

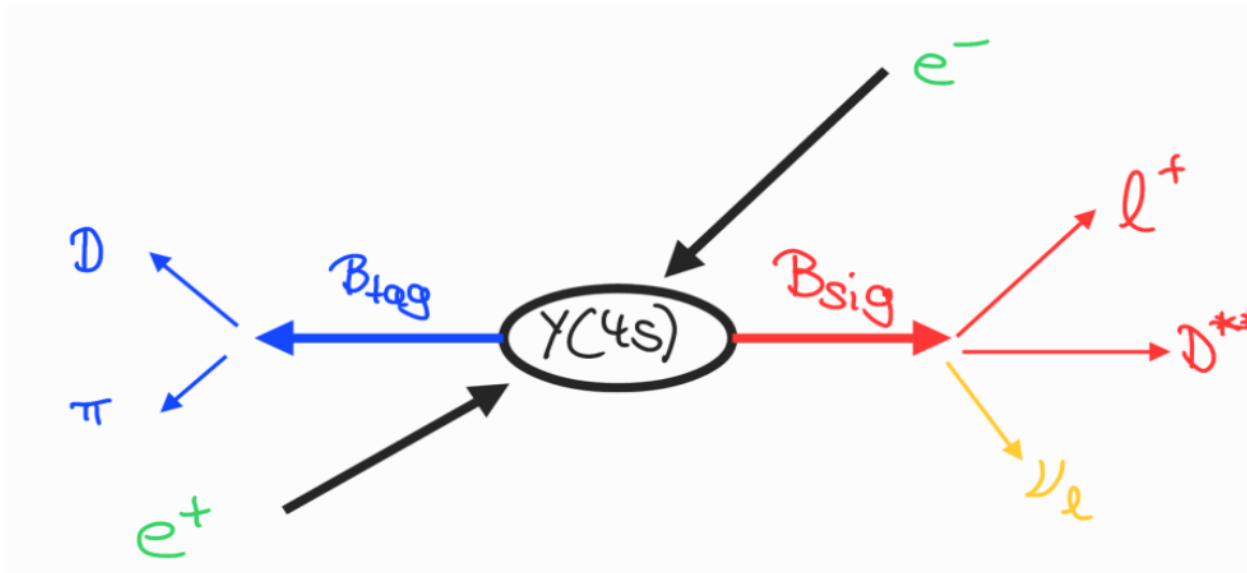
PyHF use-case: Branching Ratio Determination of

$$B \rightarrow D^{**} \ell \nu$$

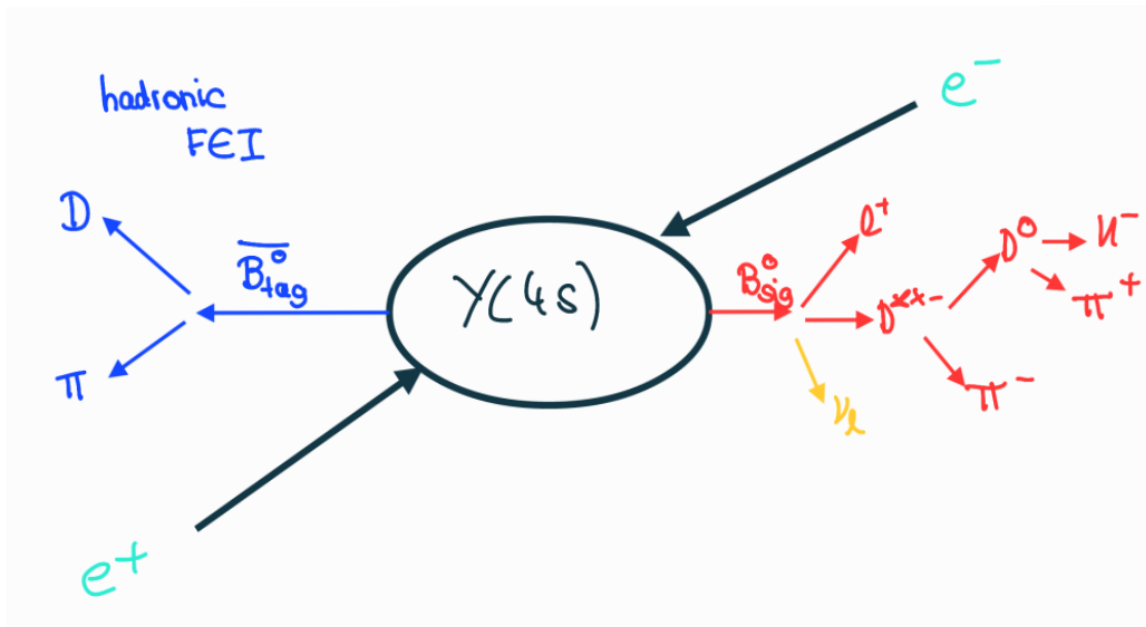
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Analysis Goal

- measurement of branching ratio $B \rightarrow D^{**} l \nu$ with hadronic FEI
- normalised to $B \rightarrow D^* l \nu$
→ in total two fits



Analysis Overview



Decay channel

Neutral

$$B^0 \rightarrow D^- \pi^0 \ell^+$$

$$B^0 \rightarrow D^{*-} \pi^0 \ell^+$$

$$B^0 \rightarrow \bar{D}^0 \pi^- \ell^+$$

$$B^0 \rightarrow \bar{D}^{*0} \pi^- \ell^+$$

Charged

$$B^- \rightarrow D^0 \pi^0 \ell^-$$

$$B^- \rightarrow D^{*0} \pi^0 \ell^-$$

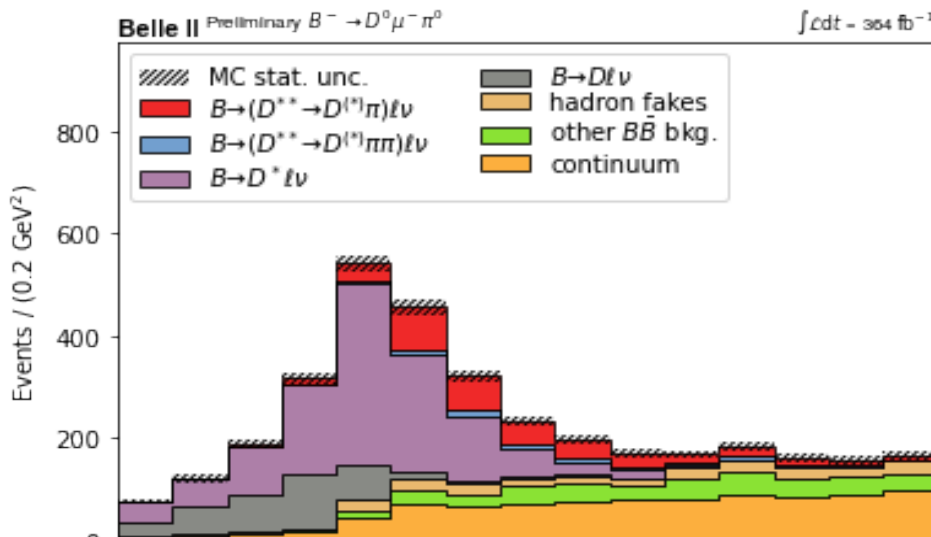
$$B^- \rightarrow D^+ \pi^- \ell^-$$

$$B^- \rightarrow D^{*+} \pi^- \ell^-$$

Neutral and charged B_{Sig} decay channels

General Fit Setup

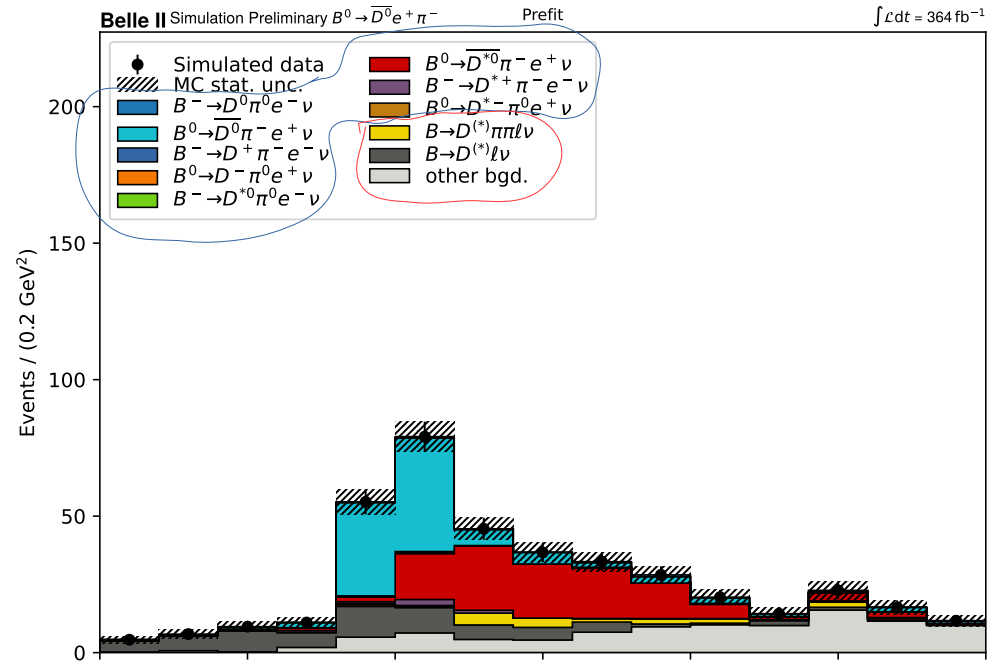
- do binned maximum likelihood fit in
with bins in range



- combine backgrounds due to similar shapes
- divide signal into individual decay channels

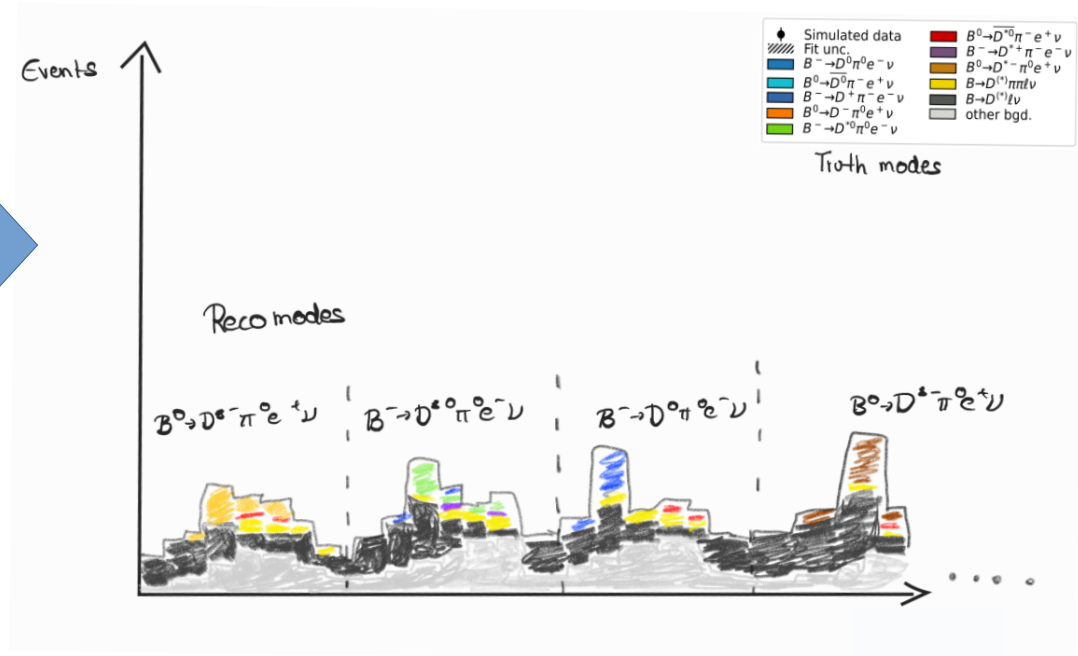
General Fit Setup

- combine backgrounds due to similar shapes
 - 8 signal categories for D^{**}
 - 3 background categories



General Fit Setup

- to incorporate between overlap between D^{**} reconstruction modes
- one overall fit for each lepton mode
- e and mu



$$B \rightarrow D^{**} l \nu$$

General Fit Setup

- include isospin constraints



- Same scaling parameter

●	Simulated data	■	$B^0 \rightarrow \bar{D}^{*0} \pi^- e^+ \nu$
////	Fit unc.	■	$B^- \rightarrow D^{*+} \pi^- e^- \nu$
■	$B^- \rightarrow D^0 \pi^0 e^- \nu$	■	$B^0 \rightarrow D^{*-} \pi^0 e^+ \nu$
■	$B^0 \rightarrow \bar{D}^0 \pi^- e^+ \nu$	■	$B \rightarrow D^{(*)} \pi \pi \ell \nu$
■	$B^- \rightarrow D^+ \pi^- e^- \nu$	■	$B \rightarrow D^{(*)} \ell \nu$
■	$B^0 \rightarrow D^- \pi^0 e^+ \nu$	■	other bgd.
■	$B^- \rightarrow D^{*0} \pi^0 e^- \nu$		

```
"modifiers": [
  {
    "name": "mu",
    "type": "normfactor",
    "data": null
  }
]
```

Systematic Uncertainties

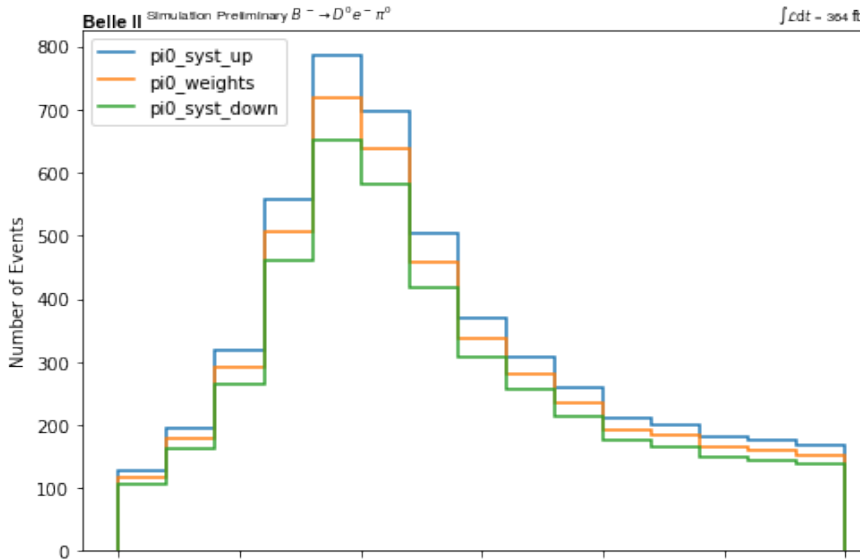
- included systematic uncertainties as nuisance parameters
 - LeptonID, pi0, HadronID, Tracking, slow pi, photon, lumi
- for lumi include as parameter

```
"parameters": [  
  {  
    "name": "lumi",  
    "auxdata": [1.0],  
    "sigmas": [0.017],  
    "bounds": [[0.915, 1.085]],  
    "inits": [1.0],  
  }  
],
```

- Statistical uncertainties from MC

```
"modifiers": [  
  {  
    "name": "my_staterror",  
    "type": "staterror",  
    "data": [1.0, 2.0],  
  }  
],
```


Systematic Uncertainties



```
"modifiers": [
  {
    "name": "my_histosys",
    "type": "histosys",
    "data": {"hi_data": [15, 22], "lo_data": [5, 18]},
  },
],
```

- per-bin shape uncertainty controlled by single nuisance parameter (gaussian constraint)
 - in Belle II: most systematic uncertainties consist of stat. and syst. component

My Model

```
{'channels': [{'name': 'measurement', 'samples': [{'name': 'other bgd.', 'data': [0.5970679330901616, 1.3137996892535455, 1.2717256755698056, 1.4321599587267346, 4.768404764908382, 5.802474698527642, 8.41263112225653, 14.083063154219614, 12.059218291109513, 16.644311234422375, 16.06636699396259, 21.543218196398243, 21.229423218210467, 30.185717718535496, 28.291736452224203, 1.280398953542008, 0.9052616897885521, 2.5445884915542245, 6.599197818761798, 10.32428133270756, 10.113429188529286, 21.018721696285162, 22.328896956071873, 25.808460073203204, 2.173208776374, 3691962496727264, 112885623735, 128485, 'dat', 641, 1.66941136203078001, 0.49529041340013, 2.150282746081515337, 100954, {'nam', 16606469778, 36.72730594757, 2.76667489261, 11.888019260866107, 13.90362, 627315326.642350706, 6, 0.2689002506125, 7.485574909292409, 0.8328054919872592, 2.065439445605206, 3.1042849437953195, 2.4393950035188037, 9.242139573325845, 11.765912298734579, 14.599793458945486, 26.807783250906894, 31.581027224451447, 33.451972700520635, 37.98349213784194, 48.789304110211305, 46.287658233786104, 47.589673673148646, 58.63434209920508, 0.19856388596687488, 0.6717074067899933, 0.23697407490247435, 1.6462592177424176, 4.796659720924173, 6.011007572753977, 4.111711923501238, 4.010731358721076, 6.195699190887513, 7.915145156440278, 8.470084053172302, 8.506
```

- Dictionary writing for model automated → many entries

$$B \rightarrow D^{**} \ell \nu$$

Running the Fit

```
def fit(
    observation: np.ndarray,
    model: pyhf.pdf.Model,
    minimiser: str,
    par_bounds: List = None,
    init_pars: Union[np.ndarray, None] = None,
):
    """
    Do not want that the program exists, if the fit failed.
    """
    # set the minimiser type, initial guess with scipy, after that use minuit, so errors included
    pyhf.set_backend("numpy", minimiser)
    if par_bounds is None:
        par_bounds = model.config.suggested_bounds()
    try:
        result = pyhf.infer.mle.fit(
            data=observation,
            pdf=model,
            par_bounds=par_bounds,
            init_pars=init_pars,
            return_uncertainties=True,
            maxiter=int(1e9),
            return_result_obj=True,
        )
        return result
    except Exception:
        pass
```

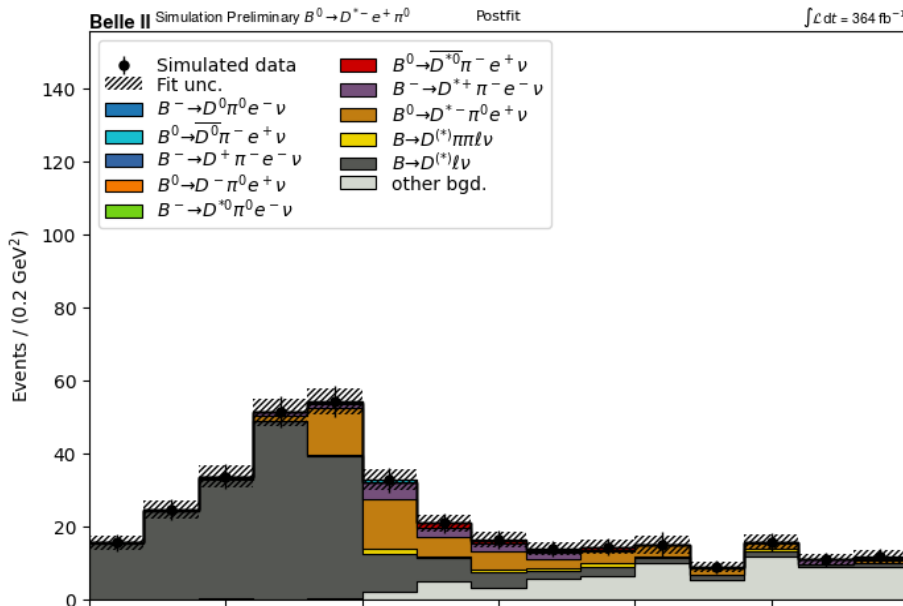
- possible to use minuit or scipy for minimising the likelihood
→ only minuit returns uncertainties



- Use scipy as initial guess
→ fit twice
→ fit converges quicker

```
result = overall_fit.fit(
    observation=observation + model.config.auxdata,
    model=model,
    minimiser="scipy",
)
# get the scipy parameters
init_pars = result[0].tolist()
# do fit with minuit
result_minuit = overall_fit.fit(
    observation + model.config.auxdata,
    model,
    init_pars=init_pars,
    minimiser="minuit",
)
```

Results with Asimov Data



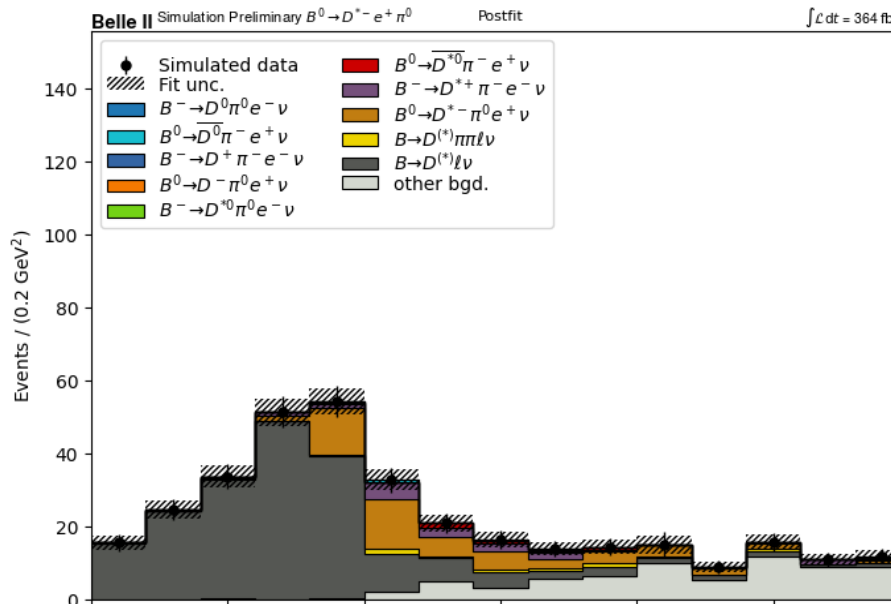
```
def get_sample_order(
    model: pyhf.pdf.Model,
    mc_data: pd.DataFrame,
    component_column: str,
) -> List:
    """
    Function to get the ordering of the samples, so that can be filled into histogram afterwards directly.
    Better to automate this, in case I change the mc matching again.
    """
    sample_order_pyhf = model.config.samples
    sample_order_mc_matching = list(mc_data[component_column].cat.categories)
    sample_order = []
    for sample in sample_order_mc_matching:
        sample_order.append(sample_order_pyhf.index(sample))
    return sample_order
```

Hist module



- Sample ordering might have changed

Results with Asimov Data



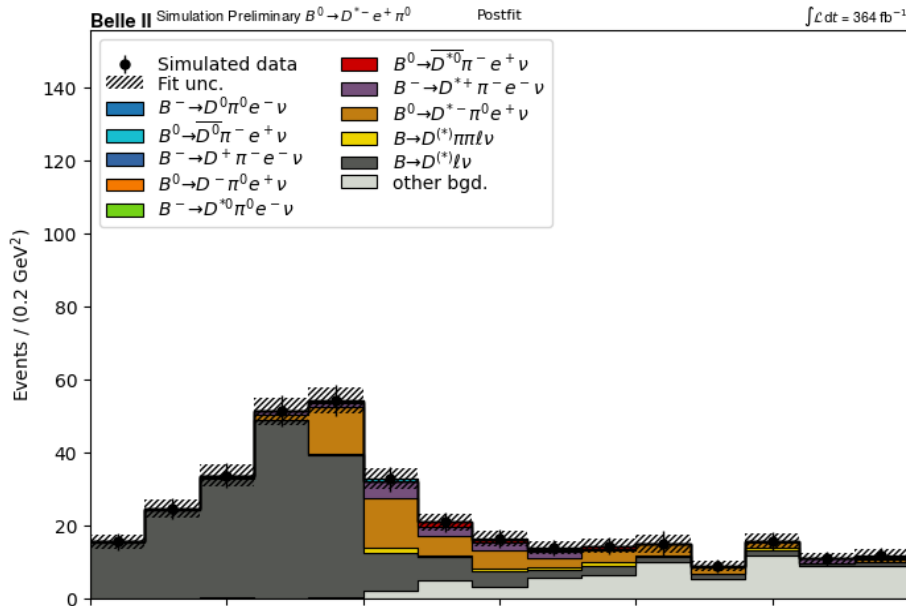
```
def get_mc_counts(
    model: pyhf.pdf.Model,
    pars: np.ndarray,
    return_by_sample: bool = False,
) -> np.ndarray:
    pars = pyhf.tensorlib.astensor(np.asarray(pars))
    deltas, factors = model.modifications(pars)
    allsum = pyhf.tensorlib.concatenate(deltas + [model.nominal_rates])
    nom_plus_delta = pyhf.tensorlib.sum(allsum, axis=0)
    nom_plus_delta = pyhf.tensorlib.reshape(
        nom_plus_delta, (1,) + pyhf.tensorlib.shape(nom_plus_delta)
    )
    allfac = pyhf.tensorlib.concatenate(factors + [nom_plus_delta])
    newbysample = pyhf.tensorlib.product(allfac, axis=0)
    if return_by_sample:
        batch_first = pyhf.tensorlib.einsum("ij...->ji...", newbysample)
        if model.batch_size is None:
            return batch_first[0]
        return batch_first

    newresults = pyhf.tensorlib.sum(newbysample, axis=0)
    if model.batch_size is None:
        return newresults[0]
    return newresults
```



- get results after the fits
 - interpolation done automatically for nuisance parameters
 - returns values per bin

Get Errors using **cabinetry**

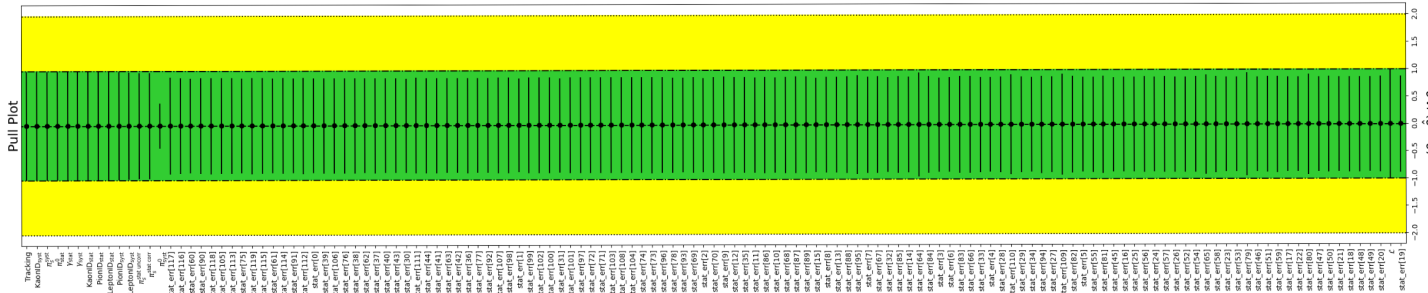


```
(
  total_stdev_model_bins,
  total_stdev_model_channels,
) = cabinetry.model_utils.yield_stdev(
  model, model_result[0][:, 0], model_result[0][:, 1], model_result[1]["corr"]
)
```

Fit value Fit uncertainty Correlation matrix

- for fit uncertainties:
- subtract statistical error from fit uncertainties in quadrature
→ one fit with scaling parameters only (statistical uncertainty)
→ then fit with everything

Pull distributions



- investigate pull distributions
→ code taken from [this example](#)
- possible to change label names

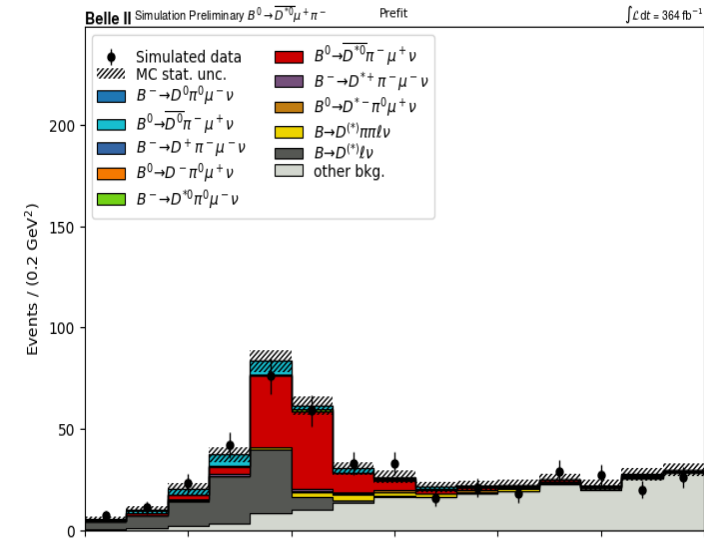
```
pulls = pyhf.tensorlib.concatenate(
    [
        bestfit[model.config.par_slice(k)]
        - model.config.param_set(k).suggested_init
    ]
    / model.config.param_set(k).width()
    for k in model.config.par_order
    if model.config.param_set(k).constrained
)
# calculate the pull errors
pullerr = pyhf.tensorlib.concatenate(
    [
        errors[model.config.par_slice(k)] / model.config.param_set(k).width()
        for k in model.config.par_order
        if model.config.param_set(k).constrained
    ]
)
# get the labels for the pull plots
labels = np.asarray(
    [
        f"{k}[{i}]" if model.config.param_set(k).n_parameters > 1 else k
        for k in model.config.par_order
        if model.config.param_set(k).constrained
        for i in range(model.config.param_set(k).n_parameters)
    ]
)
```

$$B \rightarrow D^{**} \ell \nu$$

Toy Study

```
def generate_toys(
    model: pyhf.pdf.Model,
    random_seed: int,
    n_toys: int = 500,
) -> np.ndarray:
    """
    Return a Tuple with a n_toys performed for a certain model.
    """
    np.random.seed(random_seed)
    toys = model.make_pdf(
        pyhf.tensorlib.astensor(np.asarray(model.config.suggested_init()))
    ).sample((n_toys,))
    return toys
```

- Use histogram and Poisson smear every bin
→ looks more data like

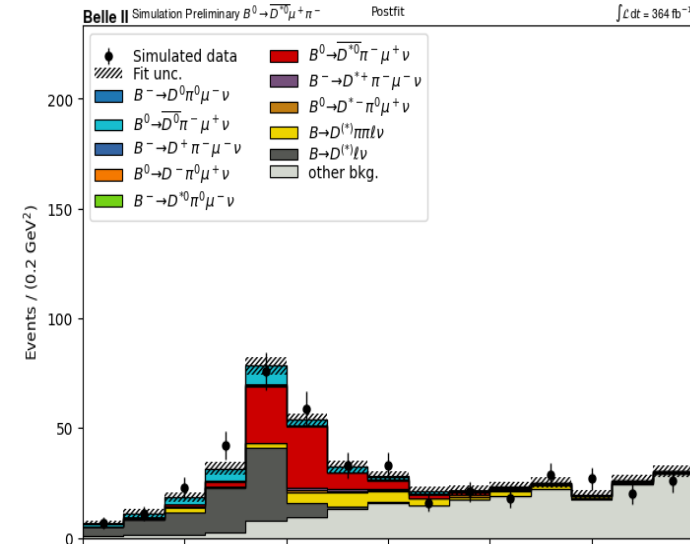


- Histogram before the fit

Toy Study

```
def generate_toys(
    model: pyhf.pdf.Model,
    random_seed: int,
    n_toys: int = 500,
) -> np.ndarray:
    """
    Return a Tuple with a n_toys performed for a certain model.
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    np.random.seed(random_seed)
    toys = model.make_pdf(
        pyhf.tensorlib.astensor(np.asarray(model.config.suggested_init()))
    ).sample((n_toys,))
    return toys
```

- Use histogram and Poisson smear every bin
→ looks more data like



- Histogram after the fit

Systematic Uncertainties

- possible to build workspace and remove particular modifier
→ use to determine effect of systematic uncertainties

```
new_workspace = workspace.prune(
    modifiers=not_considered_modifiers
)
```

- fit with all systematic uncertainties
- remove particular systematic uncertainty to determine impact on overall result
→ also automated that

```
sys_evaluation = [
    "all",
    "statistics",
    "stat_err",
    "pi0",
    "lumi",
    "LeptonID",
    "PionID",
    "KaonID",
    "slow_pion",
    "slow_gamma",
    "Tracking",
]

# loop throw the list with the considered systematic uncertainties
for exclude in sys_evaluation:
    if exclude != "all":
        if exclude == "statistics":
            not_considered_modifiers = [
                modifier
                for modifier in model.config.par_order
                if "mu" not in modifier
            ]
            new_workspace = workspace.prune(
                modifiers=not_considered_modifiers
            )
        else:
            not_considered_modifiers = [
                modifier
                for modifier in model.config.par_order
                if exclude in modifier
            ]
            new_workspace = workspace.prune(
                modifiers=not_considered_modifiers
            )
```

Conclusion

- PyHF works well to determine branching ratio of $B \rightarrow D^{**} \ell \nu$
- examples good to get a first understanding
→ more complex example for binned HEP analysis without hypotesting would be helpful
- need to determine bin counts and uncertainties yourself
→ has been automated for this analysis