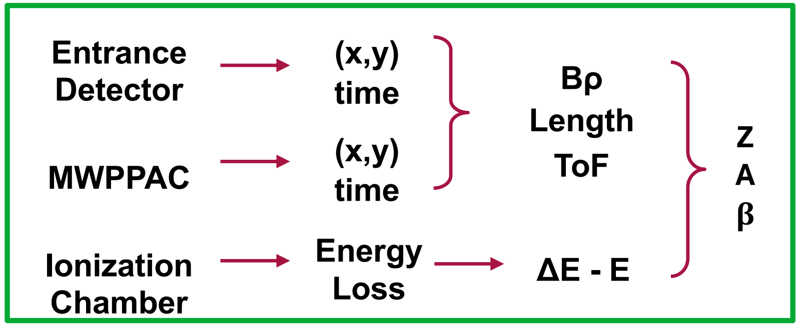
The UserSelector

- If a part of the analysis is of general interest, it should be added to the regular part of the code under src/Selector
- However, in many cases some things are experiment-specific and can be handled by the UserSelector
- The experiment specific part is set at compile time

h **UserSelector.h** 790 B

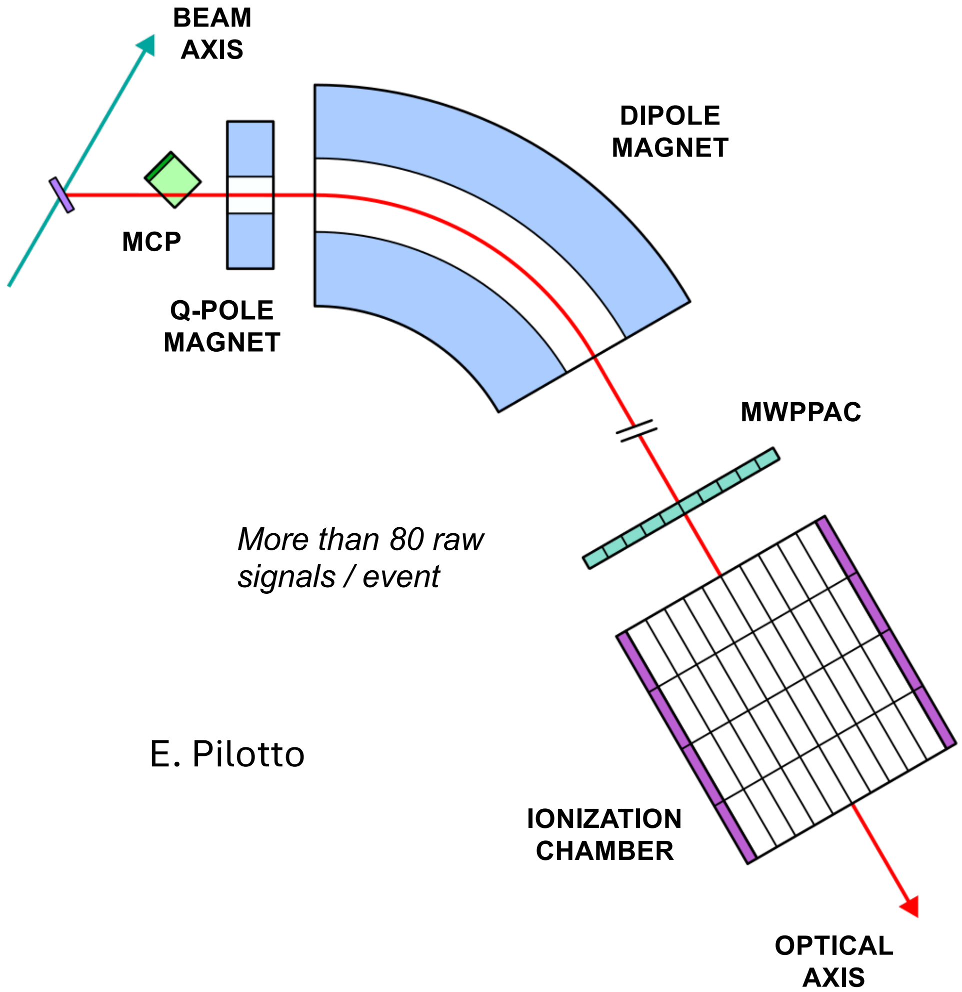
```
#pragma once
#include "AgataSelector.h"

class UserSelector : public AgataSelector {
  public:
    UserSelector(const std::string& options) : AgataSelector(options){};
    virtual Bool_t Process(Long64_t entry) override;
    virtual void   SlaveBegin(TTree* tree) override;
    virtual void   SlaveTerminate() override;

  private:
    // USER variable and histogram definition section

    unsigned long long oldTS{0};
    unsigned long long initTS{0};
    int                runNr{-1};
    int                counter{0};
    double             totCR{0};
    double             aliveT{0};

    struct UserHistograms {
        std::vector<TObject*> ptrs;
        TDirectory *dir{nullptr};
        TH1D* h_alive_time = nullptr;
        TH1D* h_avgCR      = nullptr;
    } userHistograms;
};
```

Prisma



Typical performance

- Z resolution: ~ 1/60
- A resolution: ~ 1/300



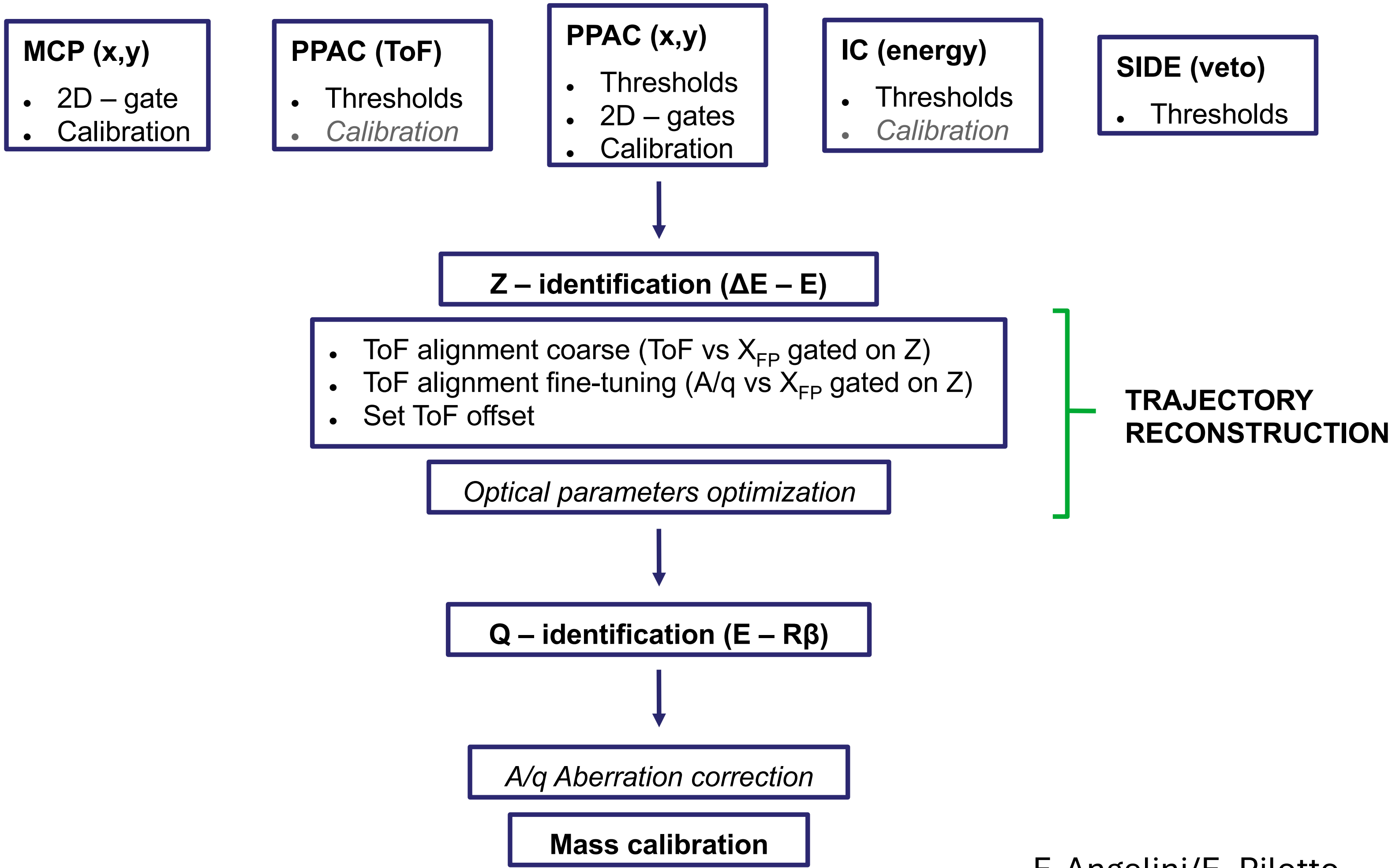
E. Pilotto

E. Pilotto

The analysis of PRISMA

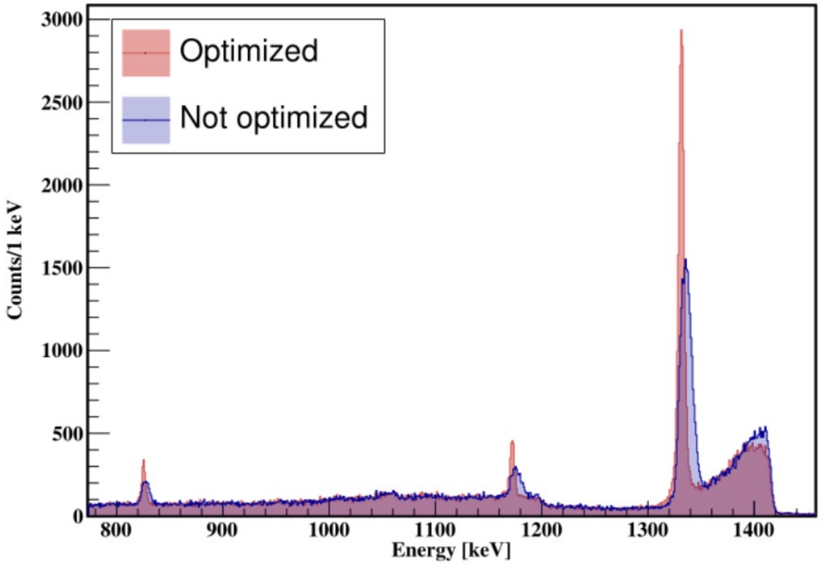
- The analysis can be handled by the Prismafilters+prisma library or by the selector
- The outcome is EQUIVALENT
- The analysis with the selector allows for more automated optimization procedures and adds some more corrections/improvements
- **If the PRISMA analysis is concluded and one is satisfied with it, there is no need to repeat it with the selector**
- The selector can take the already analyzed prisma data of the prisma library and just perform the remaining steps of the analysis

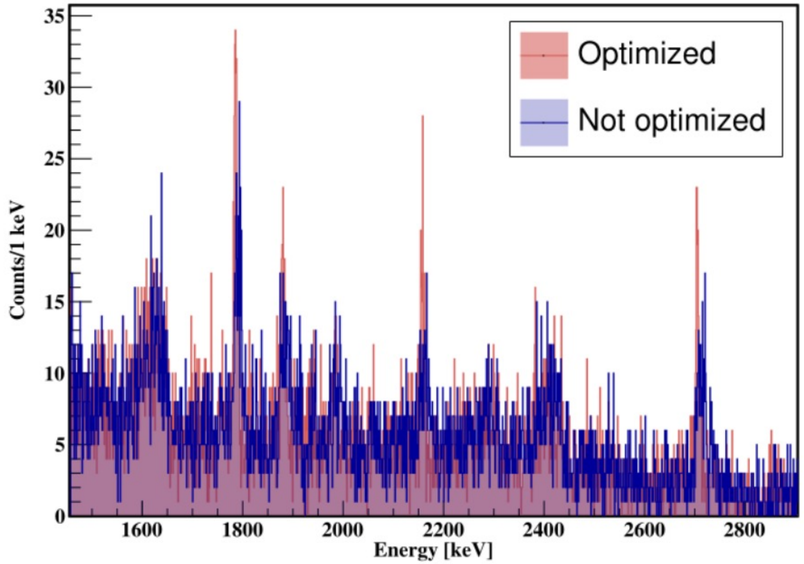
Prisma analysis schematics



F. Angelini/E. Pilotto

The optimization procedure

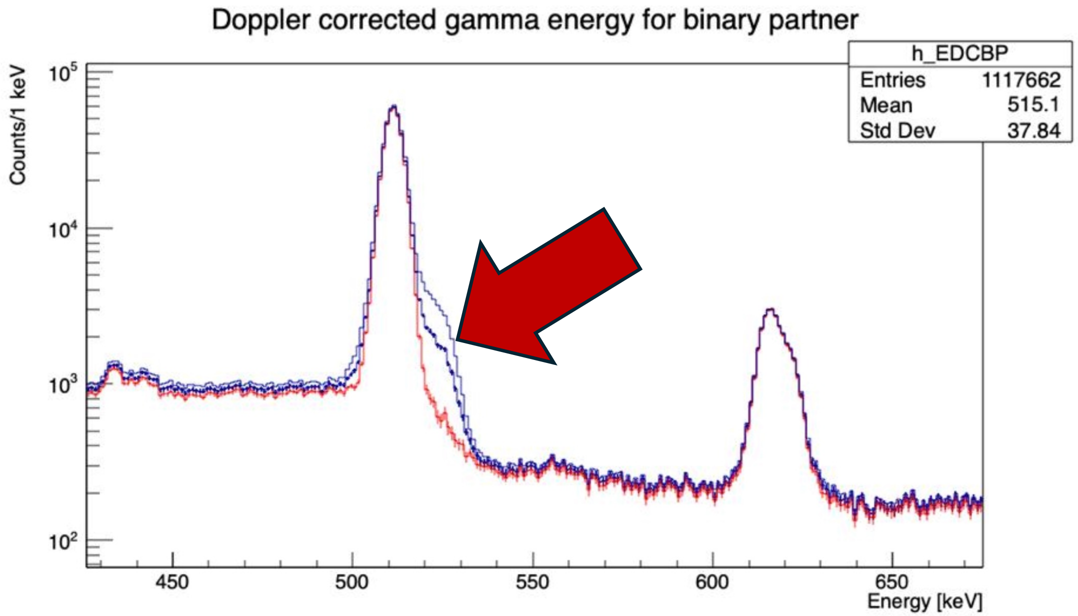




- Remarkable improvements are possible with the automatic optimization but are experiment dependent.
- There are two ways to perform it:
  - Multiparameter minimization
  - Scans of a single parameter

Background subtraction and other features

- The selector has a background subtraction option that can really improve the results in some cases
- Other things to check/features are the energy loss evaluations and kinematic reconstructions



General remarks

- You are welcome (and encouraged) to use your one data for the workshop, this will help you to debug issues and ask us questions
- You will be exposed to detectors you might not be interested in at the moment, but it’s good to know they exist for proposals/ideas
- Ask questions during the talks, let’s keep it informal