

Bounding the Higgs width using $H \Rightarrow VV$

Ciaran Williams

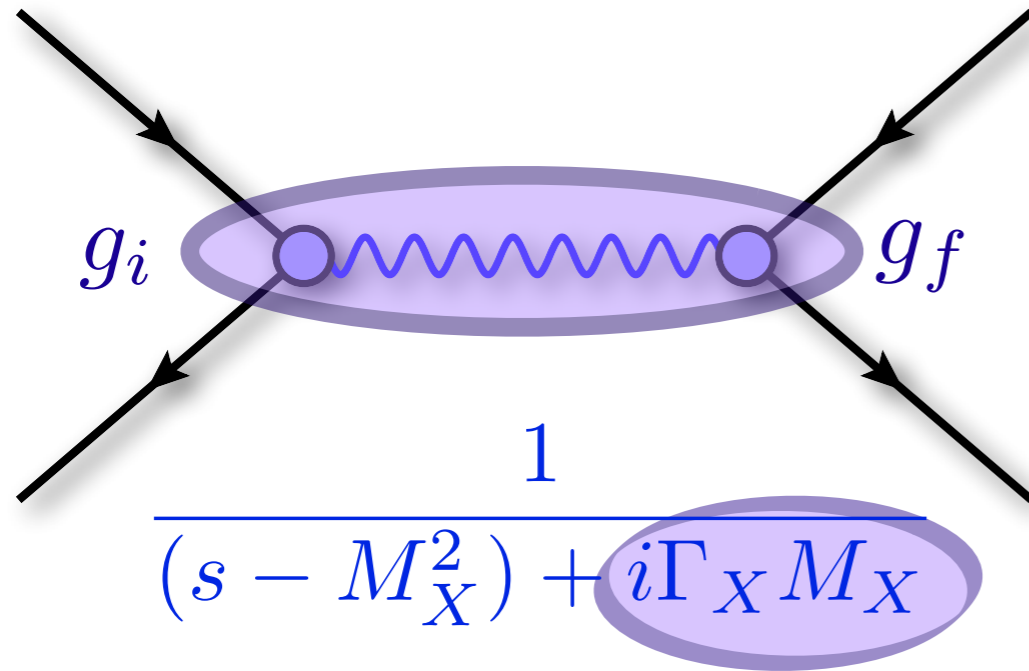
Niels Bohr Institute

With John Campbell and Keith Ellis
(1311.3589 and 1312.1628)



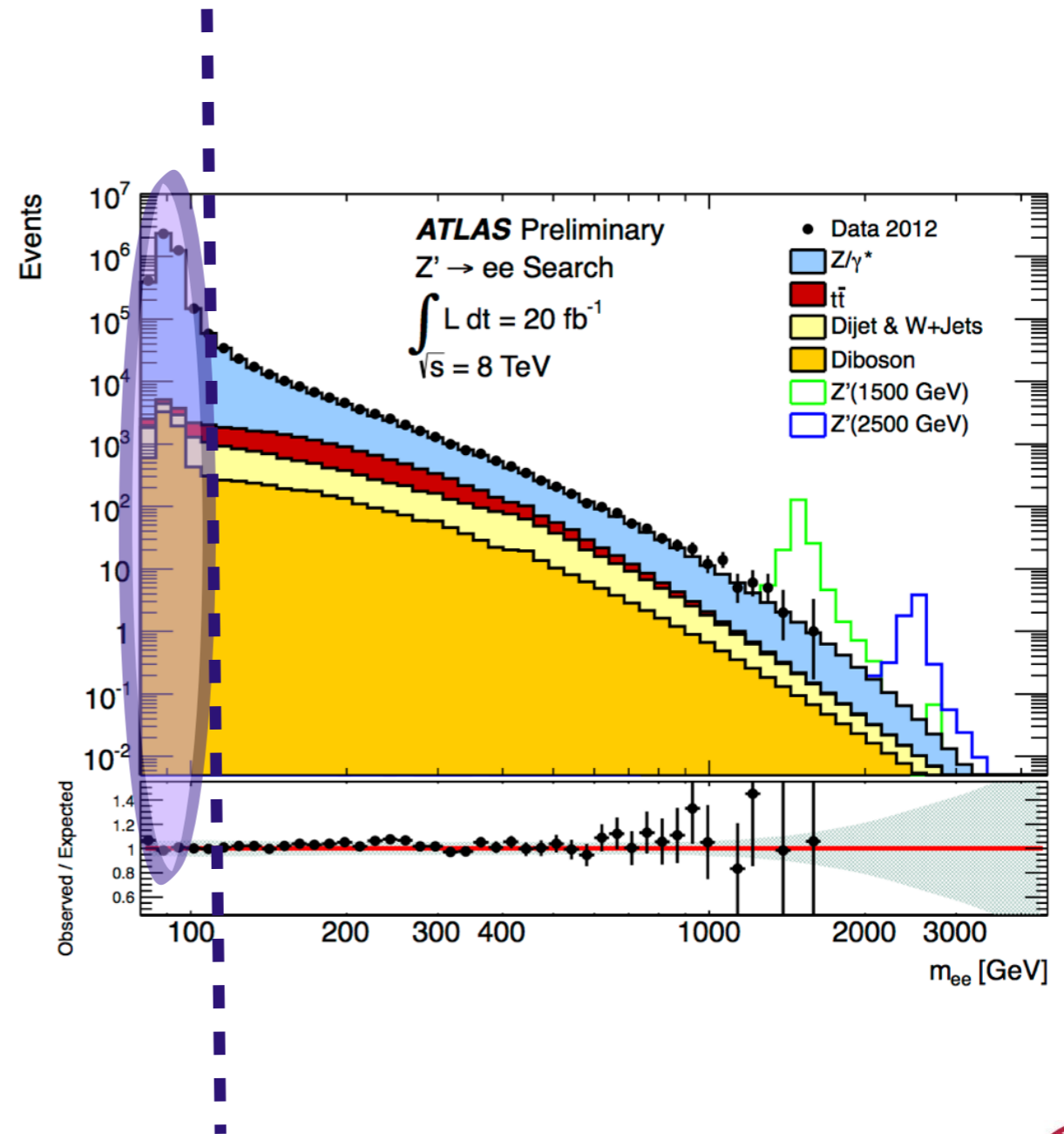
Bounding the Width Using the Off-shell Cross Section

(CW, Campbell, Ellis 11)
 (Kauer, Passarino 12)
 (Caola, Melnikov 13)
 (CW, Campbell, Ellis 13)



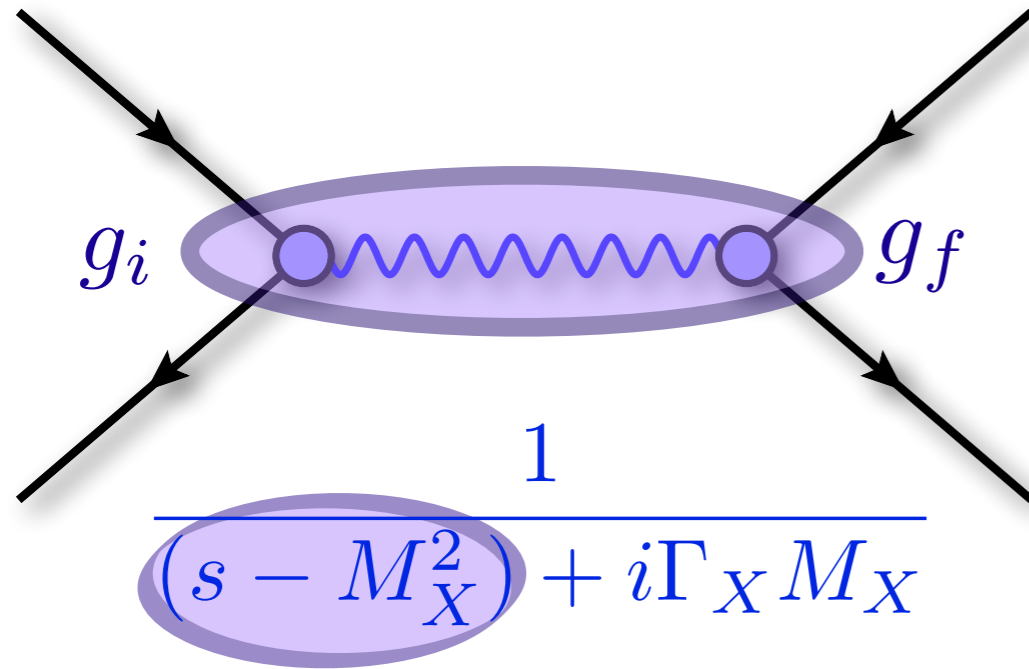
In the resonance region the “on-shell” cross section is dominated by the width.

$$\sigma_{i \rightarrow X \rightarrow f}^{on} \sim \frac{g_i^2 g_f^2}{\Gamma_X}$$



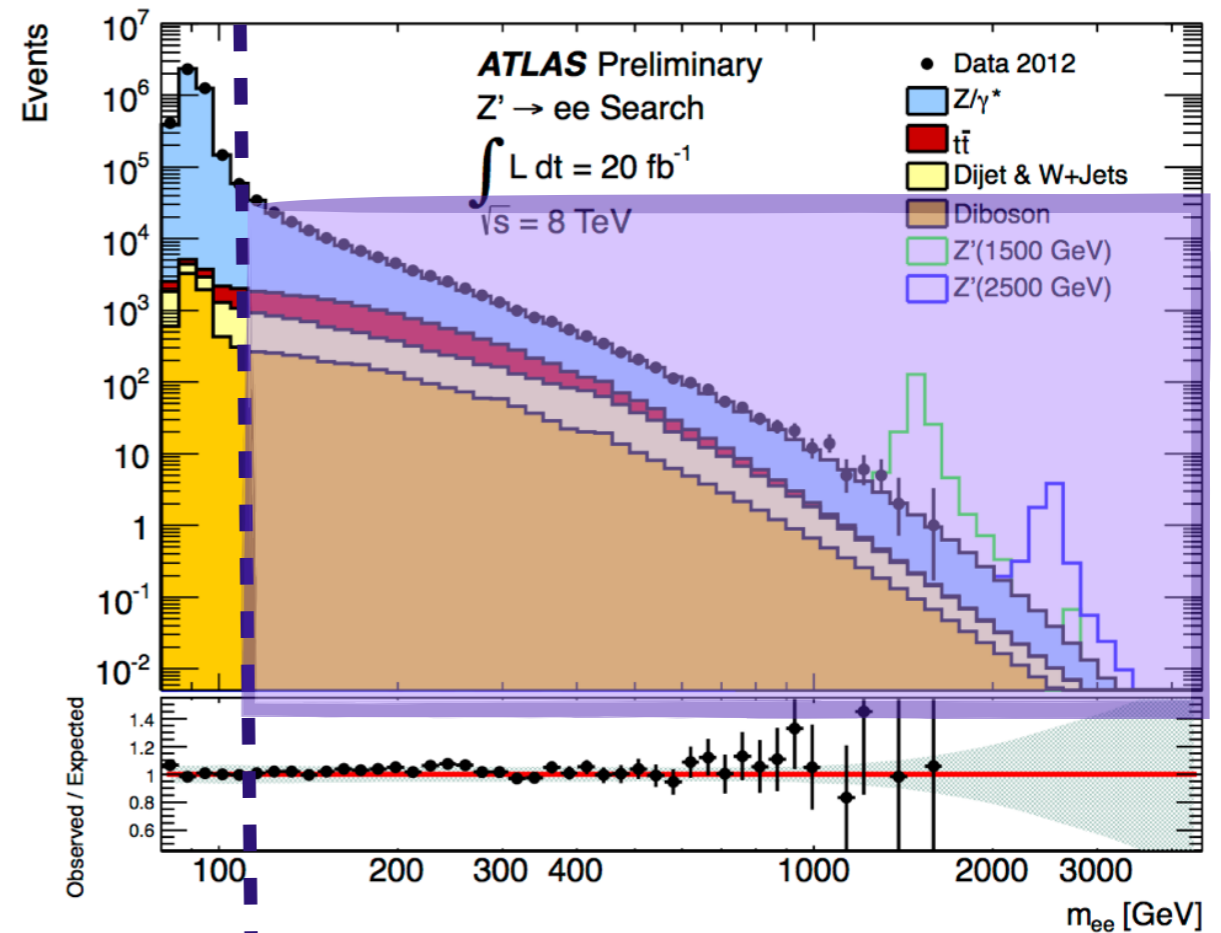
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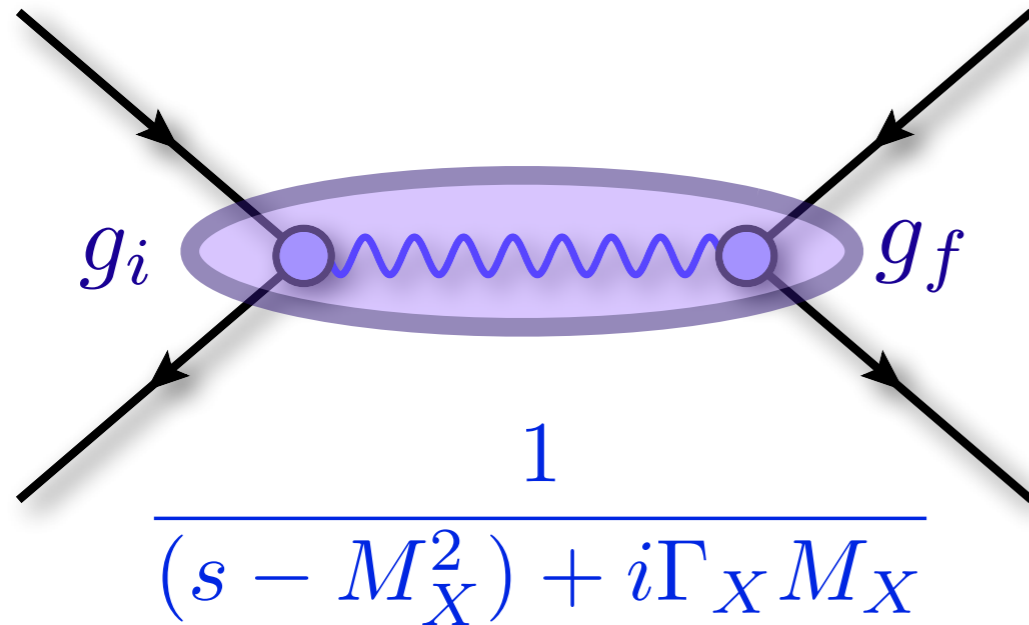
Away from the resonance region, the “off-shell” cross section does not depend on the width.

$$\sigma_{i \rightarrow X \rightarrow f}^{off} \sim g_i^2 g_f^2$$



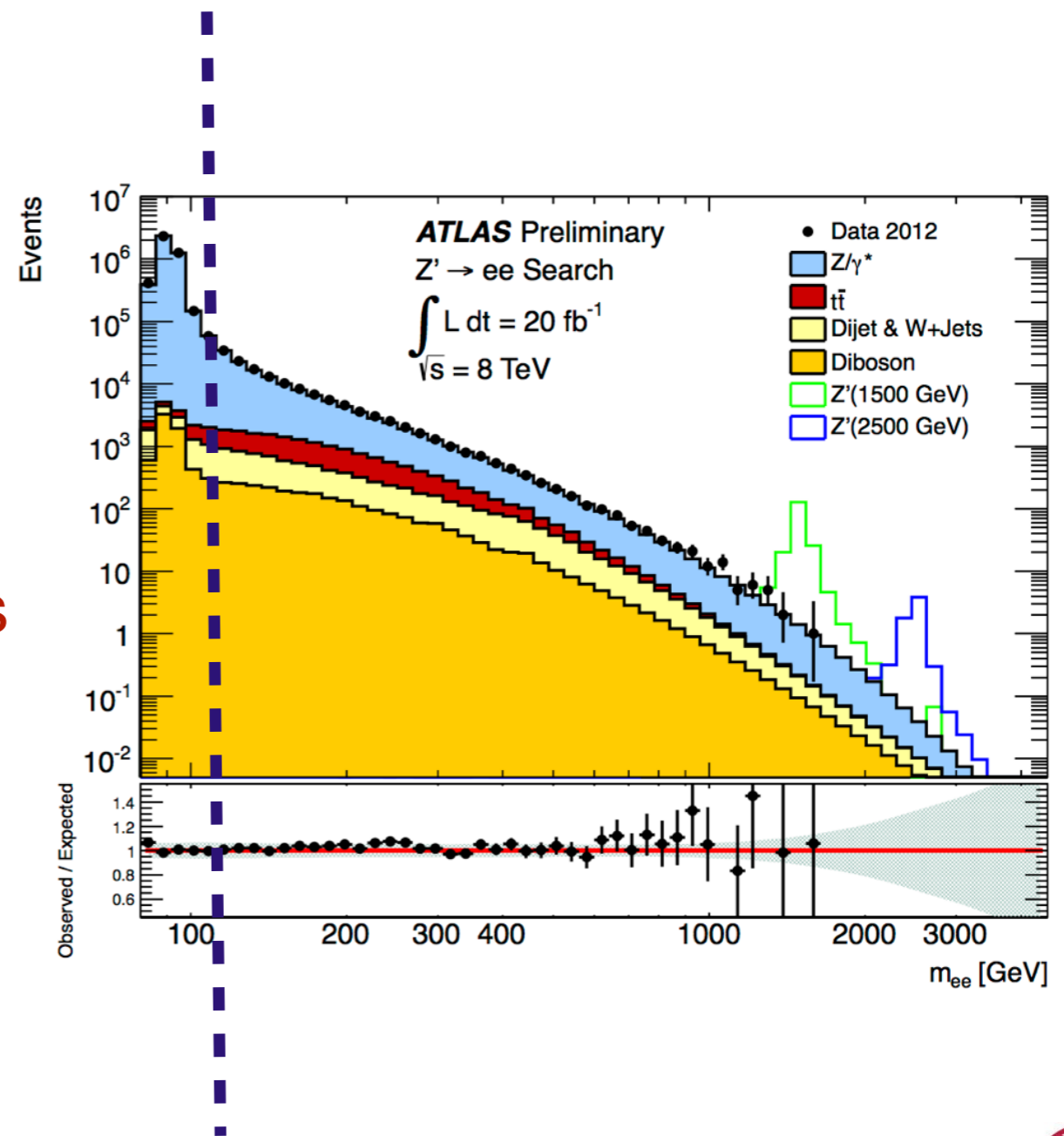
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The ratio of these cross sections is therefore dependent on the width and *independent* of the couplings.

$$\frac{\left(\frac{\sigma_{off}}{\sigma_{on}}\right)_{exp}}{\left(\frac{\sigma_{off}}{\sigma_{on}}\right)_{SM}} \propto \frac{\Gamma_X}{\Gamma_X^{SM}}$$

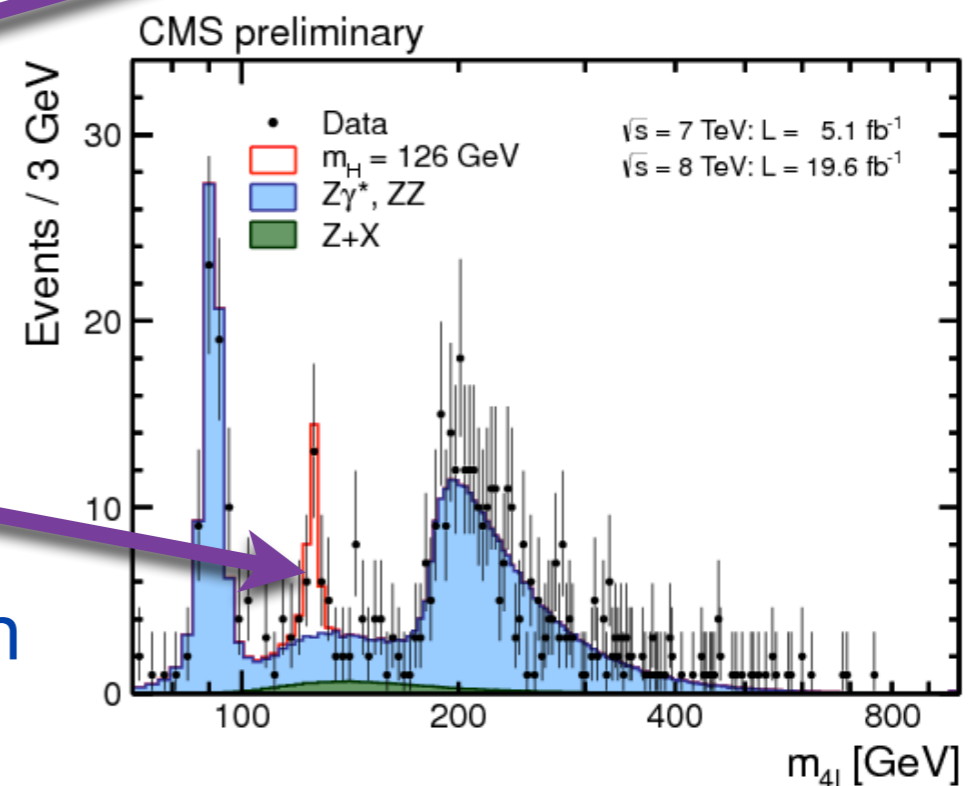
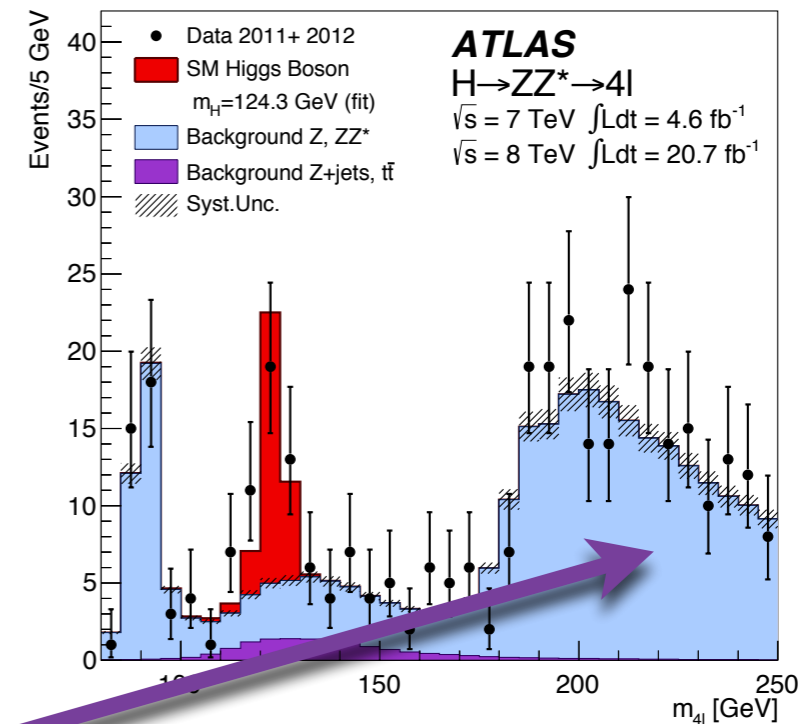


Applications to the Higgs

- Off-shell we know only at LO (incl intf)

$$\frac{\left(\frac{\sigma_{off}}{\sigma_{on}}\right)_{exp}}{\left(\frac{\sigma_{off}}{\sigma_{on}}\right)_{SM}} \propto \frac{\Gamma_X}{\Gamma_X^{SM}}$$

- We know the on-shell cross section very well, can use NNLO rate etc.



What about K-factors ?

Personally, I think that a central (dynamic) scale should be chosen such that,

$$\sigma_{LO}^{on}(\mu_{NNLO}) \sim \sigma_{NNLO}^{on}(\mu_{NNLO})$$

This is in some ways equivalent to including a NNLO K-factor (at least in the on-shell regime).

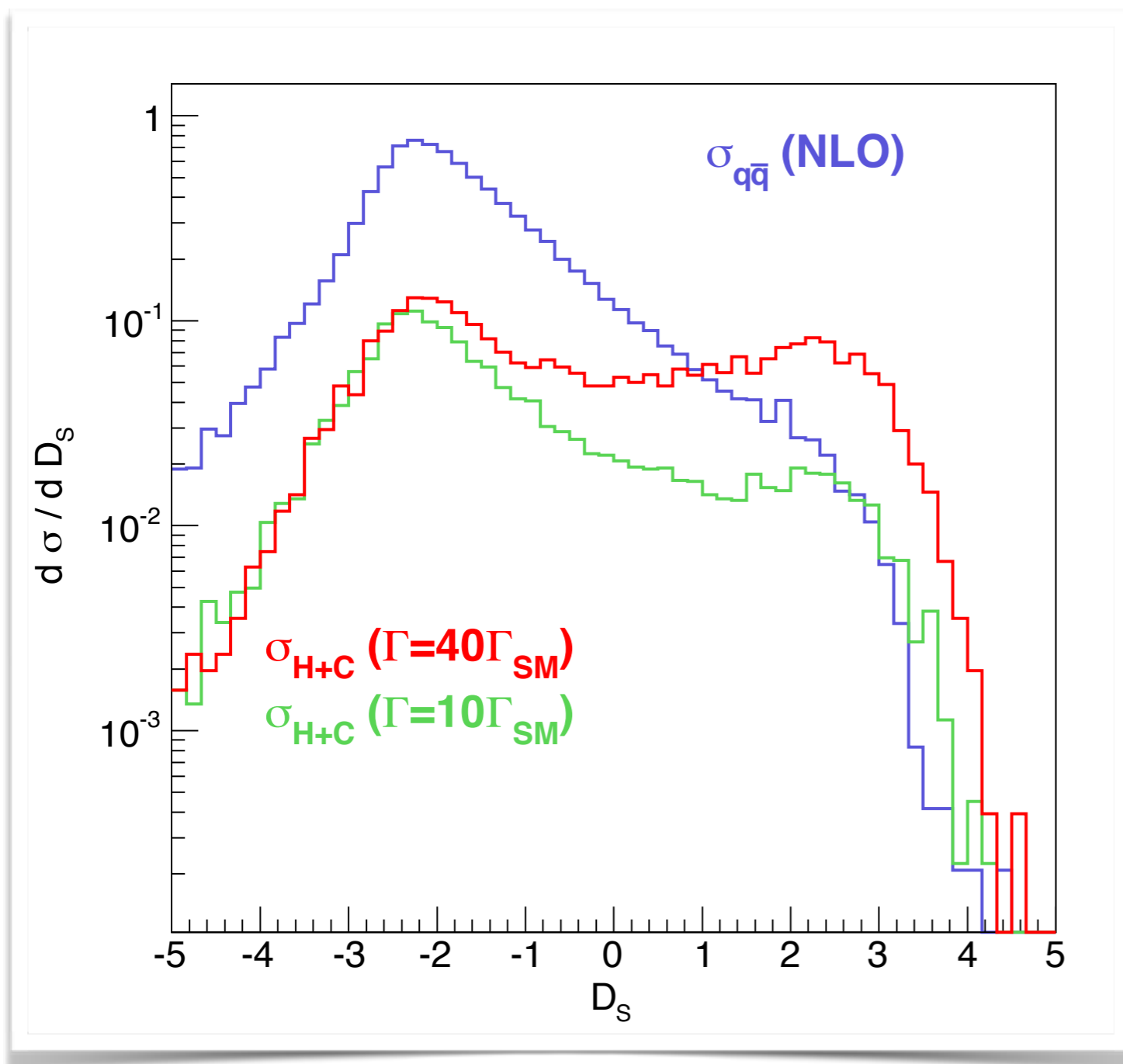
Then in the off-shell region we use the same form of scale, i.e.

$$\sigma_{LO}^{off}(\mu_{NNLO})$$

But use the usual LO scale variation as an indicator of uncertainty (i.e an envelope of $\{1/2, 2\}$)



Systematics of the MEM



MEM discriminant

$$D_S = \log \left(\frac{P_H}{P_{gg} + P_{q\bar{q}}} \right)$$

Is not sensitive to scale since

$$P_X \sim \frac{|\mathcal{M}_X|^2}{\sigma_X}$$

In fact for fixed scale choice dependence on α_S drops out.

Therefore systematics are the same as the usual analysis, i.e. normalization of gluon induced samples versus qq̄.

