The columns in the pkl files are as follows:

1: APD data which will give us the normalized population ratio or "fraction" as its called in our code

2: CA data / CA+ data

3: CA- data

4: TTL trigger data

Concerning column 2/3 CA(Classical Accelerometer data): We have a CA that outputs differential signals to be used for calculating phase difference.

For most of the time, we run the two signals through a differential amplifier, which then outputs a single signal into CH B. In this case, our CH C will be unused and hence there is no data in column 3.

On some occasions, we do not have the differential amplifier, and have to use CH B and CH C, which gives us data in column 2 and 3. In this case, we have to use column 2 - column 3 (CA+ - CA-) to get the differential signal for phase calculation.

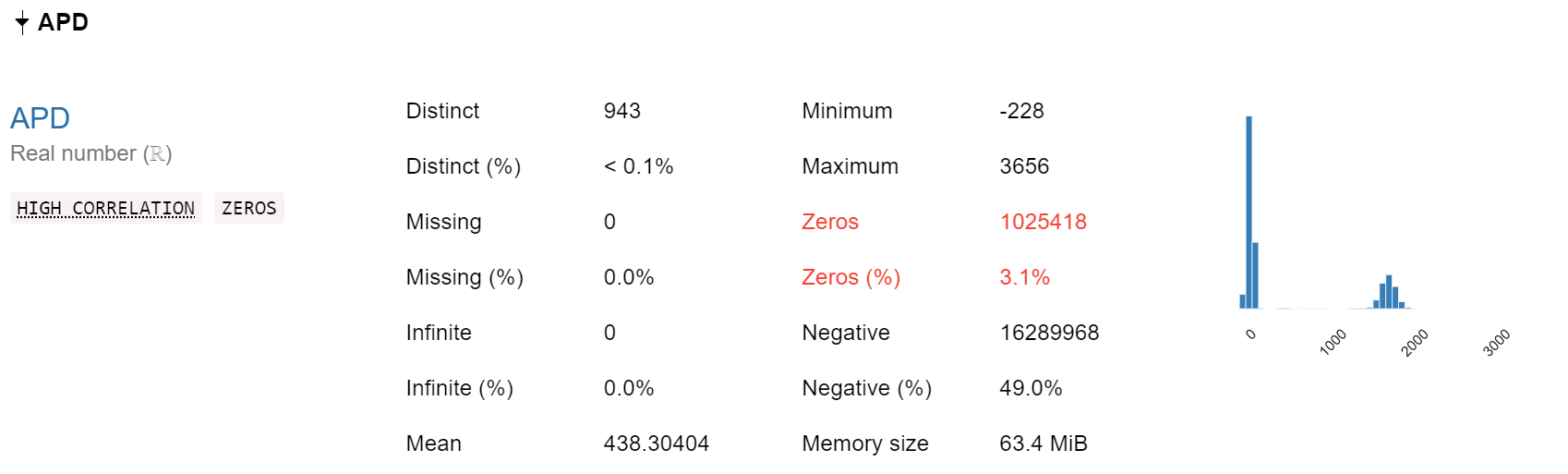
For each g measurement we have 2x79 runs, 79 for chirp up and 79 for chirp down. We scan the chirp rate at a randomized order, alternating between chirp up and down each time.

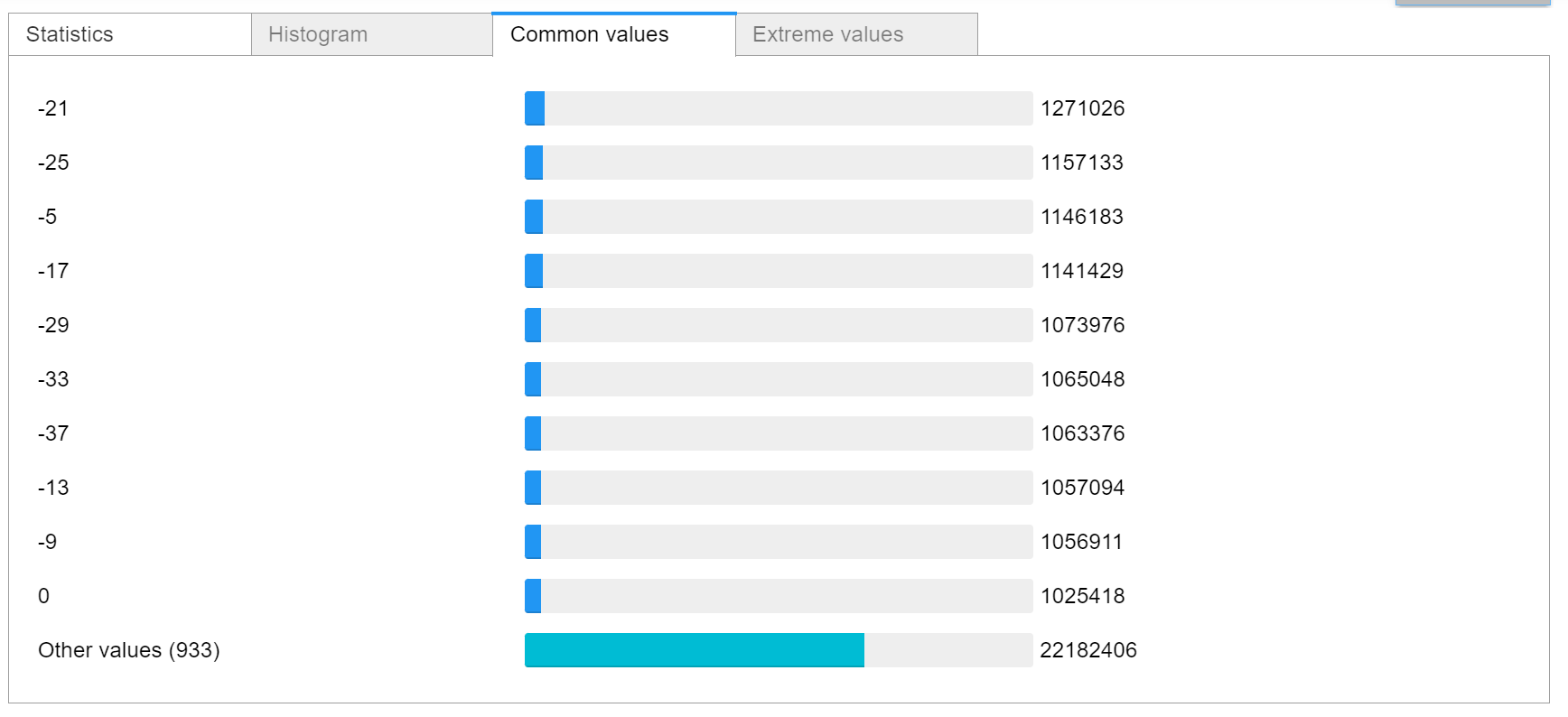
The 3 pkl files contains all the data for 2x79 runs, instead of 1 pkl file for each run. This is so that we can collect as much CA data as possible, even in-between each run.

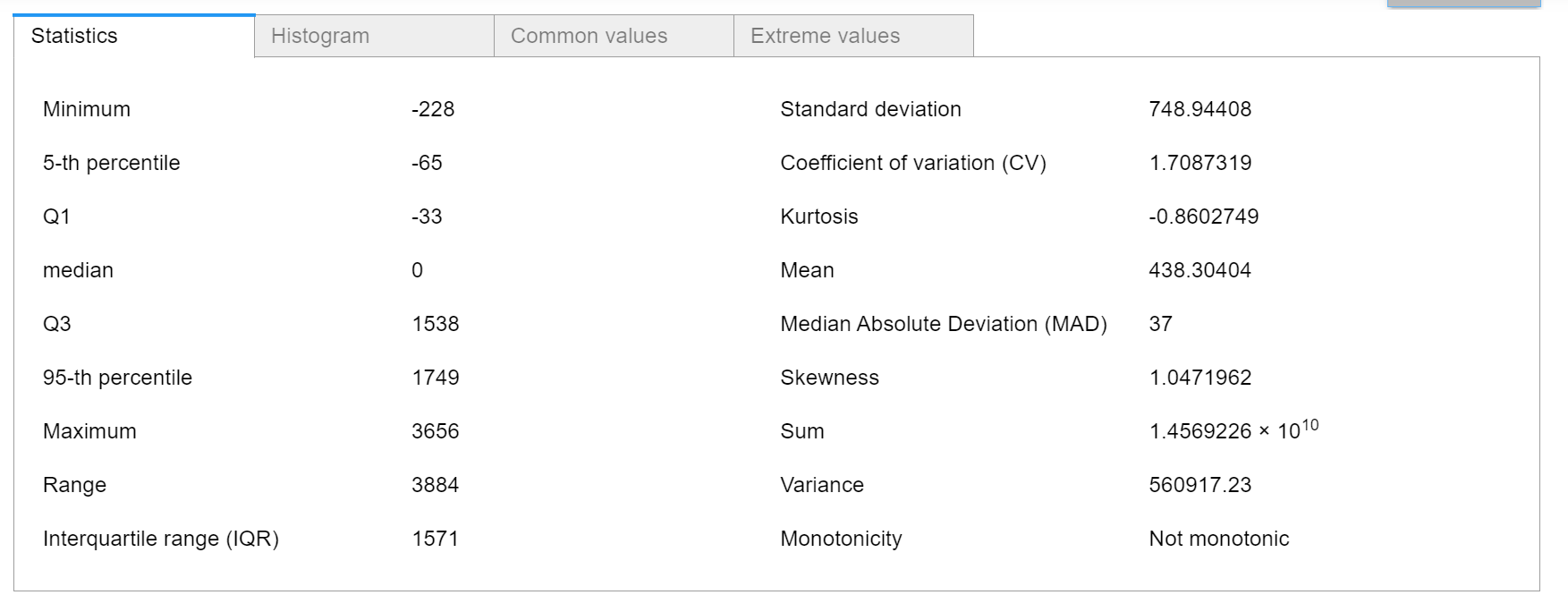
The TTL trigger in the pkl files gives us the ability to sync each experimental run and extract the relevant data that we need.

The {}runtime\_settings.json file is in each folder. This .json file gives us useful information for each run, such as the range of the picoscope channels, and the chirp scanning randomization order.

APD: Prelim Exploratory Data Analysis:









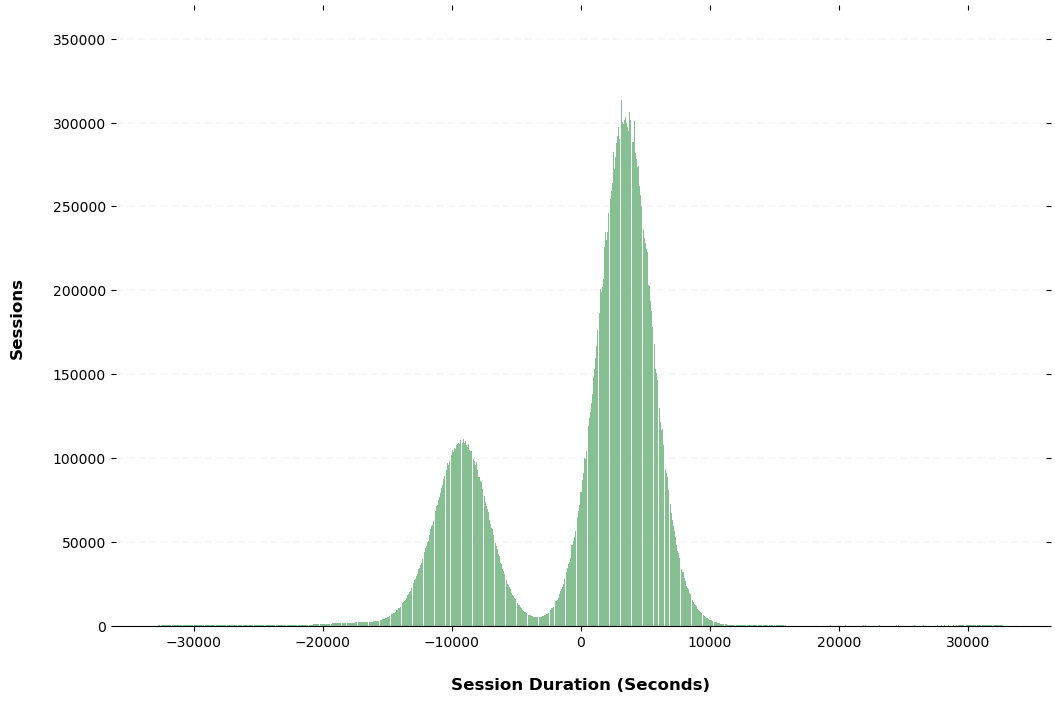


[ravi@atomionics.com](mailto:ravi@atomionics.com)Can you please write down the process to normalize the APD values.

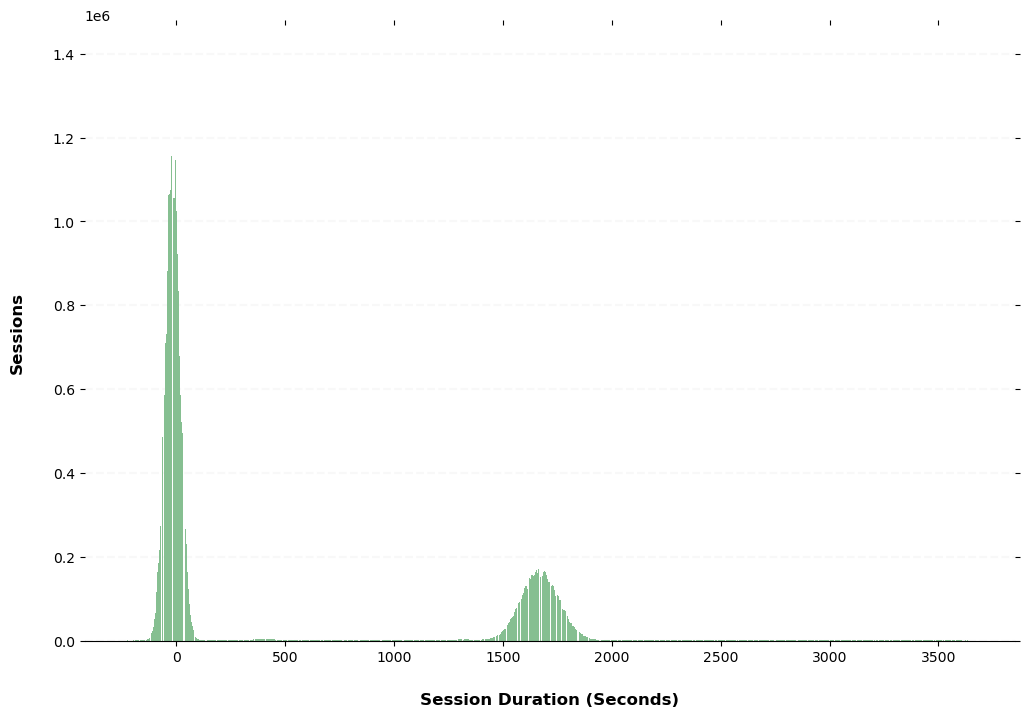
I have defined Classical\_Acc as difference between CA Plus or SRS and CA Minus

data['Classical\_Acc'] = data['CA plus or SRS']- data['CA minus']

I am getting bimodal distribution:

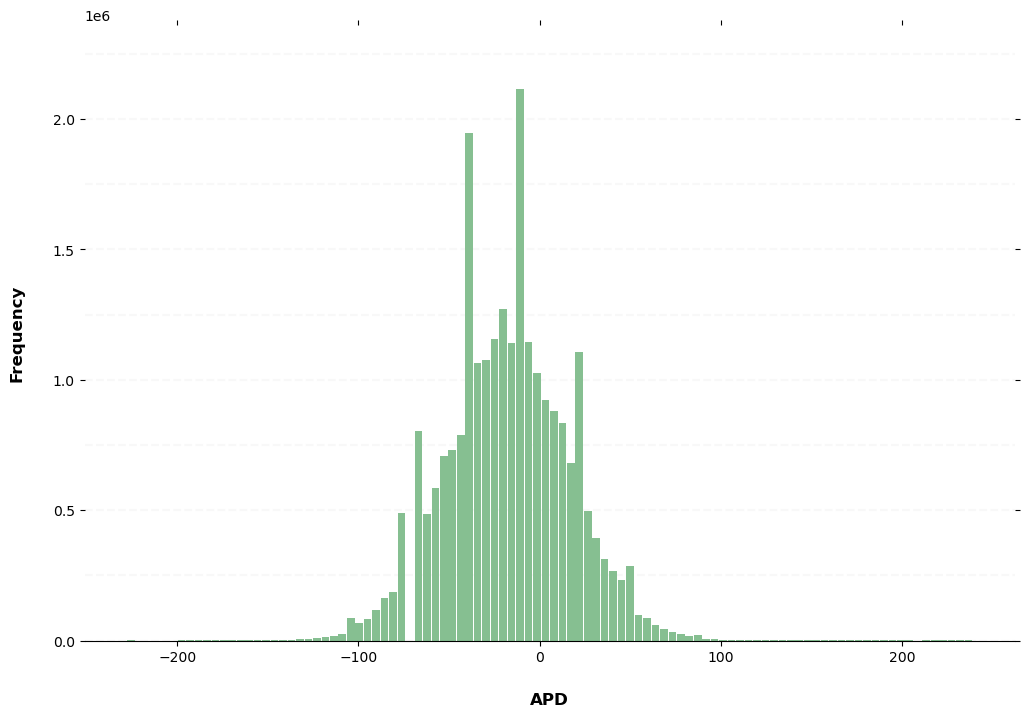


Similarly I am getting two lumps for APD Values:

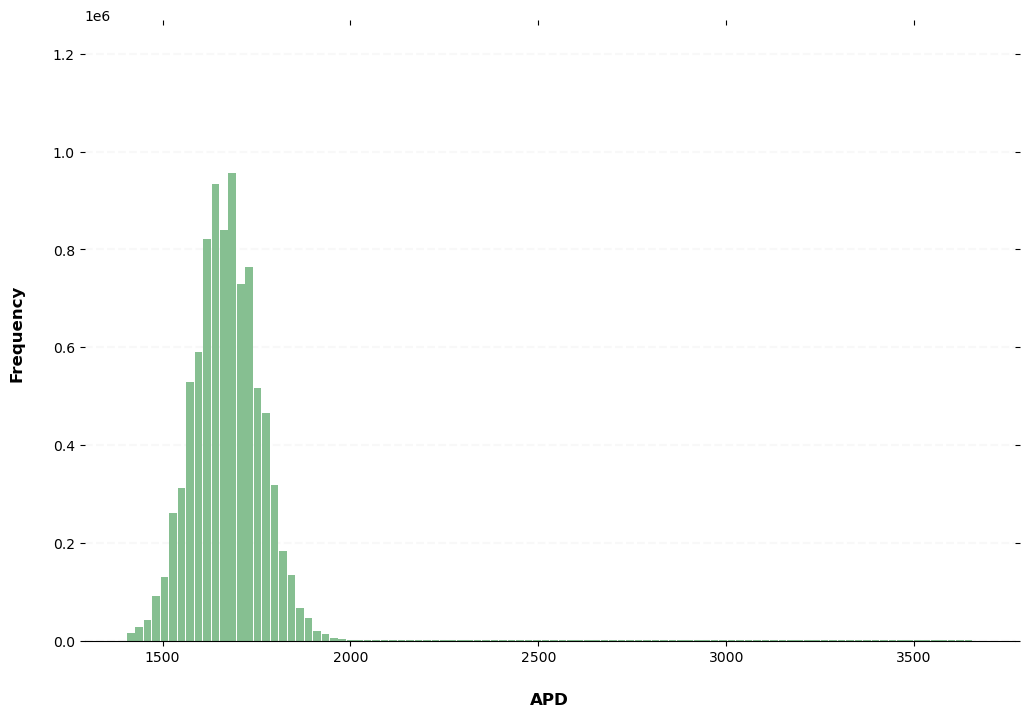


[ravi@atomionics.com](mailto:ravi@atomionics.com)Can you please write down the process to normalize the APD values.

APD Small (<240)

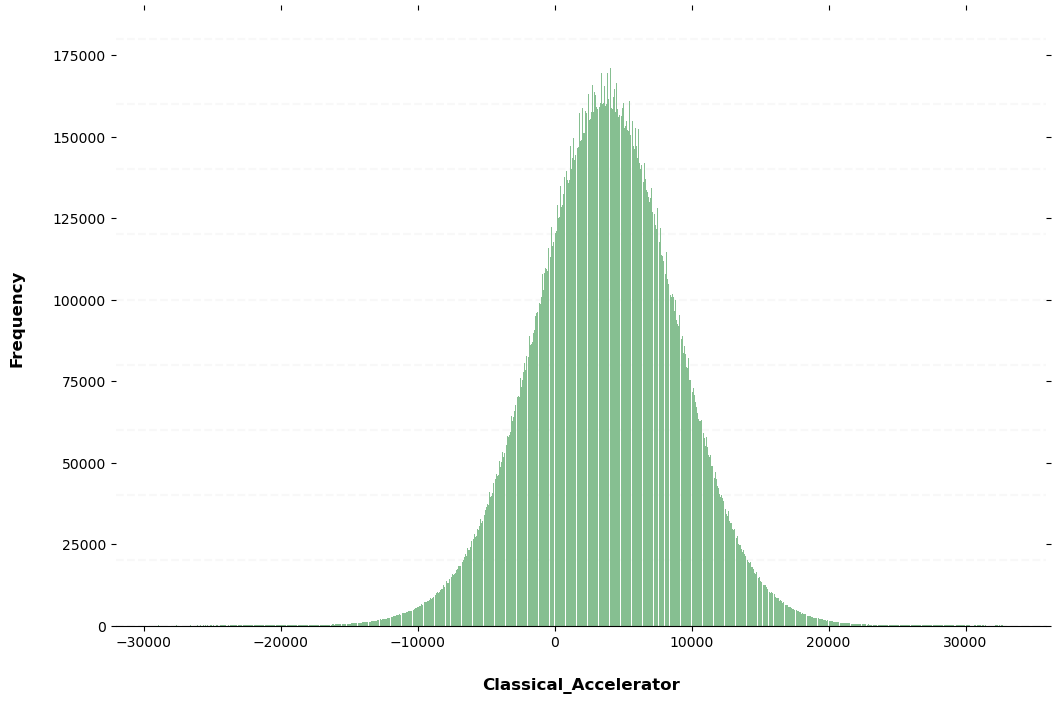


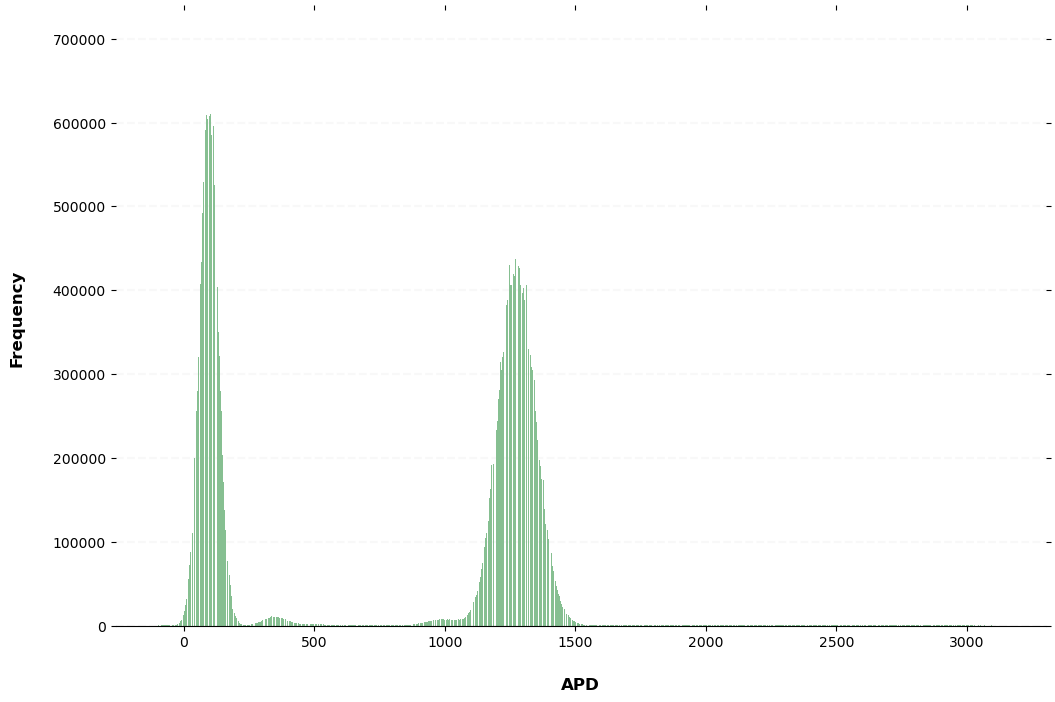
APD Big (>1400)



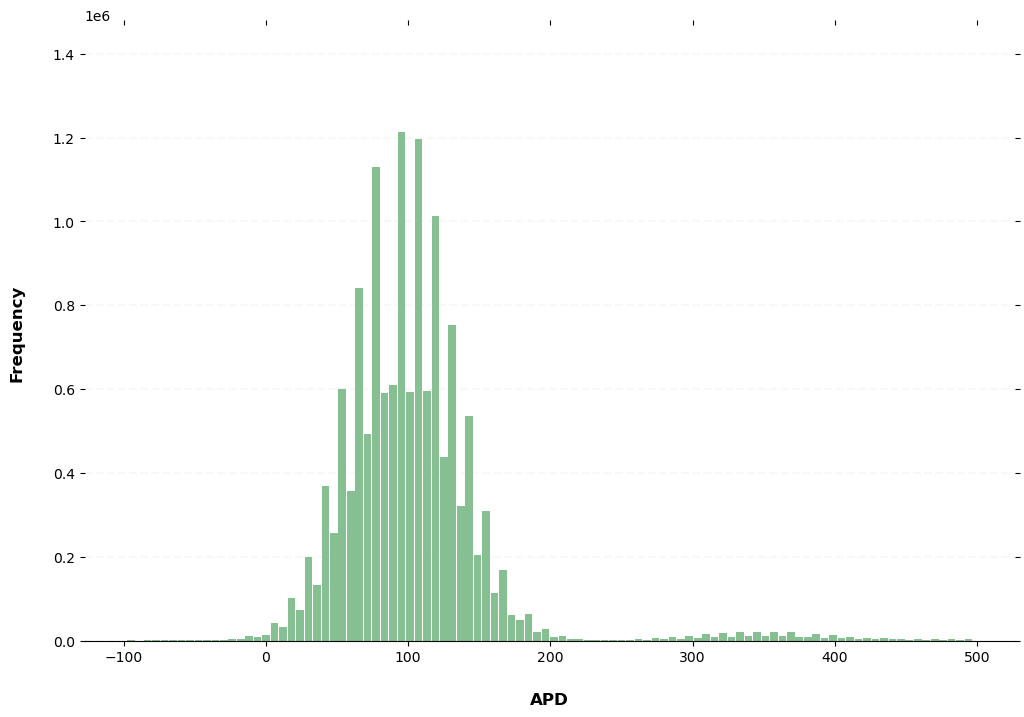
For Most recent data:

Classical Accelerator:

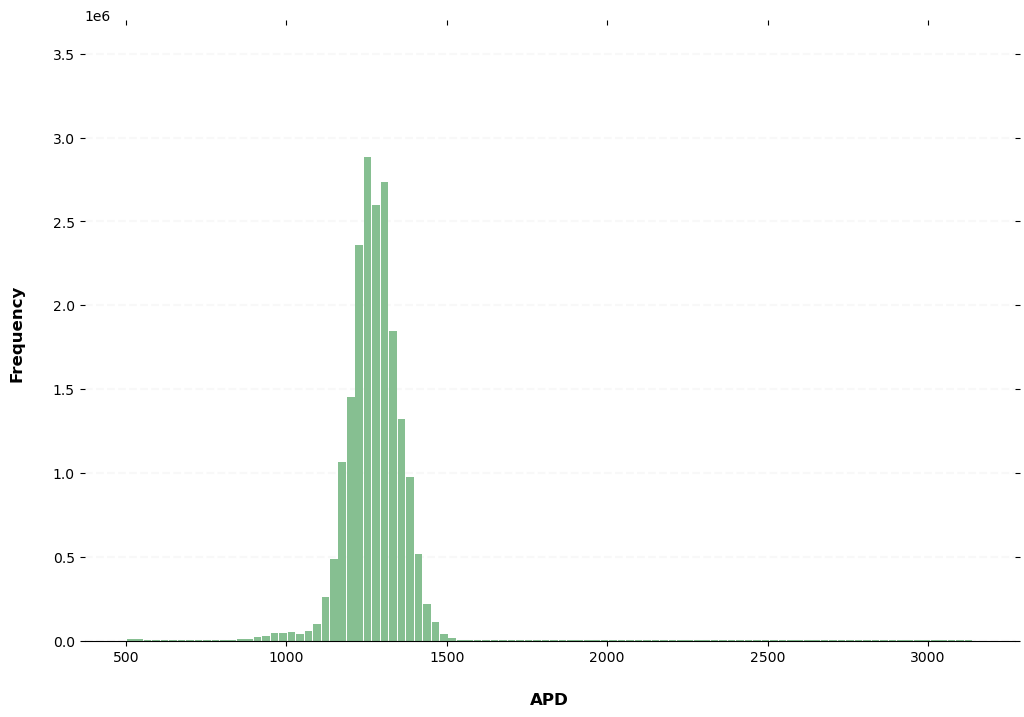


APD:  


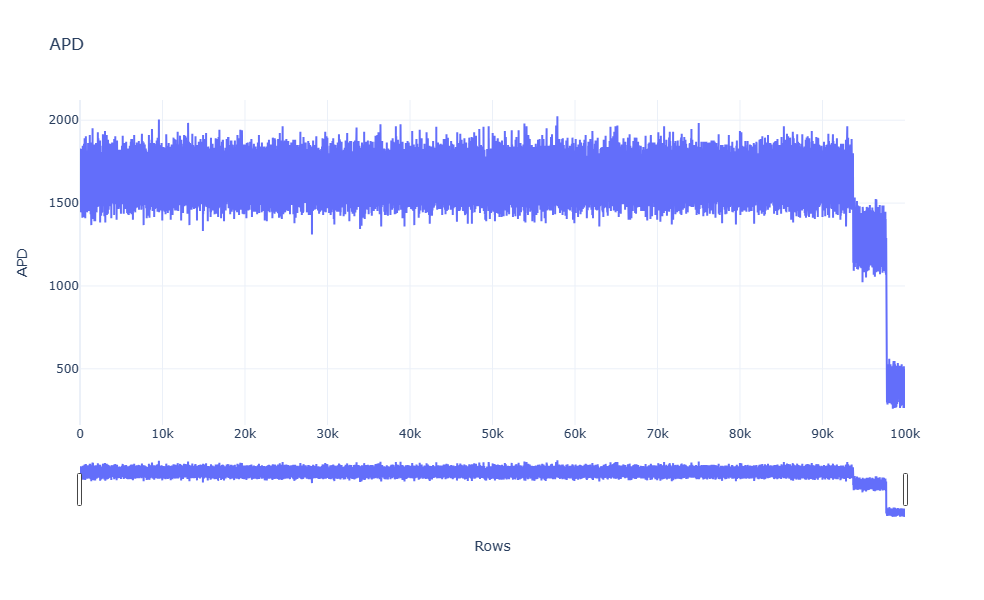
APD Small:(<500)



APD Big: (>500)



ADP Plot for first 10,000 rows



ADP Plot for first 100,000 rows

