Problem set in Applied Statistics 2020

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The philosophy of some problems is discussed with my group members Alicia, Timo and Jonas, meanwhile the code is completely written **on my own**.

I – Distributions and probabilities:

1.1 (4 points) Assuming the "El Clasico" football match is an even game (p = 0.5), what is the probability, that the score after 144 non-draw league games is exactly even?

To make it even, the number of both team's victories should be the same. Thus, we can use binomial distribution to actually calculate the probability.

$$P_x = C_n^x p^x (1-p)^{n-x}$$

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The probability of even in Barcelona verses RM is:  0.06637504645119732
If using the scipy library, the answer is:             0.06637504645119337
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1.2 (4 points) Brad Pitt and Edward Norton are shooting golf balls at a window with $p_{hit} = 0.054$ chance of hitting. How many golf balls do they need to be 90% sure of hitting the window?

To hit the window with $p_{hit} = 90\%$, we need to make sure that the former shoots don't hit, means that $p_{nohit} = 10\%$.

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The number of golf balls they use to make sure the probability over 90% is: 40
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II – Error propagation: 2.1 (10 points) The Hubble constant h has been measured by seven independent experiments: 73.5±1.4, 74.0 ± 1.4, 73.3 ± 1.8, 75.0 ± 2.0, 67.6 ± 0.7, 70.4 ± 1.4, and 67.66 ± 0.42 in (km/s)/Mpc.

- What is the weighted average of h? Do the values agree with each other?
- The first four measurements are based on a different method than the last three. Do the values from the same method agree with each other?

Answer:

1.The weighted mean is defined as

$$\hat{\mu} = \frac{\sum x_i/\sigma_i^2}{\sum 1/\sigma_i^2}$$

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68.78925107187163
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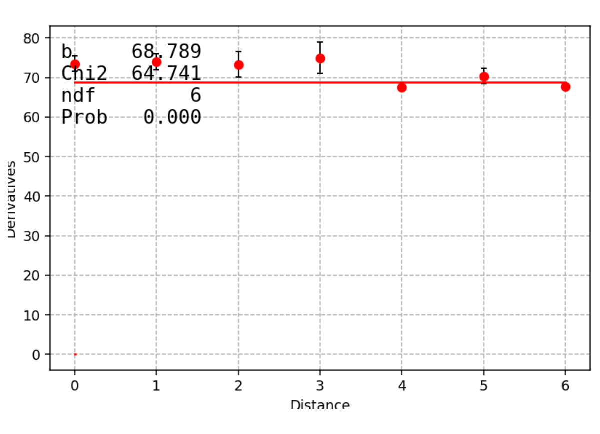
And the values don't agree with each other. The weighted mean is roughly 68.79, but we can easily see that the second and the fourth measurements need more than 3σ distance to touch the weighted average.

Meanwhile, we can do a chi2 test for the constant.



From the Chi2 regression test and numerical estimation, we can safely say that the values don't agree with each other

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The Chi2 probability of the first four values are:   0.9852357656317927

The Chi2 probability of the last three values are:   0.2584838114720961
```

Therefore, through the Chi2 test we could safely say that the first four values and the last three values agree each other within their own methods.

2.2 (10 points) Using Coulomb's law you want to measure a charge, $q_0 = Fd^2/k_eQ$. Assume that Coulomb's constant $ke = 8.99 \cdot 10^9 Nm^2/C^2$ and the instrument charge $Q = 10^{-9}C$ are known.

- Given force F = 0.87 ± 0.08 N and distance d = 0.0045 ± 0.0003 m, what is q0?
- Where does the largest contribution to the uncertainty on q0 come from? F or d?
- If you could measure F and d with uncertainties ± 0.01 N and ± 0.0001 m, respectively, at what distance should you expect to measure the charge in question q0 most precisely?

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q0 is  1.96e-06 +/- 3.17e-07 C

The uncertainty contribution on F is 1.802002224694104e-07
The uncertainty contribution on d is 2.6129032258064514e-07
Therefore the contribution mostly comes from d
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Fill the uncertainty of F and d with 0.01 and 0.0001:

$$\sigma_{q0} = \sqrt{[(\frac{d^2}{k_eQ})^2 \cdot 0.01^2 + (\frac{2Fd}{k_eQ})^2 \cdot 0.0001^2]}$$

Then plug in $F = q_0 k_e Q/d^2$:

$$\sigma_{q0} = \sqrt{\frac{d^4}{(k_eQ)^2} \cdot 0.01^2 + \frac{4 \cdot q_0^2}{d^2} \cdot 0.0001^2}$$

Take the derivatives:

$$\sigma_q^{2\prime} = \frac{4d^3}{k_e^2Q^2} \cdot (10^{-2})^2 - \frac{8 \cdot q_0^2}{d^3} \cdot (10^{-4})^2$$

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[0.00629279]
The optimal distance is  0.00629279504319142 m
In order to check, we can make a plot
Before 0.00629  m, the derivatives are all negative. Perfect
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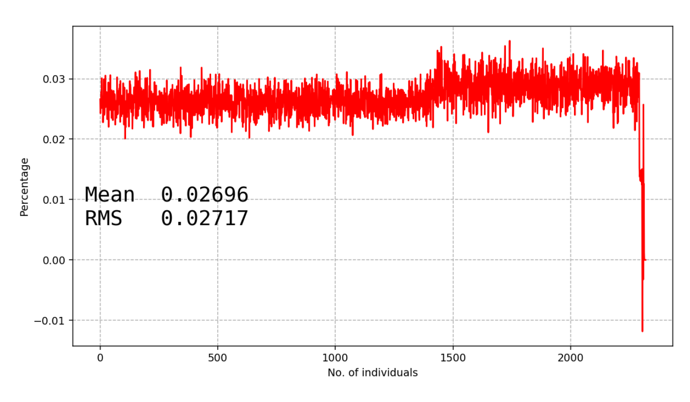
2.3 (12 points) Sub-saharan humans tend not to have any Neanderthal DNA, while all others have a few percent. The file: www.nbi.dk/~petersen/data DNAfraction.txt contains the fraction of Neanderthal DNA for 2318 Danish high school students.

- Plot the distribution of Neanderthal DNA fraction, and calculate the mean and RMS.
- Do you find any mismeasurements or outliers from the main population in the data?
- Fit the main population data with distributions of your choice, and comment on the fits.

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The outlier numbers are:  [2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 230
1 2302 2303 2304
 2305 2306 2307 2309 2310 2311 2312 2313 2314 2315 2316 2317]
Where they get the percentage deviatea away from 3 sigma(std)

Meanwhile, the mismeasurements (also includes in outliers) are: [2303 2304 2307]

Where the percentage is smaller than 0, physically not acceptable

First we move the outlier out, where they exist in 3 sigma out from average
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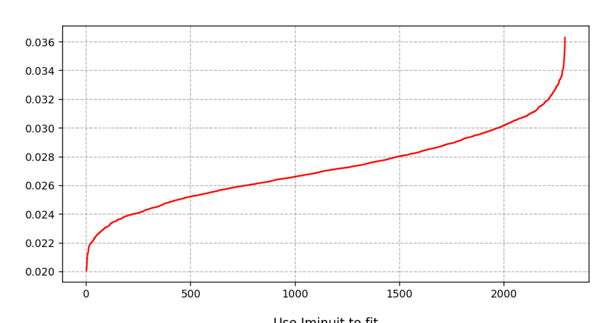

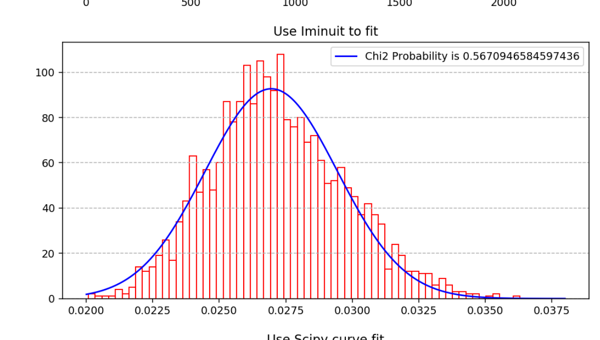

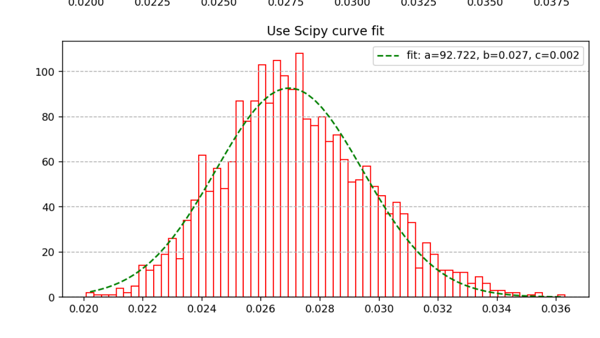


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The distribution chose is Gaussian

We create the histogram of dna_data, where array[0] is bin data's number, [1] is
bins' position
The original chi2 is:  3185.835458738805
The dof is:  61
92.7224680401674 0.026955491659177957
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The gaussian fit with Chi2 probability is ~56%, pretty neat.

III – Monte Carlo: 3.1 (15 points) Assume that the outcome of an experiment can be described by first drawing a random number x from the distribution f(x) = C(c1 + x c2) for x ∈ [1, 10], where c1 = 5 and c2 = 2 and then using this x value to calculate y = x exp(−x).

- What is the value of C? And what is the mean and RMS of f(x)?
- What method(s) can be used to produce random numbers according to f(x)? Why?
- Produce 5000 random pairs (x, y) and calculate the correlation(s) between the (x, y) values.
- Fit the distribution of the produced x values to f(x), with c1 and c2 as free parameters.
- How many measurements of x would you need, in order to determine c1 and c2, respectively, with a precision better than 1% of their values?

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The mean value of f(x) is  0.11111
The RMS is  0.0445042429662982
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Firstly, we use uniform random number generator to produce an array, then insert this random array to the distribution to get the array with specific probability.

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The correlation coefficient is : 0.002788619320464695
Therefore, x and y are highly positive correlation
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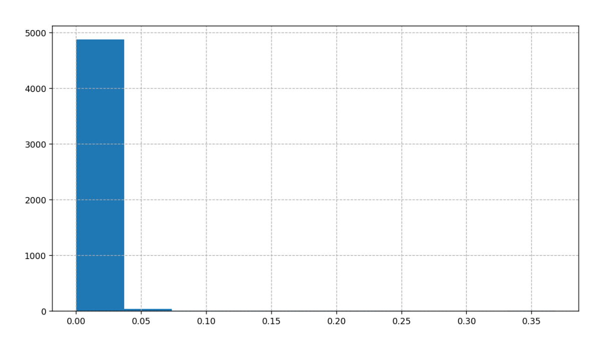

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c1 fit is:  5.001322181076822 c2 fit is:  2.0000276739729297
P chi2 is  1.0
```

IV – Statistical tests: 4.1 (15 points) The length (l in μm) and transparency (T) of two types of cells (P and E) can be found for 4690 cells in the file: www.nbi.dk/~petersen/data Cells.txt.

- Selecting P-cells by requiring l < 9 μm what is the rate of type I and type II errors?
- Which of the two variables l and T is best at distinguishing between P and E cells?
- Separate P and E cells using l and/or T, and draw a ROC curve of your result.

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The total num of P cells smaller than 9 um is : 2502
The E cells num is : 269
The total num of E cells greater than 9 um is : 1847
The P cells num is : 72
Therefore, type I error rate is:  2.7972%
The type II error rate is:  12.7127%

The type I error rate of transparency of 0.6 is:  0.03535353535353535
Type II is:  0.15359168241965973
Therefore, numerically, length is a better distinguishing variable
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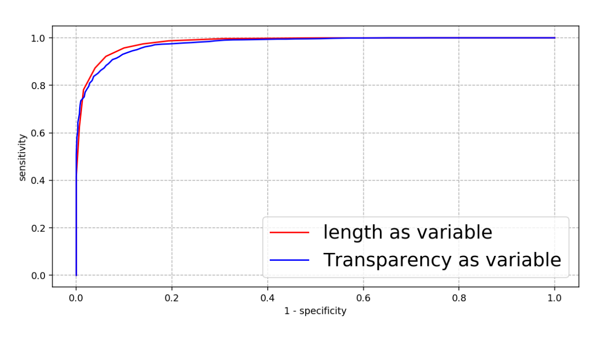

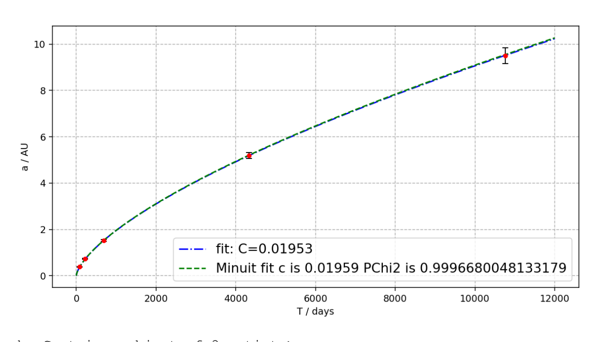

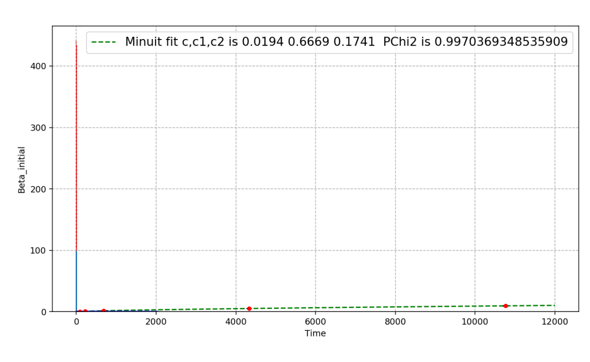

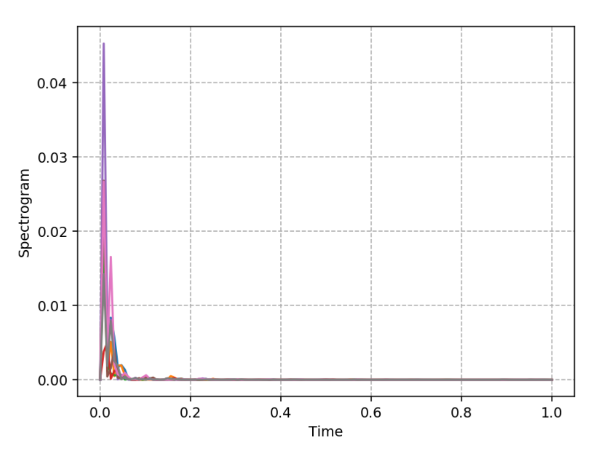

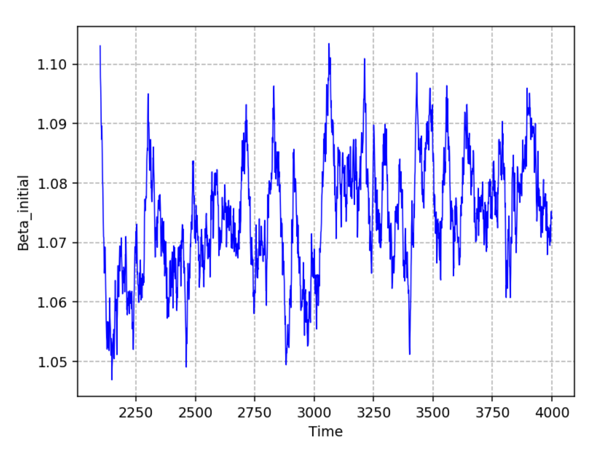

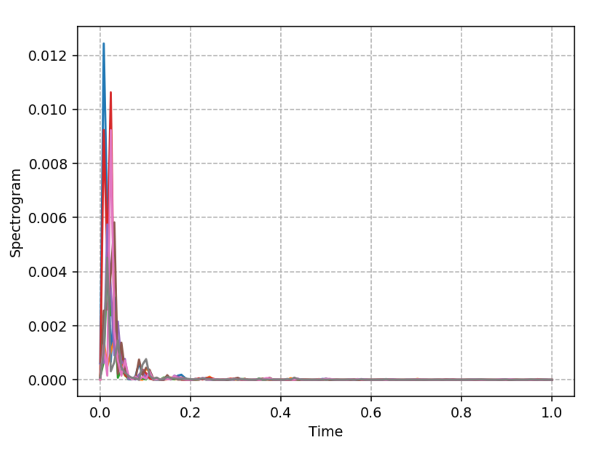

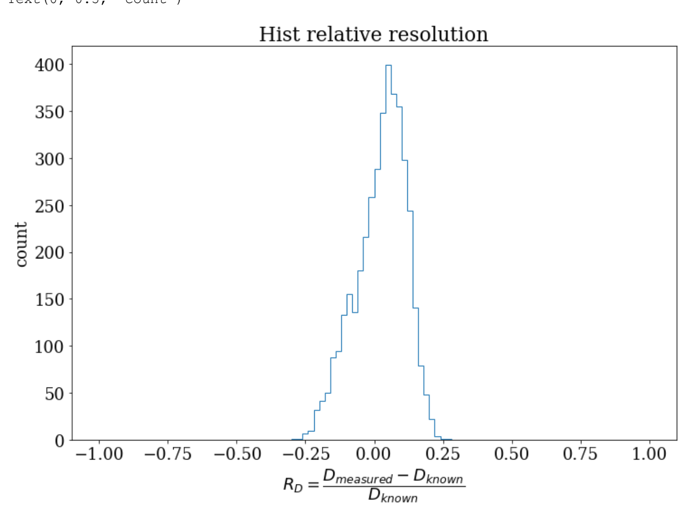

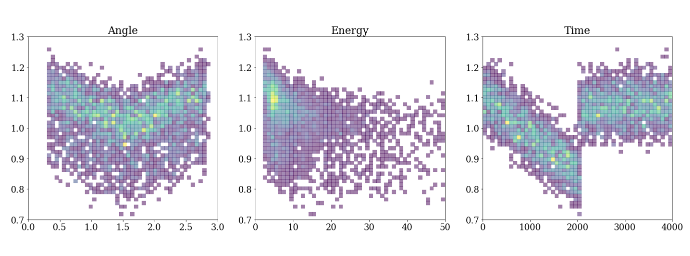

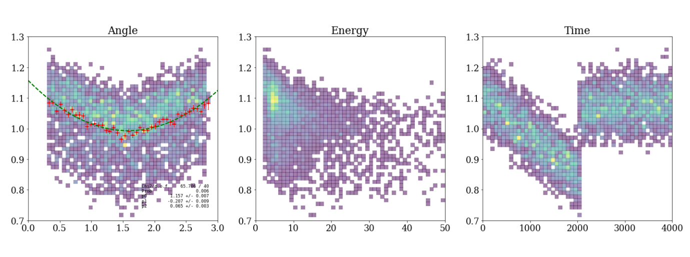

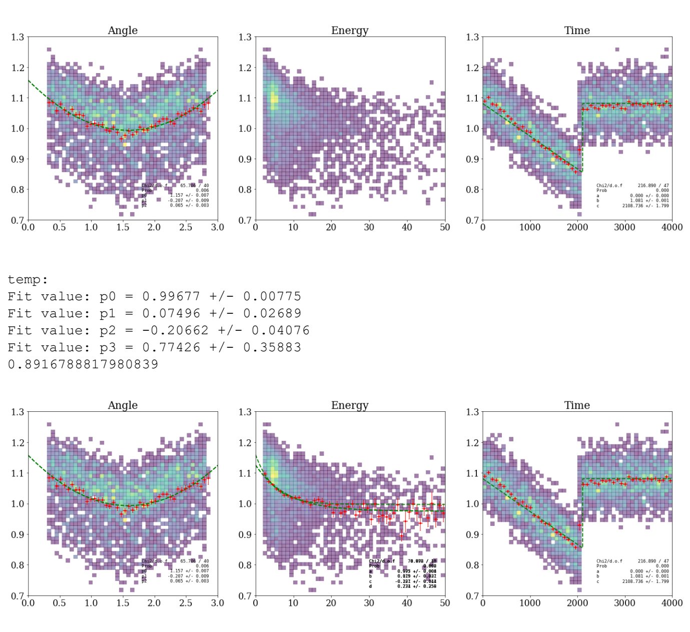

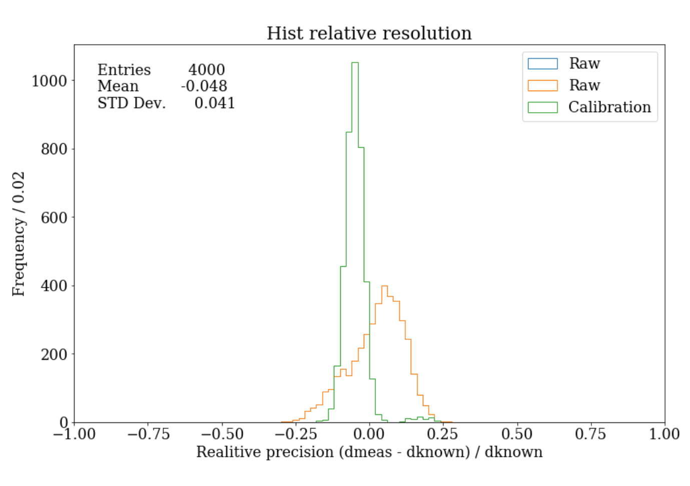

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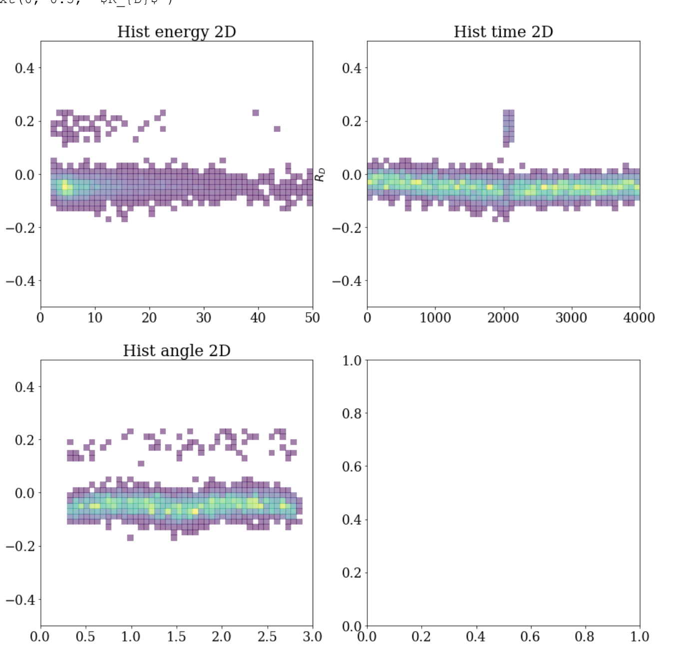


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