

Unbinned diffe cross section meas Jet Image towards a commo

Convolution	 Max-Pool

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vs for an image-





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Differential Cross Section Measurements



Differential Cross Section Measurements 39 This is the bread and butter of the measurement program at the LHC! The key component of this is the correction of detector effects. This allows for the data to be compared with other experiments and with predictions. correction of detector effects = unfolding

Want this

Measure this











There were some early proposals for unbinned unfolding* but as far as I am aware, they were not used for any measurements.

However, recent innovations in machine learning and resulted in new methods for unbinned unfolding, which are being used for data analysis+ (!)

The goal of this discussion is to propose a common way for publishing unbinned results to maximize their science potential

We need input from both experimentalist and theorists (!)

*see L. Lindemann and G. Zech, NIM A 354 (1995) 516 & related +see https://www-h1.desy.de/h1/www/publications/htmlsplit/H1prelim-21-031.long.html

How do we publish binned results?

	Repository for publication-re	EPData elated High-Energy Physics data	
	Search on 9427 publicat Search for a paper, author, experiment e.g. reaction P P> LQ LQ X, title has "pl	tions and 96116 data tables. , reaction Search Advanced hoton collisions", collaboration is LHCf or D0.	
ATLAS View Data	Data fre LICE View Data	om the LHC CMS View Data	LHCb View Data





YAML with resource files YAML YODA ROOT CSV



YAML with resource files
YAML
YODA
ROOT
CSV

ndependent_variables: header: {name: '\$\Delta R(b,b)\$'} values: - {high: 0.25, low: 0.2} - {high: 0.3, low: 0.25} - {high: 0.4, low: 0.3} - {high: 0.5, low: 0.4}

- {high: 0.6, low: 0.5}
- {high: 0.7, low: 0.6}

YAML files with metadata, bin contents, and uncertainties If the data can be fit with a function, you could publish the function (e.g. if it is a NN, you could publish the architecture and weights). 49

Another natural representation that doesn't require a function fit is to publish data sampled from the unfolded result.

My proposal is based on this idea.





As in HEPData, I propose there is a "submission" YAML file with the same measurement metadata.

Each submeasurement* also has some metadata & points to a data file. In HEPData, the data file is itself a YAML file.

The files will have data with the "shape" $[(M+1) \times N(k+1)]$

...where N is the number of sampled events and M is the number of systematic uncertainties and k is the number of dimensions per event

*this could be a single observable, or many observables





The files will have data with the "shape" $[(M+1) \times N(k+1)]$

Each event has k floats* and 1 event weight

There are N events

This is repeated for each of the M systematic uncertainties

For representations that don't have weights, the weights will be set to 1. For representations that only use weights, there will be M copies of the original array.

I have not thought deeply about file formats (npy, root, hdf5) and would be happy to hear opinions.

*For variable-length measurements, perhaps should use variable-length arrays like awkward for storage



The submission YAML should give metadata about which uncertainties are included.

For statistical uncertainties, there should be Q replicas and the uncertainty in a given bin is computed by taking the standard deviation over replicas.

For systematic uncertainties, the difference between the nominal and varied bin content is the uncertainty.

There should be warnings in metadata and/or inflated uncertainties in regions of phase space that should not be studied with the data.



Zenodo is a very natural location. Maybe the submission YAML can also be hosted on HEPData and linked to Zenodo for each searching?

Proposal - example

In [1]: import numpy as np import pandas as pd import matplotlib.pyplot as plt

In [2]: x = np.random.normal(0,1,10000)

```
In [3]: w = np.abs(x)**0.2
w_syst_up = np.abs(x)**0.3
w_syst_dn = np.abs(x)**0.1
```

```
In [4]: plt.hist(x,bins=np.linspace(-3,3,10),alpha=0.5)
plt.hist(x,bins=np.linspace(-3,3,10),weights=w,histtype="step",color="black")
n_syst_up,b=np.histogram(x,bins=np.linspace(-3,3,10),weights=w_syst_up)
n_syst_dn,_=np.histogram(x,bins=np.linspace(-3,3,10),weights=w_syst_dn)
for i in range(len(b)-1):
    plt.fill_between([b[i],b[i+1]],n_syst_dn[i],n_syst_up[i],color="black",alpha=0.3)
plt.xlabel("X")
```

```
In [5]: d = {"nominal":x,
    "nominalw":w,
    "syst_up":x,
    "syst_upw":w_syst_up,
    "syst_dn":x,
    "syst_dnw":w_syst_dn}
```

In [6]: df = pd.DataFrame(data=d)

```
In [7]: df
```

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	nominal	nominalw	syst_up	syst_upw	syst_dn	syst_dnw
0	0.731914	0.939490	0.731914	0.910622	0.731914	0.969273
1	0.146232	0.680783	0.146232	0.561711	0.146232	0.825096
2	-0.629654	0.911634	-0.629654	0.870423	-0.629654	0.954795
3	0.581001	0.897089	0.581001	0.849675	0.581001	0.947148
4	-0.321038	0.796730	-0.321038	0.711159	-0.321038	0.892597





