Prospects for future SUSY searches with SmodelS

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Contents

SmodelS

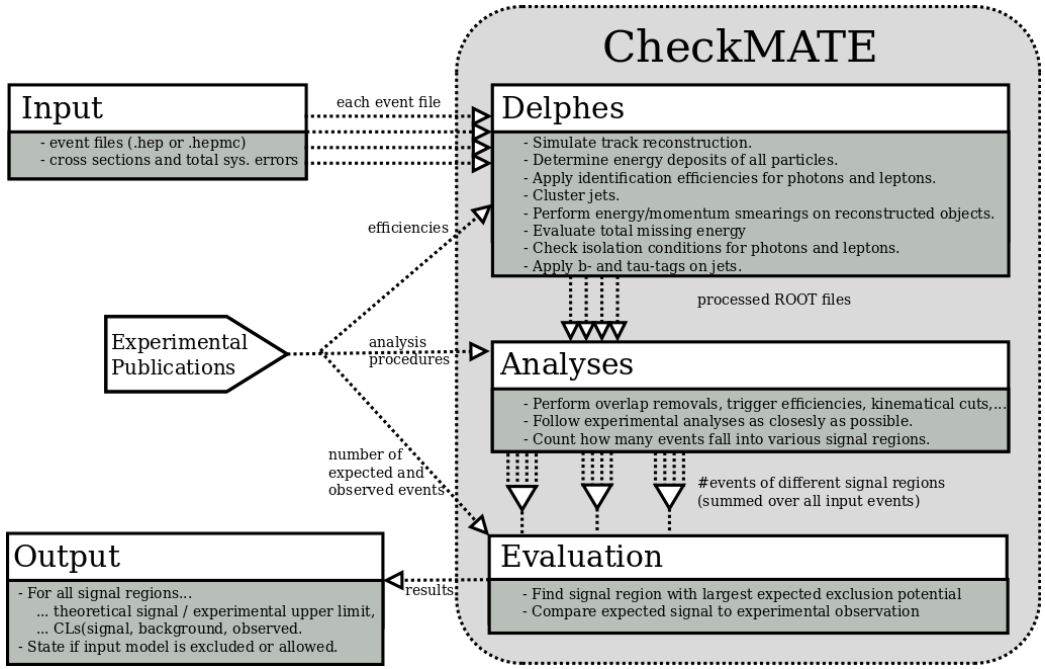
What is it good for?

- Simplified Model Spectra (SmodelS): A tool for excluding BSM models
- Similar purpose tool: CheckMATE
- Difference: No need for simulation $\rightarrow$ SmodelS is faster, not as accurate
- Can be used on BSM models with Z_2 symmetry, including the pMSSM
- Nice for experimentalists: Outputs process topologies that have not been searched for yet (missing topologies)

The CheckMATE process:

- Input: Event files (slow!), cross section
- Internally: Produces dectector simulation, reproduces analyses
- Output: Theory is (not) excluded, upper limits

Figure: CheckMATE process (arXiv:1312.2591)



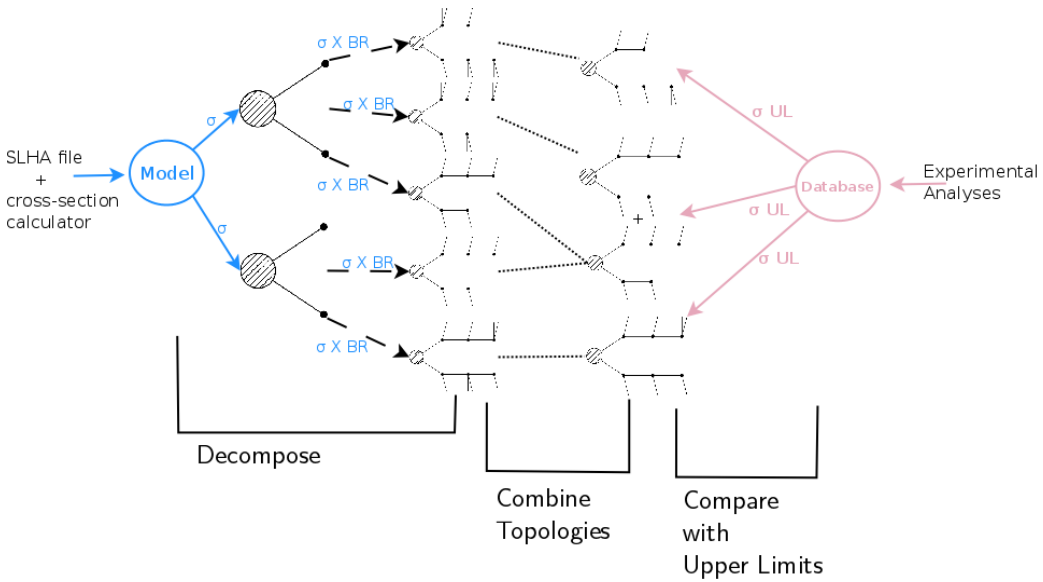
- BSM models can be huge parameter spaces $\rightarrow$ difficult to present/interpret analyses
- Simplified models reduce number of parameters/BSM particles in order to ease analyses
- Especially useful for identifying boundaries of search sensitivities
- Conclusions on simplified models can usually be generalized to complete models

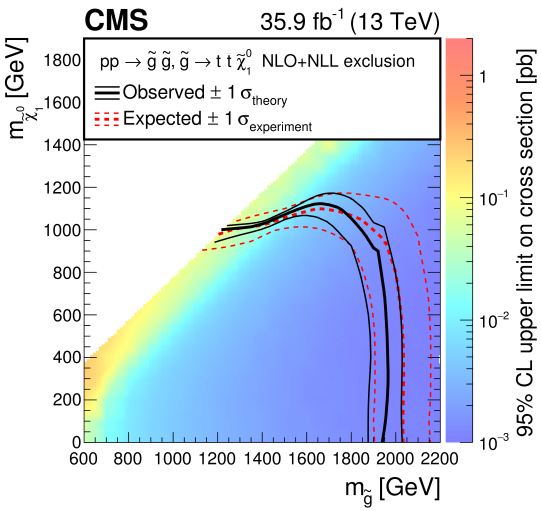
SmodelS

Excluding models with SmodelS

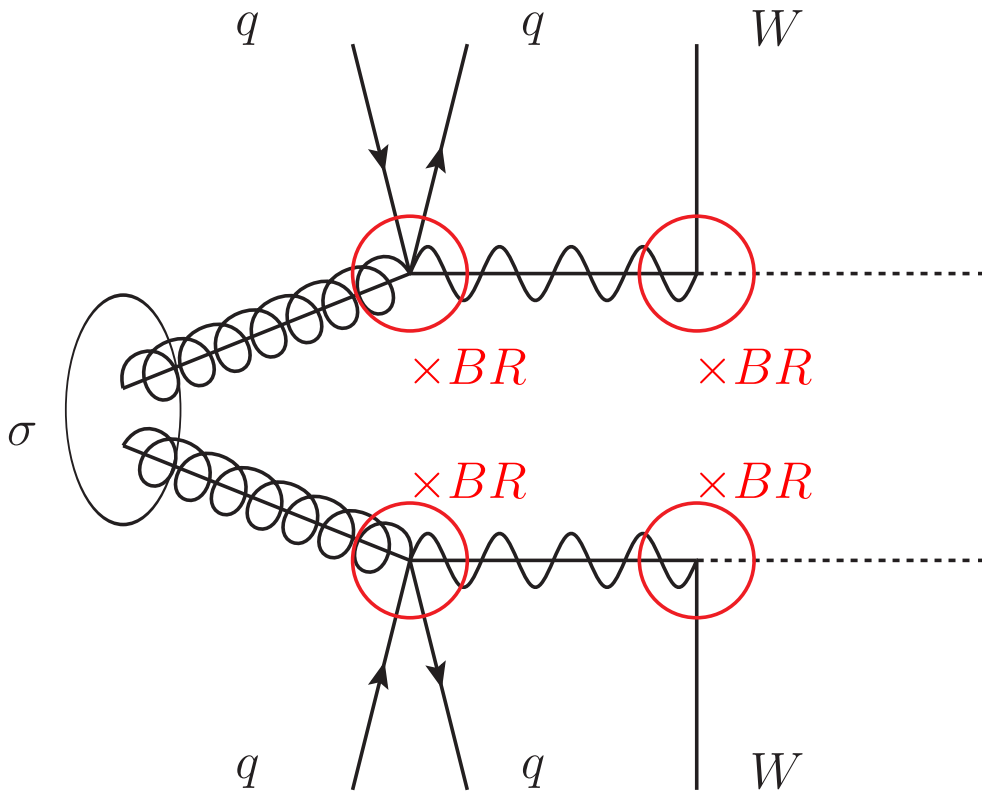
- Input: theory e.g. SLHA file (contains masses, mixing parameters etc.) and cross sections
- Decomposition into simplified model topologies, prediction of $\sigma \times BR$
- Compare with database: Upper limit maps & efficiency maps
- Assumption: Efficiencies don't change from simplified to full model

Figure: Schematic of the SmodelS process (left, arXiv:1701.06586,SmodelS manual) and example of UL map (right, arXiv:1704.07781)



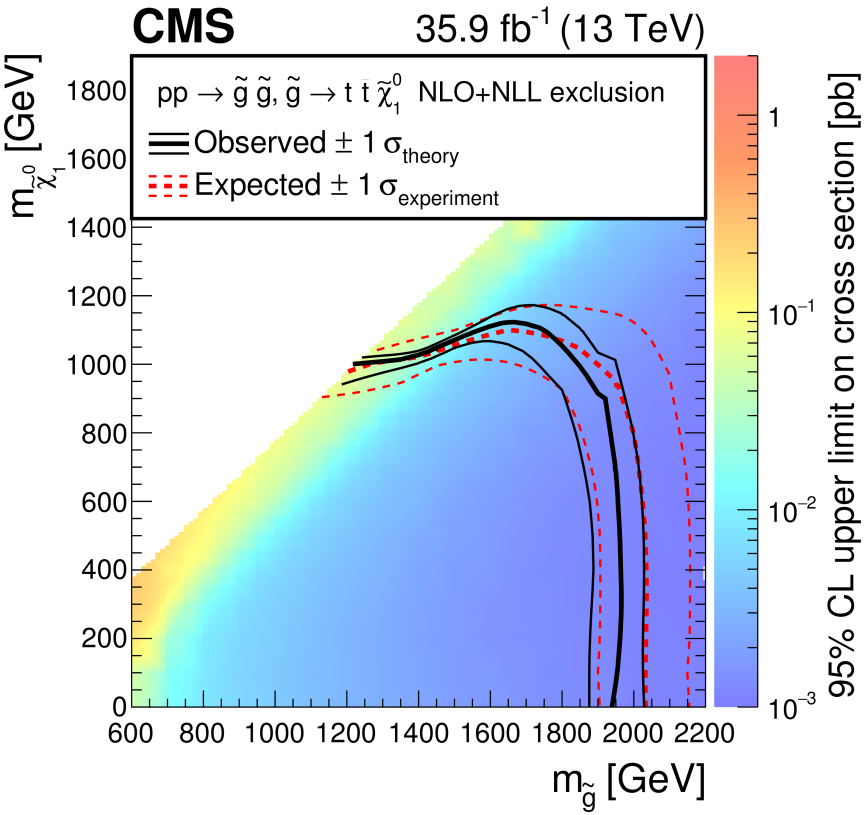


- SmodelS assigns weight to simplified models
- σ: Production cross section of branch mothers
- BR: Product of branching fractions into the exact finalstate
- weight $= \sigma \cdot \prod \mathrm{BR}$



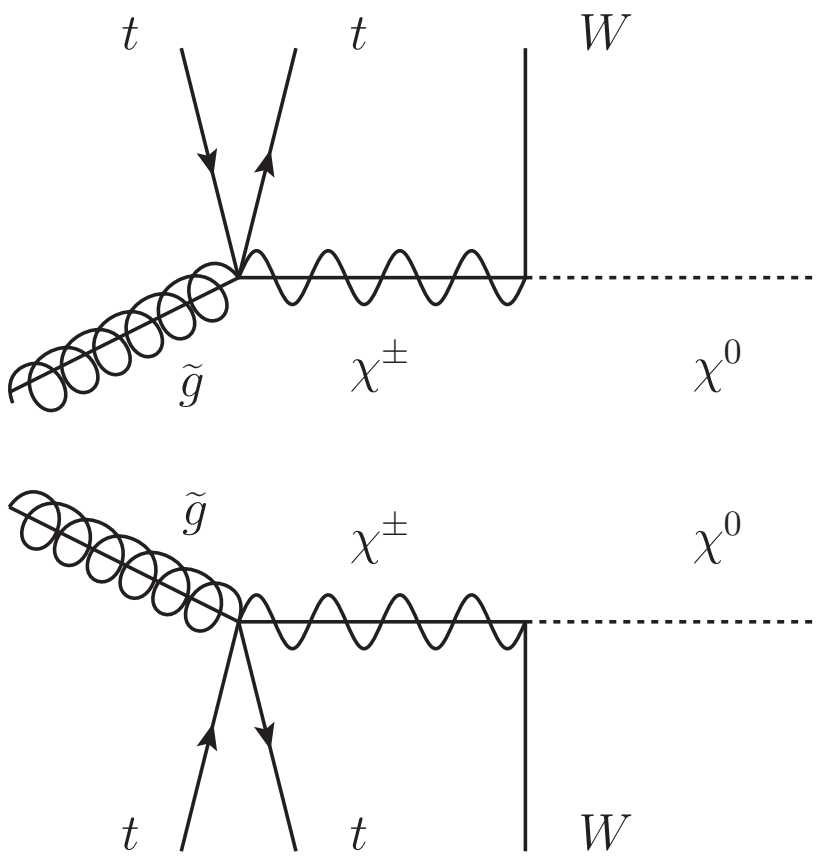
- Missing topologies: No analysis exists in the database for predicted topology
- $\rightarrow$ can help to decide on future searches! For example:
  - Run SmodelS on set of pMSSM points (e.g. from a parameter scan)
  - Find important missing topology (e.g. one that occurs in many points)
  - Perform search for topology, incorporate UL map into SmodelS database
  - Exclude parameter space
- Outside grid topologies: Analysis exists in database, but not for model

Figure: arXiv:1704.07781



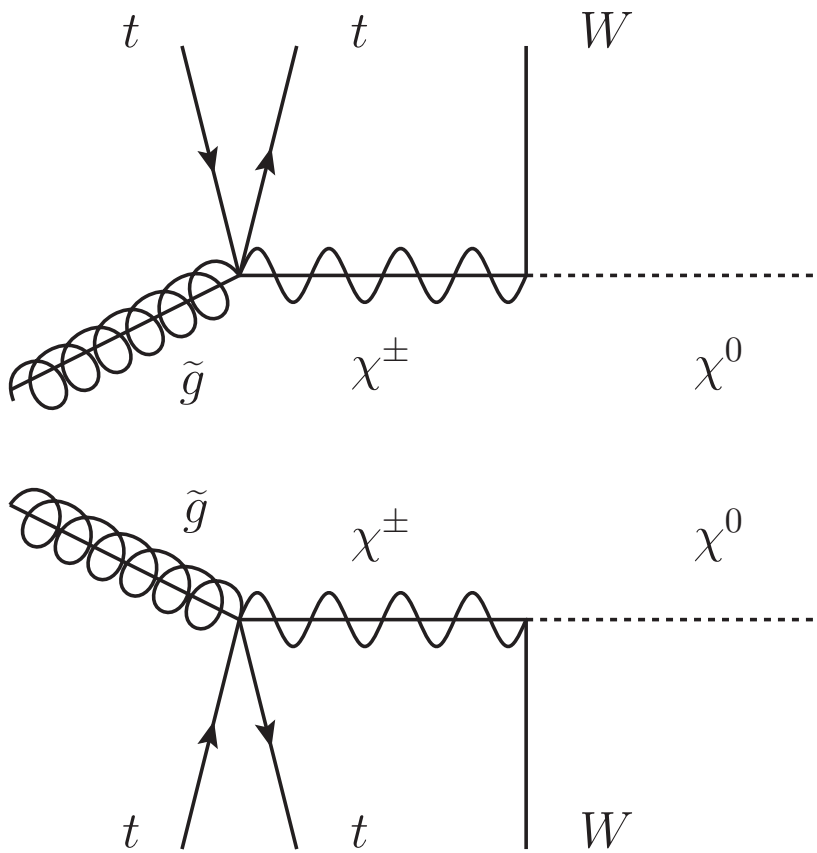
SmodelS presents missing topologies in Tx nomenclature.
Missing topologies get a Txname:

- Prefix determines the productionmode (e.g. T5 $\rightarrow$ gluino production)
- The SM finalstate is added at the end, in order of branch and occurence
- Example on the right: T5ttWttW



A process/Feynman diagram is encoded in bracket notation

(http://smodels.readthedocs.io/en/latest/TheoryDefinitior



- Bracket notation: Set of nested brackets
- From outside in: Finalstate(black), branches(red), vertices(blue)
- Example: [[[t,t],[W]],[[t,t],[W]]]
- Straightforward extension: include intermediates
- $\rightarrow$([[[q,q],[W]],[[q,q],[W]]],[[$\tilde{g}$,$\chi^{\pm}$,χ^{0}],[$\tilde{g}$,$\chi^{\pm}$,χ^{0}]])

Missing topologies

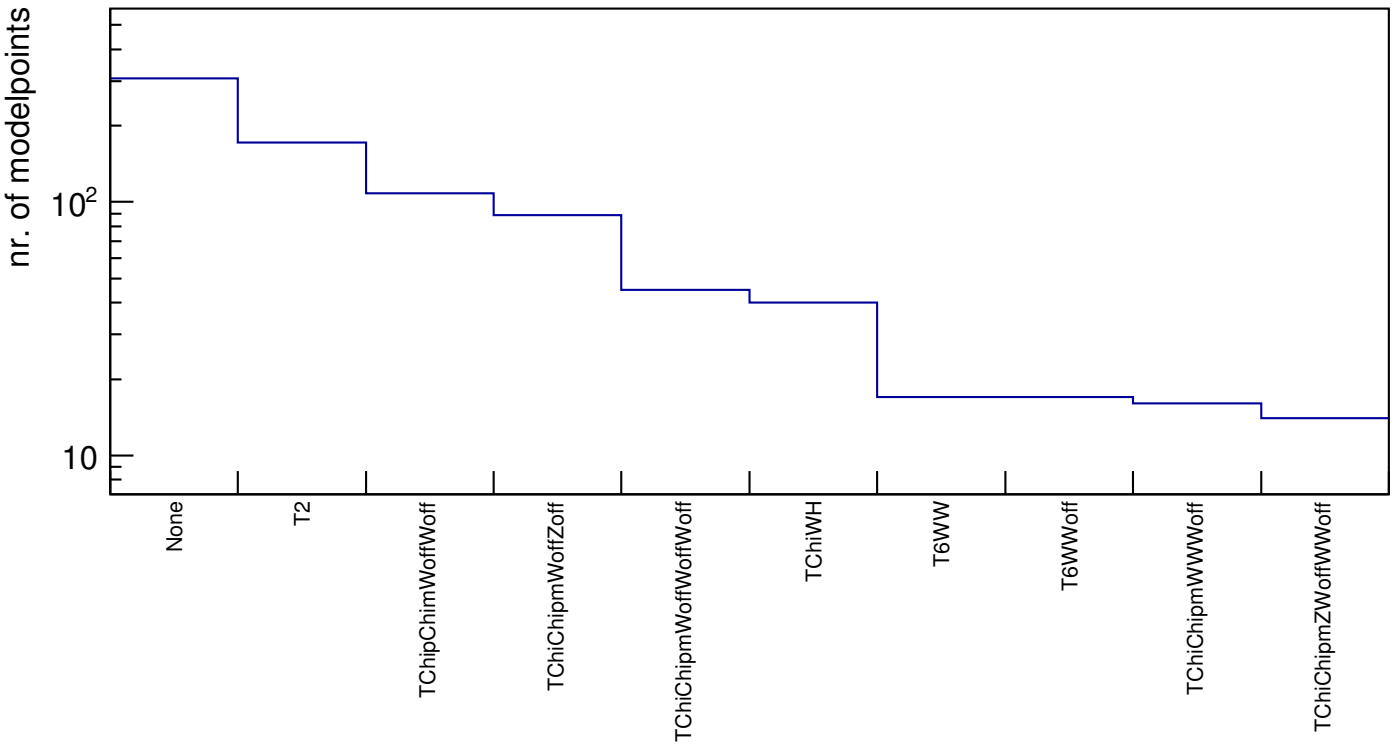
The CMS pMSSM run I parameter scan

- Monte carlo Markov chain(MCMC) scan of pMSSM parameter space
- Contains 20 million points
- Constraints: Masses < 3TeV, prompt Charginos
- $\sim$7000 points not excluded after LHC run 1
- Further exclusion by RA2b: 329 remaining points
- arXiv:1606.03577

Results of SmodelS using remaining pMSSM points

Similar studies:arXiv:1606.03577(Same scan, lists missing topologies); arXiv:1707.09036(SmodelS, ATLAS scan)

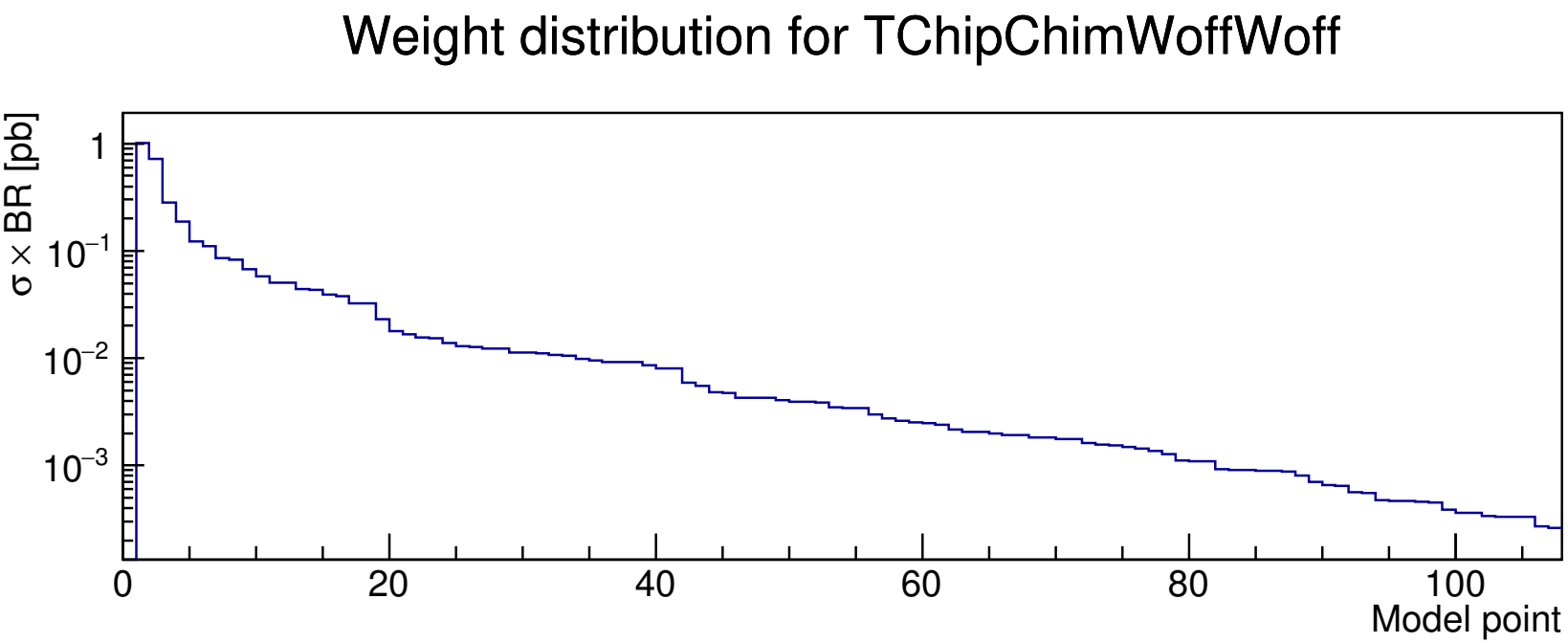
- Outside grid topologies included here
- Electroweak topologies among most occuring missing topologies
- Problem: How well can an analysis constrain these models?



Missing topologies

Further look into a Model

- Look at weight distribution for a given model
- Weight can be translated into events generated for given luminosity
- $\rightarrow$ indicator for search potential
- Each point represents a different model with different masses etc. $\rightarrow$ Success of analysis will vary from point to point



- Interested in TChipChimWoffWoff as candidate for analysis
- Added incentive to explore TChipChimWoffWoff: tends to occur in natural models
- Use ΔEW as variable for naturalness (Phys. Rev. D 88.055026)

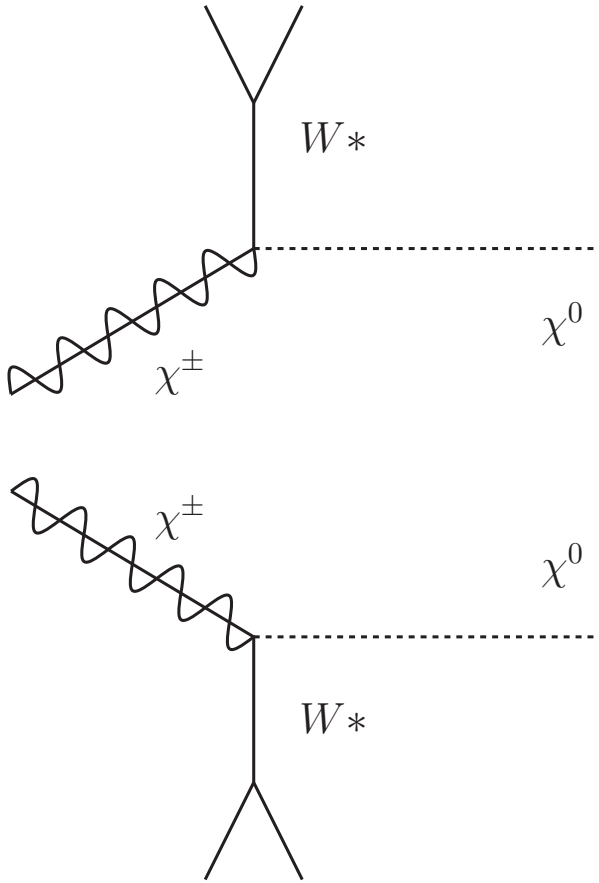
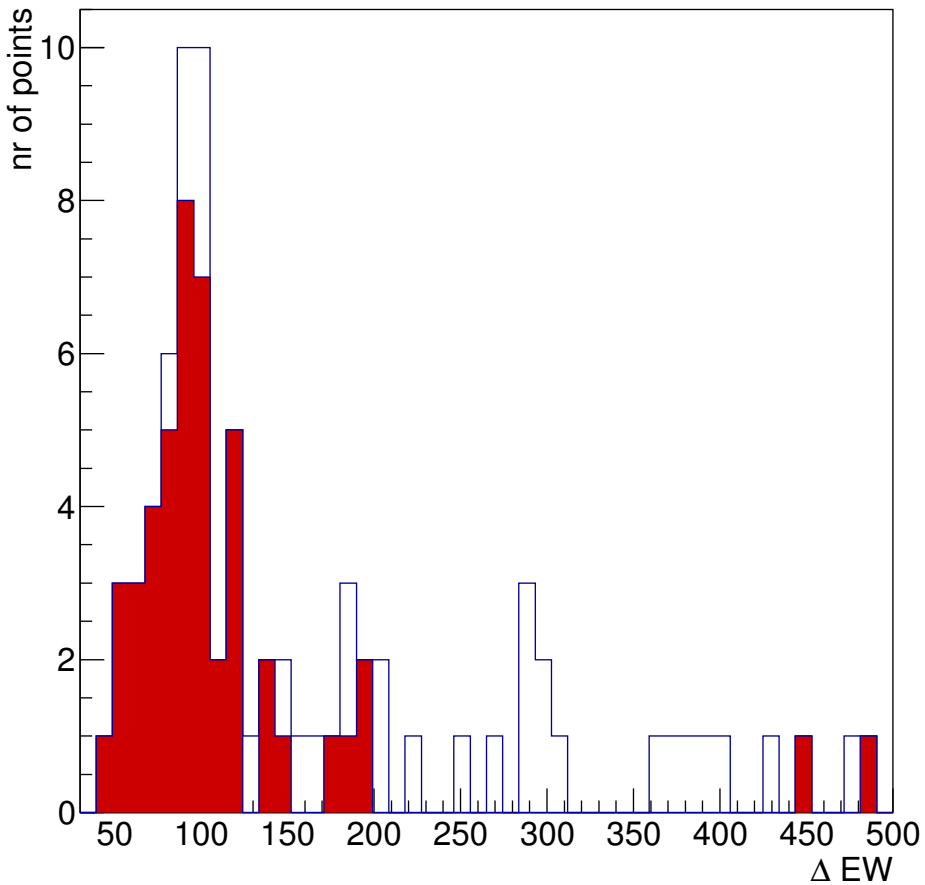


Figure: ΔEW value of model for all model points and model points containing TChipChimWoffWoff(RED)



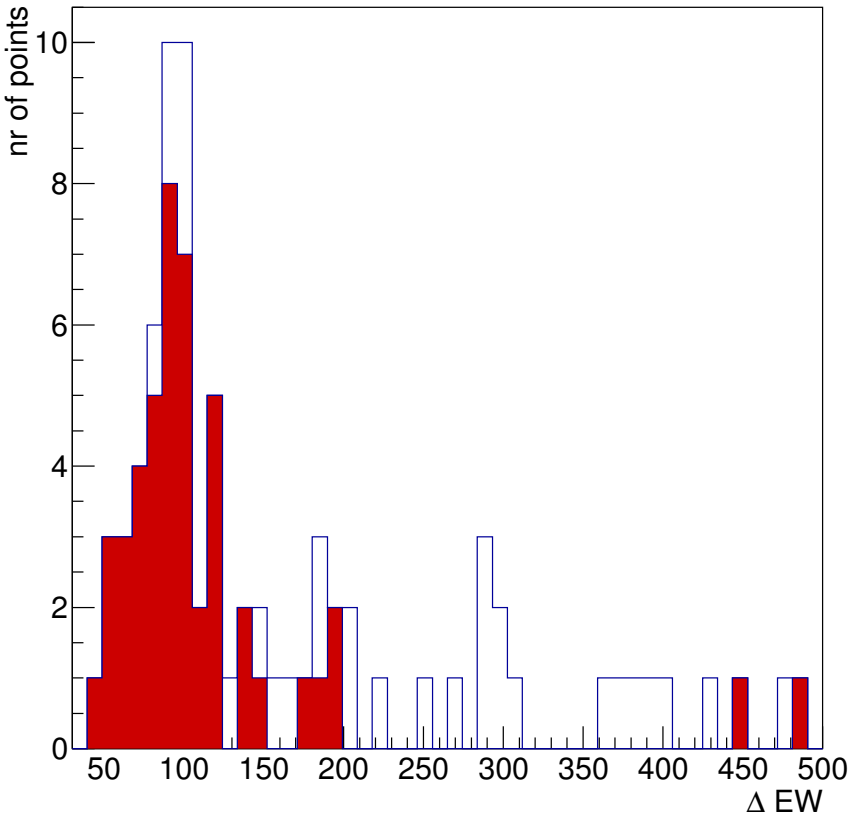
Summary

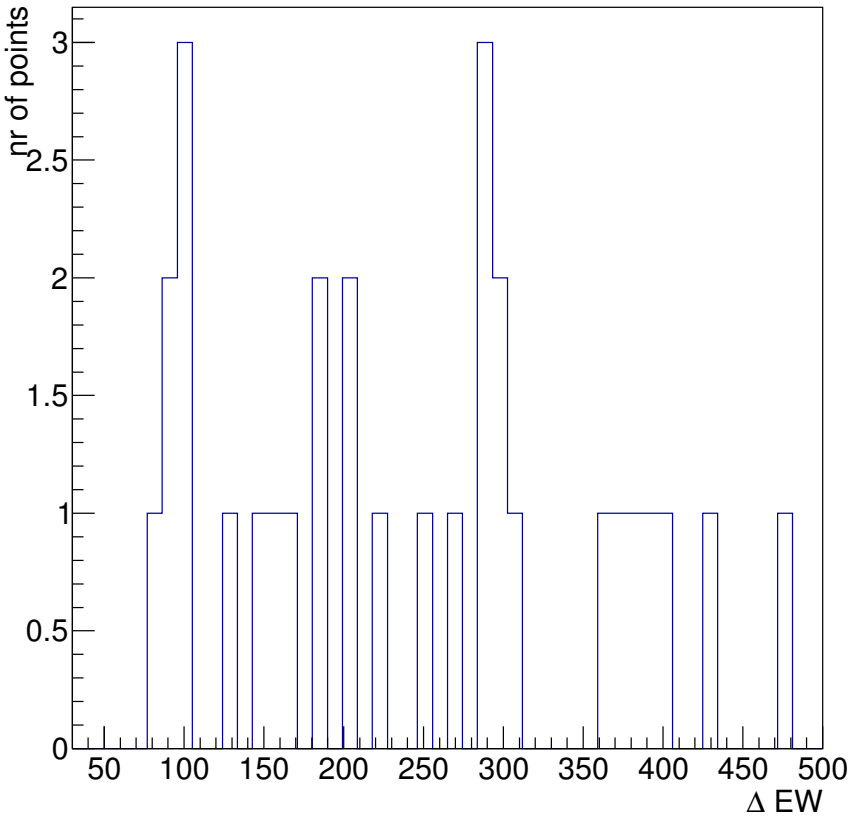
- SmodelS is a fast tool to exclude models
- SmodelS excludes theories and identifies missing topologies
- Missing topologies output can be used as a decider for future analyses
- Ran SmodelS on pMSSM run I points $\rightarrow$ interest in TChipChimWoffWoff & similar models $\rightarrow$ preliminary analysis ongoing

Outlook

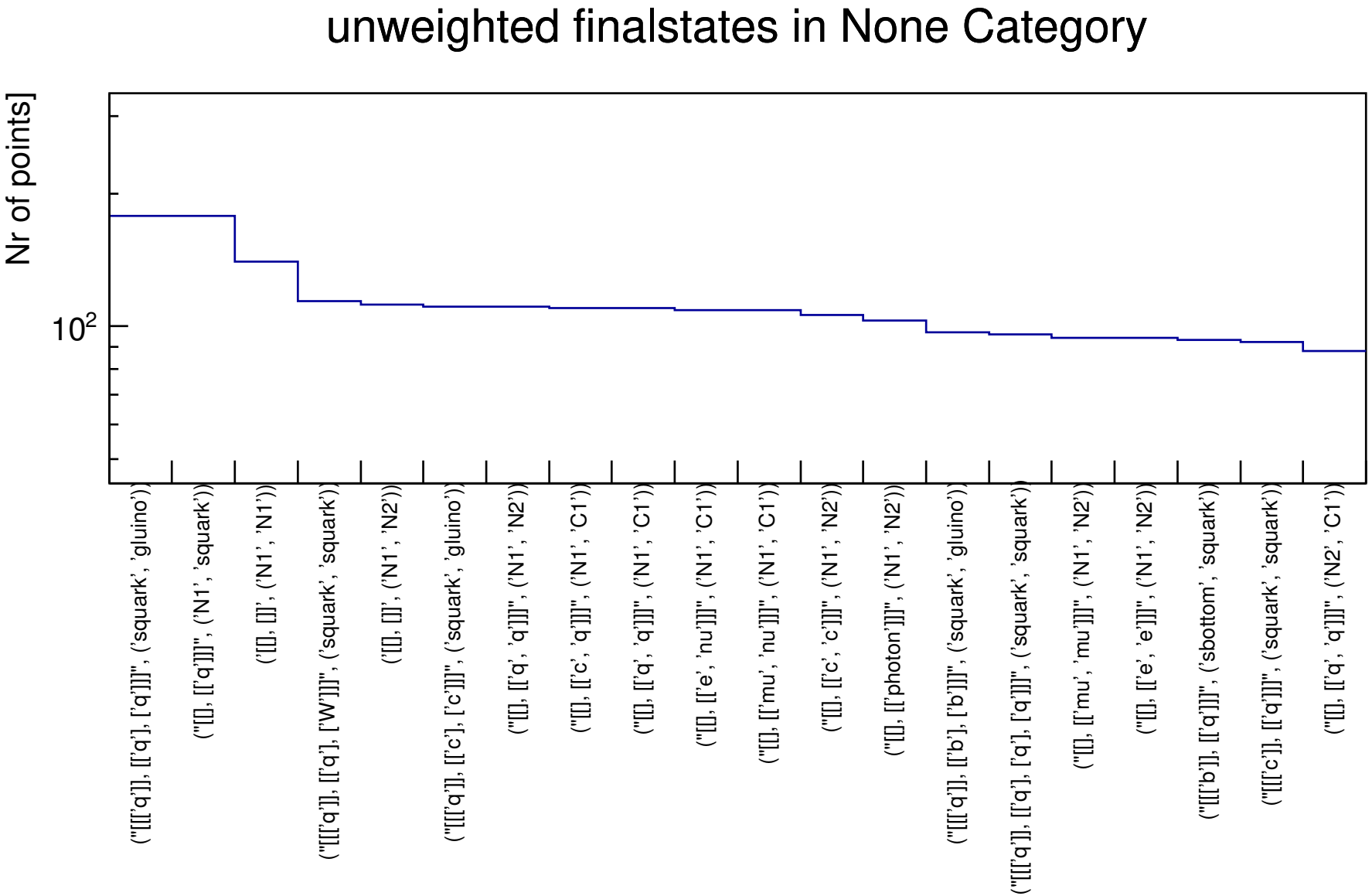
- Implement a tool in SmodelS that estimates possible sensitivity of new analysis?
- Do TChipChimWoffWoff (or similar) search
- Find SUSY in TChipChimWoffWoff.
- Party in Stockholm

Figure: Naturalness of all surviving points(left) and excluding TChipChimWoffWoff(right)



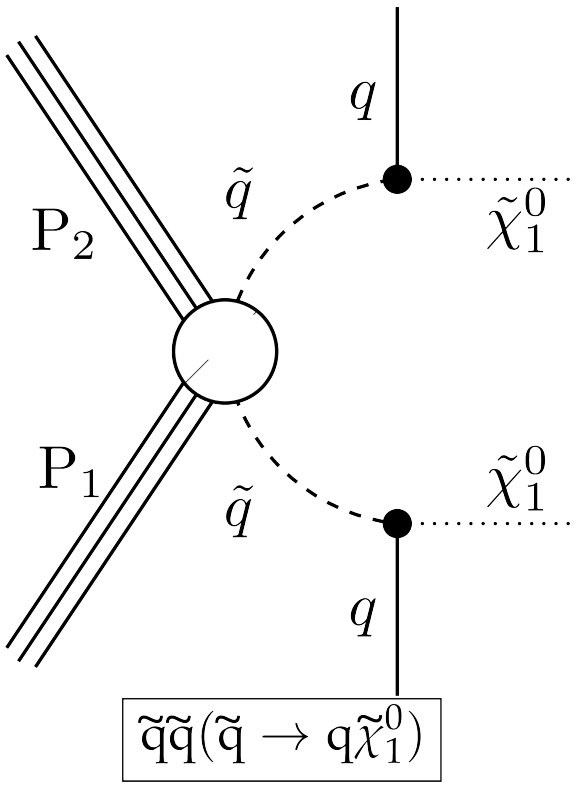


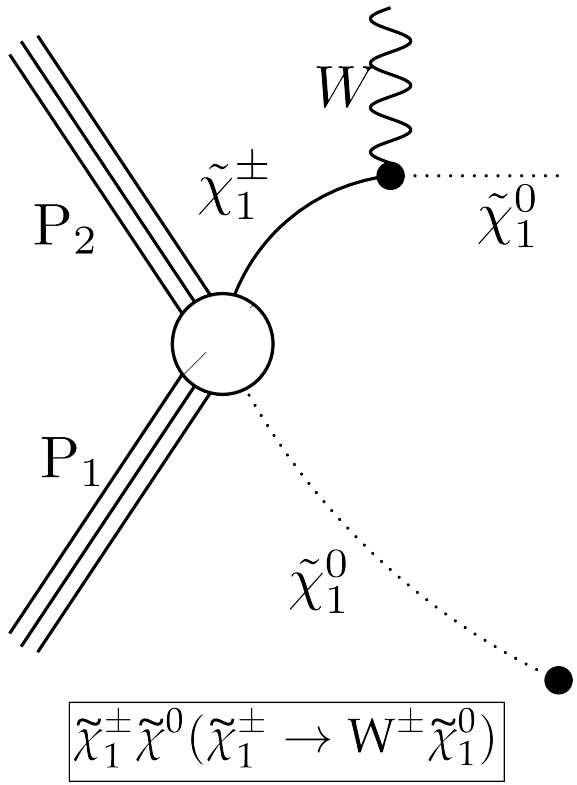
Backup

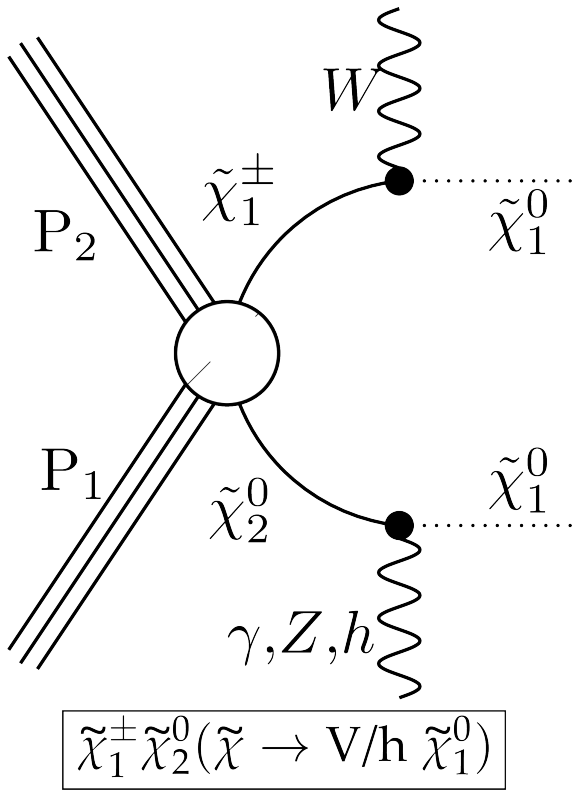

unweighted finalstates in None Category
Nr of points]
10^2
("[[['q'], ['q']]]", ('squark', 'gluino'))
("[[], [['q']]]", ('N1', 'squark'))
('[[], []]', ('N1', 'N1'))
("[[['q'], ['q'], ['W']]]", ('squark', 'squark'))
('[[], []]', ('N1', 'N2'))
("[[['q']], [['c'], ['c']]]", ('squark', 'gluino'))
("[[], [['q', 'q']]]", ('N1', 'N2'))
("[[], [['c', 'q']]]", ('N1', 'C1'))
("[[], [['q', 'q']]]", ('N1', 'C1'))
("[[], [['e', 'nu']]]", ('N1', 'C1'))
("[[], [['mu', 'nu']]]", ('N1', 'C1'))
("[[], [['c', 'c']]]", ('N1', 'N2'))
("[[], [['photon']]]", ('N1', 'N2'))
("[[[['q']], [['b']]]]", ('squark', 'gluino'))
("[[[['q']], [['q'], ['q']]]]", ('squark', 'squark'))
("[[], [['mu', 'mu']]]", ('N1', 'N2'))
("[[], [['e', 'e']]]", ('N1', 'N2'))
("[[[['b']]], [['q']]]", ('sbottom', 'squark'))
("[[[['c']], [['q']]]]", ('squark', 'squark'))
("[[], [['q', 'q']]]", ('N2', 'C1'))

Backup

- CMS analysis:arXiv:1606.03577
- Most occuring highest weight topologies in remaining points
- Left to right: T2, not categorized, TChiChipmWZ



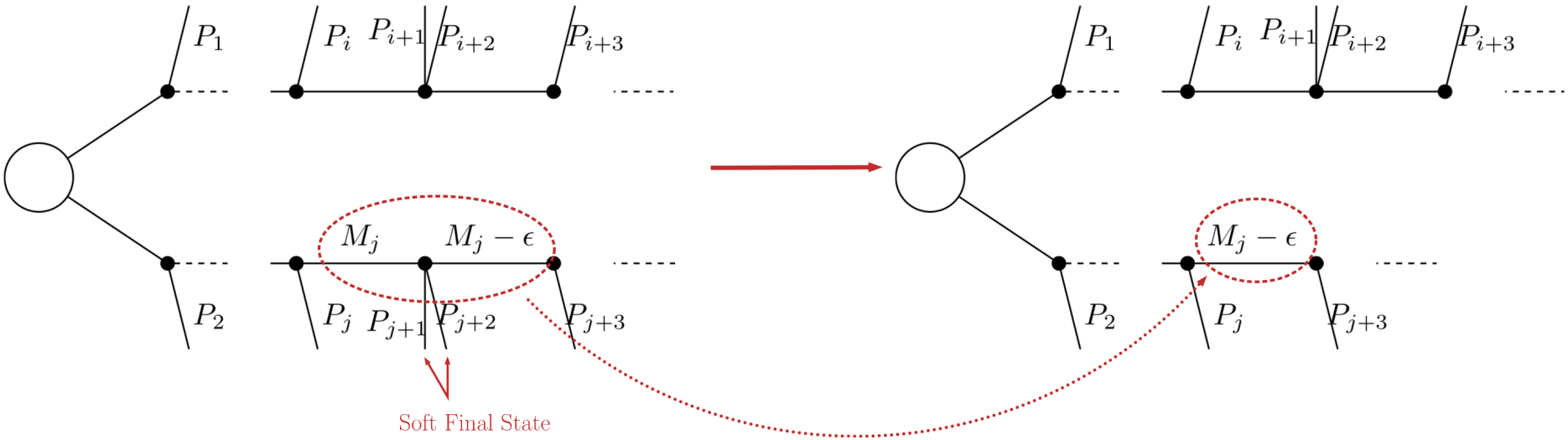




Backup

- SmodelS uses 2 types of compression:mass & invisible
- Mass compression(top): Mass difference between consecutive intermediates smaller than minmassgap(=5GeV) $\rightarrow$ Remove vertex between intermediates, intermediate further up the cascade.

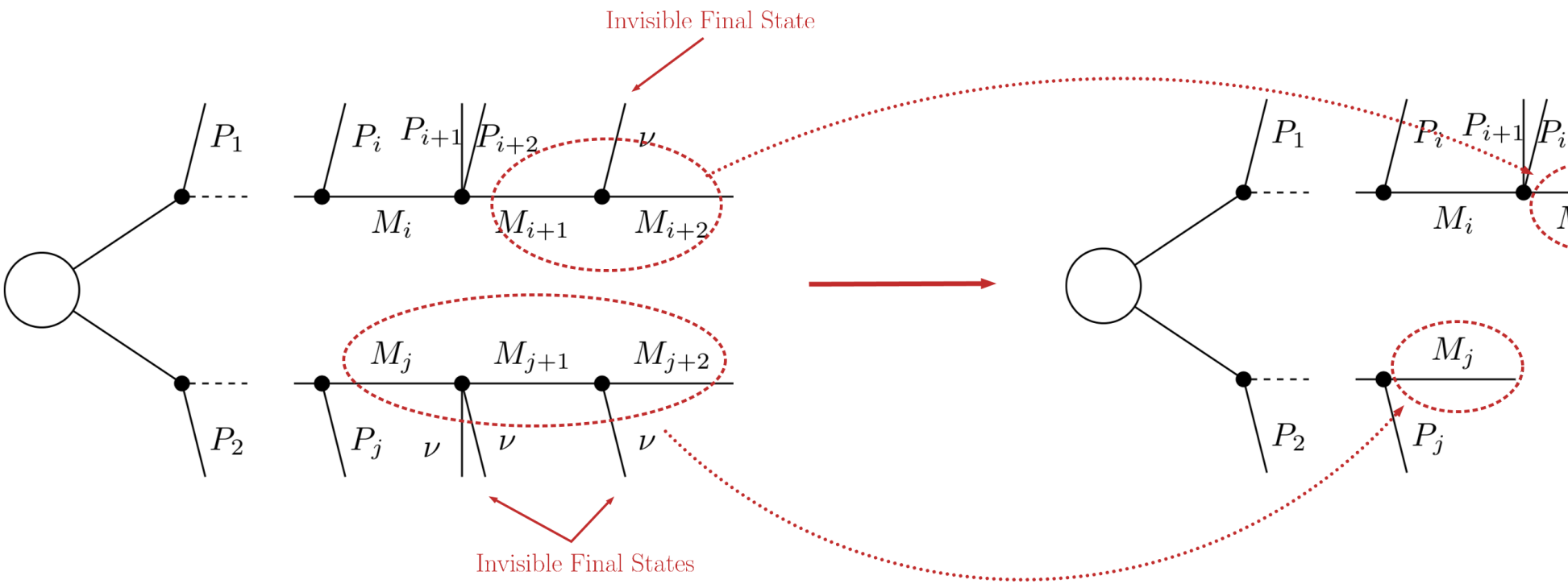
Figure: arXiv:1701.06586



Backup

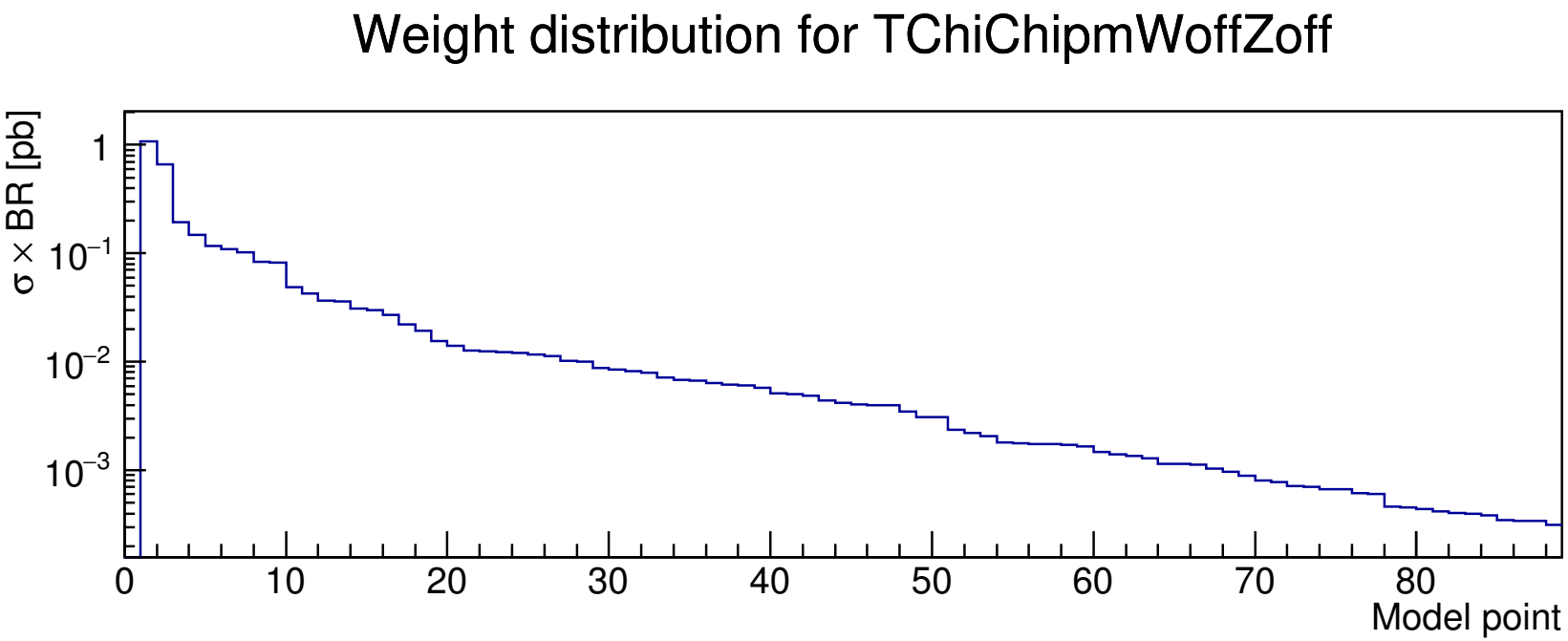
- SmodelS uses 2 types of compression:mass & invisible
- Invisible compression: Branch ends in invisible finalstate(can be more than 1 vertex): Shorten branch to last visible vertex.

Figure: arXiv:1701.06586



Backup

TChiChipmWoffZoff: Weight



Backup

TChiChipmWoffZoff: Naturalness