A new method for Depth of Interaction determination in PET detectors

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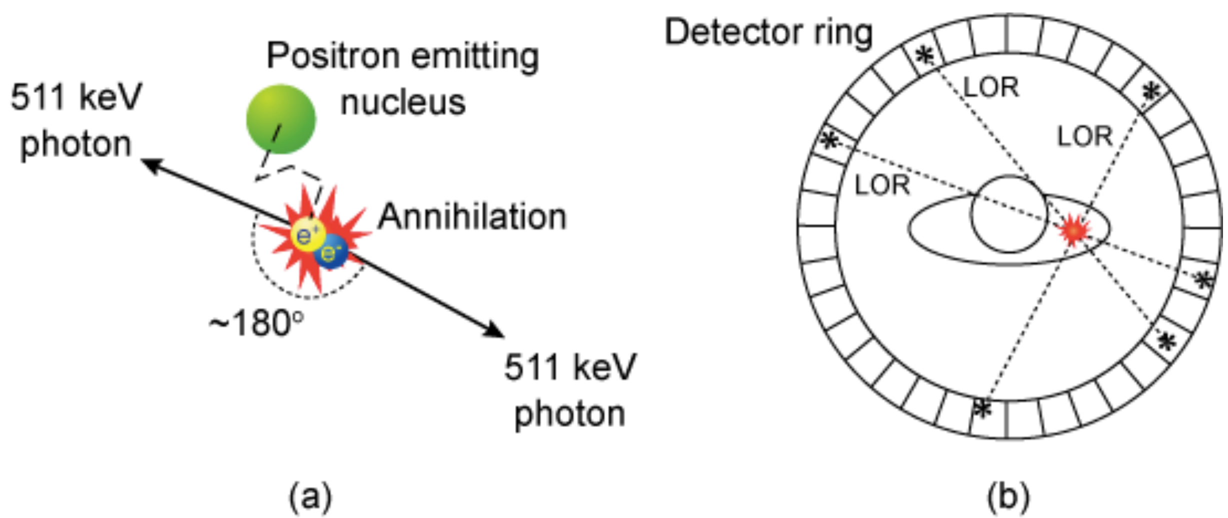
CRYSTAL CLEAR COLLABORATION

- *"Crystal Clear is an international collaboration active on **research and development on inorganic scintillation materials** for novel ionizing radiation detectors for high-energy physics, medical imaging and industrial applications."*

What are PET detectors?

- Two 511keV gamma rays due to e^+/e^- annihilation
- Interaction of photons with scintillating crystals
- Photons converted to an electrical signal via SiPM



Dilemma

- Sensitivity vs. Complexity
- Dimensions of scintillators
- One-to-one coupling vs. four-to-one coupling
- Single – sided vs. double – sided readout
- $$$

Main Idea

- sharing and redirection of scintillation light among multiple detectors, together with attenuation of light over the length of the crystals
- continuous DOI encoding with single-sided readout, and at the same time without the need for one-to-one coupling between scintillators and detectors
- good spatial, energy and timing resolutions while keeping the complexity of the system low

Set-up

- 8x8 matrix of 1.53x1.53x15mm scintillating LYSO crystals
- Top and bottom polished, other faces depolished
- 4x4 matrix of SiPMs
- Coupling of LYSO scintillator matrix to a SiPM array
- 3MBq Na-22 source
- 20 degrees Celsius

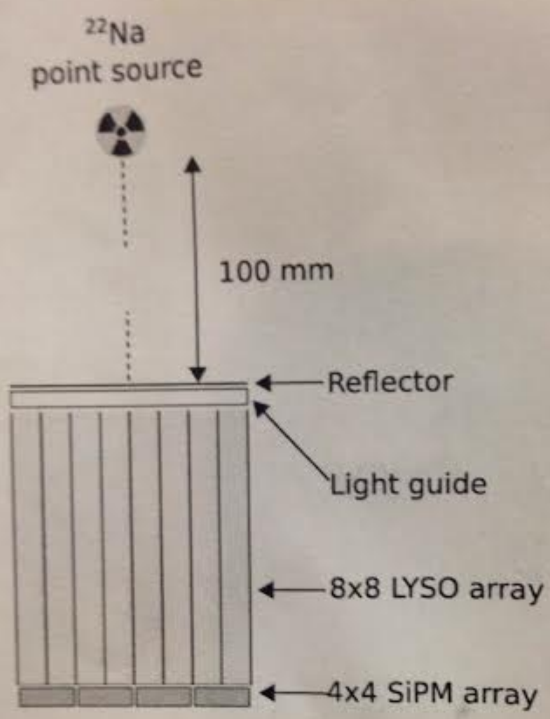


Figure 4: Schematic representation of the experimental setup used for standard characterization of the prototype module.

Light Collection

- Used for crystal separation

$$u = \frac{1}{\mathrm{P}} \sum_{i}^{N} p_i \, x_i \qquad v = \frac{1}{\mathrm{P}} \sum_{i}^{N} p_i \, y_i \qquad P = \sum_{i}^{N} p_i$$

- Finding w

$$w = \frac{p_{max}}{P}$$

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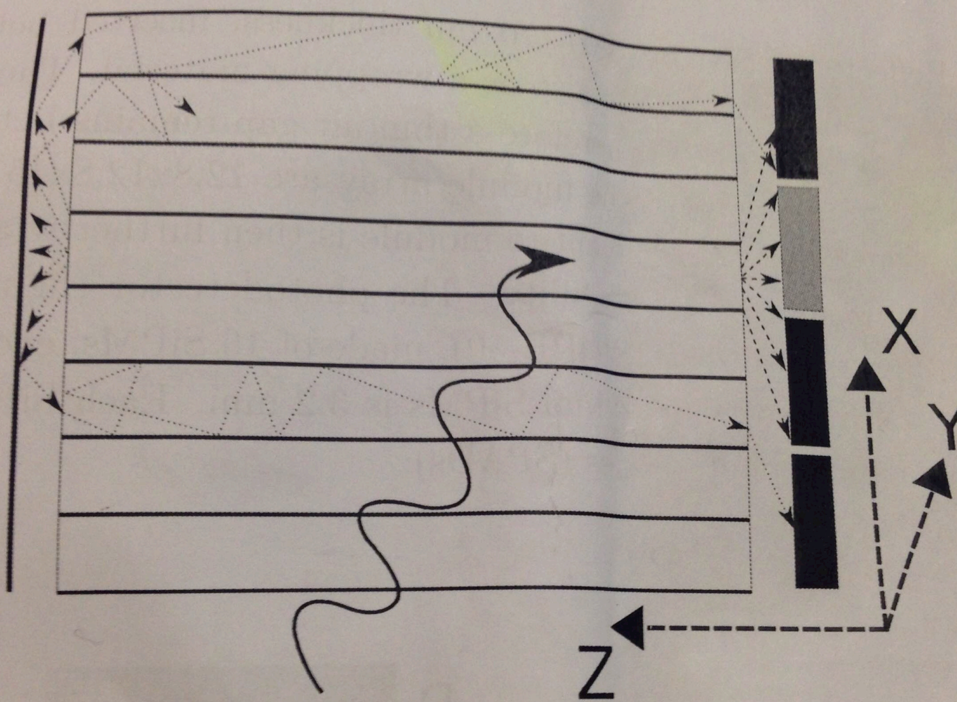
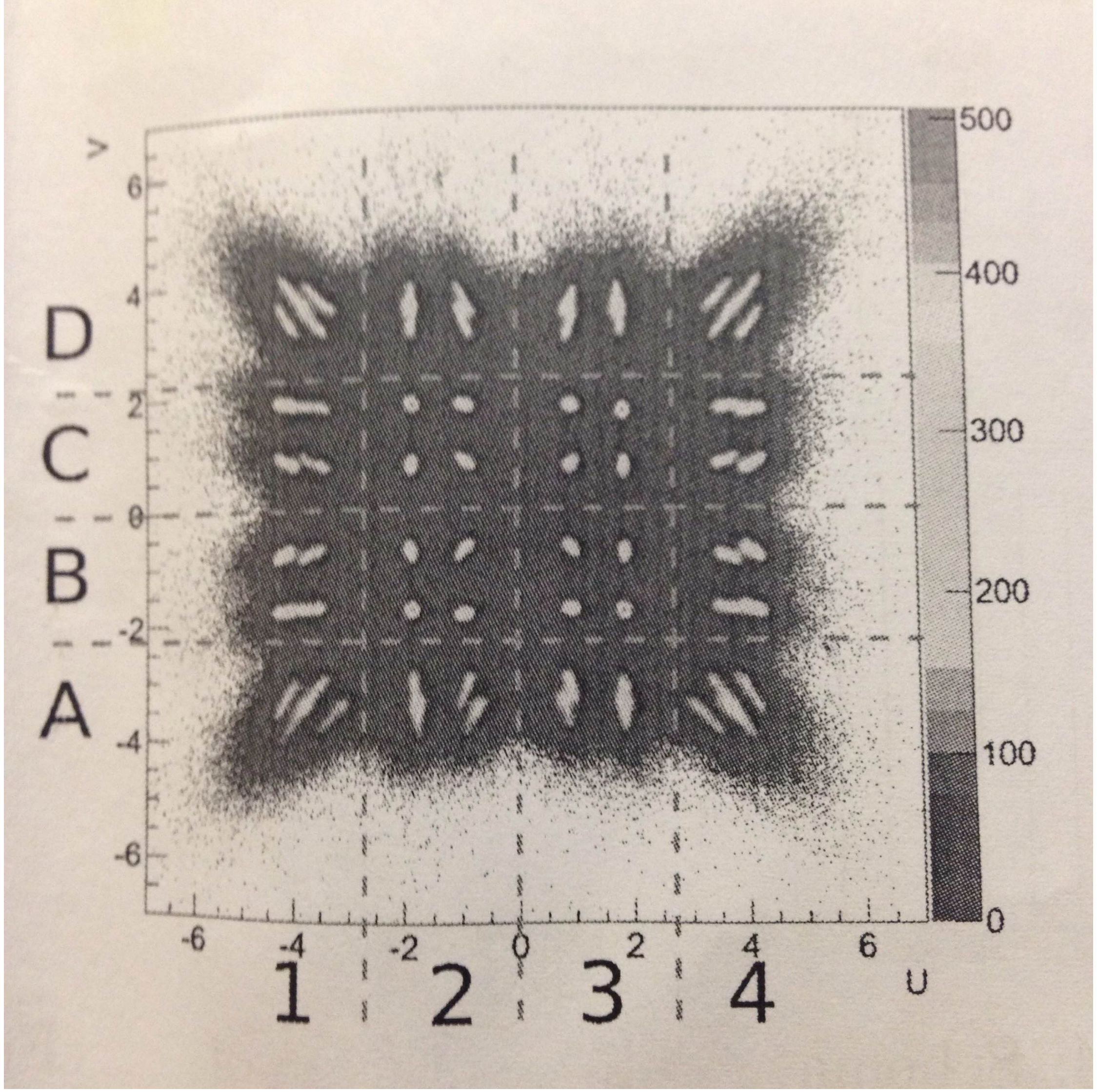


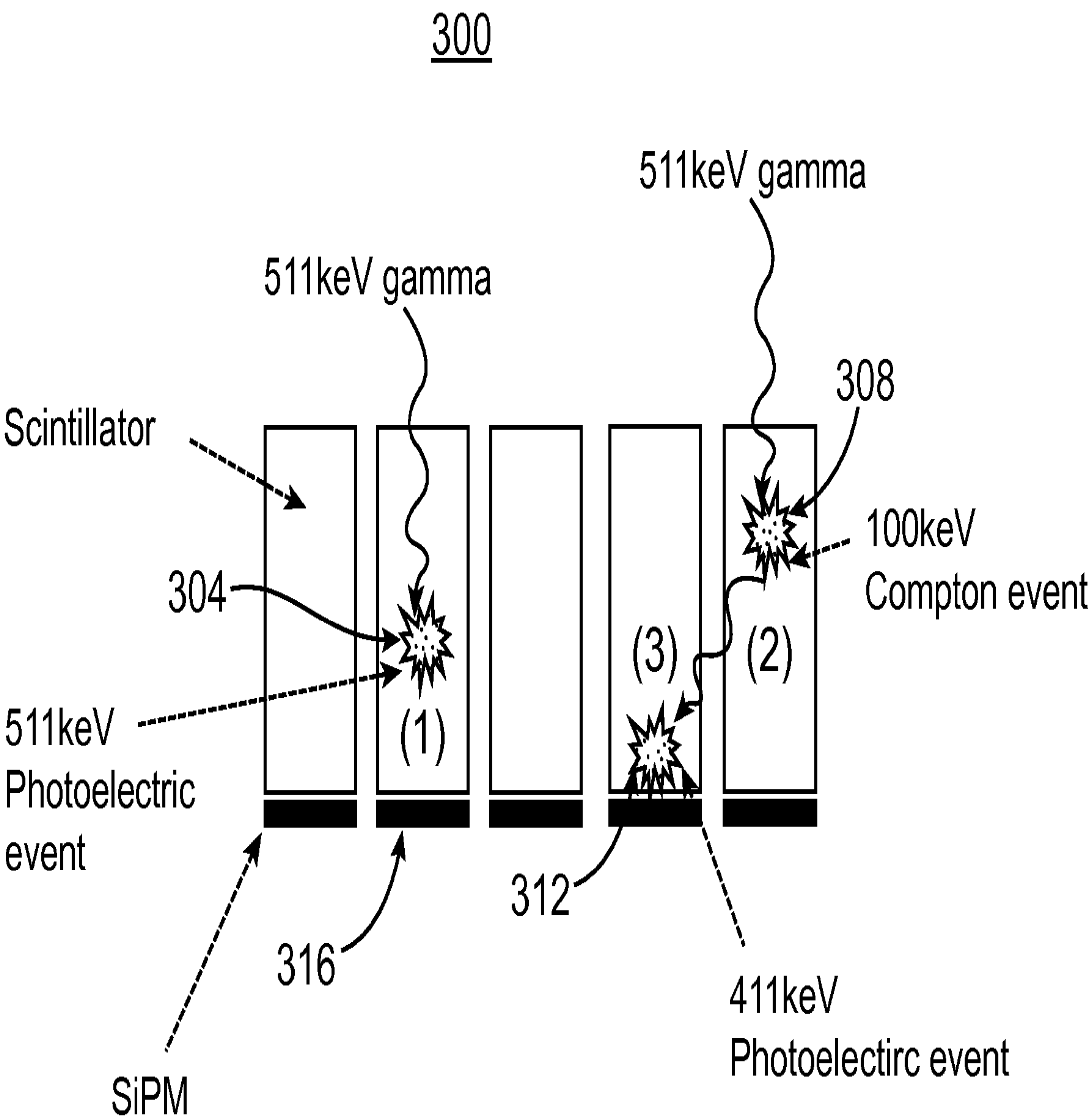
Figure 1: Schematic representation of the proposed DOI encoding method.

Crystal Separation



How it works

- excellent crystal separation is obtained for all the scintillators in the array
- DOI resolution is calculated for each crystal of the array



Electronic Tagging

- DOI encoding capability is demonstrated by means of an electronic tagging setup
- Why the z vs. w correlation is so important! Big breakthrough

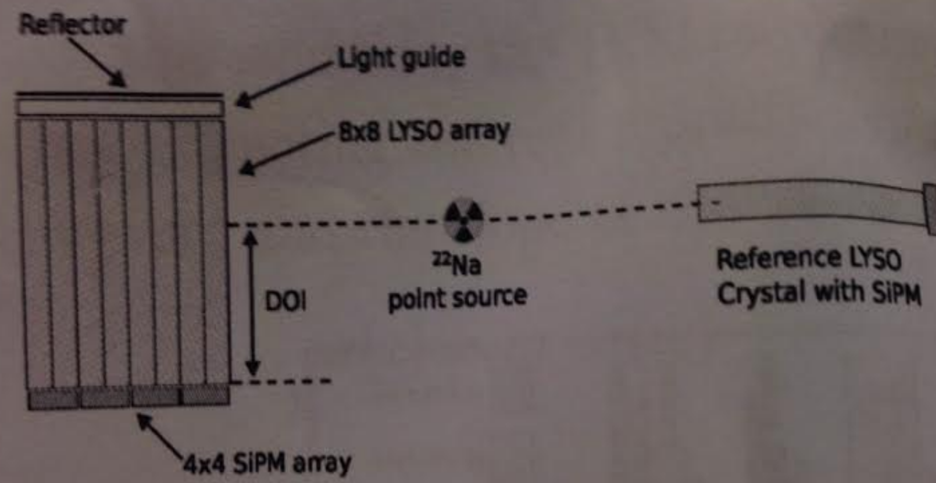
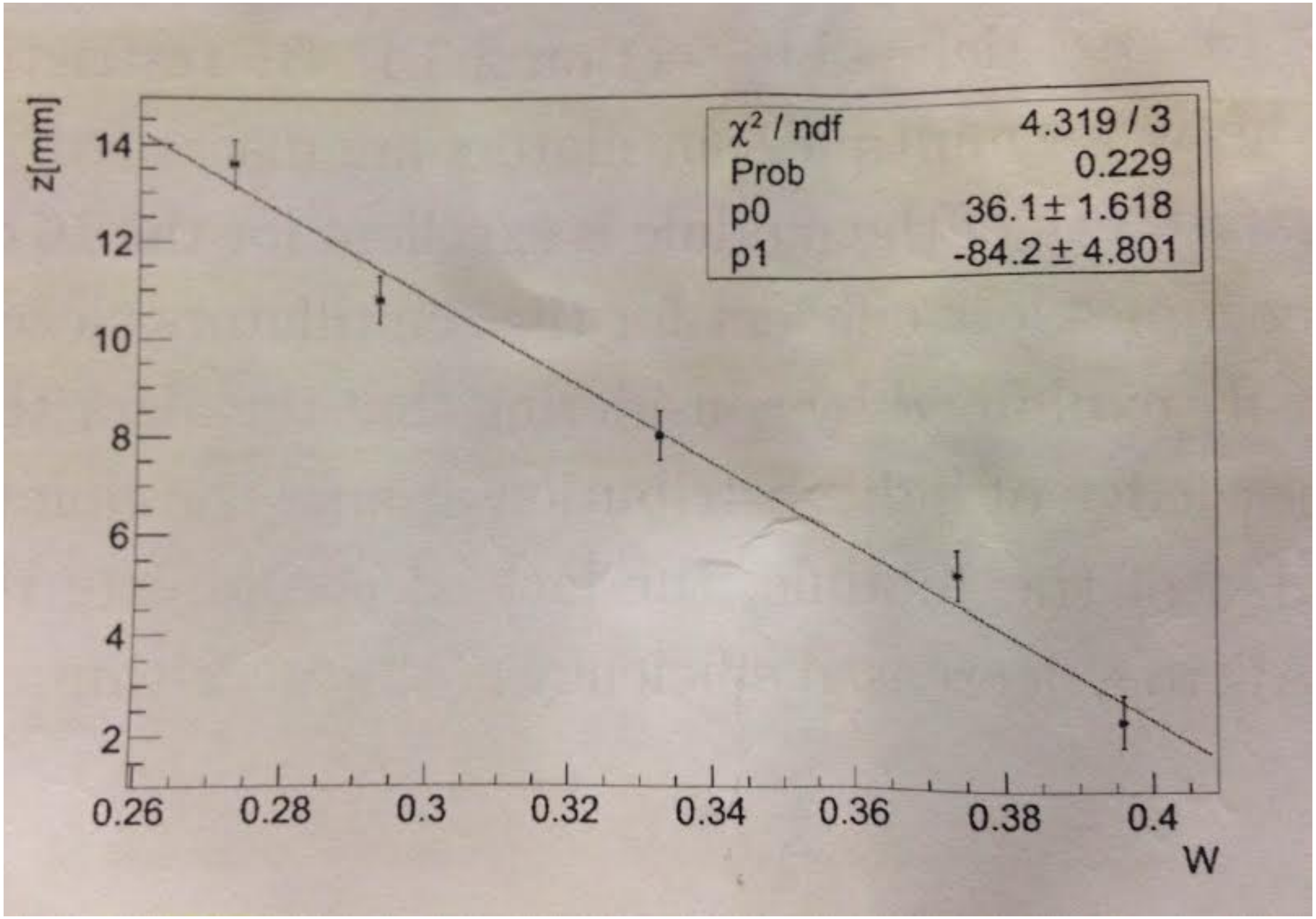


Figure 10: Schematic representation of the electronic tagging setup.

W-plot



z[mm]
14
12
10
8
6
4
2
0.26
0.28
0.3
0.32
0.34
0.36
0.38
0.4
W
χ2 / ndf 4.319 / 3
Prob 0.229
p0 36.1 ± 1.618
p1 -84.2 ± 4.801

+ Resolution

- mean energy resolution is 12.7% FWHM compared to 16.1% uncorrected
- mean DOI resolution achieved is 4.1 mm FWHM on a 15 mm long crystal

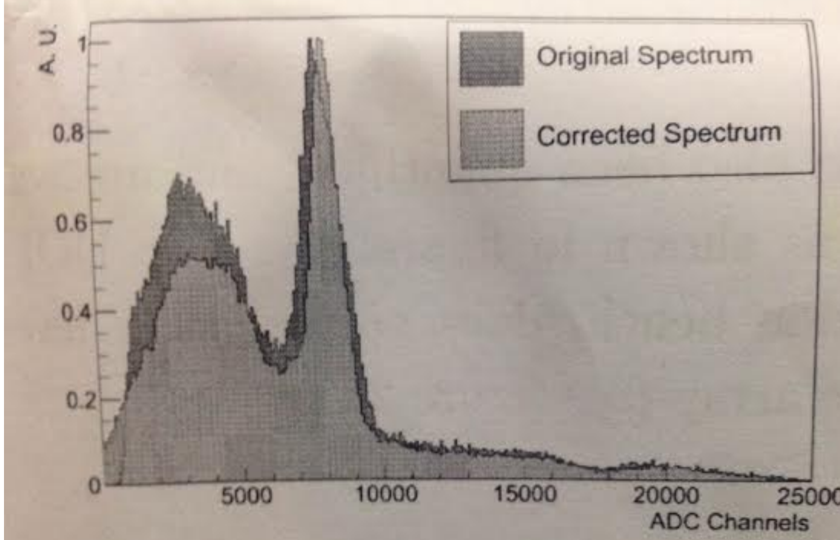
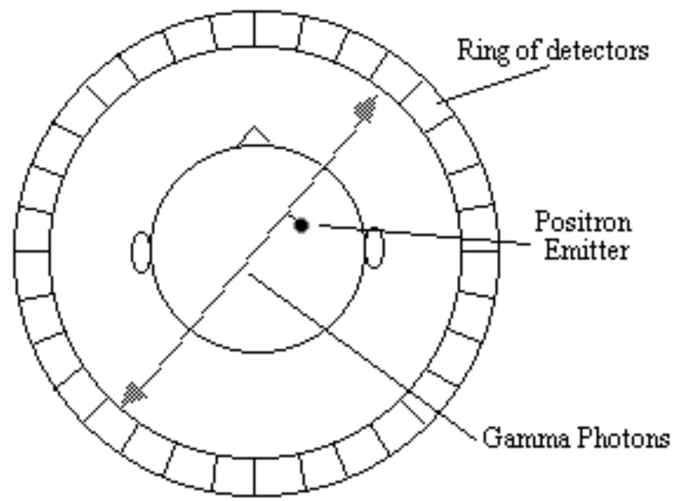


Figure 28: Comparison between standard charge spectrum (blue) and the same dataset corrected using the DOI information derived by w (red).

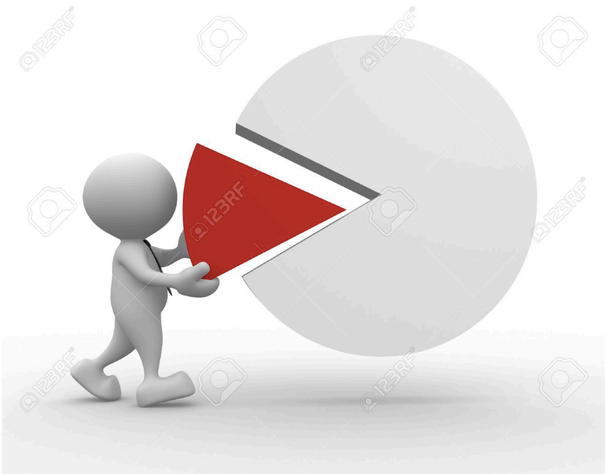
Application and Goal

- Several modules like the one described
- Light sharing and redirection mechanism described would involve the entire array of modules, rather than just one
- Shorter exams (on the order of minutes) with good spatial resolution (4.1mm)
- Organs and small animals



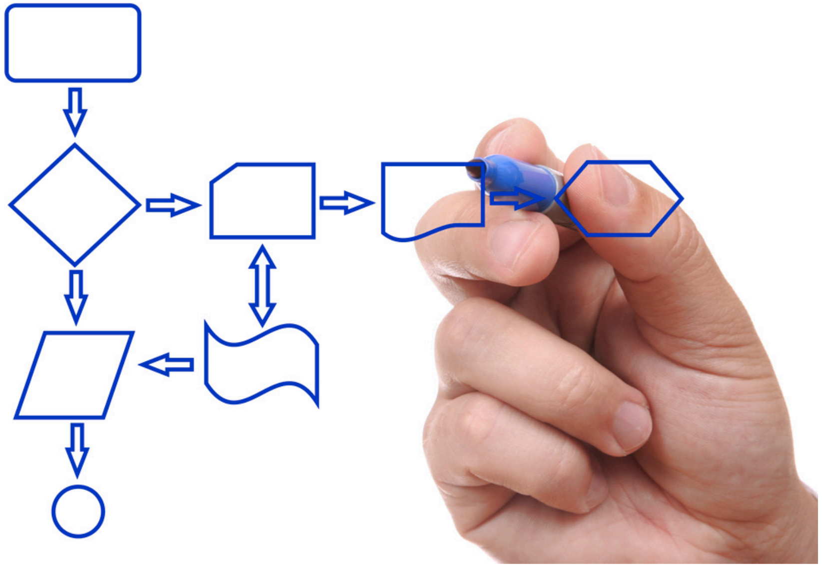
My contribution

- *Took measurements w/ source on top for best E resolution*
- Found the edge of the crystal trying with different methods
- Calibration with new DOI scan
- *Now seeing if resolution changes when threshold is increased



Finding edge of crystal

- Offset of 1.4mm in data for z vs. w plot
- One theory: physical offset
- Decide on procedure to acquire data and method for data analysis



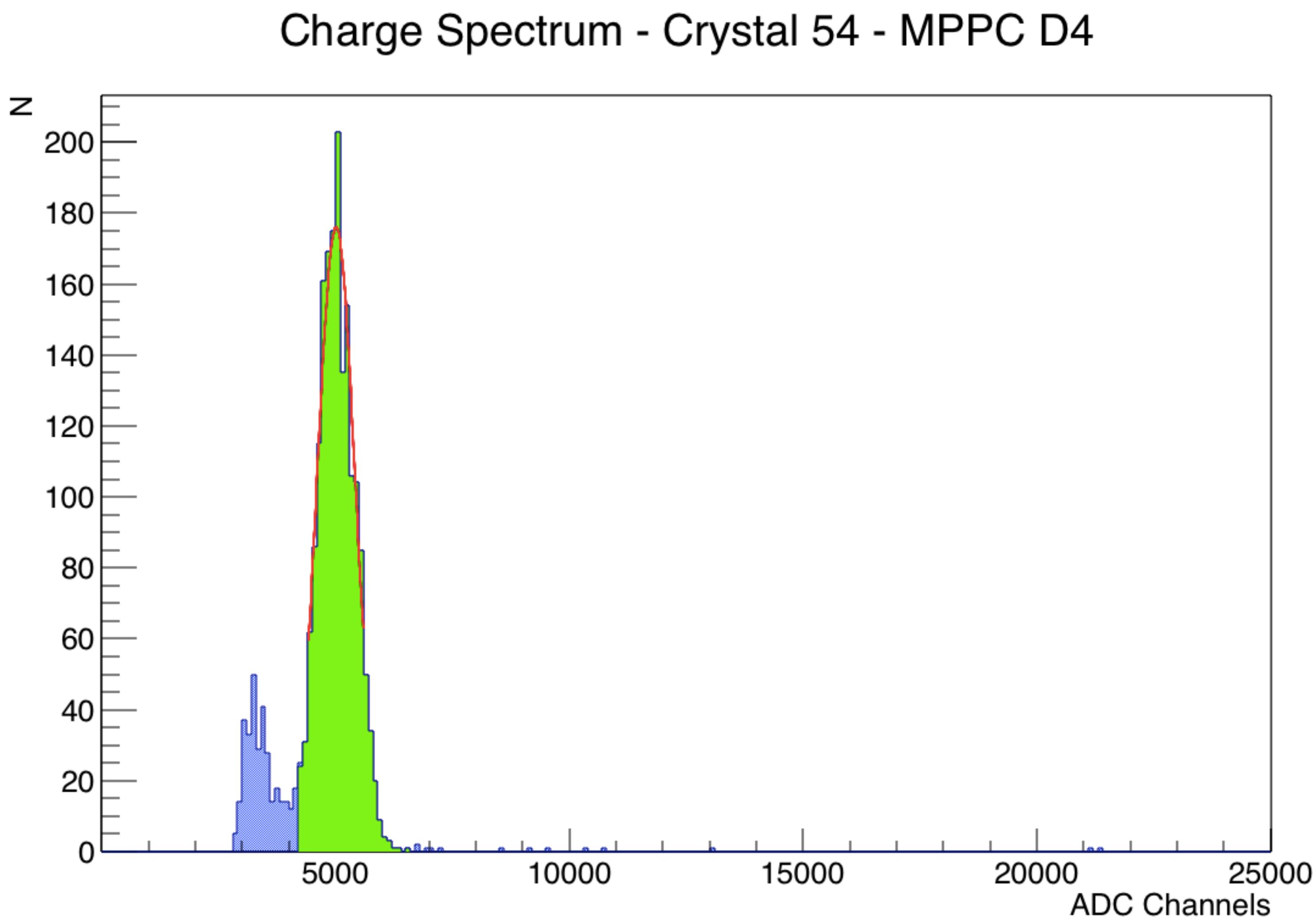
Overall Procedure

1) Use electronic tagging bench to acquire data at 0.5mm increments for z-value

2) Plot points to find drop off using different methods

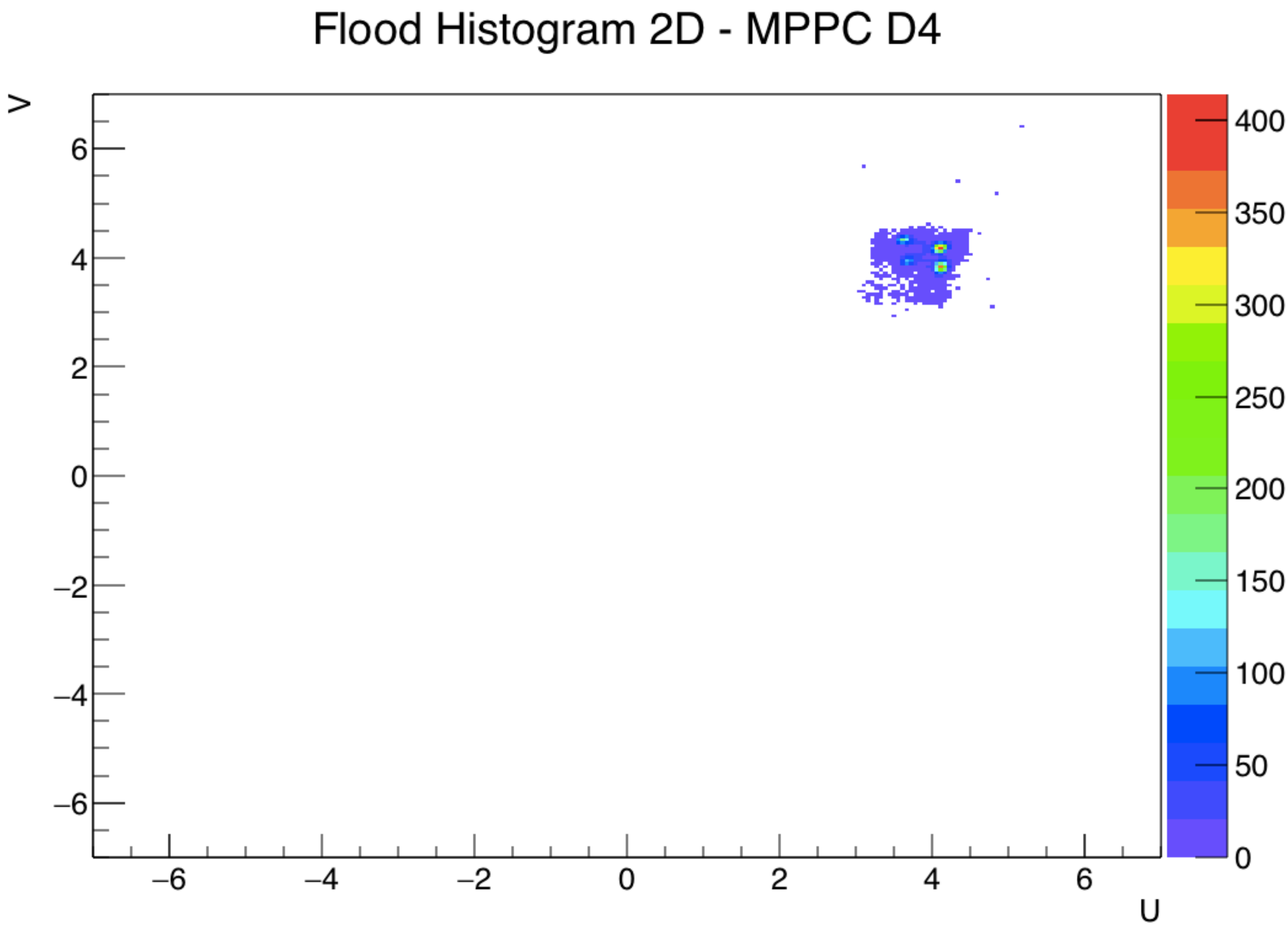
Method #1

- Started off by finding area under Gaussian in the highlighted part of the charge spectrum graph
- Not good
  - Separation of crystals changes


Charge Spectrum - Crystal 54 - MPPC D4
N
200
180
160
140
120
100
80
60
40
20
0
5000
10000
15000
20000
25000
ADC Channels

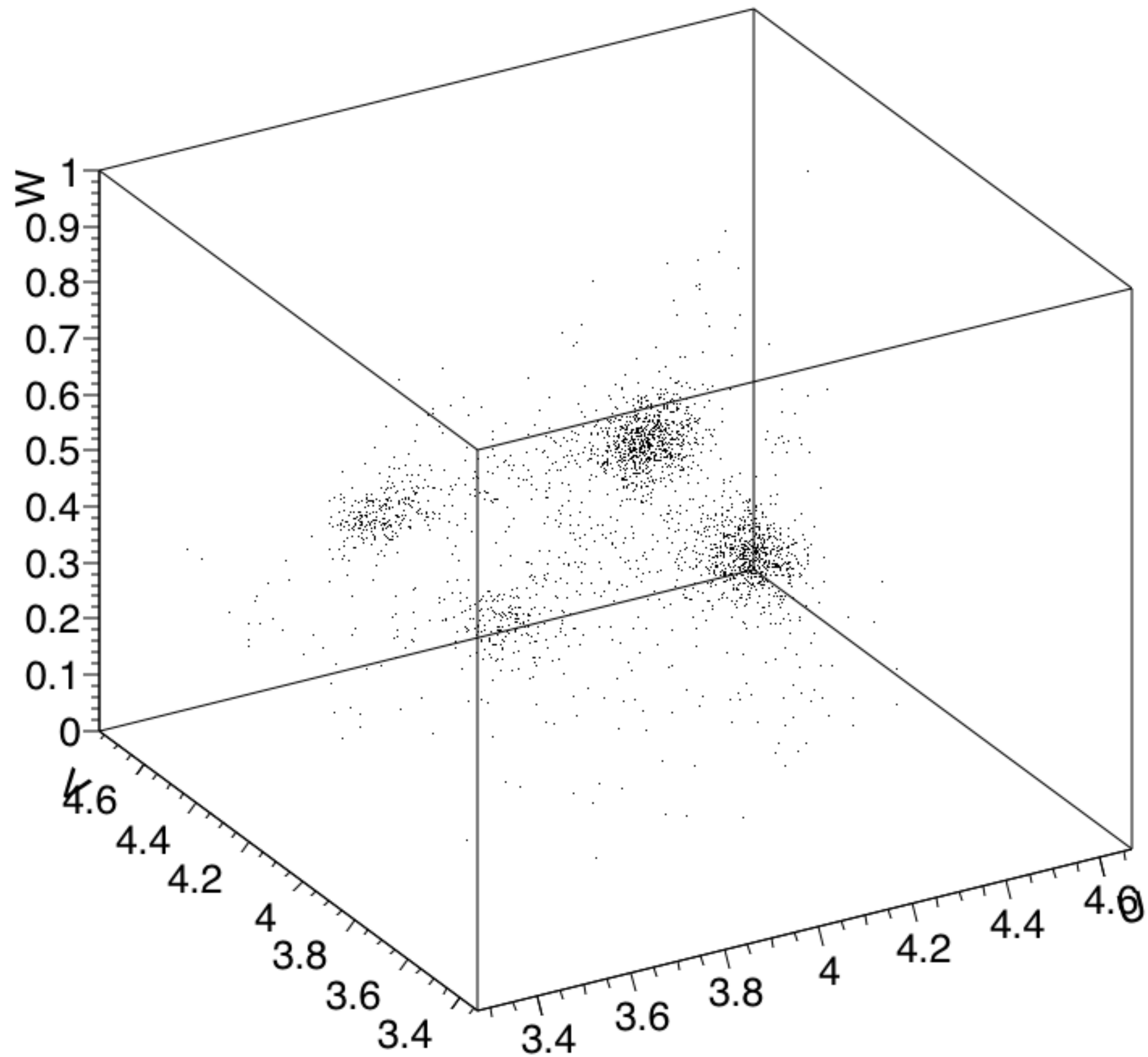
Method #2

- Then went to counting the number of events per MPPC
  - No uncertainty of the 3D cut given by the clustering algorithm
  - More consistent and no selection of "good" vs. "bad" events



Flood Histogram 2D - MPPC D4
V
6
4
2
0
−2
−4
−6
−6
−4
−2
0
2
4
6
U
400
350
300
250
200
150
100
50
0

Flood Histogram 3D - MPPC D4



Method #3

- Take number of events in flood histogram of MPPC and divide by number of events in Method #1
- Gives a normalized ratio to number of events in tagging crystal
- Best method..but time consuming

Macro used to find drop off

```
void CrystalIdentification(TString fileName){
//  TFile *f = new TFile("TTree_0_2016_22_04_12_54_51.root")
//f->ls()
//.q
TFile *f = new TFile(fileName);
//f->ls()
f->cd("Module 0.0");
//f->ls()
TCanvas* c = (TCanvas*) gDirectory->Get("TaggingCrystalSpectrum");
//c->ls()
//TH1F* f = (TH1F*) c->GetPrimitive("TriggerSpectrumHighlight")
TH1F* f1 = (TH1F*) c->GetPrimitive("TriggerSpectrumHighlight");
//f1->Draw()
//new TCanvas
//f1->Draw()

std::cout <<"///////////////////////////////////////////////////////"<< std::endl;
std::cout <<"//                TAGGING SPECTRUM                   //"<< std::endl;
std::cout <<"//                "<<f1->GetEntries()<<"                                 //"<<std::endl;
std::cout <<"///////////////////////////////////////////////////////"<< std::endl;

f->cd("Module 0.0/MPPC A4 - 0.0-3.0");
TCanvas* c1 = (TCanvas*) gDirectory->Get("Flood Histogram 2D - MPPC A4");
TH2F* f2 = (TH2F*) c1->GetPrimitive("Flood Histogram 2D - MPPC A4");
std::cout <<"//                MPPC    SPECTRUM                   //"<< std::endl;
std::cout <<"//                "<<f2->GetEntries()<<"                                  //"<<std::endl;
std::cout <<"///////////////////////////////////////////////////////"<< std::endl;
std::cout <<"//                RATIO   VALUE                      //"<< std::endl;
std::cout <<"//                "<<f2->GetEntries()/f1->GetEntries()<<"                           //"<<std::endl;
std::cout <<"///////////////////////////////////////////////////////"<< std::endl;


}
```

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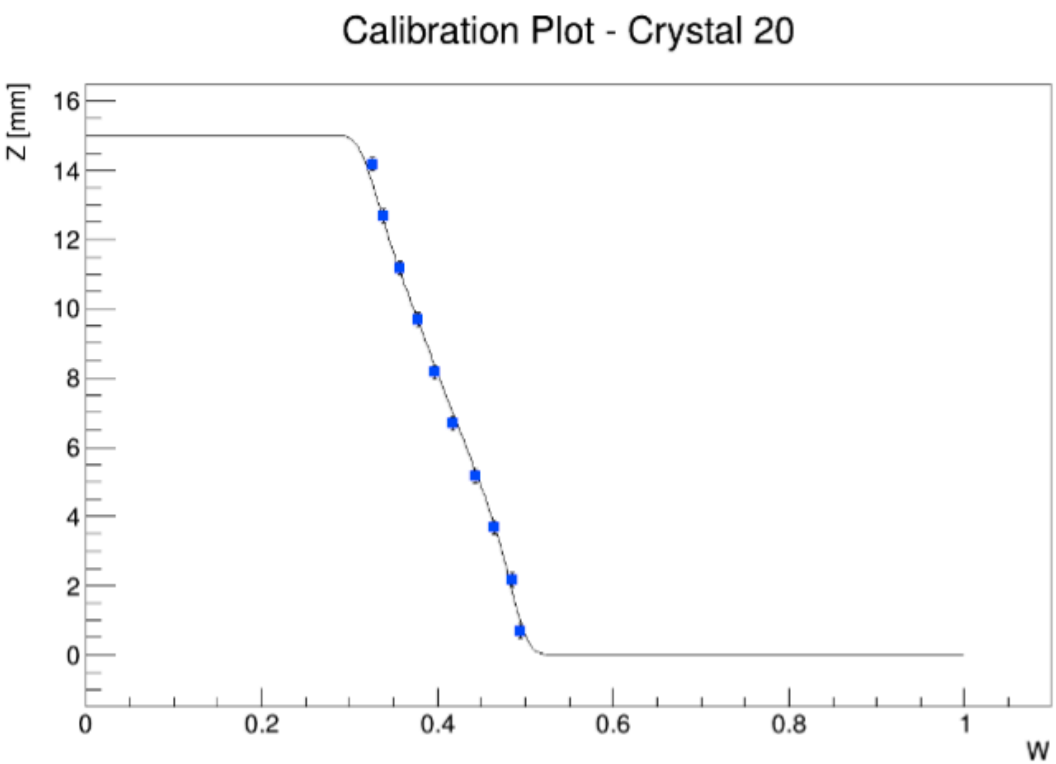
```
root [8] .x CrystalIdentification.C("../17.0/zdoi.root")
///////////////////////////////////////////////////////
//                TAGGING SPECTRUM                   //
//                36989                              //
///////////////////////////////////////////////////////
//                MPPC    SPECTRUM                   //
//                915                               //
///////////////////////////////////////////////////////
//                RATIO   VALUE                      //
//                0.0247371                          //
///////////////////////////////////////////////////////
```

Calibration

- 10 points instead of 5
- Quick mental math:
  - 10 points per column x 8 columns x 28 minutes = 37.3 hours
- Plot graphs



Present day

- Does increasing the threshold give us better energy resolution?
- Do we lose events, and therefore lower statistics?
- Compare charge spectrum histograms
- Compare w-plots and distance between test points and reference points found by algorithm

References

- M. Pizzichemi *et al.*, "A new method for DOI determantion in PET detectors," *Phys. Med. Biol*. 61(12) 4679-4798 (2016).
- C. Bircher and Y. Shao, "Use of internal scintillator radioactivity to calibrate DOI function of a PET detector with a dual-ended-scintillator readout," *Med. Phys.* 39(2) 777-787 (2012).
- S. Seifert and D. Schaart, "Improving the Time Resolution of TOF-PET Detectors by Double-Sided Readout," *IEEE Transactions on Nuclear Science* 62(1) 3-11 (2015).
- The wisdom of my advisors

Thank you

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- Marco Pizzichemi and Ginaluca Stringhini in particular