Introduction to the HistFitter framework

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+ many other people

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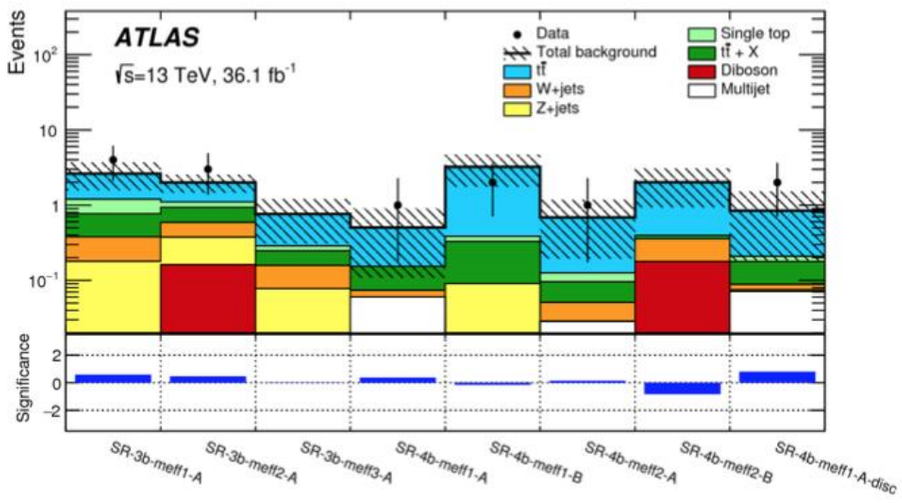
Overview of this session

1. HistFitter overview (first part of the talk)
   - Introduction & strategy
2. HistFitter tutorial (second part of the talk)
   - Running a fit & visualization
   - Calculating limits

Notes: in the interest of time, we will focus on the HistFitter framework and leave a general overview of statistics and statistical tools (i.e RooStats, RooFit, HistFactory) for further reading (some links are provided in the backup).

Some example results with HistFitter:

arXiv:1806.04030



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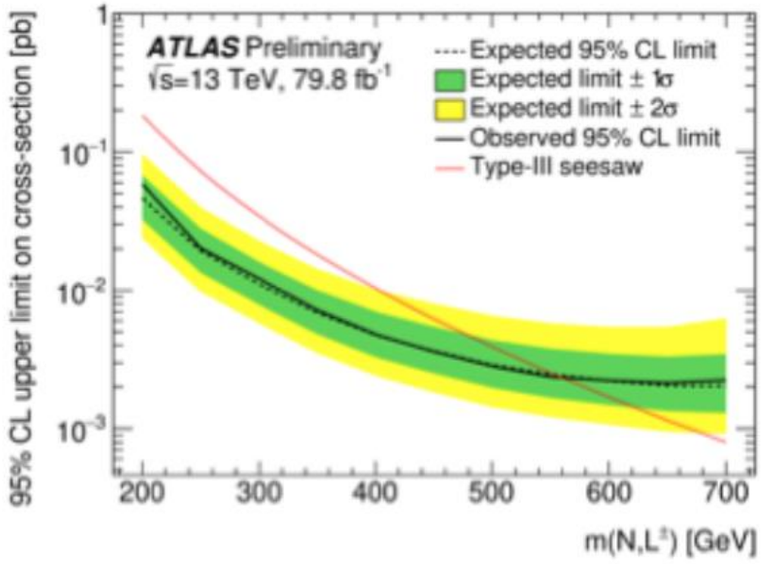

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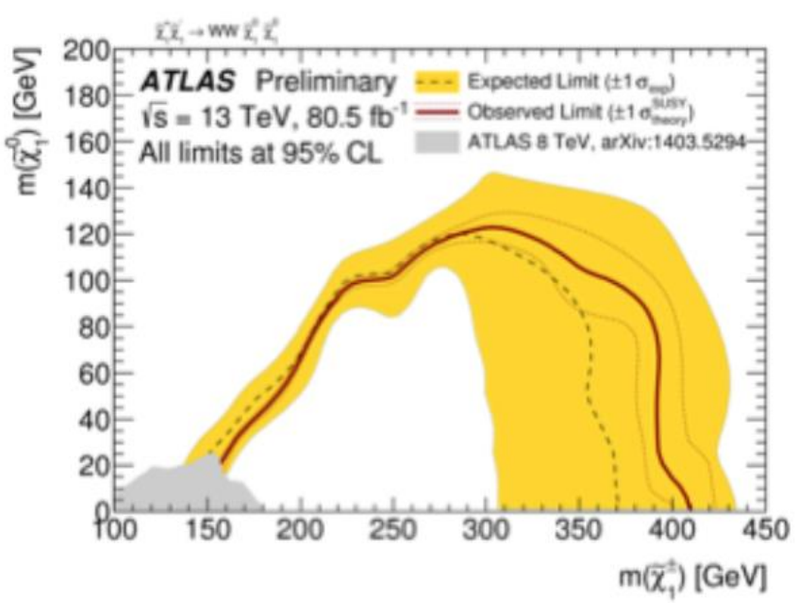


Introduction

- **HistFitter** is a statistical tool/framework used in (almost) all SUSY WG analyses since 2012 for fitting, interpretation and presentation of fit results
  - Developed in SUSY strong production 1-lepton group, quickly adopted as recommended tool
  - Initial small core team: Max Baak, Geert-Jan Besjes, David Cote, Alex Koutsman, Jeanette Lorenz and Dan Short
  - Also partly used in Higgs, Exotics and Top WGs.

- **HistFitter** is:
  - built on top of RooFit/HistFactory and RooStats
  - consists of Python part for configuration and C++ part for CPU-intensive calculations

- Why HistFitter?
- **HistFitter** extends RooFit/HistFactory and RooStats in four key areas:
  - Programmable framework: performing complete analysis from a simple configuration file
  - Analysis strategy: common physics analysis strategy concepts, such as control/signal/validation regions, woven into the fabric of HistFitter design
  - Bookkeeping: can keep track of numerous data models, from histogram production until final statistical tests → handy when working with large collections of signal hypotheses (*signal grids*)
  - Presentation and interpretation: multiple methods are provided to determine statistical significance of signal hypotheses, and produce publication-quality tables and plot summarizing the fit results.

Summary of workflow

- **Step-0:** define signal/control/validation regions
  - Input TTrees (derived from xAOD), histograms, numbers

- **Step-1:** Construct PDF and the likelihood function

  RooFit or HistFactory + RooFit
  - Result from data is a distribution
  - Model signal and background by PDF (prob. density func.)
  - Construct likelihood(s) by joining data and model(s)
  - Likelihood= Probability(data | theory) for a given hypothesis.

- ↓

- **RooWorkspace**

- ↓

- **Step-2:** Statistical tests on parameter of interest **μ** (signal strength)

  RooStats
  - Construct test statistic q_μ from likelihoods $\tilde{q}_\mu(m_H) = -2\ln\frac{L(data\,|\,\mu, m_H\hat{\hat{\theta}}_\mu)}{L(data\,|\,\hat{\mu}, m_H\hat{\theta})}$
  - Obtain expected distributions of q_μ for various **μ** values
  - Determine discovery p_0 and signal exclusion limit
  - Reminder: **p-value**= probability to get a test statistic value equal or more extreme to that observed for a given hypothesis. When setting limits LHC experiments use **CL_s technique** which gives a modified upper limit.

- **Step-3:** Repeat for each model (i.e. assumed value m_H, model parameters)

HistFitter
- adds steps-0 and 3
- allows full analysis chain from simple configuration file

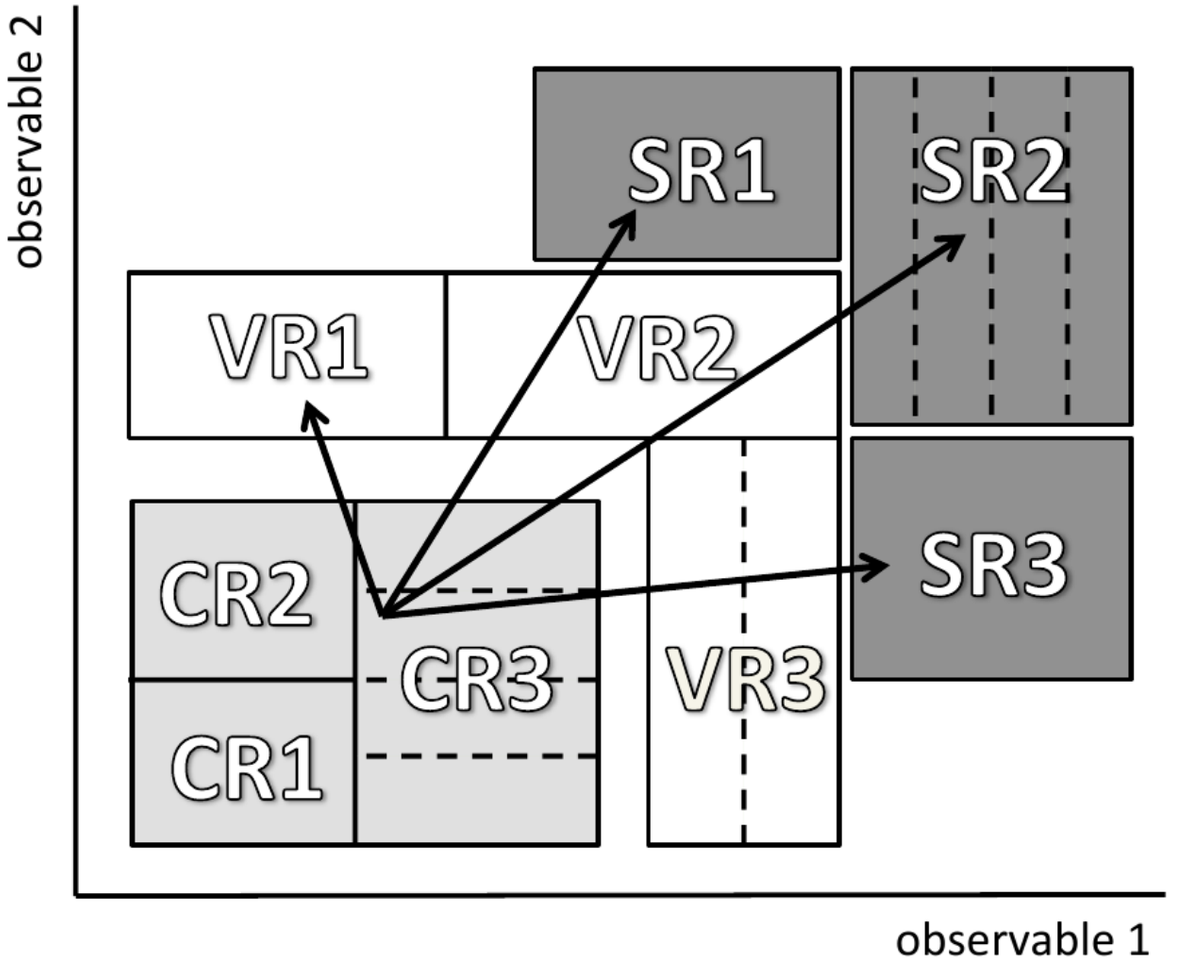
Data analysis strategy

- Particle physics analyze large data samples for measurements of discovery
- Data interpretation relies on using external - simulation, Monte Carlo (MC) - predictions for backgrounds and signal
- HistFitter configures and builds parametric models from these predictions

- Typically one defines several phase space regions to study a specific phenomenon

- Definition depends on the purpose:
  - **Signal region:** signal-rich region (SR)
  - **Control region:** background-rich region (CR), fit simulated backgrounds to data
  - **Validation region:** validation of extrapolation (VR)

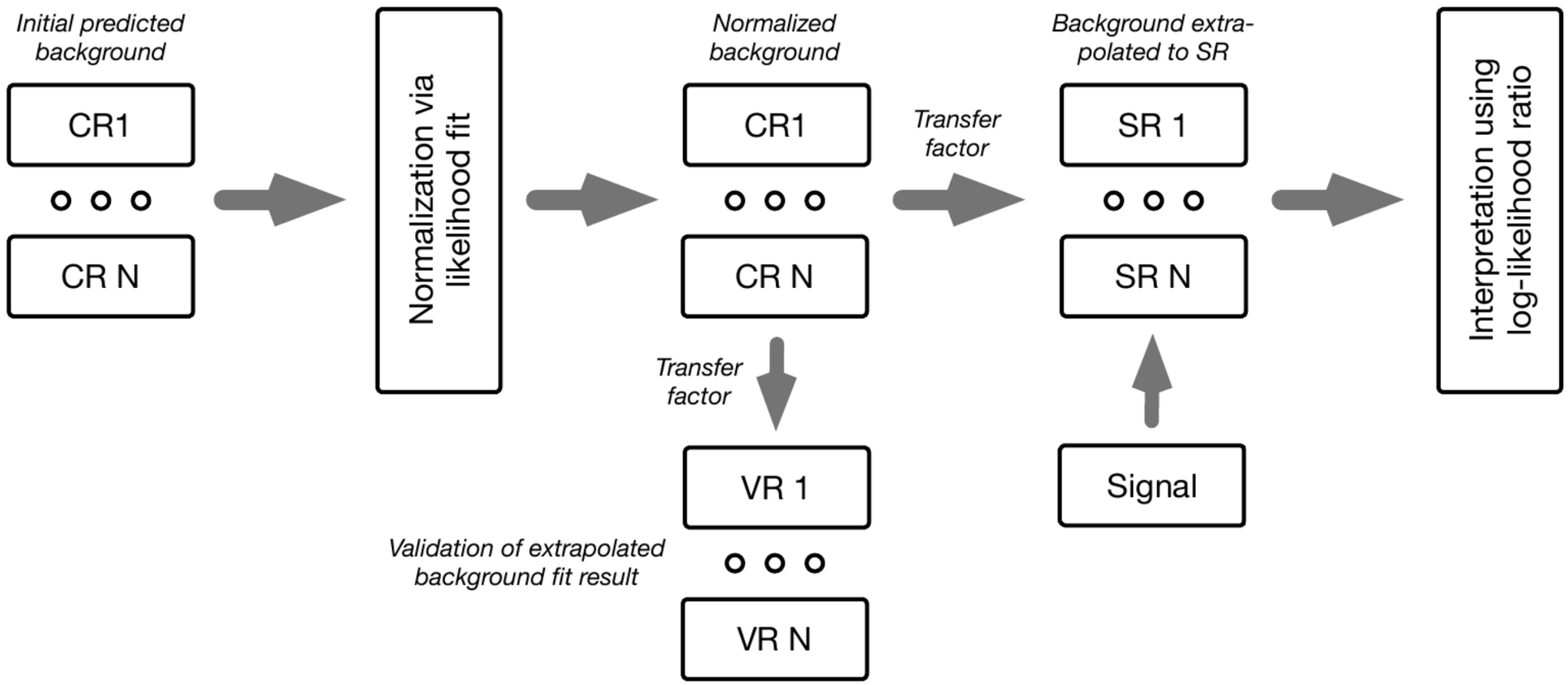
- Concepts of CR/SR/VR woven into the fabric of HistFitter



Analysis strategy flow

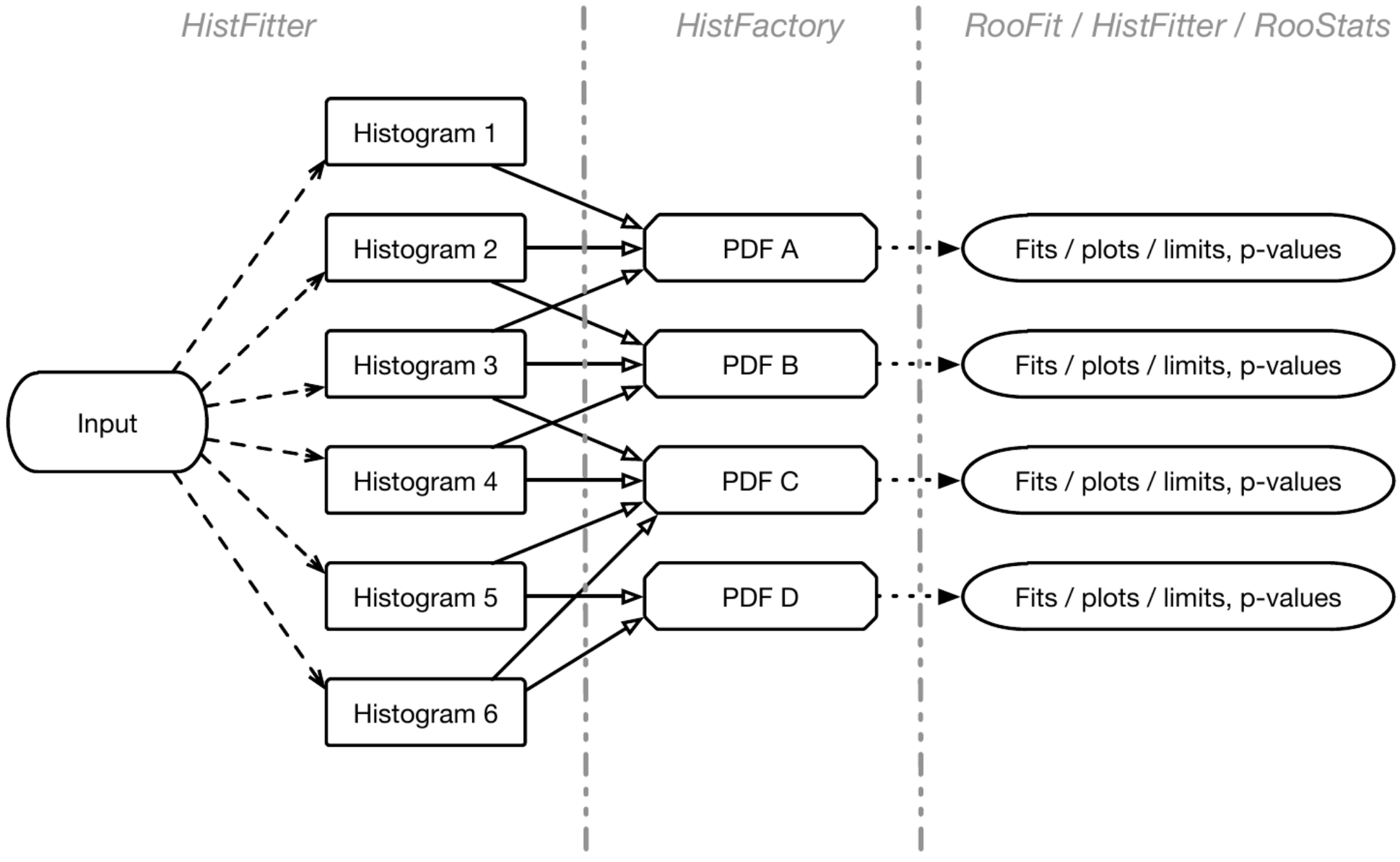
- Each CR/VR/SR modeled by a separate PDF, combined in a simultaneous fit
- Parameters shared in all regions → consistent background/signal prediction and systematics
  - Sharing user-defined

- Analysis flow:
  - Backgrounds normalized to data in a fit of control regions
  - Extrapolate to validation/signal regions using transfer factors (ratio of events between CR and SR/VR)
  - If good agreement in VR, unblind the SR
  - If no excess, add signal prediction and interpret/set limits



Processing sequence

- Based on user-defined configuration file, processing sequence of HistFitter split in three stages



step-0
Histogram production

step-1
PDF construction
Workspace building

step-2/3
Analysis of models

Model construction

- Models constructed using HistFactory from input histograms
- General form of the constructed likelihood:

$$L(\boldsymbol{n}, \boldsymbol{\theta}^0 | \mu_{\mathrm{sig}}, \boldsymbol{b}, \boldsymbol{\theta}) \;=\; P_{\mathrm{SR}} \times P_{\mathrm{CR}} \times C_{\mathrm{syst}}$$

  - P = Poisson measurements of number of observed events in CR/SR (VR)
  - C = Constraint terms for systematic uncertainties, auxiliary measurements
  - Likelihood depends on number of observed events in all regions (n), predictions for various background processes (b), the nuisance parameter (θ) parametrizing the systematic uncertainties with their central value (θ^0) and signal strength (μ_{sig})

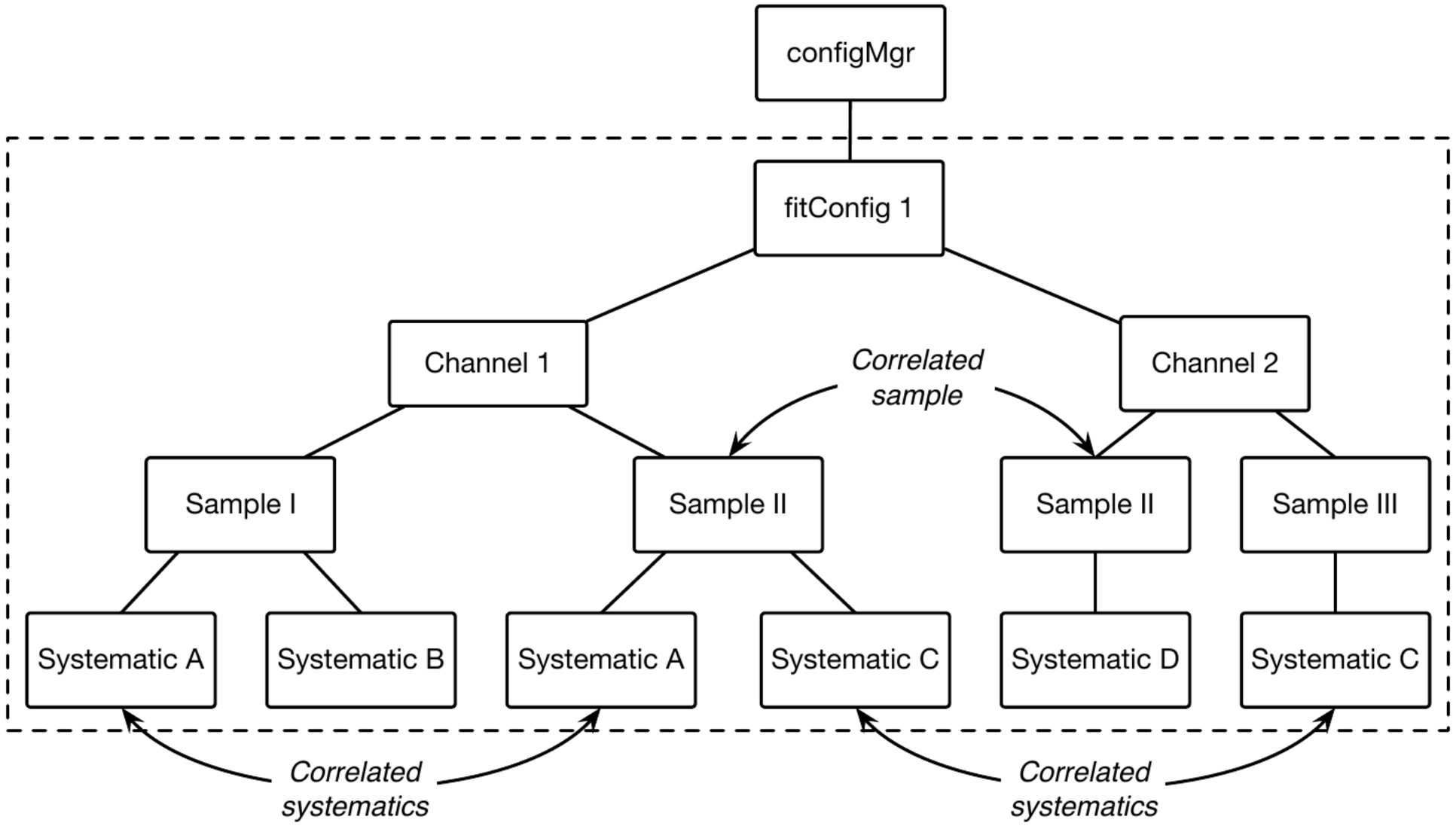
- Likelihood has multiple building blocks:
  - Control/validation/signal regions: called `channel` in HistFitter (HistFactory)
  - Signal and background processes: called `sample` in HistFitter (HistFactory)
  - Uncertainties: called `systematic` in HistFitter (HistFactory)
    - Including statistical/theory/experimental uncertainties

- HistFitter is designed to build and manipulate PDFs of nearly arbitrary complexity
- Bookkeeping/configuration machinery realized through a user-defined Python configuration file

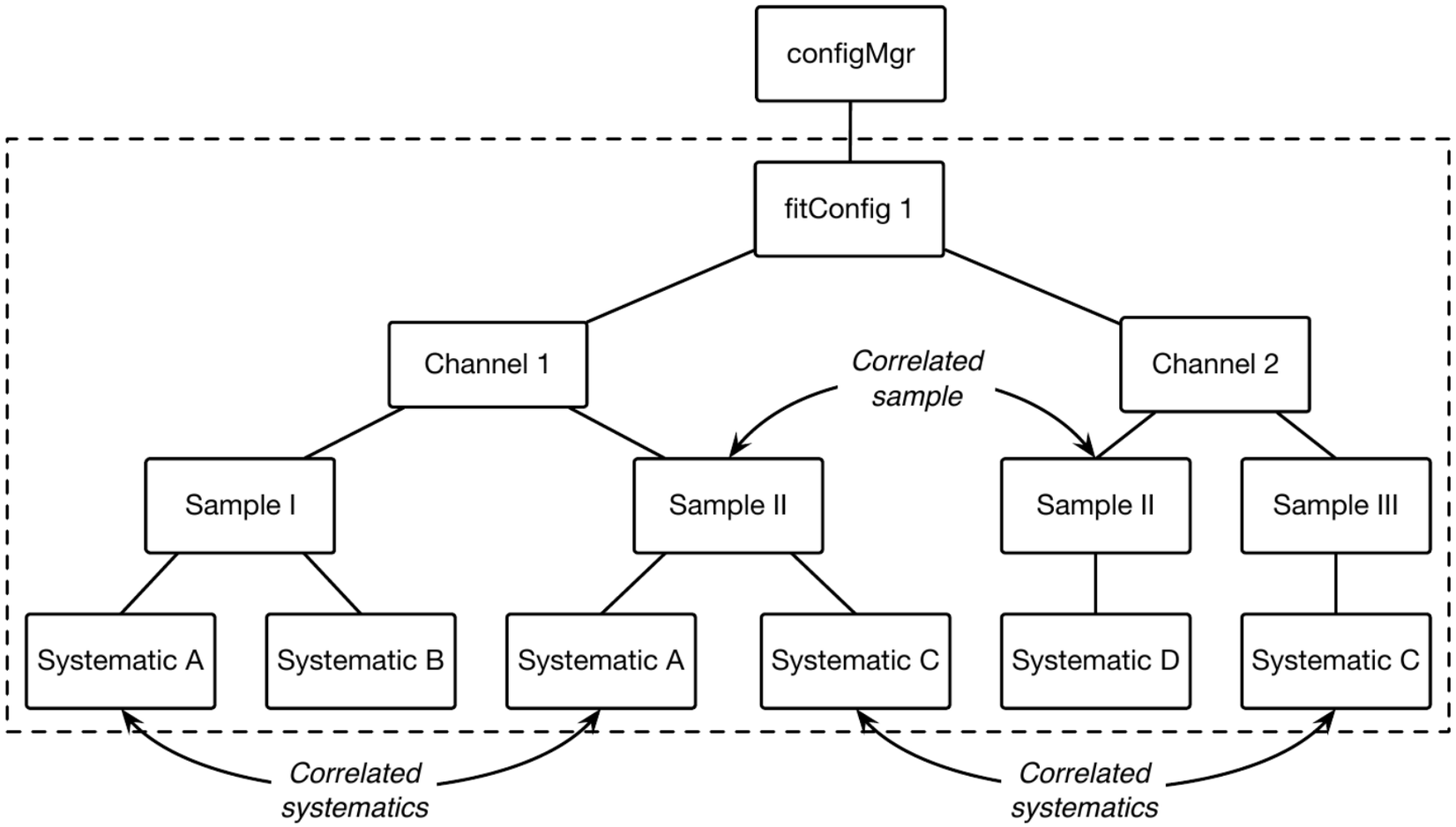
- Configuration manager (`configManager`) highest level (singleton) object in Python and C++
- Manages `fitConfig` objects that contain PDF and meta-data

Fit configuration

- `fitConfig` objects summarize `channels`, `samples` and `systematics` together with corresponding input histograms



Fit configuration properties



- `fitConfig`: can be cloned/extended (see next slide)
- `channels:` either single-bin or multi-bin (shape), property as CR/VR/SR
- `samples:` input from TTree, TH1 or raw (hard-coded) floats, correlated between channels
- `systematics`: provided as ±1σ variation of nominal histogram; input from TTree, TH1 or raw floats; can be correlated between samples and/or channels; many types available extended from HistFactory base types (see later); trickle-down mechanism (see backup)

Common fit strategies

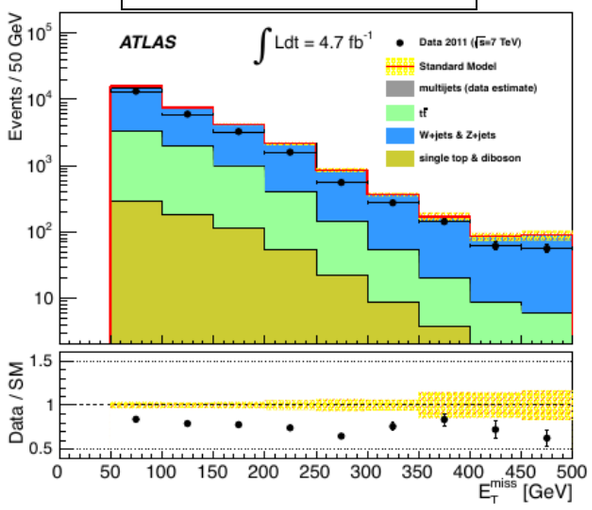
- **Background-only fit**: estimate background yields in validation/signal regions; including *only* CRs in the fit to data; no signal component included in fit configuration
- **Model-dependent signal fit**: fit signal strength and set exclusion limit on a specific signal model; possible use of multi-binned (or multi-SR) shape fit for a robust signal estimation - aka ***exclusion fit***
- **Model-*in*dependent signal fit**: to obtain model-independent upper limits on number of BSM events beyond background prediction; only usable with one single-bin SR (otherwise not model-independent). Also obtain p-value for background-only hypothesis (p_0) - aka ***discovery fit***

Fit setup	*Background-only fit*	*Model-dependent signal fit*	*Model-independent signal fit*
Samples used	backgrounds	backgrounds + signal	backgrounds + dummy signal
Fit regions	CR(s)	CR(s) + SR(s)	CR(s) + SR

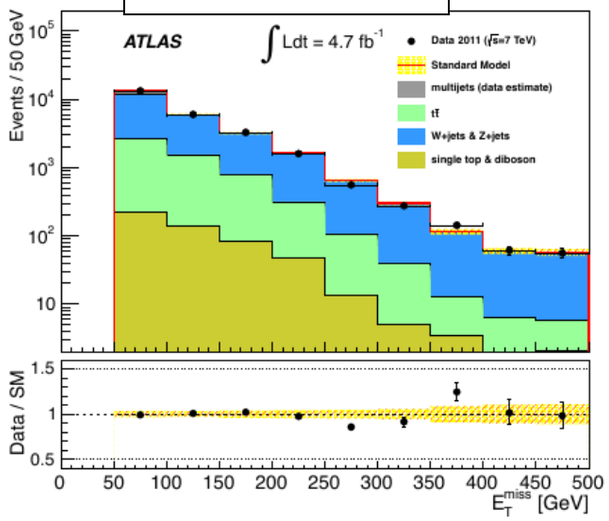
Presentation of results

- HistFitter includes a collection of tools (scripts/functions) to present/understand fit results

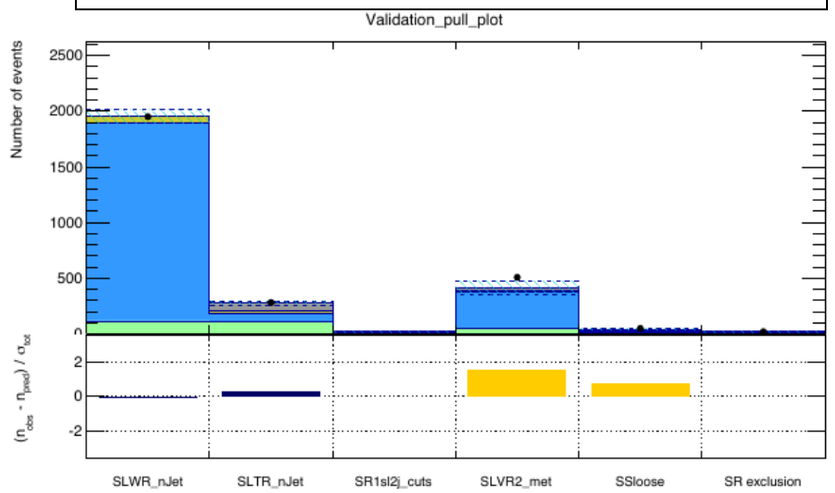
Before Fit



After Fit



After Fit VRs pull plot



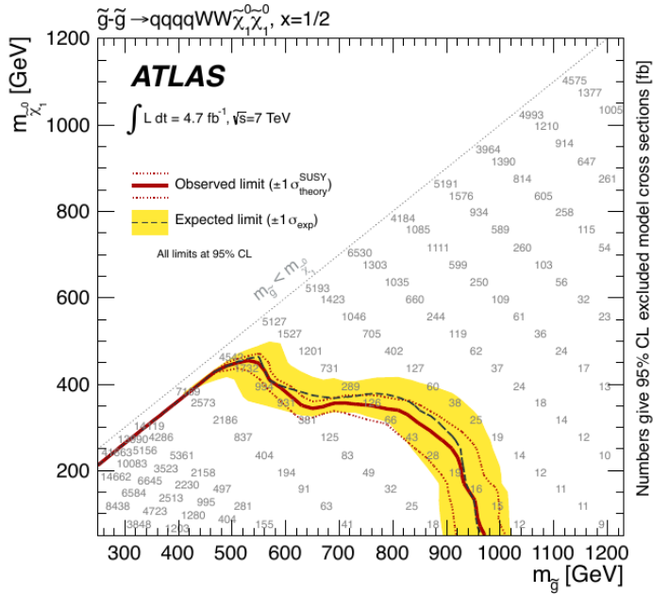
Yields Table

Signal Region	SR1	SR2
Observed events	16	19
Fitted bkg events	19.54 ± 3.93	20.47 ± 5.14
Fitted Top events	4.02 ± 0.96	4.32 ± 1.04
Fitted V+jets events	9.89 ± 1.86	10.47 ± 1.91
Fitted other background events	1.14 ± 0.15	1.19 ± 0.16
Fitted QCD events	4.49 ± 2.72	4.49 ± 4.24
MC exp. SM events	24.85	26.32
MC exp. Top events	8.42	9.11
MC exp. V+jets events	10.82	11.55
MC exp. other background events	1.13	1.17
Data-driven exp. QCD events	4.49	4.49

Systematics Table

Uncertainty of channel	SR1	SR2
Total background expectation	19.54	20.47
Total statistical ($\sqrt{N_{\text{exp}}}$)	$\pm$4.42	$\pm$4.52
Total background systematic	$\pm$3.93 [20.14%]	$\pm$5.14 [25.09%]
QCD background	$\pm$2.66	$\pm$4.20
Statistical uncertainties	$\pm$2.54	$\pm$1.86
Jet Energy Scale	$\pm$1.15	$\pm$1.17
Top yield	$\pm$0.82	$\pm$0.88
Renormalization scale (Top)	$\pm$0.34	$\pm$0.39
V+jets yields	$\pm$0.28	$\pm$0.29
Renormalization scale (V+jets)	$\pm$0.14	$\pm$0.03

Exclusion contour with upper limits



Model-independent upper limits

Signal channel	$\langle\sigma_{\text{vis}}\rangle^{95}_{\text{obs}}$[fb]	S^{95}_{obs}	S^{95}_{exp}	$p(s=0)$
SR3b	0.19	3.9	$4.4^{+1.7}_{-0.6}$	0.50
SR0b	0.80	16.3	$8.9^{+3.6}_{-2.0}$	0.03

HistFitter & documentation

- HistFitter paper on arXiv: http://arxiv.org/abs/1410.1280
- HistFitter webpage with doxgen documentation: http://cern.ch/histfitter
- Central wiki (somewhat oudated): https://twiki.cern.ch/twiki/bin/viewauth/AtlasProtected/SusyFitter
- Tutorial (to be discussed next): https://twiki.cern.ch/twiki/bin/viewauth/AtlasProtected/HistFitterTutorial
- Advanced Tutorial: https://twiki.cern.ch/twiki/bin/viewauth/AtlasProtected/HistFitterAdvancedTutorial
  - Detailed coverage of systematics.
  - Additional diagnostic tools and information for debugging failed fits.
- Mailing list ('shifts'): atlas-phys-susy-histfitter@cern.ch
- Latest recommended tag for physics: HistFitter-00-00-63 (Now on git)
- Release notes: https://twiki.cern.ch/twiki/bin/viewauth/AtlasProtected/HistFitterReleaseNotes
- Analysis check-list (SUSY WG approved): https://twiki.cern.ch/twiki/bin/view/AtlasProtected/HistFitterChecklist

- Monthly user/developer meetings: https://indico.cern.ch/event/743188/
  - To-do list and known issues can be flagged through JIRA: https://its.cern.ch/jira/projects/HISTFITTER/issues/HISTFITTER-51?filter=allopenissues

Time for questions, then onto the tutorial…

HistFitter tutorial

https://twiki.cern.ch/twiki/bin/viewauth/AtlasProtected/HistFitterTutorial

HistFitter - tutorial

- Divided into 5 parts

Setup → Get the code

Part 1 → Simple counting experiment

Start from here if you are new to HistFitter

Part 2 → More complex fits, concept of CR/SR/CR, type of systematic to choose (and "preview" of hypothesis testing)

Part 3 → Tools to visualize results (tables, pull plots)

Part 4 → Hypothesis test and upper limits

Start from here if you want to know more about limit setting

Part 5 → Contour plot

- Lots of material, you are not supposed to go through everything in one hour
- Optional parts of the HistFitter tutorial are hidden under *Show*
- Recommended parts are shown (not hidden) and carry an (*)

Setup

HistFitter tutorial start up

- Setup described on the HistFitter Tutorial twiki:
  https://twiki.cern.ch/twiki/bin/viewauth/AtlasProtected/HistFitterTutorial#Part_0_Setting_up_HistFitter

- Check out the package

```
git clone
https://:@gitlab.cern.ch:8443/HistFitter/HistFitter.git
HistFitterTutorial
 cd HistFitterTutorial
```

- Setup ROOT, setup HistFitter, compile the package, link the files needed for the tutorial

```
setupATLAS
lsetup 'root 6.06.06-x86_64-slc6-gcc49-opt'
source setup.sh
cd src
make
cd ..
ln -s $ALRB_TutorialData/samples samples
```

Work here on slc6!!!

Running HistFitter

- To run HistFitter:

  `HistFitter.py <options> <configuration_file>`

- Some options you will use:

  -t: Create histograms in all regions used for all backgrounds, signal, data from TTrees

  -w: Build workspaces from histograms

  -f: Fit

  -F: Fit type

  -D: various drawing options, to be discussed later

  -L: log level {VERBOSE,DEBUG,INFO,WARNING,ERROR,FATAL,ALWAYS}

  -l: Calculate upper limit

  -p: Calculate the CLs value for a specific signal model (for exclusion)

  -i: interactive mode, keeps you in python command line, but shows plots on your screen

- To see all options run: `HistFitter.py --help`

Part 1

Simple example

- https://gitlab.cern.ch/HistFitter/HistFitter/blob/master/analysis/tutorial/MyUserAnalysis.py
- Simple example with one region with one bin
- One background sample and one signal sample
- Number of expected and observed events provided directly in the configuration file

```
ndata     =  7.          # Number of events observed in data
nbkg      =  5.          # Number of predicted bkg events
nsig      =  5.          # Number of predicted signal events
```

- One systematic affecting only signal, one affecting only background, one both
- We want to measure the signal strength (signal normalization factor)

Part 1 Configuration file (I)

- Only showing most relevant lines

```
# Give the analysis a name
configMgr.analysisName = "MyUserAnalysis"
configMgr.outputFileName = "results/%s_Output.root"%configMgr.analysisName

# Define cuts
configMgr.cutsDict["UserRegion"] = "1."

# Define weights
configMgr.weights = "1."
```

Region selection and weights
•Here just saying "take everything with weight 1"
•Important when input is TTree (later)

- Systematic uncertainties

```
# Set uncorrelated systematics for bkg and signal (1 +- relative uncertainties)
ucb = Systematic("ucb", configMgr.weights, 1.2,0.8, "user","userOverallSys")
ucs = Systematic("ucs", configMgr.weights, 1.1,0.9, "user","userOverallSys")

# correlated systematic between background and signal (1 +- relative uncertainties)
corb = Systematic("cor",configMgr.weights, [1.1],[0.9], "user","userHistoSys")
cors = Systematic("cor",configMgr.weights, [1.15],[0.85], "user","userHistoSys")
```

Name

High and low relative effect

Type (later)

Same name→correlated

But different effect on sig and bkg

Part 1

Configuration file (II)

- Define samples: bkgSample, sigSample and dataSample

```
# Define samples
bkgSample = Sample("Bkg",kGreen-9)
bkgSample.setStatConfig(True)
bkgSample.buildHisto([nbkg],"UserRegion","cuts",0.5)
bkgSample.buildStatErrors([nbkgErr],"UserRegion","cuts")
bkgSample.addSystematic(corb)
bkgSample.addSystematic(ucb)
```

Name

Color

Set the number of background events

Add systematics

```
sigSample = Sample("Sig",kPink)
sigSample.setNormFactor("mu_Sig",1.,0.,100.)
sigSample.setStatConfig(True)
sigSample.setNormByTheory()
sigSample.buildHisto([nsig],"UserRegion","cuts",0.5)
sigSample.buildStatErrors([nsigErr],"UserRegion","cuts")
sigSample.addSystematic(cors)
sigSample.addSystematic(ucs)

dataSample = Sample("Data",kBlack)
dataSample.setData()
dataSample.buildHisto([ndata],"UserRegion","cuts",0.5)
```

Signal normalization factor

Part 1 Configuration file (III)

- Put it all together

```
# Define top-level
ana = configMgr.addFitConfig("SPlusB")
ana.addSamples([bkgSample,sigSample,dataSample])
ana.setSignalSample(sigSample)

# Define measurement
meas = ana.addMeasurement(name="NormalMeasurement",lumi=1.0,lumiErr=lumiError)
meas.addPOI("mu_Sig")

# Add the channel
chan = ana.addChannel("cuts",["UserRegion"],1,0.5,1.5)
ana.addSignalChannels([chan])
```

Define fit configuration

Add all the samples

Which one is the signal sample

Parameter of interest

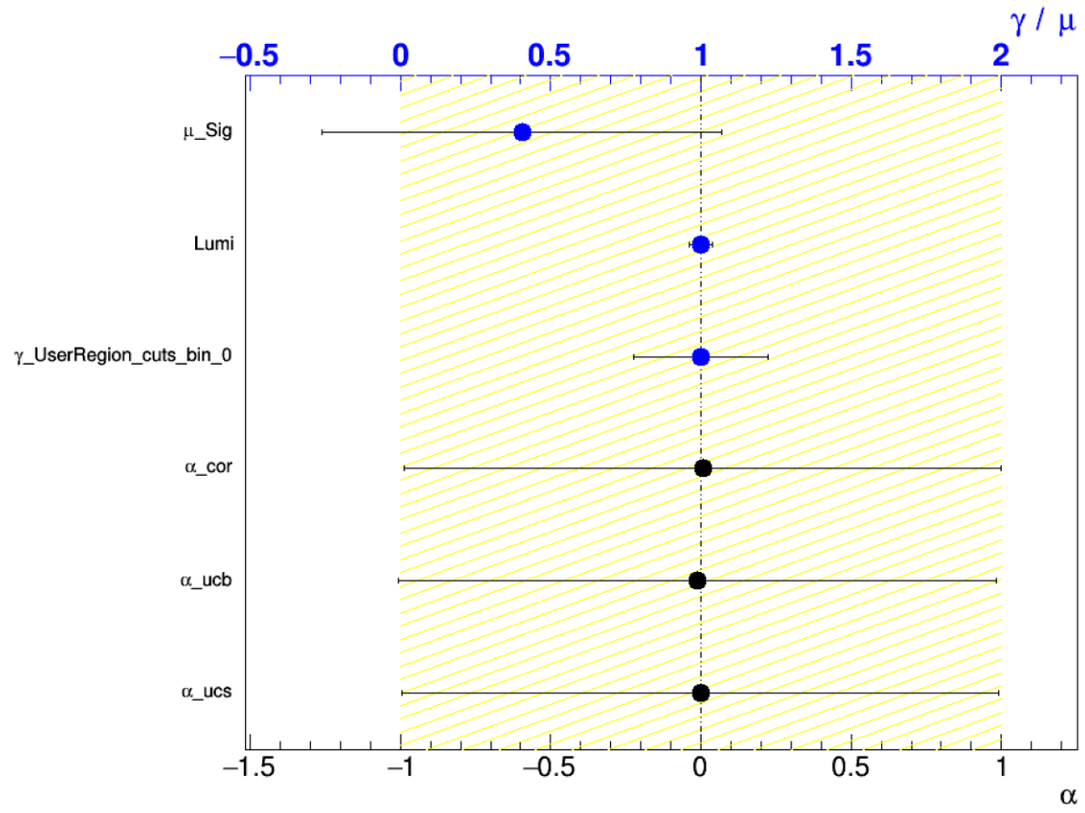
Regions to include in the fit
(only one in our case)

Part 1

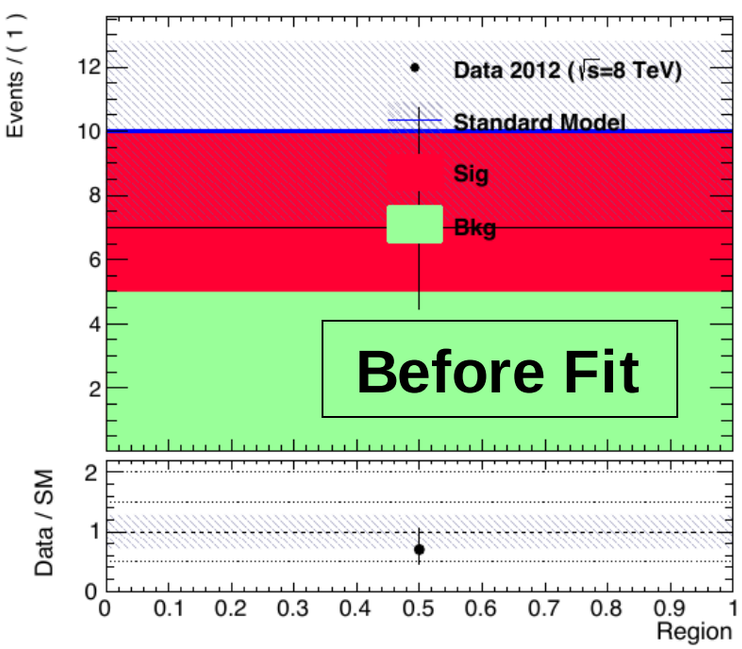
Simple Example: Results

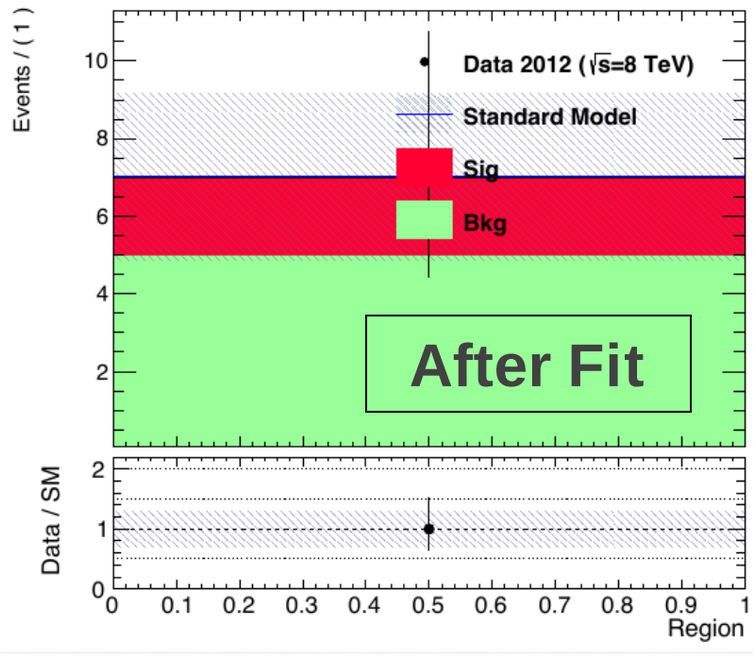
- Simple example with one region with one bin:

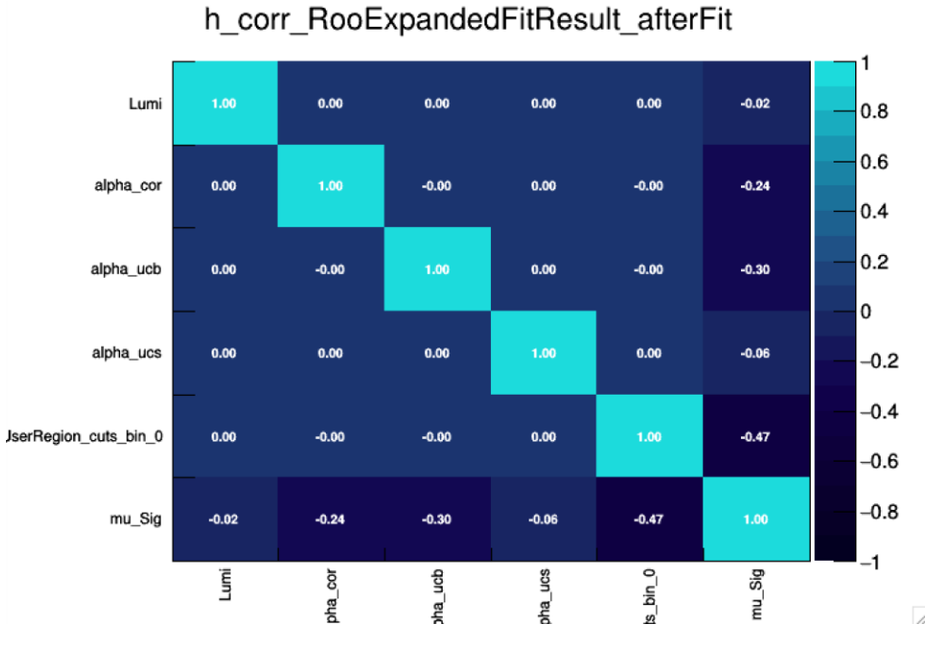
```
HistFitter.py -w -f -D "before,after,corrMatrix" -i
analysis/tutorial/MyUserAnalysis.py
```



- Creates the workspace
- Runs the fit
- Plots before/after fit regions and correlation mat
- Plots summary of fit results
- Keeps you in interactive mode







Part 1 Input from TTree

- In previous example input values provided by hand in the configuration file
- Other (better) option: read from TTree
- https://gitlab.cern.ch/HistFitter/HistFitter/blob/master/analysis/tutorial/MyOneBinExample.py
- Need to specify ROOT files with the Ttree

```
# Set the files to read from
bgdFiles = []
if configMgr.readFromTree:
    bgdFiles.append("samples/tutorial/SusyFitterTree_OneSoftEle_BG_v3.root")
    bgdFiles.append("samples/tutorial/SusyFitterTree_OneSoftMuo_BG_v3.root")
else:
    bgdFiles = [configMgr.histCacheFile]
    pass
```

- Dictionary now contains the selection

```
# Dictionnary of cuts for Tree->hist
configMgr.cutsDict["SR"] = "((lep1Pt < 20 && lep2Pt<10 && met>250 && mt>100 && jet1Pt>130 && jet2Pt>25 && AnalysisType==7) ||
      (lep1Pt < 25 && lep2Pt<10 && met>250 && mt>100 && jet1Pt>130 && jet2Pt>25 && AnalysisType==6))&& met/meff2Jet>0.5"
```

- And the weights to be applied

```
# Tuples of nominal weights without and with b-jet selection
configMgr.weights = ("genWeight","eventWeight","leptonWeight","triggerWeight","truthWptWeight","bTagWeight2Jet")
```

- Specify input file for each background sample

```
topSample.addInputs(bgdFiles)
```

Part 2 More complex fits!

- Shape fits

```
srBin = exclusionFitConfig.addChannel("met/meff2Jet",["SR"],6,0.1,0.7)
srBin.useOverflowBin=True
srBin.useUnderflowBin=True
```

Name of the variable

Look at the distribution of this variable after applying the selections of "SR"

6 equal-width bins from 0.1 to 0.7

- How shape fits can improve sensitivity

- Effect of systematic type

```
#topKtScale = Systematic("KtScaleTop",configMgr.weights,ktScaleTopHighWeights,ktScaleTopLowWeights,"weight","overallSys")
topKtScale = Systematic("KtScaleTop",configMgr.weights,ktScaleTopHighWeights,ktScaleTopLowWeights,"weight","histoSys")
#topKtScale = Systematic("KtScaleTop",configMgr.weights,ktScaleTopHighWeights,ktScaleTopLowWeights,"weight","normHistoSys")
```

Part 3

Table production

- **YieldsTable.py** produces customizable tables of yields before/after fit
- Example: `YieldsTable.py -s Top,WZ,BG,QCD -c SLWR_nJet,SLTR_nJet -w results/MyConfigExample/BkgOnly_combined_NormalMeasurement_model_afterFit.root -o MyYieldsTable.tex`

table.results.yields channel	SLWR_nJet	SLTR_nJet	SR1sl2j	SS_metmeff2Jet
Observed events	1794	269	25	26
Fitted bkg events	1800.73 ± 39.91	262.45 ± 11.47	28.53 ± 5.26	31.74 ± 8.50
Fitted Top events	117.20 ± 11.42	113.20 ± 12.53	6.17 ± 1.12	6.65 ± 1.26
Fitted WZ events	1629.37 ± 42.19	69.75 ± 6.63	13.95 ± 2.03	14.57 ± 1.98
Fitted BG events	43.49 ± 1.90	23.19 ± 1.94	0.96 ± 0.32	1.00 ± 0.32
Fitted QCD events	10.64 ± 0.51	56.30 ± 13.65	7.44 ± 3.75	9.52 ± 7.54
MC exp. SM events	1921.26	261.96	32.04	35.35
MC exp. Top events	165.16	153.98	8.75	9.38
MC exp. WZ events	1647.04	66.30	15.26	15.82
MC exp. BG events	40.96	25.03	0.59	0.63
data-driven exp. QCD events	68.06	16.64	7.44	9.52

- **SysTable.py** produces customizable tables of systematic breakdown per region (or sample)
- Example: `SysTable.py -w results/MyConfigExample/BkgOnly_combined_NormalMeasurement_model_afterFit.root -c SR1sl2j -o systable_SR1sl2j.tex`

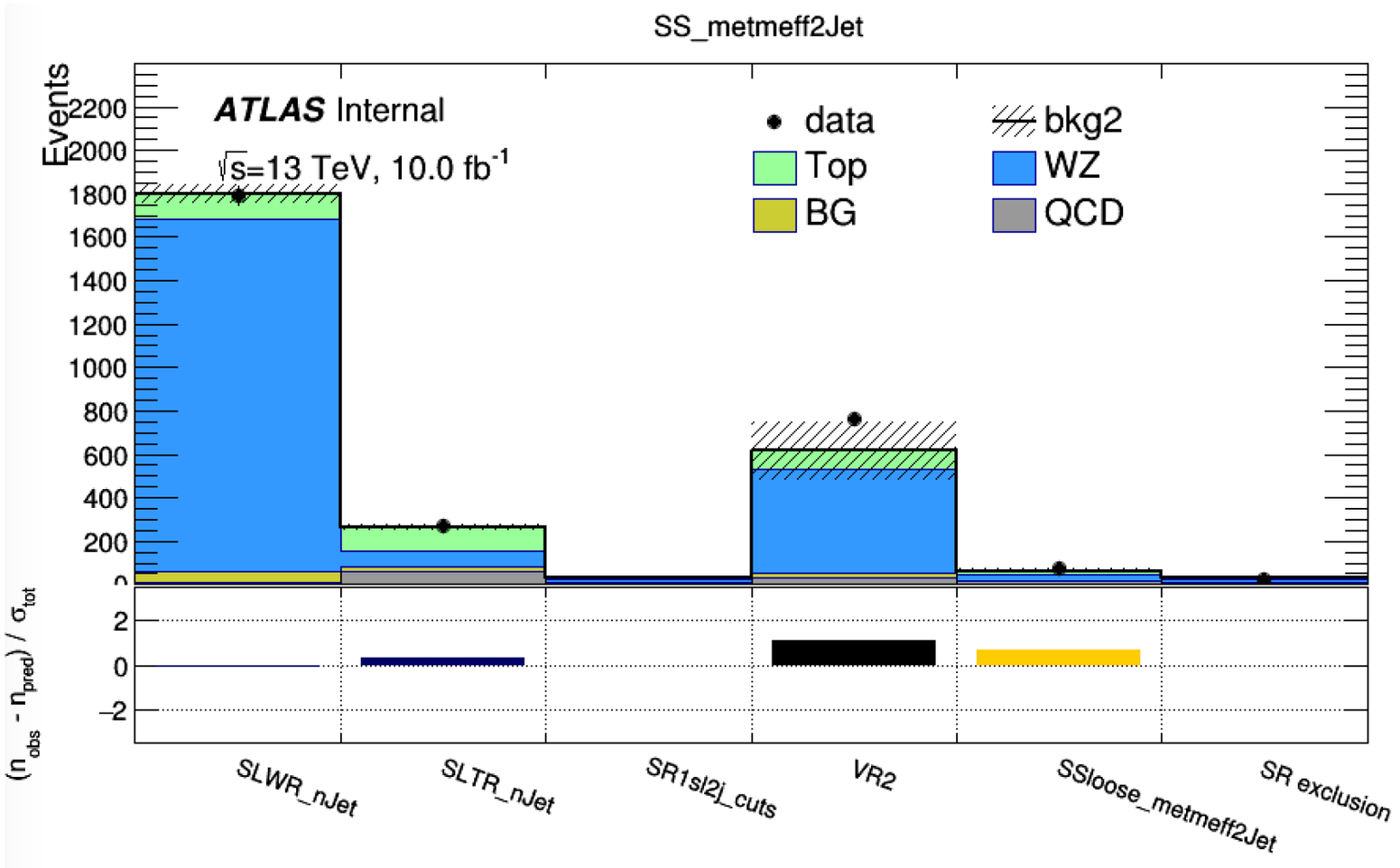
Uncertainty of channel	SR1sl2j
Total background expectation	28.53
Total statistical ($\sqrt{N_{\text{exp}}}$)	±5.34
Total background systematic	±5.26 [18.43%]
gamma_stat_SR1sl2j_cuts_bin_0	±3.63
alpha_QCDNorm_SR1sl2j	±3.63
alpha_JES	±0.93
mu_Top	±0.65
alpha_KtScaleTop	±0.52
alpha_KtScaleWZ	±0.37
mu_WZ	±0.36

Part 3

Pull plots

- You can make plots showing the agreement between expected and observed yields

```
python analysis/tutorial/examplePullPlot.py pdf
```



$$\chi = \frac{n_{\text{obs}} - n_{\text{pred}}}{\sigma_{\text{tot}}}$$

$$\sigma_{\text{tot}} = \sqrt{\sigma^2_{\text{pred}} + \sigma^2_{\text{stat, exp}}}$$

Part 4 Signal model hypothesis test

- Once you have unblinded your SR, one can calculate the CLs/p-value on specific signal models using the exclusion fit (aka model-dependent fit setup)
- As simple in HistFitter as calling:

```
HistFitter.py -p analysis/tutorial/MyUserAnalysis.py
```

- Will calculate:
  - CLs_observed = taking N observed events as data in all regions
  - CLs_expected = taking N expected events as data in all regions
  - CLs_expected ±1sigma experimental uncertainty = N expected as data, ±1sigma fit results
    - yellow band next slide
  - CLs_observed ±1sigma signal theory uncertainty = N observed as data, ±1sigma signal theory
    - need to set the name of the signal theory uncertainty systematic as `Systematic("SigXSec", ...)`
    - red-dotted lines next slide

- Setting calculator and test statistic type can be set in configManager (see backup):

```
# Setting the parameters of the hypothesis test
configMgr.doExclusion=True # True=exclusion, False=discovery
#configMgr.nTOYs=5000
configMgr.calculatorType=2 # 2=asymptotic calculator, 0=frequentist calculator
configMgr.testStatType=3   # 3=one-sided profile likelihood test statistic (LHC default)
configMgr.nPoints=20       # number of values scanned of signal-strength for upper-limit determination
```

- Result of '-p' stored in a ROOT file with 'hypotest' in the name:

```
results/MySimpleChannelAnalysis_fixSigXSecNominal_hypotest.root
```

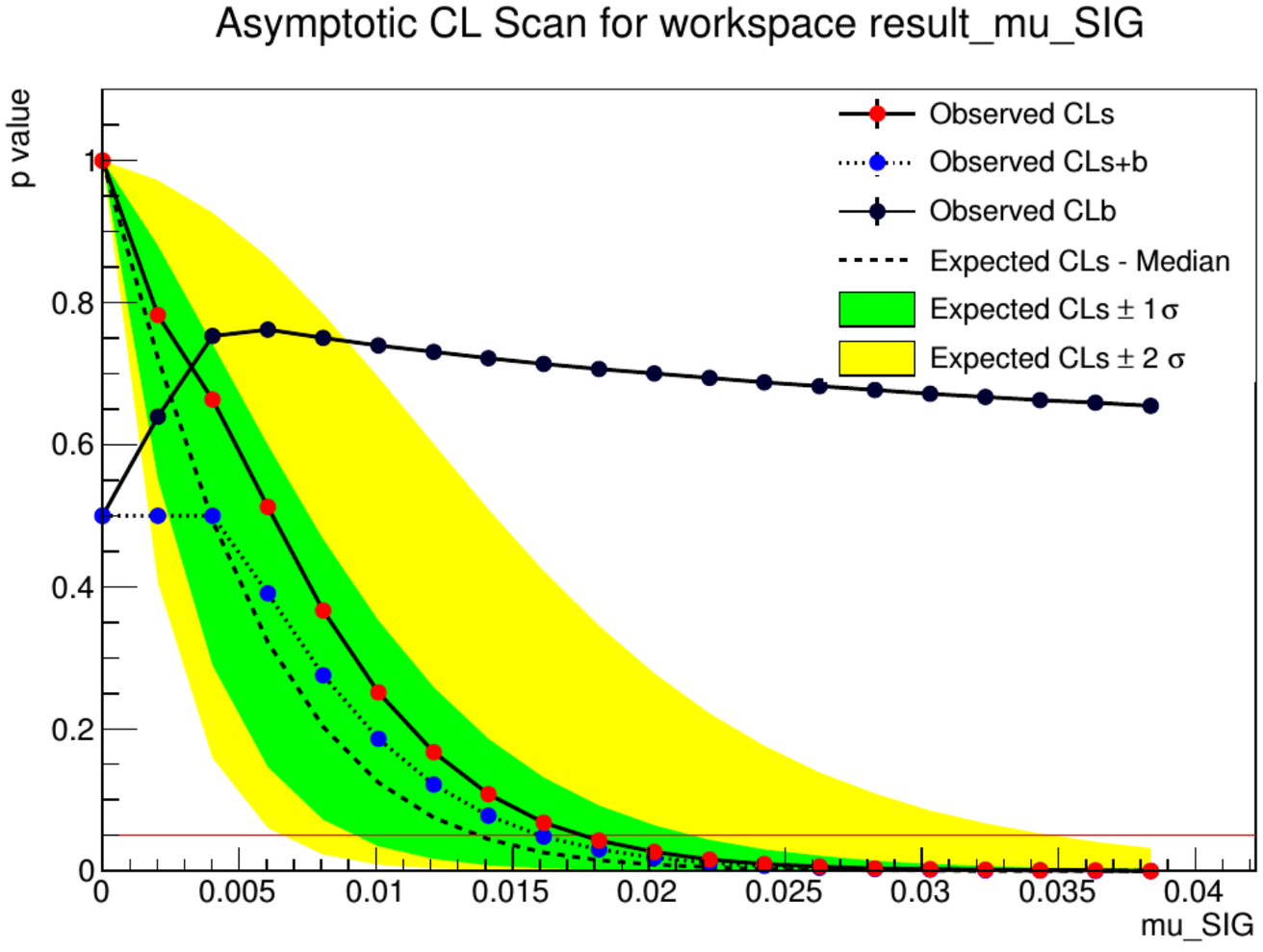
Part 4 Signal strength upper limit

- Once you have unblinded your SR, one can set upper limits on specific signal models using the exclusion fit (aka model-dependent fit setup)
- As simple in HistFitter as calling:

```
HistFitter.py -l analysis/tutorial/MyUserAnalysis.py
```

  - Technicalities similar to '-p'

- Hypothesis test ***inversion***:
  - find the value of mu_SIG for which CLs below 0.05 (or other required value)
    - instead of calculating the p-value for the specific signal
  - run the hypothesis test for increasing values of signal strength mu_SIG
    - scan range determined automatically
    - upper limit on cross section = nominal cross section × upper limit on signal strength (grey numbers in contour plots, run for each signal grid point)



Part 4 Model-independent upper limit

- Calculate the upper limit on the number of BSM physics events that we exclude in our SR
  - Typically used by theorists to check their favorite BSM model, that we have not looked at
- Requires the model-independent fit setup - aka discovery fit
  - 'dummy signal' = exactly one event in signal region (none in CRs)
  - upper limit on this 'dummy signal' = upper limit on BSM number of events
- Use the **UpperLimitTable.py** script:

  UpperLimitTable.py -c SS -w results/MyUpperLimitAnalysis_SS/SPlusB_combined_NormalMeasurement_model.root -l 4.713 -n 1000

- Results in LaTeX table:

Signal channel	$\langle \epsilon\sigma \rangle^{95}_{\text{obs}}$[fb]	S^{95}_{obs}	S^{95}_{exp}	CL_B	$p(s=0)$
SS	1.73	8.2	$6.1^{+2.3}_{-1.3}$	0.80	0.21

- ⟨σvis⟩95_obs : 95% CL upper limits on the visible cross section obs
- S95_obs :95% CL upper limits on the number of signal events obs
- S95_exp : 95% CL upper limit on the number of signal events, given the expected number (and ±1σ excursions on the expectation) of background events
- CLB: the confidence level observed for the background-only hypothesis
- p(s = 0): discovery p-value - the probability, capped at 0.5, that a background-only experiment is more signal-like than the observed number of events in a signal region

Part 5 Contour plot explained

- https://twiki.cern.ch/twiki/bin/view/AtlasProtected/SUSYLimitPlotting

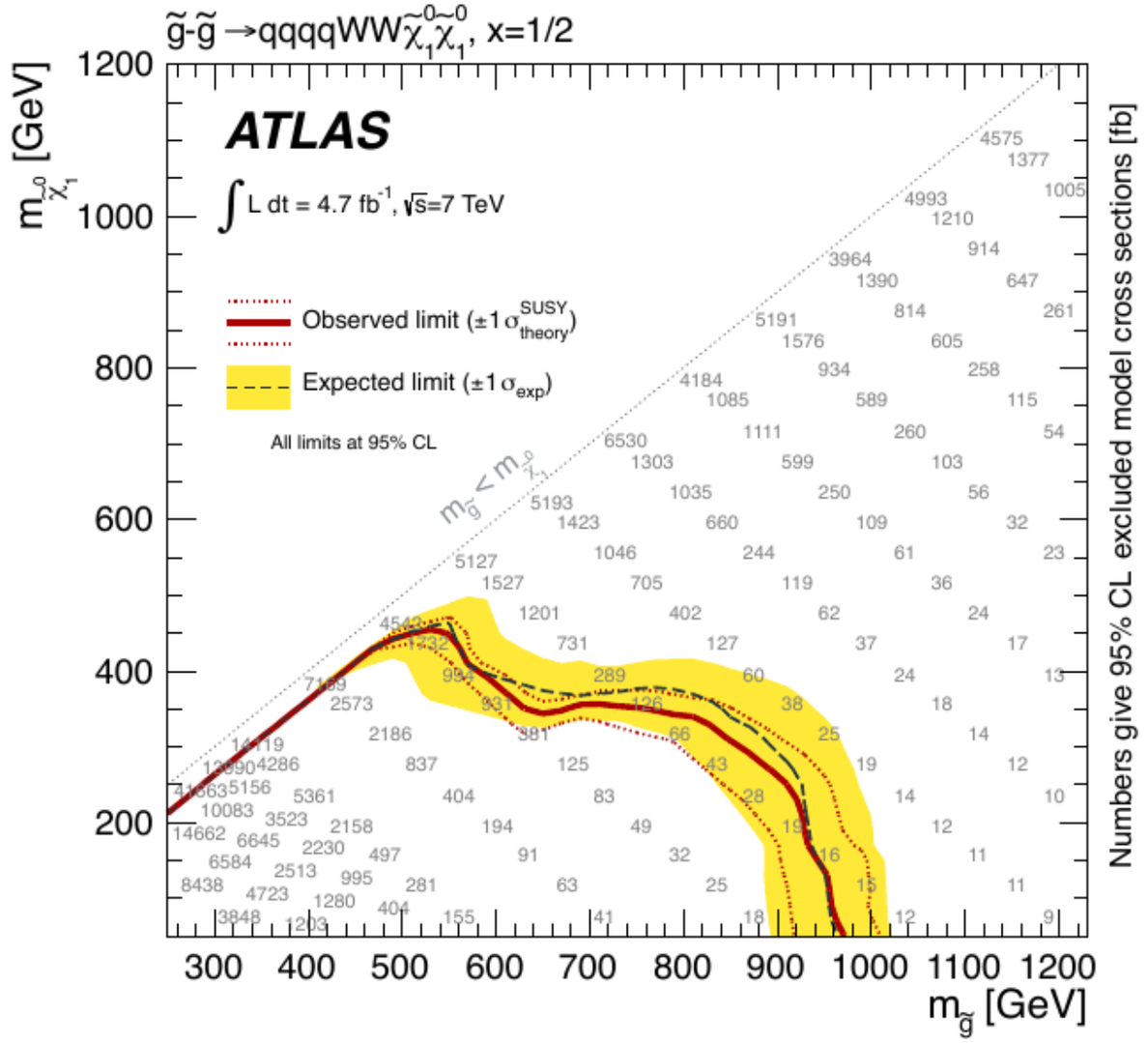
Description of limit lines

The model limits should be computed using the HistFitter package. We present the following limits:

1. **Observed limit** (thick solid dark-red line): all uncertainties are included in the fit as nuisance parameters, with the exception of the theoretical signal uncertainties (PDF, scales).
2. **Expected limit** (less thick long-dashed dark-blue line): all uncertainties are included in the fit as nuisance parameters, with the exception of the theoretical signal uncertainties (PDF, scales).

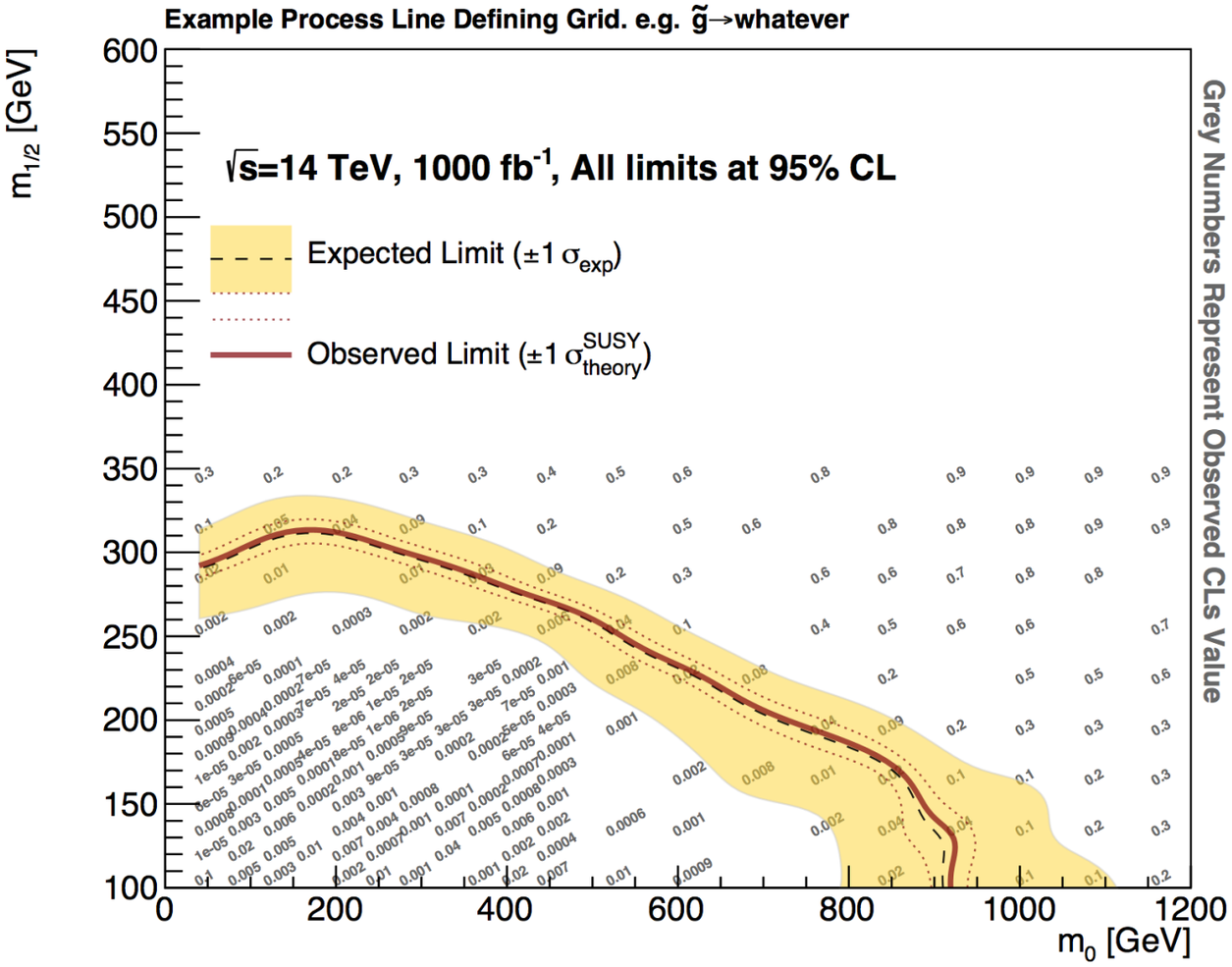
We present the following uncertainty bands:

- **±1σ lines around observed limit** (1) with style "thin dark-red dotted": re-run limit calculation (1) while increasing or decreasing the signal cross section by the theoretical signal uncertainties (PDF, scales).
- **±1σ band around expected limit** (2) with style "yellow band": the band contours are the ±1σ results of the fit (2).



Part 5 Contour plot production

- Detailed instructions in this README (linked from tutorial Twiki):
  - https://gitlab.cern.ch/HistFitter/HistFitter/tree/master/macros/Examples/contourPlotterExample
- It will guide you through these steps:
  1. Run hypothesis tests over all grid points (details for this step in tutorial Twiki)
  2. Transform this set of hypothesis tests into a JSON file
  3. If you have multiple regions, combine them in a single JSON file (Single file with "best" SR from best expected CLs value)
  4. Create the contours and store them in TGraph
  5. Make final plot



HistFitter questions

Questions answered

- How to read fit output?

- Hypothesis test/upper limit fails, what to do?

- What are the different types of systematics?
- What are 'norm' systematics?
- Which systematic should I use?
  - Flow chart for what systematic to use

- How can I use asymmetric errors?

- Why should I use shape-fits?

- How do I make pretty plots in HistFitter?

Systematics - INTERLUDE

- HistFitter extends basic HistFactory systematic types

Basic systematic methods in HistFactory	
`overallSys`	uncertainty of the global normalization, not affecting the shape
`histoSys`	correlated uncertainty of shape and normalization
`shapeSys`	uncertainty of statistical nature applied to a sum of samples, bin by bin
Additional systematic methods in HistFitter	
`overallNormSys`	overallSys constrained to conserve total event count in a list of region(s)
`normHistoSys`	histoSys constrained to conserve total event count in a list of region(s)
`normHistoSysOneSide`	one-sided normHistoSys uncertainty built from tree-based or weight-based inputs
`normHistoSysOneSideSym`	symmetrized normHistoSysOneSide
`overallHistoSys`	factorized normalization shape and uncertainty, described with `overallSys` and `histoSys` respectively
`overallNormHistoSys`	overallHistoSys in which the shape uncertainty is modeled with a normHistoSys and the global normalization uncertainty is modeled with an overallSys
`shapeStat`	shapeSys applied to an individual sample

Table 1: Sub-set of the systematic methods available in HistFitter. The methods are specified by a string argument containing a combination of basic HistFactory methods and optional HistFitter keywords: `norm`, `OneSide` and/or `Sym`. Systematic objects can be built with Tree-based, weight-based, Float or histogram input methods in all cases.

- Do **not** correlate systematics of different types: histoSys and normHistoSys should **not** be correlated
- **What systematic to use?** See guidelines in next slides

‘norm’ systematics

- **Transfer factors** are used to extrapolate from CR to SR

$$N_p(\mathrm{SR},\mathrm{est.}) = N_p(\mathrm{CR},\mathrm{obs.}) \times \left[\frac{\mathrm{MC}_p(\mathrm{SR},\mathrm{raw})}{\mathrm{MC}_p(\mathrm{CR},\mathrm{raw})}\right] = \mu_p \times \mathrm{MC}_p(\mathrm{SR},\mathrm{raw})\,,$$

  - Np(CR,obs) = number of observed events in CR
  - Np(CR/SR,raw) = number of expected MC events in CR/SR
  - The ratio in [...]-brackets is called the ***transfer factor*** **(TF)**

- An important feature of TFs is that systematic uncertainties on the background estimates can be cancelled out in the extrapolation; a virtue of using ratio of MC estimates

- Total uncertainty on the background estimate in SR is then a combination of the statistical uncertainties on the normalization in CR (smaller stat. uncert.) and residual systematic of extrapolation (shape)

- Any systematics in HistFitter with ‘norm’ in the name are uncertainties on the transfer factors (residual systematic of extrapolation, shape of extrapolation)
  - Systematics without ‘norm’ are uncertainties on event counts
- **Caution:** Care must be taken when applying ‘norm’ type systematics, as it should only be applied to samples that carry a normalization factor **μ** in the fit. Otherwise the uncertainty on the total event count or normalization is not taken into account for this sample, which can lead to an underestimation of the sample uncertainty in the signal region.
  - The correlation between the systematic alpha_X and **μ** gets removed

‘norm’ systematics implementation

Example: `overallNormaHistoSys`

Implementation:

Define the systematic uncertainty as usual, e.g.:

```
Systematic("JES","_NoSys","_JESup","_JESdown","tree","overallNormHistoSys")
```

and set regions in which the systematic uncertainties will be normalized with respect to the nominal expectation:

```
mySample.setNormRegions([region1,region2,...])
```

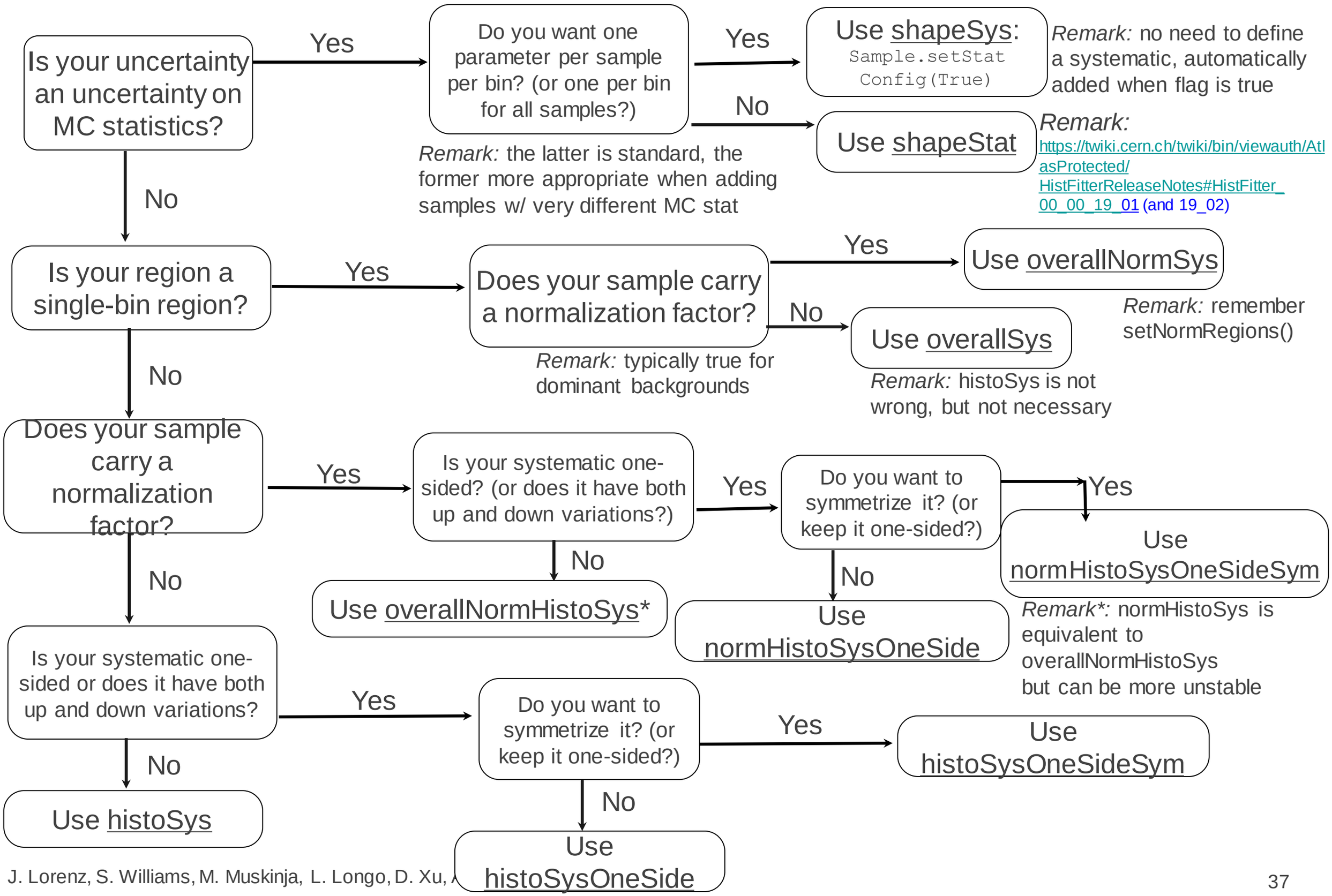
Usually the control regions are chosen for this normalization.

How does it work?

1. Temporary histograms are built containing the sum of the yields in all normalization regions (this is done for the nominal, the up and the down histogram)
2. First normalization step: Up and down temporary histograms are scaled to the yield in the nominal temporary histogram
3. The obtained scaling factor is applied to the original up and down histograms
4. If the systematics type contains an ’overall’ in the name - second normalization step: Up and down histograms are scaled to the yields in the nominal histogram. The resulting histograms are used with an `histoSys` type, the scaling factor with a `overallSys` type.

- If you do not set normalization regions (setNormRegions), the systematic will be used without being renormalized

Systematics ‘guidelines’



Understanding the fit result

- **mu_** = signal strength per sample (normalization factor), unconstrained in the fit
- **alpha_** = constrained parameter on systematic uncertainty (input alpha_ = 0 ± 1)
  - value of alpha_ represents preferred mean value of Gaussian (input value = 0)
  - error of alpha_ represents preferred gamma value of Gaussian (input value = 1) in units of input sigma
- *example*: after fit alpha_ = 0.1 ± 0.7 means
  preferred central value 0.1
  preferred uncertainty from data 0.7 x input uncertainty (30% profiled, not taking into account the correlations with other parameters)
- **gamma_stat_** = constrained parameter (Poisson), bin-by-bin uncertainty from MC statistics (mainly for propagating errors, as no information in bin to constrain)
  - value of gamma_stat_ represents width of Poisson (conversely to alpha_)
  - error of gamma_stat_ represents error on width (conversely to alpha_)
- *example*: after fit gamma_ = 0.99 ± 0.05
  preferred sigma is 0.99 x input uncertainty
- Recommendations from Stat.Forum on profiling: https://twiki.cern.ch/twiki/bin/viewauth/AtlasProtected/ProfilingChecksDraft

RooFitResult: minimized FCN value: -195178, estimated distance to minimum: 0.0201107
covariance matrix quality: Full, accurate covariance matrix Floating Parameter FinalValue +/- Error

alpha_BT	1.6742e-01 +/- 4.50e-01
alpha_JR	-4.0678e-01 +/- 5.00e-01
alpha_JR3T	-4.0670e-02 +/- 8.79e-01
alpha_JR4T	-6.8573e-02 +/- 8.91e-01
alpha_KtScaleTop	4.1254e-01 +/- 5.48e-01
alpha_KtScaleWZ	1.5158e-01 +/- 6.50e-01
alpha_LE	6.5777e-04 +/- 9.91e-01
alpha_LES	8.0288e-03 +/- 9.34e-01
alpha_LRI	9.1592e-03 +/- 9.90e-01
alpha_LRI3T	2.1968e-02 +/- 9.93e-01
alpha_LRI4T	-1.7169e-02 +/- 9.93e-01
alpha_LRM	-1.9373e-03 +/- 9.91e-01
alpha_LRM3T	6.7347e-03 +/- 1.03e+00
alpha_LRM4T	-2.0694e-03 +/- 9.99e-01
alpha_MC	2.5970e-03 +/- 9.89e-01
alpha_MC3T	-7.5278e-02 +/- 1.05e+00
alpha_MC4T	-4.0237e-02 +/- 1.01e+00
alpha_MP	1.1924e-01 +/- 6.49e-01
alpha_MP3T	-9.7037e-02 +/- 9.91e-01
alpha_MP4T	-1.5838e-01 +/- 8.81e-01
alpha_PU	-6.5987e-01 +/- 9.15e-01
alpha_PtMinTop3T	-1.3355e-02 +/- 1.03e+00
alpha_PtMinTop4T	-2.2688e-02 +/- 1.05e+00
alpha_PtMinTopC	-1.2472e-01 +/- 8.77e-01
alpha_PtMinWZ3T	-2.9269e-02 +/- 1.06e+00
alpha_PtMinWZ4T	-4.6418e-03 +/- 1.01e+00
alpha_PtMinWZC	6.9847e-02 +/- 7.28e-01
alpha_QCDNorm_SR3jT_cuts	-5.2945e-02 +/- 9.64e-01
alpha_QCDNorm_SR4jT_cuts	-2.2599e-02 +/- 9.69e-01
alpha_QCDNorm_TR_nJet	1.2121e-01 +/- 9.18e-01
alpha_QCDNorm_WR_nJet	-1.7881e-01 +/- 8.08e-01
alpha_TE	3.6969e-04 +/- 9.89e-01
gamma_stat_SR3jT_cuts_bin_0	9.6901e-01 +/- 2.22e-01
gamma_stat_SR4jT_cuts_bin_0	9.8631e-01 +/- 1.58e-01
gamma_stat_TR_nJet_bin_6	9.8506e-01 +/- 1.02e-01
gamma_stat_WR_nJet_bin_6	1.0177e+00 +/- 1.09e-01
mu_SR3jT	9.2656e-04 +/- 3.18e+00
mu_SR4jT	4.7156e-05 +/- 5.81e+00
mu_Top	9.9618e-01 +/- 1.06e-01
mu_WZ	8.8805e-01 +/- 1.07e-01

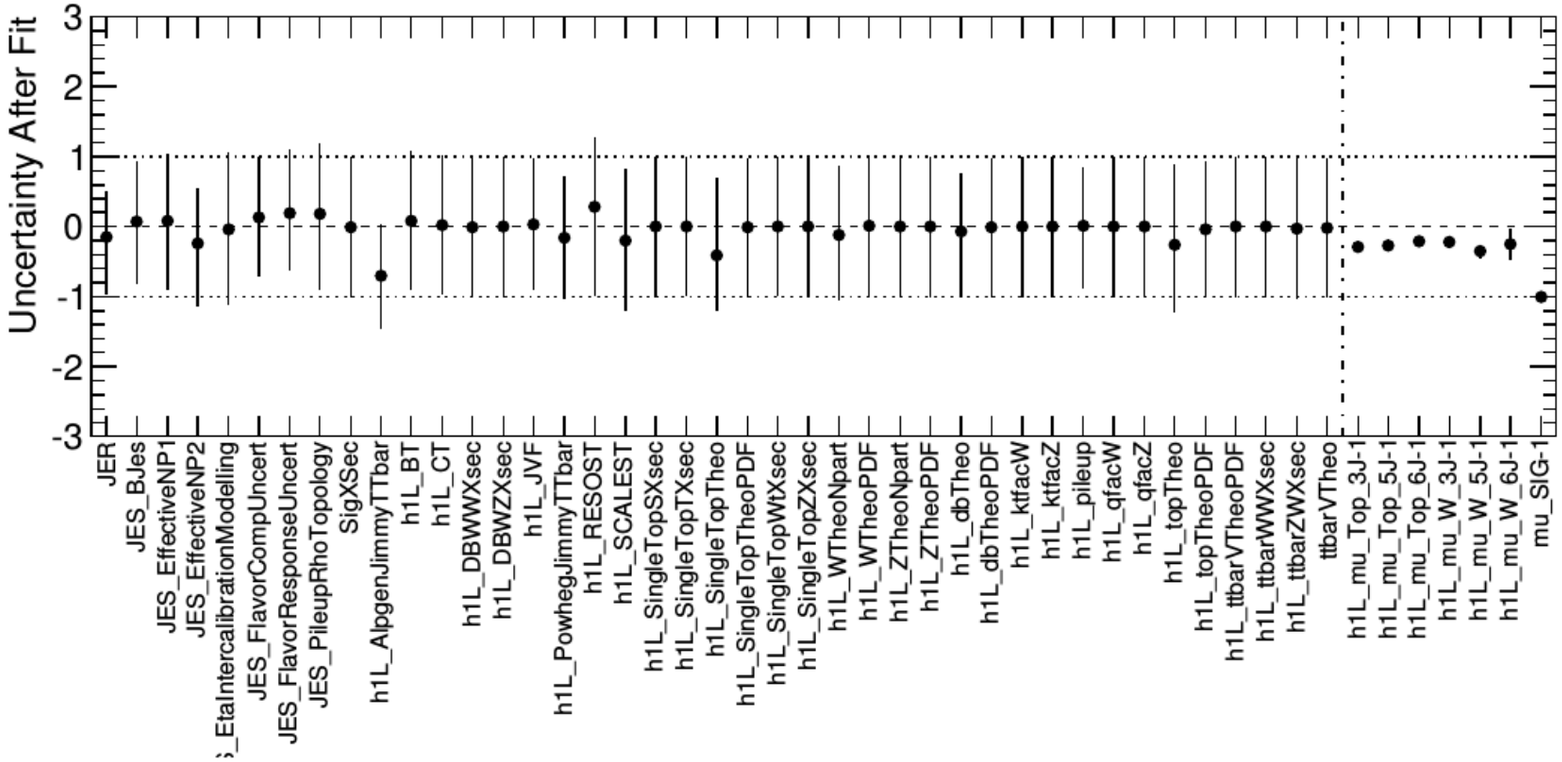
Visualizing fit results

- Script to visualize the fit results `pull_maker.py`
- Input is fit log (HistFitter log):

  `pull_maker.py -i myBkgFit.log -o myBkgFitResult`
- Output are .eps/.pdf plots as shown below

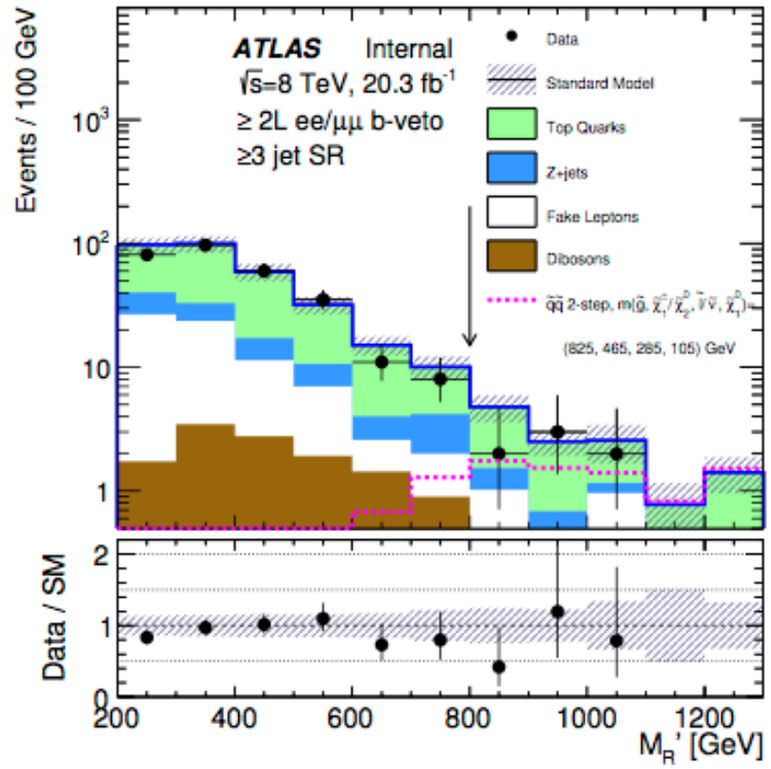
Some analyses use a simple macro to interpret the text output of -f, and converting the fit results into a plot:

Some current example from the 1-lepton strong production analysis:



Cosmetics of plots

- Several cosmetics options for your plots (before/after fit) can be set from your configuration file
- In particular:
  - Per fitConfig:
    - data color
    - total pdf color
    - error fill (line) color/style
    - a TLegend
  - Per channel:
    - min/max y-axis for the nominal plot (not for ratio plot)
    - title x/y-axis
    - logy
    - ATLAS label x/y-position & additional text eg. "for approval"
    - show lumi (off by default)



- See example: https://svnweb.cern.ch/trac/atlasphys/browser/Physics/SUSY/Analyses/HistFitterUser/trunk/MET_jets_leptons/python/OneHardLepton_ForCombination_wid_elmu_v12_SRplots.py#L1411
- Further changes are possible to be made in the src/Utils.cxx file, inside the PlotPdfWithComponents() function: https://svnweb.cern.ch/trac/atlasphys/browser/Physics/SUSY/Analyses/HistFitter/tags/HistFitter-00-00-42/src/Utils.cxx#L755
  - Do not forget to recompile when you change things in src
- **Note:** When changing cosmetics in config file or in Utils.cxx you do ***NOT*** need to re-run '-t' or '-w'
  - Unless you changed the binning or added/removed systematics

Asymmetric errors - Minos

- Run the fit as usual, but adding -m “ALL” (or -m “all” or a comma-separated list):

```
HistFitter.py -t -w -f -m all -F bkg --fitname Validation <your config file>
```

Further fitting options: Using Minos

Last year we encountered various problems with instable fits and with an artificial large profiling. A detailed summary of all problems was given by Max: `https://indico.cern.ch/event/245778/contribution/3/material/slides/0.pdf`

Main conclusions:

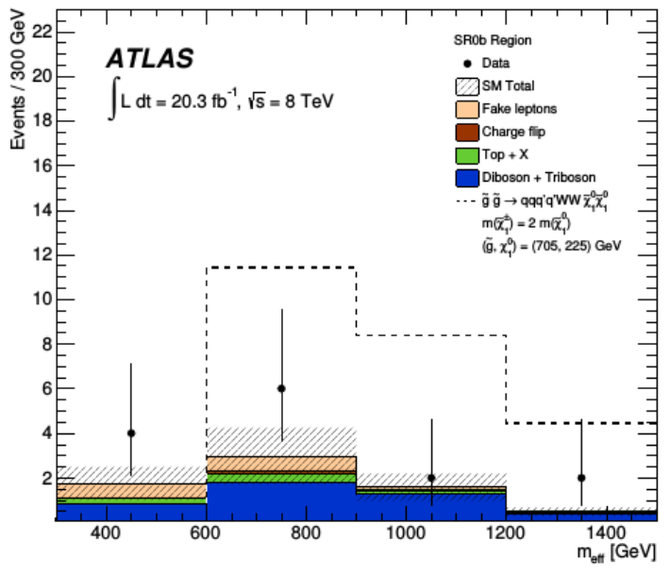
- If observing profiling check the fit by using Minos, the profiling may be artificial and point to an incorrect error given back by the Hesse calculation
  - Activate Minos by using -m PARAM, where PARAM is a comma separated list of all parameters for which the Minos calculation should be performed. Usually taking ’ALL’
- We are using Minuit 2 now, instead of Minuit. This seems to be more stable, but gives the same result.
- In addition the interpolation method between up and down systematic variations was changed to “polynomial interpolation + linear extrapolation”, which avoids kinks in the profile log-likelihood curve. More details in Max’ slides.

Some (anti-)profiling may still occur. If so: recommendation to check the profile log-likelihood curves.

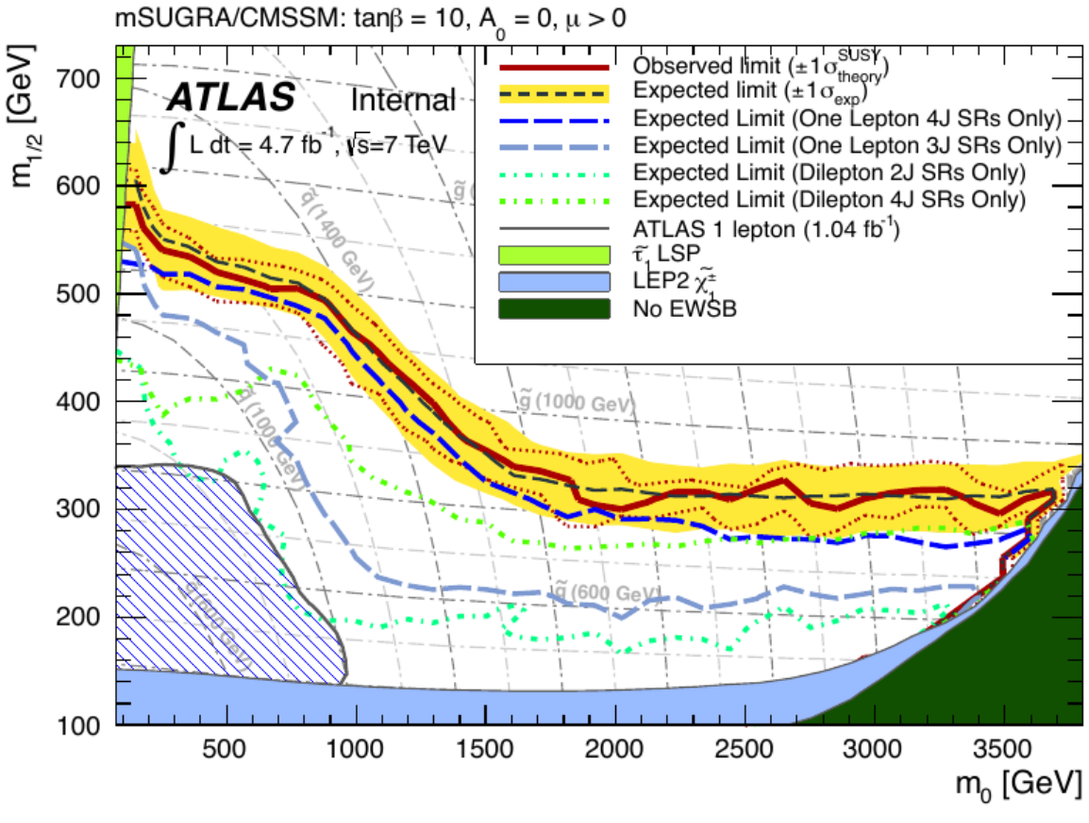
Power of shape fits - combining SRs

- Many analyses now doing shape fits or combining exclusive SRs to boost performance or be more ‘general’

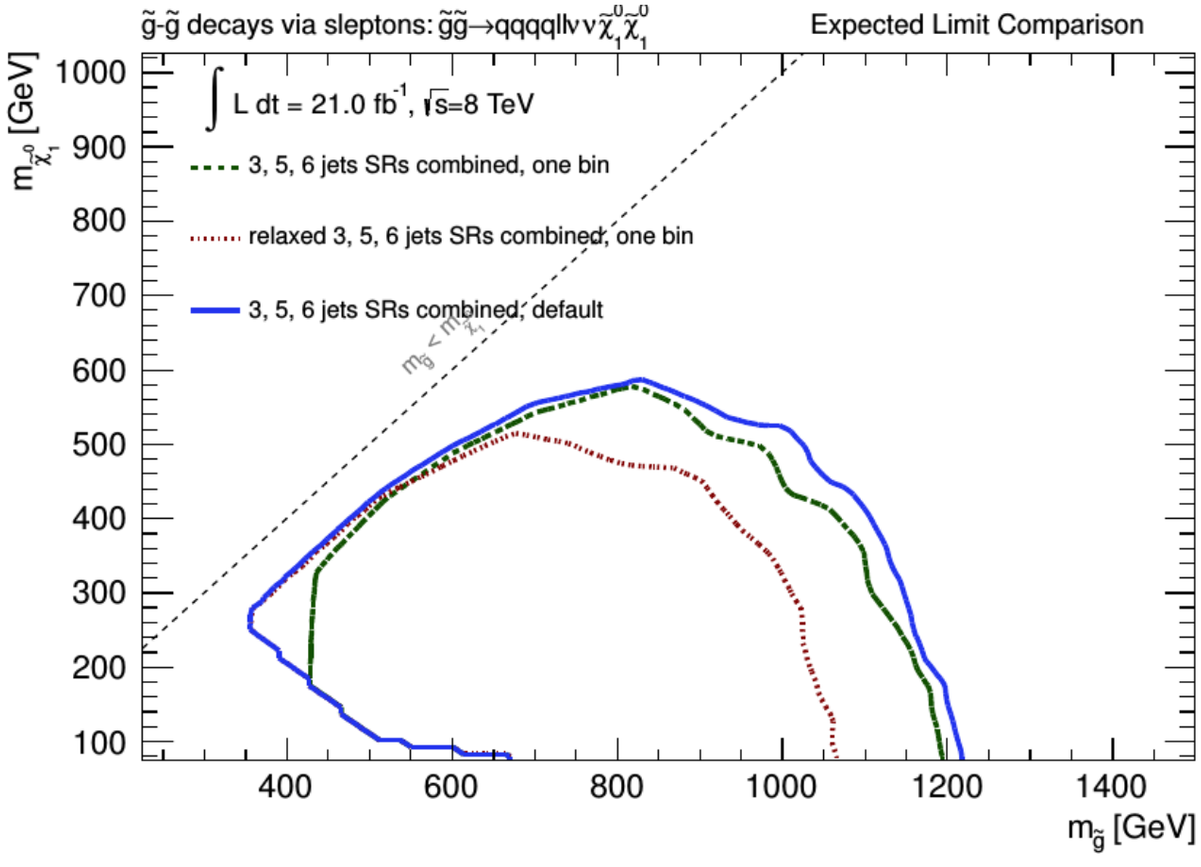
- Examples from SUSY 1-lepton searches
- Left-bottom: power of combining exclusive SRs (mSUGRA)
  - each SR optimized for specific signature on different models (mSUGRA/GMSB/Simplified Models)
  - much more powerful exclusion reach in mSUGRA when used simultaneously
  - useful for many other models not used in optimization
- Right-bottom: power of shape fits (Simplified 2-step Model)
  - using shape fits, multi-bin SRs (top right), while extending the exclusion reach (keeping the reach in worst case)



https://cds.cern.ch/record/1488897? Carsten Meyer



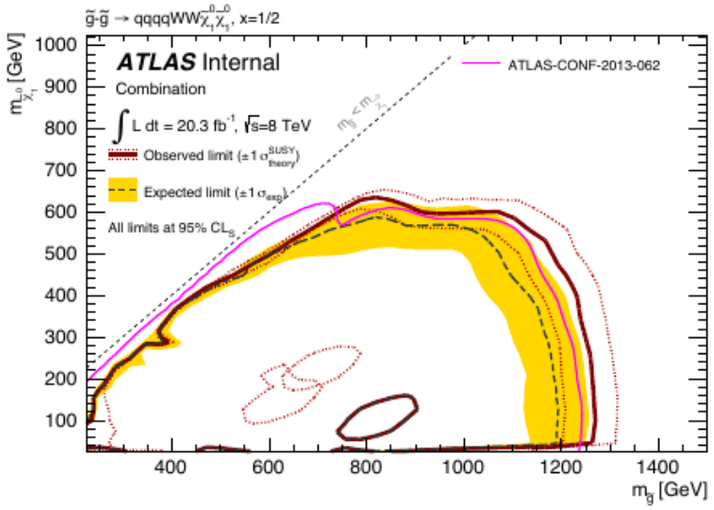
https://cds.cern.ch/record/1509517? Jeanette Lorenz



Hypothesis test failure modes

Some failures may occur in the calculation of hypothesis tests, e.g. see the output from the previous example.

The statistics forum offers OTP credit for "Improved error flagging / handling by the asymptotic calculator."



Possible failures and how to analyze them:

- The Hypothesis test is failing to due to a too large signal contribution
  - How to recognize: Only happens for points that should be clearly excluded. Output of '-p' is not giving sensible results back. The results are automatically removed during the creation of the list files.
  - What to do: Only a problem if the affected point is close to the contour. In such a case run an upper limit scan (see next slide), and check which signal strength is excluded. Possibly the point can be removed by hand.
- The output of '-p' is giving 'nan' values as result.
  - Usually multiple fits did not converge properly.
- The CLs values are exactly 1.
  - These points are not automatically removed during the list creation. Check that the hypothesis test was failing for them and remove them by hand if fit setup cannot be fixed.
  - Most likely one of the fits did not converge during the hypothesis tests.

In summary: the cause for failures needs to be debugged analysis specific with analysis specific solutions

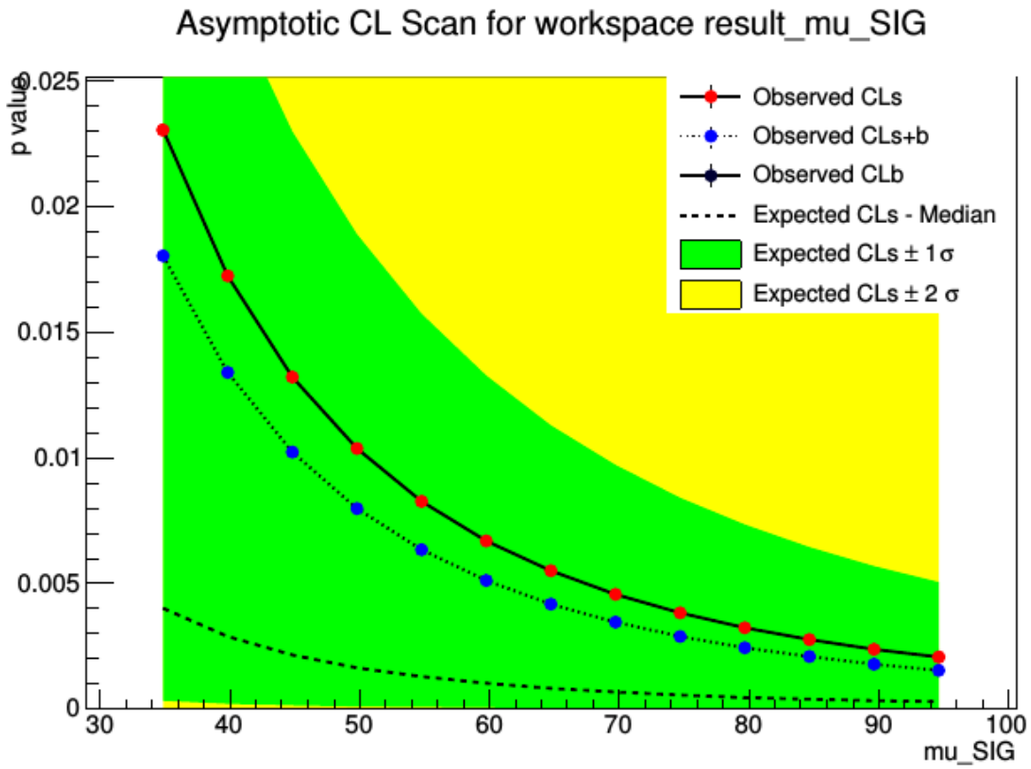
- Typically one needs to run the exclusion fit by hand with '-F excl -f' and try to see what parameters fail the fit
- Check the input histograms for these parameters
- Try running the fit without the problematic parameter/systematic to be sure it is the culprit

Upper limit failures

Some of the upper limits are not working properly, as the scan range is not sufficiently large.

Some of the upper limits (observed, expected, up, down etc.) have the same numerical values, e.g.

```
<INFO> HypoTestTool: The computed upper limit is: 55.5461 +- 0
<INFO> HypoTestTool:  expected limit (median) 55.5461
<INFO> HypoTestTool:  expected limit (-1 sig) 55.5461
<INFO> HypoTestTool:  expected limit (+1 sig) 55.5461
<INFO> HypoTestTool:  expected limit (-2 sig) 55.5461
<INFO> HypoTestTool:  expected limit (+2 sig) 55.5461
```



This problem is being fixed in the trunk by adding a dynamical extension of the scan range. Signal points still failing after this fix will be automatically removed.

Backup

Links- statistical methods

- Statistics lectures (CERN school, 2014, W. Verkerke):
  - Part-1: https://indico.cern.ch/event/287744/contribution/7/material/slides/0.pdf
  - Part-2: https://indico.cern.ch/event/287744/contribution/11/material/slides/1.pdf
  - Part-3: https://indico.cern.ch/event/287744/contribution/14/material/slides/0.pdf

- Plotting the Differences Between Data and Expectation, G. Choudalakis, D. Casadei http://arxiv.org/abs/1111.2062

- CLs: https://twiki.cern.ch/twiki/pub/AtlasProtected/StatisticsTools/CLsInfo.pdf

[28] A. Read, Presentation of search results: the CL s technique, Journal of Physics G: Nuclear and Particle Physics 28 (10) (2002) 2693.

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[30] S. Wilks, The large-sample distribution of the likelihood ratio for testing composite hypotheses, Ann. Math. Statist. 9 (1938) 60–62.

Links- statistical tools

- RooFit overview (2004): http://www.nikhef.nl/~verkerke/talks/chep03/chep2003_v4.pdf
- ATLAS Statistics Forum page on Stat. Tools: https://twiki.cern.ch/twiki/bin/viewauth/AtlasProtected/StatisticsTools
- RooFit/RooStats at ACAT 2014: https://indico.cern.ch/event/258092/session/0/contribution/140/material/slides/1.pdf
- Higgs Combination procedure/explanation of CLs observed/expected and error bands: http://cds.cern.ch/record/1375842
- HistFactory documentation: https://cdsweb.cern.ch/record/1456844/ https://twiki.cern.ch/twiki/bin/view/RooStats/HistFactory

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[24] L. Moneta, K. Belasco, K. S. Cranmer, S. Kreiss, A. Lazzaro, et al., The RooStats Project, PoS ACAT2010 (2010) 057. arXiv:1009.1003.

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Test statistic/ calculator types

- Setting calculator and test statistic type can be set in configManager:

```
## setting the parameters of the hypothesis test
#configMgr.nTOYs=5000
configMgr.calculatorType=2 # 2=asymptotic calculator, 0=frequentist calculator
configMgr.testStatType=3   # 3=one-sided profile likelihood test statistic (LHC
default)
configMgr.nPoints=20       # number of values scanned of signal-strength for upper-
limit determination of signal strength.
```

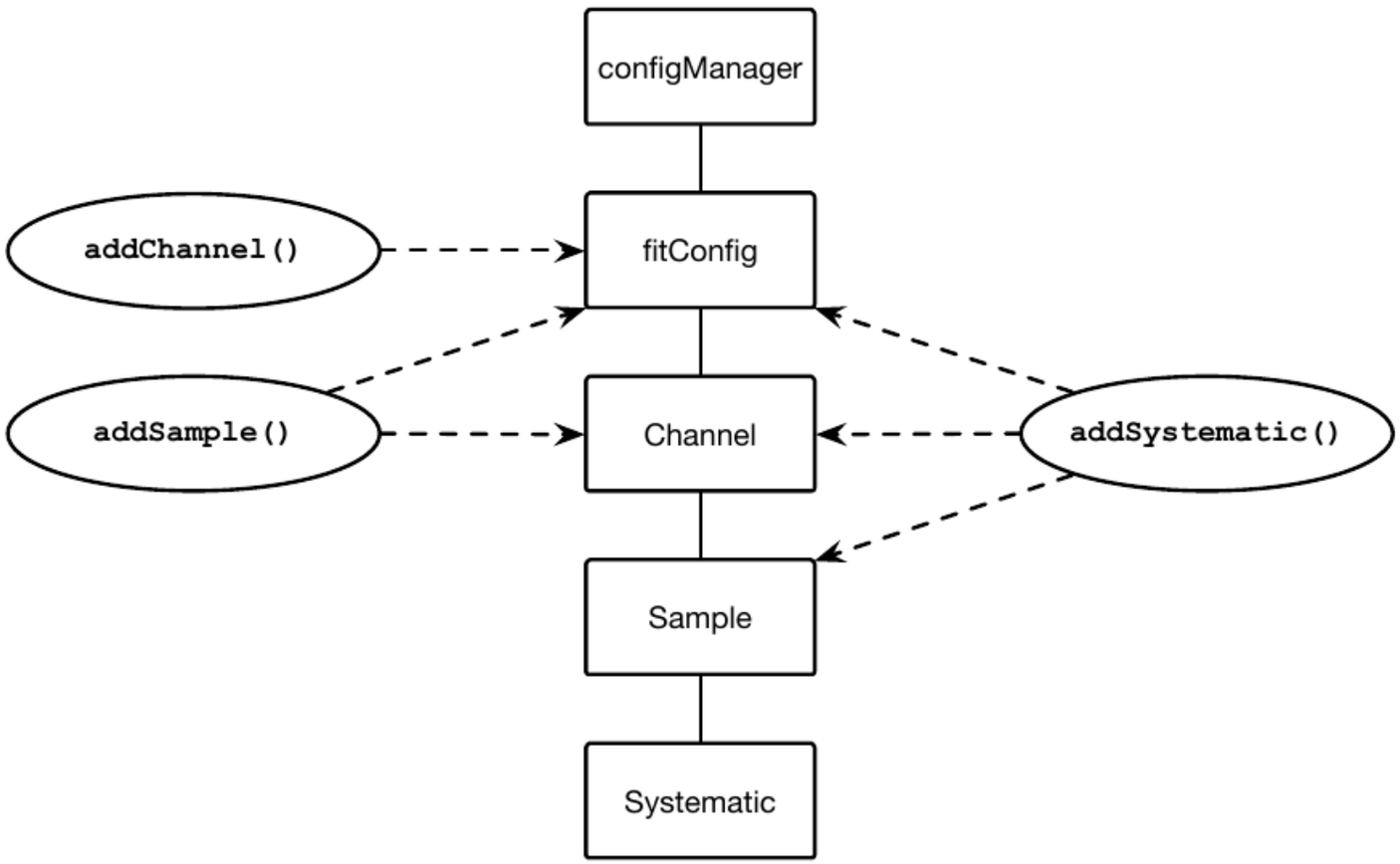
Available methods:

- calculatortype = 0 Freq calculator (= limit using toy experiments, using a fully Frequentist approach)
- type = 1 Hybrid calculator (= limit using toy experiments, using a Bayesian-Frequentist hybrid approach)
- type = 2 Asymptotic calculator (= limit using asymptotic formula)
- type = 3 Asymptotic calculator using nominal Asimov data sets (not using fitted parameter values but nominal ones)

The calculators typically used in ATLAS are 0, or 2.
When choosing the Frequentist or Hybrid calculator, one needs to specify the number of toy experiments.

- testStatType = 0 LEP
- = 1 Tevatron
- = 2 Profile Likelihood
- = 3 Profile Likelihood one sided (i.e. = 0 if mu $<$ mu_hat)

Trickle-down mechanism



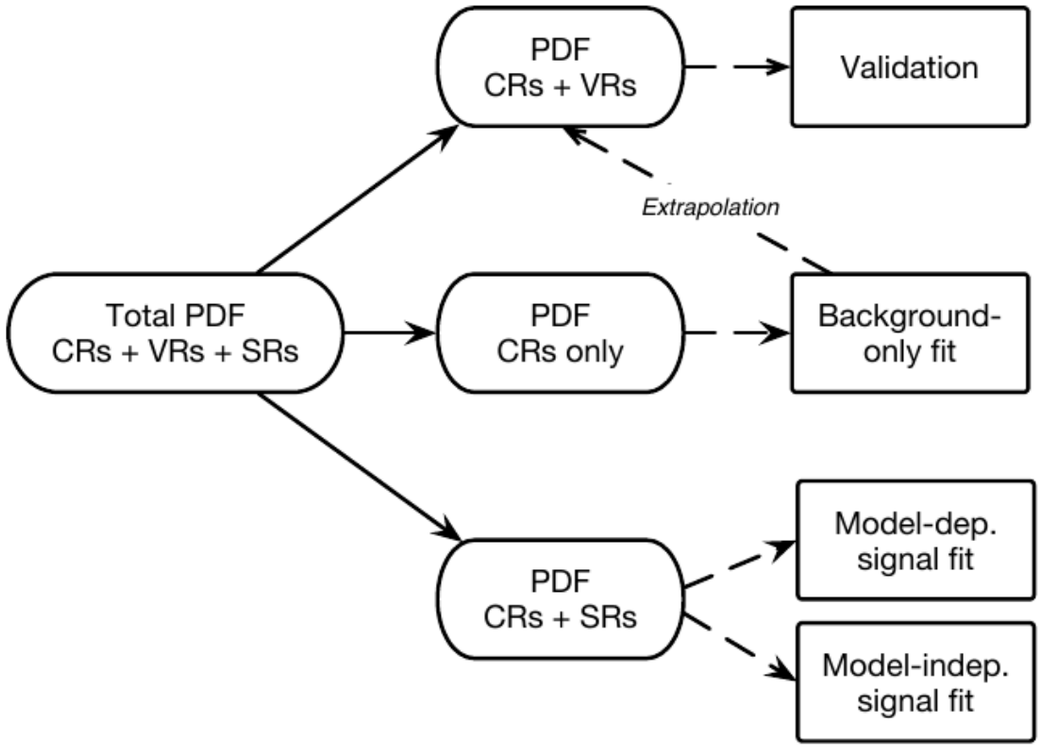
`Channels` are added to a `fitConfig`.

Samples can be added to either a `fitConfig` or a `channel`. If adding to `fitConfig` also added to all depending `channels`.

Similar for **systematics**. Can be added to `fitConfig` and then propagated to all `channels` and `samples`. Or added to a `channel` and then propagated to all depending `samples`. Or just added to a specific `sample`.

⇒ A complicated PDF can be described by few lines of code.

Extrapolation/error propagation



Extrapolation into validation and signal regions:

- Deconstruction of full likelihood containing CRs and VRs/SRs into smaller likelihood only containing CRs for use in the background-only fit.
- Incorporation of fitted parameters after background-only fit into full likelihood.
- Evaluation of the extrapolated uncertainty in validation/signal regions through standard error propagation.

Extrapolation into signal and validation regions particularly rigorous in HistFitter due to use of `RooExpandedFitResult` class:

- Standard `RooFitResult` contains only the parameters used in the background-only fit.
- Using instead the `RooExpandedFitResult` class allows to extrapolate **all** parameters, such that a correct evaluation of the uncertainties through error propagation is possible.

Region/fit type definition

More advanced fit 1: explicit use of control, validation and signal regions

Every channel in a config file should be specified as either control, validation or signal region:

- `yourFitConfig.setSignalChannels([SR1,SR2,...])`
- `yourFitConfig.setBkgConstrainChannels([CR1,CR2,...])`
- `yourFitConfig.setValidationChannels([VR1,VR2,...])`

Using this, different fit strategies can be separated:

- **Background-only fit:** Only the CRs are used to constrain the fit parameters. Any potential signal contribution is neglected everywhere. Only regions set in `setBkgConstrainChannels` are used to constrain the backgrounds. The fit result may be extrapolated to regions defined in `setValidationChannels` (signal regions also need to be included here, if an extrapolation the signal regions is wished)
- **Exclusion fit:** CRs and SRs are used in the fit. The potential signal contribution is taken into account as predicted by the tested model in all the regions. This option considers only the signal and control regions. No validation regions may be set.
- **Discovery fit:** Both CRs and SRs are used in the fit. The signal is independently considered in each SR, but is neglected in the CRs. In this way, one total background prediction in the signal regions is achieved. This background prediction is conservative since any signal contribution in the CRs is attributed to background and thus yields a possible overestimation of the background in the SRs. Dedicated SRs (and signal samples) need to be used, which are one bin counting-experiments. A 'dummy' signal model that is a single bin histogram with the bin value at 1 is used. (The discovery fit should not have any model dependence.) Validation regions may not be used in this fit configuration.

The fit type can be defined by the option -F {excl,disc,bkg}. This sets the variable myFitType to FitType.Exclusion, FitType.Discovery, FitType.Background, respectively, which can be propagated to the configuration file.

RooStats HistFactory tool

- Builds PDFs from histograms using XML configuration
  - Supports multiple regions (=channels)
  - Systematics defined in a variety of ways

$$P(n_{cb}, a_p \mid \phi_p, \alpha_p, \gamma_b) = \prod_c \prod_b \text{Pois}(n_{cb} \mid \nu_{cb}) \text{G}(L_0 \mid \lambda, \Delta_L) \prod_p \text{P}_P(a_p \mid \alpha_p)$$

$$\nu_{cb}(\phi_p, \alpha_p, \gamma_b) = \lambda_{cs} \gamma_{cb} \phi_{cs} \eta_{cs}(\vec{\alpha}) \sigma_{csb}(\vec{\alpha})$$

Lumi

ShapeSys
MC stats
ShapeFactor

NormFactor

OverallSys

HistoSys

- Central disadvantage: PDFs cannot be contructed in *flexible* way
- Solution: HistFitter acts as flexible wrapper to build and analyze PDFs.

- https://twiki.cern.ch/twiki/pub/RooStats/WebHome/HistFactoryLikelihood.pdf

Blinding & selection optimization

- Some people are starting to use HistFitter for optimization of signal selection.
- Need to be careful not to include the data under investigation.

- New option: blinding of data.

- Possibility to blind CRs and/or SR.
  - If blinded, MC expectation is chosen for data.

- Select in configuration file with:
  - configMgr.blindSR = True
  - configMgr.blindCR = True

ROOSTATS example

- **RooStats** project/tools suite delivers a series of tools that can calculate intervals and perform hypothesis tests using a variety of statistical techniques

An example of a custom RooStats driver script

Tool to calculate p-values for a given hypothesis

$$\int_{q_{\mu,obs}}^{\infty} f(q_\mu \mid \mu')dq_\mu$$

```
// create first HypoTest calculator (N.B null is s+b model)
FrequentistCalculator fc(*data, *bModel, *sbModel);

// configure  ToyMCSampler and set the test statistics
ToyMCSampler *toymcs = (ToyMCSampler*)fc.GetTestStatSampler();

ProfileLikelihoodTestStat profll(*sbModel->GetPdf());
// for CLs (bounded intervals) use one-sided profile likelihood
profll.SetOneSided(true);
toymcs->SetTestStatistic(&profll);

HypoTestInverter calc(*fc);
calc.UseCLs(true);

// configure and run the scan
calc.SetFixedScan(npoints,poimin,poimax);
HypoTestInverterResult * r = calc.GetInterval();

// get result and plot it
double upperLimit = r->UpperLimit();
double expectedLimit = r->GetExpectedUpperLimit(0);

HypoTestInverterPlot *plot = new HypoTestInverterPlot("hi","",r);
plot->Draw();
```

$f(q_\mu \mid \mu')$
Tool to construct test statistic distribution

$q_\mu(\mu')$
The test statistic to be used for the calculation of p-values

Tool to construct interval from hypo test results

‘exclusion’ vs ‘discovery’

‘exclusion’

‘discovery’

‘likelihood assuming μ signal strength’

$$\tilde{q}_\mu = -2\ln\frac{L(data\,|\,\mu,\hat{\hat{\theta}}_\mu)}{L(data\,|\,\hat{\mu},\hat{\theta})}$$

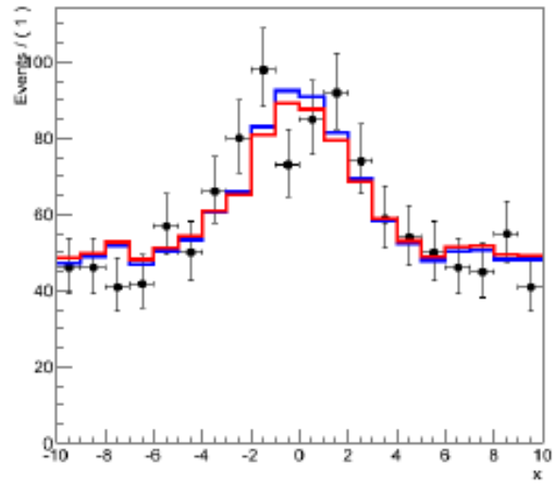
‘likelihood of best fit’

‘likelihood assuming background only’

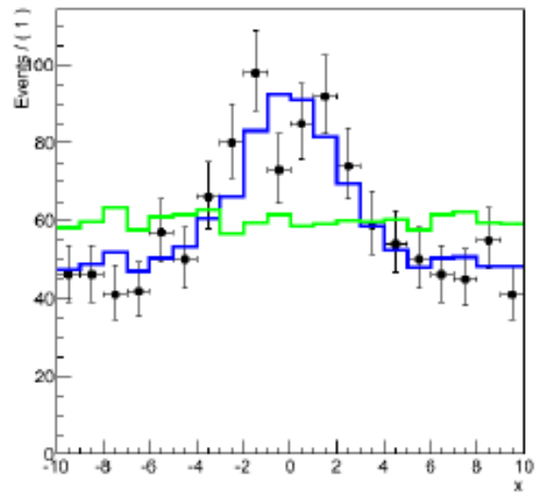
$$\tilde{q}_0 = -2\ln\frac{L(data\,|\,\mu=0,\hat{\hat{\theta}}_0)}{L(data\,|\,\hat{\mu},\hat{\theta})}$$

‘likelihood of best fit’

$\tilde{q}_1 = 0.77$

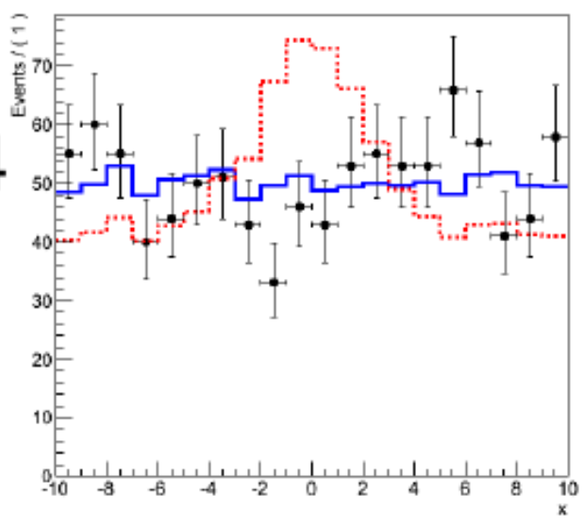


simulated data with signal+bkg

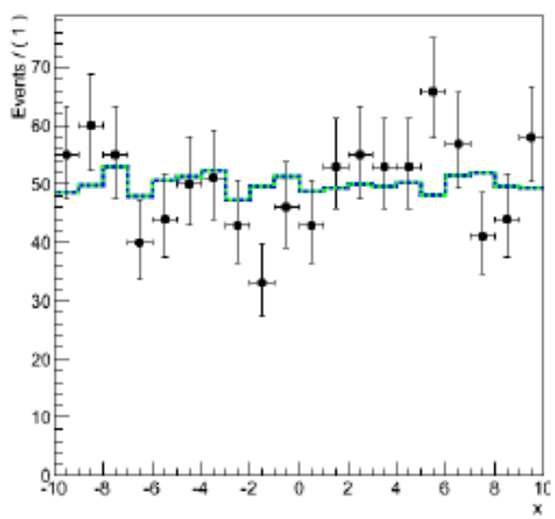


$\tilde{q}_0 = 34.7$

$\tilde{q}_1 = 52.34$



simulated data with bkg only



$\tilde{q}_0 = 0$

A real life example

- A real life example of a HistFitter configuration file used inside the SUSY strong production with 1-lepton team can be seen here: https://svnweb.cern.ch/trac/atlasphys/browser/Physics/SUSY/Analyses/HistFitterUser/trunk/MET_jets_leptons/python/OneHardLepton_ForCombination_notower.py

- It contains several orthogonal CRs/VRs and shape-fit/multi-bin SRs
- It contains all the recommended systematics
- It has a background-only fit setup and an exclusion fit setup
- It can run the exclusion fit setup over many signal model grids

- The analysis and results are described here: https://cds.cern.ch/record/1626588