

Software for processing and analyzing data obtained from hybrid pixel detectors of the Medipix family

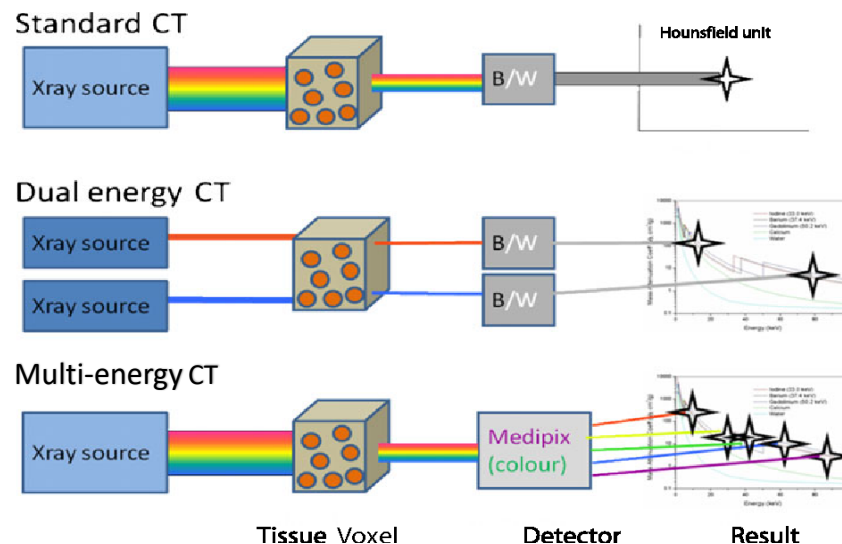
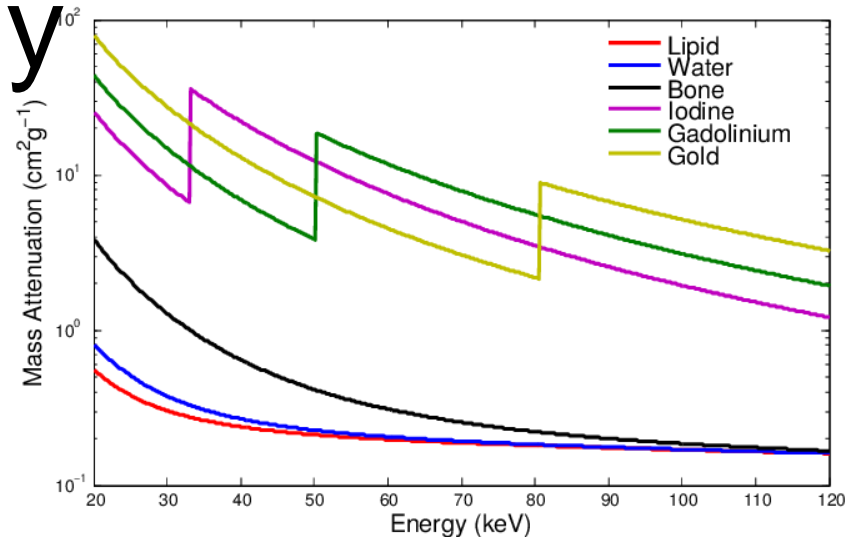
Aleksandr Lapkin (JINR)(lapkin@jinr.ru)

Nucleus-2022

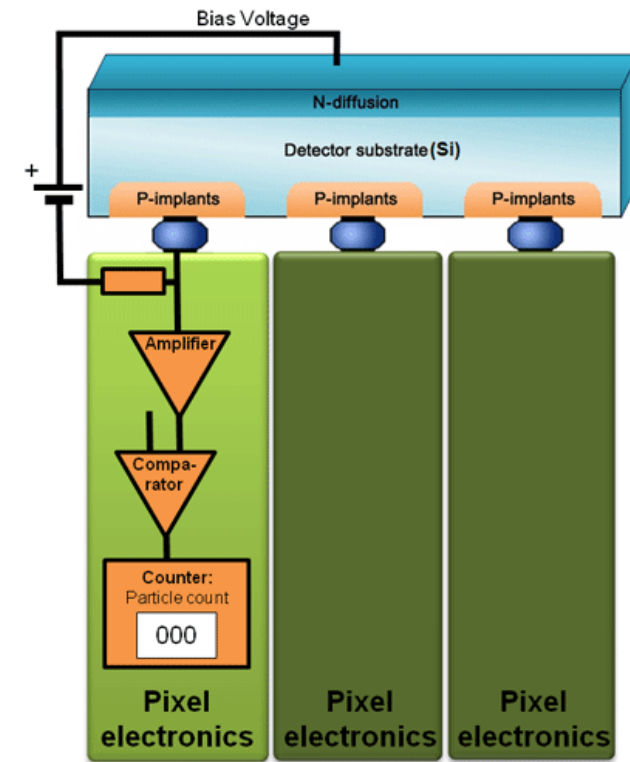
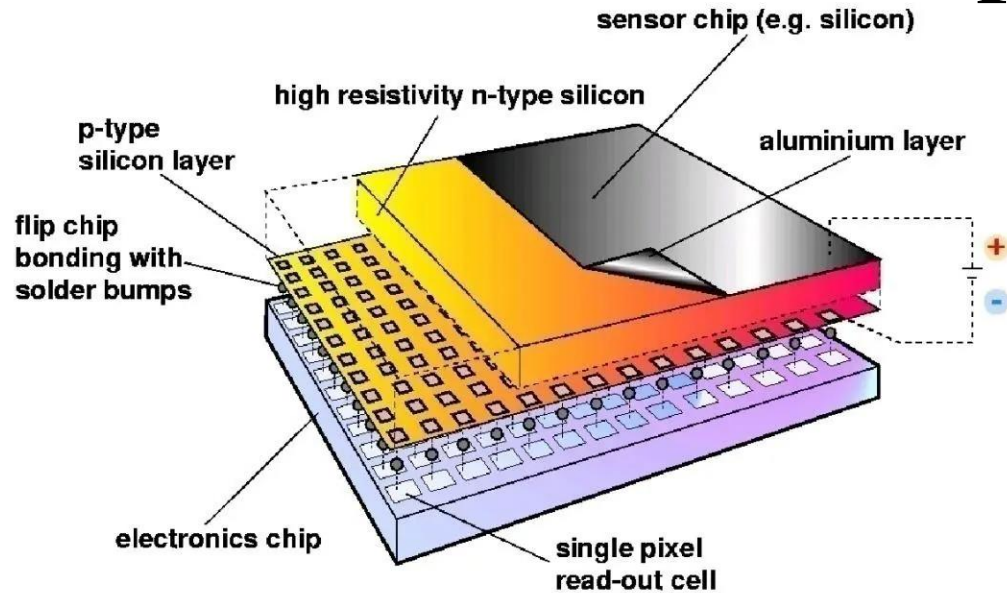
15.07.2022

Multi-energy tomography

- Our group is developing a multi-energy tomograph using Medipix family detectors
- To obtain energy information Medipix detectors perform threshold scans (series of frames of the object with different thresholds)
- We need a tool to operate threshold scan data

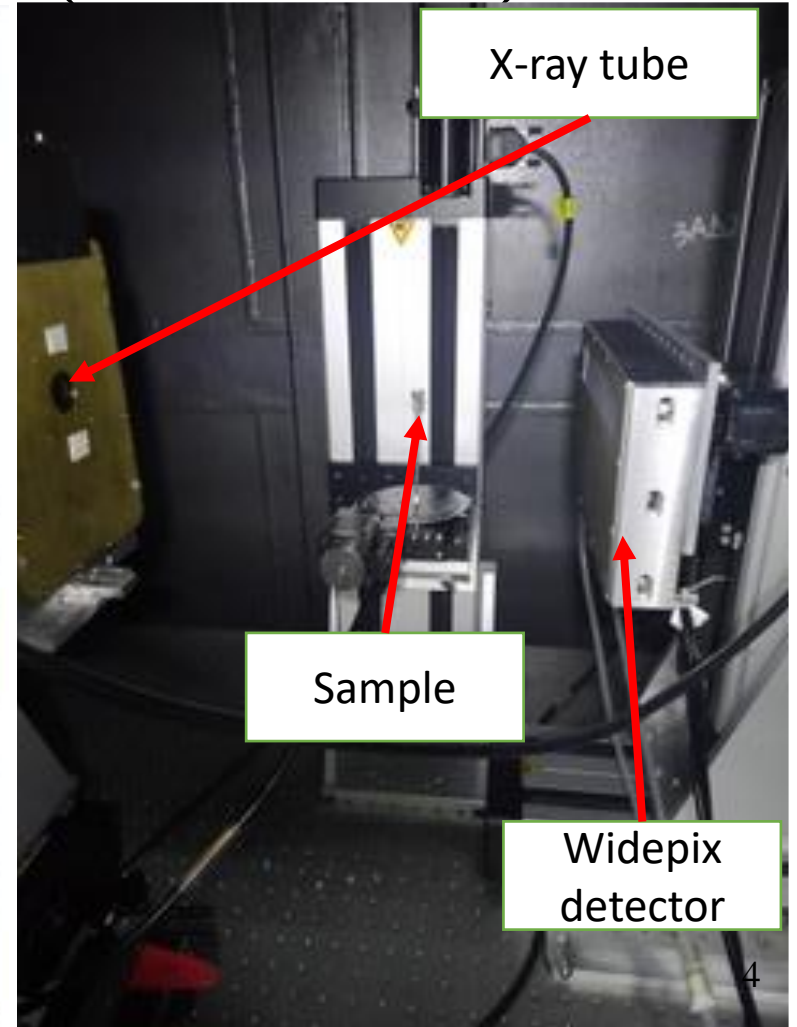


Medipix

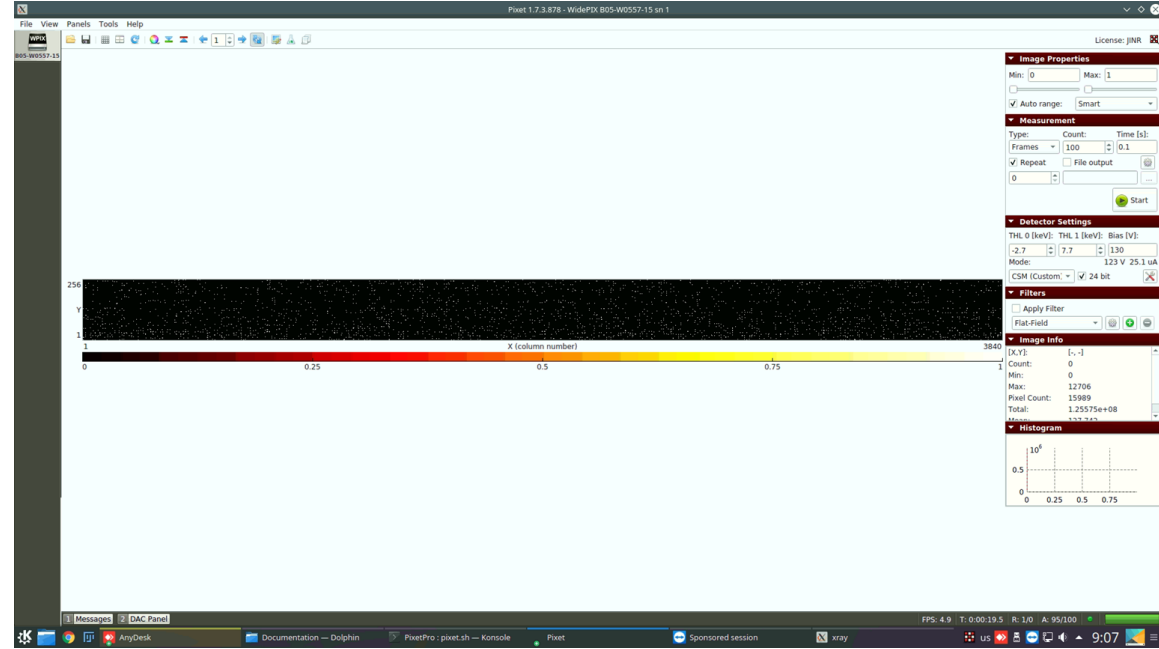


- Medipix series detectors are hybrid semiconductor pixel detector
- Developed by Medipix collaboration (<https://medipix.web.cern.ch/>)
- Consists of a semiconductor sensor and a readout integrated circuit
- Photons are detected by their transferring energy to electrons. The appeared free electrons move to the pixel contact pads, causing a signal
- The signal is digitized and compared with the threshold in a pixel. Pixels operate independent

Experimental Setup (“Kalan”)



Widepix



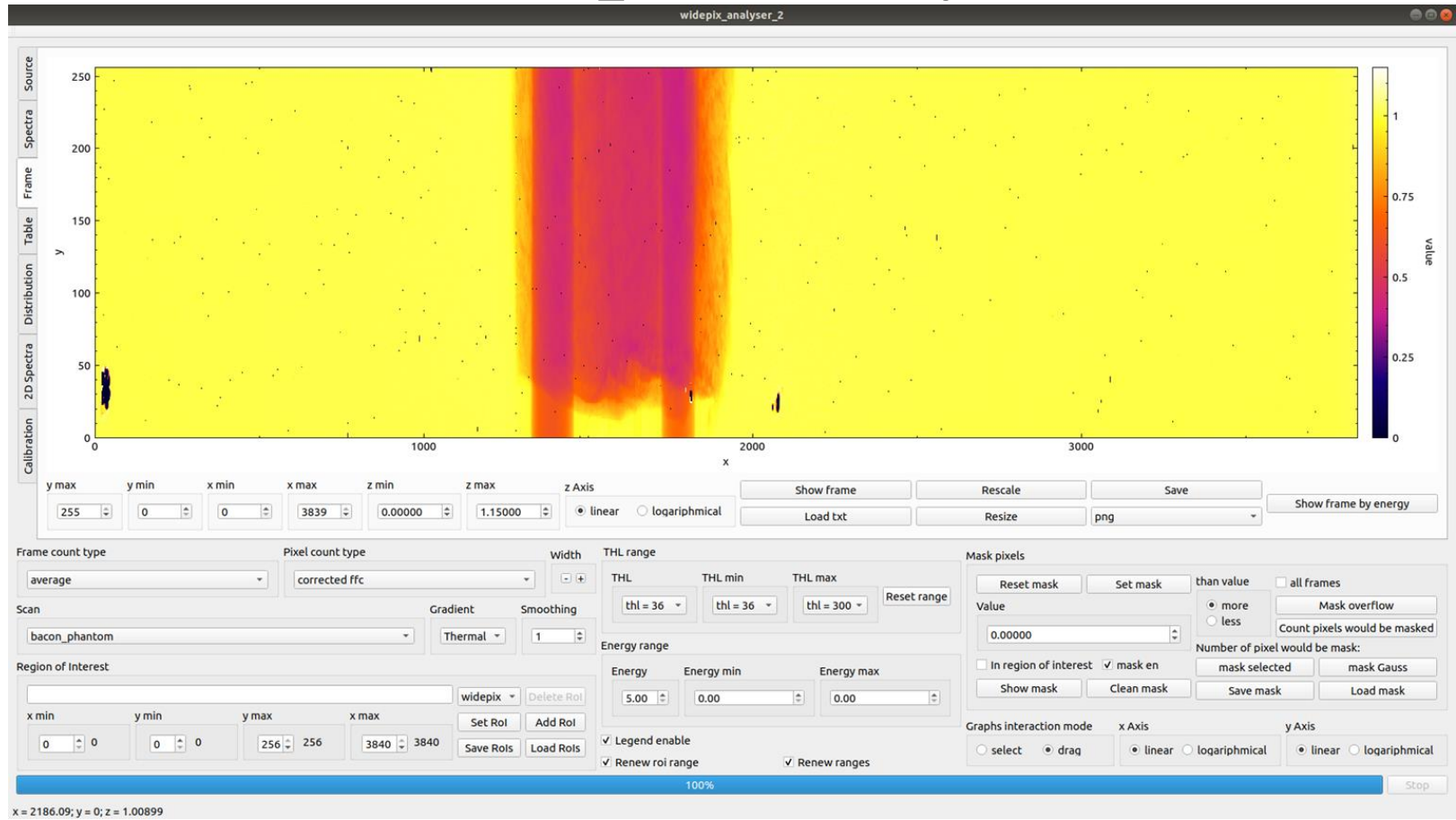
Widepix detector (15x1):

- 15 Medipix3RX in one row
- Charge Summing Mode for compensation the effect of charge spreading
- $256 \times 3840 = 983040$ pixels
- Two registration channels with one counter for each channel
- CdTe sensor

Pixet Software:

- Standard software for driving of Medipix detectors
- Allows to make readout of frames series, threshold scans, equalization and detector setup
- Python interpreter
- Pixet cannot provide analysis which is required for our researches

Widepix analyser



- The program was written to analyze threshold scans data
- It was written in C++ language using Qt and CERN ROOT libraries
- There is the phantom with tubes with La and Gd and pork fat on the frame (the phantom is showing in the next slide)

Phantoms



Phantom with tubes and pork fat



Phantom with tubes. There are I, Gd, La solutions and H₂O in the tubes (Cocktail phantom)

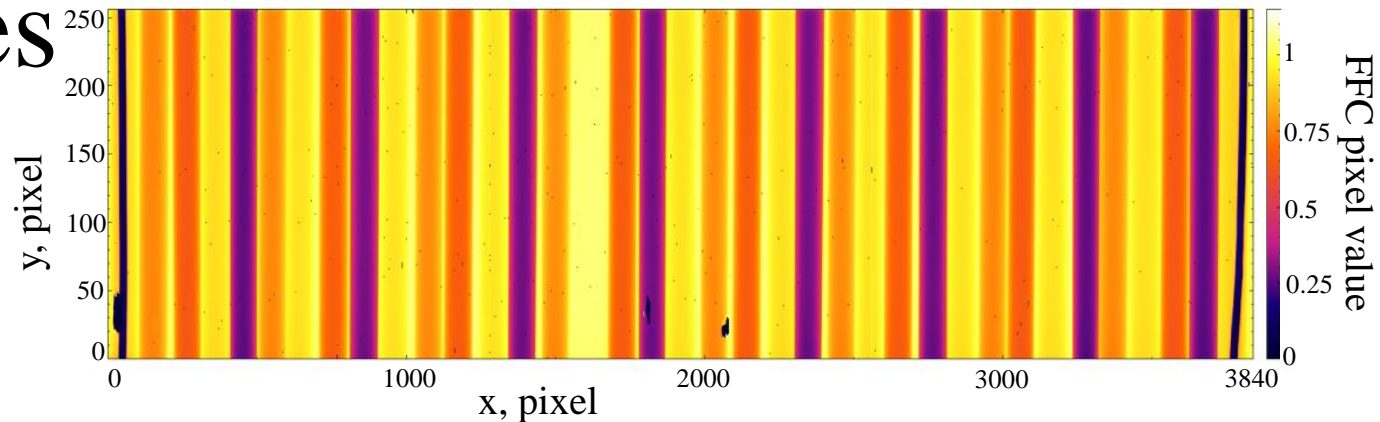
- These phantoms allow to compare X-ray energy absorption of different materials in different concentrations
- Pork fat emulates soft tissue

Frames

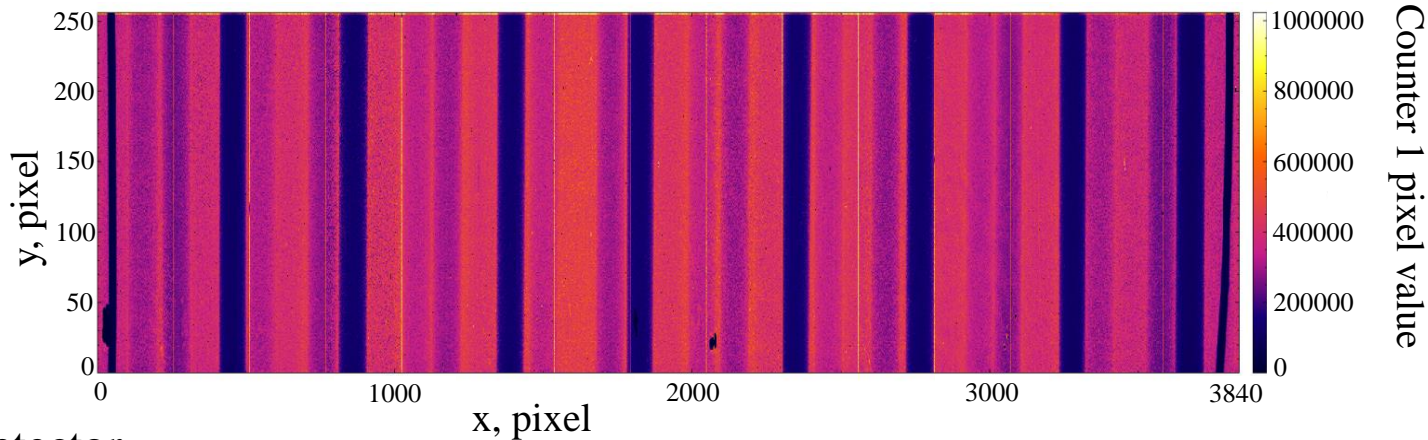


Cocktail phantom

FFC frame THL = 36

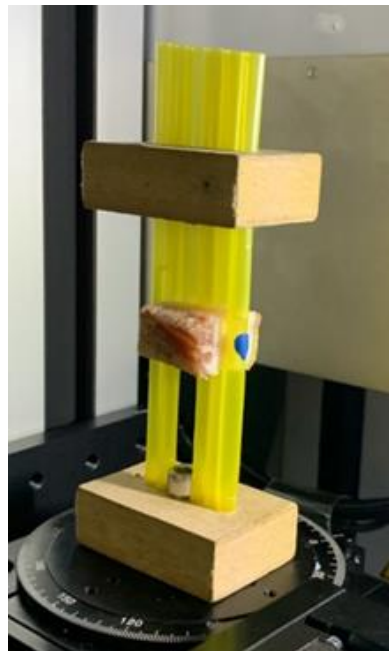


Raw data frame THL = 36



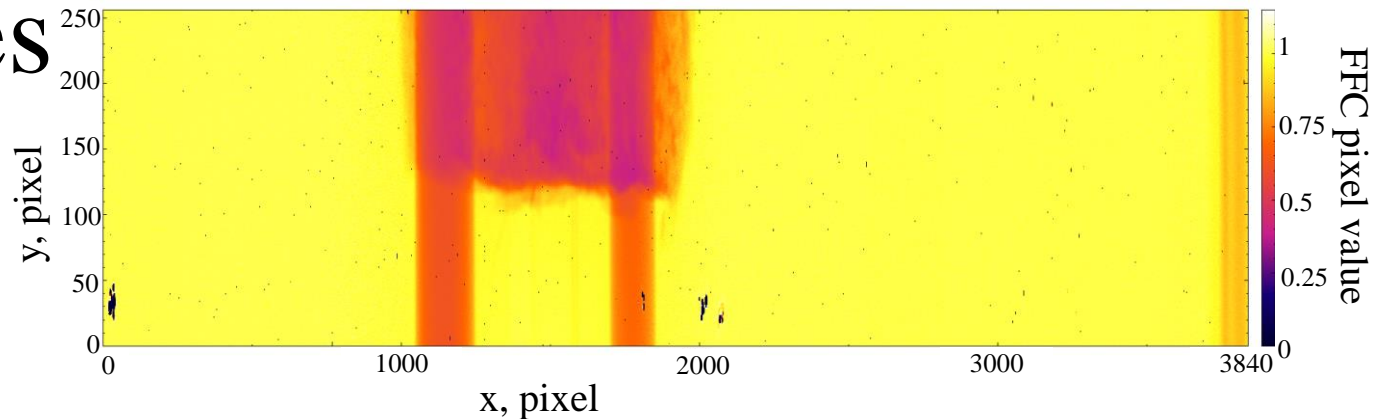
- Frame is an image from the detector
- Frame is a 2D histogram
- A bin value is calculated from the counter values of the corresponding pixels (raw data, FFC,...)

Frames

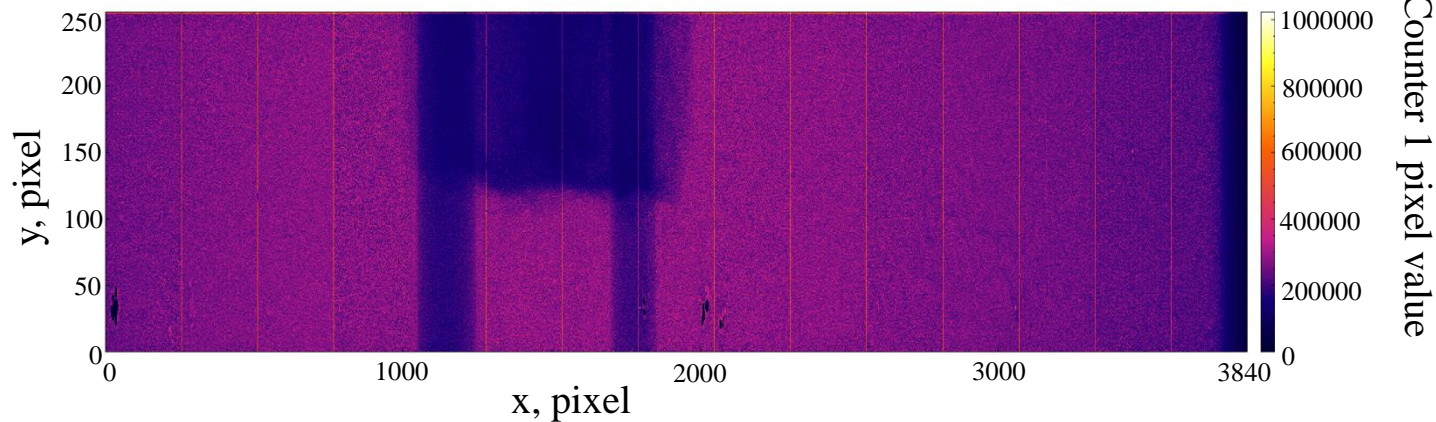


Phantom with
pork fat

FFC frame THL = 36



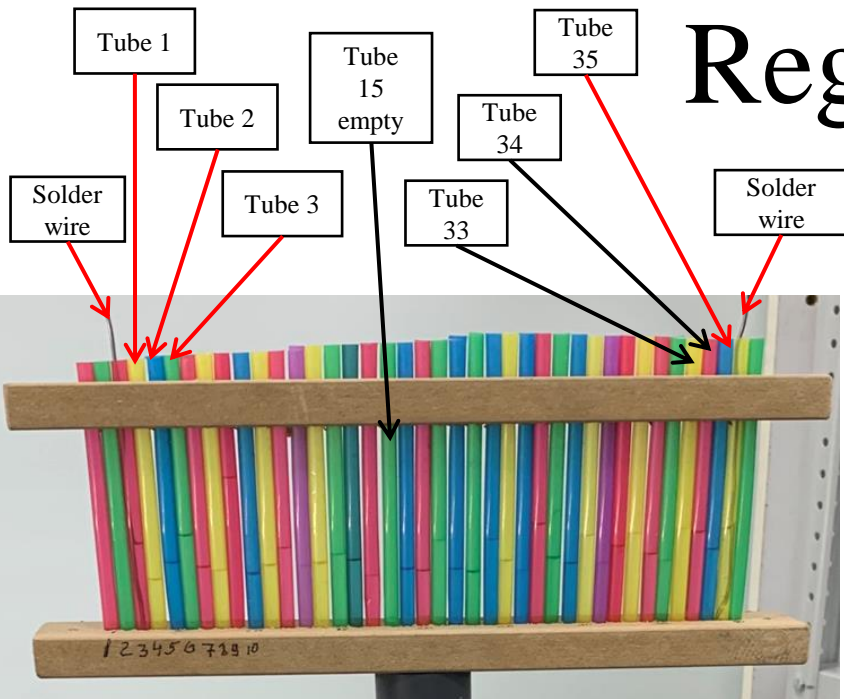
Raw data frame THL = 36



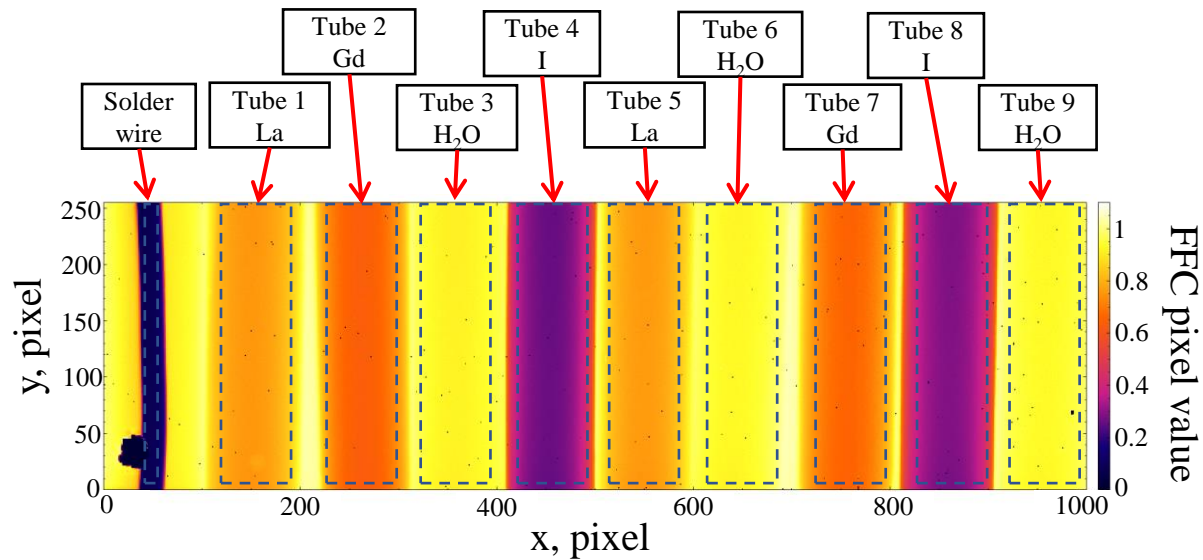
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Regions of Interest (RoI)

Frame area, FFC, THL = 36



Cocktail phantom

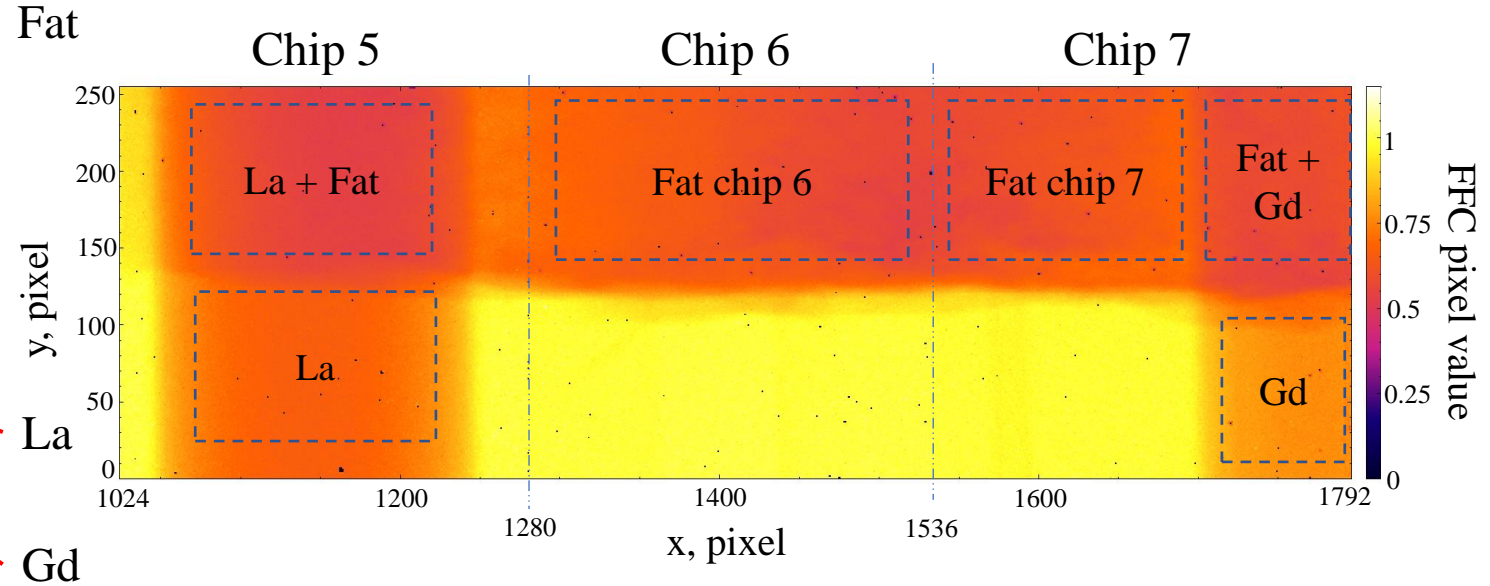


There are 35 tubes and 2 solder wires on the frame

- The program can operate a set of different RoI
- Region of interest is a detector area which is processed independently

Regions of Interest (RoI)

Frame area, FFC, THL = 36

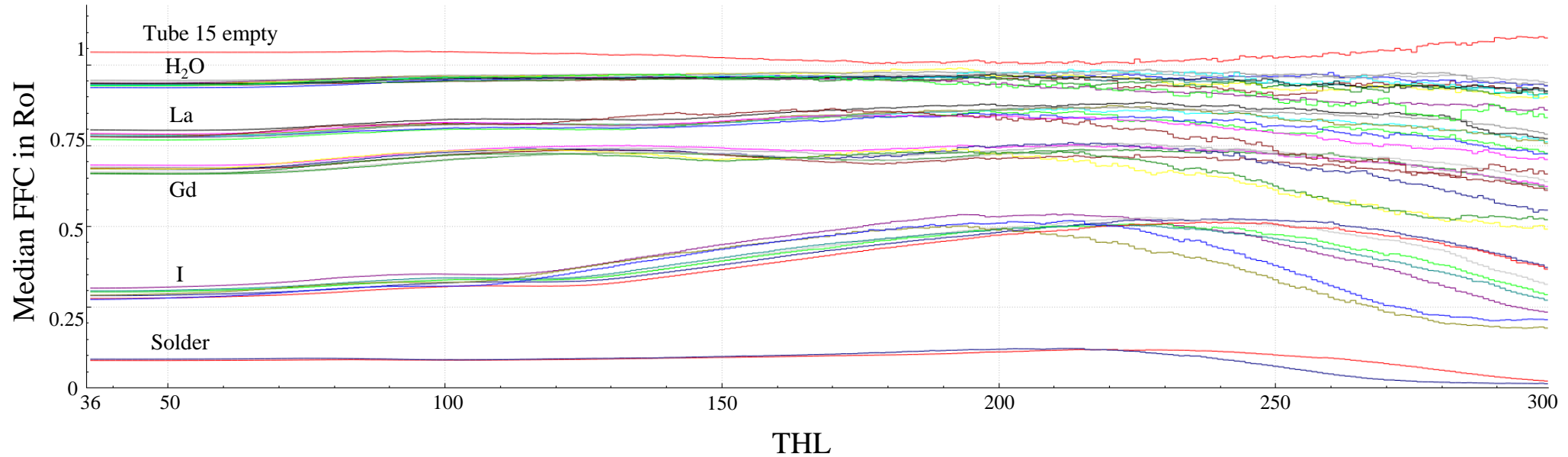


Phantom with pork fat

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- Region of interest is a detector area which is processed independently

Spectra

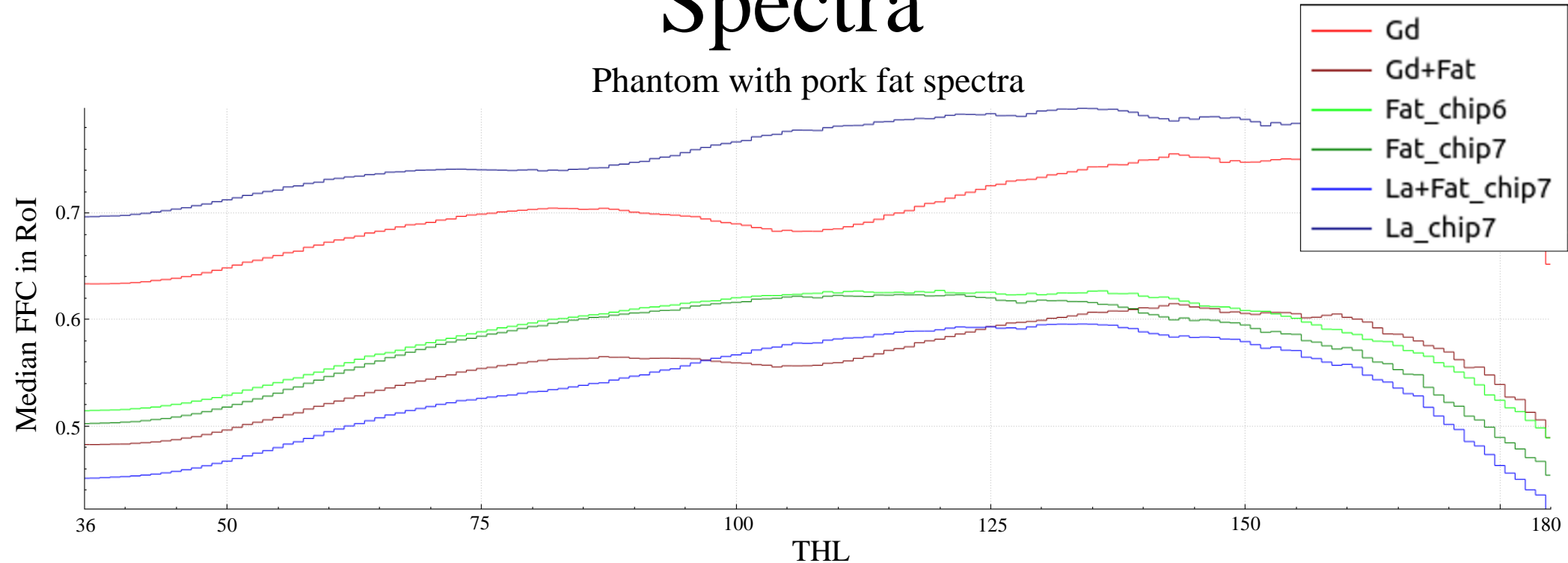
Cocktail phantom spectra by tubes



- Spectrum means the dependence of the frame value on the threshold value
- The frame value is calculated from pixel values (sum, mean, median, min, max,...)
- Spectra can be calculated for RoI

Spectra

Phantom with pork fat spectra



- Spectrum means the dependence of the frame value on the threshold value
- The frame value is calculated from pixel values (sum, mean, median, min, max,...)
- Spectra can be calculated for ROI

Statistic data

Cocktail phantom data, THL = 100,
pixel value is FFC

RoI	Number of pixels	Sum	Mean	Median	Standard deviation	Signal to noise resolution
Tube 1 (La)	17466	14091.2	0.806778	0.799718	0.03115	28.8349
Tube 2 (Gd)	17834	12761.3	0.715558	0.704645	0.0377045	22.4352
Tube 3 (H ₂ O)	22140	21153.9	0.955462	0.952464	0.00329717	29.6459
Tube 4 (I)	18772	6430.13	0.342539	0.324684	0.0486977	12.0184

The program calculates data:

- Number of pixels
- Minimum
- Maximum
- Sum
- Mean
- Median
- Number of zero pixels
- Number of filtered pixels
- Number of overflowed pixels
- Standard deviation
- Signal to noise resolution
- Variance
- Most probable value of pixel in RoI

- The statistic data is calculated on the whole Widepix detector, each Medipix3RX chip and each regions of interest
- The statistic analysis is made pixel by pixel. The pixel value is calculated on the counter values (counter1, counter0, FFC, counter1/counter0,...)

Table of statistical values

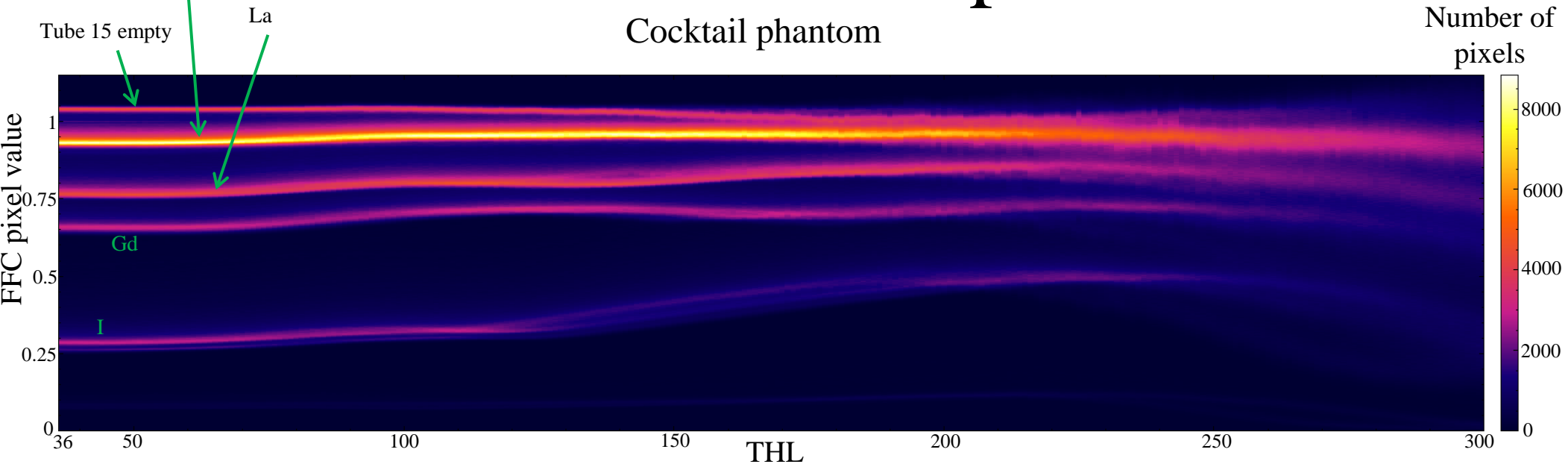
Cocktail phantom data, THL = 100, pixel value is FFC

Name of area ^	Number of pixel	Minimum	Maximum	Sum	Mean	Median	Zeros	Overflows	Masked	Standard deviation	Signal to noise resolution	Maximum density	Variance	x min	x max	y min	y max
18 tube 1	7230	0	1.01362	6879.23	0.951485	0.948819	2	0	0	0.0245465	39.7385	0.936188	0.000602529	70	100	6	247
19 tube 2	17466	0	0.975341	14091.2	0.806778	0.799718	10	0	0	0.03115	28.8349	0.78756	0.000970324	121	192	1	247
20 tube 3	17834	0	0.842464	12761.3	0.715558	0.704645	8	0	0	0.0377045	22.4352	0.683911	0.00142163	228	302	7	248
21 tube 4	22140	0	1.02073	21153.9	0.955462	0.952464	20	0	0	0.0329717	29.6459	0.944526	0.00108713	317	407	4	250
22 tube 5	18772	0	0.492701	6430.13	0.342539	0.324684	13	0	0	0.0486977	12.0184	0.299046	0.00237147	416	492	6	253
23 tube 6	20900	0	0.949474	17282.7	0.826923	0.816721	17	16	0	0.0408455	22.2633	0.801829	0.00166835	509	592	1	253
24 tube 7	20995	0	1.06358	20246.1	0.964328	0.959145	11	0	0	0.029727	33.034	0.954172	0.000883696	607	692	4	251
25 tube 8	20417	0	0.88232	15178.5	0.743424	0.733615	16	1	0	0.0482381	17.8743	0.698503	0.00232691	715	798	6	252
26 tube 9	18352	0	0.490074	6692.69	0.364684	0.351674	17	0	0	0.0394066	15.3246	0.333411	0.00155288	823	897	4	252
27 tube 10	22000	0	1.04476	21269	0.966775	0.964564	36	0	0	0.0424051	23.187	0.956904	0.0017982	917	1005	2	252
28 tube 11	19422	0	0.919378	16020.8	0.824879	0.816106	7	0	0	0.032472	27.9696	0.803271	0.00105443	1037	1115	3	252
29 tube 12	20000	0	0.962446	14669.9	0.733497	0.721715	20	0	0	0.0443152	19.3262	0.704992	0.00196384	1135	1215	1	251
30 tube 13	23500	0	1.08771	22877.7	0.973519	0.966778	23	359	0	0.0399426	24.7022	0.955793	0.00159541	1239	1338	10	251
31 tube 14	15808	0	0.438571	5443.1	0.344325	0.335448	12	0	0	0.0294615	19.9173	0.320601	0.000867978	1358	1422	4	251
32 tube 15	21131	0	1.03145	17848.7	0.844667	0.830393	28	25	0	0.0546976	16.8025	0.809025	0.00299183	1453	1539	4	250
33 tube 16	25602	0	1.10633	26602.4	1.03908	1.03991	13	0	0	0.0245447	41.5303	1.03934	0.000602444	1570	1672	2	253
34 tube 17	19276	0	0.863371	14121.8	0.732611	0.719633	15	0	0	0.0460273	18.5961	0.69924	0.00211851	1687	1766	5	249
35 tube 18	12789	0	0.444263	4381.23	0.342578	0.333459	8	0	0	0.0287074	20.3885	0.32008	0.000824114	1796	1859	50	253
36 tube 19	22814	0	1.04724	21769.2	0.954202	0.949451	19	2	0	0.0337396	28.9521	0.939296	0.00113836	1881	1973	1	249

- The program generates statistic data in the form of a table

Two dimension spectra

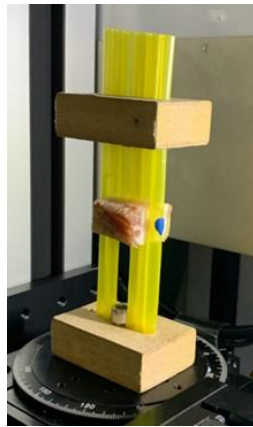
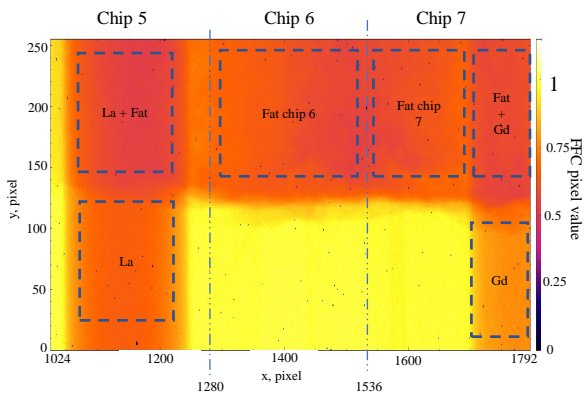
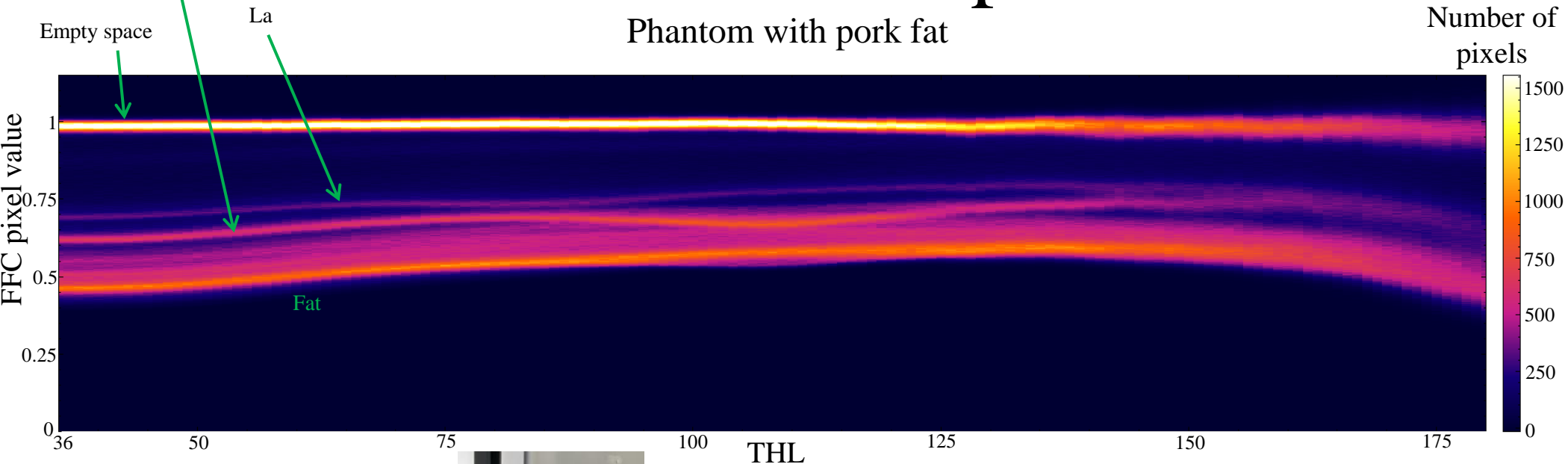
Cocktail phantom



- Two dimension spectrum is a 2D histogram
 - X axis is the threshold value
 - Y axis is the pixel value
- The bin value is the number of pixels with the corresponding value at the given threshold.
- Two dimension spectra show the dependence of the pixel distribution by the threshold value
- Ranges and numbers of bins can be set by user

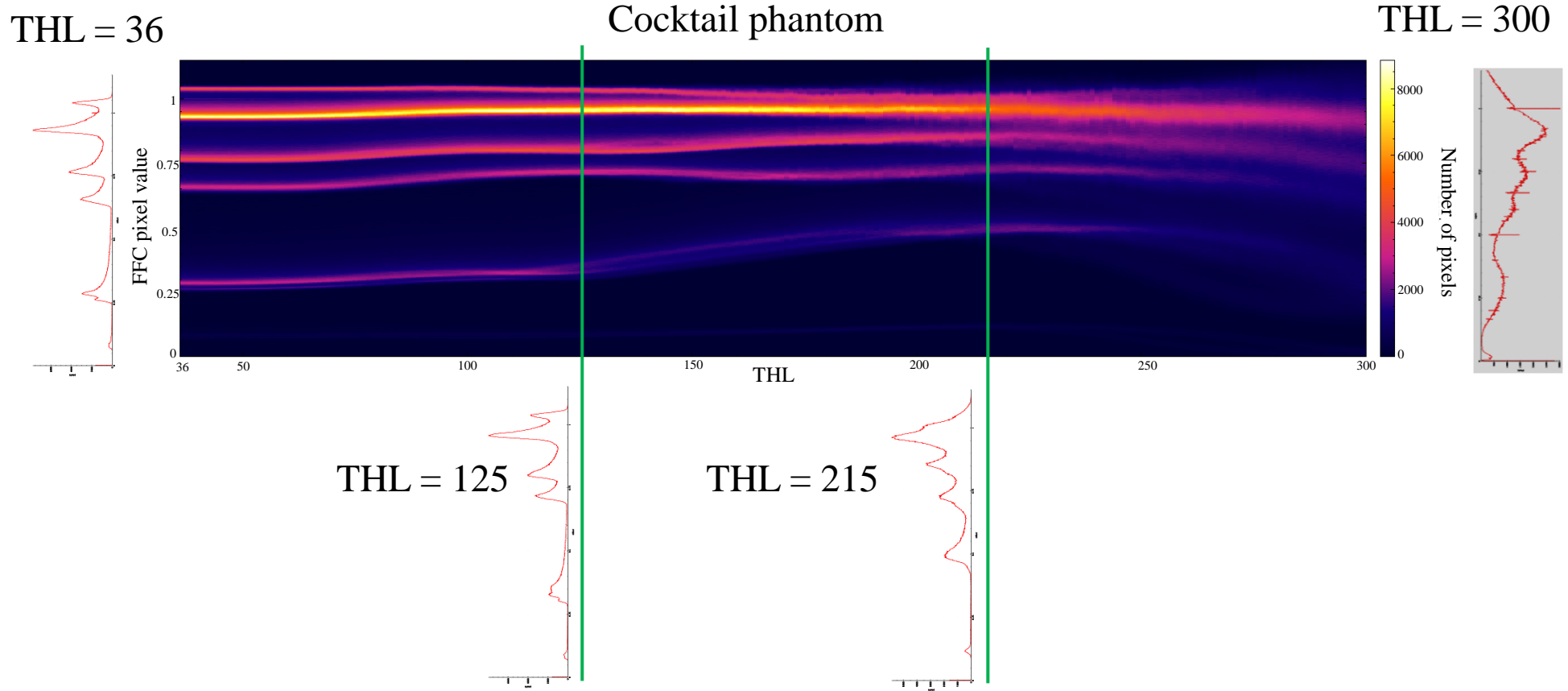
Two dimension spectra

Phantom with pork fat



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Distribution



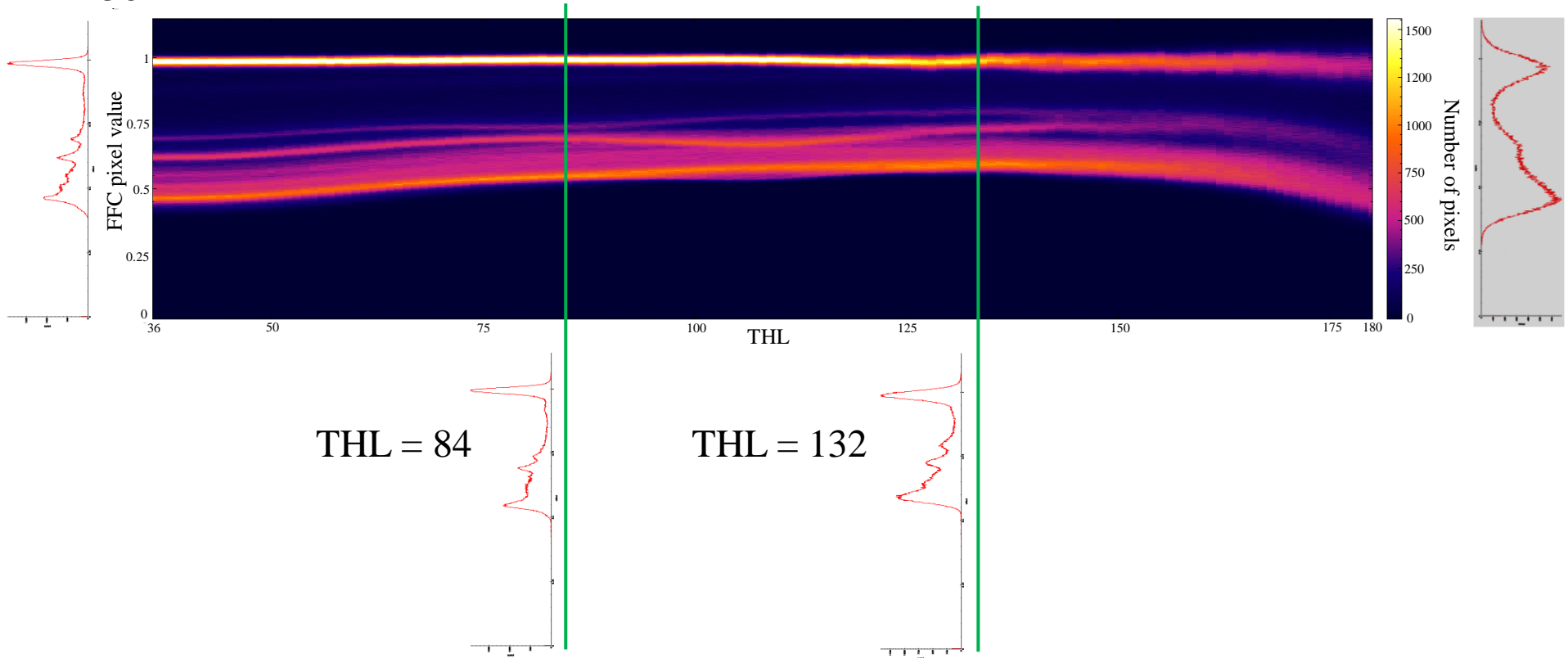
Distribution is a y-profile of 2D-Spectrum

Distribution

Pork fat phantom

THL = 36

THL = 180



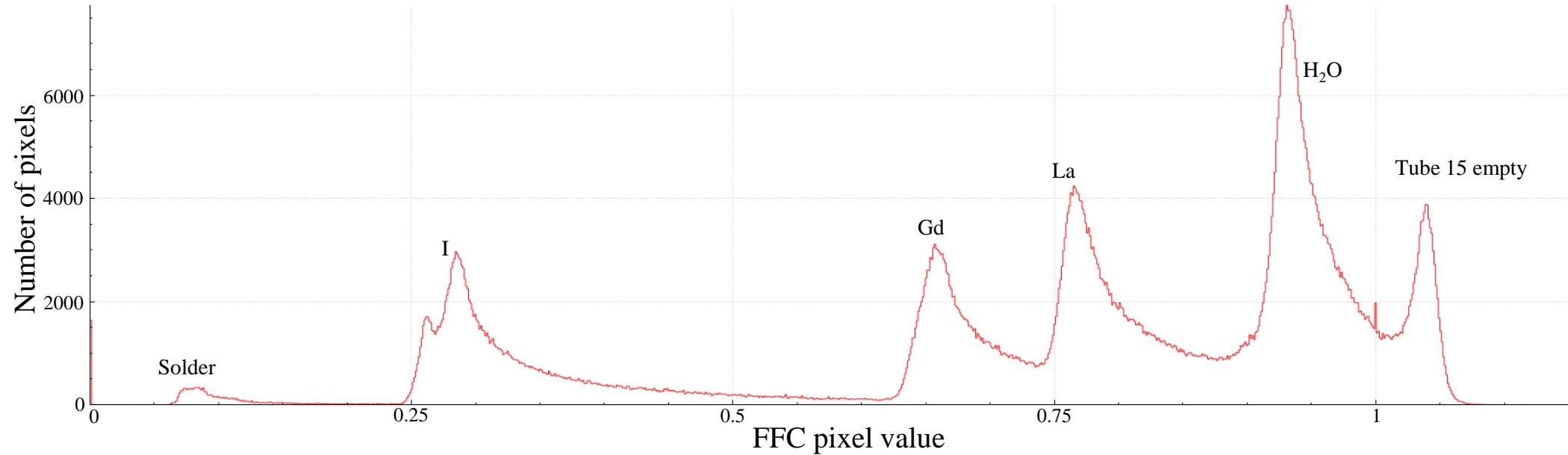
THL = 84

THL = 132

Distribution is a y-profile of 2D-Spectrum

Distribution

Cocktail phantom, THL = 36



- The distribution is a histogram

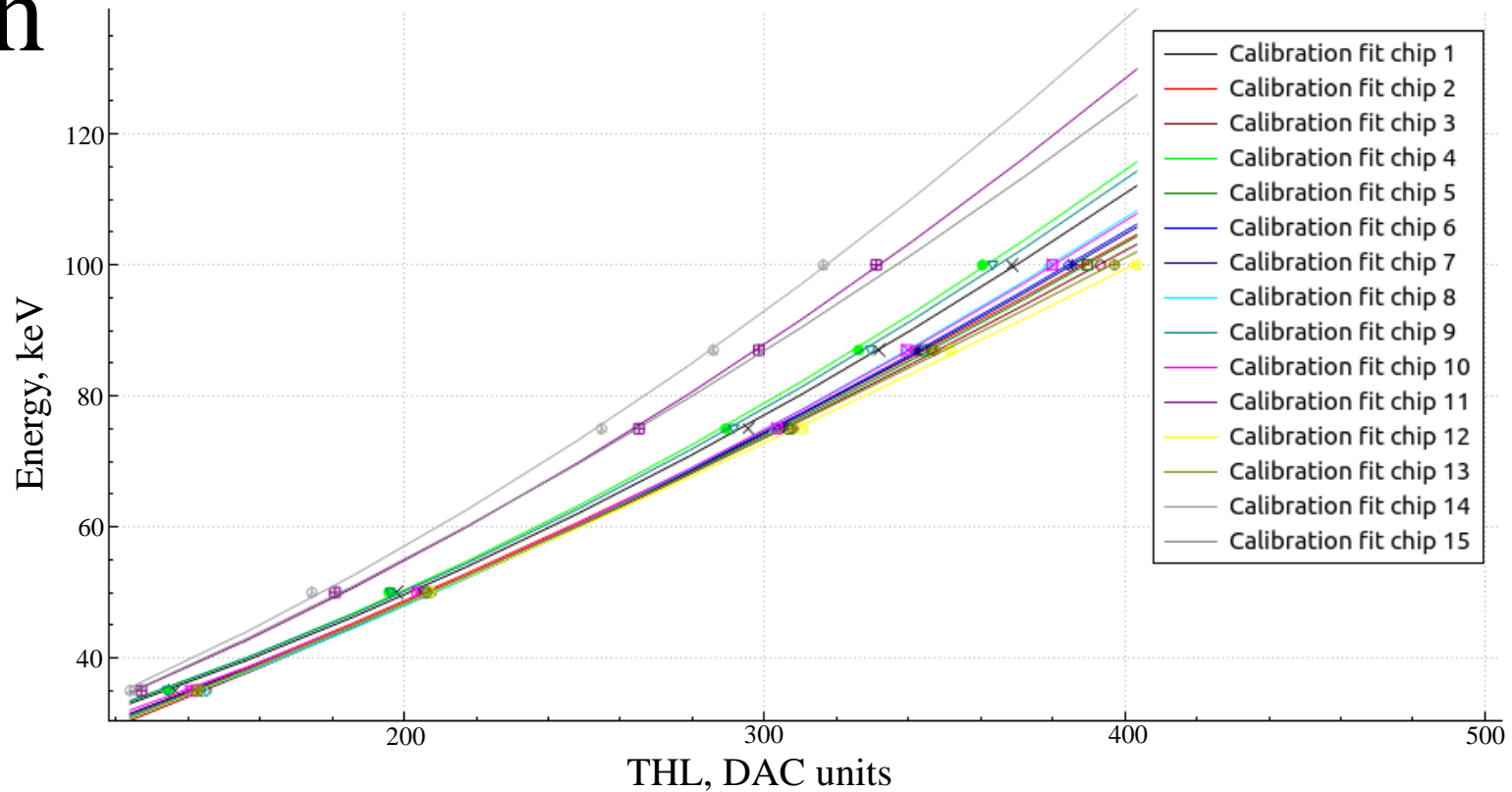
- X axis is the pixel value

- Y axis is the number of pixels

- The distribution provides a probability distribution of pixel value

- The distribution of the frame with threshold THL = 36 with cocktail phantom is shown on the figure

Calibration



- The program provides possibilities to make calibration for Medipix3RX in Widepix detector
- The calibration is calculated from a series of open-beam threshold scans with different X-ray tube voltage
- The calibration data is used to align Medipix3RX detector with each other
- The calibration data allows to plot spectra using energy scale

Additional features of the program

- Pixel filtering (filtering by a condition for pixel value, filtering by deviation from mean value, filtering areas,...)
- Saving pictures in different formats
- Mathematical operations with spectra

Further plans

- Writing documentation
- Embedding of material identification algorithms
- Rebinning
- Porting on Windows system
- Modification to work with other Medipix detectors (on demand)

All source code is available to all interested colleagues for free.

https://github.com/lapkinspjnr/widepix_analyser_2.git

Any suggestion for adding features to the program are welcome
(lapkin@jinr.ru)

The program is available at (unzip, run widepix_analyser_2.sh):

<https://drive.google.com/file/d/1DxxsUFTb3vQFS9L-cpTprQJD-n9RQ4fi/view?usp=sharing>

Thanks for your attention

Are there any questions?