

Flavor-violating squarks @ the LHC

Abishek, Amit, Benjamin, Björn, Giacomo, Mihoko, Motoi, Priscilla, Ramona

- Squarks are admixtures of different flavors
- Simplified model: right stop-scharm mixing

$$\begin{pmatrix} \tilde{u}_1 \\ \tilde{u}_2 \end{pmatrix} = \begin{pmatrix} \cos \theta_{tc} & \sin \theta_{tc} \\ -\sin \theta_{tc} & \cos \theta_{tc} \end{pmatrix} \begin{pmatrix} \tilde{c}_R \\ \tilde{t}_R \end{pmatrix}$$

- 3D parameter space (2 masses, one mixing angle)
 $m_{\tilde{u}_1}, m_{\tilde{u}_2}, \theta_{tc}$

- Possible flavor-violating decays: $\tilde{u}_i \rightarrow t + \cancel{E}_T$ or $c + \cancel{E}_T$

- Signatures

$$t\bar{t} + E_T^{miss} \triangleright 1407.0583$$

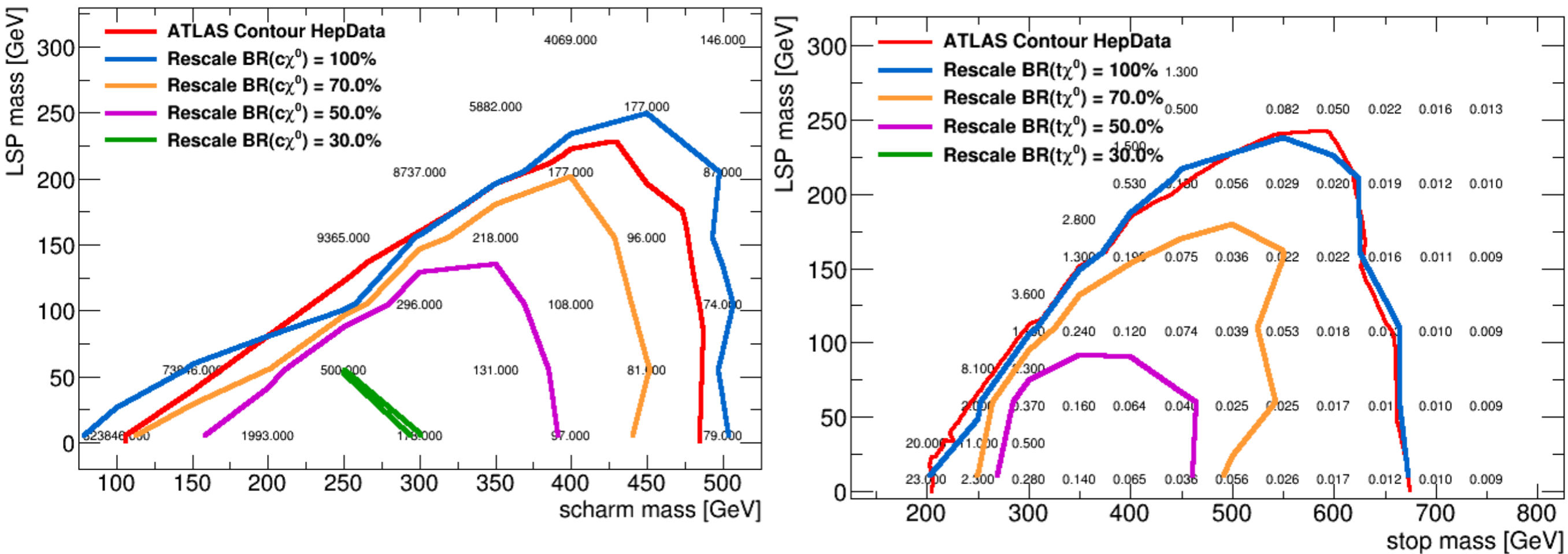
$$c\bar{c} + E_T^{miss} \triangleright 1501.01325$$

$$c + t + E_T^{miss} \triangleright \text{Monotops?}$$

Objectives:

- Coverage of current searches ?
- Potential of a dedicated top-charm analysis

Rescaling the limits



Rescaled using HepData from Run 1 references

Assumptions:

- Only one particle (u1)
- No contamination of $tt+\text{MET}$ from $cc+\text{MET}$ and $ct+\text{MET}$ and viceversa

Next steps

- Prepared a code that calculates all BR for all $u1/u1$ assumptions
- Implementing acceptance x efficiency from HepData of stop and scharm analyses
- Obtaining exclusions vs $u1/u2/\alpha$ from UL

```
BR1 BR2 alpha, u1, u2, signal, accepted?  
1.0 500 800 signal = 6.46800075688 excluded  
1.0 550 800 signal = 6.41650897439 excluded  
1.0 600 800 signal = 5.39521717792 excluded  
1.0 650 800 signal = 4.08024491753 not excluded  
1.0 700 800 signal = 3.06534614271 not excluded  
1.0 750 800 signal = 2.25312782681 not excluded  
1.0 800 800 signal = 1.47807430705 not excluded
```