

# EFT interpretation and benchmarks



+

shape interpolation techniques

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Based on the works:

[1] Higgs Pair Production: Choosing Benchmarks With Cluster Analysis

—> A.C. Martino Dall’Osso, Tommaso Dorigo, Florian Goertz, Carlo A. Gottardo, Mia Tosi

[2] Analytical parametrization and shape classification of anomalous HH production in the EFT approach

—> A. C., Martino Dall'Osso, Pablo de Castro Manzano, Tommaso Dorigo, Florian Goertz, Maxime Gouzevich, Mia Tosi

[3] On the reinterpretation of non-resonant searches for Higgs boson pairs

—> A. C. , Florian Goertz , Ken Mimasu , Maxime Gouzevitch , and Anamika Aggarwal

# Outline

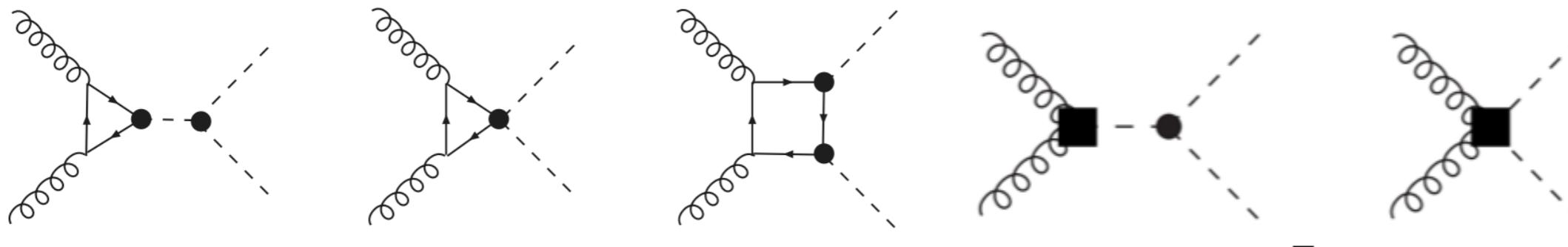
## Part I

- Defining shape benchmarks
- A method for “fast-food” reinterpretation
  - comparison between explicit results and shape benchmarks

## Part II

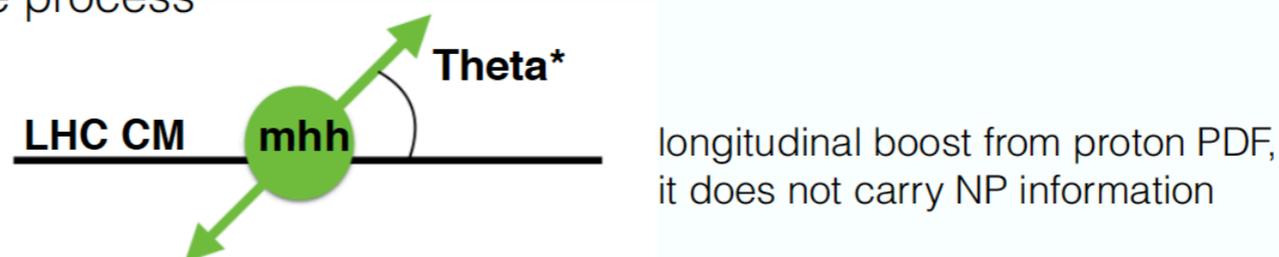
- Methods of shape interpolation
  
- Conclusions

# The process @ LO



Modifications of the higgs couplings wrt its SM values can dramatically change signal topology  
=> Interference patterns from theory parameters  
=> Modifications from trigger acceptances to definition of the best analysis methods

At LO we have a simple 2 -> 2 process, where only two kinematic variables define the BSM piece of the process



A purely statistical method to define benchmarks for non-resonant HH production at LHC, mapping the BSM H couplings to the signal kinematical properties in different points of parameter space.

The samples similarity is tested with a likelihood ratio based on Poisson counts

We test samples similarity with a likelihood ratio based on Poisson counts

If two samples under test share the same parent distribution the probability to observe  $n_{1,i}$  and  $n_{2,i}$  in the  $i$ -th bin is given by:

$$Pois(n_{i,1}) \times Pois(n_{i,2}) = Pois(n_{i,1} + n_{i,2}) \times Binomial(n_{i,1}/(n_{i,1} + n_{i,2}))$$

All information about samples similarity is contained here

Ancillary information not relevant to sample comparison

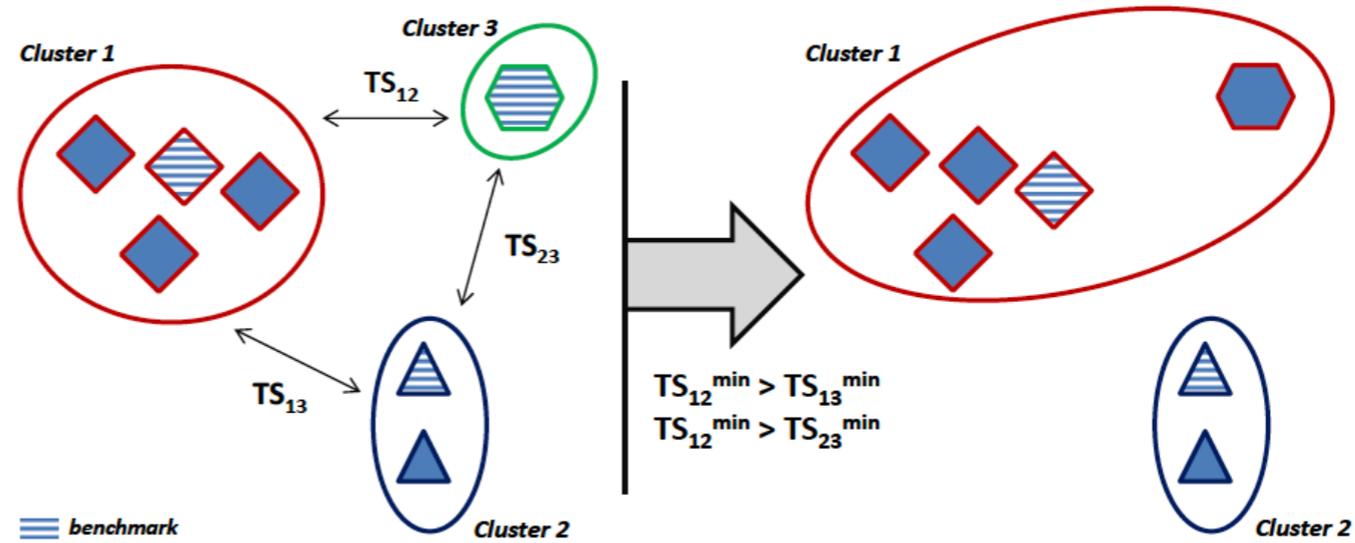
It is possible to define the log-likelihood ratio (Test Statistic):

$$TS(1,2) = 2 \log \left( \frac{L}{L_S} \right) = 2 \sum_{i=1}^{N_{bins}} \log(n_{i,1}!) + \log(n_{i,2}!) - 2 \log \left( \frac{n_{i,1} + n_{i,2}}{2}! \right)$$

the denominator in the TS is the "saturated model" ( $n_{i,1} = n_{i,2}$ )

The TS is chi2 distributed, and can be used as an ordering parameter when comparing two samples (Wilks theorem !)

Given 3 samples (i,j,k) if  $TS(i,k) > TS(j,k)$  then the samples (i,k) are more similar between than than (j,k)



Steps for clustering samples:

- 1 - each sample is identified as one-element cluster
- 2 - the cluster to cluster similarity is defined as  $TS_{min} = \min( TS(i,j) )$  where i runs on the first cluster elements and j in the second one

3 - The pair of clusters with the highest  $TS_{min}$  is clustered together

==> repeat steps 2 and 3 up to a fixed number of clusters (**Nclus**) is reached

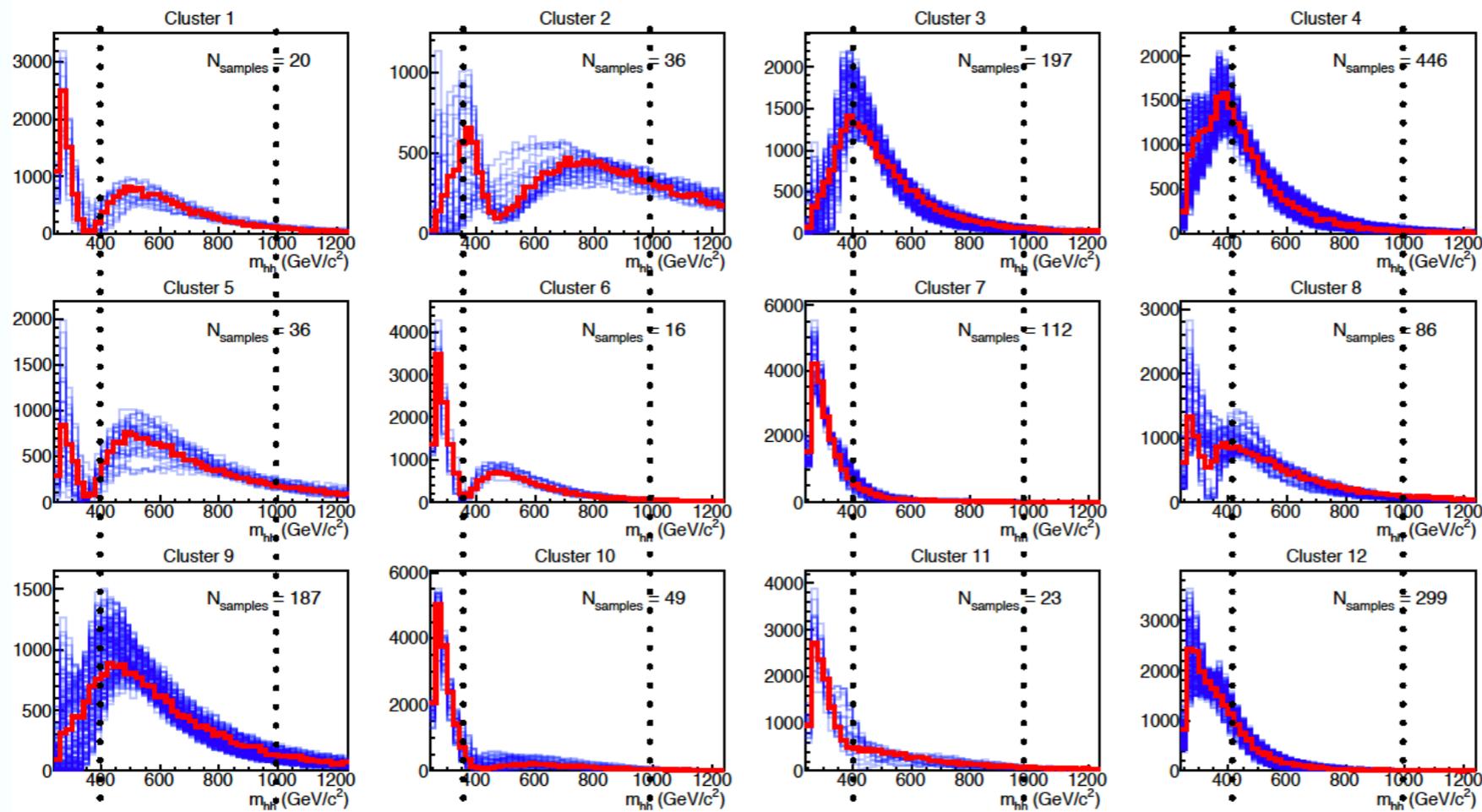
The **benchmark** is defined as the element with the highest  $TS_{min}(k) = \min( TS(k,i) )$  where i runs over the elements of the cluster k

**= the element most similar to all the other samples of the cluster**

# Resulting shape benchmarks

From a scan of 1507 parameter space points smartly chosen to spam the 5D parameter space, and using LO MC simulations we arrive in automated way to a kinematic classification to define benchmark points.

The  $M_{hh}$  distributions in the clusters:



**Red:** the benchmark  
**Blue:** the other samples in the cluster

The benchmarks are part of the LHCXSWG YR4

$M_{hh} = 400, 1000,$

$400, 1000,$

$400, 1000,$

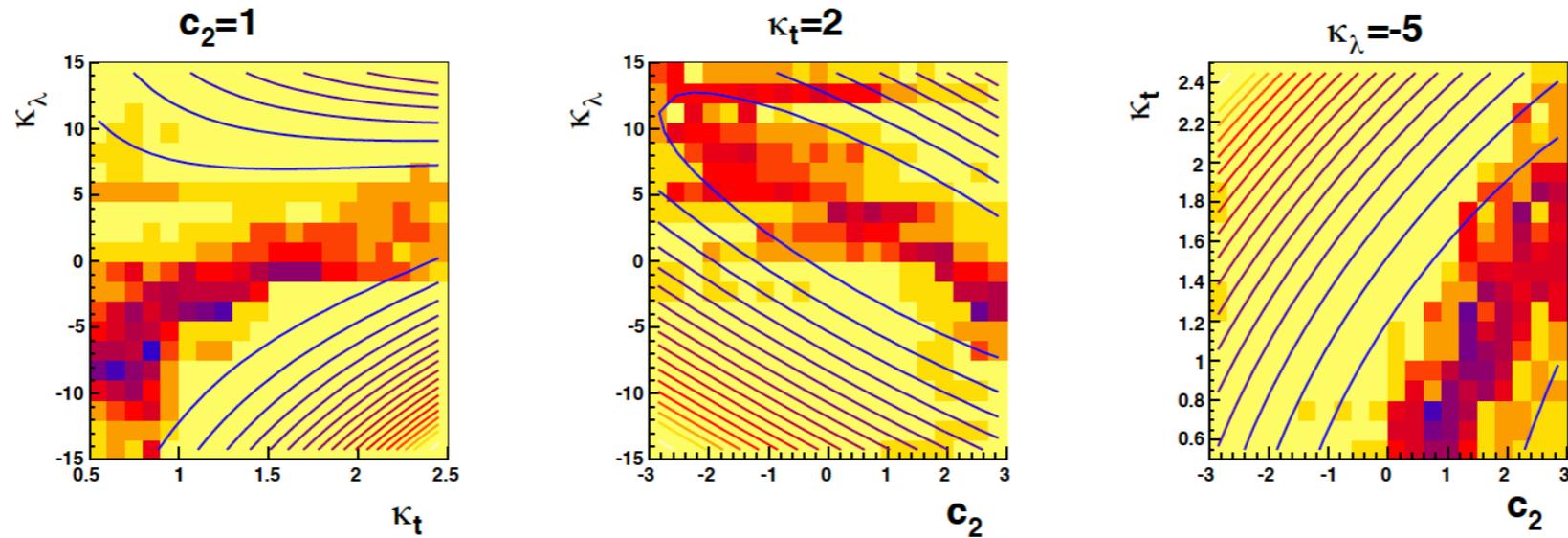
$400, 1000, \text{GeV}$

# Shape benchmarks distributions on parameter space

[1]

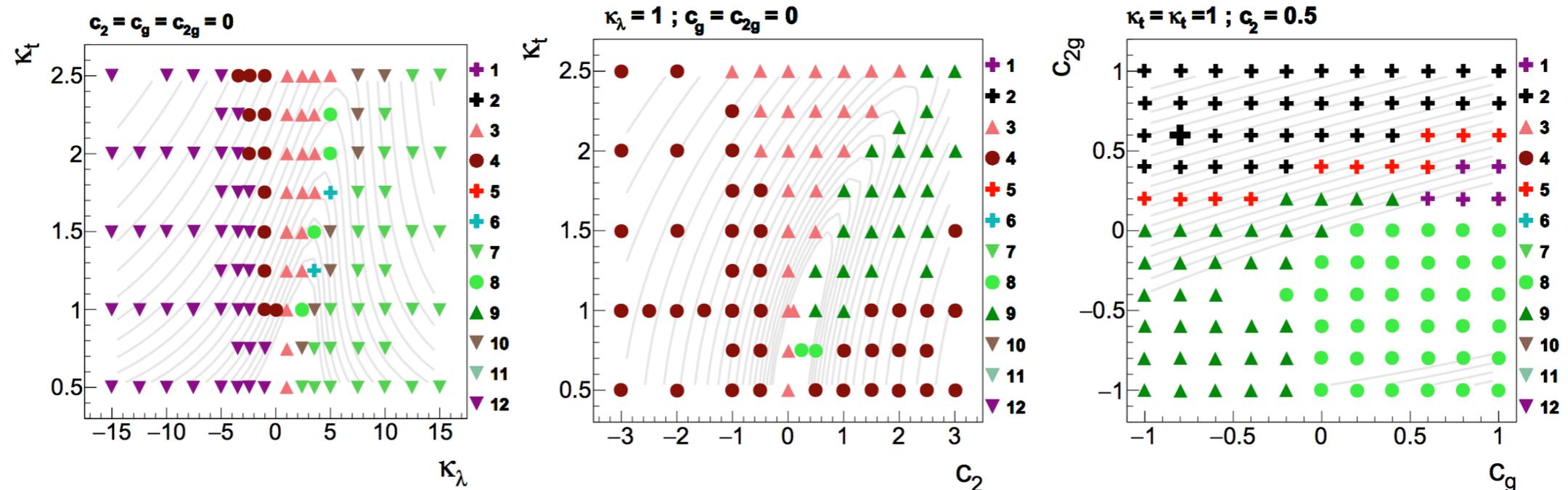
A larger variability in kinematic topologies is correlated with local minima of cross sections (where apparent cancelations among different processes holds)

When we overlap the values of the TS between two nearest neighbors samples with the isolines of cross section we directly see the correlation

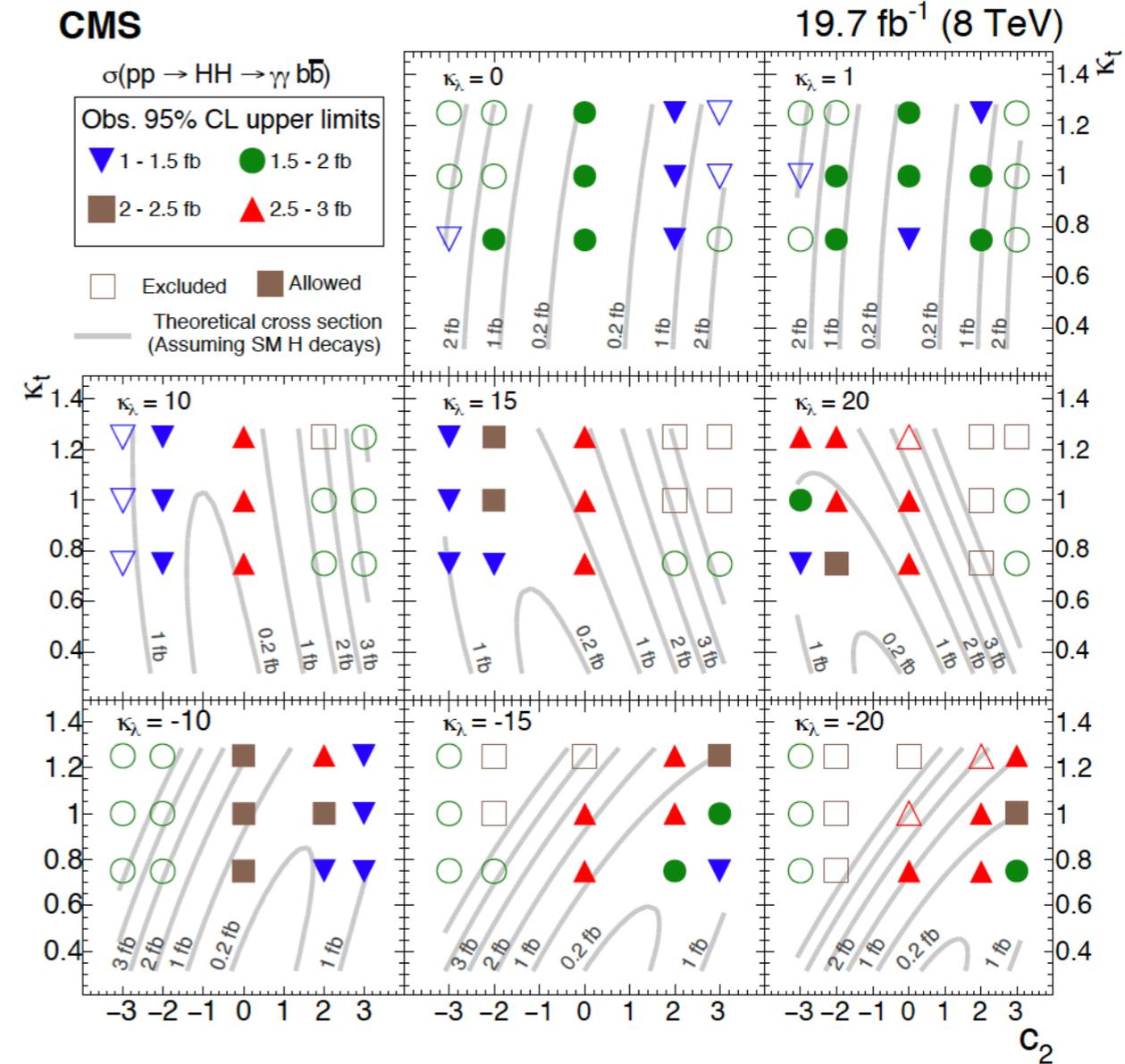
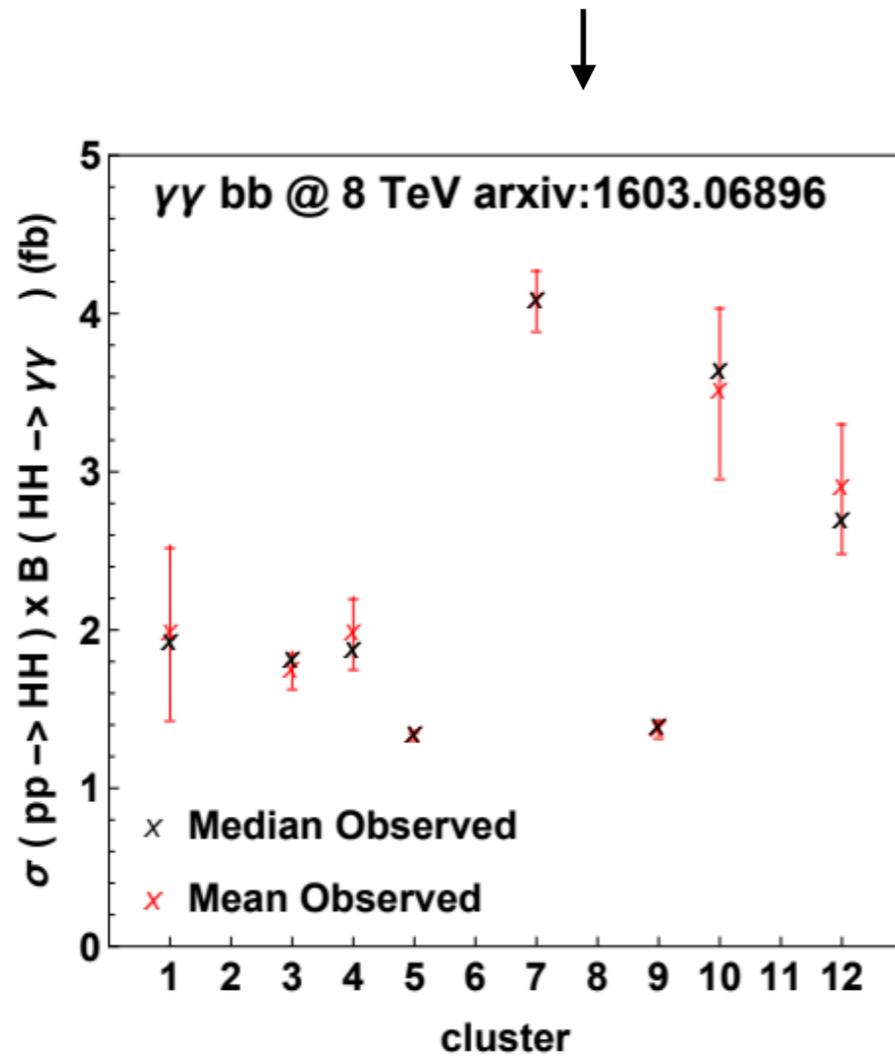


Blue/Red stand for higher values of the TS between nearest neighbors

As result, the distributions of benchmarks usually enclose simply connected regions of couplings



- In the 8 TeV CMS analysis an explicit scan on some anomalous couplings was done
- We organize these points in clusters
  - Even if there is spread on the final result, there is a clear pattern on the spread of the limits



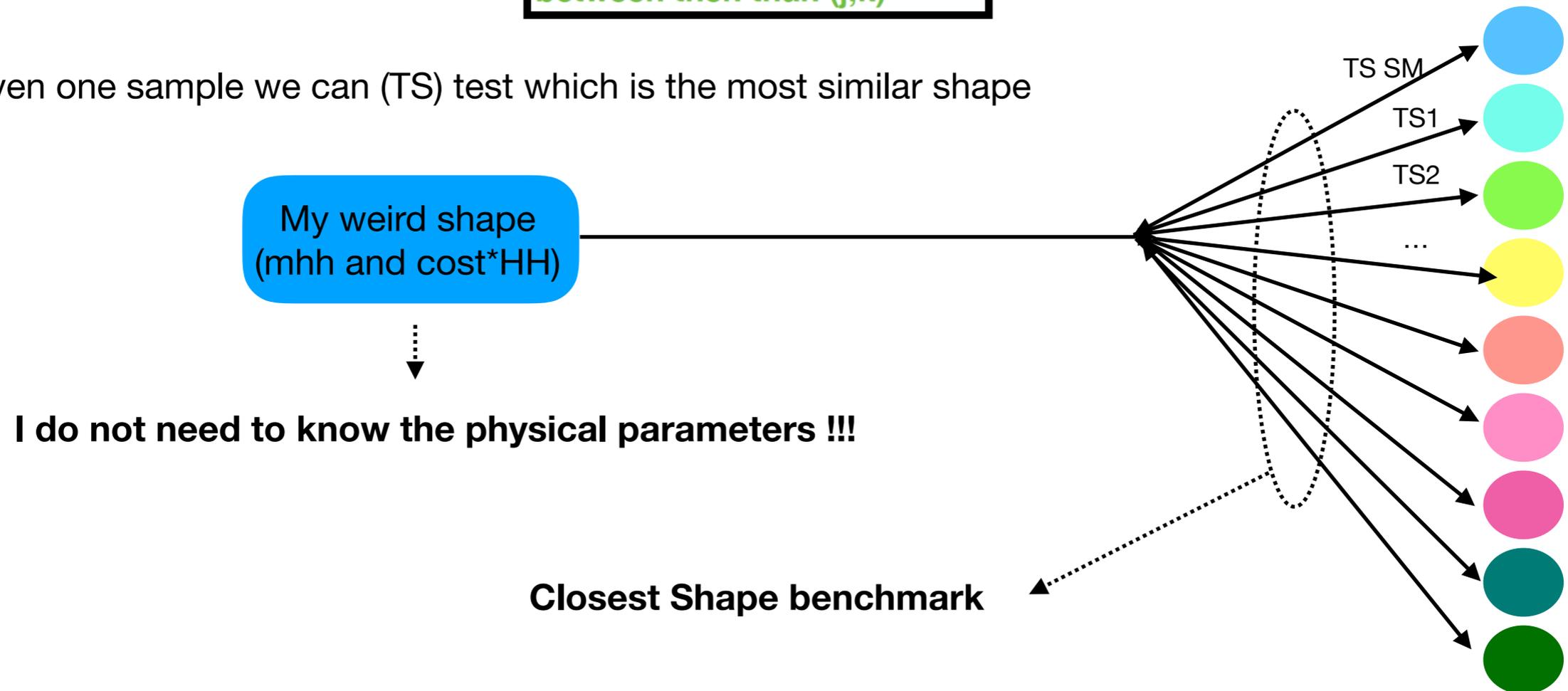
For the 2016 version of this analysis we will make the reverse exercise

# Fast reinterpretation method

The TS test can also be used as a fast reinterpretation method

Given 3 samples (i,j,k) if  
 $TS(i,k) > TS(j,k)$  then the  
 samples (i,k) are more similar  
 between then than (j,k)

—> Given one sample we can (TS) test which is the most similar shape

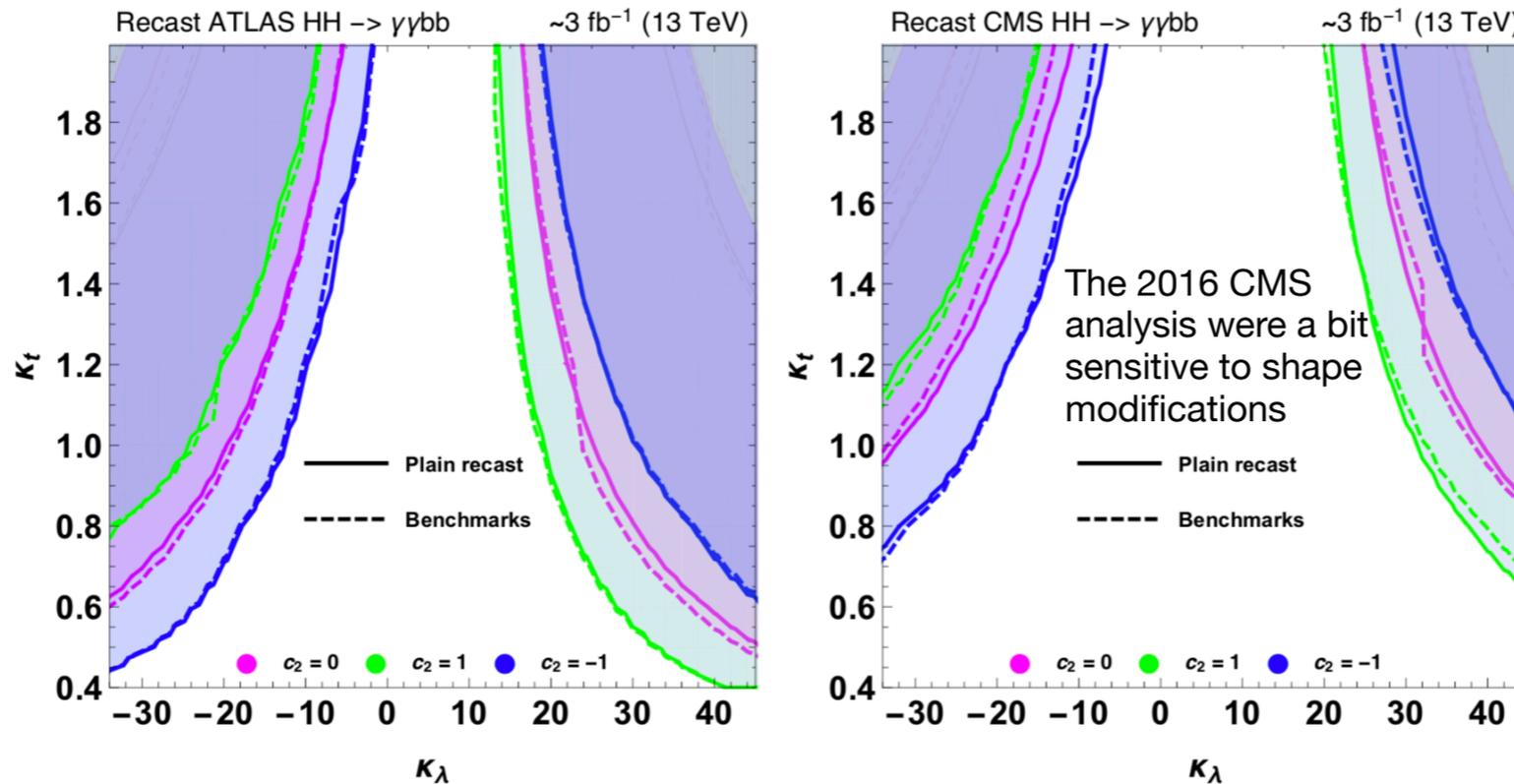


An implementation of the TS test just entering the 5 anomalous couplings mentioned here can be found on:

<https://github.com/kenmimasu/Rosetta/tree/dev/dihiggs> [1]

This was made possible because we have an analytical parametrization of the HH topology in terms of these 5 parameters

We compare with the sensitivity of an explicit scan and of using the benchmarks results  
 -> calculated with Delphes recast of the  $\sim 3/\text{fb}$  CMS and ATLAS analyses  
 (see Anamika's talk + backup for validation on shape benchmarks)



- The result/benchmark seems a fair for an **first assessment**

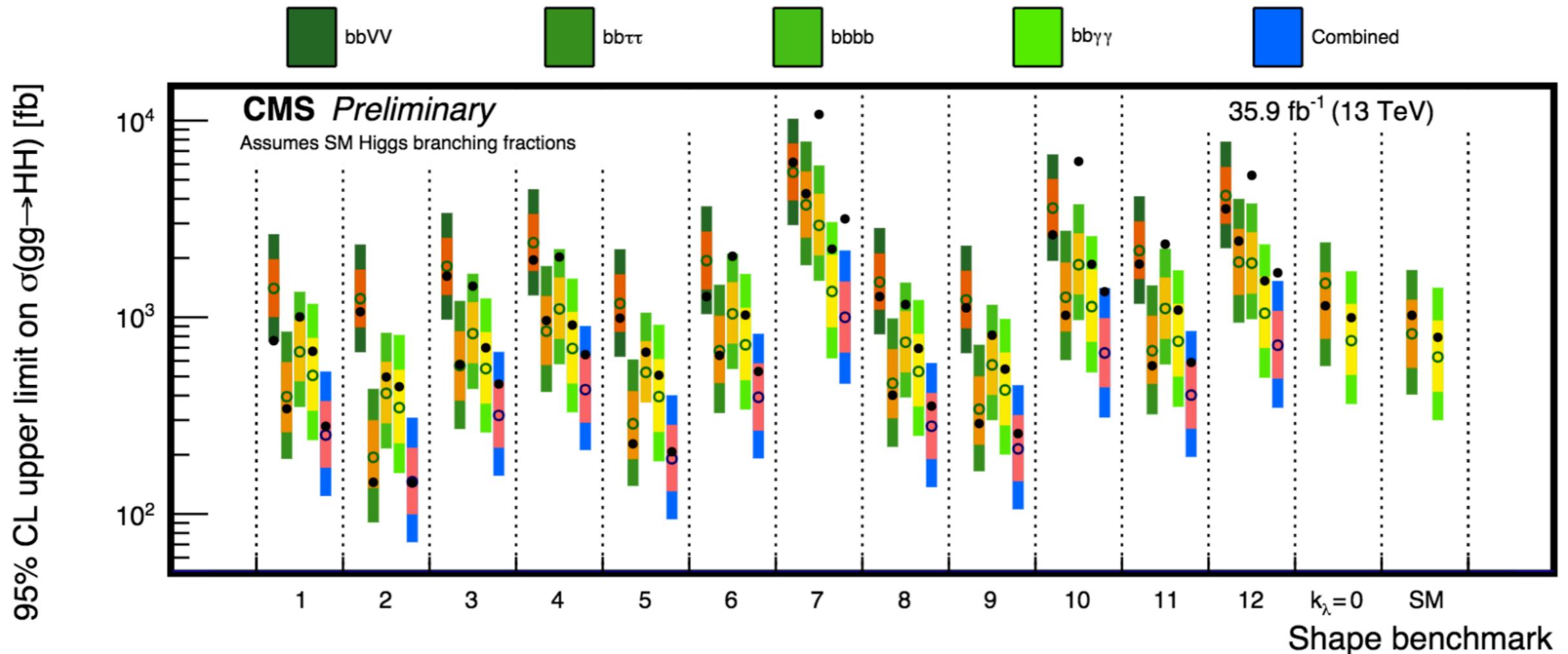
Let's take a leap of confidence

The kl-kt scan is just an demonstration focussed on the sensitivity of shape modifications. There are caveats!!!!

- SM HH BR
- Ignoring anomalous couplings effect on the contamination of signal on single H

# Using CMS combo

CMS released a limits from the combination of the hh-channels calculated on the shape benchmarks (see L. Cadamuro talk)



It is clear that the relative impact of each channel for different signal topologies changes  
 $\Rightarrow$  They are complimentary on the parameter space of anomalous couplings

# Where the limits on some anomalous couplings combinations would be?

The idea is to make possible to **estimate** the effects of the experimental results on your favorite model in case ATLAS and CMS did not consider it

$C2 = +1$

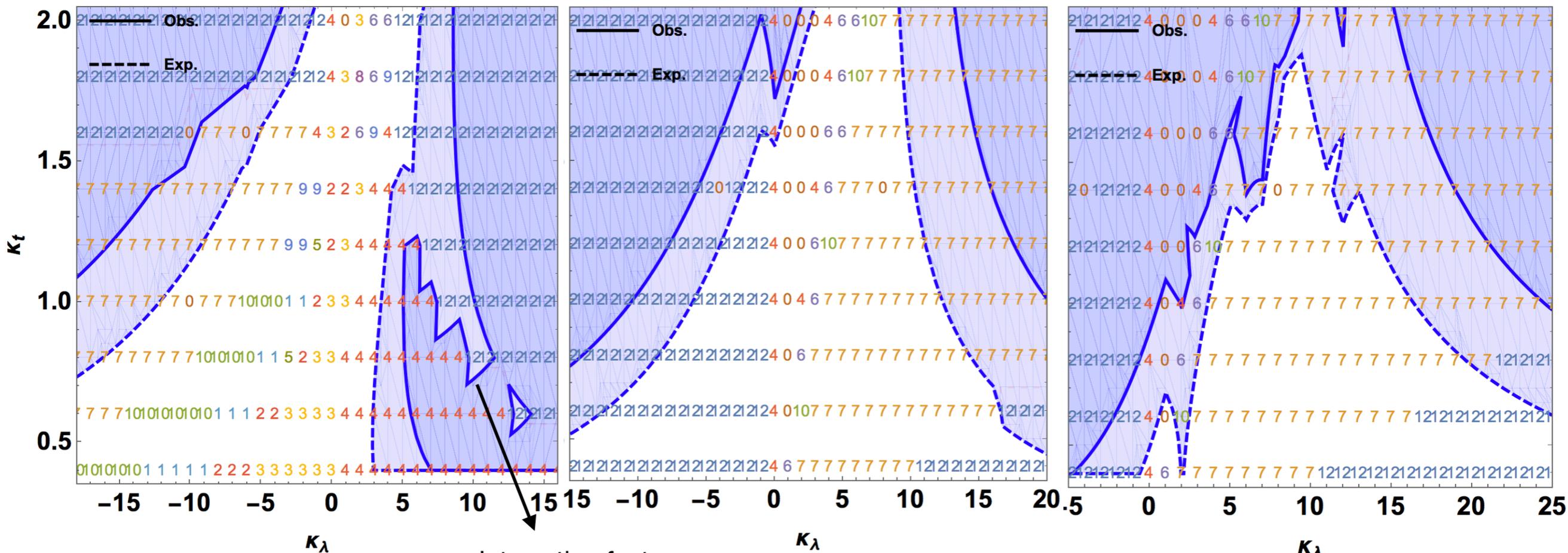
$C2 = 0$

$C2 = -1$

$c_2 = 1; c_g = c_{2g} = 0$  (CMS combo) 35.9 fb<sup>-1</sup> (13 TeV)

$c_2 = c_g = c_{2g} = 0$  (CMS combo) 35.9 fb<sup>-1</sup> (13 TeV)

$c_2 = -1; c_g = c_{2g} = 0$  (CMS combo) 35.9 fb<sup>-1</sup> (13 TeV)



Interesting features can be found on boundaries

0 = SM-like

- Am I suggesting the experiments should use benchmarks to access anomalous couplings ??? —> **NO!!!!!!!**
- Easy handles to estimation **outside** experiment

This is a demonstration of usage!!!!

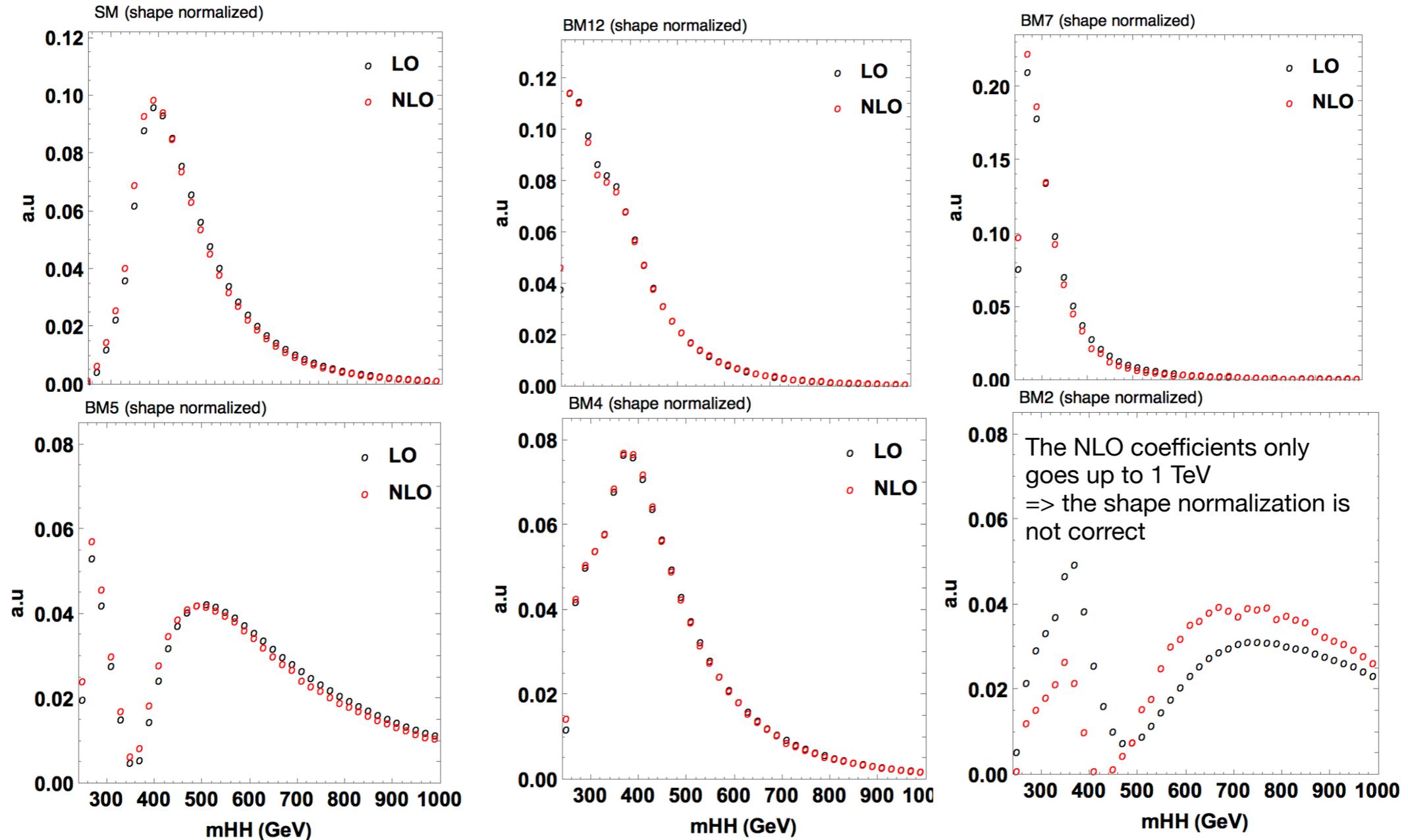
- Assuming SM HH BR
- Ignoring anomalous single H processes

See Anamika's talk for the effect of correlations

# Shape benchmarks @ QCD NLO

The authors of [1] calculated reweighing coefficients to QCD NLO (parametrized only by  $m_{hh}$ )

- The shapes of the BMs with LO after shape normalization maintain the characteristics **up to the degree of precision that we can claim with the method!**



Request to the authors (see part II of this talk)

—> Have the coefficients up to higher  $m_{hh}$  (~3 TeV?)

—> Make the coefficients to cover the 3D kinematics of the Higgs pair

—>  $\cos^2 \theta_{hh}$  is approximately flat, but after analysis selection it is not completely flat — see backup

—>  $m_{hh} \cos^2 \theta_{hh}$  can still be a good approximation to reconstruct the hh system, one can add thought  $p_z(hh)$  to complete the 3D

—> have the same result at 14TeV = future studies

# Fast reinterpretation method

The TS test can also be used as a fast reinterpretation method

Given 3 samples (i,j,k) if  
 $TS(i,k) > TS(j,k)$  then the  
 samples (i,k) are more similar  
 between then than (j,k)

—> Given one sample we can (TS) test which is the most similar shape

My weird shape  
(mhh and cost\*HH)

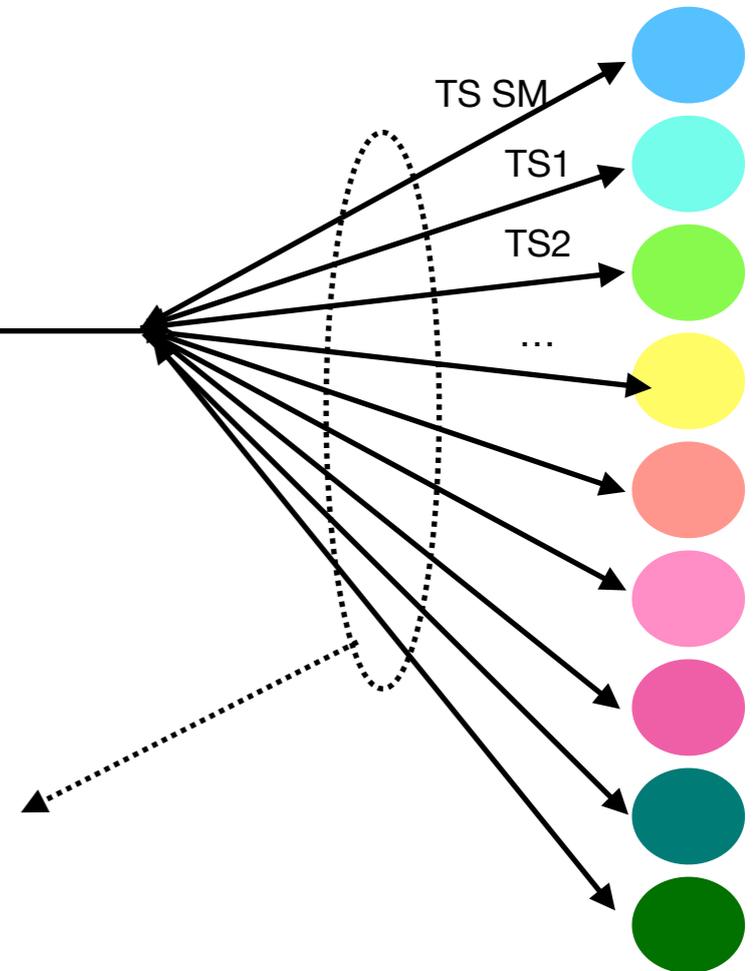


**I do not need to know the physical parameters !!!**

**Closest Shape benchmark**

If you want to use different input from 5 anomalous couplings  
(e.g Chromomagnetic, new physics on the loop, off shell  
resonances, HH+X...) you just have some coding homework,  
but the mapping is technically possible

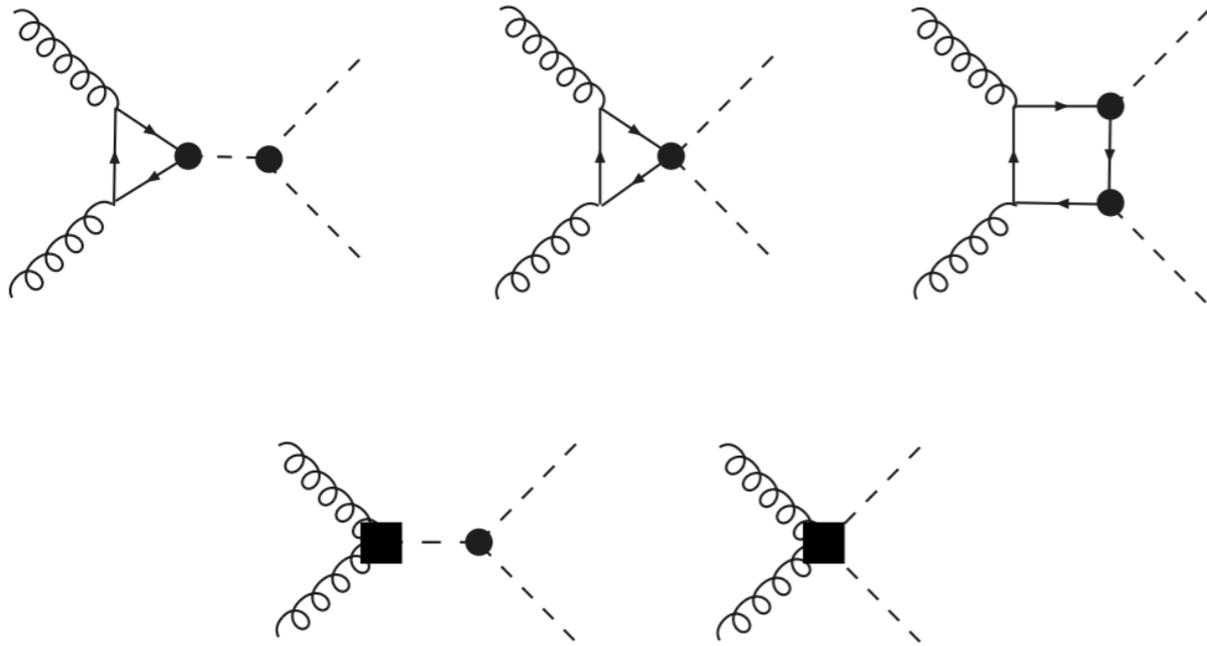
**the user should have conscience if it is physically possible !!!! ;-)**



## **Part II**

**The official results of the experiments must be precise  
== How to make precise scans with finite computing time? ==**

# The process



Pieces of the modifications of the total cross section:

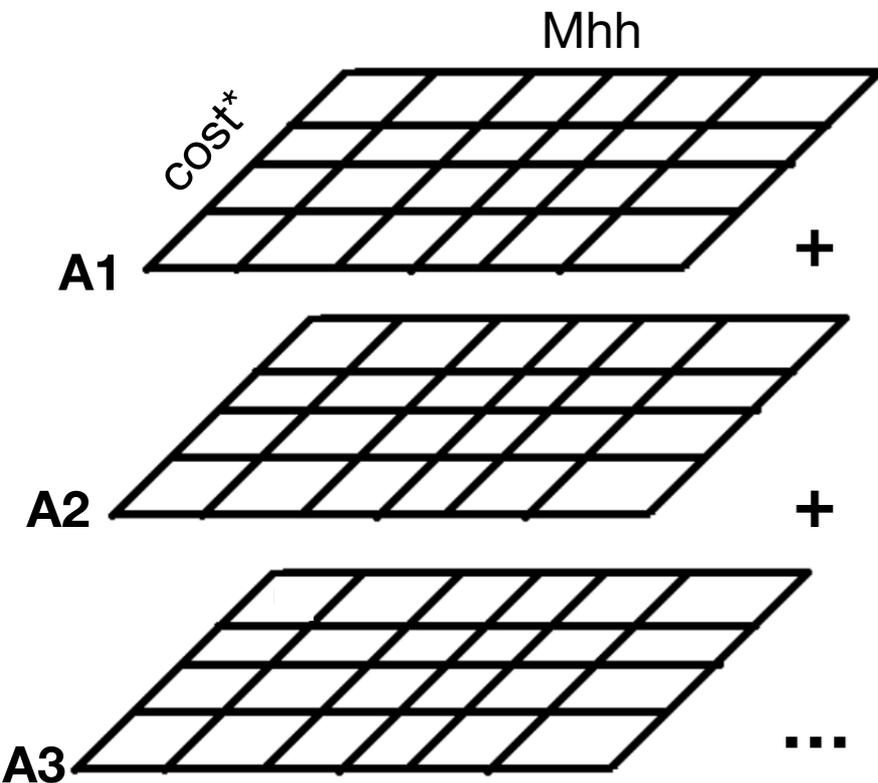
$$R_{hh} \equiv \frac{\sigma_{hh}}{\sigma_{hh}^{SM}}$$

$$= A_1 \kappa_t^4 + A_2 c_2^2 + (A_3 \kappa_t^2 + A_4 c_g^2) \kappa_\lambda^2 + A_5 c_{2g}^2 + (A_6 c_2 + A_7 \kappa_t \kappa_\lambda) \kappa_t^2$$

$$+ (A_8 \kappa_t \kappa_\lambda + A_9 c_g \kappa_\lambda) c_2 + A_{10} c_2 c_{2g} + (A_{11} c_g \kappa_\lambda + A_{12} c_{2g}) \kappa_t^2$$

$$+ (A_{13} \kappa_\lambda c_g + A_{14} c_{2g}) \kappa_t \kappa_\lambda + A_{15} c_g c_{2g} \kappa_\lambda$$

Those coefficients can also be viewed as differential  
(15 at LO and 23 at NLO)



That is a simple concept! How to use it?

# What can we do to extrapolate shapes of a finite collection of MC samples?

I will comment on two methods:

	<p><b>Reweighting event by event using representative matrix of events (e.g. the shape benchmarks)</b></p>	<p><b>Treating the parts of the cross section as different samples to be combined</b></p>
<b>Pros</b>	<p>All the generated event statistics has positive weights = Maximal use of MC stats</p>	<p>More intuitive for setting limits on parameters given the statistical tools available on experiments</p>
<b>Cons</b>	<p>To set limits on parameters one must adapt a framework for doing limits on from scans/ shape morphings</p>	<p>Part of the generated MC stats. may have negative weights, according with the point Some weights can be large.</p>
	<p>CMS analyses has been doing up to now</p>	<p>ATLAS has been doing up to now</p>

**Matrix Element reweighting:** Built-in method on MG\_aMC@NLO

# Analytical parametrization of shapes

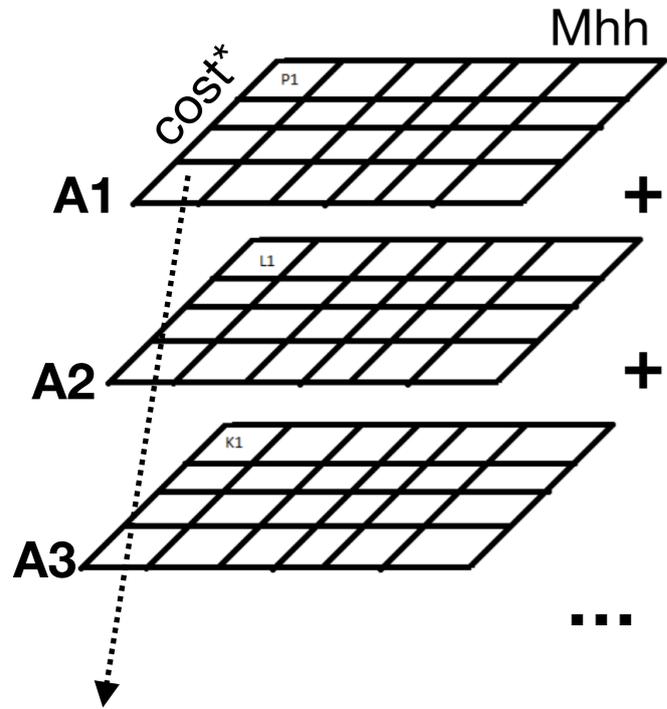
## Reweighting event by event shape benchmarks

[3]

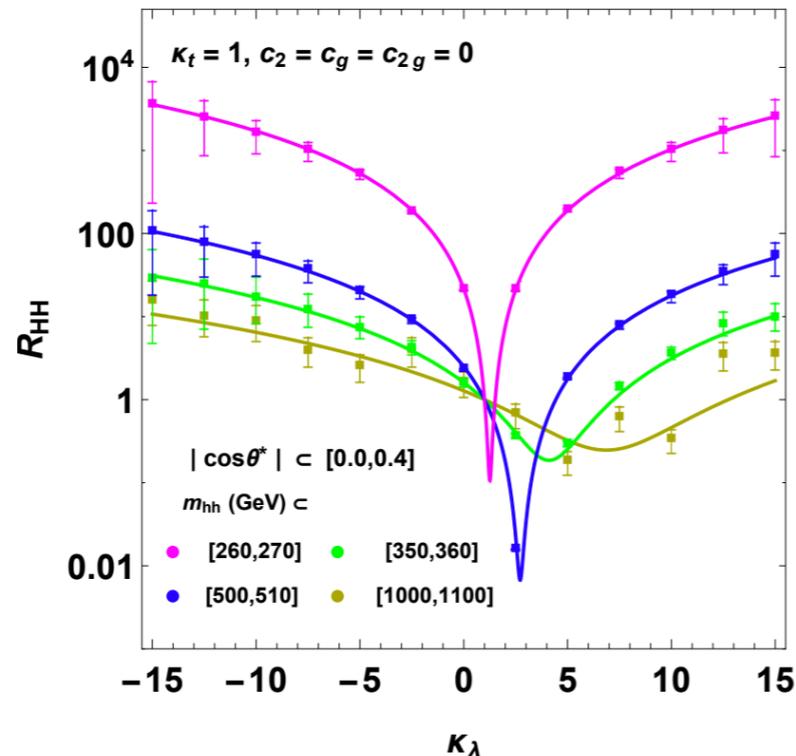
There are 2 practical ways to get the coefficients/bin:

- 1) Using an MC model that allow simulation of different parts of the matrix element squared and binning it
  - in MG\_MC@NLO it means using coupling orders
  - There is model ready @5D
- 2) Brute force: generating a large grid of parameter space and fitting the above formula in each kinematical bin
  - This was done when the tools (1) were not available
  - MC simulations do have statistical uncertainties

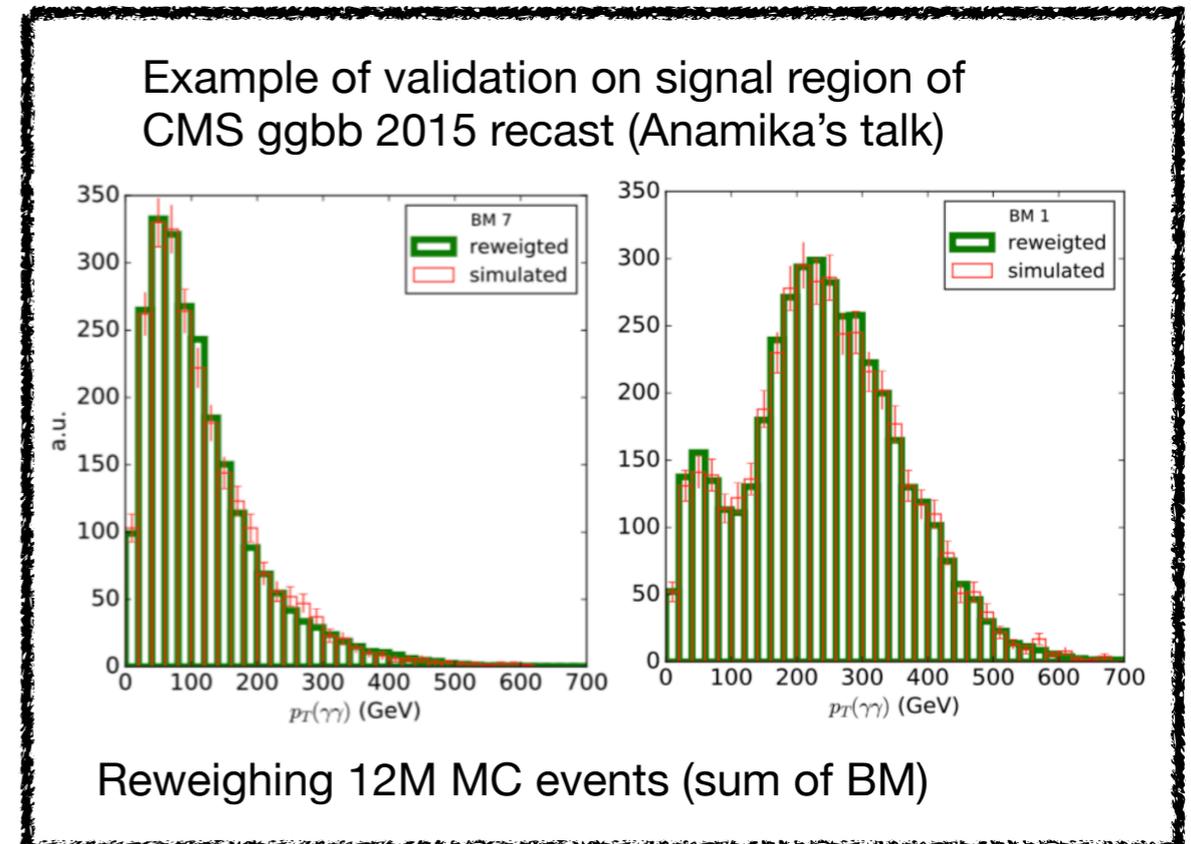
=> The more number of samples on a scan more precise the fit, e.g.



$$R_{hh} \equiv \frac{\sigma_{hh}}{\sigma_{hh}^{SM}}$$



=> This method is not so precise in tails of  $m_{hh}$ , but for the kinematics space of resolved analyses it was well validated and used on all CMS analyzes (but bbWW)



# Treating pieces of cross section as different samples to be combined

Total shape = all the interference parts summed up, with proper coefficients

There are 2 practical ways to get the shape parts:

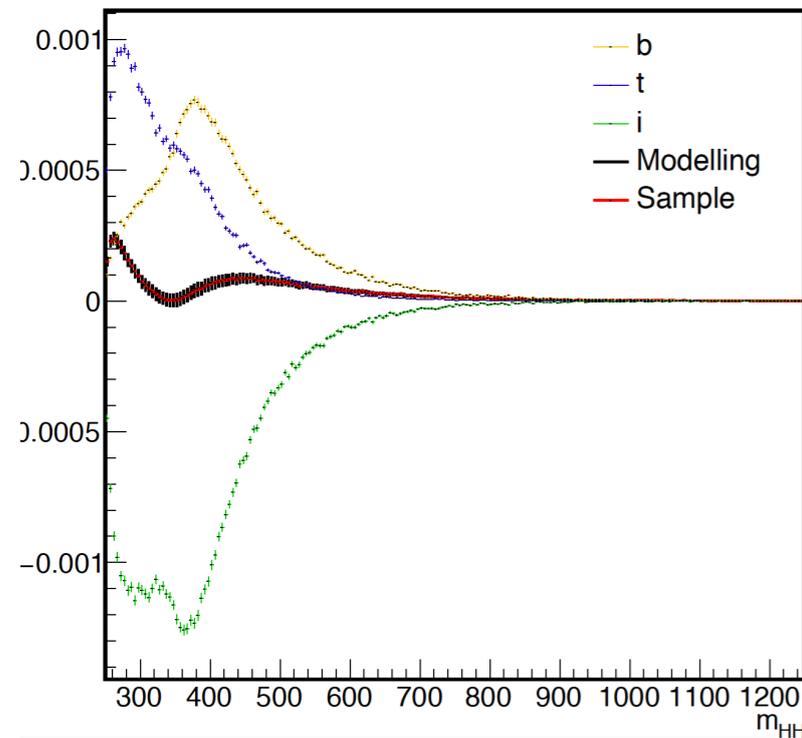
- 1) Using analytical formulas to isolate them from few simulations on different points (see P. Bokan talk)
- 2) Using an MC model that allow simulation of different parts of the matrix element squared

Validation done by L. Cadamuro

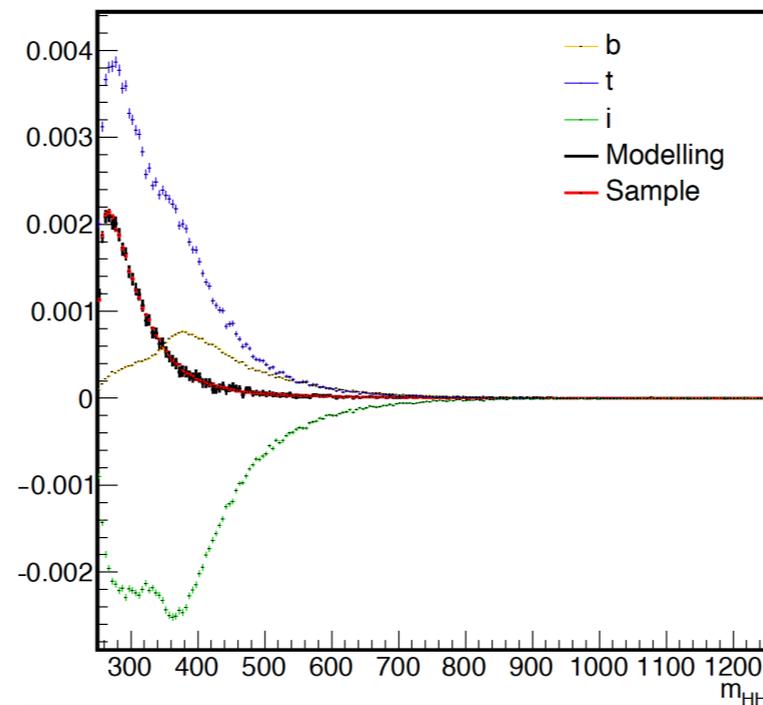
Only the model with kt-kl animals couplings were available at the time of validation (LO)

=> triangle (t) + box (b) + interference (i)

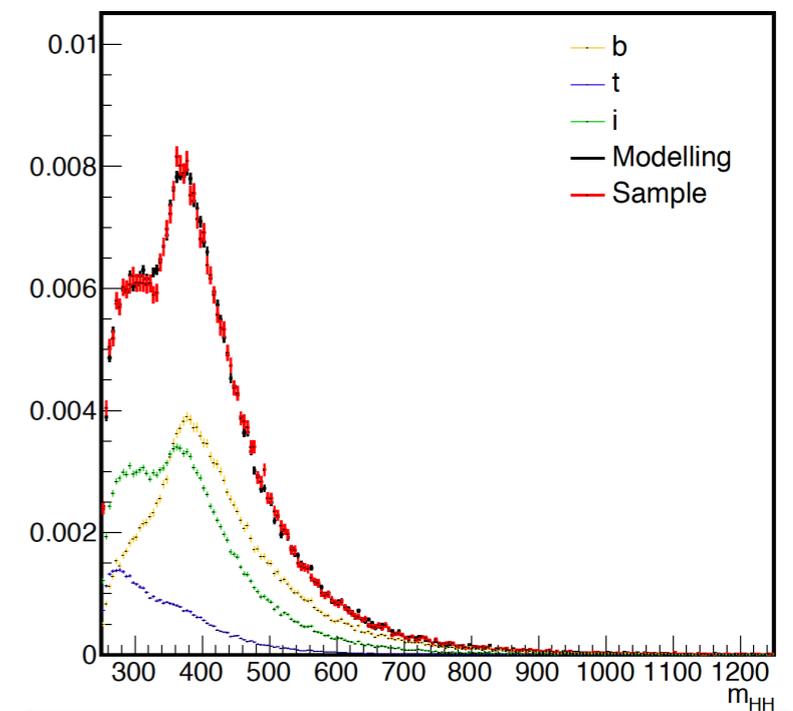
$k_\lambda = 2.5, k_t = 1$



$k_\lambda = 5, k_t = 1$



$k_\lambda = -2, k_t = 1.5$



Made with the default MGaMC@NLO SM loop model + coupling orders (kindly done by Eleni Vryonidou)  
The 5D version (LO) is done (see backup), just ask me out

# Conclusions

## The method of defining shape benchmarks for HH non-resonant searches (only!)

- It is based on a pure statistical method
  - It really does not matter which couplings correspond to them
  - There is no need to redefine them @NLO
    - Different of saying that they do not need to be generated @NLO for studies!!
- The main goal of it:
  - Allow discovery as soon as possible (or not miss it)
    - What is this something precisely (precision on coupling)? To be defined upon discovery
- In the meanwhile, it appears also to be the simplest solution for:
  - Experimental usage: MC tool, sanity checks and optimizations with limited CPU usage
  - Theory usage: until a better solution is found, it provides an estimate of the limit on your preferred combination of anomalous Higgs couplings.

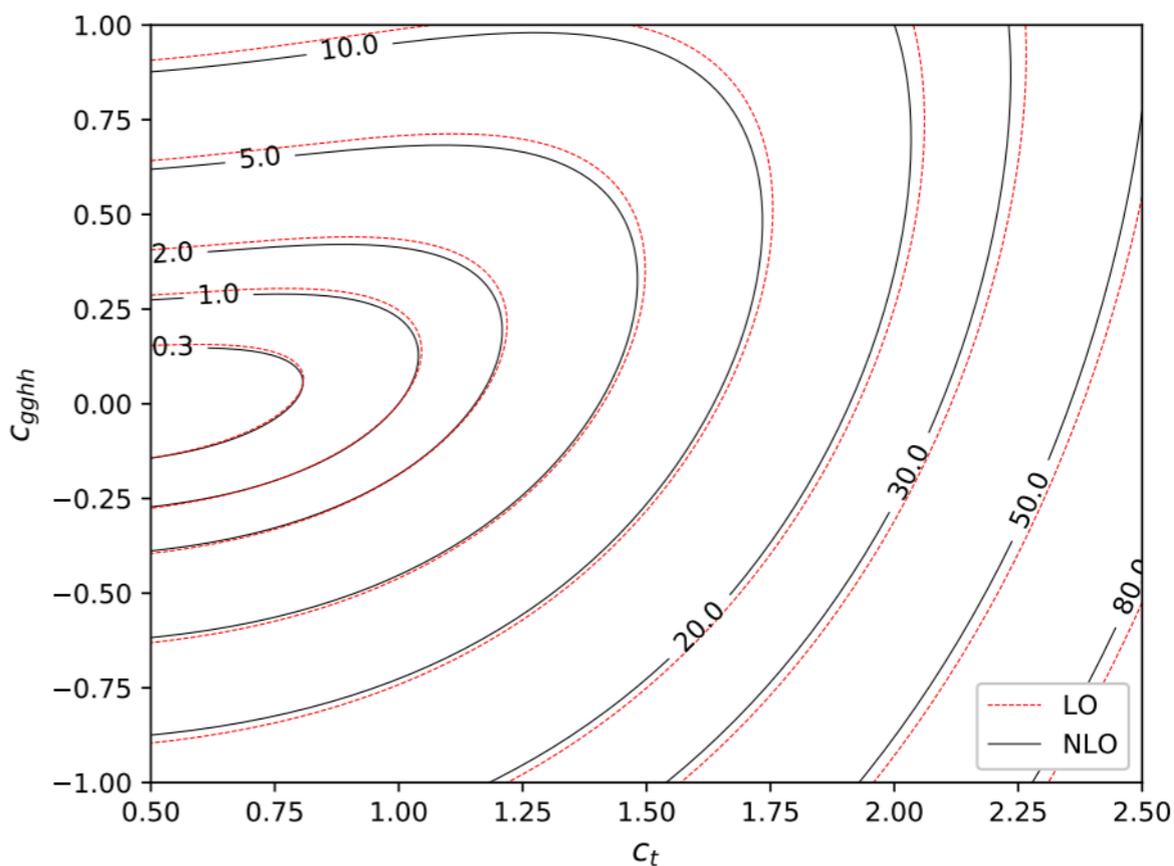
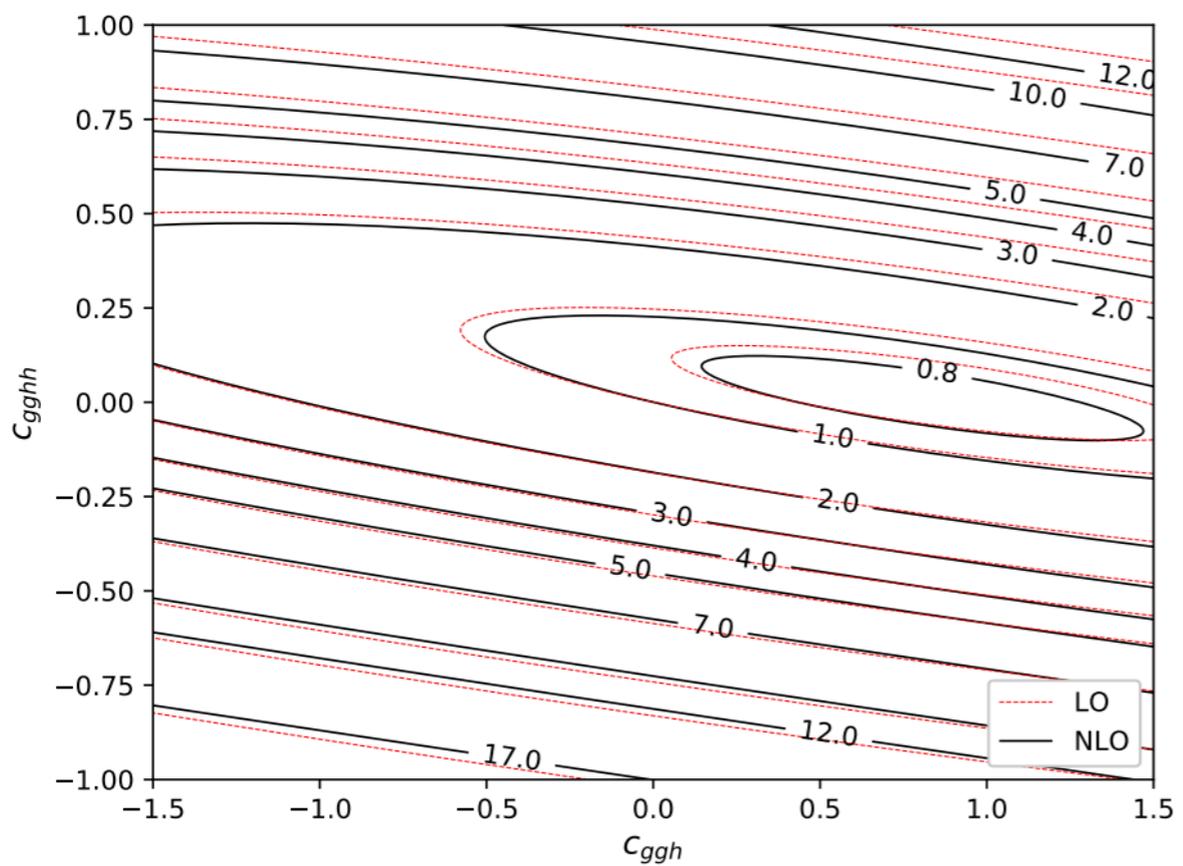
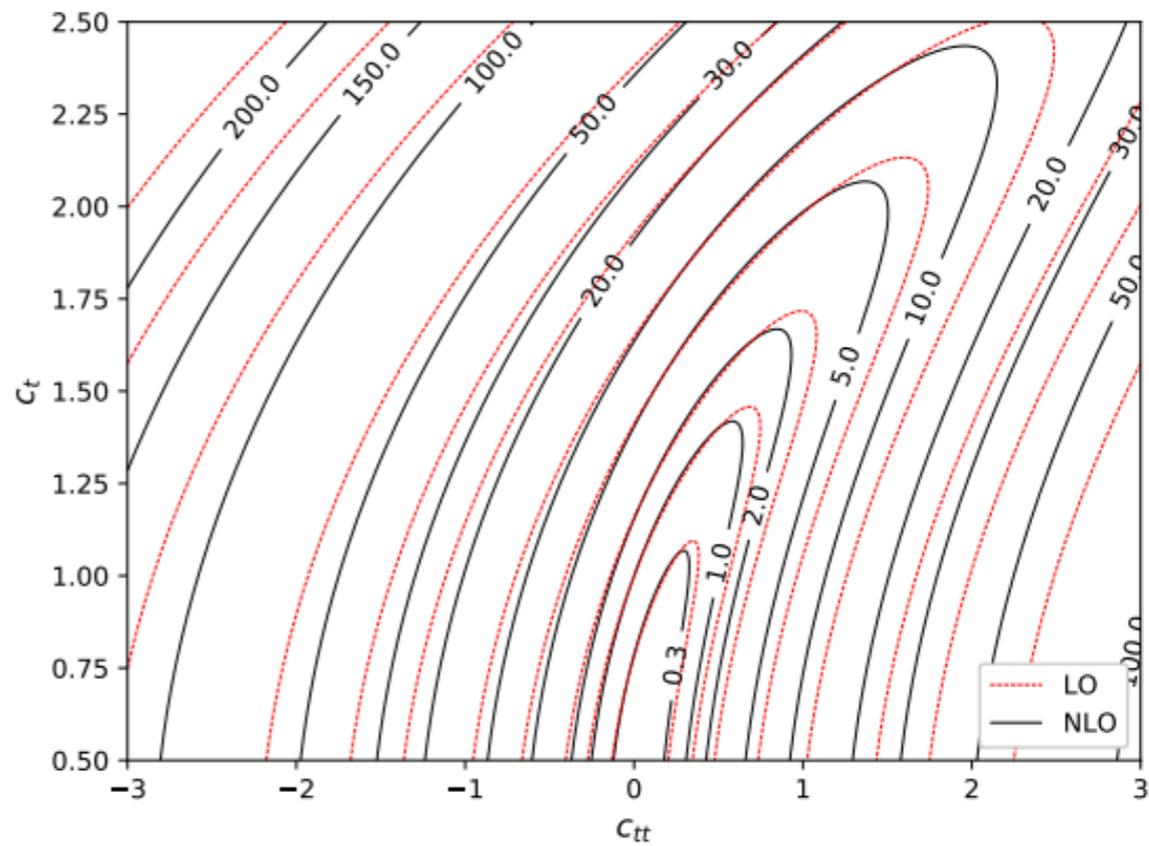
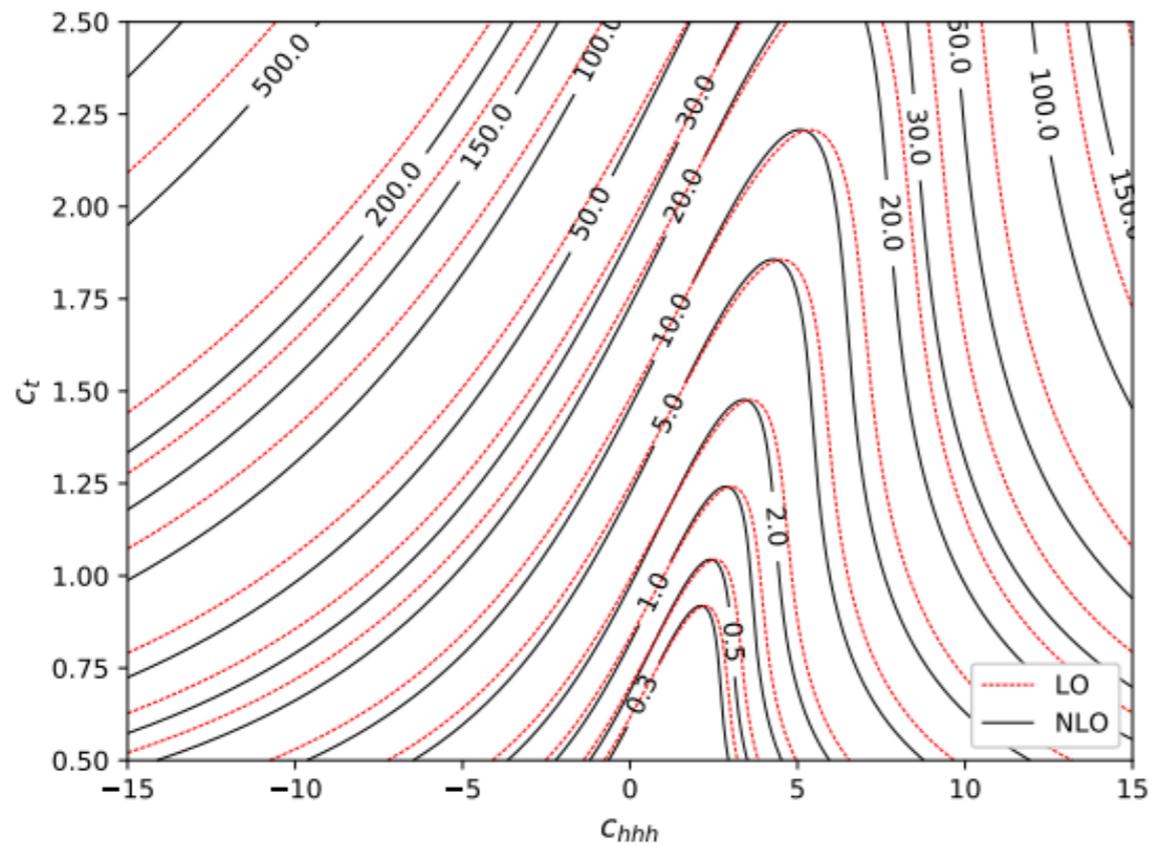
## Experimental results on physics can/need to be more precise

(eg, for a combination of HH and H in some model framework)

- Two methods for scan of parameters using finite computing resources were discussed
  - Technically both methods can be extended to NLO
    - MC guys: to have a model that can separate  $ME^2$  parts makes all easier!
  - Does ATLAS and CMS need to uniform the method of BSM scan?
    - Maybe, for a BSM combination
- The very same shape extrapolation methods can be used for any process
  - Including VBF HH !!!

# Backup

# Cross sections @NLO

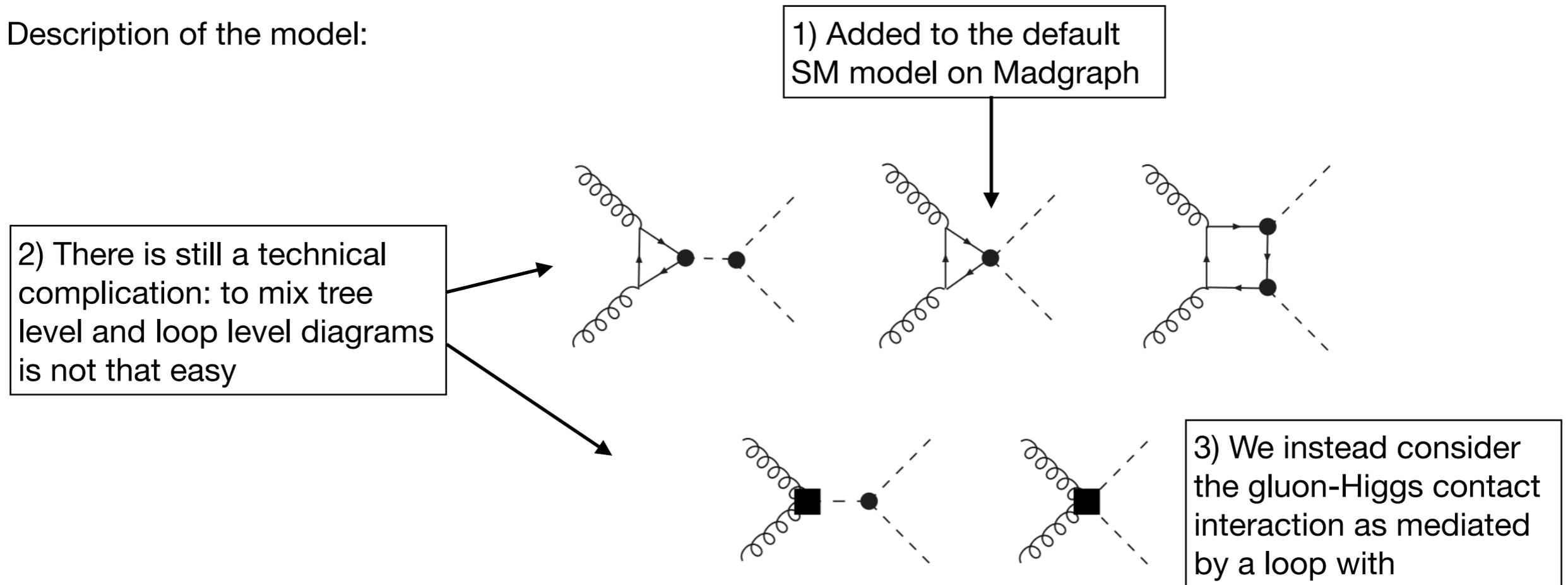


# The model (LO)

The model file we were based on form factors to emulate the kinematics of the ggHH \*loop induced\* process

The possibility construct a model that is capable of of generate the \*loop induced\* process in Madgraph is somehow recent. Only like this we could think on generating the different pieces of the matrix element separately

Description of the model:



Temporary location: /afs/cern.ch/work/a/acarvalh/public/toHH\_BSM/loop\_sm\_5D.tar.gz

To generate the different parts of the Matrix element take a look [here](#)

# Reweighting event by event shape benchmarks - some validation

We validate how well can we reweighs events to the shape benchmarks on the CMS analyses  
Using the coefficients from the brute force calculation

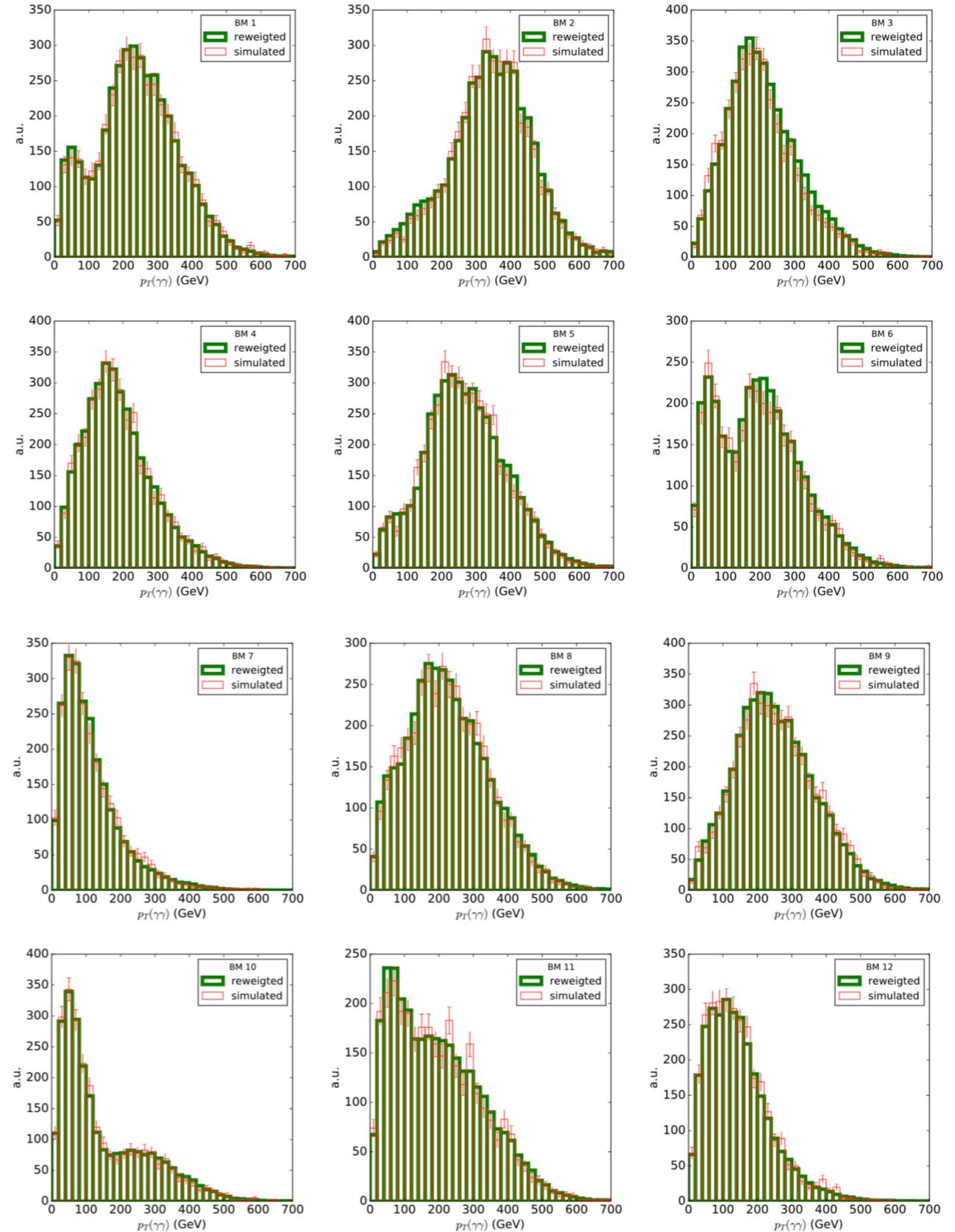
Example of validation:

Efficiencies after  
ggbb analysis cuts

Shapes on  
signal region

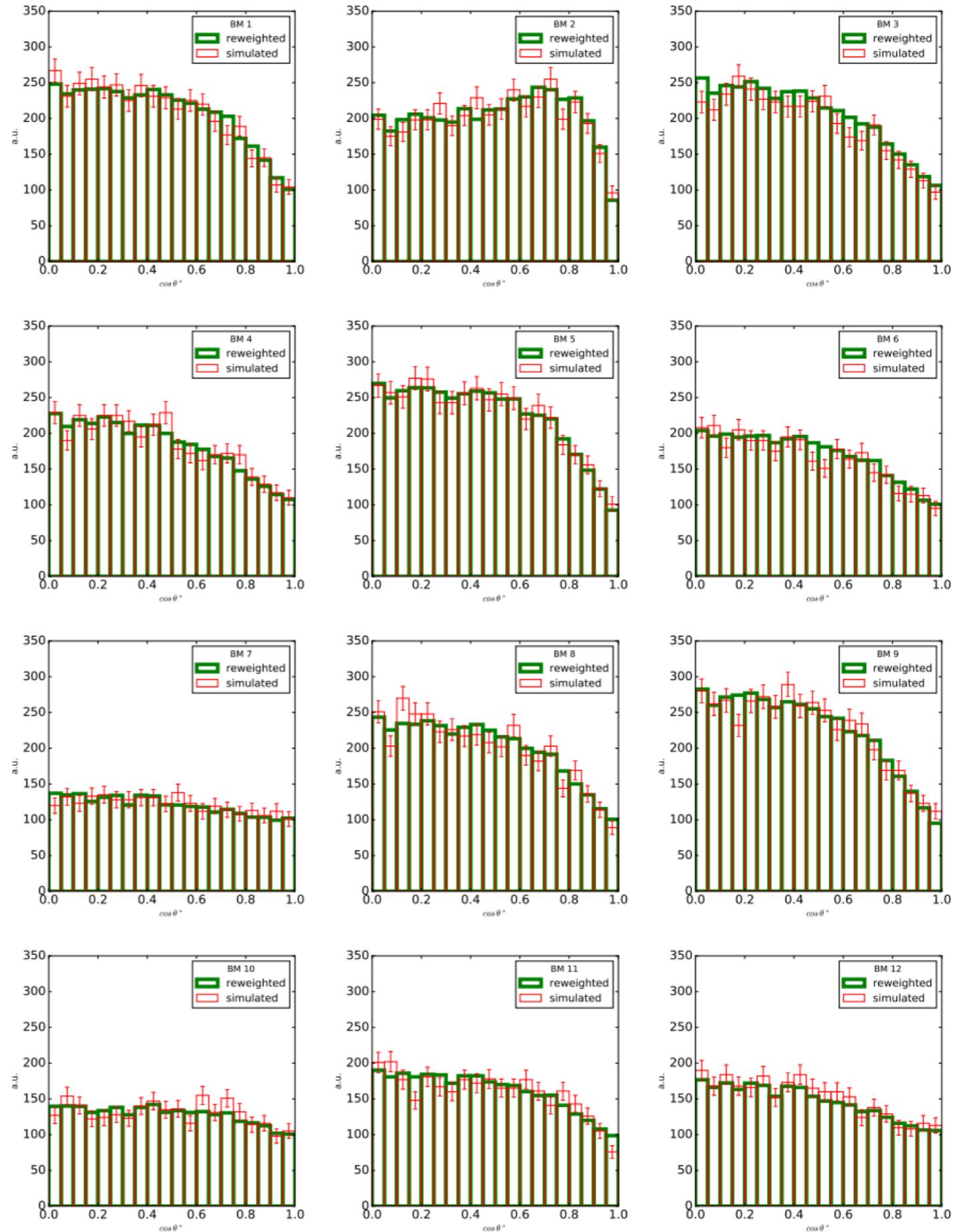
$N$	$\kappa_\lambda$	$\kappa_t$	$c_2$	$c_g$	$c_{2g}$	$C_{\text{norm}}$	ATLAS-like		CMS-like	
							$\epsilon_{\text{MC}}$	$\epsilon_{\text{rew}}$	$\epsilon_{\text{MC}}$	$\epsilon_{\text{rew}}$
0	1.0	1.0	0.0	0.0	0.0	1.0	10.0	10.0	11.46	11.47
1	7.5	1.0	-1.0	0.0	0.0	0.94	10.6	10.6	10.83	10.79
2	1.0	1.0	0.5	-0.8	0.6	0.71	10.3	10.4	11.46	11.26
3	1.0	1.5	-1.5	0.0	-0.8	0.96	9.93	10.5	10.89	11.68
4	-3.5	1.0	-3.0	0.0	0.0	0.98	9.42	9.37	9.89	9.72
5	1.0	1.0	0.0	0.8	-1.0	0.88	11.6	11.5	12.47	12.50
6	2.4	1.0	0.0	0.2	-0.2	0.96	8.47	8.73	7.27	7.74
7	5.0	1.0	0.0	0.2	-0.2	1.01	6.24	6.17	3.30	3.23
8	15.0	1.0	0.0	-1.0	1.0	0.92	10.2	10.3	10.64	10.74
9	1.0	1.0	1.0	-0.6	0.6	0.86	11.6	11.6	12.92	12.79
10	10.0	1.5	-1.0	0.0	0.0	1.01	6.67	6.60	3.48	3.48
11	2.4	1.0	0.0	1.0	-1.0	0.95	8.16	8.26	6.72	6.81
12	15.0	1.0	1.0	0.0	0.0	1.0	7.80	7.52	6.23	6.17

Similar results are found with the method (1)

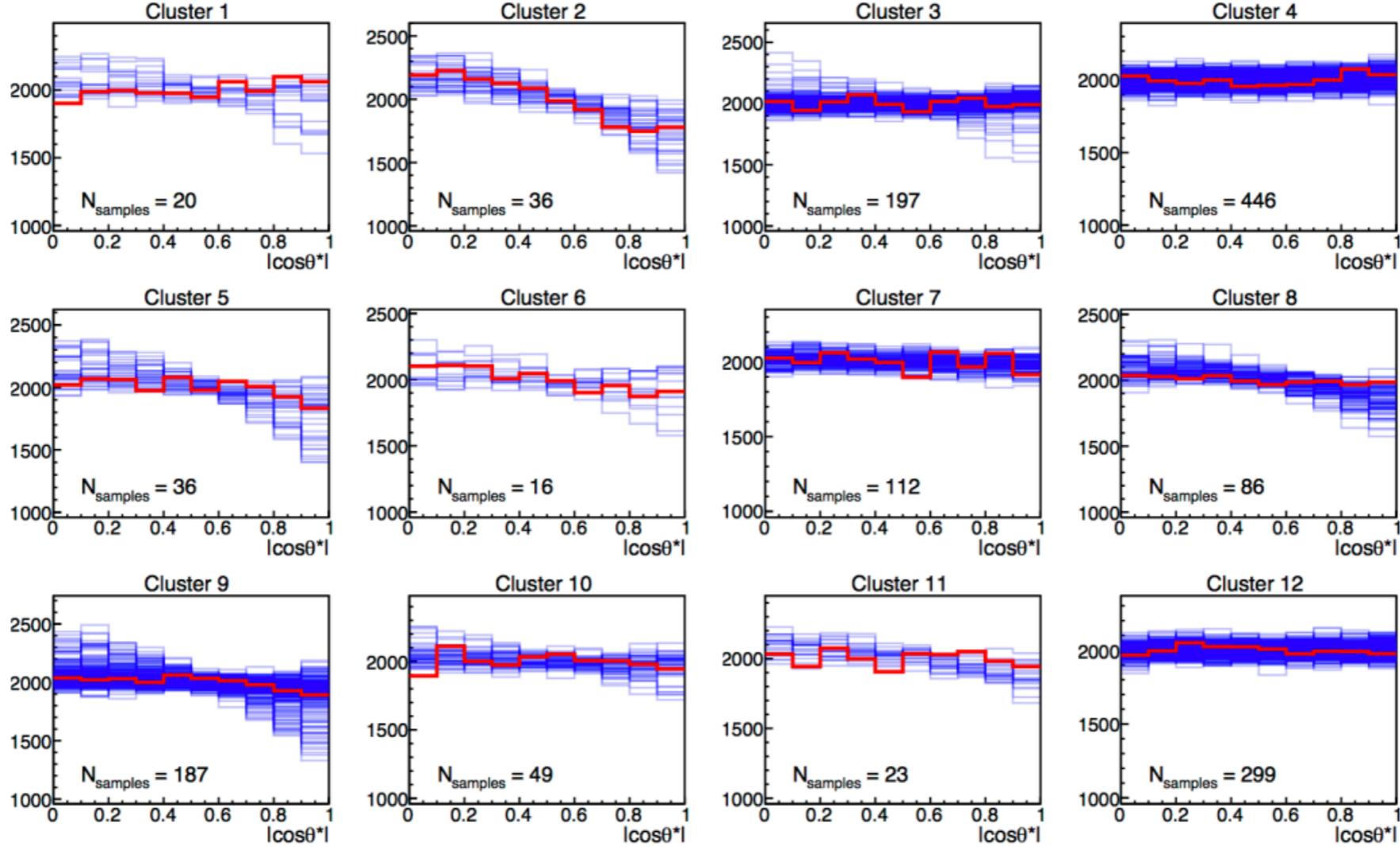


# Reweighting event by event shape benchmarks - some validation

Shapes on  
signal region

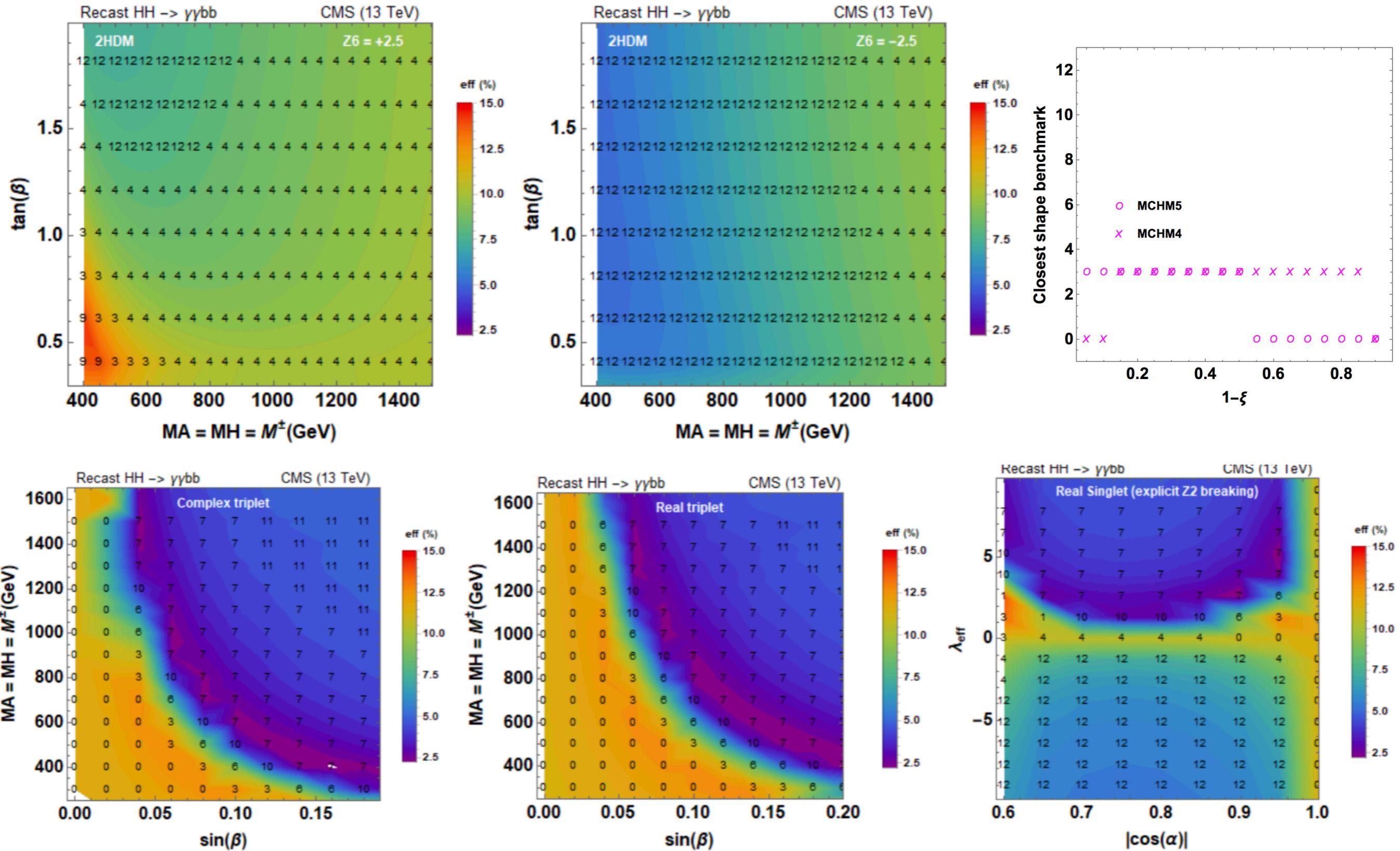


# Cost\*HH gen-level @ LO



**Figure 5.** Generation-level distributions of di-Higgs boson mass  $m_{hh}$  (top three rows) and emission angle  $|\cos \theta^*|$  (bottom three rows) for the clusters identified by the choice  $N_{clus} = 12$ . The red distributions correspond to the benchmark sample in each cluster, while the blue ones describe the other members of each cluster. Cluster 3 contains the SM sample.

# Reweighting event by event shape benchmarks - some validation

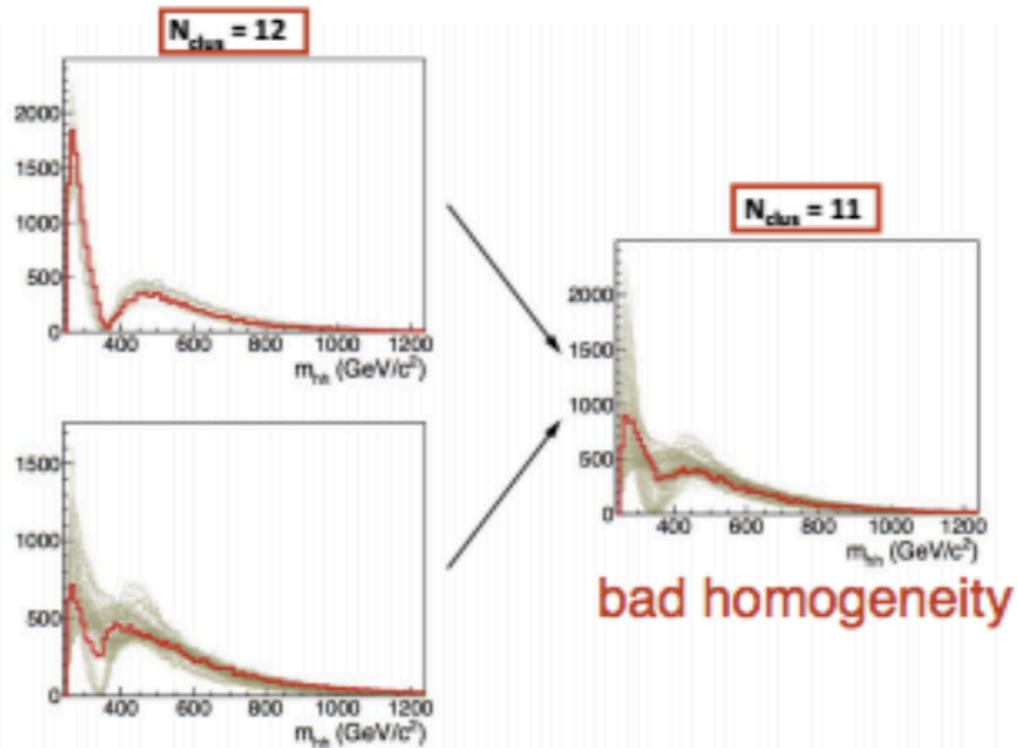


## Binning used for TS test on reinterpretation

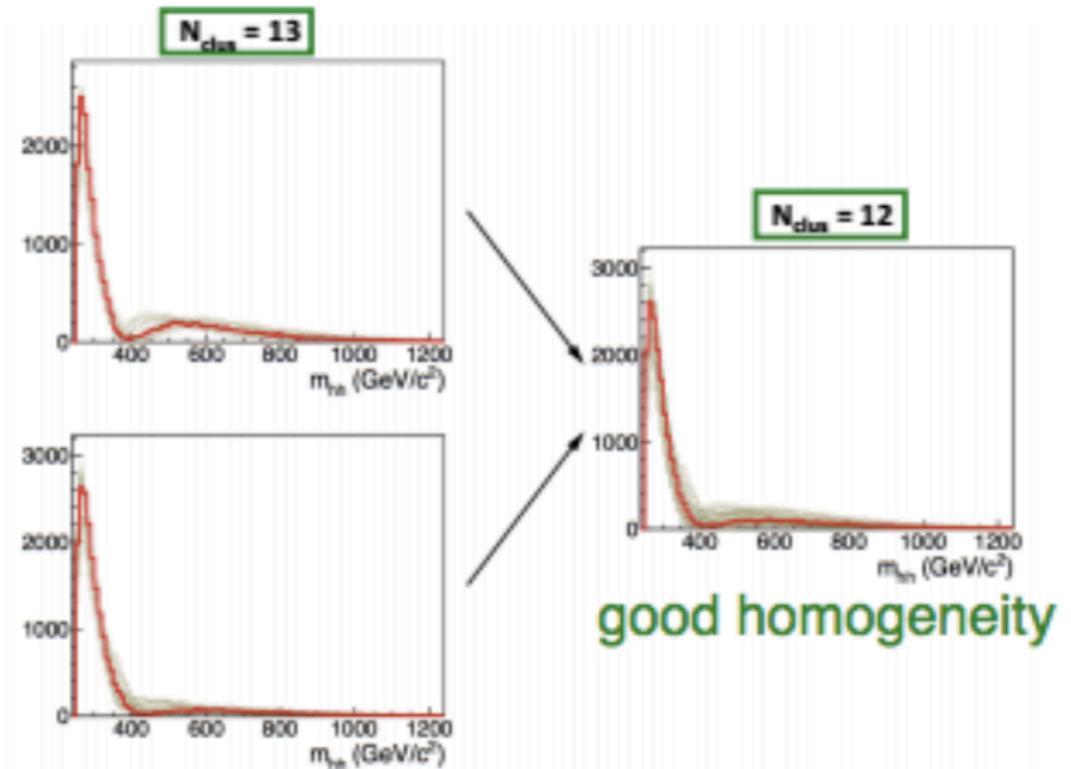
```
bins = ([[ 250., 260., 270., 280., 290., 300., 310.,  
320., 330., 340., 350., 360., 370., 380.,  
390., 400., 410., 420., 430., 440., 450.,  
460., 470., 480., 490., 500., 510., 520.,  
530., 540., 550., 560., 570., 580., 590.,  
600., 610., 620., 630., 640., 650., 660.,  
670., 680., 690., 700., 750., 800., 850.,  
900., 950., 1000., 1100., 1200., 1300., 1400.,  
1500., 1750., 2000., 50000.]), ([ 0., 0.40000001, 0.60000002, 0.80000001, 1. ])]
```

# Why to stop with 12 clusters?

11 clusters are visually too few

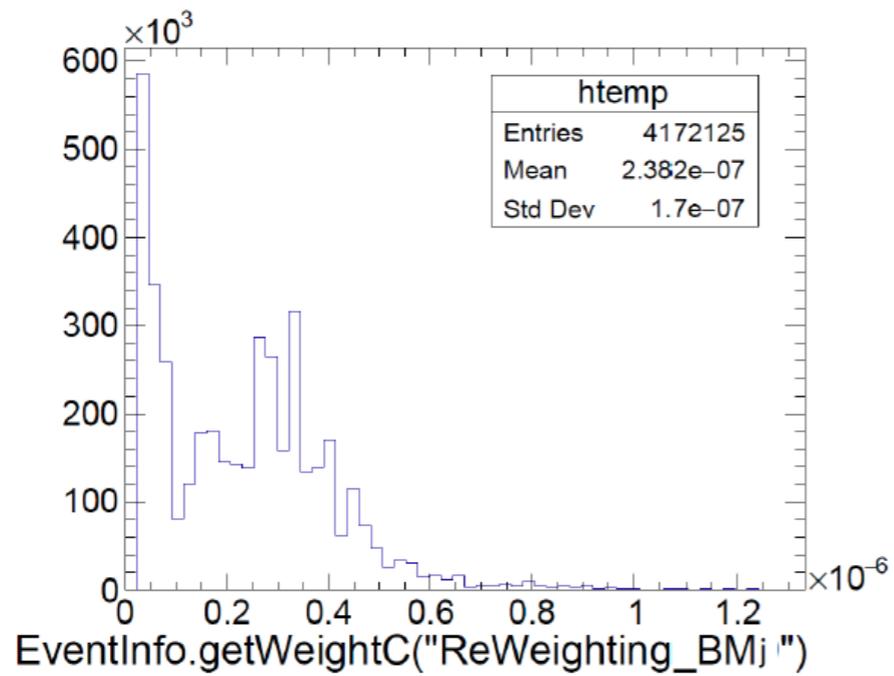
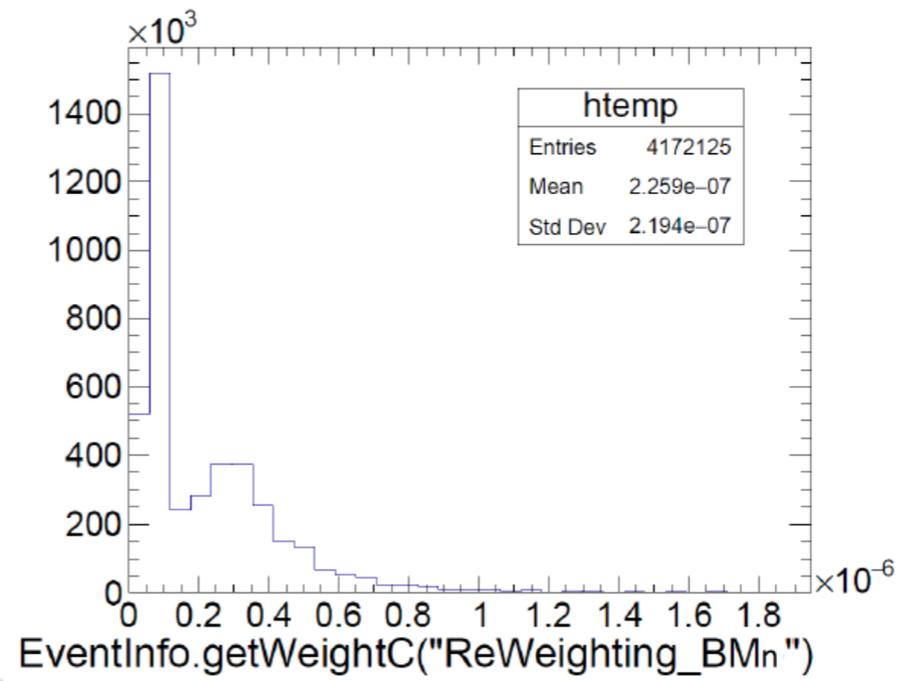
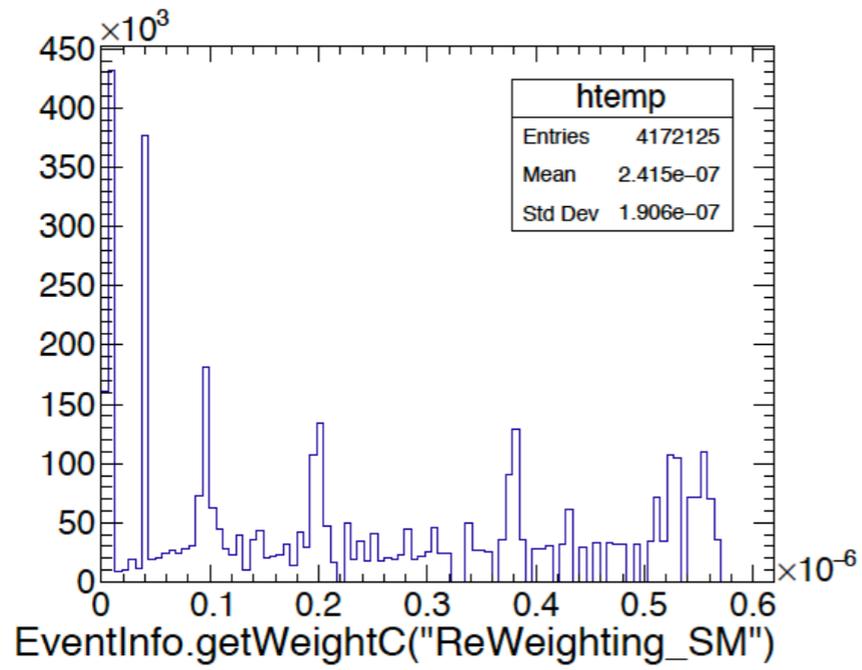


13 clusters are visually too much



Trade off between number of benchmarks and intra-cluster homogeneity

# Examples of size of weights



~400k events/sample

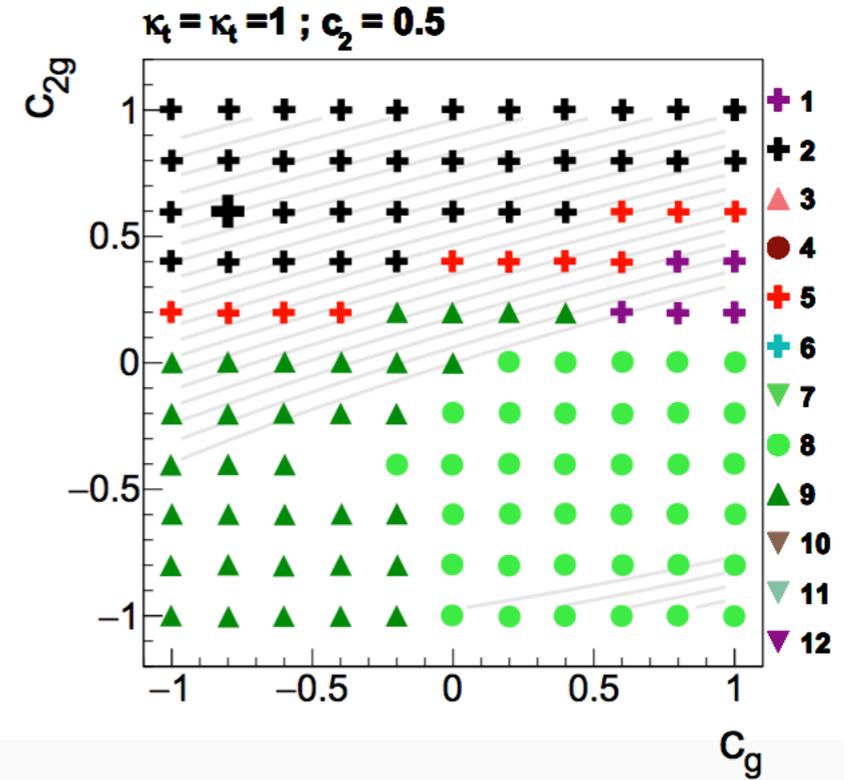
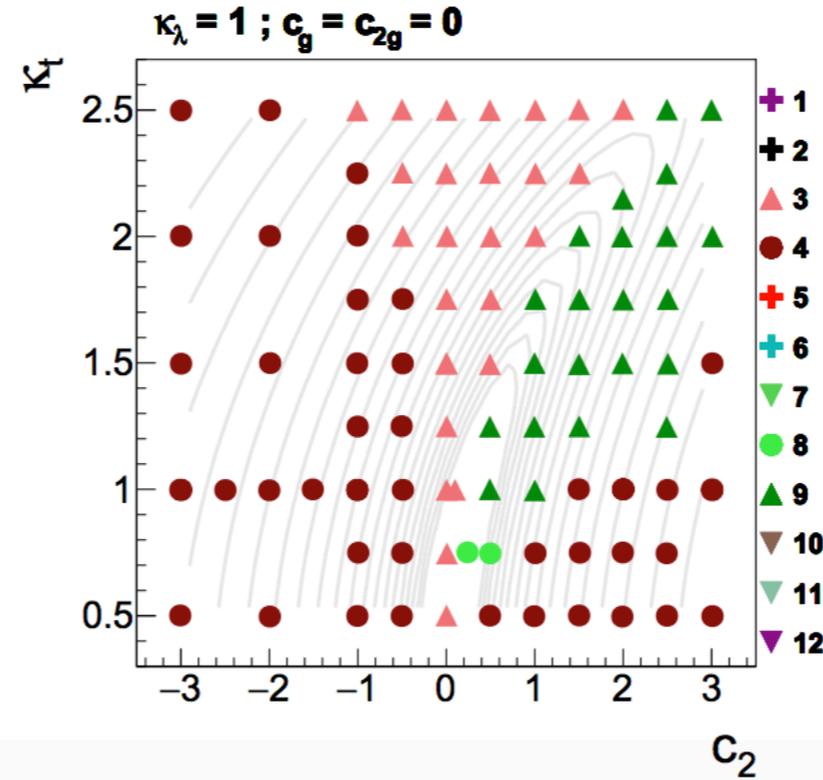
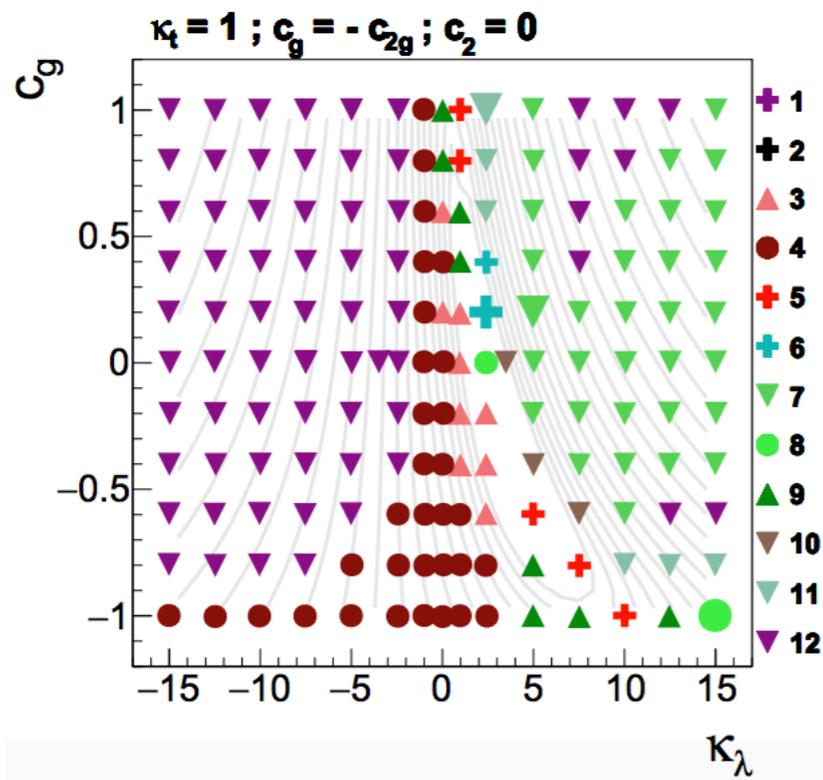
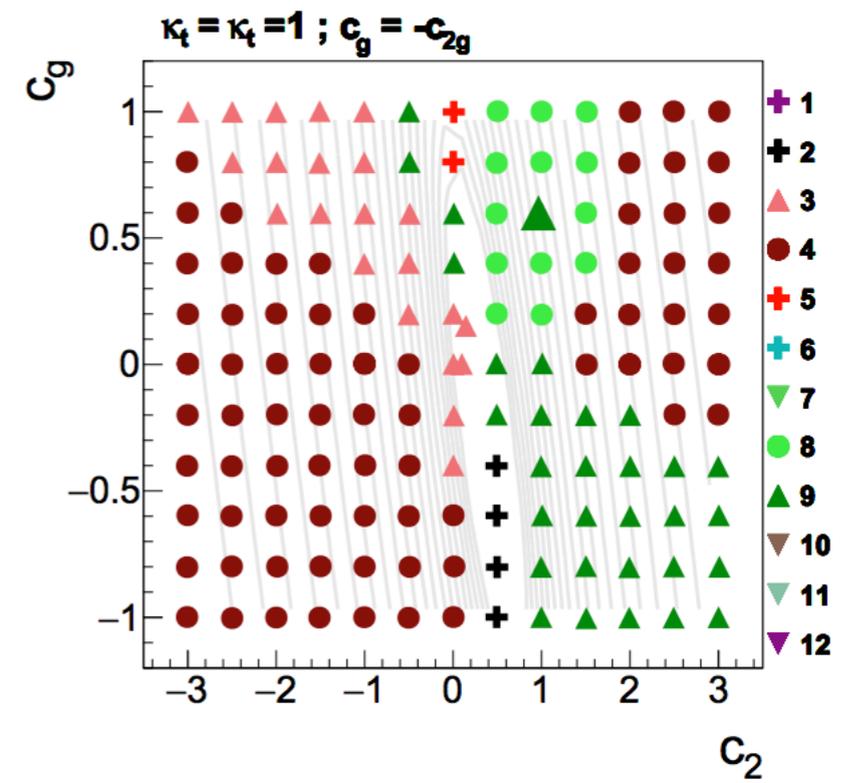
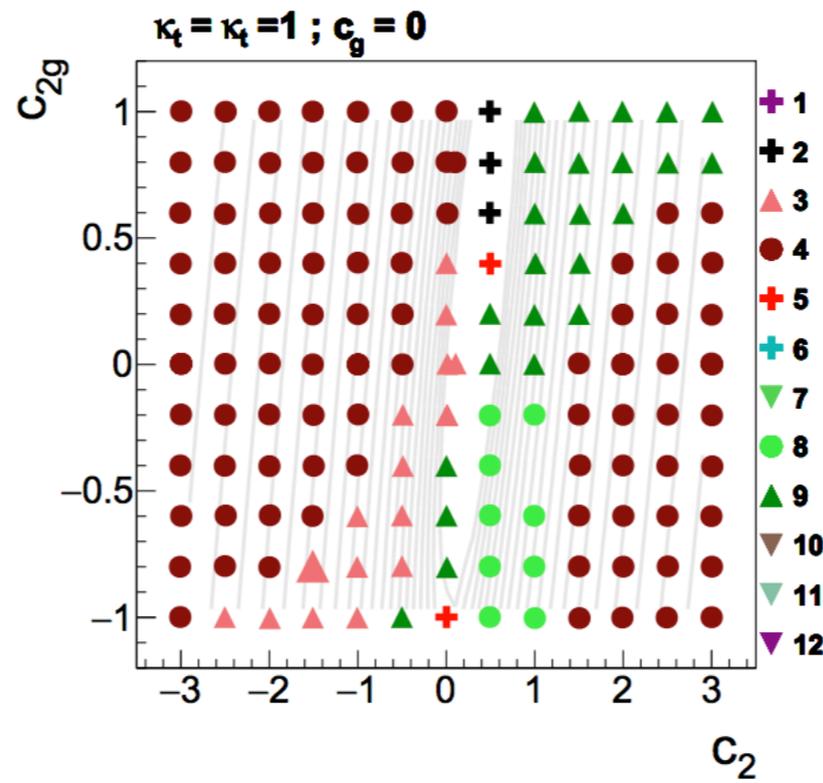
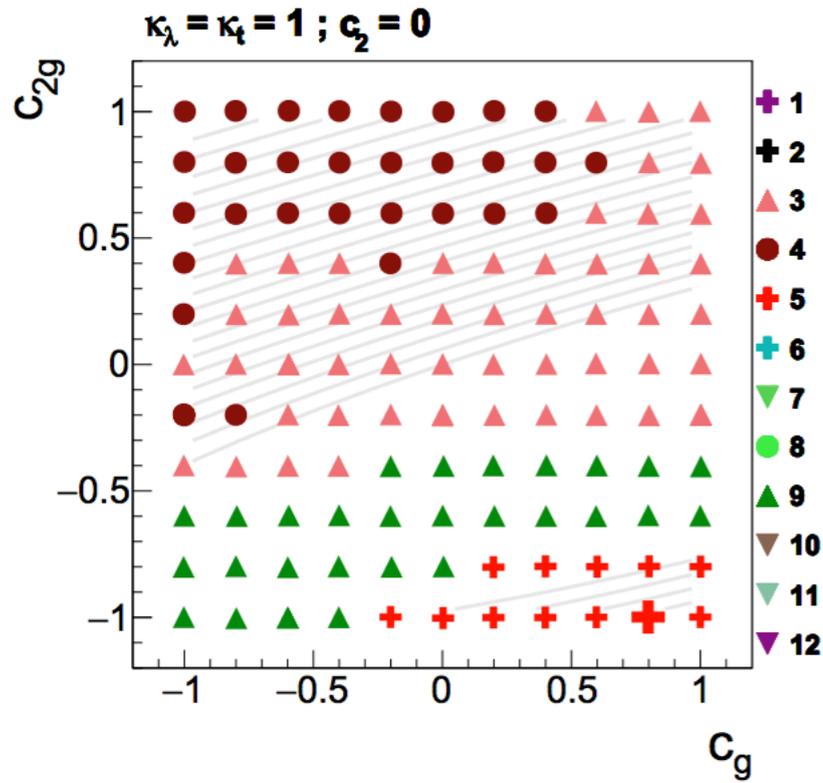
Similar weights distributions to all BMs

# Parameter space scan for clustering

The resulting population of the five-dimensional grid is admittedly arbitrary; however it is seen *a posteriori* to be able to picture reasonably well the varied spectrum of topologies of GF di-Higgs boson production. It includes  $N_{sample} = 1507$  points of the five-dimensional parameter space, composed of the following three subsets:

- We start with a geometrically well-spaced grid in the slices of Fig. 2, identified by values of  $\kappa_\lambda = 0, \pm 1, \pm 2.4, \pm 3.5, \pm 5, \pm 10, \pm 15$ ;  $\kappa_t$  from 0.5 to 2.5 in steps of 0.25 when  $|\kappa_\lambda| < 5$ , and steps of 0.5 elsewhere;  $c_2$  between  $-3.0$  and  $3.0$  in steps of 0.5;  $c_g$  and  $c_{2g}$  between  $-1.0$  and  $1.0$  in steps of 0.2.
- In some regions of parameter space (especially those with  $c_2 = 0.5$  and  $c_{2g} = \mathcal{O}(1)$ ) there is a strong cancellation between the different operators in the threshold  $m_{hh}$  region. This leads to topologies where the distribution of  $m_{hh}$  exhibits a long tail to high values<sup>9</sup>. In order to have a better kinematic description of this topology (and as well of the cancellation pattern between operators) we add to the grid one slice of parameter space with  $c_2 = 0.5$  and  $\kappa_\lambda = \kappa_t = 1$ , maintaining the previous binning in the  $c_g - c_{2g}$  plane.
- Finally, we also consider a three-dimensional grid of points described by the parameters  $\kappa_\lambda$ ,  $\kappa_t$ , and  $c_2$  in the hyperplane defined by  $c_g = c_{2g} = 0$ . The points are identified by combinations of the following parameter values:  $\kappa_\lambda = \pm 1, \pm 2.4, \pm 3.5, \pm 5, \pm 7.5, \pm 10, \pm 12.5, \pm 15$ ;  $\kappa_t$  from 0.5 to 2.5 in steps of 0.25; and  $c_2$  between  $-3.0$  and  $3.0$  in steps of 0.5. An increased density of points is allocated near the point corresponding to the SM hypothesis ( $|c_2| < 1$ ).

# Some more cluster mappings...



# Some more cluster mappings...

