Analysis of darknoise measurements in Valencia Statistical characterization of HPK SiPMs for FD1

Julio Ureña

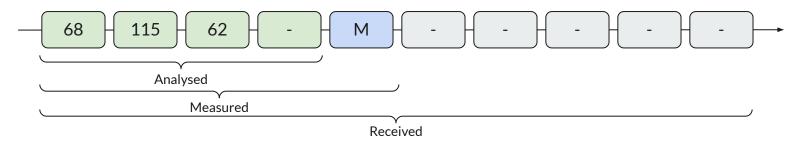
Photosensor WG meeting - 17 Dec 2024



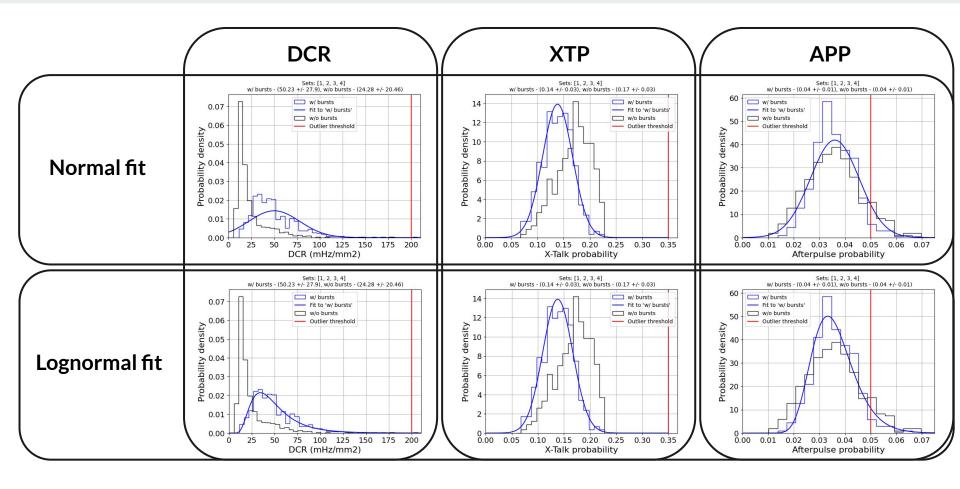
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Introduction

- 5 trays have been measured so far
- The first three trays (68, 115 and 62) have already been analysed and presented Results from tray 68 (set 1), Photosensor WG meeting on 2024/02/13 - https://indico.fnal.gov/event/63323/ Results from tray 68 (set 1), Photosensor WG meeting on 2024/02/27 - https://indico.fnal.gov/event/63509/ Results from tray 115 (set 2), Photosensor WG meeting on 2024/05/07 - <u>https://indico.fnal.gov/event/64609/</u> Results from tray 62 (set 3), Photosensor WG meeting on 2024/05/07 - https://indico.fnal.gov/event/66372/
- The fourth tray contains a mixture of boards from different trays. From now on, we will refer to the former-trays as sets.
- Although we have used the results from the analysis of the fourth set in this presentation, we have not devoted a particular presentation to show them yet. We will do so in coming photosensor meetings.
- In this presentation we show the results of an statistical study performed to assess the number of SiPMs which we need to measure in order to achieve a certain relative error in the statistical characterization of the DCR, XTP and APP for the full HPK production of FD1

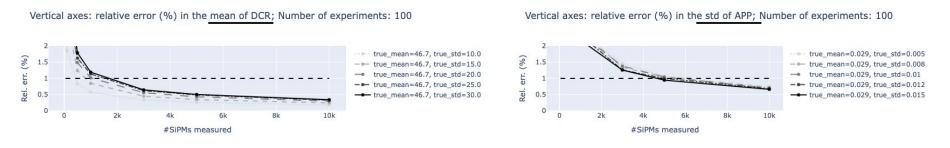


DCR, XTP and APP distributions so far (sets 1, 2, 3 & 4)



Procedure

- For every distribution in ('normal', 'lognormal'):
 - For every magnitude in ('DCR', 'XTP', 'APP'):
 - Fit the chosen distribution to the histogram of the chosen magnitude using our results from the first four trays
 - Compute a set of mean-values and sigma-values covering a vicinity of the fitted mean and sigma
 - For every (mean, sigma) pair:
 - For every number-of-SiPMs, N, in (50, 100, ..., 5000, 10000):
 - Repeat 100 times:
 - Sample the fixed distribution with the fixed (mean, sigma) pair N times
 - Histogram the resulting samples and fit them to a distribution of the chosen kind
 - Compute the fit error for the fit mean and sigma
 - Make it relative to the (true) fixed mean and sigma of the underlying distribution
 - Compute the average relative fit errors for mean and sigma over the 100 experiments



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DCR (normal fit)

Vertical axes: relative error (%) in the std of DCR; Number of experiments: 100

err. (%)

Rel.

err. (%)

Rel.

(%)

err.

Rel.

err. (%)

Rel.

err. (%)

Rel.

0.5

1.5

0.5

0

0

0

0

15

0.5

0

1.5

05

0

1.5

0.5

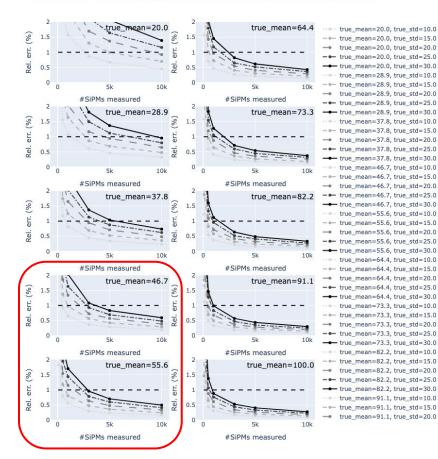
0

0

0

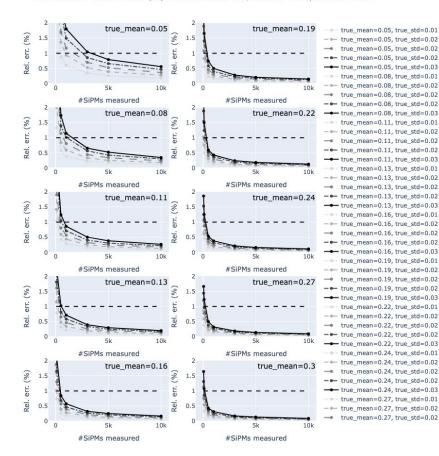
true_mean=20.0 true_mean=64.4 true mean=20.0, true std=10.0 (%) 1.5 --- true mean=20.0, true std=15.0 - true mean=20.0, true std=20.0 --- true mean=20.0, true std=25.0 true mean=20.0, true std=30.0 0.5 true_mean=28.9, true_std=10.0 --- true mean=28.9, true std=15.0 5k 10k 5k 10k —• true mean=28.9, true std=20.0 #SiPMs measured #SiPMs measured -- true mean=28.9, true std=25.0 true_mean=28.9 true mean=73.3 (%) 1.5 true mean=37.8, true std=10.0 --- true mean=37.8, true std=15.0 —• true mean=37.8, true std=20.0 --- true mean=37.8, true std=25.0 0 5 true_mean=37.8, true_std=30.0 0 true mean=46.7, true std=10.0 10k 5k 10k 5k --- true mean=46.7, true std=15.0 #SiPMs measured #SiPMs measured — true mean=46.7, true std=20.0 true mean=37.8 true mean=82.2 -- true_mean=46.7, true_std=25.0 (%) ---- true mean=46.7, true std=30.0 1.5 true mean=55.6, true std=10.0 --- true mean=55.6, true std=15.0 — true mean=55.6, true std=20.0 --- true mean=55.6, true std=25.0 0 true mean=55.6, true std=30.0 5k 10k 5k 10k true mean=64.4, true std=10.0 #SiPMs measured #SiPMs measured -- true mean=64.4, true std=15.0 true_mean=64.4, true_std=20.0 true mean=46.7 true mean=91.1 (%) --- true mean=64.4, true std=25.0 1.5 ----- true mean=64.4, true std=30.0 true mean=73.3, true std=10.0 --- true mean=73.3, true std=15.0 0.5 —• true mean=73.3, true std=20.0 -- true mean=73.3, true std=25.0 0 5k 10k 5k 10k 0 true mean=73.3, true std=30.0 #SiPMs measured true_mean=82.2, true_std=10.0 #SiPMs measured --- true_mean=82.2, true_std=15.0 true mean=55.6 true mean=100.0 (%) -- true mean=82.2, true std=20.0 1.5 --- true mean=82.2, true std=25.0 true mean=82.2, true std=30.0 true mean=91.1, true std=10.0 --- true mean=91.1, true std=15.0 - true mean=91.1, true std=20.0 10k 10k 5k 5k #SiPMs measured #SiPMs measured

Vertical axes: relative error (%) in the mean of DCR; Number of experiments: 100

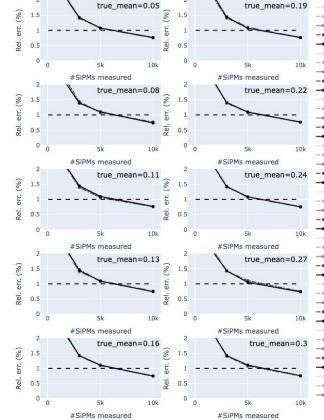


XTP (normal fit)

Vertical axes: relative error (%) in the mean of XTP; Number of experiments: 100



Vertical axes: relative error (%) in the std of XTP; Number of experiments: 100

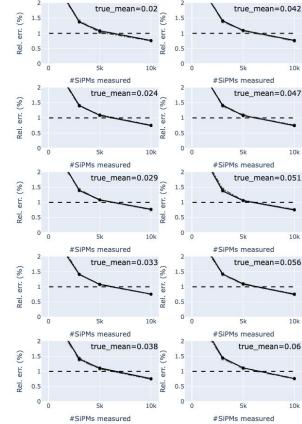


true mean=0.05, true std=0.01 --- true mean=0.05, true std=0.02 —• true mean=0.05, true std=0.02 -- true mean=0.05, true std=0.02 true mean=0.05, true std=0.03 true mean=0.08, true std=0.01 --- true mean=0.08, true std=0.02 true mean=0.08, true std=0.02 -- true mean=0.08, true std=0.02 true mean=0.11, true std=0.01 -- true mean=0.11. true std=0.02 true_mean=0.11, true_std=0.02 -- true_mean=0.11, true_std=0.02 ---- true mean=0.11, true std=0.03 true mean=0.13, true std=0.01 --- true_mean=0.13, true_std=0.02 true_mean=0.13, true_std=0.02 -- true mean=0.13, true std=0.02 ----- true mean=0.16, true std=0.01 --- true mean=0.16, true std=0.02 —• true mean=0.16, true std=0.02 -- true mean=0.16, true std=0.02 ••• true mean=0.19, true std=0.01 --- true_mean=0.19, true_std=0.02 true_mean=0.19, true_std=0.02 --- true_mean=0.19, true_std=0.02 true_mean=0.22, true_std=0.01 --- true mean=0.22, true std=0.02 — true mean=0.22, true std=0.02 -- true mean=0.22, true std=0.02 true_mean=0.22, true_std=0.03 true mean=0.24, true_std=0.01 --- true mean=0.24, true std=0.02 true mean=0.24, true std=0.02 -- true mean=0.24, true std=0.02 ----- true_mean=0.24, true_std=0.03 true mean=0.27, true std=0.01 -- true mean=0.27, true std=0.02 —• true mean=0.27, true std=0.02

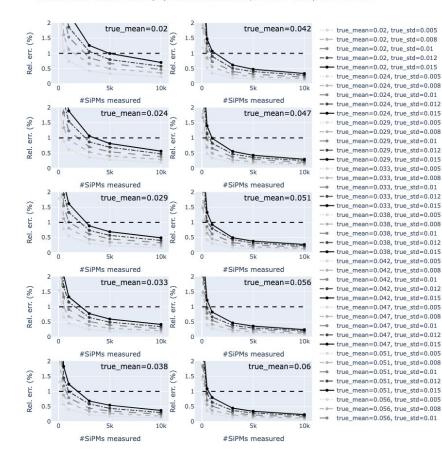
APP (normal fit)

Vertical axes: relative error (%) in the std of APP; Number of experiments: 100

true mean=0.02, true std=0.005 --- true mean=0.02, true std=0.008 —• true mean=0.02, true std=0.01 --- true mean=0.02, true std=0.012 true_mean=0.02, true_std=0.015 true mean=0.024, true std=0.005 --- true mean=0.024, true std=0.008 10k true mean=0.024, true std=0.01 -- true mean=0.024, true std=0.012 ----- true_mean=0.024, true_std=0.015 true mean=0.029, true std=0.005 --- true mean=0.029, true std=0.008 true_mean=0.029, true_std=0.01 --- true_mean=0.029, true_std=0.012 true mean=0.029, true std=0.015 true mean=0.033, true std=0.005 10k --- true mean=0.033, true std=0.008 true_mean=0.033, true_std=0.01 --- true mean=0.033, true std=0.012 true mean=0.033, true std=0.015 true mean=0.038, true std=0.005 --- true mean=0.038, true std=0.008 true mean=0.038, true std=0.01 --- true_mean=0.038, true_std=0.012 true mean=0.038, true std=0.015 10k true_mean=0.042, true_std=0.005 --- true_mean=0.042, true_std=0.008 true mean=0.042, true std=0.01 --- true mean=0.042, true std=0.012 true mean=0.042, true std=0.015 true_mean=0.047, true_std=0.005 --- true mean=0.047, true std=0.008 - true_mean=0.047, true_std=0.01 --- true_mean=0.047, true_std=0.012 10k true_mean=0.047, true_std=0.015 ----- true mean=0.051, true std=0.005 --- true mean=0.051, true std=0.008 —• true mean=0.051, true std=0.01 --- true mean=0.051, true std=0.012 true mean=0.051, true std=0.015 true mean=0.056, true std=0.005 --- true mean=0.056, true std=0.008 true mean=0.056, true std=0.01



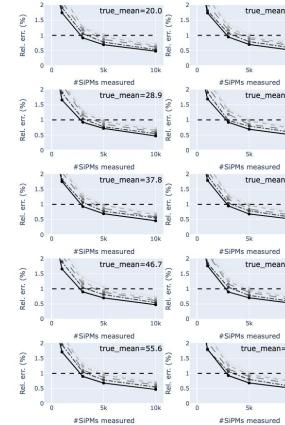
Vertical axes: relative error (%) in the mean of APP; Number of experiments: 100



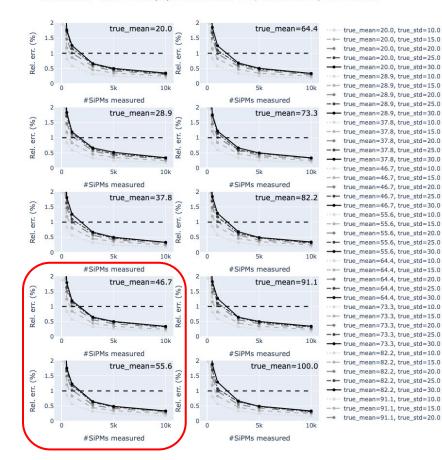
DCR (log-normal fit)

Vertical axes: relative error (%) in the std of DCR; Number of experiments: 100

true_mean=64.4 true mean=20.0, true std=10.0 --- true mean=20.0, true std=15.0 —• true mean=20.0, true std=20.0 --- true mean=20.0, true std=25.0 true mean=20.0, true std=30.0 true mean=28.9, true std=10.0 --- true mean=28.9, true std=15.0 10k 5k 10k —• true mean=28.9, true std=20.0 #SiPMs measured --- true mean=28.9, true std=25.0 true mean=73.3 (% 1.5 true mean=37.8, true std=10.0 --- true mean=37.8, true std=15.0 - true_mean=37.8, true_std=20.0 --- true_mean=37.8, true_std=25.0 true mean=37.8, true std=30.0 true mean=46.7, true std=10.0 10k 10k 5k --- true mean=46.7, true std=15.0 #SiPMs measured — true mean=46.7, true std=20.0 true mean=82.2 --- true mean=46.7, true std=25.0 ----- true mean=46.7, true std=30.0 % 1.5 true mean=55.6, true std=10.0 --- true mean=55.6, true std=15.0 true_mean=55.6, true_std=20.0 --- true mean=55.6, true std=25.0 true mean=55.6, true std=30.0 0 10k 5k 10k true mean=64.4, true std=10.0 #SiPMs measured --- true_mean=64.4, true_std=15.0 2 —• true mean=64.4, true std=20.0 true mean=91.1 --- true mean=64.4, true std=25.0 true mean=64.4, true std=30.0 true_mean=73.3, true_std=10.0 --- true mean=73.3, true std=15.0 0 5 —• true mean=73.3, true std=20.0 --- true mean=73.3, true std=25.0 0 10k 54 10k ----- true_mean=73.3, true_std=30.0 #SiPMs measured true mean=82.2, true std=10.0 --- true mean=82.2, true std=15.0 true mean=100.0 —• true mean=82.2, true std=20.0 1.5 -- true mean=82.2, true std=25.0 true mean=82.2, true std=30.0 true mean=91.1, true std=10.0 --- true mean=91.1, true std=15.0 —• true mean=91.1, true std=20.0 10k 10k 5k

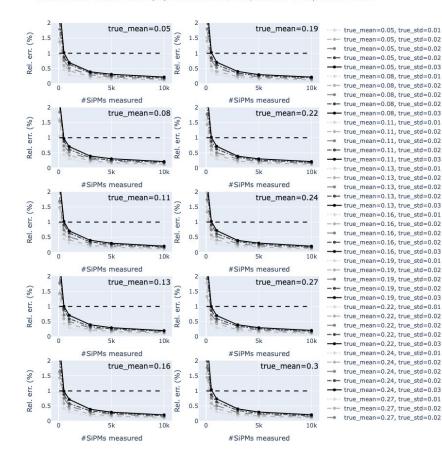


Vertical axes: relative error (%) in the mean of DCR; Number of experiments: 100

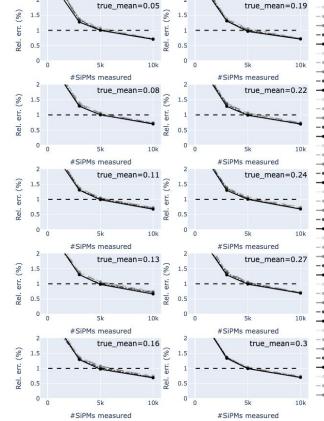


XTP (log-normal fit)

Vertical axes: relative error (%) in the mean of XTP; Number of experiments: 100

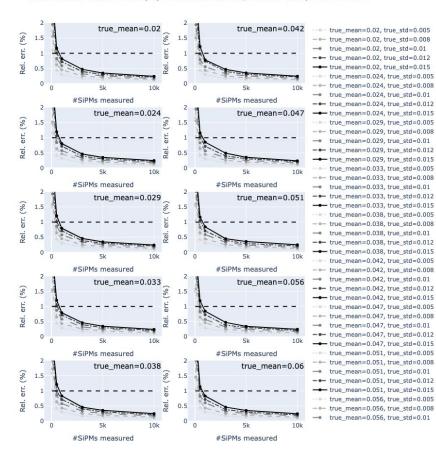


Vertical axes: relative error (%) in the std of XTP; Number of experiments: 100



true mean=0.05, true std=0.01 --- true mean=0.05, true std=0.02 —• true mean=0.05, true std=0.02 -- true mean=0.05, true std=0.02 true mean=0.05, true std=0.03 true mean=0.08, true std=0.01 --- true mean=0.08, true std=0.02 true mean=0.08, true std=0.02 -- true mean=0.08, true std=0.02 true mean=0.11, true std=0.01 --- true mean=0.11. true std=0.02 true_mean=0.11, true_std=0.02 -- true_mean=0.11, true_std=0.02 ---- true mean=0.11, true std=0.03 true mean=0.13, true std=0.01 --- true_mean=0.13, true_std=0.02 true_mean=0.13, true_std=0.02 -- true mean=0.13, true std=0.02 ----- true mean=0.16, true std=0.01 --- true mean=0.16, true std=0.02 true_mean=0.16, true_std=0.02 -- true mean=0.16, true std=0.02 true mean=0.19, true std=0.01 --- true_mean=0.19, true_std=0.02 true_mean=0.19, true_std=0.02 --- true_mean=0.19, true_std=0.02 true_mean=0.22, true_std=0.01 --- true mean=0.22, true std=0.02 — true mean=0.22, true std=0.02 -- true mean=0.22, true std=0.02 true_mean=0.22, true_std=0.03 true mean=0.24, true_std=0.01 --- true mean=0.24, true std=0.02 true mean=0.24, true std=0.02 -- true mean=0.24, true std=0.02 ----- true_mean=0.24, true_std=0.03 true mean=0.27, true std=0.01 --- true mean=0.27, true std=0.02 —• true mean=0.27, true std=0.02

Vertical axes: relative error (%) in the mean of APP; Number of experiments: 100



true_mean=0.024, true_std=0.005 0 --- true mean=0.024, true std=0.008 5k 10k 5k 10k 0 —• true mean=0.024, true std=0.01 #SiPMs measured #SiPMs measured -- true mean=0.024, true std=0.012 true mean=0.024 true mean=0.047 ---- true_mean=0.024, true_std=0.015 err. (%) 10% 1.5 1.5 true mean=0.029, true std=0.005 --- true mean=0.029, true std=0.008 true mean=0.029, true std=0.01 Rel. --- true_mean=0.029, true_std=0.012 0.5 0.5 true_mean=0.029, true_std=0.015 0 true mean=0.033, true std=0.005 0 5k 10k 5k 10k --- true mean=0.033, true std=0.008 #SiPMs measured #SiPMs measured true_mean=0.033, true_std=0.01 true mean=0.029 true_mean=0.051 -- true_mean=0.033, true_std=0.012 err. (%) (%) ----- true mean=0.033, true std=0.015 1.5 1.5 true mean=0.038, true std=0.005 --- true mean=0.038, true std=0.008 Rel. true mean=0.038, true std=0.01 0.5 0.5 --- true_mean=0.038, true_std=0.012 0 true mean=0.038, true std=0.015 0 5k 10k 5k 10k true mean=0.042, true std=0.005 #SiPMs measured #SiPMs measured --- true_mean=0.042, true_std=0.008 true_mean=0.042, true_std=0.01 true mean=0.033 true_mean=0.056 err. (%) (%) --- true mean=0.042, true std=0.012 1.5 1.5 true mean=0.042, true std=0.015 true mean=0.047, true std=0.005 --- true_mean=0.047, true_std=0.008 Rel. 0.5 0.5 true mean=0.047, true std=0.01 -- true mean=0.047, true std=0.012 0 0 5k 10k 5k 10k true_mean=0.047, true_std=0.015 #SiPMs measured #SiPMs measured true_mean=0.051, true_std=0.005 --- true_mean=0.051, true_std=0.008 true mean=0.038 true mean=0.06 true mean=0.051, true std=0.01 err. (%) 1.5 --- true mean=0.051, true std=0.012

5k 10k 5k 10k #SiPMs measured #SiPMs measured

Vertical axes: relative error (%) in the std of APP; Number of experiments: 100

1.5

0.5

true_mean=0.042

true mean=0.02, true std=0.005

--- true mean=0.02, true std=0.008

—• true mean=0.02, true std=0.01

--- true mean=0.02, true std=0.012

true mean=0.02, true std=0.015

true mean=0.051, true std=0.015

true_mean=0.056, true_std=0.005

--- true mean=0.056, true std=0.008

true mean=0.056, true std=0.01

true mean=0.02

(%)

ELT.

Rel.

Rel.

0.5

0

0

0.5

How many SiPMs do we need to measure? (normal/log-normal distribution assumption)

- As far as the mean is concerned, the limiting factor (the one which requires a bigger number of measured SiPMs to achieve a fixed relative error) is the DCR. Assuming a DCR of ~50 mHz/mm2 mean with a 28 mHz/mm2 sigma (typical value from sets 1, 2, 3 and 4) we would need to measure 3000 SiPMs to achieve a ~1% relative error in the mean.
- The relative error for the **sigma** seems *almost* unaffected by the true mean and sigma. In whichever case, we would need to measure 3000 SiPMs to achieve a ~<1.5% relative error, and 5000 SiPMs to achieve a ~1% relative error.

3000 SiPMs add up to a ~1% of the FD1 SiPMs. Equivalently, they are 25 trays (so far we have received 10 trays, from which Carlos has measured 5 and I have analysed 4) An SP module is instrumented with three module-length (58.2 m) anode planes constructed from 6 m high by 2.3 m wide anode plane assemblies (APAs), stacked two APAs high and 25 wide, for 50 APAs per plane, and 150 total. Each APA consists of an alumninum frame with three layers of active wires, strung at angles chosen to reduce ambiguities in event reconstruction, that form a grid on each side of the APA. The relative voltage between the layers is chosen to ensure

Introduction to DUNE

The DUNE Technical Design Report

From DUNE TDR Vol. I: Introduction to DUNE

Novel silicon photomultiplier (SiPM) based photon detectors (PDs) called ARAPUCAs^{\ddagger} are placed in the inactive space between the innermost wire planes of the APAs, installed through slots in the <u>APA</u> frame. Each <u>APA</u> holds ten <u>PD</u> modules, for a total of 1500 per <u>SP module</u>] Of these, 500 are mounted in the <u>APAs</u> of the central anode plane and collect light from both directions, and 500 each are mounted in the outer <u>APA</u> frames and collect light from only the inner-facing direction.

48 SiPMs/supercell x 4 supercells/PD module x 10 PD modules/APA x 50 APAs/plane x 3 planes/FD1 = 288000 SiPMs/FD1

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Summary and further questions

- The measured DCR distribution is better fit by a lognormal PDF rather than a normal one. Although less significant, XTP and APP also show heavier tails towards bigger values. For the moment we lack a fundamental reason to explain this.
- Based on the 480 SiPMs measured and analyzed in Valencia so far, we estimate that in order to characterize the DCR, XTP and APP distributions within a ~1% error for the full HPK FD1 production (without batch distinction) we need to measure 3000 (HPK) SiPMs. This is our current baseline goal.
- Additionally, do we want to discriminate between batches?
 - If so, how do we define a production batch?
 - Can we track production batches? I.e. SiPMs that were manufactured simultaneously
 - If that's not the case, then do we want to define a batch as the 1600 boards that are sent by HPK in the same delivery?
 - Is this definition useful from an sipm-characterization point of view?
- Do we want to discard entire batches based on the measurements?
 - If so, what should be the threshold for the fraction of SiMPs not fulfilling requirements in order to discard a batch?
- Do we want to discard individual boards based on measurements?
 - In this case, notice that our results would not be representative of the accepted sample (we'll be only measuring a 1% of the HPK production)



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