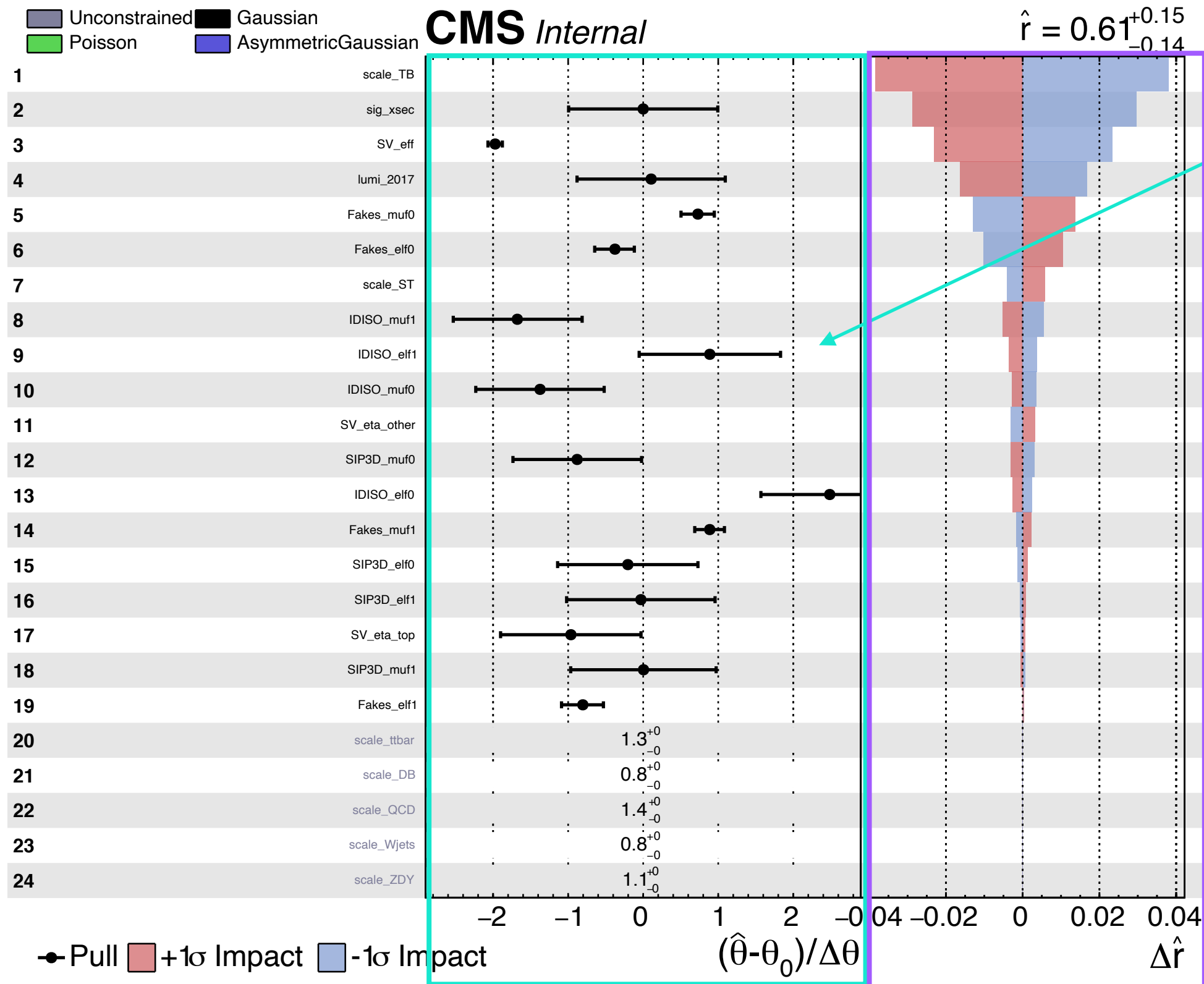


How to: Impact plots with HiggsCombine

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KU SUSY meeting
7 June 2021

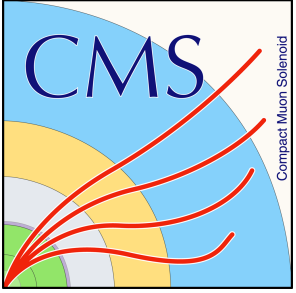
What are impacts?



Comparison of
pre + post fit
value (pull)

Effect of 1 sigma
shift on POI

KUEwkino workflow

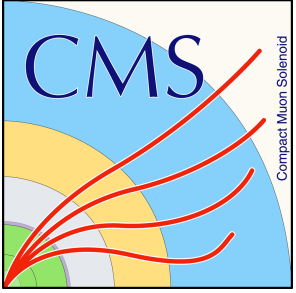


- see Zach's talk [here](#) about how to get from NANO to limits
- BuildFit(Condor) step will produce datacards in directories corresponding to signal mass splittings
- These datacards will be the input to the start of the impact plot workflow
- HiggsCombine makes the impact plots, installation instructions [here](#)

text2workspace

- Choose one mass point to convert the datacard to a RooWorkspace
 - `text2workspace.py -d [datacard.txt] -o [workspace.root] -m [mass point]`
 - Or `combineTool.py -M T2W -i [datacard.txt] -m [mass point] -o [workspace.root]`
 - Only need `-m` argument if running inside directory
 - Can be run on condor using `--job-mode condor --sub-opts='request_memory = 8 GB'`

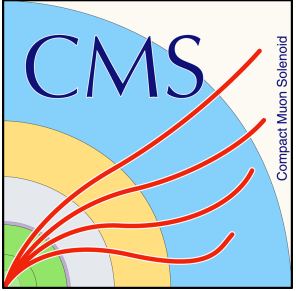
doInitialFits



- Do fits to POI first
- `combineTool.py -M Impacts -d [workspace.root] --doInitialFit --robustFit 1 -m [mass point]`
 - robustFit flag does a more robust likelihood scan (fit more likely to converge, step size controlled with `--stepSize` argument)
- Output: `higgsCombine_initialFit_Test.MultiDimFit.mH[mass].root` file with limit TTree and toys TDirectory
- Can be run on condor using `--job-mode condor --sub-opts='request_memory = 8 GB'`

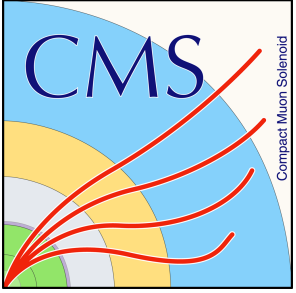
- Does likelihood scans for each nuisance parameter
- `combineTool.py -M Impacts -d [workspace.root] --doFits --robustFit 1 -m [mass point]`
 - Mass point must match mass in file name of initialFit root file
 - Output:
`higgsCombine_paramFit_Test_[NPname].MultiDimFit.mH[
mass point].root` with same structure as initialFit.root file
- Can be run on condor using `--job-mode condor --sub-opts='request_memory = 8 GB'`

Impacts + plotting



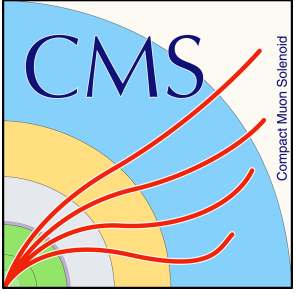
- `combineTool.py -M Impacts -d [workspace] -m [mass point] -o impacts.json`
 - Collects information from previous steps and outputs to json file
 - Mass point must match mass in file name of initialFit root file
- `plotImpacts.py -i impacts.json -o impacts`
 - Produces .pdf plot with NP pulls and impact on POI

Individual impacts



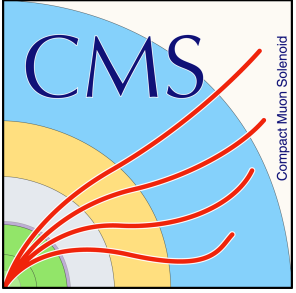
- `python diffNuisances.py fitDiagnostics.root --all`
 - Script is in `HiggsAnalysis/CombinedLimit/test`
 - To get `fitDiganostics.root` file:
 - `combineTool.py -M FitDiagnostics -d [datacard.txt or workspace.root] -m [mass splitting]`
 - Has information about output and behavior of bkg-only and s+b fits
- `diffNuisances` prints impacts and s+b and bkg-only pulls for all parameters (with `--all` flag)

Current issues



- Datacards with all shape systematics segfaulting during text2workspace
 - Separate by channel to run fits with all shape systematics
 - fakes+QCD systematics ok for all channels
 - MET Trig + BTag systematics not playing nice
 - Under investigation - run impacts for lnN systematics only
- flatParam cannot be added with CombineHarvester

Overview of steps



1. KUEwkino workflow
2. `text2workspace.py [datacard.txt] -m [mass point] -o [workspace.root]`
3. `combineTool.py -M Impacts -d [workspace.root] --doInitialFit --robustFit 1 -m [mass point]`
4. `combineTool.py -M Impacts -d [workspace.root] --doFits --robustFit 1 -m [mass point]`
5. `combineTool.py -M Impacts -d [workspace.root] -m [mass point] -o impacts.json`
6. `plotImpacts.py -i impacts.json -o impacts`