Learning more about Simplified Models with 3D parameter scans

Thomas Jacques
Amelia Brennan
Johanna Gramling
Millie McDonald
Karl Nordstrom

JHEP 1506 (2015) 142 (arXiv:1502.05721), arXiv:1603.01366

2016-06-22 DM WG

Introduction

Thomas Jacques

- We simply do not know the correct model and properties of the dark sector, so experimental searches should convey as much information as possible

- This is best done through searches for a series of EFTs, simplified models and UV complete theories, as well as presenting the information necessary for a recast
  *See talks from "Reinterpreting LHC searches for DM models" workshop last week, including talk by Felix Kahlhoefer, for more context on the role of simplified models

- As part of this effort, how can we convey more information about simplified models?

Simplified Models

Thomas Jacques

- At the most general level, even the simplest of simplified models has a large number of parameters; e.g. in a naive Z' model, including couplings to both quarks and leptons, there are up to 28 free parameters

- Necessary to make simplifying assumptions to keep the number of parameters small; e.g. in monojet Z' searches,

I. Examine vector and axial-vector individually: $c^q_A = c^\chi_A = 0$ or $c^q_V = c^\chi_V = 0$

II. MET searches for quark coupling, so assume $g_l = 0$

III. 'Minimal Flavor Violation': g_q equal for each quark

$$\mathcal{L} \supset g_\chi Z'_\mu (c^\chi_V \bar{\chi}\gamma^\mu\chi + c^\chi_A \bar{\chi}\gamma^\mu\gamma^5\chi)$$
$$+ \sum_q g_q Z'_\mu (c^q_V \bar{q}\gamma^\mu q + c^q_A \bar{q}\gamma^\mu\gamma^5 q)$$
$$+ \sum_l g_l Z'_\mu (c^l_V \bar{l}\gamma^\mu l + c^l_A \bar{l}\gamma^\mu\gamma^5 l)$$

Vector

Axial-vector

Simplified Models

Thomas Jacques

- Given these simplifying assumptions, we should convey as much info as possible about the remaining parameters

- Currently, the recommendation is to start with one set of semi-arbitrary couplings (e.g. g_q=0.25, g_{DM}=1) and scan over masses (m_{DM}, M_{med})

- Alternative is to reparameterise to

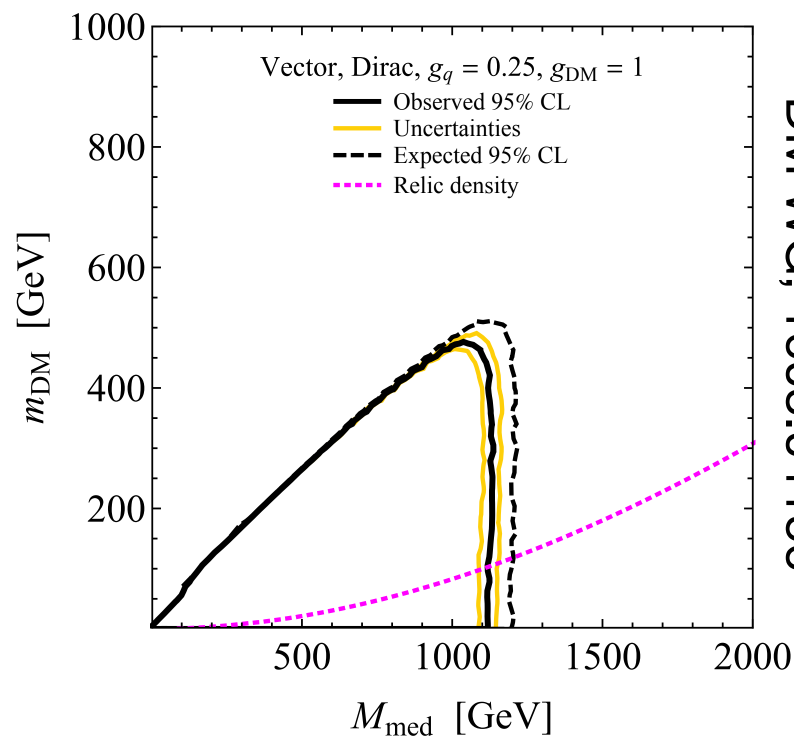
$$\left\{m_{\rm DM},\, M_{\rm med},\, g_{\rm DM},\, g_{\rm SM}\right\} \to \left\{m_{\rm DM},\, M_{\rm med},\, g_{\rm DM}{\cdot}g_{\rm SM},\, g_{\rm DM}/g_{\rm SM}\right\}$$

and scan over (m_{DM}, M_{med}, $g_{DM}.g_q$) for fixed g_{DM}/g_q

Comparing the options

Thomas Jacques

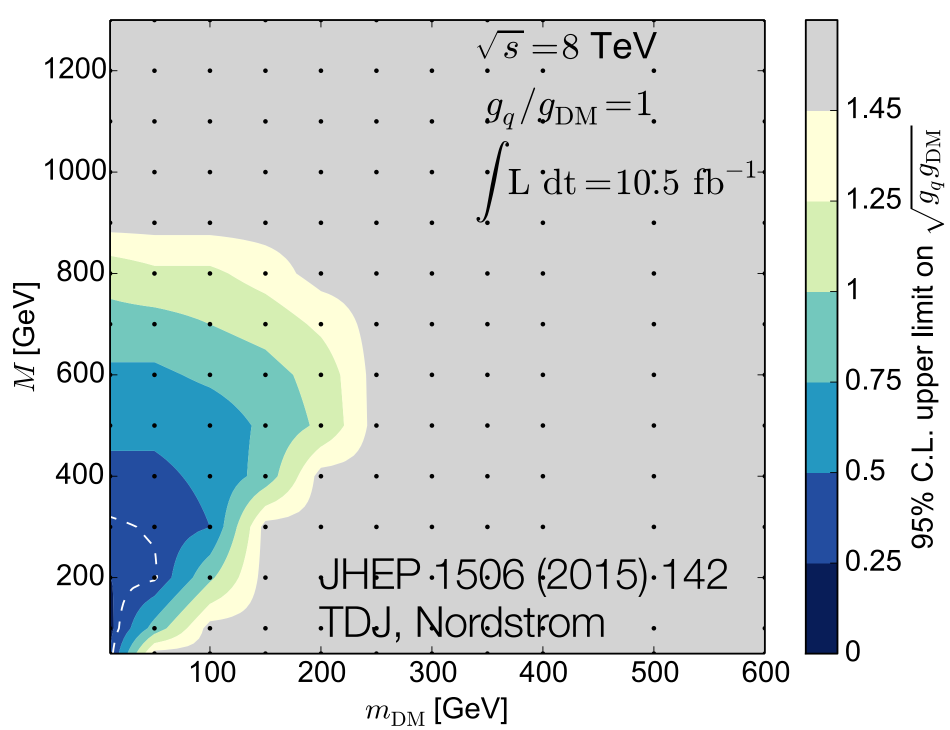
Benchmark coupling



DM WG, 1603.04156

- ✓ Only 2 parameters to scan
- ✓ Easier comparison between experiments
- ✗ Semi-arbitrary choice of coupling
- ✗ Less comprehensive: Difficult to translate to other couplings

3-D scan

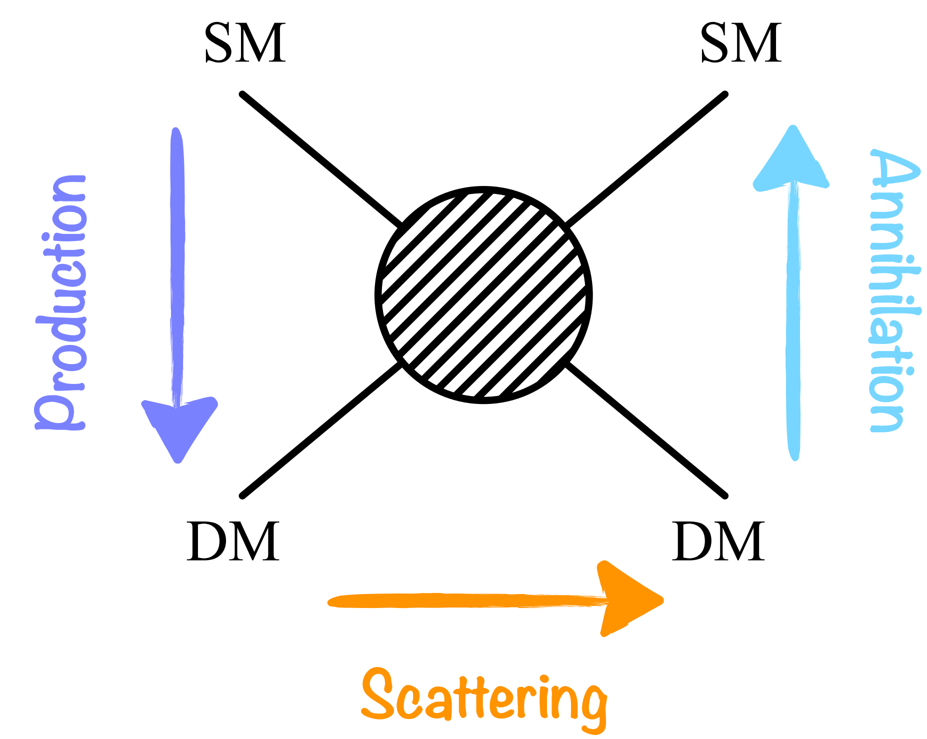


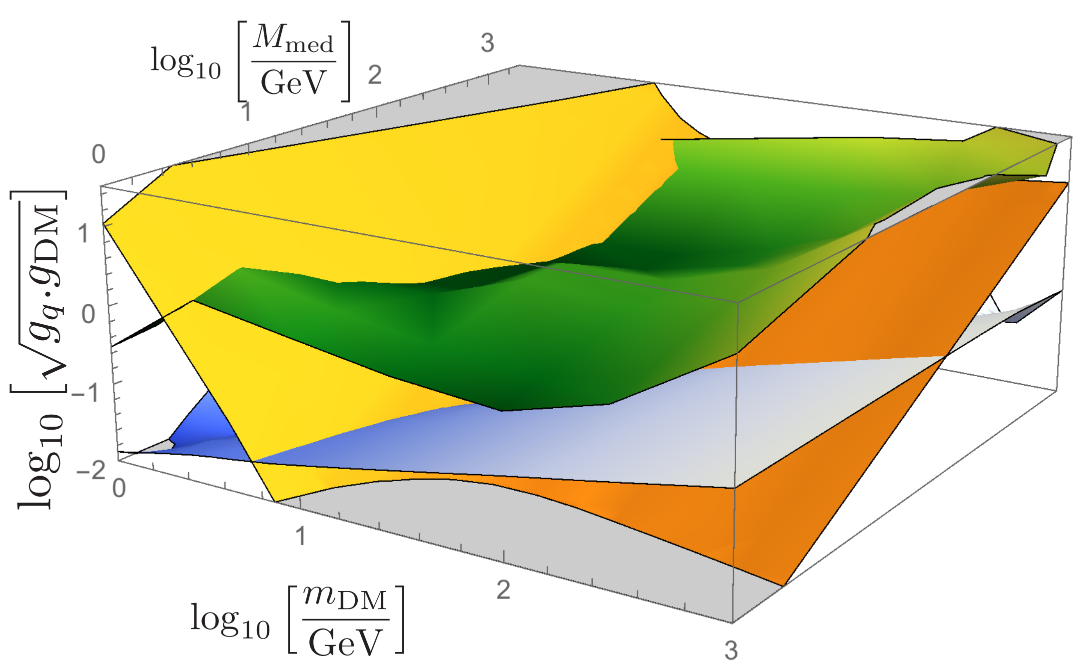
- ✓ Easy to interpret
- ✓ More comprehensive
- ✗ Difficult to compare results
- ✗ Scan over parameter space more challenging

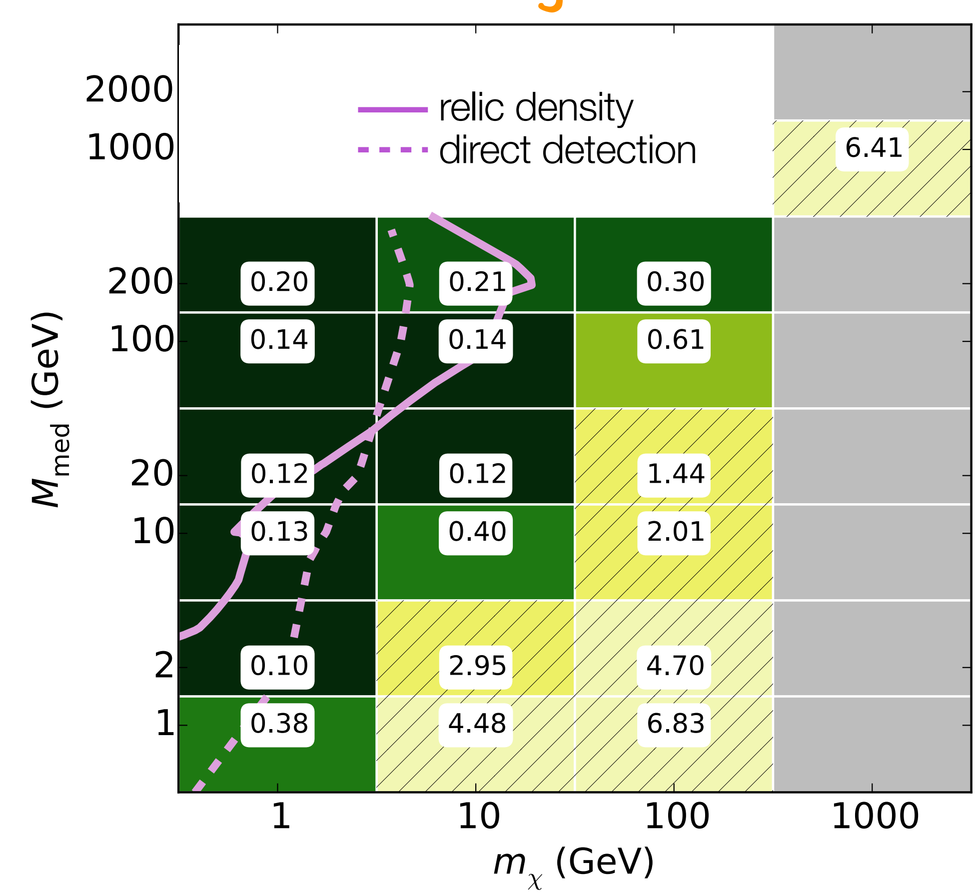
Comparing to other constraints

Thomas Jacques

- Difficult to compare multiple constraints in 3D parameter space!
- Intercept shows the boundary where one constraint becomes stronger than another, indicating the region where each class of constraints performs best







Brennan et al. arXiv:1603.01366

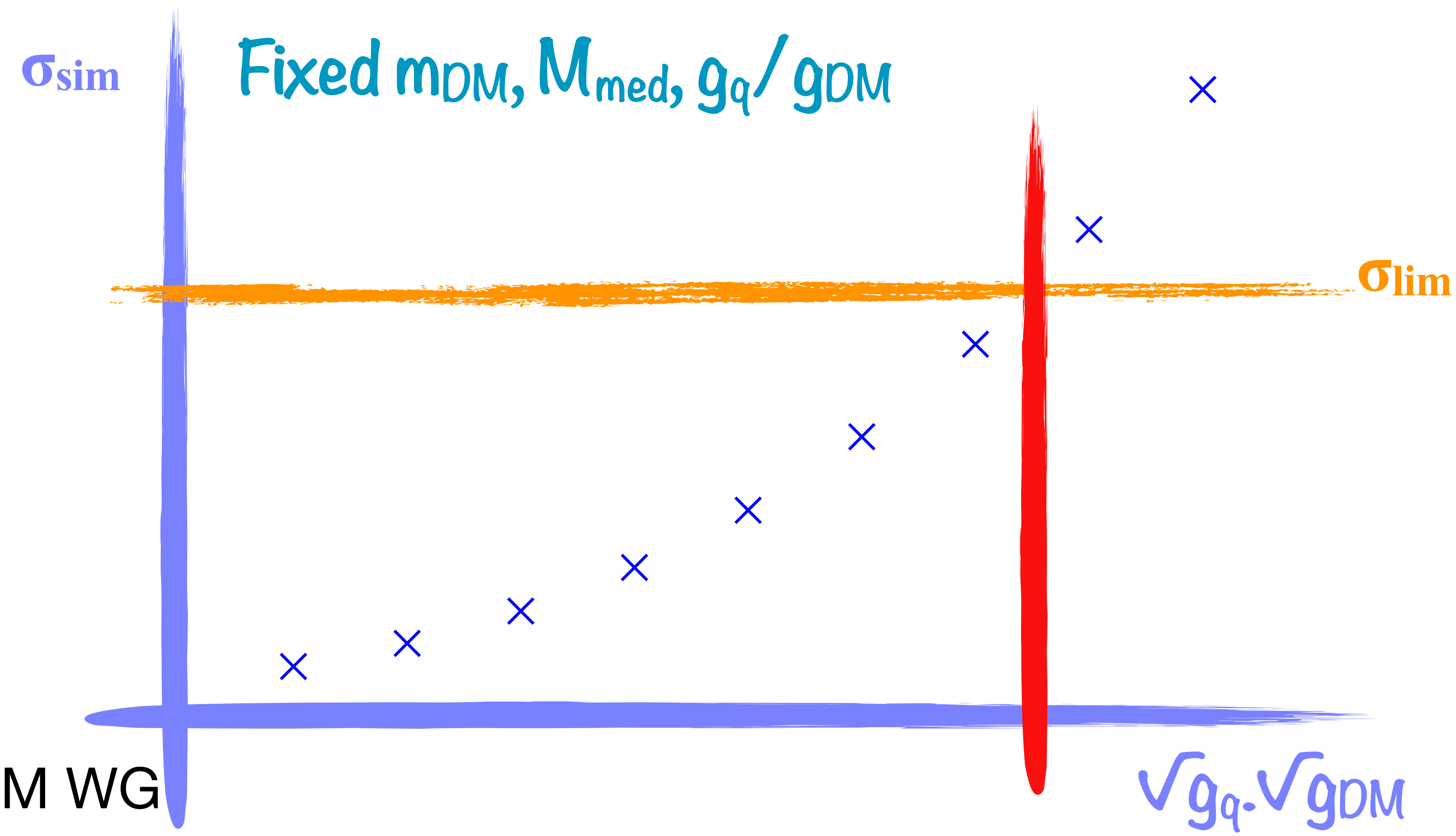
Rescaling relations

Thomas Jacques

$$\left\{m_{\rm DM},\, M_{\rm med},\, g_{\rm DM},\, g_{\rm SM}\right\} \rightarrow \left\{m_{\rm DM},\, M_{\rm med},\, g_{\rm DM}{\cdot}g_{\rm SM},\, g_{\rm DM}/g_{\rm SM}\right\}$$

For each $\{m_{DM}, M_{med}, g_q/g_{DM}\}$, simulate signal cross section σ_{sim} for a range of $g_q.g_{DM}$, compare with the experimental limit σ_{lim}.

Value of $g_q.g_{DM}$ where $\sigma_{sim} = \sigma_{lim}$ defines the constraint on $g_q.g_{DM}$.

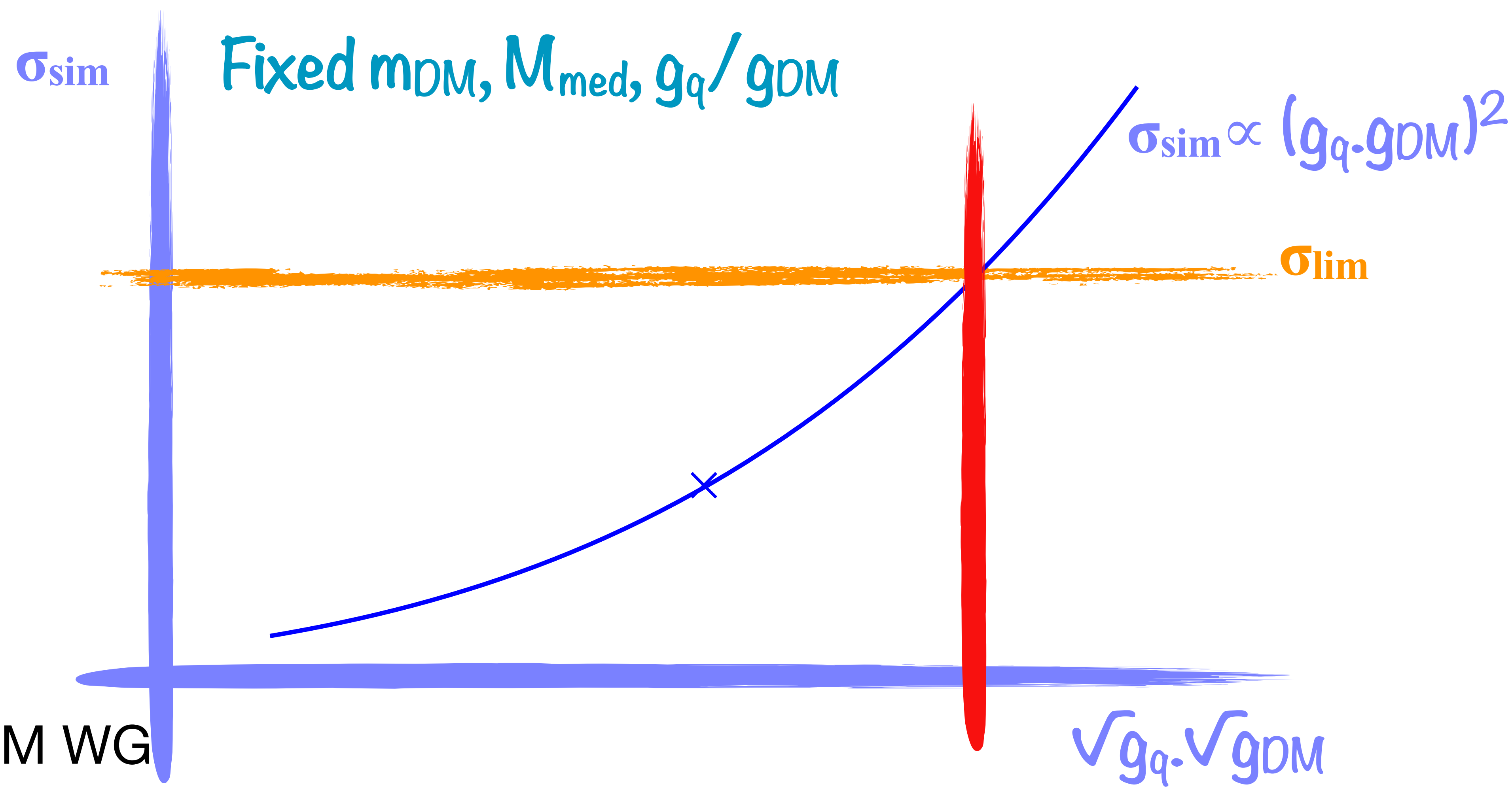


Rescaling relations

Thomas Jacques

If we know how σ_{sim} varies with $g_q.g_{DM}$, we can simulate for one value of $g_q.g_{DM}$, avoiding the full scan

This is not always straightforward!



How good is the rescaling?

Thomas Jacques

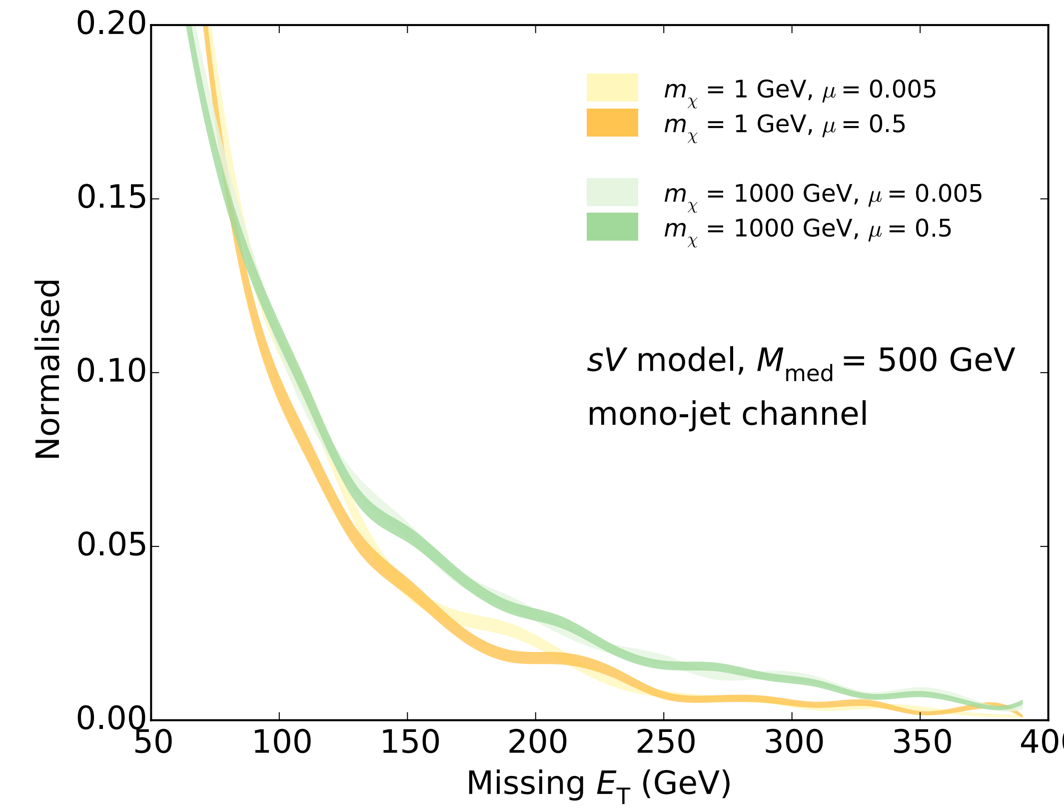
- What is the rescaling relation?

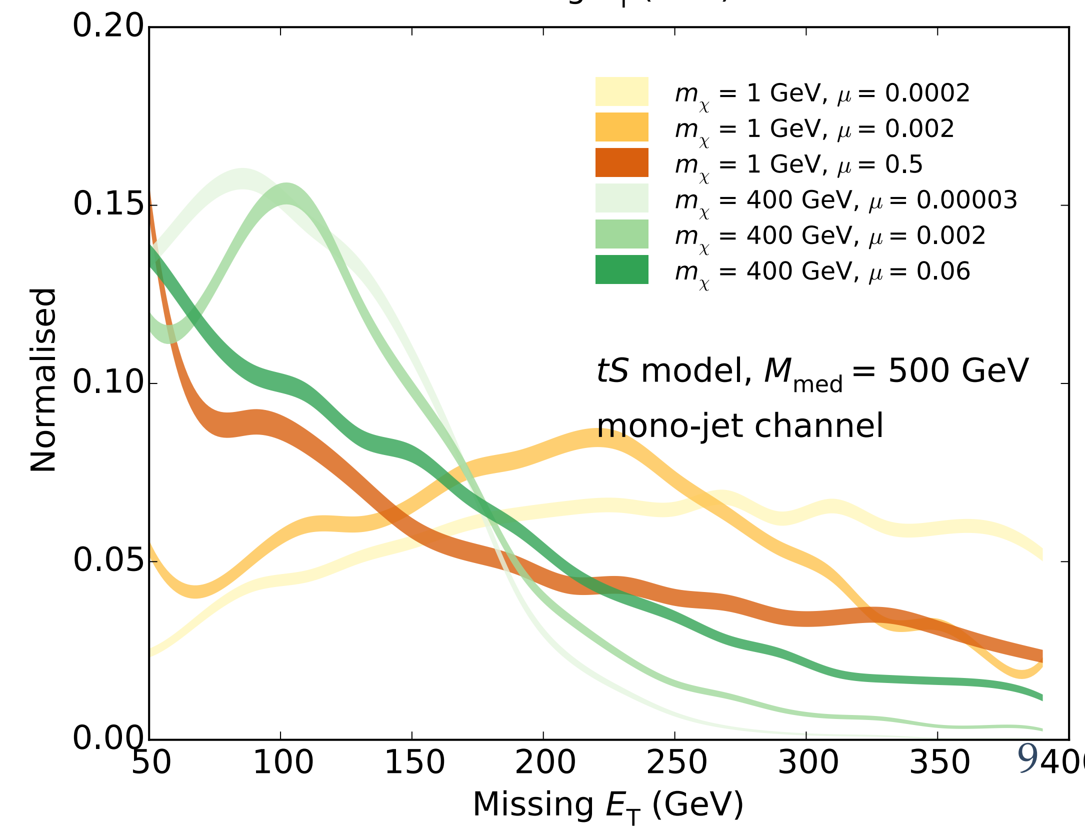
$$\sigma \propto \begin{cases} g_q^2 g_{\rm DM}^2/\Gamma_{\rm OS} & \text{if } M > 2m_{\rm DM} \\ g_q^2 g_{\rm DM}^2 & \text{if } M < 2m_{\rm DM} \end{cases}$$

- Holds only if the kinematic distribution of missing energy is independent of the width

$$\sigma \propto \frac{g_{\rm DM}^2 g_q^2}{(s-M^2)^2 + M^2\Gamma^2},$$

- Kinematic behaviour not greatly affected for on-shell s-channel models when $\Gamma/M_{med}<0.5$
- t-channel: additional monojet diagrams with on-shell mediator
    - Peak shape strongly depends on Γ/M_{med}! Coupling scan absolutely needed



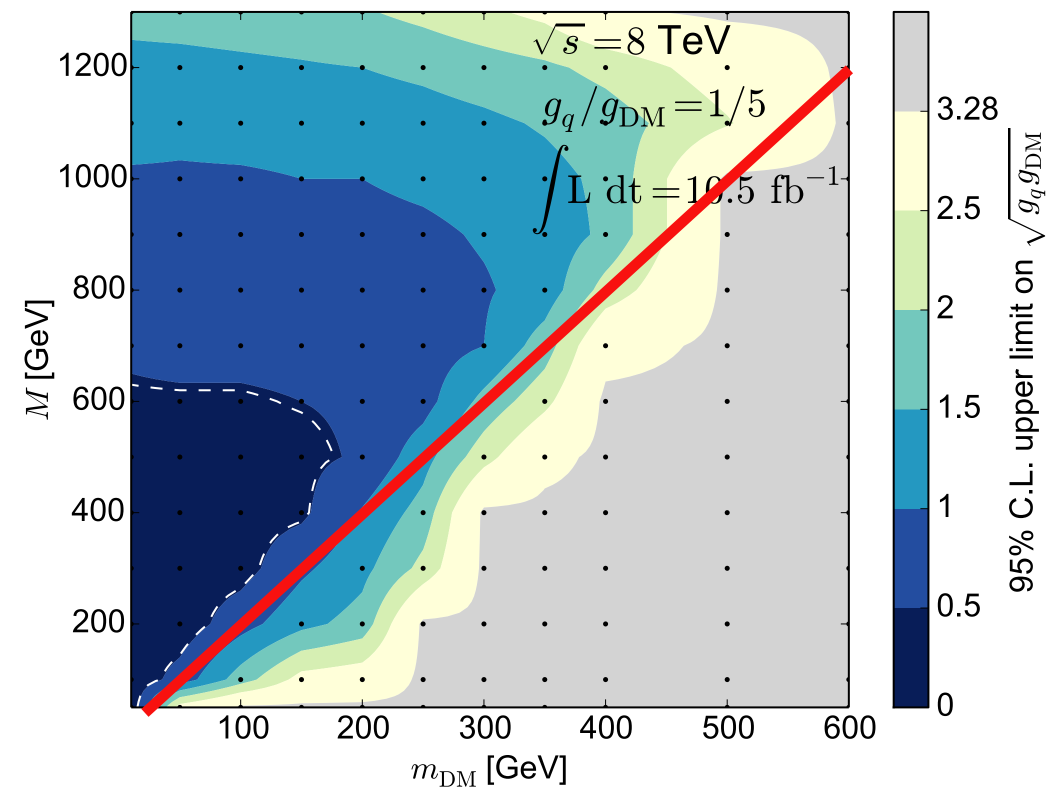


Brennan et al. arXiv:1603.01366

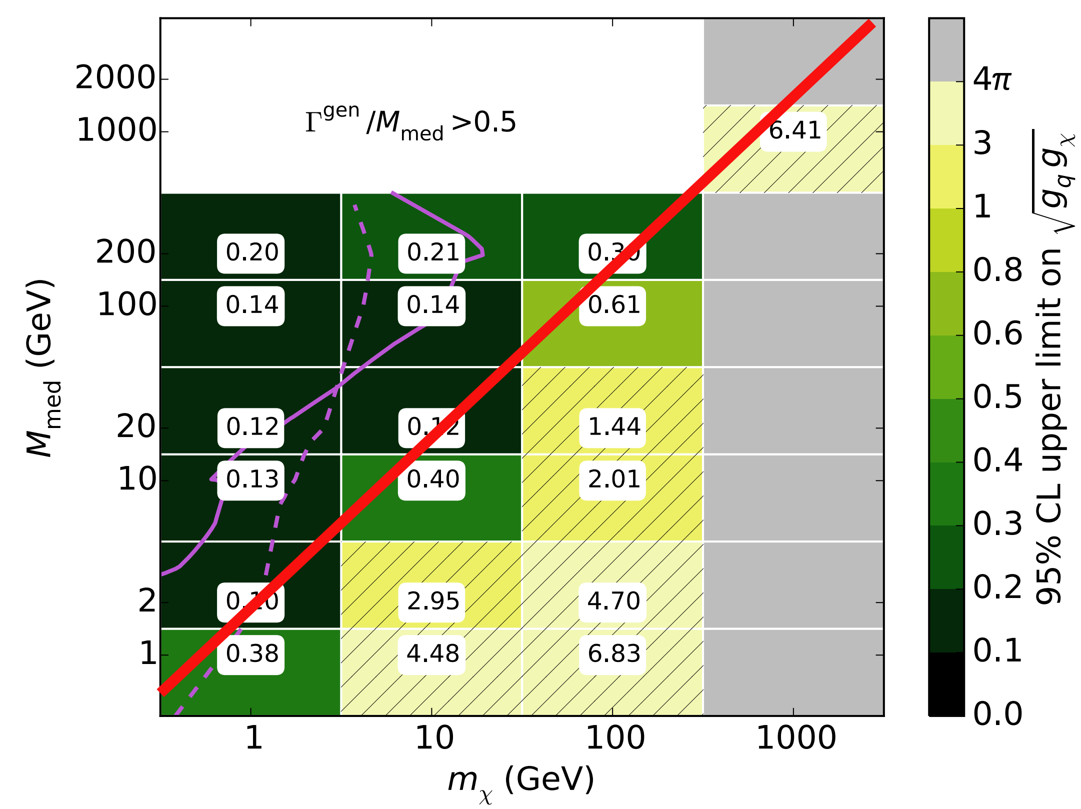
How good is the rescaling?

Thomas Jacques

- Distinguish 3 regions:
  - **On shell** ($M_{med} > 2m_{DM}$)
    → above red line
    - strong limits, weaker for high masses
    - Ensure Γ/M_{med}<0.5 at generation
  - **Off shell** ($M_{med} < 2m_{DM}$)
    →below red line
    - Pair production of DM turns off, limits weaken
    - Many points with $\Gamma/M_{med} > 0.5$
  - **Transition region**
    →near red line



TJ, Nordstrom arXiv:1502.05721

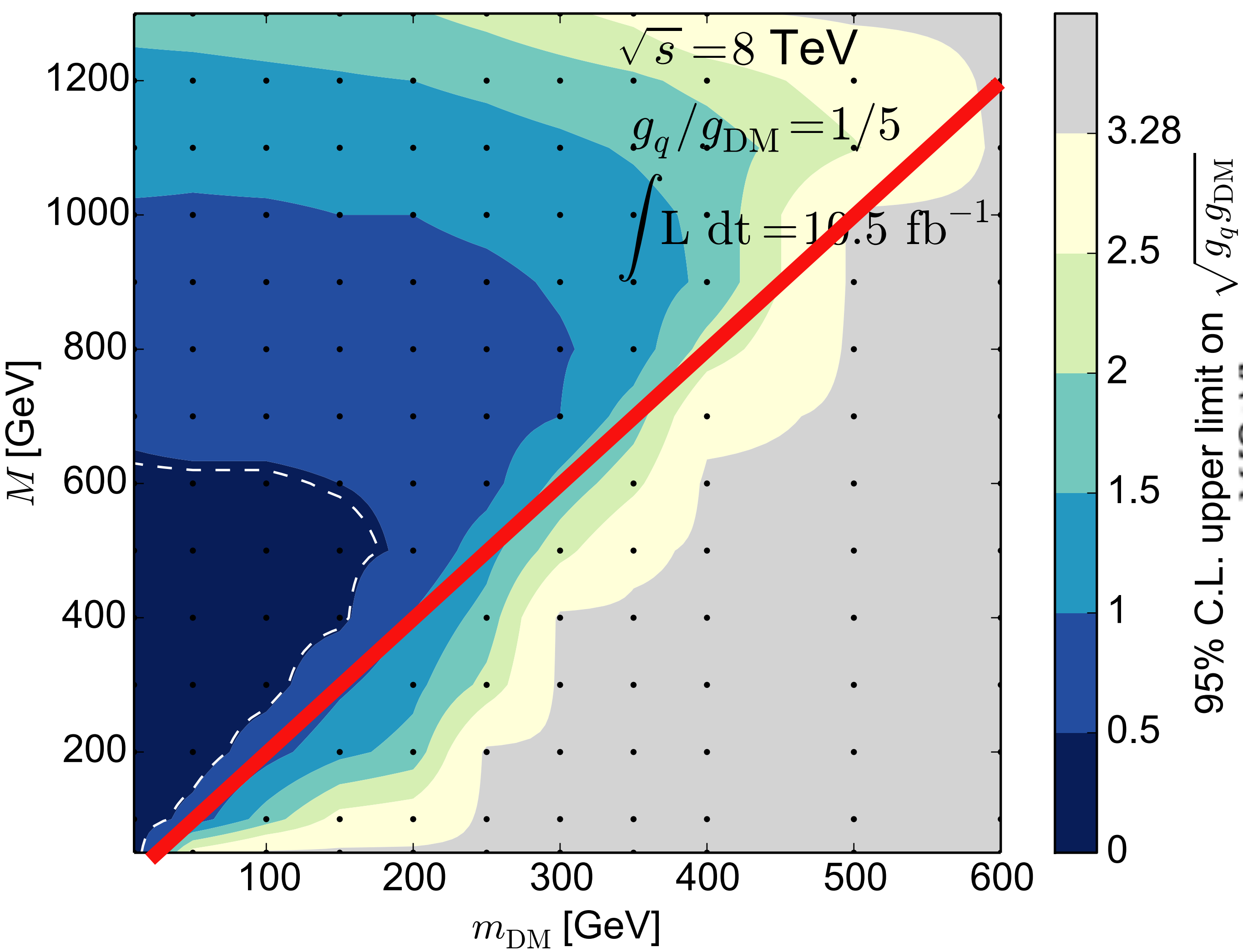


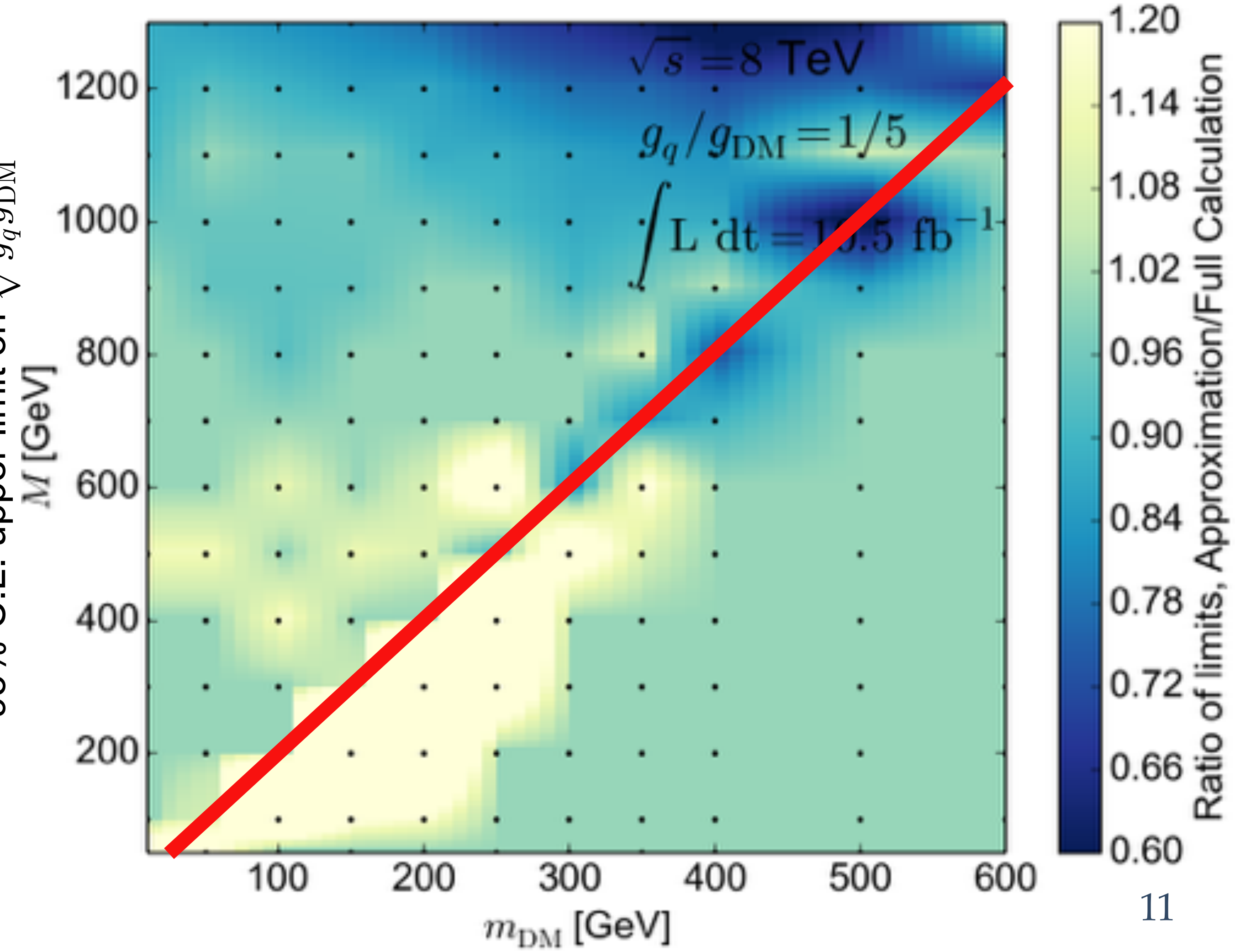
Brennan et al. arXiv:1603.01366

How good is the rescaling?

SISSA
Thomas Jacques

- Main indicator for validity of the rescaling is the **size of the width**
- OK for central **on-shell** region where constraints are strong and width is small
    - At large mediator masses, constraint becomes weaker, width becomes large, rescaling breaks down
- In **off-shell** region, rescaling works well if width is small, but constraints are weak and width is usually large
- Rescaling breaks down in **transition region**





Morphing

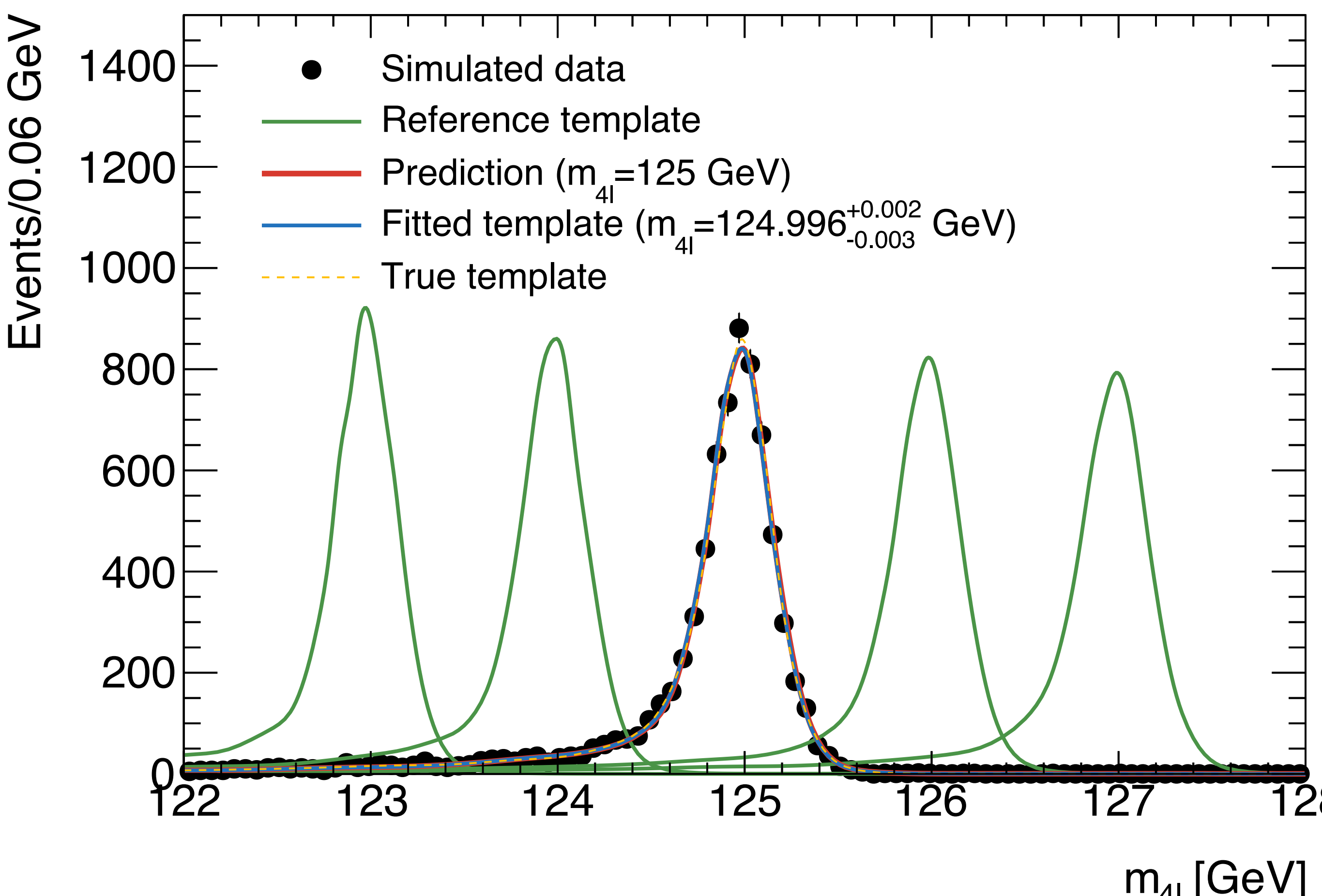
Thomas Jacques

- Method for estimating physical distributions as a continuous function of an arbitrary number of theoretical parameters using non-linear interpolation between a number of input distributions, or factorising out dependence on mediator mass before generation

- Would allow regions where rescaling fails to be investigated for a reasonable computational cost

- Only works in regions with smooth change in distribution

- In use by other analyses



Baak et al, arXiv:1410.7388

Conclusion

Thomas Jacques

- Current DMWG recommendation of benchmark couplings severely limits the scope of constraints on simplified models
- To get constraints on a 3D parameter space, it will be necessary to increase the dimension of the scan in some regions
- A combination of rescaling and morphing can offset this cost by reducing the size of the scan
- Rescaling works well when iff: the width is small, the model is FSR only, and away from transition between on- and off-shell region
- Further study required to determine how tight the scan points need to be for morphing to be effective
- Complementary to other efforts to convey more information to the community