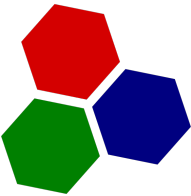


Selector analysis: AGATA+ $\{\text{ancillary}\}$ analysis

D. Brugnara

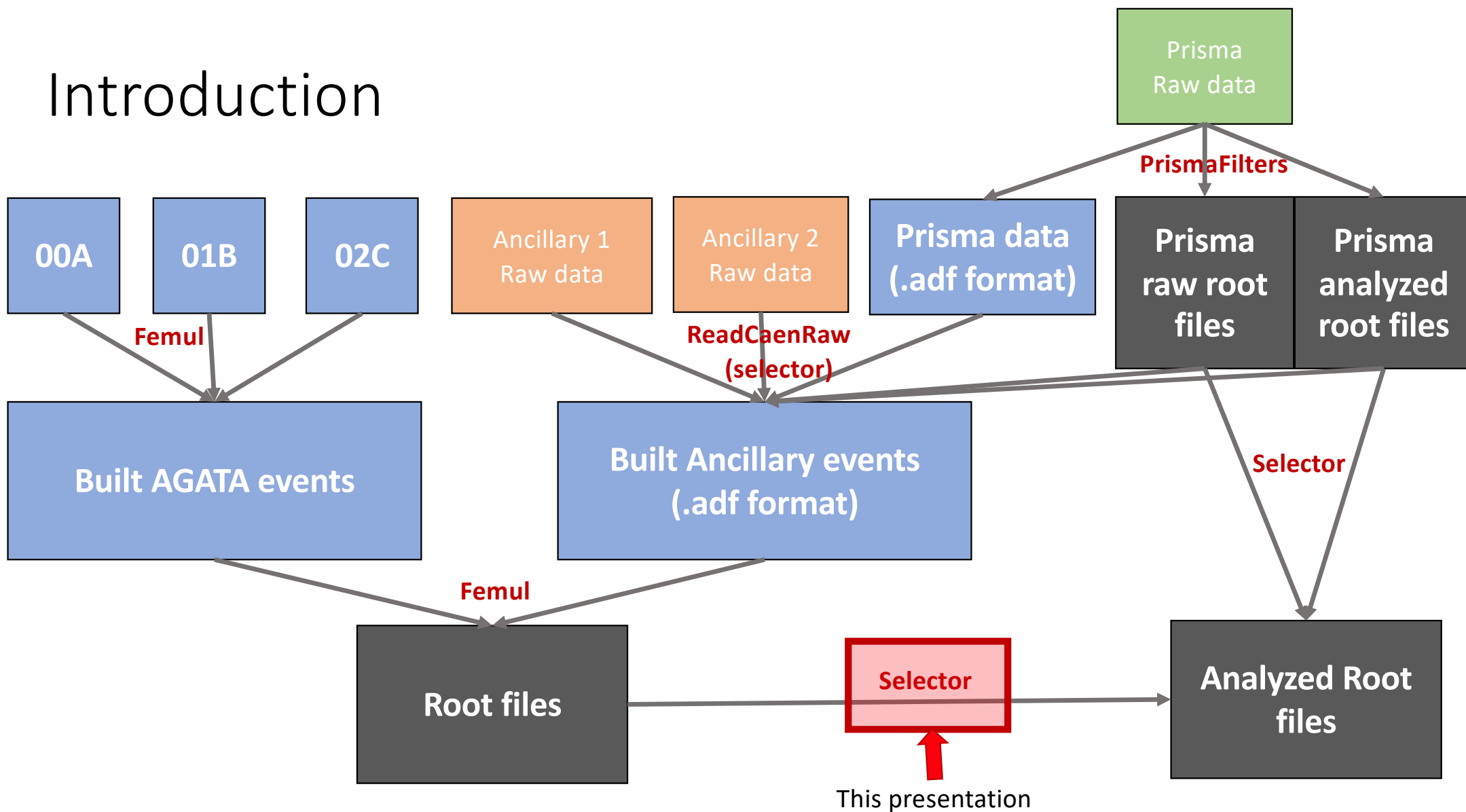


Outline

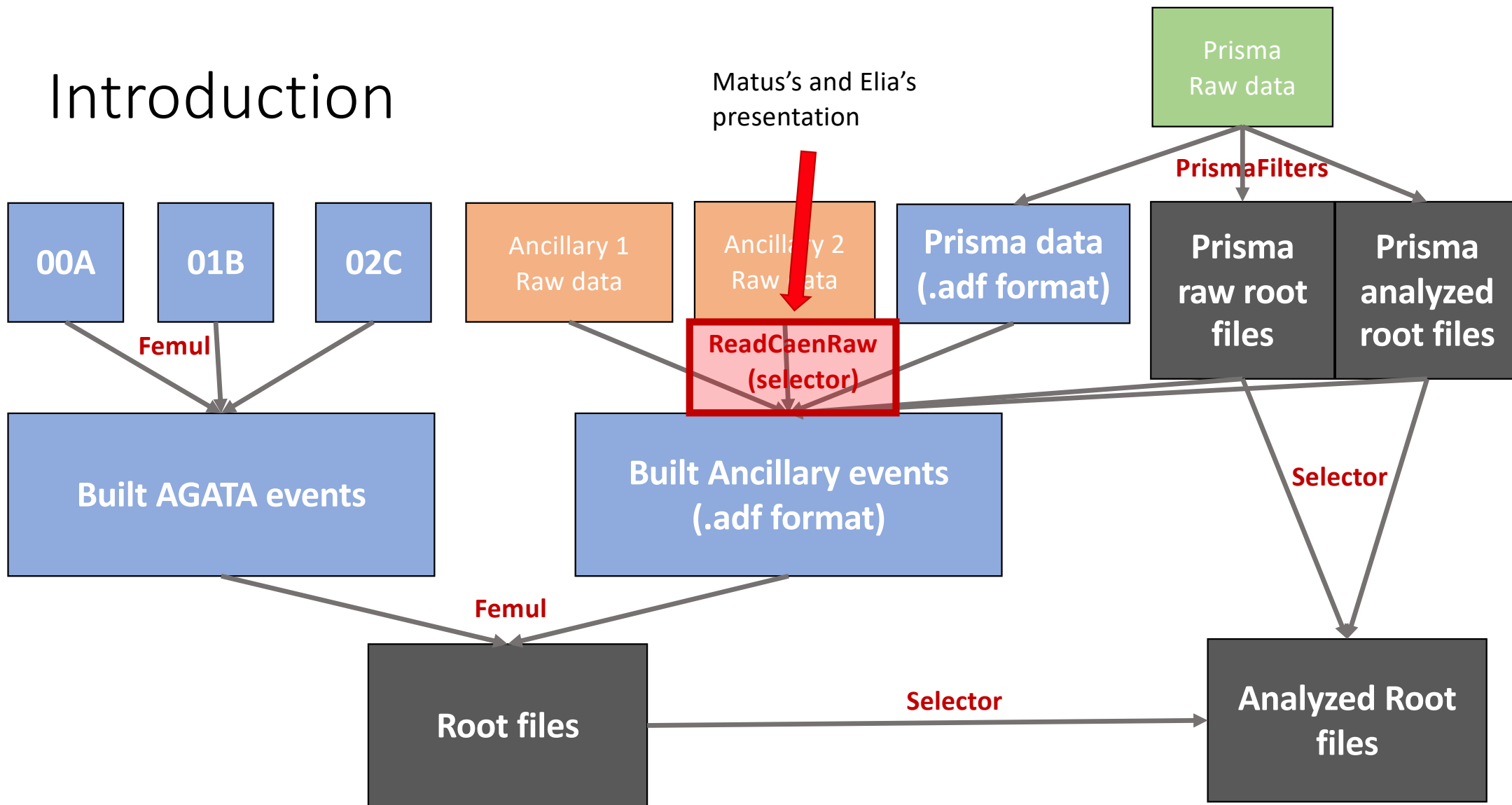
09:00	12 - Global data replay Global replays <i>RDC-202 - 202, CCIN2P3</i>		<i>Jeremie Dudouet</i> 09:00 - 10:00
10:00	coffee break <i>RDC-202 - 202, CCIN2P3</i> 10:00 - 10:30		
11:00	13 - Selector General info on the selector: what it is and what can you do with it <i>RDC-202 - 202, CCIN2P3</i> 10:30 - 12:00		
12:00	Lunch <i>RDC-202 - 202, CCIN2P3</i> 12:00 - 13:30		
13:00	9 - PRISMA: general introduction <i>Filippo Angelini</i> Detailed description of PRISMA and the data analysis <i>RDC-202 - 202, CCIN2P3</i> 13:30 - 15:00		
14:00	18 - Other ancillaries <i>Matus Balogh</i> General information on the ancillaries, data format and DAQ <i>RDC-202 - 202, CCIN2P3</i> 13:30 - 15:00		
15:00	coffee break <i>RDC-202 - 202, CCIN2P3</i> 15:00 - 15:30		
16:00	10 - PRISMA: steps of the analysis with examples <i>Filippo Angelini</i> Step-by-step guide on the PRISMA analysis <i>RDC-202 - 202, CCIN2P3</i> 15:30 - 17:00		11 - Other ancillaries <i>Elia Pilotto</i> Information on handling the RAW data of the ancillaries and the optimization procedure <i>RDC-202 - 202, CCIN2P3</i> 15:30 - 17:00
17:00			

Installation and introduction

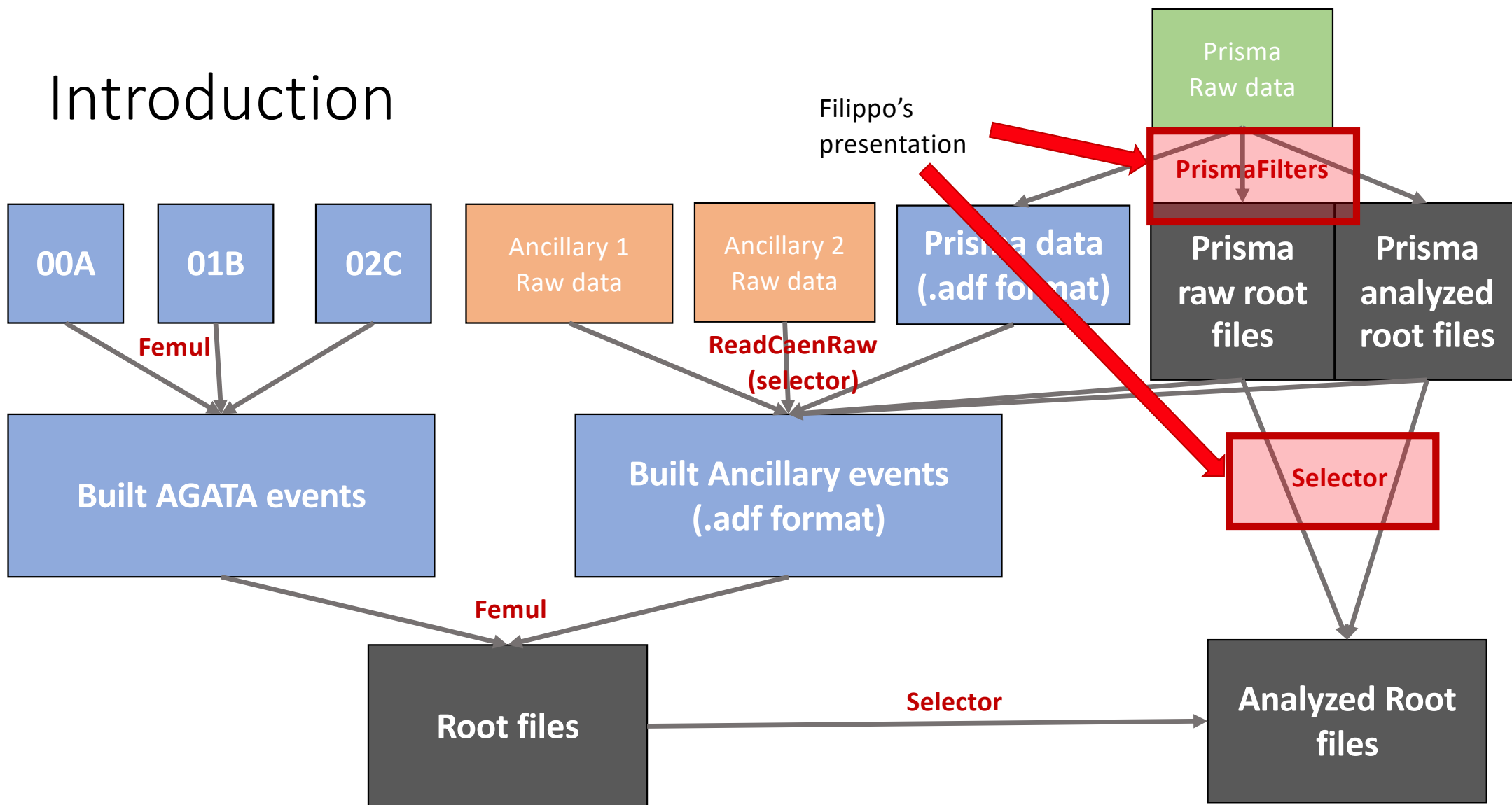
Introduction



Introduction



Introduction





The starting point

- Femul produces a root file containing MANY leaves
- 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 a quick near-line analysis and has since evolved with more refinements with full analysis capabilities
- This also means that sometimes some changes/improvements are made and could break backward compatibility (for instance for the configuration file). Since the program is more stable now it does not happen often
- We try to log on the CHANGELOG.md significant changes in different versions
- Other README.md files are located in the Conf folder, explaining the meaning of the files.
- **You are meant to modify the code**

Agata leaves

- In general, the leaves contain the following information for:
 - Single hit (within a segment)
 - Single core
 - Addback (nearest cores)
 - Tracking

Leaf name	Data type	Content
nb	int	Number of gammas/interactions
id	int[nb]	Id of the core/segment
Energy	float[nb]	Energy of the gamma/hit
TS	unsigned long /[nb]	Lowest timestamp/array of all triggered channels
(G)X/(G)Y/(G)Z	float[nb]	Position of the hit/first interaction
T	float[nb]	Cfd time, needs to be added to TS

Agata leaves

- Some leaves are more specific

Leaf name	Data type	Content
trackX2/trackY2/trackZ2	float[nb]	Position of the second interaction of the gamma (for polarization analysis purposes)
hitX/hitY/hitZ	float[nb]	Position of a hit in the crystal frame of reference
trackFOM	float[nb]	Figure of merit of tracking
trackType	float[nb]	Compton/photoelectric/pair production

Prisma

- Prisma has several leaves, but the data format is divided in raw and analyzed leaves.
- If you perform the analysis with the PrismaFilters+Prisma Library, the selector need the the analyzed variables
- If you need to create the histograms for the PRISMA analysis or to do all analysis with the selector, you only need the raw variables

```
*.....*
*Br 43 :MCP_raw : MCP_raw[3]/s
*Entries : 1388002 : Total Size= 8331627 bytes File Size = 5649710
*Baskets : 33 : Basket Size= 556544 bytes Compression= 1.47
*.....*
*Br 44 :PPAC_Xleft_raw : PPAC_Xleft_raw[10]/s
*Entries : 1388002 : Total Size= 27768196 bytes File Size = 9274837
*Baskets : 73 : Basket Size= 1855488 bytes Compression= 2.99
*.....*
*Br 45 :PPAC_Xright_raw : PPAC_Xright_raw[10]/s
*Entries : 1388002 : Total Size= 27768273 bytes File Size = 9214345
*Baskets : 73 : Basket Size= 1855488 bytes Compression= 3.01
*.....*
*Br 46 :PPAC_Cathode_raw : PPAC_Cathode_raw[10]/s
*Entries : 1388002 : Total Size= 27768350 bytes File Size = 14873215
*Baskets : 73 : Basket Size= 1855488 bytes Compression= 1.87
*.....*
*Br 47 :PPAC_Y_raw : PPAC_Y_raw[2]/s
*Entries : 1388002 : Total Size= 5555116 bytes File Size = 4108603
*Baskets : 27 : Basket Size= 371200 bytes Compression= 1.35
*.....*
*Br 48 :TOF_raw : TOF_raw[10]/s
*Entries : 1388002 : Total Size= 27767657 bytes File Size = 17433268
*Baskets : 73 : Basket Size= 1854976 bytes Compression= 1.59
*.....*
*Br 49 :IC_A_raw : IC_A_raw[10]/s
*Entries : 1388002 : Total Size= 27767734 bytes File Size = 14831556
*Baskets : 73 : Basket Size= 1854976 bytes Compression= 1.87
*.....*
*Br 50 :IC_B_raw : IC_B_raw[10]/s
*Entries : 1388002 : Total Size= 27767734 bytes File Size = 14322170
*Baskets : 73 : Basket Size= 1854976 bytes Compression= 1.94
*.....*
*Br 51 :IC_C_raw : IC_C_raw[10]/s
*Entries : 1388002 : Total Size= 27767734 bytes File Size = 11970373
*Baskets : 73 : Basket Size= 1854976 bytes Compression= 2.32
*.....*
*Br 52 :IC_D_raw : IC_D_raw[10]/s
*Entries : 1388002 : Total Size= 27767734 bytes File Size = 11614686
*Baskets : 73 : Basket Size= 1854976 bytes Compression= 2.39
*.....*
```

Prisma: gen_conf.py

```
TB_PRISMA=(  
  "ConfPath      $CONFDIR/prisma",          #Path to Prisma configuration files  
  "LUTFile       lutPRISMA.txt",           #LUT file name (default is : lutPRISMA.txt)  
  "ManagerFile   manager.conf",          #Manager file name (default is : manager.conf)  
  "WriteRawTree",                          #Store the raw data in the output Tree (default 1)  
  "WriteAnaTree",                          #Store the analyzed data in the output Tree (default 1)  
  #"DoPrismaAnalysis",                    #Ignore the input analyzed data (if present) and process the prisma lib on the raw data (default 0)  
  #"Verbose",                               # Print warnings in the processing  
)
```

- You can choose what to write in the root file based on your analysis strategy
- If you are feeding raw PRISMA data to femul (f10201a0), you can also perform the analysis during the replay with the “DoPrismaAnalysis” keyword
- Otherwise, it is recommended to only write the data that you need not to double the space on disk

Other ancillaries (aka CAEN digitizers)

- Data from CAEN digitizers has the same format and requires a lookup table (LUT)

Leaf name	Data type	Content
nb	int	Number of channels in an event
Channel	int[nb]	Channel that has triggered
Board	int[nb]	Board that has triggered
TS	unsigned long	Lowest timestamp of all triggered channels
TSHit	unsigned long[nb]	Timestamp of the single hit
Time	float[nb]	Interpolated time, needs to be added to TSHit
Energy	float[nb]	Energy of trapezoid (PHA) of Qlong (PSD)
QShort	float[nb]	Short integration (PSD only)

The output

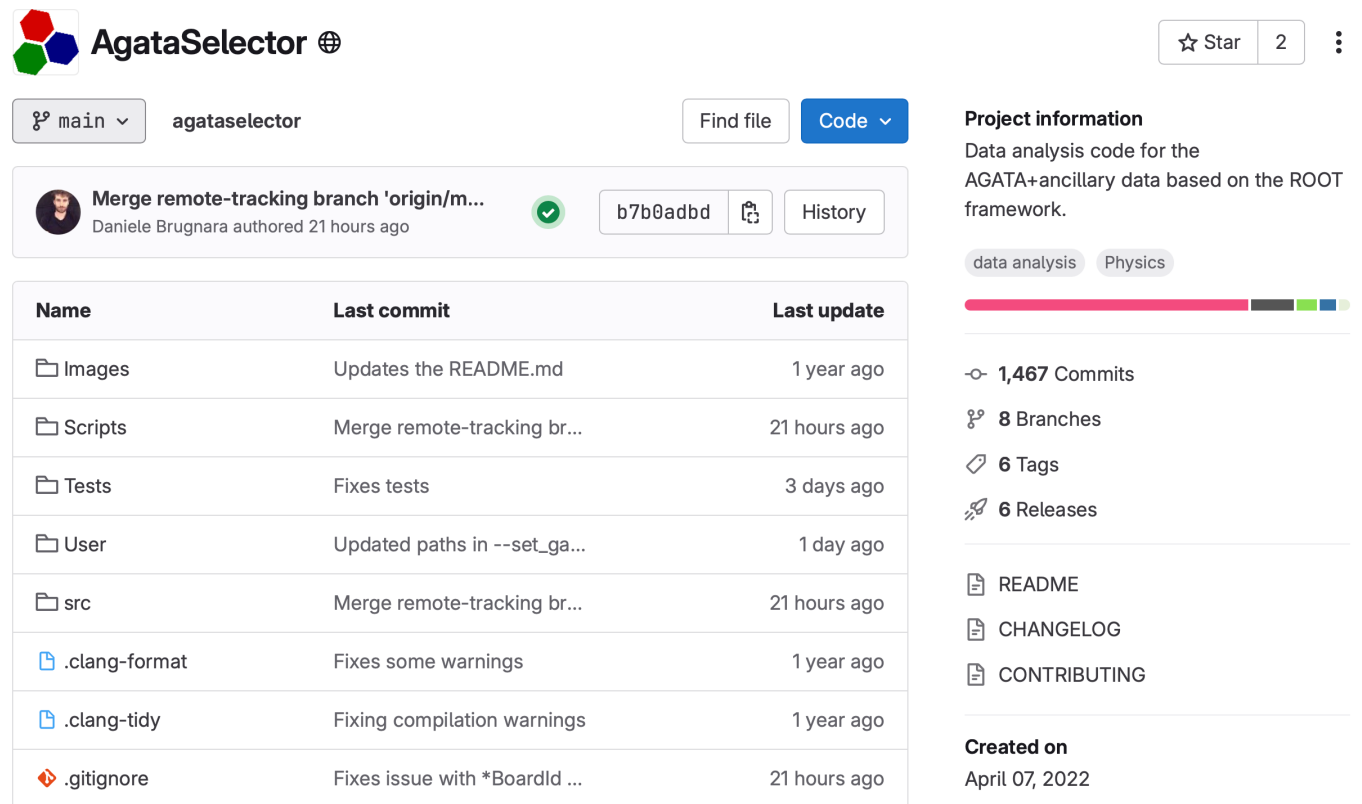
- The selector produces ROOT files containing:
 - Histograms (each analysis is contained within a folder):
 - Single detector analysis
 - Coincidence analysis
 - TTrees of:
 - High level data of a single detector. For instance, Spider provides things such as excitation energy or angles
 - Doppler correction based on the analysis of the agata+ancillary coincidence
- Generally, TTrees take up a considerable amount of disk space and are not very useful since histograms provide the high-level analysis already

The output

- For each input file an output file is produced in the output folder. The files of each run are added in a single file called `sum_xxx-yyy.root`, where `xxx` is the run number and `yyy` is the number of input files.
- Different runs can be also added with `--sum_all`
- The partial files can be discarded with the option `--rm_partial`
- Additionally to the “regular” output it is possible to personalize the analysis with the `UserSelector` which will in turn produce additional output in the `User` folder.

Installation procedure

- The repository can be found here:
<https://baltig.infn.it/gamma/agataselector>



The screenshot shows the GitHub repository page for AgataSelector. At the top, there is a repository header with the name "AgataSelector" and a globe icon. Below this, there are navigation elements including a branch selector set to "main", the repository name "agataselector", a "Find file" button, and a "Code" button. A recent commit is displayed, titled "Merge remote-tracking branch 'origin/m..." by Daniele Brugnara, with a green checkmark icon and a commit hash "b7b0adbd". Below the commit information is a table listing the repository's files and folders, including "Images", "Scripts", "Tests", "User", "src", ".clang-format", ".clang-tidy", and ".gitignore", each with its last commit message and update time. On the right side, there is a "Project information" section with a star button showing 2 stars, a progress bar, and statistics for commits (1,467), branches (8), tags (6), and releases (6). Below this, there are links to the README, CHANGELOG, and CONTRIBUTING files, and a "Created on" date of April 07, 2022.

AgataSelector 🌐

main agataselector Find file Code

Merge remote-tracking branch 'origin/m...
Daniele Brugnara authored 21 hours ago

Name	Last commit	Last update
Images	Updates the README.md	1 year ago
Scripts	Merge remote-tracking br...	21 hours ago
Tests	Fixes tests	3 days ago
User	Updated paths in --set_ga...	1 day ago
src	Merge remote-tracking br...	21 hours ago
.clang-format	Fixes some warnings	1 year ago
.clang-tidy	Fixing compilation warnings	1 year ago
.gitignore	Fixes issue with *BoardId ...	21 hours ago

Project information
Data analysis code for the AGATA+ancillary data based on the ROOT framework.

data analysis Physics

1,467 Commits

8 Branches

6 Tags

6 Releases

README

CHANGELOG

CONTRIBUTING

Created on
April 07, 2022

Installation procedure

- ✓ Clone the repository
- ✓ Create a build folder
- ✓ Configure with cmake
- ✓ Compile

Note: root needs to be installed and compiled with a c++ version > 14

```
git clone https://baltig.infn.it/gamma/agataselector.git
cd agataselector
mkdir build; cd build
cmake ..
make -j4
```

If you want to perform a personalized analysis for your experiment, before compiling with make, specify the proper experiment name. For instance for EXP_001 you would specify:

```
cmake -DEXP_NAME=EXP_001 .
```

```
source Scripts/selector.sh
```



























(Optional) Adds the build directory to \$PATH and adds tab-completion

Known troubles and how to solve them

- Make sure to compile root with at least c++14:
 - `DCMAKE_CXX_STANDARD=17` (or 14 if you prefer)
- In some cases, the selector remain stuck when reading one of the ancillary branches called `*ChannelId` or `*BoardId`. This is due to a ROOT problem with the TTreeReader because there is a name mismatch when writing the TTrees. The newest version of femul is writing the TTrees with no mismatch, in case you experience this problem, make sure to update femul and the selector.

Tests

- At each commit the code is tested.
- The test include:
 - Does the code build properly?
 - Additionally does the prisma-agata analysis work?
 - At last, two spectra (DC, DCBP) are fitted for fully identified isotopes
 - The test passes if integral, mean and sigma of the peaks of interest is within the parameters
- This helps us in controlling that nothing was broken in the process
- An X marked commit means that the test was not passed

Aug 09, 2023	 Bug fix with beta vs betaBP in gammadetectorPrisma Matúš Sedlák authored 3 weeks ago		✓	8acc674		
Aug 02, 2023	 EXP014 changes Julgen authored 4 weeks ago		✓	02e2196f		
Jul 14, 2023	 Adds the possibility of saving the doppler correction in the output tree Daniele authored 1 month ago		✓	b2eba252		
Jul 11, 2023	 Prisma-dante was missing Daniele Brugnara authored 1 month ago		✓	dfa2344a		
	 Clang format Daniele Brugnara authored 1 month ago		✓	1a1e8b9a		
	 Merge branch 'devel-3' into 'main' ... Daniele Brugnara authored 1 month ago		✓	789c10de		
Jun 22, 2023	 Improves startup time Agata Analysis authored 2 months ago		✗	8a6521fe		
Jun 21, 2023	 Merge branch 'main' of https://battig.infn.it/gamma/agataselector into main Agata Analysis authored 2 months ago		✓	eef32eca		

Documentation

- Several README.md files are present in the root folder and serve as a reference
- Not everything is contained in these README files

README.md

AgataSelector

DOI: 10.5281/zenodo.8329198

This analysis code is meant for the data of AGATA+ $\text{\$Ancillary}$, producing var performing kinematic calculations and other operations useful for Doppler correction analysis tasks. The starting point of the selector are the ROOT files produced a work in progress and is meant to be updated and modified by both users as log the bug fixes, improvements and broken compatibility issues in the CHANNEL based on ROOT and requires an installed version where ROOT has been corrected. Our intent is to make the analysis procedure straightforward and reproducible. will contain a configuration folder that contains the configuration file of the selector, the calculations, the lookup tables, the date and the git hash. This means the outcome of the analysis is reproducible.

Contents

1. Installation procedure
2. Run the selector
3. Performing the analysis
4. Selector options
5. Prisma
6. Notes on user selectors
7. Advanced options
8. Optimizers
 - Selector's builtin optimization
 - Scan of the LUT parameters
 - Grid search of the LUT parameters

Installation procedure

- ✓ Clone the repository
- ✓ Create a build folder
- ✓ Configure with cmake
- ✓ Compile

```
git clone https://baltig.infn.it/gamma/agataselector.git
cd agataselector
mkdir build; cd build
cmake ..
make -j4
```

If you want to perform a personalized analysis for your experiment, before you specify the proper experiment name. For instance for EXP_001 you would specify:

```
cmake -DEXP_NAME=EXP_001 ..
```

In this case the code will look for a folder called EXP_001 under User/EXP, will expect a new selector with your additions. You should copy the template folder. Add histograms to the struct defined in the .h file. If the experiment is with the required name will be created.

In the root files you can write the TTree for a given detector. On top of that, the configuration used to analyze it. However, ROOT needs the dictionaries to use functionalities of the classes serialized in the file. To support this feature you code to the `~/./bashrc`. You need to call it from the build directory:

```
source Scripts/selector.sh
```

This also adds the bash completion and the possibility to use some things interactively.

If you want to be extra careful and check if your installation is done correctly test. To do so, compile with the correct flag and run the following commands:

```
cmake -B build -DENABLE_TESTING=ON -S .
cmake --build build -j4
cd build/Tests
ctest --output-on-failure -j6
```

Prisma

The selector can now run the full analysis of prisma. This allows to run the parameters of the spectrometer. Please refer to this PRISMA_README.md for documentation is still preliminary and is not complete.

Selector options

This is a list with a brief description of the various command-line options:

Option	expected input	Description
--help	-	Prints a help menu
--nrevs	[#]	Specify number of events to analyze
--nrthr	[#]	Specify maximum number of thread that if the selector is killed by the OS there is not enough memory and you reduce the number of threads of dis produced histograms if possible.
--conf	[file]	Specify a conf file, default is in ../
--iofile	[infile, outfile]	Specify an input and an output file, if conf.
--iolistfile	[file]	Specify a file where to read a list of line by line.
--verb	[#]	Verbosity: 0 (prints progress Sel), 1 info).
--no_user_sel	-	Runs standard selector without the User/UserSelector.cxx.
--print_conf	[out_file]	Prints the default conf file with default parameters. Note that some of the present, an example is EX_VALUES_AGATASPIDER_CONF.
--rm_partial	-	Removes partial output files that are in the input folder.
--optimize	-	Runs optimizer on the given peak by multiple times.
--only_enabled_histograms	-	Creates and fills only the histograms: \${CONF_FOLDER}/enabled_histograms
--debug_canvas	-	Shows a canvas at each fit (at the moment in the optimization procedure)
--reduction_cond	[reduction condition]	Creates a new reduced data TTree with reduction condition. Bash special character escaped with the backslash character on Z in PRISMA and the gammas to reduce the input file, only nbTrack>0&&Z_Nr>0 262. In folder of run 262 one would find new files with the prefix red_ the condition "nbTrack>0&&Z_Nr>0".
--set_gates	[selector file]	Starts the automatic procedure to set gates are then read automatically. Call a TCutG and close it with a double-c then ask you to input the id of the cut.
--no_hadd	-	Does not hadd to sum up the statistics
--update_runs	-	Run the selector only for trees not processed
--update_prisma	-	Updates the prisma part of the analysis
--sum_all	-	Runs hadd of all runs processed in the file will be called runs-#-#.root
--subtract_bkg	-	Subtracts the background based on windows set up in the configuration
--window_size	-	Size of the progress window. If not set, calculated automatically

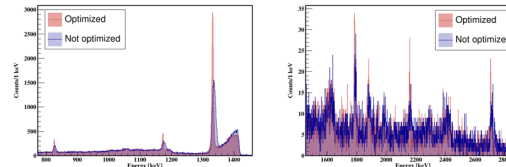
If you create a file:

```
touch StopFile
```

Optimizers

There are several ways to optimize the outcome of the data with the selector. Here we report a description of each.

Selector's builtin optimization



The `--optimize` option runs the selector multiple times trying to minimize a figure of merit which is a combination of the centroid min and the sigma of the peak. The bias on the two conditions is set in the selector configuration file with SIGMA_WEIGHT. The fitter class can fit at the same multiple peaks and combine them in the figure of merit. The parameters to be optimized are those included in the configuration file such as Z_SHIFT, PHE, ... In practice, any parameter that is a floating point number can be optimized. Different minimizer algorithms can be tried by choosing them in the configuration file. The outcome is a matter of trial and error. It is advised to run the optimization procedure on data which has been reduced with the --reduction_cond option speed up the procedure. For instance, if one wants to optimize the coincidence spectrum between agata and prisma, it will be faster to select only good coincidence events between prisma and agata. This can be done by setting the condition on nbTrack>0 and A_Nr==32 (for instance) on.

Use `--debug_canvas` to check the quality of the fit at the first steps.

Check the progress of the minimizer during each step in the file `./Conf/Optimizer/Log.txt` whatever specified in the selector configuration file.

The parameters of the fit, if the default ones are not ok can be set in the file called `./Conf/Optimizer/parameters.dat` or the name indicated with the keyword FIT_PAR_FILE. This file will be created with the default parameters if nothing is found in the right folder. Be careful if the file is there the parameters will be read from it. This means that when the fit does not make sense it is probably because the parameters are not ok, so you can just delete the file so that it generated automatically.

The optimization procedure is not limited to the improvement of the Doppler correction but can be applied for the improvement of Q-value or excitation energy distributions.

Parameters part of the user configuration are also accessible. Generally, one should try to optimize multiple transition at once to obtain the most stable results.

The range of variation of the parameters should be gradually reduced as one converges to a solution. To do so, it is often useful to plot the gradient of a parameter. This is done with the SC parameter in the configuration file. This will vary the specified parameter with the selected step ultimately produce a root file (specified as ROOT_FILE) with as many TGraphs as the number scanned parameters. The SCAN option will also add a TH2D histogram with the parameter on the x-axis (in internal units) and the spectrum on the y-axis. This allows to inspect the effect of the parameter on the whole spectrum. It is also possible to create a contour plot (with the keyword CONTOUR) to check the correlation of different minimized parameters. This, however, requires a lot of iterations and does not often converge to something that makes sense.

Scan of the LUT parameters

The previous selector can only optimize parameters in the selector.conf file. However, other important parameters are contained on some detector's lookup tables. If this is the case there are two options, the grid search optimizer (see next section Grid-search optimizer) or the LUT_OPTIMIZER. The latter is a workaround that uses a special type of user selector to perform scan of the LUT parameters. In this case one can scan parameters independently, but the algorithm is very general and can be used on many detectors. Please find a step-by-step guide in the User/EXP/LUT_OPTIMIZER.

Grid-search optimizer for silicon detectors

This program will perform a grid search of the optimal parameters in the lookup table of the detectors allowing for the fine-tuning.

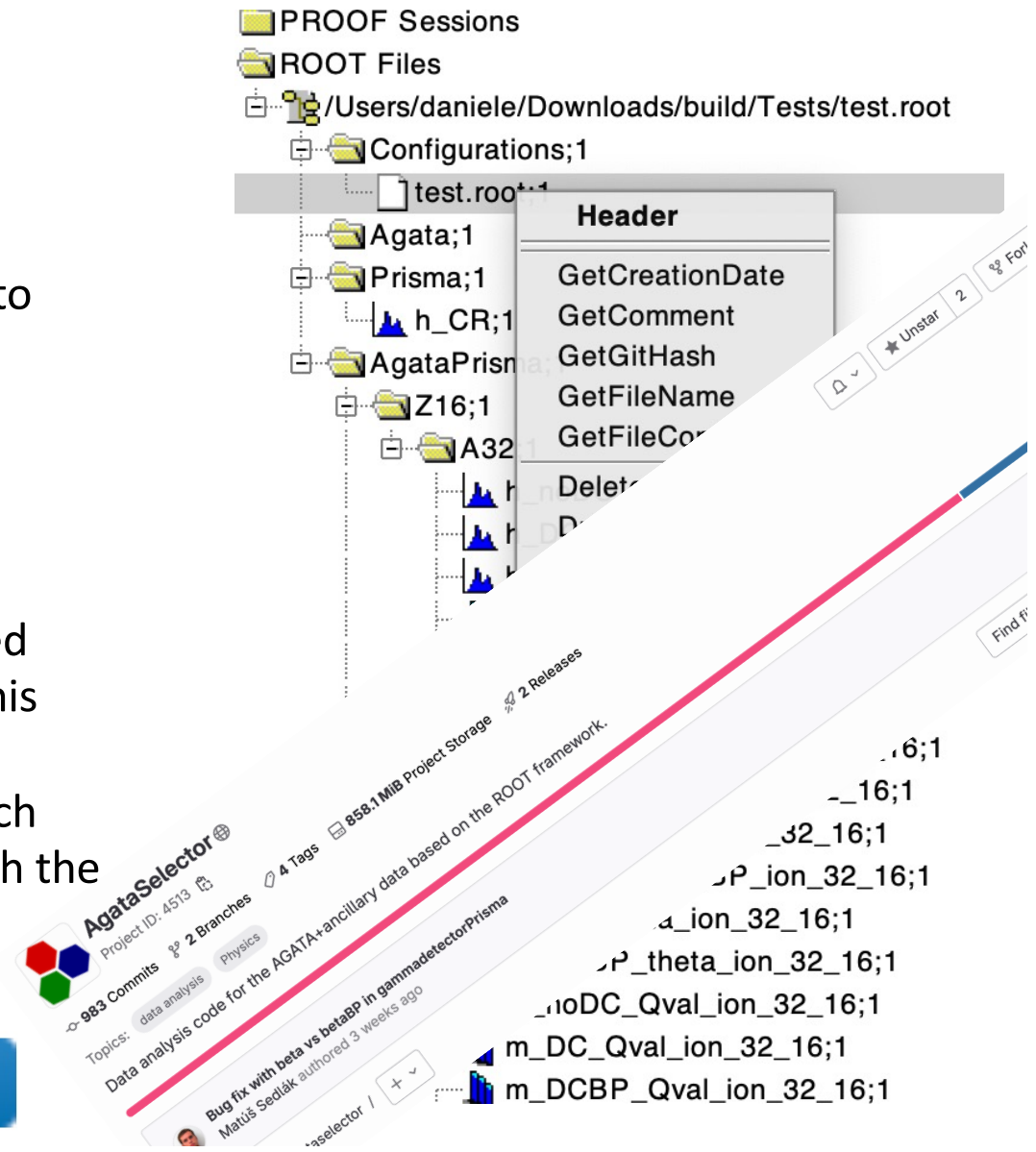
Requirements

This application requires a compiler that supports C++17 or newer, with ROOT compiled against the system. The system must be compiled with the CMAKE_BUILD_TYPE=Release flag.

Reproducibility

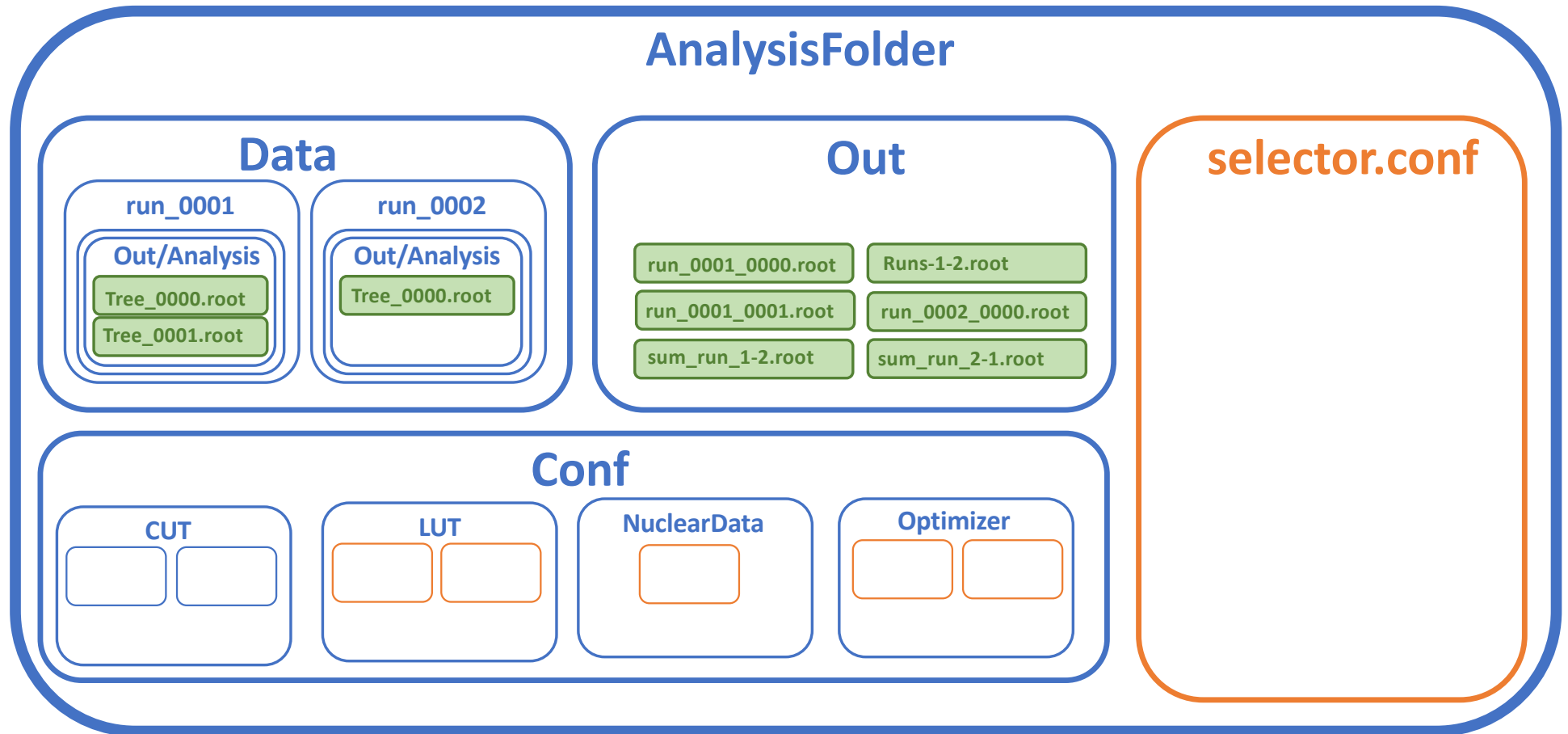
- The output files contain the parameters used to generate it:
 - The entire selector.conf
 - The lookup tables
 - The git hash
 - The date of creation
- This means that the analysis can be reproduced simply by printing the selector.conf used for this specific file and checking out the correct hash
-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

DOI [10.5281/zenodo.8329198](https://doi.org/10.5281/zenodo.8329198)



Setup of the analysis

Setup of the analysis folder



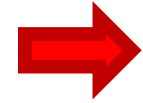
Generate/retrieve the default selector.conf

- The default selector.conf can be generated typing:
 - `RunSelector - - print_conf selector.conf`
- In all experiments, a nearline analysis was performed, it is a good starting point for the offline analysis.
- To “recall” the analysis you should have compiled the selector with the cmake option “`-DEXP_NAME=EXP ###`”. This will compile the UserSelector that you can find in `agataselector/User/EXP/EXP_###`
- The configuration folder adapted for your experiment is `agataselector/User/EXP/EXP_###/Conf`
- The selector.conf is in `agataselector/User/EXP/EXP_###/selector.conf` (you might have multiple versions if the setup was changed during the experiment)

In general, the selector is being constantly updated with bug fixes and improvements. This could mean that some features could have been added and some changes need to be applied to the selector.conf if you have pulled from origin. In order to get access to all options you can print the default configuration file with the option `RunSelector - -print_conf my_selector.conf`. Each conf parameter will contain a comment with some infos on the effect of the parameter

Options

How to run the code:
`./RunSelector [options, ...] \`
`[#run, ...]`



Option	expected input	Description
--help	-	Prints a help menu
--nrevts	[#]	Specify number of events to analyze, default is all.
--nrthr	[#]	Specify maximum number of threads, default is 6. Note that if the selector is killed by the OS, it might mean that there is not enough memory and you might have to reduce the number of threads or disable some of the produced histograms if possible.
--conf	[file]	Specify a conf file, default is in <code>../Conf/</code> .
--iofile	[infile, outfile]	Specify an input and an output file, this will disregard the conf.
--iolistfile	[file]	Specify a file where to read a list of inputFile outputFile line by line.
--verb	[#]	Verbosity: 0 (prints progress Sel), 1 (prints debugging info).
--no_user_sel	-	Runs standard selector without the analysis contained in <code>User/UserSelector.cxx</code> .
--print_conf	[out_file]	Prints the default conf file with default values for each parameters. Note that some of the options might not be present, an example is <code>EX_VALUES</code> of <code>AGATASPIDER_CONF</code> .
--rm_partial	-	Removes partial output files that correspond to each file in the input folder.
--optimize	-	Runs optimizer on the given peak by running the selector multiple times.
--only_enabled_histos	-	Creates and fills only the histograms present in the file <code>\${CONF_FOLDER}/enabled_histos.conf</code>
--debug_canvas	-	Shows a canvas at each fit (at the moment it is used only in the optimization procedure)
--reduction_cond	[reduction condition]	Creates a new reduced data TTree based on the given reduction condition. Bash special characters should be escaped with the backslash character. For instance to set a condition on Z in PRISMA and the number of tracked gammas to reduce the input file, one would add <code>./RunSelector --reduction_cond nbTrack>0&&Z_Nr>0 262</code> . In this case in the data folder of run 262 one would find new reduced ROOT files with the prefix <code>red_</code> the condition <code>"nbTrack>0&&Z_Nr>0"</code> .
--no_hadd	-	Does not hadd to sum up the statistics
--update_runs	-	Run the selector only for trees not present in the output folder procedure)
--update_prisma	-	Updates the prisma part of the analysis
--sum_all	-	Runs hadd of all runs processed in the current session, the file will be called <code>runs-#-#.root</code>
--window_size	-	Size of the progress window. If not present it is calculated automatically

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 calculations. 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      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          Degradrer distance in um
DEG_THICKNESS     0      mg/cm2       Degradrer 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      #          Degradrer present YES/NO
DEG_MATERIAL      none #          Degradrer material
MATERIAL          none #          Target material
DEG_POS           AFTER #          Degradrer position BEFORE/AFTER
#-----
```

Example of Detector Conf: Agata

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

- Enable/disable histograms or TTrees
- Speficy LUT (if necessary)
- Set some global angles and psitions
- Sets parameters of the histograms such as bin width
- Sets other detector-dependent parameters

```

#-----
AGATA_CONF
BIN_WIDTH          1      #      Bin width in gamma histograms
COINC_W_RIGHT      10     #      Time window right with with the same type of det
COINC_W_LEFT       0     #      Time window left with the same type of det
TRACKING_FOM_THR   0      #      Threshold for the figure of merit of the tracking (0-1.02)
GAMMA_E_MAX        4000   keV     Maximum gamma energy in histograms
BETA_AVG_PHI       180    deg     Average beta phi Doppler correction for detector
BETA_AVG_MAG       0.1    #      Average beta magnitude Doppler correction for detector
ANGLE              0      deg     Detector angle. For AGATA should be 180-prisma_angle
BETA_AVG_THETA     20     deg     Average beta theta Doppler correction for detector
PHI                0      deg     Detector phi rotation for optimization purposes
THETA_Y            0      deg     Detector rotation on the vertical plane for optimization purposes
CFD_UNIT           10     ns      Cfd units
THETA_X            0      deg     Detector rotation on the horizontal plane for optimization purposes
Z_SHIFT            0      mm      Detector z shift for optimization purposes
TIME_UNIT          10     ns      Timestamp unit, should 10*ns
Y_SHIFT            0      mm      Detector y shift for optimization purposes
X_SHIFT            0      mm      Detector x shift for optimization purposes
EXCLUDE_ANCILLARY  NO     #      Only analyze event in anticoincidence with ancillaries
ENABLE_TREE        NO     #      Ebable or disable detector TTree to save memory (strongly encouraged)
ENABLE_HISTS       YES    #      Ebable or disable detector histos to save memory
EXCLUDE_TS         0 0    ms      Exclude events in this timestamp region, beginning of run is TS=0
LUT                #      Lookup table path
SPECTRA_TYPE       TRACKED          Spectra type: SEGMENT, CORE, CORE1, ADDBACK, TRACKED, CALORIMETER
#-----

```

Example of Coincidence Conf: Agata+Spider

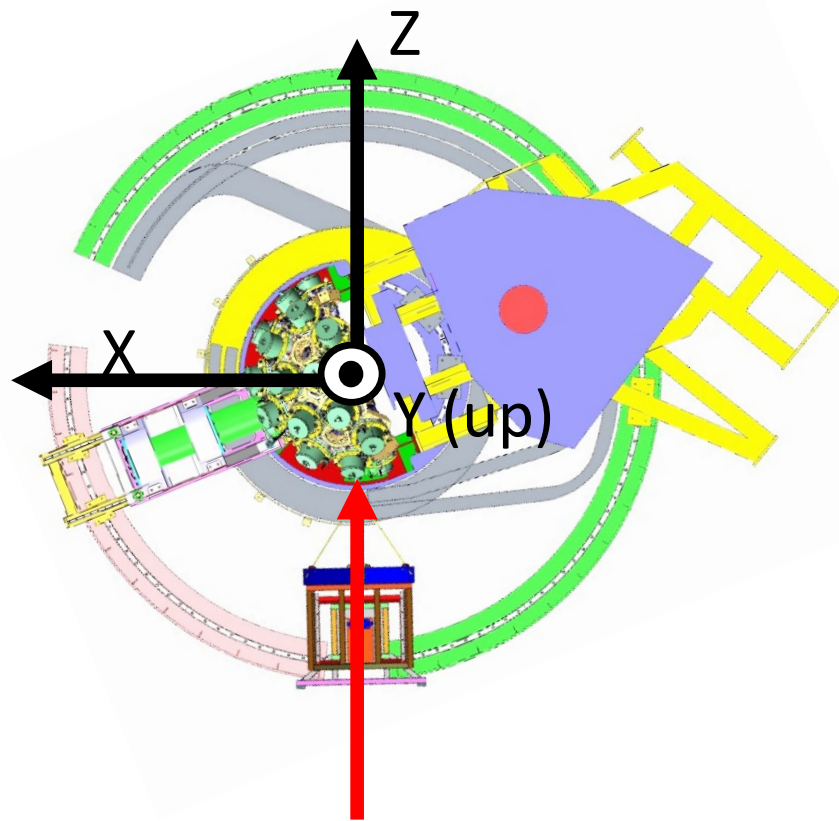
KEYWORD | value(s) | unit of measure | comment

- Set the coincidence window based on the peak position
- Enable histograms and trees
- Set Doppler correction position
- Other detector-dependent parameters



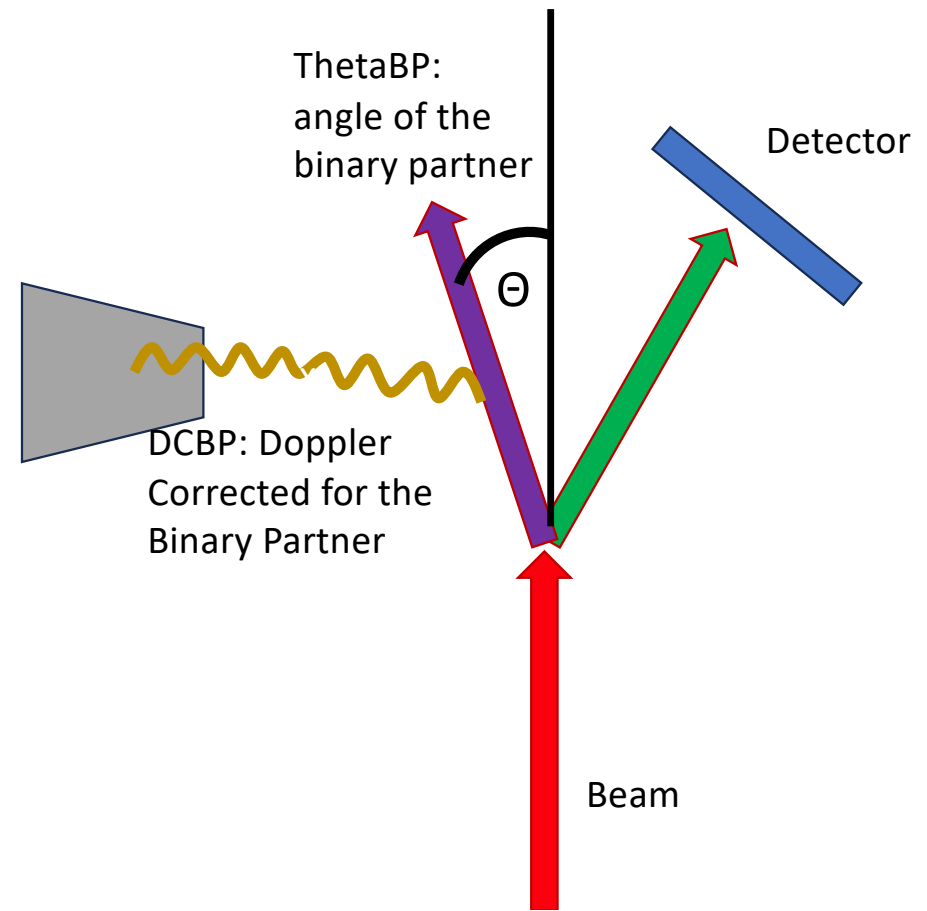
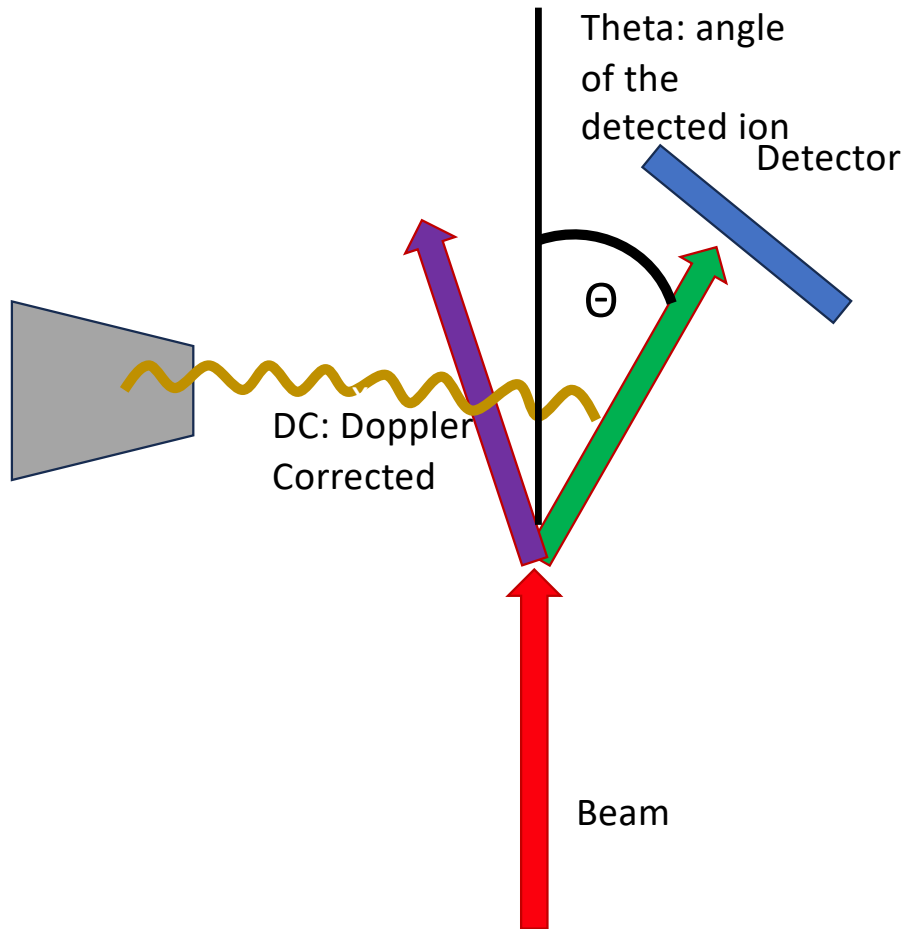
```
#-----
AGATASPIDER_CONF
COINC_W_RIGHT      0      #      Time window right
COINC_W_LEFT       0      #      Time window left
ENABLE_TREE        NO     #      Enable or disable coincidence TTree branch to save memory (strongly encouraged)
ENABLE_HISTS       YES    #      Enable histograms of coincidence
EX_VALUES          0 1    MeV      Excitation energy gates, first value is the min, second value is the max
EX_VALUES_FILE     NONE   #      File name in the folder LUT containing the channel by channel gate in excitation energy
BP_FRAGMENT_POSITION      MID_TARGET      Doppler correction position for binary partner
FRAGMENT_POSITION      MID_TARGET      Doppler correction position for detected ion
EX_VALUES_FILE         NONE   #      File name in the folder LUT containing the channel by channel gate in excitation energy
#-----
```

Frame of reference



- The frame of reference with respect to the beam is necessary for reaction calculations
- It is common to all detectors.
- Z points in the direction of the beam and Y points upwards

Naming Conventions



Energy loss corrections

- The energy loss corrections for the target are calculated for the kinematics reconstruction and the doppler correction. The kinematics reconstruction is done in at the reaction point specified in the REACTION_CONF ([0-1]).
- They are calculated **only if the eloss table is present** under Conf/EnergyLoss with the naming scheme given by the keyword MATERIAL/DEGRADER_MATERIAL under TARGET_CONF (check with - - verb 2).
- They need to be calculated with SRIM, and can be generated with the Script under Scripts/Srim

How to add histograms and personalize
the analysis

The source code

- Conf: parameters that can be read from the selector.conf
- Container: classes that represent the analyzed detector
- Core: things unrelated to the analysis
- Lut: classes that read the lookup tables of various detectors
- Optimizer: fitter class and minimizer for optimization
- Physics: nuclear data class, energy loss and reaction calculator
- Selector: analysis code

Name
..
Conf
Container
Core
DataStructures
Lut
Optimizer
Physics
Selector
Tools
main.cxx
mainMpi.cxx

The source code

- The analysis is contained in src/Selector
- In the newest version, the detector analysis is separated from the coincidence analysis

main ▾ agataselector / src / Selector / + ▾ History Find file Edit ▾ ↓ ▾ Clone ▾

Name	Last commit	Last update
→ CoincidenceAnalysis	Bug fix with beta vs betaBP in gammadetectorPrisma	3 weeks ago
→ DetectorAnalysis	Adds the possibility of saving the doppler correction in the output tree	1 month ago
➤ AgataSelector.cxx	Prisma-dante was missing	1 month ago
h AgataSelector.h	Fixes bug in previous commit	1 month ago
📄 CMakeLists.txt	Starting to move analysis in different classes	1 month ago

Take a look at the code relative to your detector here!

The analyzed data

- The "Analyzed" data is saved in classes that can be accessed in later steps of the analysis.
- These classes are the ones that can be saved in TTrees
- The Doppler correction is also saved for each detector that can provide it
- These classes are the ones that can be saved also in root files
- They are kept in the directory: src/Container/

```
// Container classes
Agata          agataOutput;
Labr           labrOutput;
Prisma        prismaOutput;
Spider        spiderOutput;
Dante         danteOutput;
Euclides      euclidesOutput;

GammaDC       gammaAgataPrisma;
GammaDC       gammaAgataPrismaDante;
std::vector<GammaDC> gammaAgataSpider;
std::vector<GammaDC> gammaAgataDante;
GammaDC       gammaAgataEuclides;
GammaDC       gammaLabrPrisma;
GammaDC       gammaLabrPrismaDante;
std::vector<GammaDC> gammaLabrSpider;
std::vector<GammaDC> gammaLabrDante;
GammaDC       gammaLabrEuclides;
```

Basic steps of the analysis procedure

- Each analysis is associated to a different folder and all have some steps:

At the start

- **Istantiate**->Associates to a detector the correct input
- **AllocateHistos**->Allocates memory for the histograms if they are enabled

Every event

- **Clear** -> Clears the containers of each detector
- **Analyze** ->Fills the container based on the analysis
- **FillHistos** -> Fills the histograms with the data in the containers

At the end

- **Finalize** -> Performs operations on the final histogram

```
public:  
    virtual void Istantiate();  
    virtual bool AllocateHistos();  
    virtual void Clear();  
    virtual void Analyze();  
    virtual bool FillHistos();  
    virtual void Finalize();
```

How to add a histogram

- If you want to add an histogram you have to declare it in the correct analysis class's header
- The histogram are placed in a struct that correspond to the analysis folder
- Sub structs and subfolders are also present

```
main ▾ agataselector / src / Selector / DetectorAnalysis / AgataAnalysis.h
```

```
h AgataAnalysis.h 5.15 KiB
```

```
1 #pragma once
2
3 #include "Agata.h"
4 #include "DetectorAnalysis.h"
5
6 class AgataAnalysis : public DetectorAnalysis {
7     public:
8         explicit AgataAnalysis(Inputs, Agata&);
9         void Istantiate() override;
10        bool AllocateHistos() override;
11        void Analyze() override;
12        bool FillHistos() override;
13        void Finalize() override;
14
15    protected:
16        // Container data
17        Agata& agata;
18
19        // Histograms
20        struct AgataHistograms : public DetectorHistograms {
21            TH1D* h_trackE{nullptr};
```

How to add a histogram

- Use the specific functions that ensure functionalities such as the detection of not enabled histograms:
 - **Allocate the memory with `Initialize<TH*D>(...)`**
 - **Fill with the `Fill(...)` function**

```
11
12 bool AgataAnalysis::AllocateHistos() {
13     AgataHistograms& h = agataHistograms;
14     h.dir = input.outFile.mkdir("Agata", "Agata standalone histograms");
15     h.dir->cd();
16
17     if(!DetectorAnalysis::AllocateHistos()) return false;
18
19     // 1-D histograms
20     Initialize<TH1D>(
21         h.h_trackE,
22         new TH1D("h_trackE",
23                 Form("gamma tracked;Energy [keV];Counts/%d keV",
24                     conf.agata.binWidth),
25                 static_cast<int>(conf.agata.gammaEmax / UNITS::keV
26                                 / conf.agata.binWidth),
27                 0, conf.agata.gammaEmax / UNITS::keV),
```

```
735
736 bool AgataAnalysis::FillHistos() {
737     if(!DetectorAnalysis::FillHistos()) return false;
738
739     for(int i{0}; i < **agataReader.nbTrack; ++i) {
740         Fill(h.h_trackE, agataReader.trackE->At(i));
741         if(i != lowestTrackIdx)
```

The Conf folder

- Contains the parameters used by the selector
- In case the selector performs the prisma analys, additional folders are present

📄 README.md

Contents

Folder	Content description
CUT	Cuts (TGraphs) needed for the analysis. Each detector has its own folder.
EnergyLoss	Energy loss tables generated in SRIM
LUT	Lookup table configuration files for various experiments
NuclearData	Nuclear masses files
Optimizer	Files to perform the optimization

About configuration files

The default configuration file can be generated with

```
./RunSelector --print_conf my_conf.conf
```

Please note that old configuration files are no longer compatible with the updated version of the selector.

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
- Histograms can be added to the struct in the header

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

private:
    // USER variable and histogram definition section

    // unsigned long long timeRef = 0;

    TH1D *h_agataCR = nullptr;
}
```



The UserSelector

- Memory is allocated in the SlaveBegin
- Histograms are filled in the Process function
- You will find the result in the user folder!

```
void UserSelector::SlaveBegin(TTree* treeToRead) {
    AgataSelector::SlaveBegin(treeToRead);

    // User selector initialisation - done just once per file

    // std::cout << "Example value retrieved from conf file: "<<
    // conf.user.example/UNITS:mm << " mm" << std::endl;

    outFile.mkdir("User","User's custom analysis");
    outFile.cd("User");

    UserHistograms& hu = userHistograms;
    hu.h_agataCR = new TH1D("h_agataCR","Count Rate per minute of"
        "AGATA;Time[min];Counts per min",10080,0,10080);
}

Bool_t UserSelector::Process(Long64_t entry) {
    AgataSelector::Process(entry);

    UserHistograms& hu = userHistograms;

    if(!agataOutput.E.empty())
        hu.h_agataCR->Fill(agataOutput.TS);

    return kTRUE;
}
```


The UserConf

```
C++ UserConf.cxx 229 B
1 #include "UserConf.h"
2
3 UserConf::UserConf() : Conf("USER_CONF") {
4     parD.emplace("EXAMPLE",
5                 Conf::Property<double>{example, "mm",
6                                         "Example of configuration value"});
7 }
8
```

- It adds the possibility of reading custom parameters from the selector.conf
- You can declare a parameter in the .h and read it in the .cxx
- In this case the parameter to read is a double (parD), other types are also present such as strings (parS)
- Checkout src/Conf/Conf.h for other types

```
h UserConf.h 126 B
1 #pragma once
2
3 #include "Conf.h"
4
5 class UserConf : public Conf {
6     public:
7         UserConf();
8
9     public:
10         double example{0};
11 };
```

Your Experiment's configuration

- You will find your experiment's configuration under `agataselector/User/EXP/EXP_***`
- Link this directory in your analysis
- Recall the experiment specific code with:

```
cmake -DEXP_NAME=EXP_*** .
```

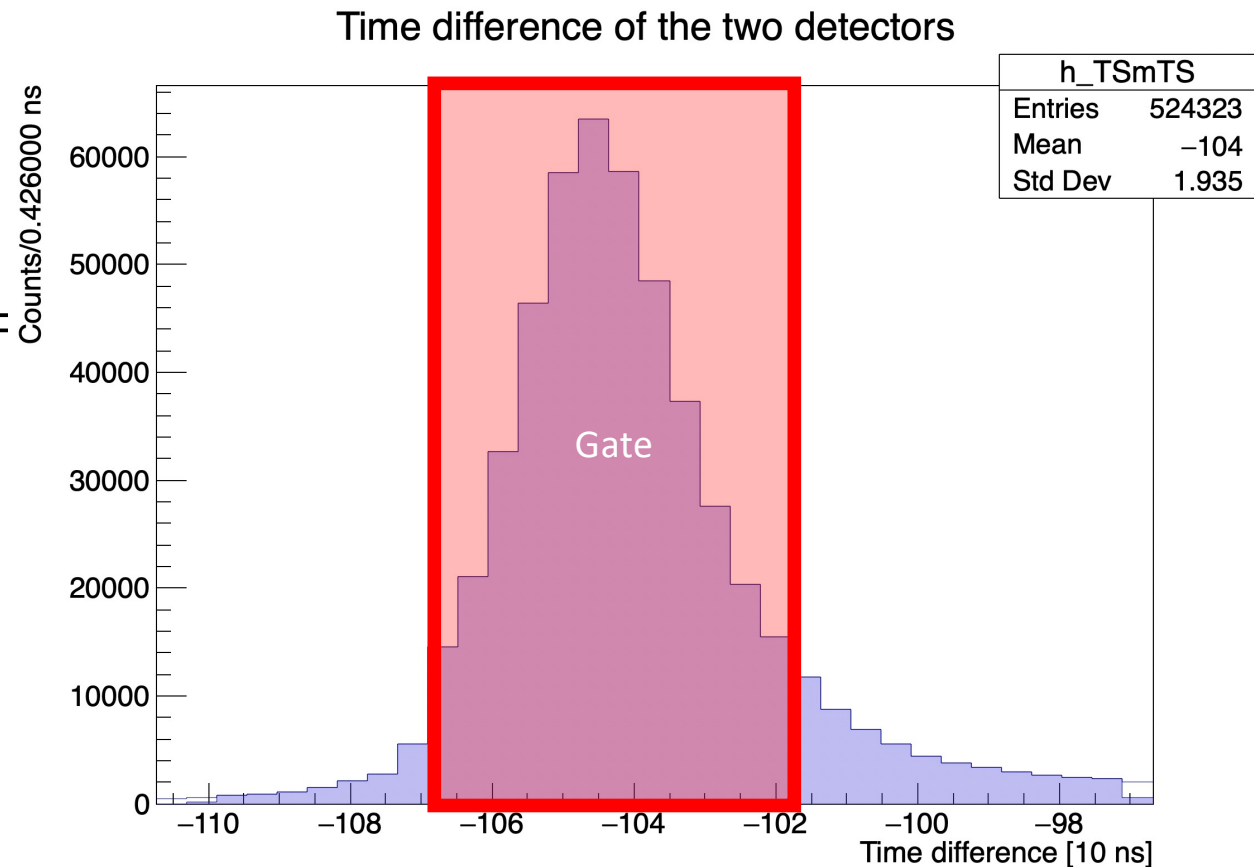
main ▾ agataselector / User / EX

Updated paths in `--set_gates, chan`
Filippo Angelini authored 2 days ago

Name	Name
..	..
COM_001	Conf
COM_002	CMakeLists.txt
COM_003	C++ UserConf.cxx
EXP_001	h UserConf.h
EXP_002	C++ UserSelector.cxx
EXP_003	h UserSelector.h
EXP_004	
EXP_005	

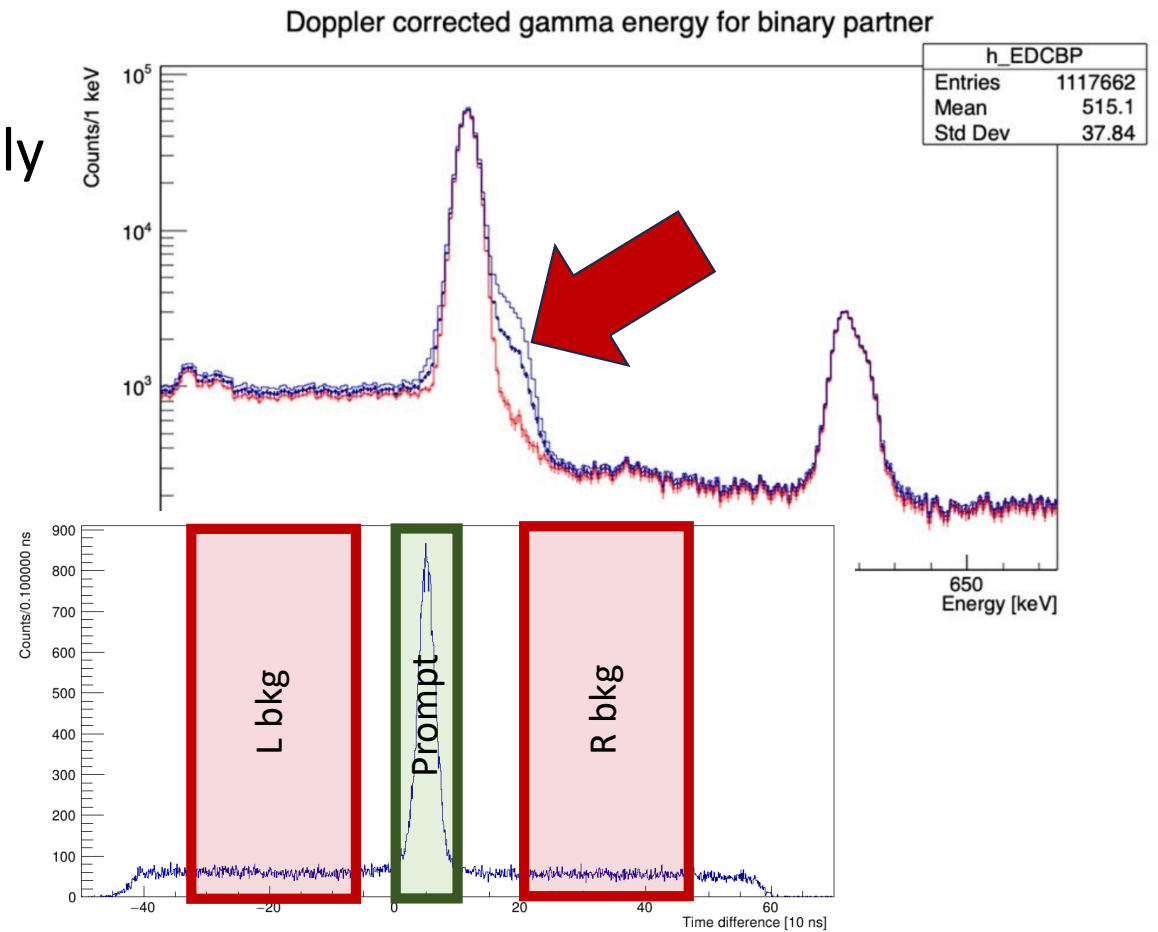
Time coincidences

- All ancillary detectors need to be time-gated
- All coincidences will have a time difference histogram that is used to select the gate in the `***_CONF`
- Some detectors such as Euclides, Agata have an internal time gate
- All time gates are set with the parameter:
 - `COINC_W_LEFT`
 - `COINC_W_RIGHT`



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



Background subtraction: details

- Each coincidence and detector has three time gates:

```
#-----  
AGATASPIDER_CONF  
COINC_W_RIGHT_RIGHT_BKG      0      #      Right Background time window on the right side of the coincidence peak  
COINC_W_LEFT_RIGHT_BKG       0      #      Left Background time window on the right side of the coincidence peak  
COINC_W_RIGHT_LEFT_BKG       0      #      Right Background time window on the left side of the coincidence peak  
COINC_W_LEFT_LEFT_BKG        0      #      Left Background time window on the left side of the coincidence peak  
COINC_W_LEFT                  -6     #      Time window left  
COINC_W_RIGHT                  4     #      Time window right
```

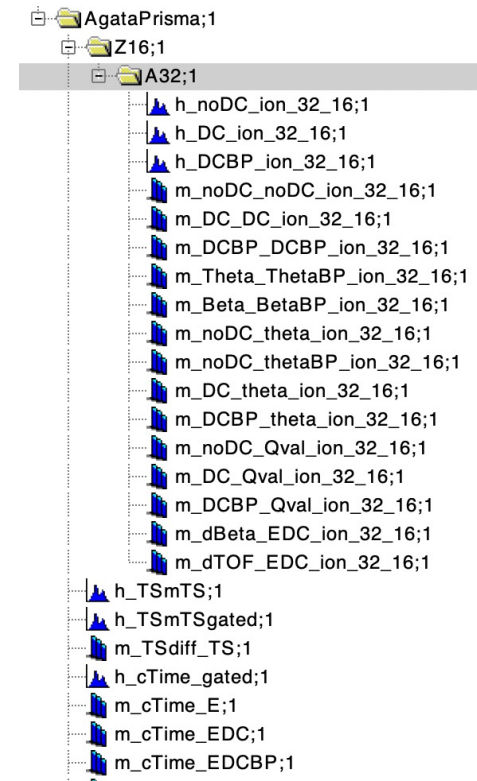
- The selector with the option - - subtract_bkg will run three times one for the left background, one for the right background and once for the prompt peak
- It will then rescale the background based on the time interval and add the total with a negative sign
- Note that if you want to subtract the random AGATA-SPIDER coincidences, the left and right background should be set only in the AGATASPIDER_CONF. In the other time gates, such as the one in AGATA, the interval of left and right background should be the same as the prompt

Detector specific analysis

Agata-Prisma analysis

See Filippo's presentation

- The analysis of PRISMA is handled by the prisma library or the selector
- The selector produces most of the histograms necessary for the analysis also for the prisma library
- It then handles the coincidences
- Ion-gated histograms can be found in the Z##/A## folder.
- Important histograms include:
 - The DC(BP)_Qval which allows to gate on the total excitation energy of the system
 - The DC(BP,noDC)_Theta(BP) that allows to check the Doppler correction as a function of the angles
 - The various gamma-gamma matrices

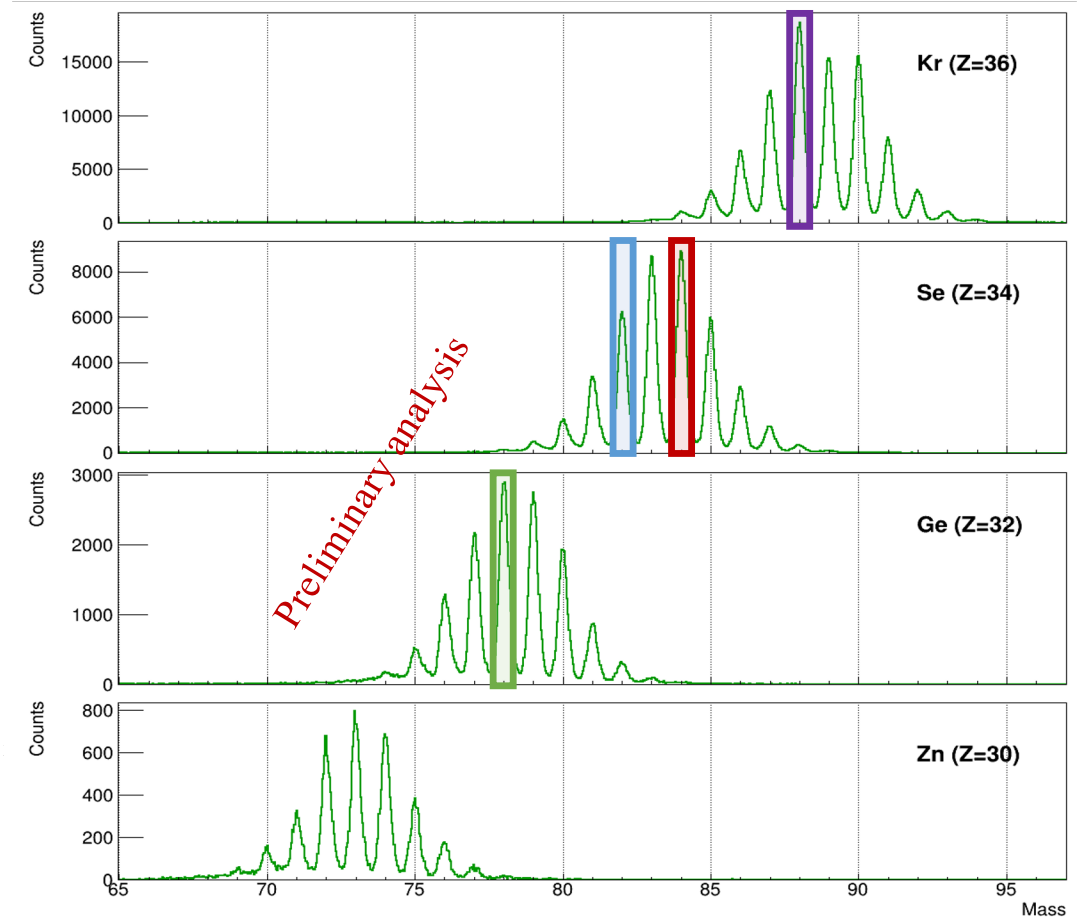
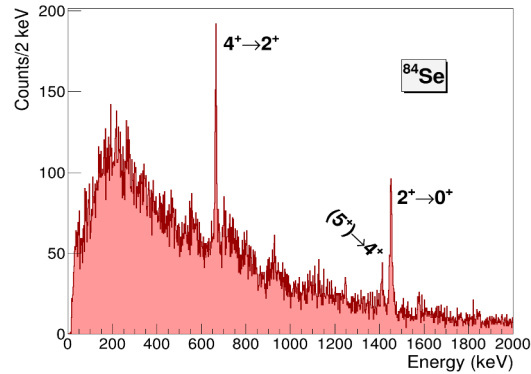
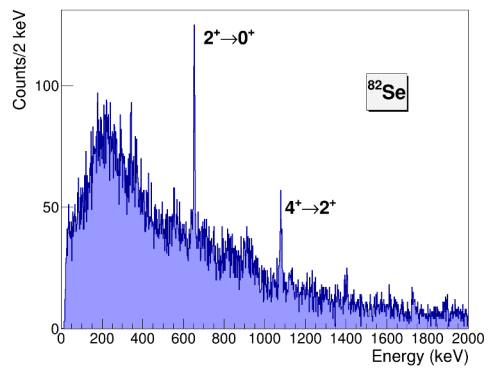
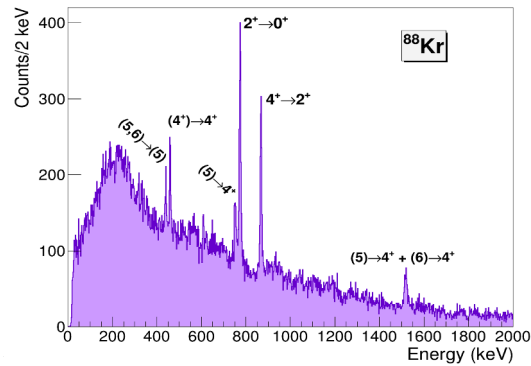
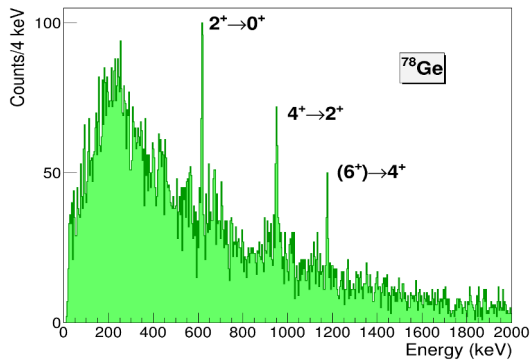


Prisma

- Broken IC or PPAC channels can be disabled
- The TOF offset can be set in the selector to optimize the Doppler correction without disrupting the identification
- One can require or discard some parameters such as TOF_OK, IC_OK to perform the analysis
- Cuts in Z can be placed in Conf/CUT/Prisma/IC/ to produce histograms in coincidence
- In AGATAPRISMA_CONF it is possible to set EX_VALUES to gate on specific values of TKEL and generate additional histograms

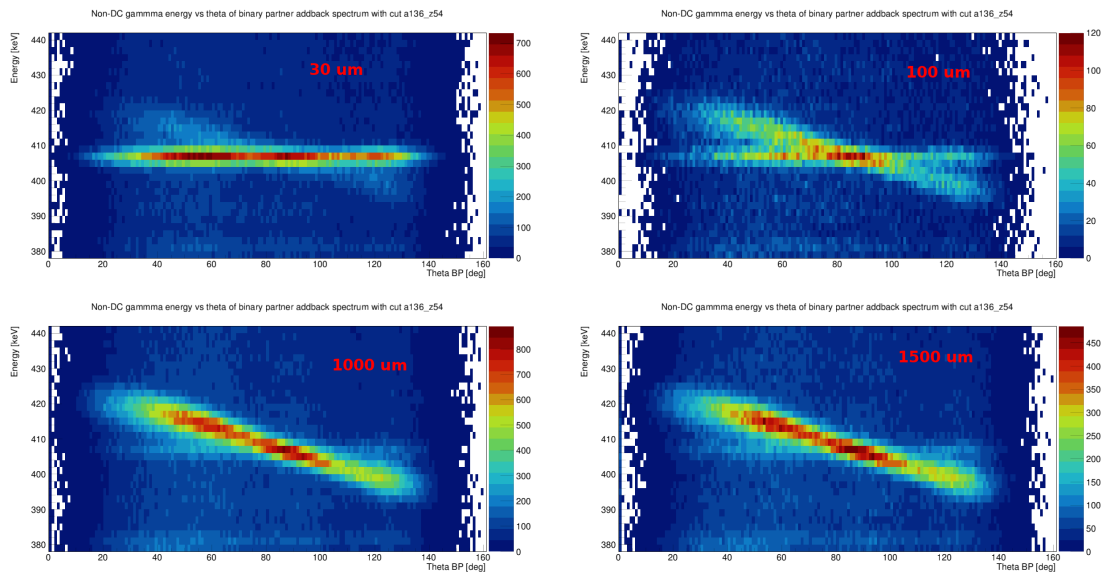
Prisma: some examples

- Example of identification



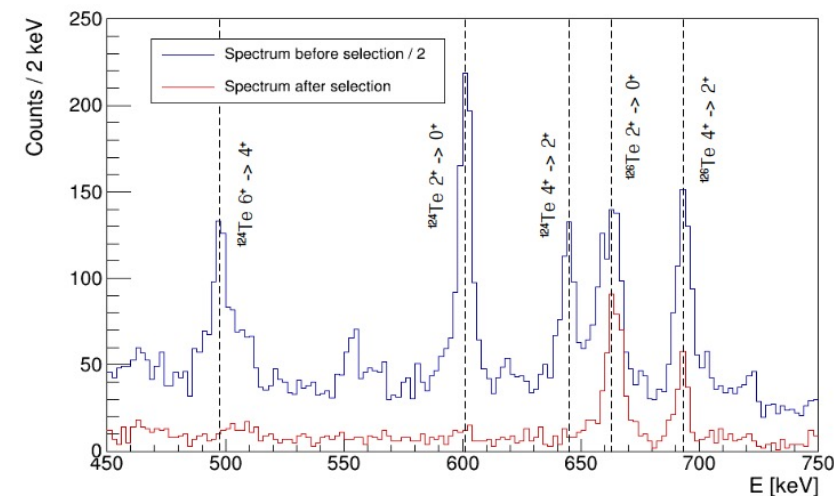
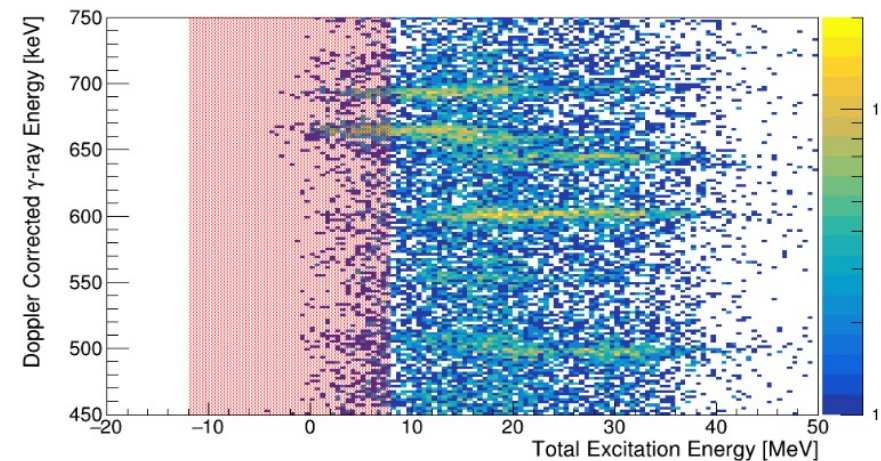
Prisma example

- Prisma provides the possibility of a fine kinematics reconstruction
- The Q-value matrices are often a very powerful tool
- The angle reconstruction is also great



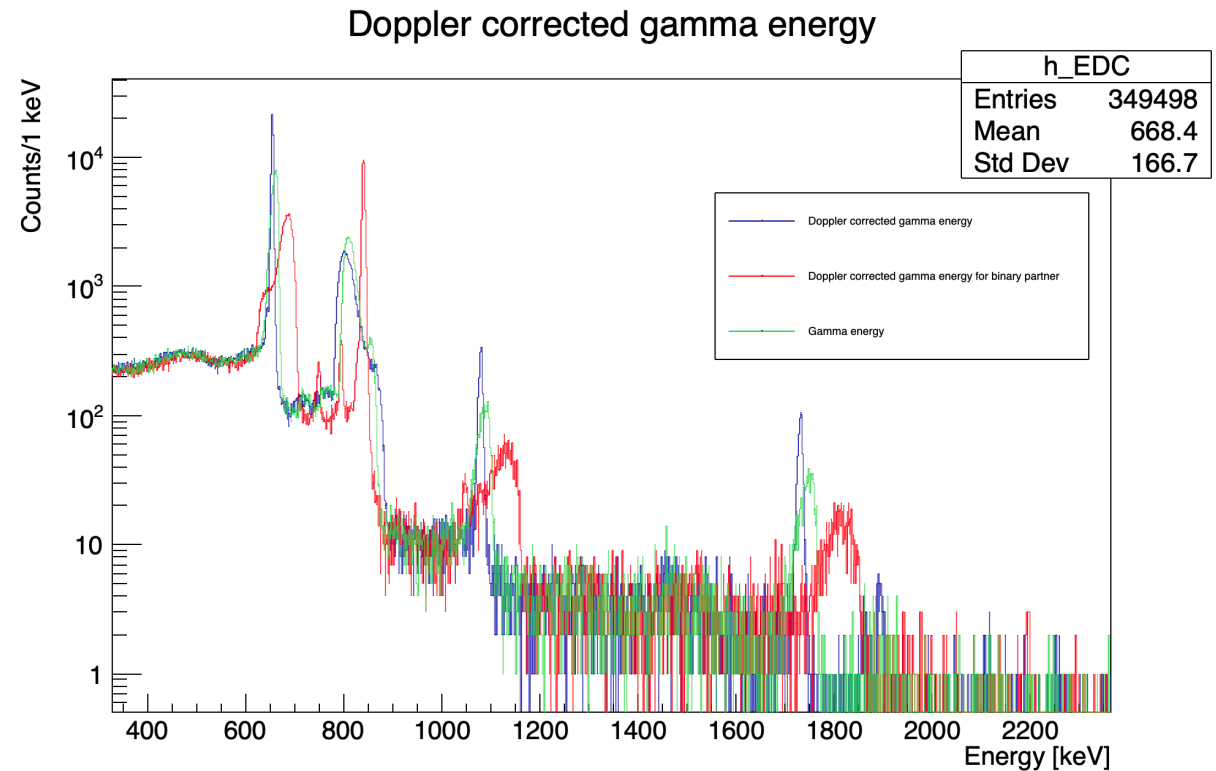
See Filippo's presentation

E. Pilotto Master Thesis



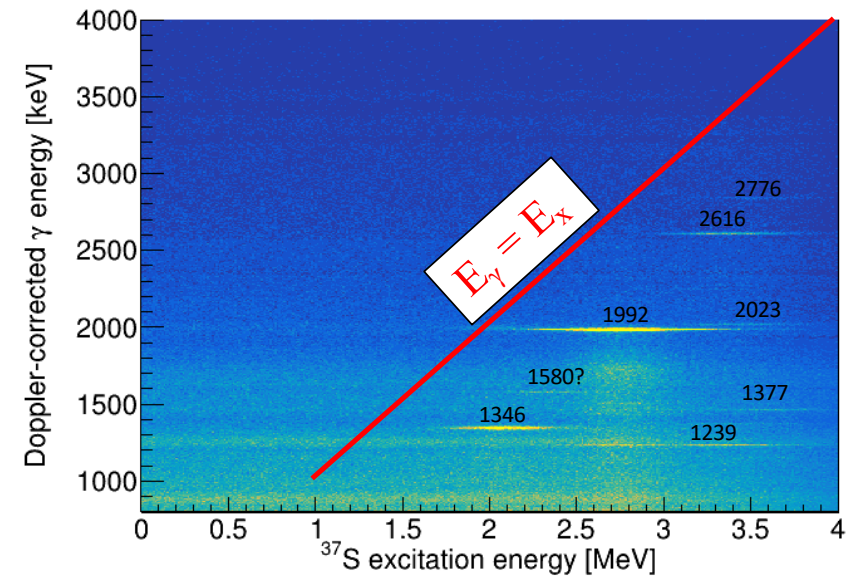
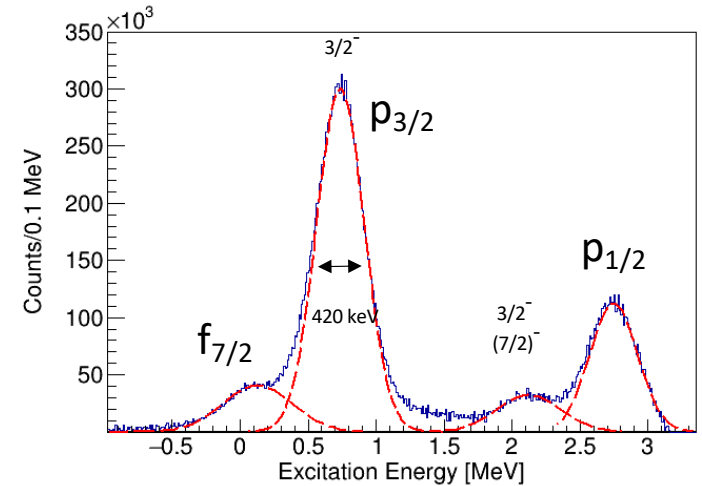
Spider

- Spider uses the measured energy and angles to reconstruct the reaction kinematics
- You can set the assumed detected ion with the ION keyword
- The basic output are doppler corrected spectra for the various ions



Spider

- Since we reconstruct the kinematics, we also calculate the excitation energy
- This can be useful, depending on the reaction
- Also for Coulomb excitation it can be helpful to remove contaminants from fusion evaporation from contaminants in the target



Spider

- Detector dependent parameters:
 - Theta
 - Phi
- Channel names are not important but are helpful for the user
- Global rotation and shifts are set in the selector.conf and can be optimized (more on that later)

LUT_SPIDER.dat 4.93 KiB

```
1 ##### SPIDER #####
2 #
3 # the "map" number conversion into detector and strip:
4 # strip = (map % 10) + 1
5 # detector = (map / 10) + 1
6 #
7 # Board  channel  map  name  thr_lo  thr_hi  theta  phi  TimeOffset  ncalpar  calpars
8 1  0  1  D2S2  0.2    100    155.2  103.99  0  2  -0.725279350  0.009017265
9 1  1  0  D2S1  0.2    100    159.6  103.99  0  2  -0.737257684  0.008884174
10 1  2  3  D2S4  0.2    100    146.0  103.99  0  2  -0.720283915  0.009107212
11 1  3  2  D2S3  0.2    100    150.6  103.99  0  2  -0.731441192  0.008929393
12 1  4  5  D2S6  0.2    100    136.8  103.99  0  2  -0.782888331  0.009167317
13 1  5  4  D2S5  0.2    100    141.4  103.99  0  2  -0.711211883  0.008914951
14 1  6  7  D2S8  0.2    100    128.0  103.99  0  2  0.439492218  0.008844957
15 1  7  6  D2S7  0.2    100    132.3  103.99  0  2  -0.774363174  0.008928424
16 1  8  11  D1S2  0.2    100    155.2  52.56  0  2  -0.755972829  0.008866296
17 1  9  10  D1S1  0.2    100    159.6  52.56  0  2  -0.758290619  0.009060886
18 1  10  13  D1S4  0.2    100    146.0  52.56  0  2  -0.796959980  0.009098155
19 1  11  12  D1S3  0.2    100    150.6  52.56  0  2  -0.789661853  0.009081235
20 1  12  15  D1S6  0.2    100    136.8  52.56  0  2  -0.913507112  0.009238220
21 1  13  14  D1S5  0.2    100    141.4  52.56  0  2  -0.812225239  0.009063498
```

Things you care about: the calibration parameters

Spider

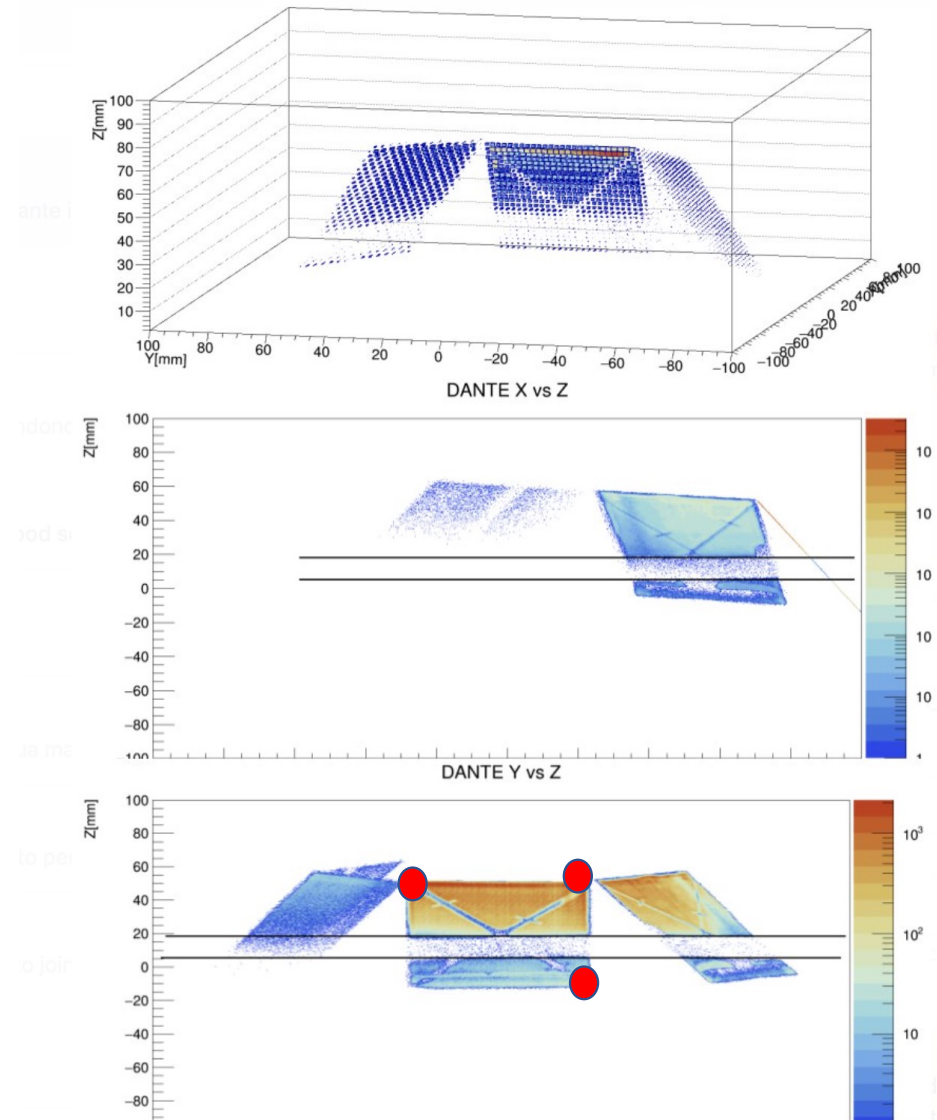
- The EX_VALUES keyword allows to generate histograms gated on a specific excitation energy value
- Additionally, it is possible to gate on a gamma-ray to generate additional histograms in coincidence with it such as additional gamma-gamma matrices with the keyword GAMMA_GATE of AGATASPIDER_CONF
- Kinematic line TCuts can be placed in the Conf/CUT/SPIDER/ThetaLabELab folder
- To extract the optimal results it is possible to tune theta and phi of each spider channel to optimize the Doppler correction. This feature is under construction and testing and can be compiled running cmake with the option – DSPIDER_ANGCAL=On (for more info contact Matus)
- Another option is to use a specific user selector called LUT_OPTIMIZER, refer to the readme for more information: https://baltig.infn.it/gamma/agataselector/-/tree/main/User/EXP/LUT_OPTIMIZER?ref_type=heads

Dante

- In general, a “perfect” Dante event should contain at least 3 events, corresponding to x, y (TACS) and T (cfid logic signal)
- Additionally, a TAC can be placed between Dante and Prisma, this is also handled by the analysis
- This does not happen all the time and the selector should handle this, some options are present in the selector.conf file
- The spatial calibration is performed by selecting the (x,y) points of the extremities of the
- The analysis should be expanded and improved for Dante




DANTE

- DANTE can be used as a standalone detector (for DANTE-DANTE coincidences) or combined with PRISMA
- The selector handles both cases
- It is possible to set gates in Conf/Cuts/PrismaDante/TOF_TKEL
- In this case of the triple coincidence AGATA-PRISMA-DANTE it is necessary to set two time gates: agata-prisma and agata-dante

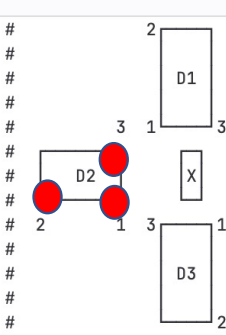


Dante Lookup table

main ▾ agataselector / User / EXP / Template / Conf / LUT / LUT_DANTE_3det_0deg.dat Find file Blame History Permalink

LUT_DANTE_3det_0deg.dat 2.75 KiB Edit ▾   

#	#		X	Y	Z							
1	#	2										
2	#	D1	D1P1	72.8361	25.3272	23.7575						
3	#		D1P2	41.2708	77.7189	-11.2993						
4	#		D1P3	35.3073	25.3272	57.5486						
5	#	3										
6	#	1	D2	D2P1	72.8935	-25.2499	23.7059					
7	#	X	D2P2	80.2628	-25.2499	-46.4078						
8	#		D2P3	72.8935	25.2500	23.7059						
9	#	2										
10	#	3										
11	#	1	D3	D3P1	35.3073	-25.3272	57.5486					
12	#		D3P2	3.7420	-77.7189	22.4917						
13	#		D3P3	72.8361	-25.3272	23.7575						
14	#	2										
15	#Board	channel	name	thr_lo	thr_hi	P1(x,y,z)	P2(x,y,z)	P3(x,y,z)	pos1	pos2	po3	Time Offset
16	1	0	D1X	4726	6700	72.8361	41.2708	35.3073	6700	4726	6700	0
17	1	1	D1Y	3110	4535	25.3272	77.7189	25.3272	3110	3110	4535	0
18	1	2	D1T	0	2000	23.7575	-11.2993	57.5486	0	0	0	0
19	#											
20	1	4	D2X	4060	5990	72.8935	80.2628	72.8935	5990	4060	5990	0
21	1	5	D2Y	3850	5570	-25.2499	-25.2499	25.2500	3850	3850	5570	0
22	1	6	D2T	0	2000	23.7059	-46.4078	23.7059	0	0	0	0
23	#											
24	1	8	D3X	4381	6597	35.3073	3.7420	72.8361	6597	4381	6597	0
25	1	9	D3Y	3605	5625	-25.3272	-77.7189	-25.3272	3605	3605	5625	0
26	1	10	D3T	0	2000	57.5486	22.4917	23.7575	0	0	0	0
27	#											
28	1	12	D4X	10000	5000	36.0146	-24.5866	59.1902	5000	2200	5000	0
29	1	13	D4Y	10000	3500	-27.7491	-60.1032	-52.9991	2100	2100	3500	0
30	1	14	D4T	0	2000	56.3766	40.5354	19.2878	0	0	0	0



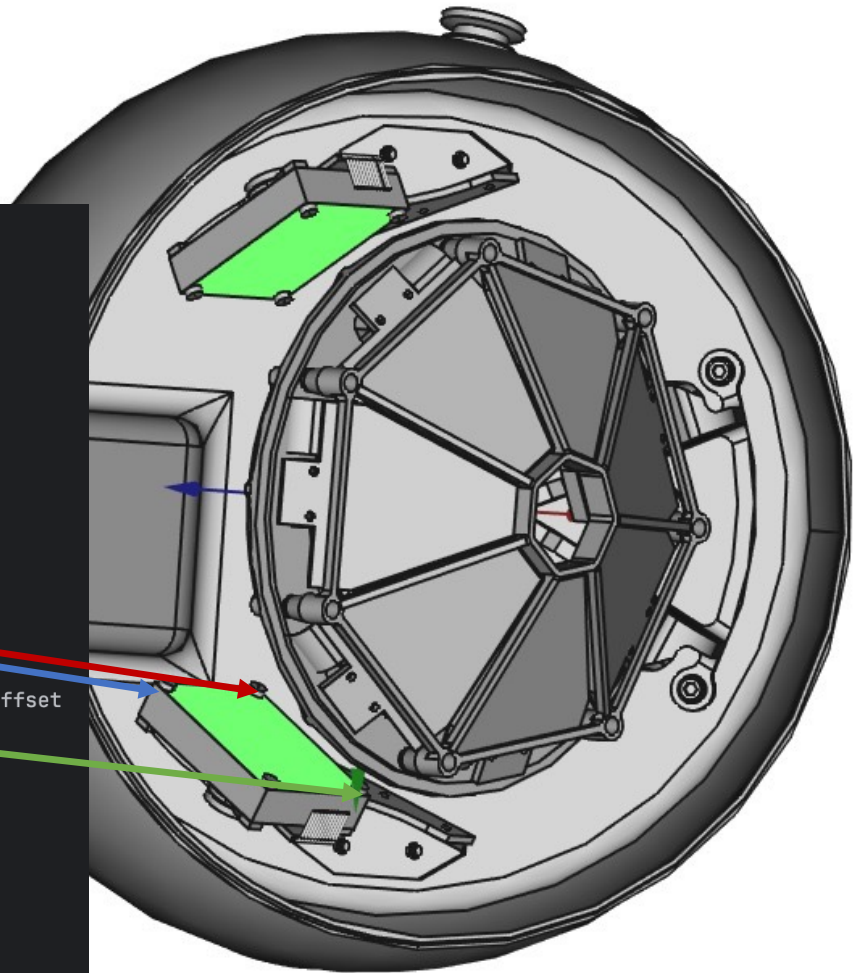
- Detector dependent parameters:
 - P1, P2, P3
 - pos1, pos2, pos3
- Channel names distinguish X, Y, T and TOF

The lookup table also performs the 3D position reconstruction of DANTE, mapping 2D points (pos1, pos2, pos2) to 3D points (P1, P2, P3)

DANTE

- The positions of the points of reference are extracted from the CAD, you should probably not change this points

```
#
#
# 2
#  D1
#  1 3
#  X
#
# 3
#  D0
#
#
#Board channel name thr_lo thr_hi P1(x,y,z) P2(x,y,z) P3(x,y,z) pos1 pos2 po3 Time Offset
5 4 D1X 5000 30000 23.331110 22.363780 -20.662189 29013 7516 29328 0
5 5 D1Y 5000 30000 68.437477 100.43748 68.437477 5396 5396 27773 0
5 6 D1T 0 65000 76.067215 20.650030 76.835121 0 0 0 0
#
5 0 D0X 5000 30000 -20.662189 -21.629499 23.331110 27290 4472 27023 0
5 1 D0Y 5000 30000 -68.437477 -100.43748 -68.437477 29396 29396 5410 0
5 2 D0T 0 65000 76.835121 21.417936 76.067215 0 0 0 0
#
5 8 D1TOFDANTE 0 16000 -127 0.01714 0 0 0 0 0 0
```

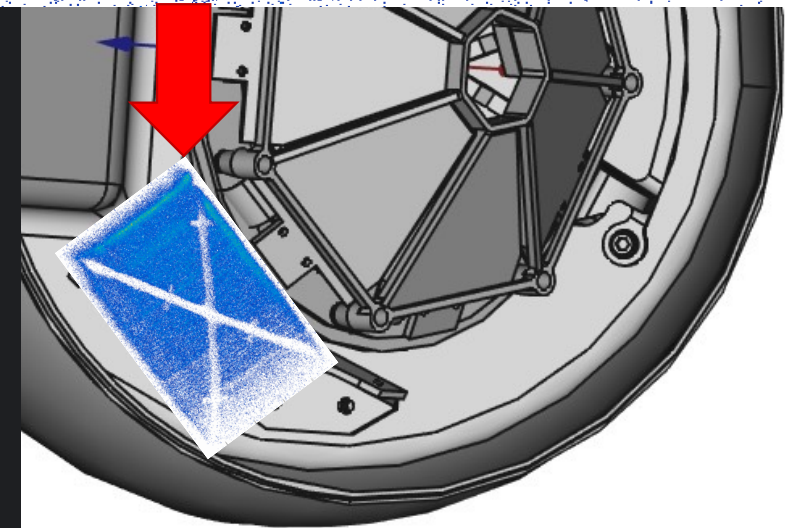


DANTE

- The thresholds are set to remove the retrigger and consider only positions that do make sense



```
#
#      2
#      ┌───┐
#      │ D1 │
#      └───┘
#      1   3
#
#      ┌───┐
#      │ X  │
#      └───┘
#
#      3   1
#      ┌───┐
#      │ D0 │
#      └───┘
#      2
#
#Board channel name thr_lo thr_hi P1(x,y,z) P2(x,y,z) P3(x,y,z) pos1 pos2 po3 Time Offset
5      4      D1X  5000  30000  23.331110  22.363780  -20.662189  29013  7518  29328  0
5      5      D1Y  5000  30000  68.437477  100.43748  68.437477  5396  5396  27773  0
5      6      D1T   0    65000  76.067215  20.650030  76.835121  0     0     0     0
#
5      0      D0X  5000  30000  -20.662189 -21.629499  23.331110  27290  4472  27023  0
5      1      D0Y  5000  30000  -68.437477 -100.43748 -68.437477  29396  29396  5410  0
5      2      D0T   0    65000  76.835121  21.417936  76.067215  0     0     0     0
#
5      8      D1TOFDANTE 0    16000  -127    0.01714  0     0     0     0     0
```

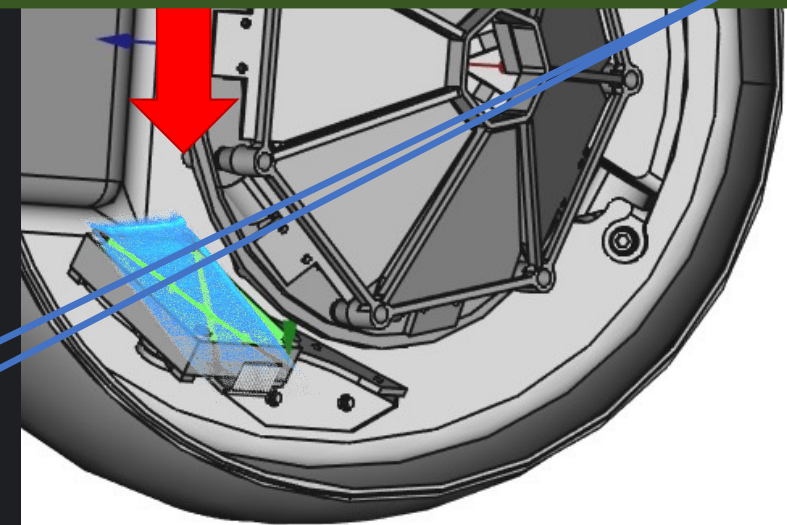


DANTE

- The thresholds are set to remove the retrigger and consider only positions that do make sense

```

#          2
#          ┌───┐
#          │ D1 │
#          └───┘
#          1   3
#
#          ┌───┐
#          │ X  │
#          └───┘
#
#          3   1
#          ┌───┐
#          │ D0 │
#          └───┘
#          2
#
#Board channel name thr_lo thr_hi P1(x,y,z) P2(x,y,z) P3(x,y,z) pos1 pos2 po3 Time Offset
5      4      D1X  5000  30000  23.331110  22.363780  -20.662189  29013  7518  29328  0
5      5      D1Y  5000  30000  68.437477  100.43748  68.437477  5396  5396  27773  0
5      6      D1T   0    65000  76.067215  20.650030  76.835121  0     0     0     0
#
5      0      D0X  5000  30000  -20.662189  -21.629499  23.331110  27290  4472  27023  0
5      1      D0Y  5000  30000  -68.437477  -100.43748  -68.437477  29396  29396  5410  0
5      2      D0T   0    65000  76.835121  21.417936  76.067215  0     0     0     0
#
5      8      D1TOFDANTE 0    16000  -127    0.01714  0     0     0     0     0
  
```

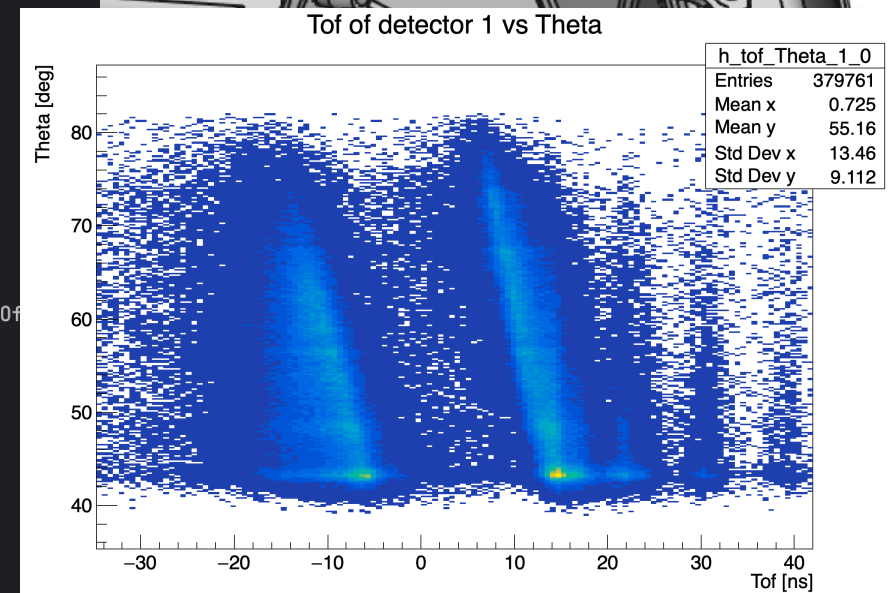
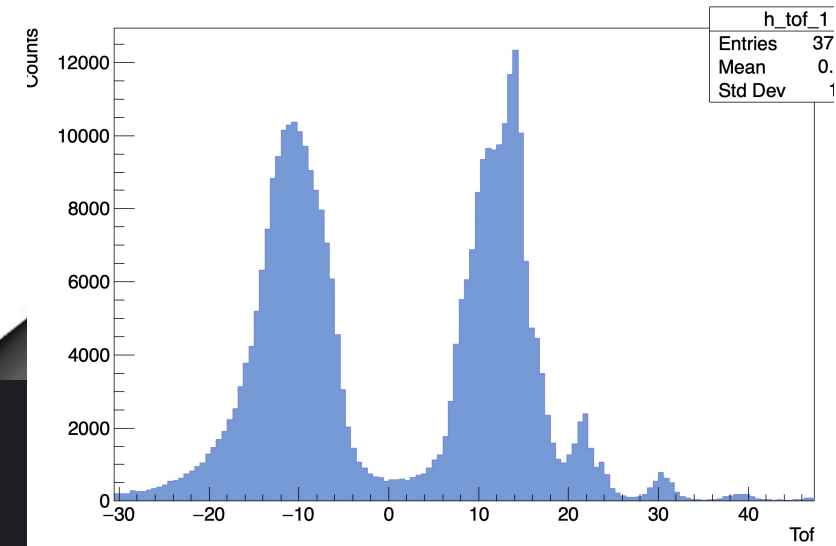


DANTE

- The TOF between two symmetric DANTEs should be centered in 0 and calibrated to the right scale based on simulations

```

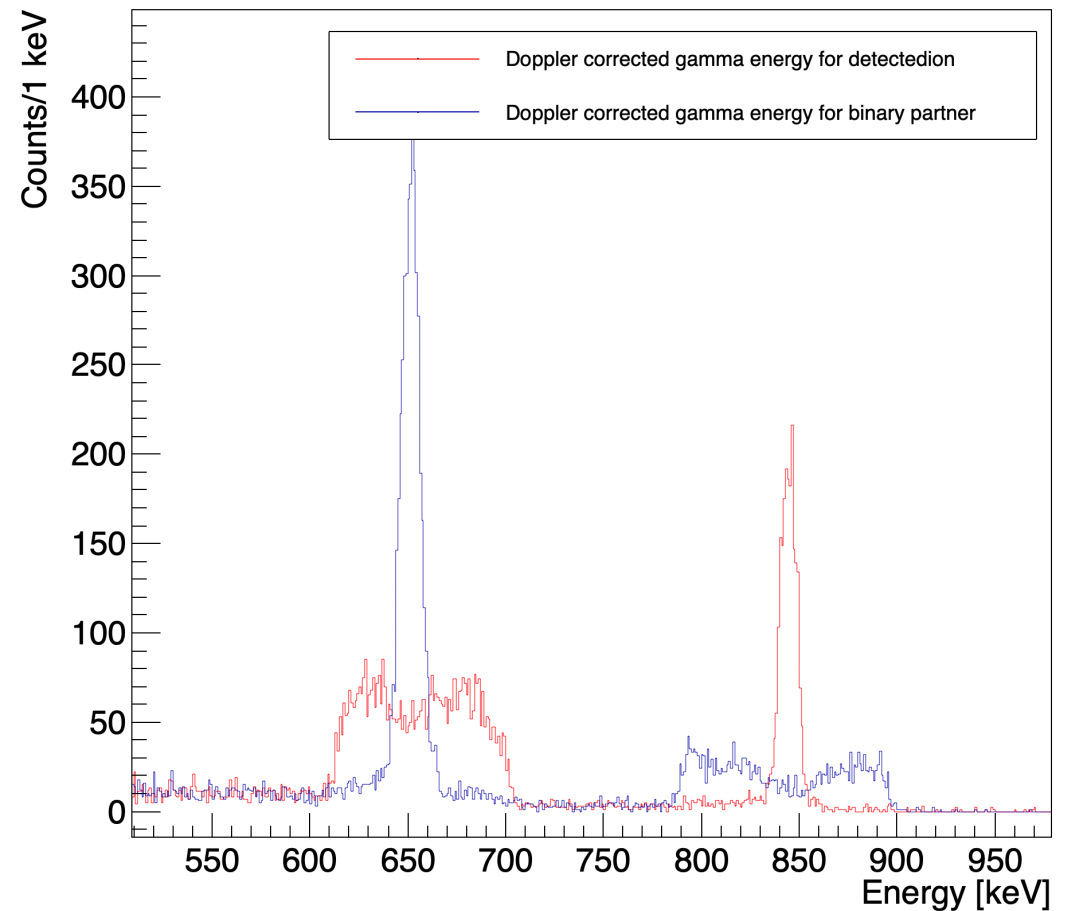
#          2
#          ┌───┐
#          │ D1 │
#          └───┘
#          1   3
#
#          ┌───┐
#          │ X  │
#          └───┘
#
#          3   1
#          ┌───┐
#          │ D0 │
#          └───┘
#          2
#
#Board  channel  name  thr_lo  thr_hi  P1(x,y,z)  P2(x,y,z)  P3(x,y,z)  pos1  pos2  po3  Time Of
5       4       D1X    5000   30000   23.331110  22.363780  -20.662189  29013  7518  29328  0
5       5       D1Y    5000   30000   68.437477  100.43748  68.437477  5396  5396  27773  0
5       6       D1T     0      65000   76.067215  20.650030  76.835121  0      0      0      0
#
5       0       D0X    5000   30000   -20.662189 -21.629499  23.331110  27290  4472  27023  0
5       1       D0Y    5000   30000   -68.437477 -100.43748 -68.437477  29396  29396  5410  0
5       2       D0T     0      65000   76.835121  21.417936  76.067215  0      0      0      0
#
5       8       D1TOFDANTE  0      16000   -127    0.01714  0      0      0      0      0
  
```



DANTE Gates

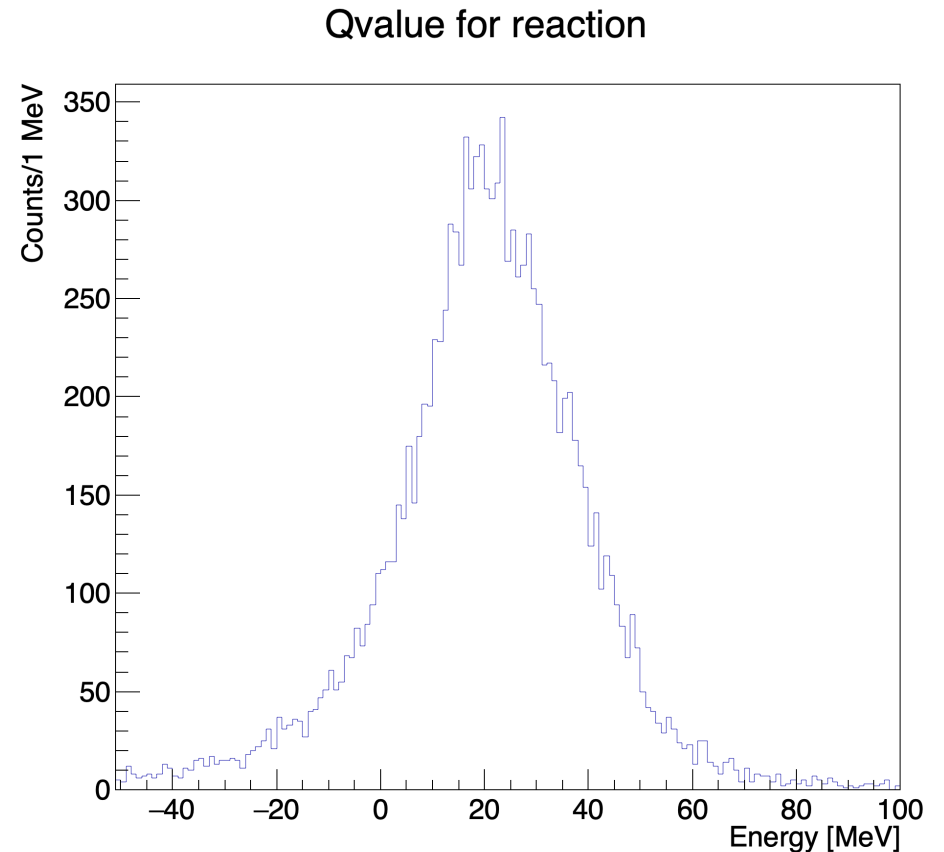
- For DANTE-DANTE coincidences you can set a gate on the TOF vs Theta matrix. In this case you can use the `-- set_gates` option to set them interactively
- For DANTE-PRISMA coincidences, you can set the gates in the `Conf/Cuts/PrismaDante/TOF_TK` EL folder, but it will soon be standardized with the `-- set_gates` option

Doppler corrected gamma energy for detectedion



DANTE Gates

- For DANTE-DANTE coincidences you can set a gate on the TOF vs Theta matrix. In this case you can use the `-- set_gates` option to set them interactively
- For DANTE-PRISMA coincidences, you can set the gates in the `Conf/Cuts/PrismaDante/TOF_TK` EL folder, but it will soon be standardized with the `-- set_gates` option



LaBr

- They share the same base class of Agata: GammaDetector
- As a consequence, the analysis of coincidences with Agata is exactly the same, so you can perform the same analysis as for Agata.
- In some cases, they were acquired without external trigger, meaning that they will have a lot of data. In this case you can use the --labr_slave option of ReadCaenRaw and/or the mandatoryKey of femul to process their data only if it is in coincidence with other ancillaries in the first case or femul in the second.
- In the case of experiments with Prisma, we discovered that they are strongly affected by the magnetic field despite the shielding so they require a calibration when the magnet was on

Labr

- Detector dependent parameters:

- Theta
- Phi

main ▾ agataselector / User / EXP / Template / Conf / LUT / LUT_LABR.dat Find file Blame History Permalink

LUT_LABR.dat 1.16 KIB Edit ▾


	#LaBr	Co+Cs				thr_lo	thr_hi	theta	phi	TimeOffset	npar_gl	p0_qL	p1_q2	npar_qs	p0_qs	p1_qs
1																
2	#board	(V1730)	channel	map	name											
3	1	0	0	D0	0	16000	90.422684	124.92098	0	2	0.37834748	0.38837488	2	10.01488	0.384881	
4	1	1	1	D1	0	16000	84.308418	97.489398	0	2	4.994643769	0.441859949	2	0.570262	0.443247	
5	1	2	2	D2	0	16000	90.572804	73.768608	0	2	-4.882700373	0.4567364497	2	9.782321	0.473778	
6	1	3	3	D3	0	16000	99.968116	51.748253	0	2	-2.68135951	0.4616749283	2	9.040133	0.473527	
7	1	4	4	D4	0	16000	93.353077	26.901224	0	2	-3.368474921	0.4774816369	2	.609657	0.481297	
8	1	9	9	D5	0	16000	94.007297	1.3778600	0	2	0	1	2	2	1	
9	1	5	5	D6	0	16000	99.883486	-28.723198	0	2	10.52197059	0.4435828877	2	8.918459	0.444711	
10	1	6	6	D7	0	16000	86.180070	-45.908423	0	2	12.53667474	0.4240481389	2	8.411274	0.421525	
11	1	7	7	D8	0	16000	91.699165	-66.505287	0	2	16.78408614	0.3897415818	2	5.049303	0.387539	
12	1	8	8	D9	0	16000	85.591641	-95.344627	0	2	-12.39452343	0.4289130669	2	8.673472	0.452371	
13	#####															
14	1	15	15	monitor	0	16000	0		0	0	2	0	1	2	0	1
15																
16																

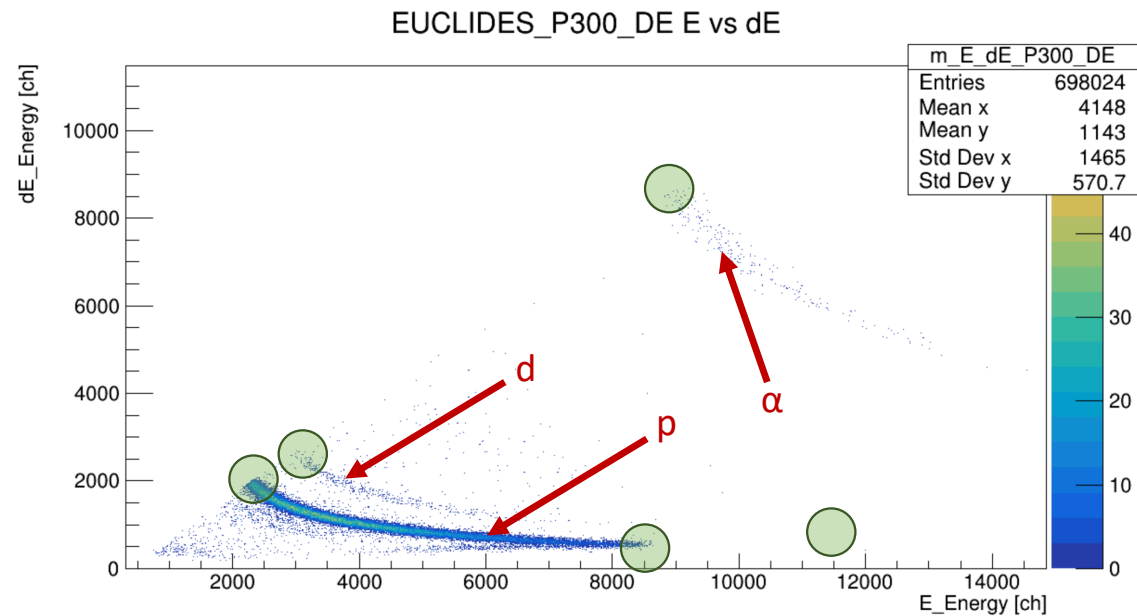
- The calibration coefficients are needed for the short and long integration
- Another parameter that can be tuned is the timestamp offset
- Be careful with PRISMA: the source data might/will have different gains with respect to the data due to the magnets

Things you care about: the calibration parameters

Other ancillaries

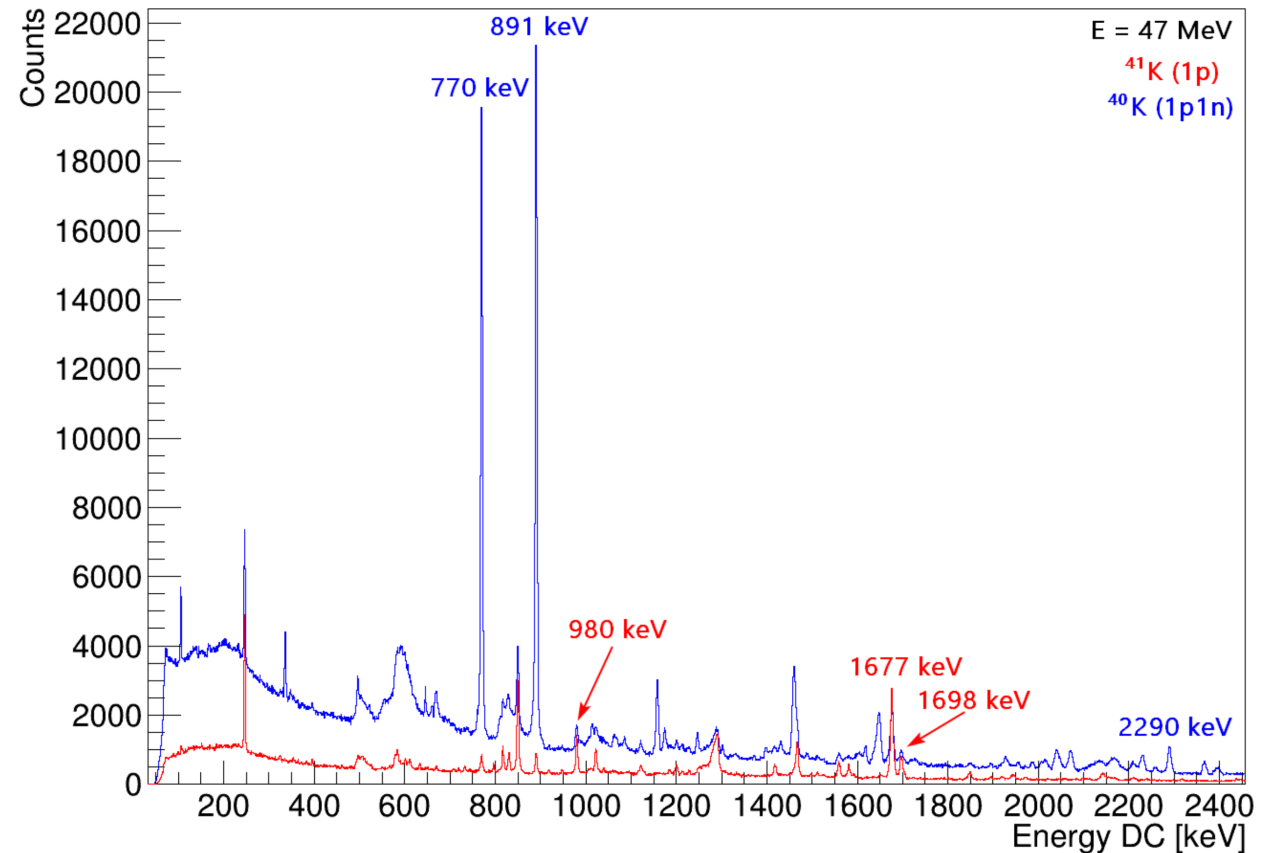
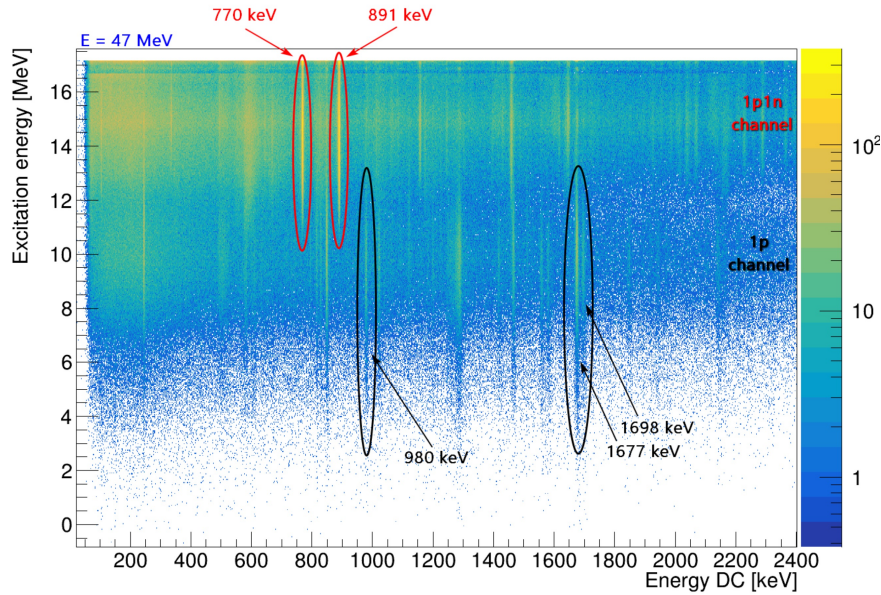
Euclides

- Set gates for all telescopes in `Conf/CUT/EUCLIDES/EdE/`
- The naming scheme to adopt should be `z1_m1_mapnr` for while for alphas it should be `z2_m2_mapnr`
- Check the time alignment
- Calibrate with alpha run or with punch trough points 
- In this case the reaction of interest could be a Nbody reaction. In this case the ions of interest need to be specified with:
`IONS A1 Z1 A2 Z2 A3 Z3 END Comment`



Mirco Del Fabbro PhD Thesis

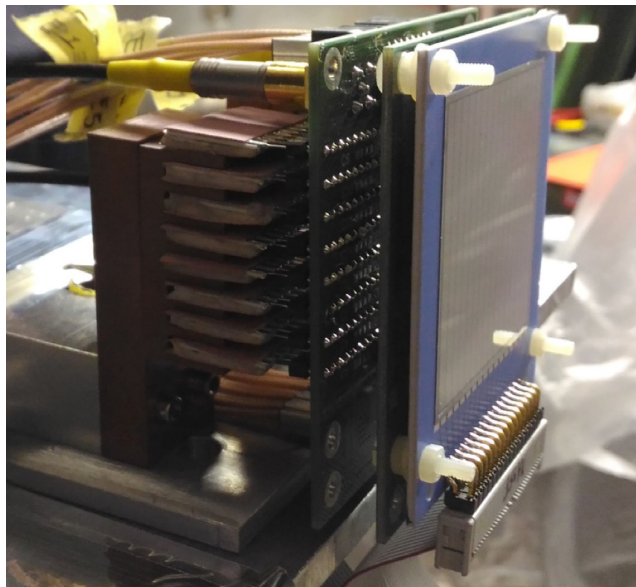
Euclides



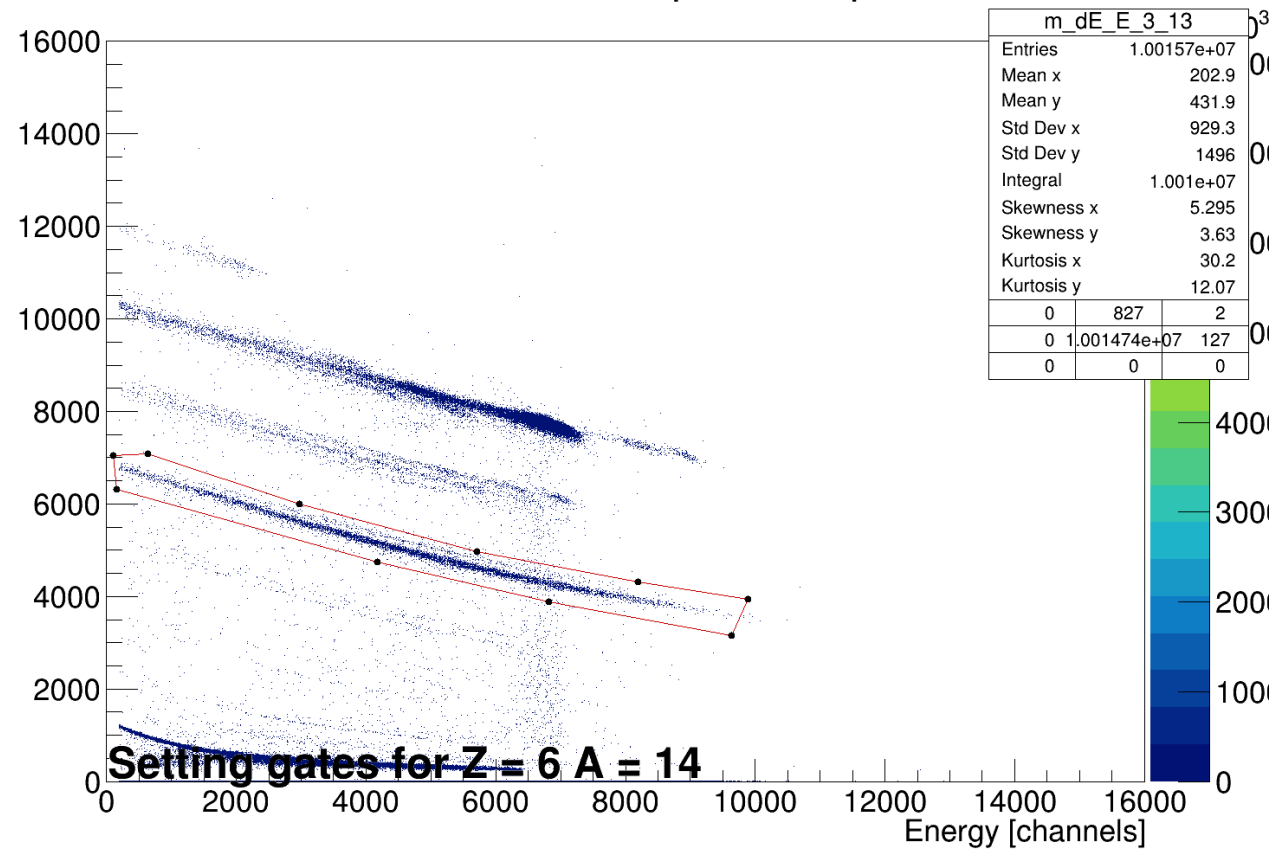
- Constructing a “rough” compound system excitation energy it is possible to discriminate not only protons, neutrons and alphas but also the $1p1n$ channel from the $1p$ channel (as an example)

Oscar

- Particle identification with ΔE -E correlation matrix
- Good position sensitivity thanks to stripped ΔE detector
- The analysis is developed in the selector but will probably need refinements



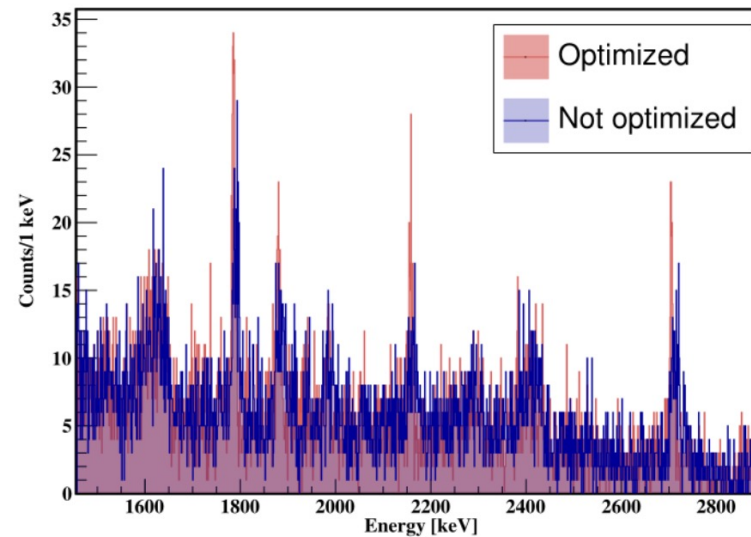
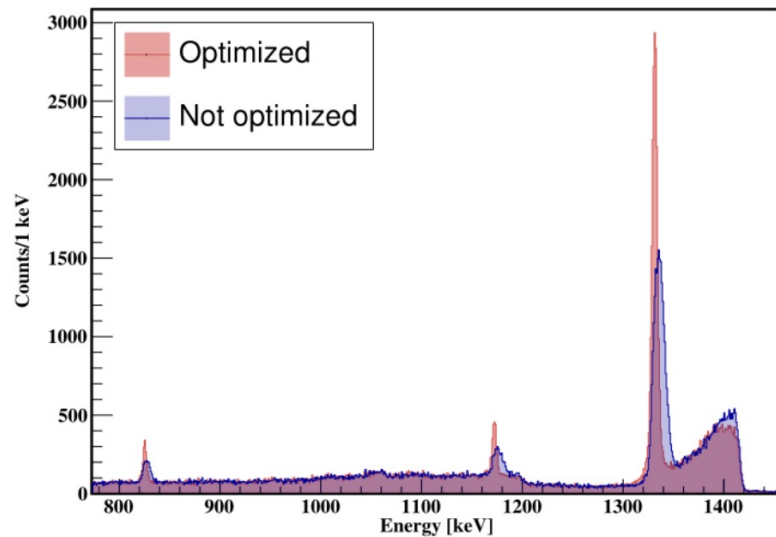
OSCAR dE vs E - pad 3 strip 13



Optimization

The optimization procedure

See Elia's talk



- Remarkable improvements are possible with the optimization but are experiment dependent.
- The selector contains a procedure to find the optimal parameters by running `RunSelector -optimize 2`

The optimization procedure

- Checkout the “OPTIMIZER_CONF” parameters in the selector.conf
- Any parameter contained in the selector.conf that is a single float number can be optimized (target thickness, angles, calibration coefficients). Parameters are minimized simultaneously
- This can be used to improve the doppler correction or the q-value/excitation energy to the right position based on the user’s insight
- It is done with a root minimizer (multiple ones are available: Migrad, Simplex, ...)

Reducing the data

- Since the selector will run multiple times, one must reduce the data to the one of interest. To do so, it is possible to apply a reduction condition on the data such as:

```
./RunSelector --reduction_cond nbTrack\>0\&\&Z_Nr\>0 262
```
- For every input file, a reduced file will be created in the folder where the original tree is, called `red_TREENAME_####.root`. The files can be then added to create a single file with the data of interest of few MB that will allow the selector to run with high frequency.
- The optimizer should be run on this file by changing the input file pattern in the `selector.conf`

Running the optimizer

- The parameter(s) to be optimized can be specified adding one (or multiple lines) in the selector.conf:

```
PARAMETER |detector|par_name|initial_value|min|max|step| ->
```

```
PARAMETER AGATA_CONF ANGLE 31 25 25 1 deg
```

```
PARAMETER TARGET_CONF THICKNESS 1 0.5 2 0.1 mg/cm2
```

- The “line(s)” to optimize can be specified adding one (or multiple lines) in the selector.conf :

```
TRANSITION |folder|spec_name|centroid|sigma|tail|bias ->
```

```
TRANSITION /AgataPrisma/Z16/A32 h_DC_ion_32_16 2230 4 0.1 0.5 keV
```

- The fit can be done without a tail, with a left, right, left+right and left+right symmetric tail (parameter TAIL).
- The SIGMA_WEIGHT is a parameter that goes from 0 to 1. It adds weight to the sigma in the cost function.
- The SCAN option will create a root file with the gradient scanned by the parameter, multiple scans can be performed.

Checking the results

- If the Conf/Optimizer/parameters.dat is present it will be created. If it is present the parameters for the fit (mean, sigma, tau, xmin, xmax, integral) will be read from there, otherwise the default ones will be used. You can simply remove it to start from the default ones.
- At each step some lines will be added to the Conf/Optimizer/log.txt with the current value of each parameter as well as the current cost (gradient value)
- At the end an optimized conf will be created in the folder based on the optimal value.
- The results of the fit can be checked step by step with the option:
-- debug_canvas

Reading raw data and building ancillary
events

Generating the .adf files from the raw data

- The script to read the raw data and build ancillary events is contained in Scripts/AncMerging. To build it, run “cmake -DBUILD_SCRIPTS=On .”
- It builds events within the ancillary within a window
- It handles coincidences also with prisma+other ancillary
- It adds time offset based on the necessary delays
- It applies the correct key for each detector
- The output can then be used by femul to build Agata+ancillary events

Configuration options

ReadCaenRaw.set_labrdantespider 2.63 KIB

```
1 #window: width of the time window used for the event building (in ns)
2 window 500
3
4 #boardDef:
5 # arg 1: boardId
6 # arg 2 :boardVersion(V1725/V1730==1 - VX2740 ==2)
7 # arg 3 :number of channels
8 # arg 4: FWVersion (PHA or PSD)
9 # arg 5: ns per timestamp
10 # arg 6: ns per sample
11 # arg 7: data key: 0xFA0201A2 = SPIDER ; LABR = 0xFA0201A5 ; DANTE = 0x
12 boardDef 0 1 16 PSD 2 2 labr
13 boardDef 1 2 64 PHA 8 8 spider
14 boardDef 5 1 16 PHA 4 4 dante
15
16
17 #minFold:
18 # arg 1: minFold for this detector
19 # arg 2: keep only events if coincidence with other board
20 minFold 2 0
21 minFold 1 0
22 minFold 1 0
23
24
25 # board   channel   timeOffset
26 tsoffset 0 0      121
27 tsoffset 0 1      121
28 tsoffset 0 2      121
29 tsoffset 0 3      121
```

See Elia's presentation for all the details

- **window** [time window width in nanoseconds, usually around 500]
- **board** [board number] [firmware version: 1 or 2] [number of channels: normally 16 or 64] [firmware type: PSD or PHA] [nanoseconds per timestamp] [nanoseconds per sample] [detector name]
- **tsoffset** [board number][channel] [value of offset in timestamps (multiples of 10 ns)]
- **minfold**: [board number] [minimum fold of a board to write an event in the output]

Troubleshooting

See Elia's presentation for
all the details

Coincidences stop at
some point

Online building problem

Loss of statistics

Online building problem

Multiple peaks

Ancillaries or cores not aligned

Align with `genconf.py` or
`ReadCaenRaw.set`

Exponential shape

The global time offset is wrong

Find the coincidence peak as
explained in
`Scripts/TimeOffsetPeak`

No peak

There is no global offset

Run
`ReadCaenRaw` and
`femul`

Finding the coincidence peak

- It is not straightforward and is strongly dependent on the trigger processor settings
- If LaBr are present and acquired as slaves of other ancillaries they can be used to find the right offset
- The offset can be found by randomly correlating all events as explained in Scripts/TimeOffsetFix:

Finding the offset

You should have the agapro package installed with the `ListFrames` program installed. Locate your ancillary BU file which should be named like `ancillaryBU_i***_***_0000.adf`. Chose one good AGATA crystal and locate the `psa_0000.adf` file under the data folder such as `Data/00A/psa_0000.adf`.

Modify the script `generate.sh` to point to those files and run it with `sh generate.sh`. Two files called `anc.txt` and `agata.txt` should be generated.

Now it's the time to run `./fix` which will read these two files and generate a root file called `out.root`. Inside this file there should be a big histogram, locate the peak in the histogram and note precisely the x-axis position. This is your offset number. You may have to modify the `fix.C` script to change the limits and binning of the histogram of the dimension of the vectors in case no peak is present. Then recompile the script.

You can use the macro `drawHist.cxx` for help in finding the peak.

Applying the offset

Now that you have an offset, use the `ReadCaenRaw` as you normally would but with the option `--global-anc-tsoffset value`, where value is the position of the peak.

Other useful scripts

Generation of SRIM tables

📄 README.md

Energy loss table production using SRIM

`ELoss_table_for_AgataSelector.bat` is windows script, which uses module of `SRIM` called `SRModule.exe` to produce tables of energy loss tables used by AgataSelector

Running the script

Locate your installation of `SRIM` and its subdirectory `SR Module`, which you can copy wherever you want to run it

Make sure that files `SNUC03.dat` and `SC0EF03.dat` are present and named accordingly

Copy files `ELoss_table_for_AgataSelector.bat` and `target.dat` into your `SR Module` folder

Edit `target.dat` file with parameters of your target in the form: A Z name Density(g/cm3)

Open `cmd` (press `win+R`, type `cmd` and press enter) and navigate to your `SR Module` folder by `cd /d X:\path\to\your\folder`

Run command `ELoss_table_for_AgataSelector.bat Amin Amax Zmin Zmax Emax`, where from Amin to Amax is mass number range of impinging ions, where from Zmin to Zmax is proton number range of impinging ions and Emax is maximum energy in keV of impinging ion to be calculated.

The output are .txt files named as Target-A-Z_Ion-A-Z.txt for each ion - target combination. This files needs to be transferred to `agataselector/User/EXP/Your_EXP_NAME/Conf/EnergyLoss` folder and you are good to go

MPI

- The selector can be distributed on multiple machines if they have a common file system and boost-mpi installed.
- To enable MPI compile with:

```
cmake -DCMAKE_CXX_COMPILER=mpic++ -DUSE_MPI=On .
```

- It is also necessary to add a file called “hfile” with the ip of each machine that will contribute
- To distribute simply add the option - -distribute when launching the selector.
- Note that the machine where you launch it from will be only assigning jobs and thus will not be under load.

Perspectives and foreseen updates

- S1 (Sauron) and Oscar will be added to the analysis
- Tests should be added for other detectors
- If you find a bug or have a feature please help us, it benefits the community! You can contact us by email or open an issue on baltig:
<https://baltig.infn.it/gamma/agataselector/-/issues>

