



# AGATA ancillaries analysis: rebuilding events and selector optimization

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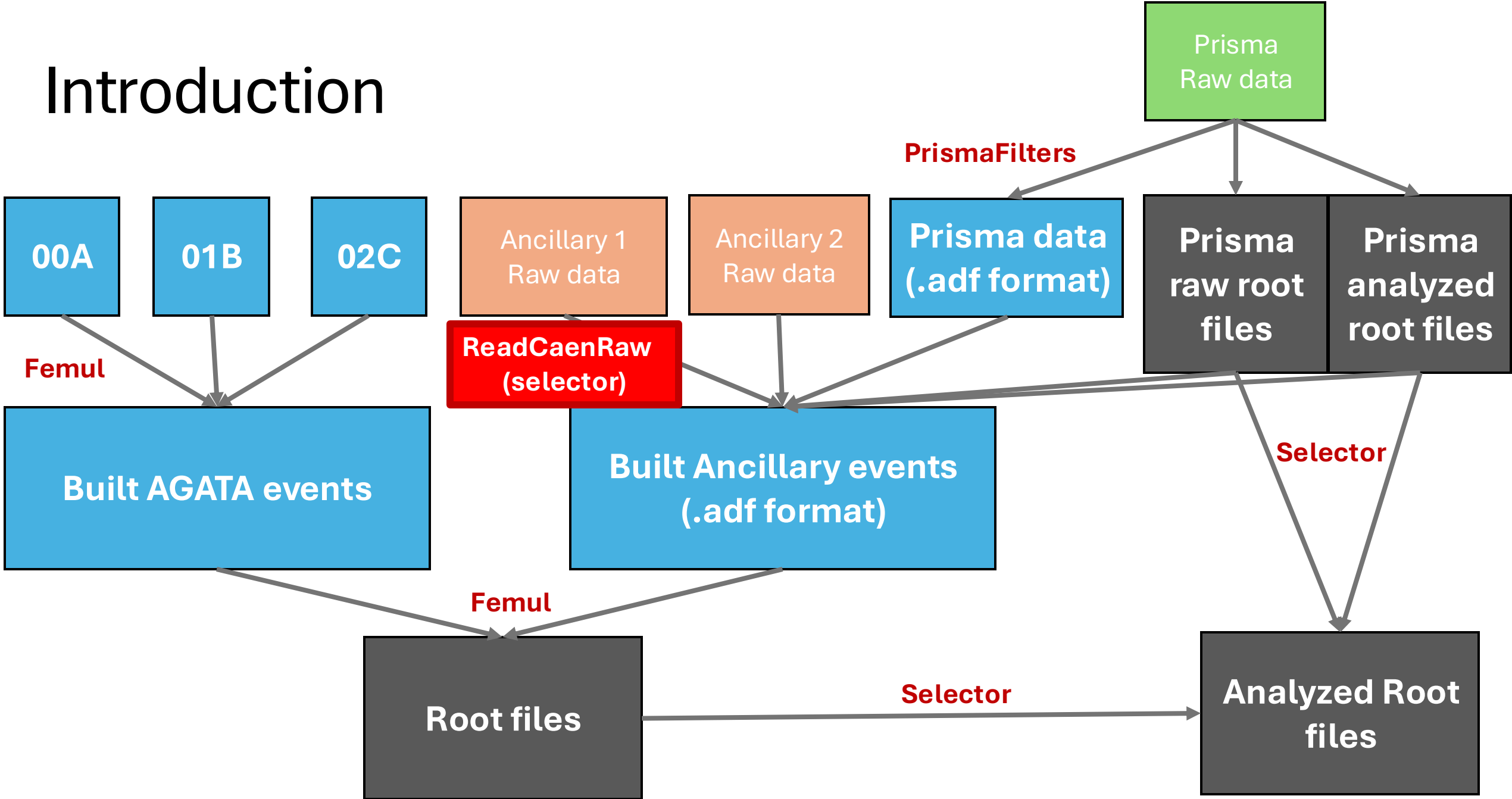
*On behalf of the AGATA collaboration*

- Part 1: Reading raw data and building the ancillary events
- Part 2 : Using the optimization of the selector and other features

# Rebuilding events

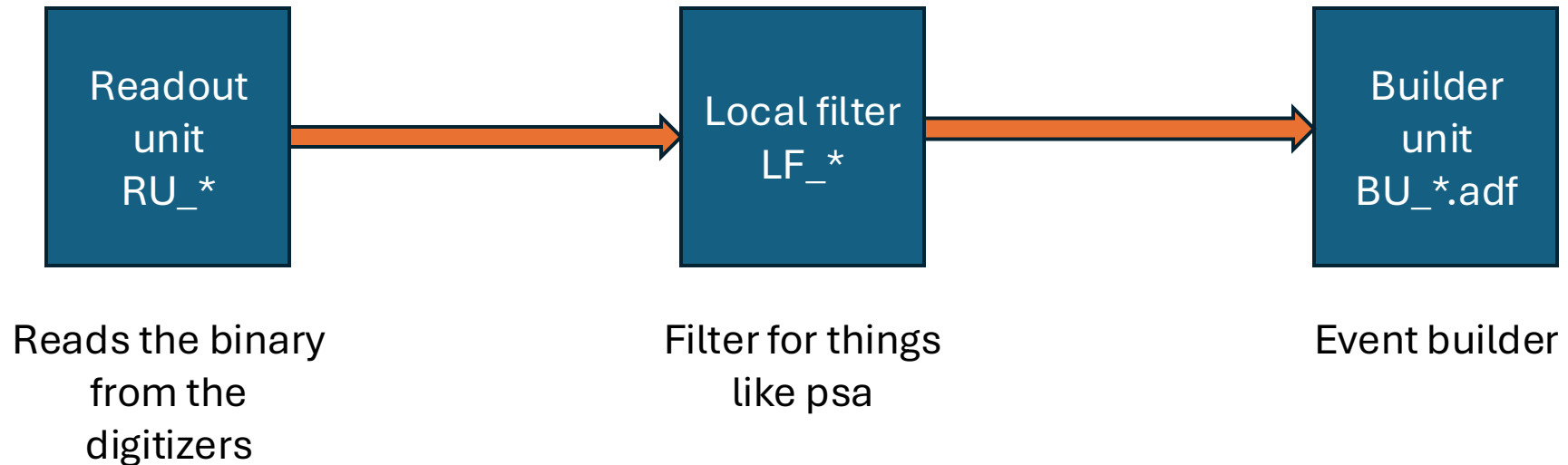
- This will be a bit technical, but it is important to understand what is happening "under the hood" do debug issues and understand how the data flow works
- We need to produce an adf file to feed to femul to produce the root trees
- The EventMerger of femul requires built events (with composite frames), so we need to produce

# Introduction



# 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



- Reads the binary output from the CAEN digitizers
  - There are two different firmware types: PHA and PSD
  - There are also two different firmware versions which we will call 1 and 2
- Builds the time coincidences with a simple event builder, we can set the time window
- Can also include and build PRISMA events both for analyzed and raw data

# ReadCaenRaw: how to run

```
daniele@ccvisit15 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 --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
```

- The ReadCaenRaw is contained in the agataselector and can be compiled running `cmake -DBUILD_SCRIPTS=On`.
- You will find the executable in your build folder under `Scripts/AncMerging/`

# Configuration file: PRISMA-LABR conf

ReadCaenRaw.set\_labrprisma 825 B

```
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 board 1 1 16 PSD 2 2 labr
13
14 #minFold:
15 # arg 1: detector
16 # arg 2: minFold for this detector
17 # arg 3: keep only events if coincidence with other board
18 minfold 1 0
19
20 # board   channel   timeOffset
21 tsoffset 1 0 130
22 tsoffset 1 1 130
23 tsoffset 1 2 130
24 tsoffset 1 3 130
25 tsoffset 1 4 130
26 tsoffset 1 5 130
27 tsoffset 1 6 130
28 tsoffset 1 7 130
```

- **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]



# Configuration file: SPIDER-DANTE-LABR conf

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
```

- **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]

# ListFrames: Labr only

Gamma-gamma  
coincidence of the labr  
(fa0201a5)

235	11476	76	ca020100	257	0	26784040305	4145	event:ranc
		28	fa0201a5	259	0			
		28	fa0201a5	271	3			
236	11552	48	ca020100	0	0	26784053342	13037	event:ranc
		28	fa0201a5	260	0			
237	11600	48	ca020100	0	0	26784056728	3386	event:ranc
		28	fa0201a5	259	0			
238	11648	48	ca020100	0	0	26784065158	8430	event:ranc
		28	fa0201a5	256	0			
239	11696	48	ca020100	0	0	26784069669	4511	event:ranc
		28	fa0201a5	256	0			
240	11744	48	ca020100	0	0	26784102553	32884	event:ranc
		28	fa0201a5	264	0			
241	11792	48	ca020100	0	0	26784108471	5918	event:ranc
		28	fa0201a5	271	0			

Composite frame  
Labr hit

The eventnumber slot in the adf headers for the ancillaries is misleading. Since it is not used, to save space, it has been exploited to save the board and channel info of the hit. To extract board and channel can be done with a bit mask and bit shift:

# Minfold 2

Setting minfold 2 for the LABR board, we only store gamma-gamma coincidences, this can be useful to reduce the data or to find coincidence peaks

First timestamp of the ancillaries

Time difference with respect to the previous frame

#	event	bOffset	bSize	0xKeyADF	eventNum	timeStamp	dTstamp	keyADFname
	0	0	76	ca020100	0	26781315390	0	event:ranc
			28	fa0201a5	261	0		
			28	fa0201a5	262	0		
	1	76	76	ca020100	0	26781898753	583363	event:ranc
			28	fa0201a5	259	0		
			28	fa0201a5	260	0		
	2	152	76	ca020100	0	26782083333	184580	event:ranc
			28	fa0201a5	258	0		
			28	fa0201a5	261	0		
	3	228	76	ca020100	0	26782431032	347699	event:ranc
			28	fa0201a5	263	0		
			28	fa0201a5	264	2		
	4	304	76	ca020100	0	26783123146	692114	event:ranc
			28	fa0201a5	256	0		
			28	fa0201a5	264	1		
	5	380	76	ca020100	0	26783165714	42568	event:ranc
			28	fa0201a5	257	0		
			28	fa0201a5	261	0		
	6	456	76	ca020100	0	26783570632	404918	event:ranc
			28	fa0201a5	256	0		
			28	fa0201a5	263	0		
	7	532	76	ca020100	0	26784040305	469673	event:ranc
			28	fa0201a5	259	0		

# Prisma-Labr coincidence

- We are now interested in merging the PRISMA data with the other ancillaries
- This is useful for DANTE and the LABR so far
- We just need to use the --prisma option:  
./ReadCaenRaw --input [files] --prisma [files]
- You have several options:
  - Include only the raw PRISMA data (if you are doing the analysis with the selector) → fa0201a0
  - Include only the analyzed PRISMA data (if you have already done the analysis with the prisma filters) → fa0201a1
  - Include both of them if you want to keep all options. Note that this will double the amount of space on disk used by prisma

Prisma-labr time coincidence



83442	4122628	48	ca020100	0	27798784921	13011	event:ranc
		28	fa0201a5	264	0		
83443	4122676	580	ca020100	0	27798787167	2246	event:ranc
		532	fa0201a0	0	19		.data:ranc0
		28	fa0201a5	271	0		
83444	4123256	48	ca020100	0	27798801217	14050	event:ranc
		28	fa0201a5	260	0		
83445	4123304	552	ca020100	1	27798805668	4451	event:ranc
		532	fa0201a0	0	0		.data:ranc0
83446	4123856	552	ca020100	1	27798824875	19207	event:ranc
		532	fa0201a0	0	0		.data:ranc0

# Example of a DANTE-DANTE coincidence

- A “perfect” DANTE event should have X, Y and T. In this specific case with two dante detectors at forward angles, an event can be a DANTE-DANTE coincidence that should have X1, Y1, T1, X2, Y2, T2, TOF for a total of 7 hits in a single event

This is a good DANTE-DANTE event

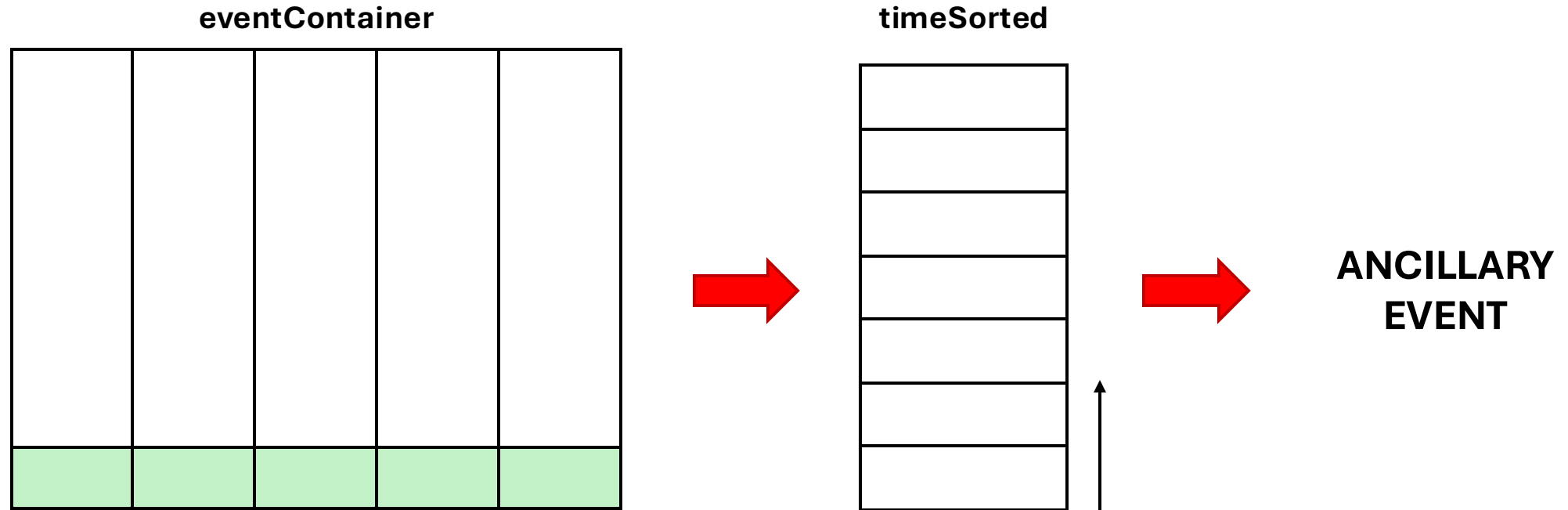


Time alignment looks good



18	1108	188	ca020100	0	6156700534505	16257	event : ranc
		24	fa0201a3	1282	0		
		24	fa0201a3	1286	4		
		24	fa0201a3	1280	8		
		24	fa0201a3	1281	10		
		24	fa0201a3	1285	11		
		24	fa0201a3	1284	12		
		24	fa0201a3	1288	15		
19	1296	48	ca020100	0	6156700535810	1305	event : ranc
		28	fa0201a5	3	0		
20	1344	48	ca020100	0	6156700537112	1302	event : ranc
		28	fa0201a5	6	0		
21	1392	48	ca020100	0	6156700563064	25952	event : ranc
		28	fa0201a5	0	0		

# Event building in ReadCaenRaw



"eventContainer" size in ReadCaenRaw.h

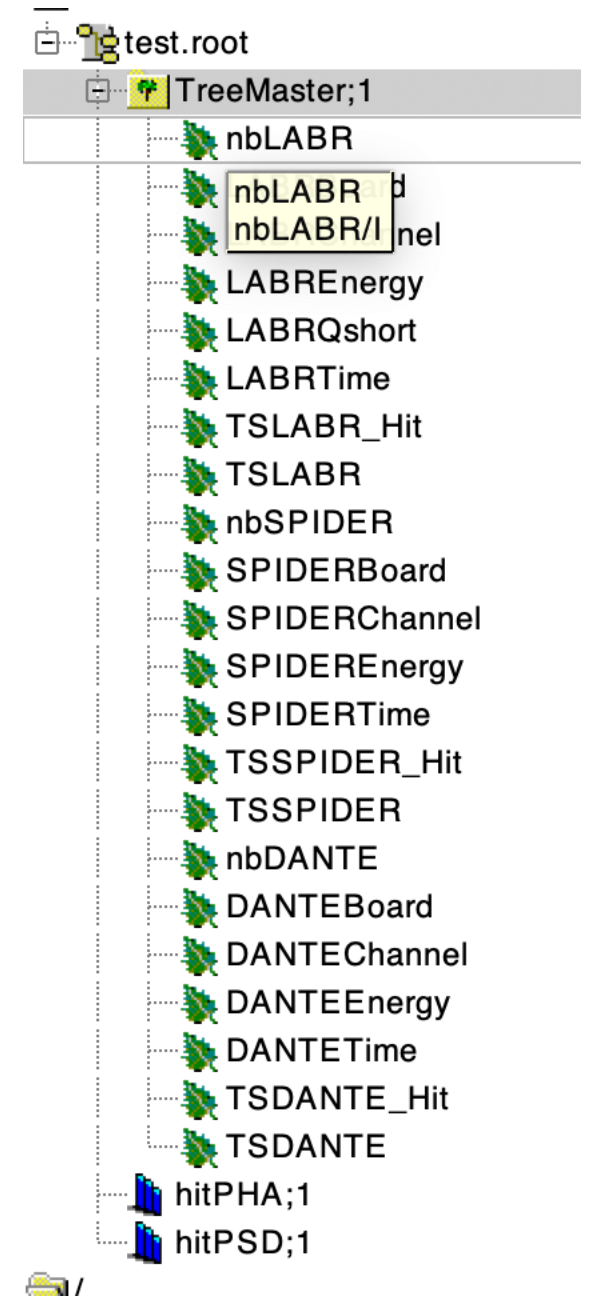
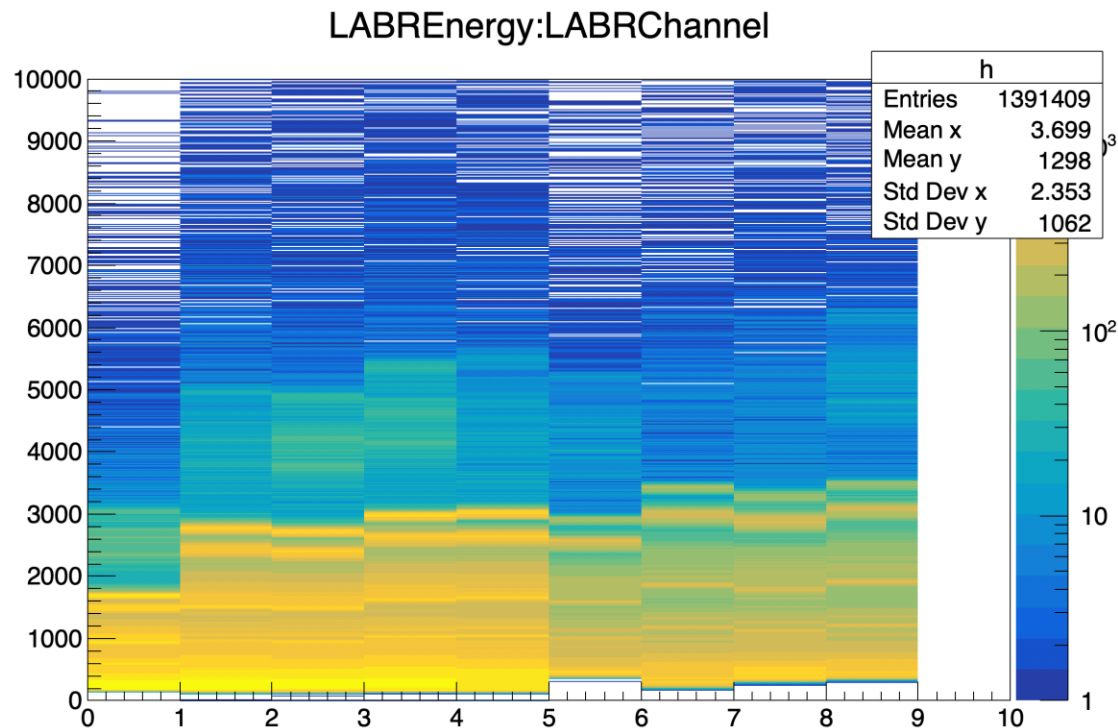
```
301  
302 int channelsBuffersSize{50000};  
303 std::map<uint16_t, std::deque<intern
```

"timeSorted" size in ReadCaenRaw.cxx

```
416 if(timeSorted.size() > 1000) {  
417     if(verbose) std::cout <<
```

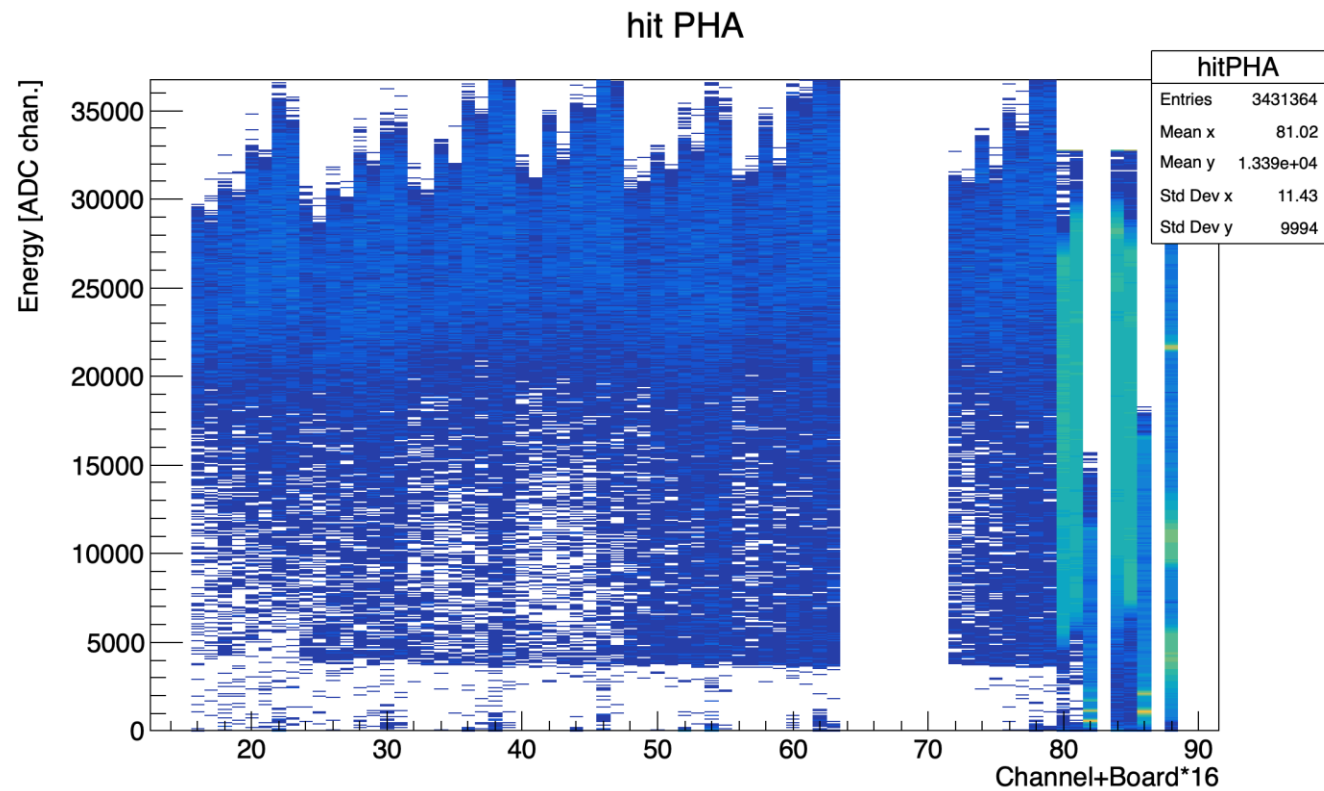
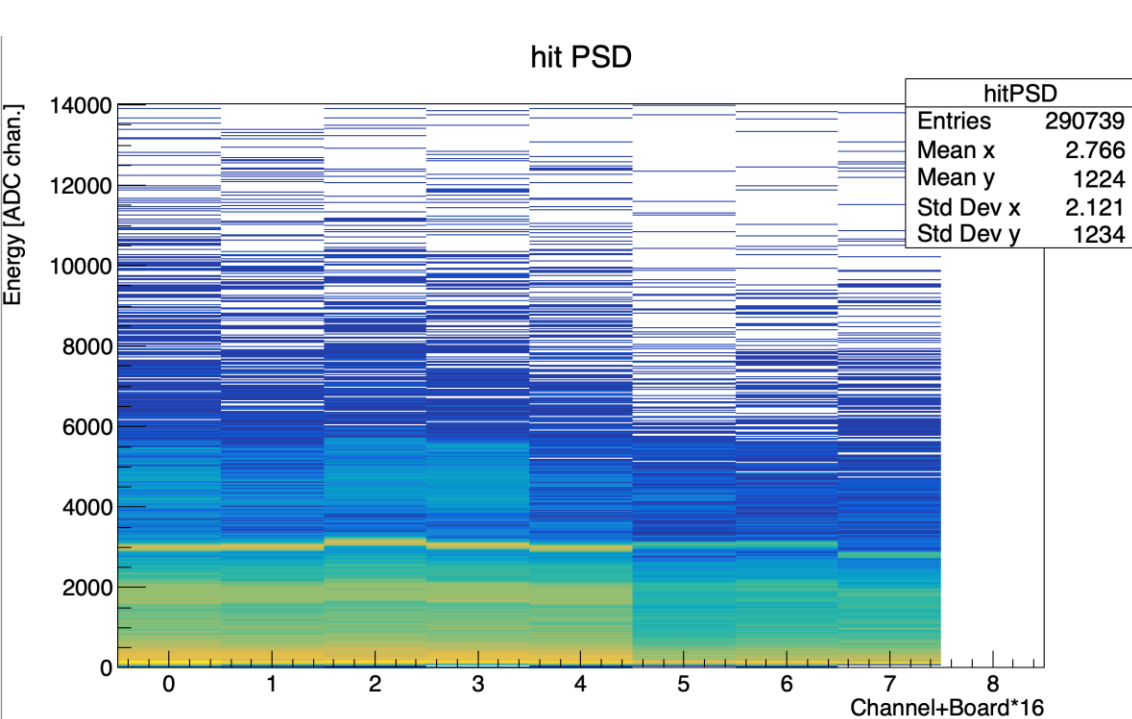
# Root output

- It has the same format of the TreeBuilder
- You can run the selector on it
- It's good to check the ancillary data before going through femul



# Root output

- In the example data you will see both data from both PSD (labr) and PHA (SPIDER and DANTE)

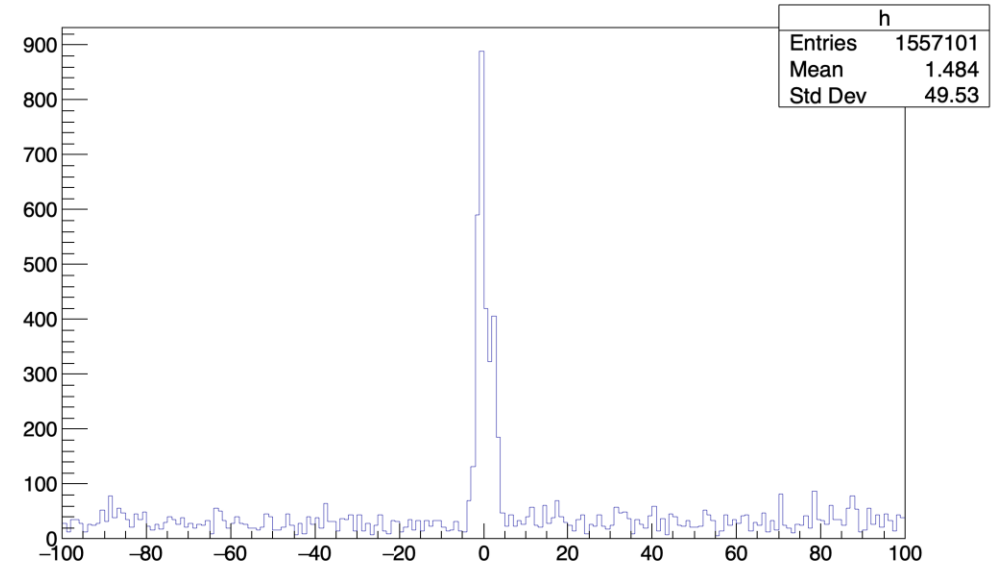




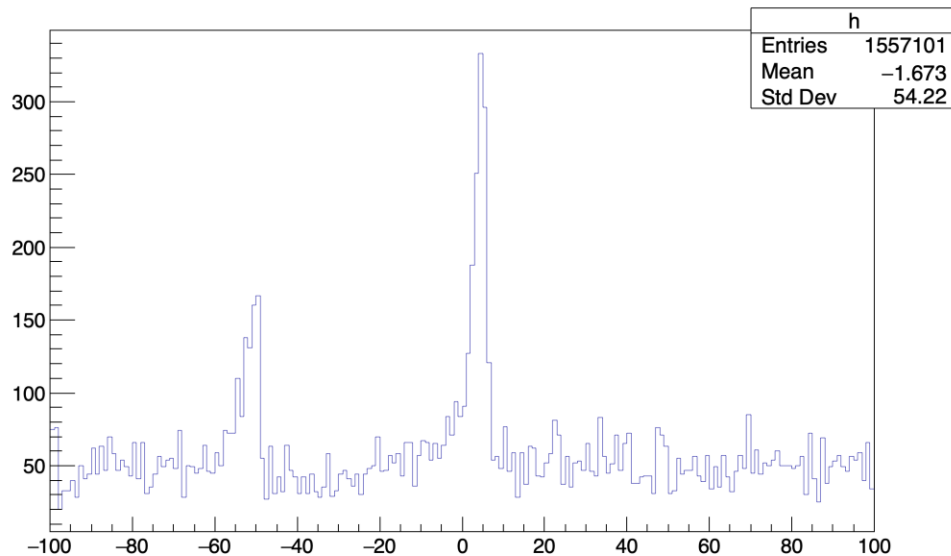
# Time coincidence peaks

- You can now check the time alignment of all detectors
- You should aim to have all peaks at 0
- If this is not the case, change the ReadCaenRaw.set, specifically the tsoffset keyword for the channel that is not aligned

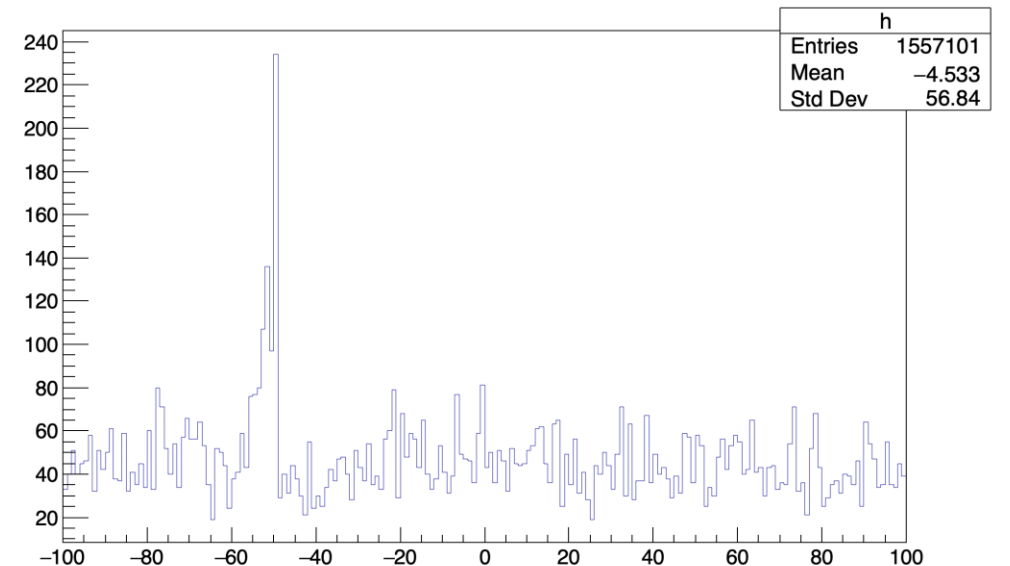
TSSPIDER-TSLABR



TSLABR-TSDANTE



TSSPIDER-TSDANTE



# Things to check

- There is coincidence peak between agata and the ancillaries
- There is a coincidence peak between the ancillaries themselves
- The coincidence peak remains during the whole experiment
- The coincidence peak has a shape that makes sense

# Possible issues and how to solve them

Symptoms

Disease

Cure

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`

# Time offset fix

- If you need to find the time coincidence peak, you can follow the instructions in the README.md in `agataselector/Scripts/TimeOffsetFix`

First of all, compile the script with

```
sh compile.sh
```



You should get an executable called `fix` to find the offset. This correlates all possible events and generates a histogram where a peak should be present. The x-position of the peak corresponds to the peak value.

## 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`. Choose 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.

# Time offset fix

```
[daniele@ccvisit15 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 --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
```

# Selector Optimization

- Data reduction / selection
- Scanning parameters
- Multiparameter minimization
  
- Grid – search optimization
  - Not well tested yet
  - Fine tuning
  - See main README.md of agataselector (or ask Matus Balogh)

# Data reduction

First we reduce the amount of data to use for optimization. The best condition to achieve this is experiment dependent, but usually you:

- Require coincidence
- May require to be in the coincidence peak (reject background)
- Select an energy range
- ...

Example:

```
RunSelector --conf selector.conf --nrthr 10 --reduction_cond "nbSPIDER > 0 && nbCores > 0 && trackE > 900" 628 MB -> 23 MB
```

This will create reduced files in the data folder, with the same name as the old ones with the "red\_" prefix. You should then sum them all into one:

```
hadd optData_0000.root Data/run_0034/Out/Analysis/red_Tree_000*
```

OBS: multiple runs can be used

# Scan a parameter

- Choose the spectrum (and transition) to optimize
- Choose the parameter(s) to optimize
- In the "selector.conf", in "OPTIMIZER\_CONF" you add both

```
PARAMETER SPIDER_CONF X_SHIFT 0 -20 20 1 mm      #PARAMETER |detector|par_name|initial_value|min|max|step|
SCAN SPIDER_CONF X_SHIFT 0 -20 20 4 mm          #SCAN |detector|par_name|initial_value|min|max|step|
TRANSITION AgataSpider h_EDC 991.5 3 0.1 0.5 keV #TRANSITION |folder|spec_name|centroid|sigma|tail|bias|
ONLY_SCAN YES                                   #optional
```



# Scan a parameter

- Choose the spectrum (and transition) to optimize
- Choose the parameter(s) to optimize
- In the "selector.conf", in "OPTIMIZER\_CONF" you add both

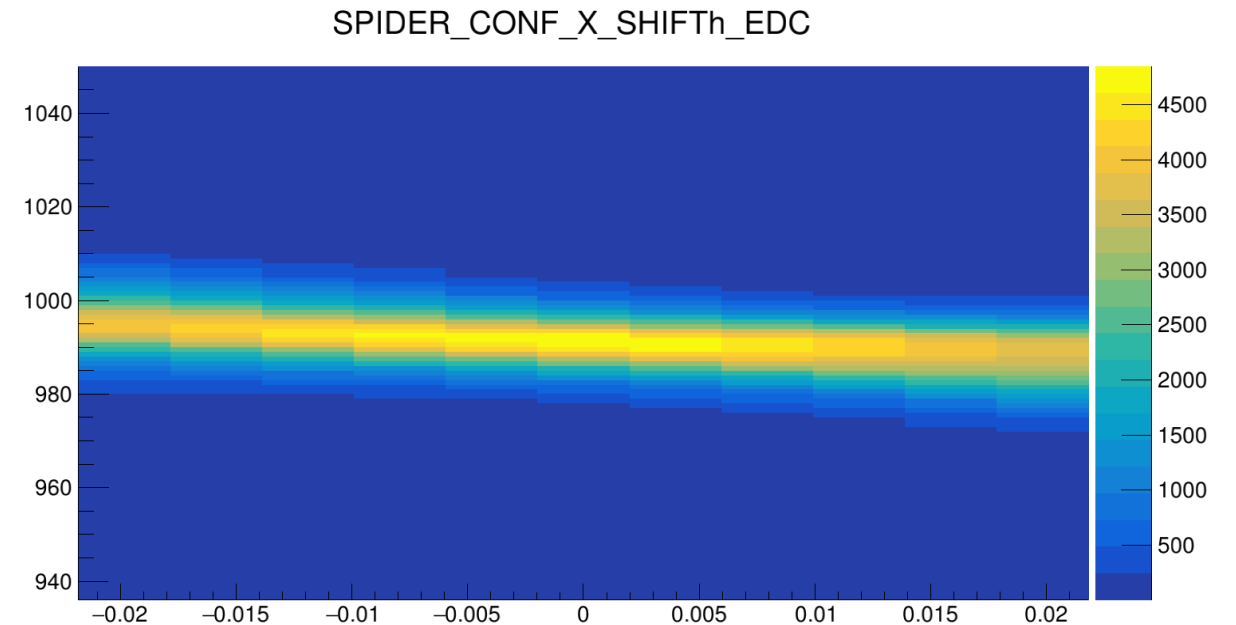
```
PARAMETER SPIDER_CONF X_SHIFT 0 -20 20 1 mm
SCAN SPIDER_CONF X_SHIFT 0 -20 20 4 mm
TRANSITION AgataSpider h_EDC 991.5 3 0.1 0.5 keV
ONLY_SCAN YES
```

```
#PARAMETER |detector|par_name|initial_value|min|max|step|
#SCAN |detector|par_name|initial_value|min|max|step|
#TRANSITION |folder|spec_name|centroid|sigma|tail|bias|
#optional
```

- Run the selector (scans in file "out.root")

```
RunSelector 9999 --conf selector.conf \
  --nrthr 1 --verb -1 --only_enabled_histos \
  --optimize
```

OBS: "only\_enabled\_histos" option activated,  
you should modify accordingly the file  
"Conf/enabled\_histos.conf"



# Fit with multiparameter optimization

- Similar notation to scan:

```
PARAMETER SPIDER_CONF X_SHIFT 0 -20 20 1 mm  
PARAMETER SPIDER_CONF Y_SHIFT 0 -20 20 1 mm  
PARAMETER SPIDER_CONF Z_SHIFT 0 -20 20 1 mm  
TRANSITION AgataSpider h_EDC 991.5 3 0.1 0.5 keV
```

# Fit with multiparameter optimization

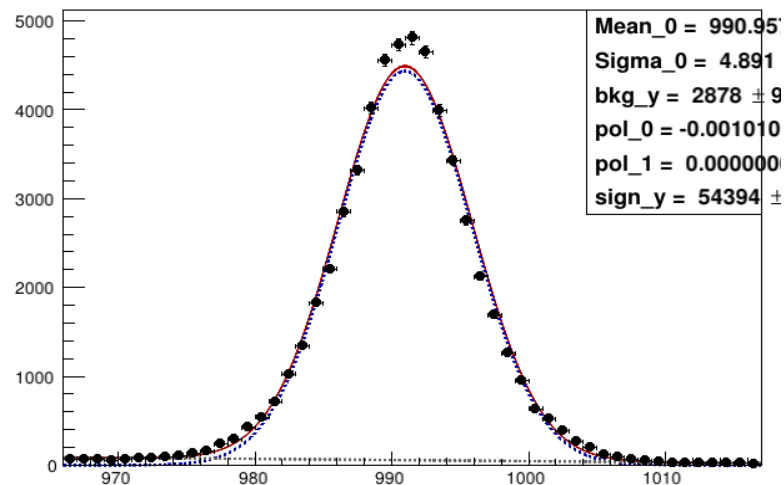
- Similar notation to scan:

```
PARAMETER SPIDER_CONF X_SHIFT 0 -20 20 1 mm  
PARAMETER SPIDER_CONF Y_SHIFT 0 -20 20 1 mm  
PARAMETER SPIDER_CONF Z_SHIFT 0 -20 20 1 mm  
TRANSITION AgataSpider h_EDC 991.5 3 0.1 0.5 keV
```

- If fits are not good, you change parameters in file "Conf/Optimizer/parameters.dat"

- Run selector with "debug canvas" option

```
RunSelector 9999 --conf selector.conf \  
--nrthr 1 --verb -1 --only_enabled_histos \  
--optimize --debug_canvas
```



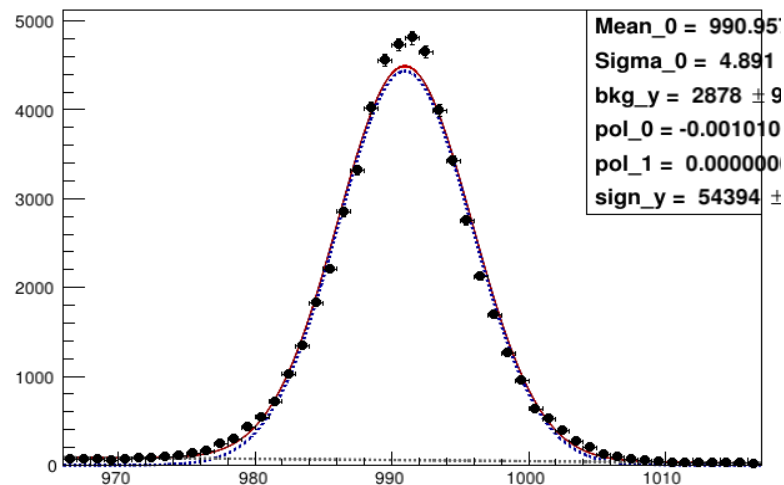
# Fit with multiparameter optimization

- Similar notation to scan:

```
PARAMETER SPIDER_CONF X_SHIFT 0 -20 20 1 mm
PARAMETER SPIDER_CONF Y_SHIFT 0 -20 20 1 mm
PARAMETER SPIDER_CONF Z_SHIFT 0 -20 20 1 mm
TRANSITION AgataSpider h_EDC 991.5 3 0.1 0.5 keV
```

- Run selector with "debug canvas" option

```
RunSelector 9999 --conf selector.conf \
--nrthr 1 --verb -1 --only_enabled_histos \
--optimize --debug_canvas
```



- If fits are not good, you change parameters in file "Conf/Optimizer/parameters.dat"
- Once fits are good, run optimization without option "debug\_canvas" option

```
RunSelector 9999 --conf selector.conf \
--nrthr 1 --verb -1 --only_enabled_histos \
--optimize
```

- While it is running, you can monitor with  

```
tail -f Conf/Optimizer/log.txt
```
- At the end output file is run with best parameters

# Cost function

The cost function takes into account many factors:

- The fitted energies
- The fitted sigmas (+ tails)
- The reference energy
- The bias on each transition
- The number of non-converging fits
- A weight factor

$$C = (1 - W) \sqrt{\sum_{i=1}^N (\mu_i - \epsilon_i)^2 \cdot b_i} + W \sqrt{\sum_{i=1}^N \tilde{\sigma}_i^2 \cdot b_i} + N_{nc} C_{nc}$$

$$\tilde{\sigma}_i = \sigma_i + \tau_{l,i} + \tau_{r,i}$$

# Cost function

Keywords:

TAIL 0 # 0: notail, 1: right, 2: left, 3: left+right, 4: symmetric

NON\_CONVERGENCE\_COST 5 # Multiplier cost for fits that did not converge

SIGMA\_WEIGHT 0.5 # 0 for pure centroid optimization, 1 for pure width optimization

$$C = (1 - W) \sqrt{\sum_{i=1}^N (\mu_i - \epsilon_i)^2 \cdot b_i} + W \sqrt{\sum_{i=1}^N \tilde{\sigma}_i^2 \cdot b_i} + N_{nc} C_{nc}$$

$$\tilde{\sigma}_i = \sigma_i + \tau_{l,i} + \tau_{r,i}$$

# Additional files

File: Conf/Optimizer/parameters.dat

FIT\_PAR\_FILE parameters.dat [#Name of parameter file](#)

```
-----  
idx: 0  
name : init_val min max fixed  
AmpL_0 1.000000e+04 0.000000e+00 1.000000e+08 0  
Mean_0 9.915000e+02 9.865000e+02 9.965000e+02 0  
Sigma_0 5.000000e+00 1.650000e+00 1.500000e+01 0  
Tau_left_0 1.000000e-04 1.000000e-03 1.000000e+01 0  
Tau_right_0 1.000000e-04 1.000000e-03 1.000000e+01 0  
pol_0 0.000000e+00 -1.000000e-01 1.000000e-01 0  
pol_1 0.000000e+00 -1.000000e-01 1.000000e-01 0  
min_max 9.665000e+02 1.016500e+03
```

OBS: If not present it's created,  
otherwise it's read

File: Conf/Optimizer/log.txt

LOG\_FILE log.txt [#Name of log file](#)

```
#####End of minimizer#####  
#####Running with optimal parameters  
===== it: 74 =====  
par: SPIDER_CONF X_SHIFT ---> val: -0.00187371  
par: SPIDER_CONF Y_SHIFT ---> val: 0.00157457  
par: SPIDER_CONF Z_SHIFT ---> val: 0.000614222  
COST 2.47316  
FITTED MEAN 991.501  
FITTED SIGMA 4.92468
```

# Final remarks on optimization

- You can **should** play with hyper-parameters

```
ALGORITHM Simplex # Name of algorithm (Migrad, Simplex,...)
MINIMIZER Minuit   # Name of minimizer (Minuit/Minuit2, Fumili, GLSMultiMin, Genetic)
BKG_POL_ORDER 1   # Polynomial order for background
MAX_CALLS 1000    # Maximum number of minimizer calls
TOLERANCE 0.1     # Minimizer tolerance
PRECISION 0.01    # Minimizer precision (likely leave 0 for optimally calculated value)
USE_INTERVALS NO  # Use intervals in minimization (try what is best)
VALID_ERRORS NO   # Performs error analysis (e.g. run Hesse for Minuit)
...
```



# Background subtraction

- The selector has a background subtraction option that can really improve the results in some cases
- This can be done for each detectors or for the coincidence between detectors (NOT BOTH)
- To activate you run the selector with "--subtract\_bkg" option and you have to set background regions in configuration file "selector.conf"

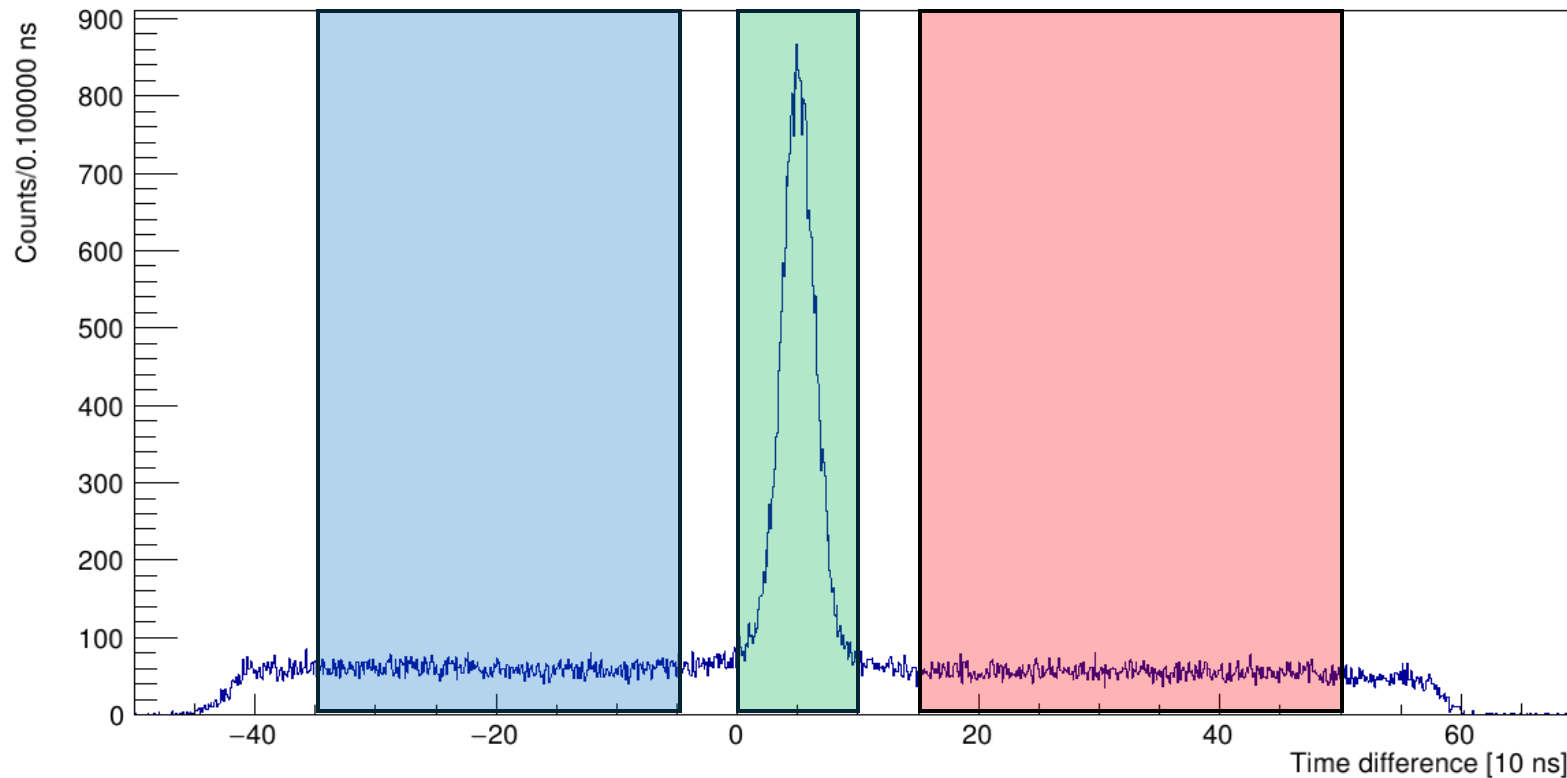
```
RunSelector 34 --conf selector.conf --subtract_bkg
```

```
COINC_W_RIGHT_RIGHT_BKG 50 # Right Background time window on the right side of the coincidence peak
COINC_W_LEFT_RIGHT_BKG 15 # Left Background time window on the right side of the coincidence peak
COINC_W_RIGHT_LEFT_BKG -5 # Right Background time window on the left side of the coincidence peak
COINC_W_LEFT_LEFT_BKG -35 # Left Background time window on the left side of the coincidence peak
COINC_W_LEFT 0 # Time window left with the same type of det
COINC_W_RIGHT 10 # Time window right with with the same type of det
```

# Background subtraction

How it works:

- Selector is run 3 times, selecting events in each region
- The corresponding spectra are then normalized on the width of the region
- Finally the background subtraction takes place (on each plot)



# Background subtraction

## Asymmetric peaks

Example: AGATA

```
AGATA_CONF
```

```
...
```

```
COINC_W_RIGHT_RIGHT_BKG 7
```

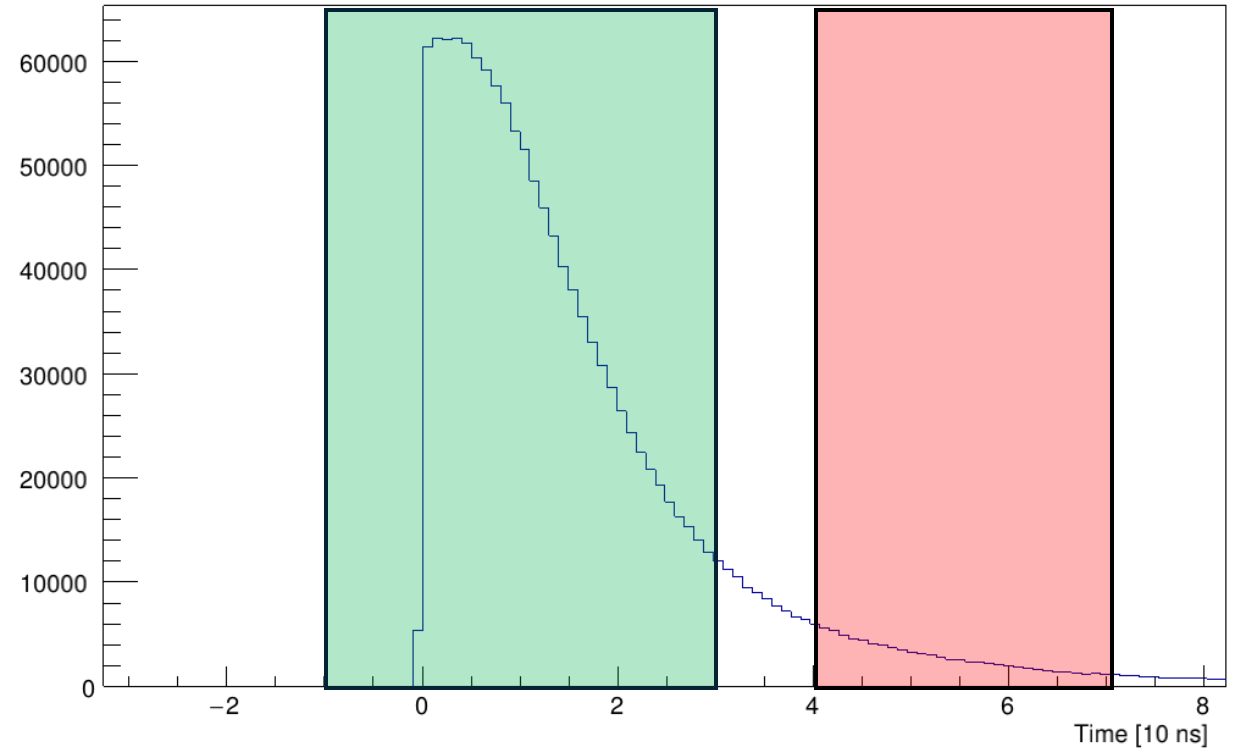
```
COINC_W_LEFT_RIGHT_BKG 4
```

```
COINC_W_RIGHT_LEFT_BKG -2
```

```
COINC_W_LEFT_LEFT_BKG -2
```

```
COINC_W_LEFT -1
```

```
COINC_W_RIGHT 3
```



# Background subtraction

## Coincidence

Example: AGATA – DANTE

- In this case you should put the values for all three regions in the AGATA\_CONF and DANTE\_CONF
- Now you can define your normal regions in the AGATADANTE\_CONF

AGATA\_CONF

...

COINC\_W\_RIGHT\_RIGHT\_BKG 5  
COINC\_W\_LEFT\_RIGHT\_BKG -1  
COINC\_W\_RIGHT\_LEFT\_BKG 5  
COINC\_W\_LEFT\_LEFT\_BKG -1  
COINC\_W\_LEFT -1  
COINC\_W\_RIGHT 5

DANTE\_CONF

...

COINC\_W\_RIGHT\_RIGHT\_BKG 20  
COINC\_W\_LEFT\_RIGHT\_BKG -20  
COINC\_W\_RIGHT\_LEFT\_BKG 20  
COINC\_W\_LEFT\_LEFT\_BKG -20  
COINC\_W\_LEFT -20  
COINC\_W\_RIGHT 20

AGATADANTE\_CONF

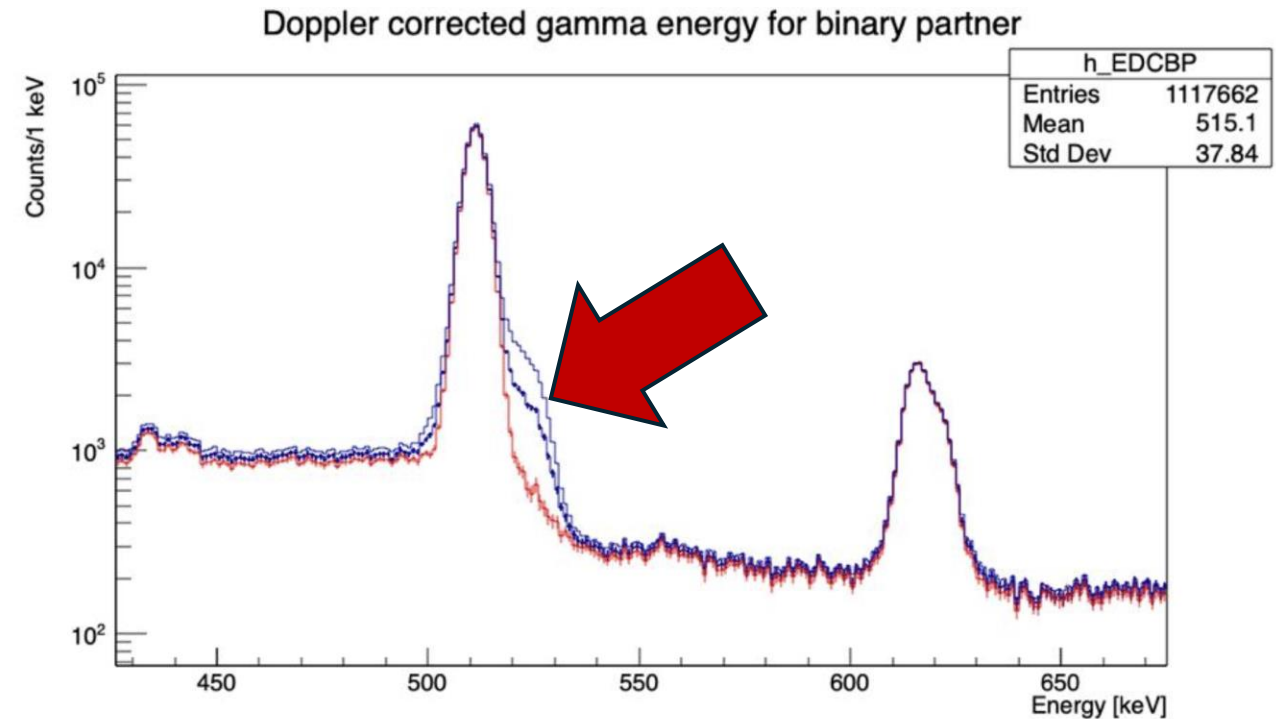
...

COINC\_W\_RIGHT\_RIGHT\_BKG 50  
COINC\_W\_LEFT\_RIGHT\_BKG 15  
COINC\_W\_RIGHT\_LEFT\_BKG -5  
COINC\_W\_LEFT\_LEFT\_BKG -35  
COINC\_W\_LEFT 0  
COINC\_W\_RIGHT 10

# Background subtraction

Example of results:

- Coulex experiment
- Transition of interest in binary partner close to 511 keV
- Have to remove background from 511 keV



# Thank you for your attention



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Special thanks to: Daniele Brugnara

*On behalf of the AGATA collaboration*

