SMoDelS is an automatised tool for the interpretation of simplified model results from the LHC. It allows to decompose models of new physics obeying a $\mathbb{Z}_2$ symmetry into simplified model components, and to compare these against a large database of experimental results. The first release of SMoDelS, v1.0, used only cross section upper limit maps provided by the experimental collaborations. In this new release, v1.1, we extend the functionality of SMoDelS to efficiency maps. This increases the constraining power of the software, as efficiency maps allow to combine contributions to the same signal region from different simplified models. Other new features of version 1.1 include likelihood and $\chi^2$ calculations, extended information on the topology coverage, an extended database of experimental results as well as major speed upgrades for both the code and the database. We describe in detail the concepts and procedures used in SMoDelS v1.1, explaining in particular how upper limits and efficiency map results are dealt with in parallel. Detailed instructions for code usage are also provided.
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1 Introduction

The ATLAS and CMS experiments at the Large Hadron Collider (LHC) are searching for new physics beyond the Standard Model (BSM) in many different channels. An important class of these searches considers final states with large missing transverse energy (MET), targeting supersymmetry (SUSY) with R-parity conservation or other models with a new conserved parity. In order to design optimal analyses that look for specific final states and to communicate the results, the concept of simplified models [1–5] has been widely adopted by the experimental collaborations.

While limits in terms of simplified model spectra (SMS) are a convenient way to illustrate and compare the reach of specific analyses, understanding how they constrain a realistic model with a multitude of relevant production channels and decay modes quickly becomes a non-trivial task. To tackle this issue we have created SModelS [6, 7], an automatised tool for interpreting simplified model results from the LHC. The principle of SModelS is to decompose BSM collider signatures featuring a $\mathbb{Z}_2$ symmetry into simplified model topologies, using a generic procedure where each SMS is defined by the vertex structure and the SM final state particles; BSM particles are described only by their masses, production cross sections and branching ratios.

The SModelS decomposition corresponds to an approximate mapping of the original model signatures to a coherent sum of simplified model topologies. The underlying assumption [6] is that differences in the event kinematics (e.g. from different production mechanisms or from the spin of the BSM particle) do not significantly affect the signal selection efficiencies. The tool can then be used for any BSM model with a $\mathbb{Z}_2$-like symmetry as long as all heavier R-odd particles (cascade-)decay promptly to the lightest one, which should be electrically and colour neutral.\(^2\) Note that due to the $\mathbb{Z}_2$ symmetry only pair production or associated production of two BSM particles is considered, and MET is always implied in the final state description. Regarding experimental results, the tool contains a large database of SMS results from ATLAS and CMS SUSY searches.

Since the publication of SModelS v1.0 [7] in December 2014, the code base has undergone significant structural changes. Version 1.1 comes with many new features, the most important one being the extension to efficiency maps.

The advantage of efficiency maps (EM) over the previously (and still) used cross section upper limit (UL) maps is that they allow to combine contributions from different SMS topologies to the same signal region (SR) of a given experimental analysis. This significantly enhances the coverage and constraining power of the SMS results. Further novelties of this release include:

- a new and more flexible database format;
- extended information on the topology coverage;
- inclusion of likelihood and $\chi^2$ calculation for EM-type results;
- inclusion of a database browser tool for easy access to the information stored in the database;
- performance improvement for the decomposition of the input model;

\(^2\)Charged tracks may also be treated in an SMS context [8] and will be available in future versions of SModelS.
– inclusion of new simplified model results to the database, including a few 13 TeV results;
– overall significant speedups of the code and the database.

The purpose of this paper is to present these new features, describing in detail the concepts and procedures used in the code and the database. Particular attention is given to how upper limits and efficiency maps are dealt with simultaneously.

The (re-)interpretation of LHC searches, which is the main goal of SModelS, has recently become a very active field. Several other public tools have been developed by different groups. In particular, FastLim [9] and XQCAT [10] employ pre-computed efficiency maps to constrain, respectively, the minimal supersymmetric standard model (MSSM) and extra heavy quark scenarios. SUSY-AI [11] is a code which has been trained with machine learning techniques to reproduce the ATLAS exclusion for the phenomenological MSSM. Finally, CHECKMATE [12, 13], MADANALYSIS 5 [14, 15], Rivet (≥ 2.5) [16] and GAMBIT’s ColliderBit [17, 18] allow for more general recasting of ATLAS and CMS searches based on Monte Carlo event simulation. Last but not least, Contur [19] aims at constraining BSM scenarios from differential Standard Model measurements based on the Rivet [16] toolkit.

The rest of the paper is organised as follows. We start in Section 2 by explaining the basic concepts of SModelS, including the structure of UL-type and EM-type results and of the database of experimental results. In Section 3, we then discuss in detail the decomposition procedure, the computation of the theory predictions, the comparison of theory predictions against the experimental results, and how missing topologies are identified. How to run SModelS is shown in Section 4. Section 5 contains conclusions and an outlook.

Installation instructions are provided in Appendix A. Appendix B describes some useful SModelS-internal tools, while Appendix C provides information about ‘home-grown’ efficiency maps included in the database. A complete, browsable manual and an extensive code documentation are provided in html format in the ‘docs’ folder of the distribution; they are also available online at [20].

In case of problems using SModelS, we kindly ask the user to contact the authors via smodels-users@lists.oeaw.ac.at.

Note:

When using SModelS v1.1 for scientific work (or any other purposes), please cite this paper as well as the original SModelS publication [6]. In scientific publications, please also cite the programs SModelS v1.1 makes use of: PYTHIA 6.4 [21] and/or PYTHIA 8.2 [21, 22], NLLFAST [23–29], and PySLHA [30]. For convenience, these citations are provided as a bibtex file in the SModelS distribution.

We also strongly recommend to cite all the experimental results used; a separate bibtex file is provided to that effect in the SModelS database folder. In case you use the FastLim efficiency maps in SModelS (see ‘adding FastLim data’ in Appendix B), please also properly cite FastLim [9] and the relevant experimental results. These references are also provided in a bibtex file with the distribution.
2 Basic Concepts and Structure

A central task of SModelS is the decomposition of a complex BSM model into its set of simplified model topologies. As mentioned in the introduction, this decomposition relies on several assumptions [6]: first, the production channel is not taken into account, and only on-shell particles are considered in cascade decays. Virtual particles are replaced by an effective vertex, where only the on-shell decay products are specified. Additionally, new states are described only by their masses, neglecting all other quantum numbers, thus disregarding potential influences of the spin and coupling structure on the selection efficiencies. Finally it should be noted that the SMS approach is only valid within the narrow width approximation. For a safe application of SModelS (in particular to non-MSSM or non-SUSY scenarios), these assumptions should be understood and, if needed, verified.

A few studies on the validity of the SMS assumptions are available. For example, the effects of alternative production channels in squark simplified models were studied in [31]. The effect of a different spin structure was studied for the case of the dijet+MET final state in [32], for the dilepton+MET final state in [33] and for $t\bar{t}$+MET final states in [34]. For all these cases it was found that the application of SMS limits is safe. Generally, however, the validity of the SMS assumptions will depend on the concrete model under consideration, as well as details of the experimental search. In particular, an inclusive cut-and-count search might be less sensitive to differences than a shape-based analysis. Examples for which the SMS assumptions do not hold include the mono-X analyses performed in the context of dark matter searches. Dark matter simplified model results are therefore not included in SModelS v1.1.

In this section we first explain the basic concepts and language used in SModelS v1.1 to describe simplified model topologies. This is followed by detailed descriptions of UL-type and EM-type results and of the database of experimental results.

2.1 Simplified Model Definitions

Elements A simplified model topology representing a specific cascade decay of a pair of BSM states produced in the hard scattering is called an ‘element’ in the SModelS language. Elements contain the final states ($Z_2$-even) particles appearing in the cascade decay as well as the masses of the BSM ($Z_2$-odd) states in the decay chain. An element may also hold information about its corresponding ‘weight’ (cross section times branching ratio times efficiency). Figure 1 illustrates an element and its properties.

SModelS works under the inherent assumption that, for collider purposes, all the essential properties of a BSM model can be encapsulated by its elements. While some caveats apply (see above), such an assumption is extremely helpful to cast the theoretical predictions of a specific BSM model in a model-independent framework, which can then be compared against the corresponding experimental limits. For instance, as shown in Figure 1, only the masses of the BSM states are used; other properties,

---

3In order to treat the UL and EM map results on the same footing, SModelS v1.1 applies a trivial binary efficiency to elements for UL-type results as will be explained later.
such as their spins or other quantum numbers are ignored (the PID’s are, however, stored for book-
keeping).

Below we describe in more detail the element properties and their implementation in SModelS.

**Vertices** Each $\mathbb{Z}_2$-odd decay is represented by a vertex containing its final states (one $\mathbb{Z}_2$-odd state and the $\mathbb{Z}_2$-even particles).

**Final States ($\mathbb{Z}_2$-even)** Final states indicate all $\mathbb{Z}_2$-even states coming out of a vertex. In most cases, these correspond to Standard Model particles (leptons, gauge bosons, Higgs,...). Note that, if the input model contains BSM states which are $\mathbb{Z}_2$-even, such as additional Higgs bosons, these are also treated as final states. In contrast, stable or long-lived $\mathbb{Z}_2$-odd particles which might appear in the detector (either as MET or charged tracks) are *not* classified as final states.

**Intermediate States ($\mathbb{Z}_2$-odd)** The $\mathbb{Z}_2$-odd states are always assumed to consist of BSM particles with $\mathbb{Z}_2$ conserving decays of the form: ($\mathbb{Z}_2$-odd state) $\rightarrow$ ($\mathbb{Z}_2$-odd state) + final states. The only information kept from the intermediate states are their masses, see Figure 1 (right). If an intermediate state is stable and neutral, it is considered as a MET signal.

**Branches** A branch is the basic substructure of an element. It represents the cascade decays of a single initial $\mathbb{Z}_2$-odd state. The diagram in Figure 2 illustrates an example of a branch.

The structure of each branch is fully defined by its number of vertices and the number of final states coming out of each vertex. Furthermore, the branch also holds the information about the final states originating from each vertex and the masses of the intermediate states, as shown in Figure 2 (right).

**Element Representation: Bracket Notation** The structure and final states of elements can conveniently be represented in textual form using a notation of nested brackets. Figure 3 shows how to convert between the graphical and bracket representations of an element.
Figure 2: Representation of a branch, including its overall structure (left) and a concrete example with all the information it holds in the SModelS scheme (right).

Figure 3: Conversion of an element to the bracket notation used in SModelS.

The brackets are ordered and nested in the following way. The outermost brackets correspond to the branches of the element. The branches are sorted according to their size and each branch contains an ordered list of vertices. Each vertex contains a list of the final states originating from it. Schematically, for the example in Figure 3, we have:

```
| element = [branch1, branch2] |
| branch1 = [vertex1] |
| vertex1 = [l+, l-] |
| branch2 = [vertex1, vertex2] |
| vertex1 = [l+] |
| vertex2 = [nu] |
```

Using the above scheme it is possible to unambiguously describe each element with a simple list of nested brackets. However, in order to fully specify all the information relative to a single element, we must also include the list of intermediate state masses and the element weight. The intermediate state masses are represented by a mass array for each branch, as shown in Figure 4.

**Topologies**

It is often useful to classify elements according to their overall structure or topology. Each topology corresponds to an *undressed* element, removed of its final states and $\mathbb{Z}_2$-odd masses. Therefore the topology is fully determined by its number of branches, number of vertices in each branch and number of final states coming out of each vertex. An example of a topology is shown in Figure 5.

Within SModelS, elements are grouped according to their topology. Hence topologies represent a list
of elements sharing a common basic structure (same number of branches, vertices and final states in each vertex).

2.2 Database Definitions and Structure

SModelS contains a large database of SMS results from ATLAS and CMS SUSY searches.\(^4\) Starting with version 1.1, two types of experimental constraints are used:

- **Upper Limit (UL)** constraints: constrains on \(\sigma \times BR\) of simplified models, usually provided by the experimental collaborations;

- **Efficiency Map (EM)** constraints: constrains the total signal \((\sum \sigma \times BR \times \varepsilon)\) in a specific signal region. Here \(\varepsilon\) denotes the acceptance times efficiency. These are either directly provided by the experimental collaborations or computed by theory groups.

Although the two types of constraints above are very distinct, both the folder structure and the object structure of SModelS are sufficiently flexible to simultaneously handle both UL-type and EM-type results. The database itself can be seen as a collection of experimental results, each of which obey the following hierarchical structure:

\(^4\)Extensions to non-MET searches are foreseen for future SModelS releases.
• **Experimental Result:** corresponds to an experimental publication (published paper or preliminary result like a conference note or analysis summary) and contains a list of Data Sets as well as general information about the result (luminosity, publication reference, ...).

  – **Data Set:** represents a distinct signal region for a given experimental result. For EM-type results, there is one data set per signal region, each containing the relevant efficiency maps. UL-type results are treated analogously, but, since they correspond to the best signal region or a combination of signal regions, they have just one data set containing the relevant upper limit map.

    * **Upper Limit map:** contains the upper limit constraints for UL-type results. Each map refers to a single simplified model (or more precisely to a single element or sum of elements).

    * **Efficiency map:** contains the efficiencies for EM-type results. Each map refers to a single element or sum of elements.

A schematic summary of the above structure is shown in Figure 6. Below we describe in more detail the main concepts and building blocks of the SModelS database.

### Upper Limit Results

Upper Limit experimental results contain the experimental constraints on the cross section times branching ratio ($\sigma \times BR$) for simplified models from a specific experimental publication or preliminary result. These constraints are typically given in the format of UL maps, which correspond to 95% confidence level (CL) upper limit values on $\sigma \times BR$ as a function of the respective parameter space (usually BSM masses or slices over mass planes). The UL values usually assume the best signal...
region (for a given point in parameter space), a combination of signal regions or more involved limits from other methods. An example of an UL map is shown in Figure 7.

Within SModelS, the UL map shown in Figure 7 is used to constrain the simplified model \( \tilde{q} + \tilde{q} \rightarrow (jet + \tilde{\chi}_1^0) + (jet + \tilde{\chi}_1^0) \). Using the SModelS notation this simplified model is mapped to the element \([[[jet]], [[[jet]]]]\), using the notation defined in Section 2.1. Usually a single experimental publication contains several UL maps, each one constraining different simplified models. We stress that the exclusion curve shown in the UL map above is never used by SModelS.

**Upper Limit Constraint**  The upper limit constraint specifies which simplified model is constrained by the respective UL map. For simple constraints, as the one shown in Figure 7, it corresponds to a single element \([[[jet]], [[[jet]]]]\). In some cases, however, the constraint corresponds to a sum of elements. As an example, consider the ATLAS upper limit map shown in Figure 8.

Here, the upper limits apply to the sum of the cross sections:

\[
\sigma = \sigma([[e^+],[e^-]]) + \sigma([[\mu^+],[\mu^-]])
\]

In this case the UL constraint is:

\([[[e^+],[e^-]]] + [[[\mu^+],[\mu^-]]]\)

where it is understood that the sum is over the weights of the respective elements and not over the elements themselves.

Note that the sum can be over particle charges, flavors or more complex combinations of elements. However, almost all experimental results sum only over elements sharing a common topology.
Upper Limit Conditions When the analysis constraints are non-trivial (refer to a sum of elements), it is often the case that there are implicit (or explicit) assumptions about the contribution of each element. For instance, in Figure 8, it is implicitly assumed that each lepton flavor contributes equally to the summed cross section:

\[ \sigma([e^+], [e^-]) = \sigma([\mu^+], [\mu^-]) \] (condition)

Therefore, when applying these constraints to general models, one must also verify that these conditions are satisfied. Once again we can express these conditions in bracket notation:

\[ [([e^+]], [e^-])] = [([\mu^+]], [\mu^-])] \] (condition)

where it is understood that the condition refers to the weights of the respective elements and not to the elements themselves.

In several cases it is desirable to relax the analysis conditions, so the analysis upper limits can be applied to a broader spectrum of models. Once again, for the example mentioned above, it might be reasonable to impose instead:

\[ [([e^+]], [e^-])] \approx [([\mu^+]], [\mu^-])] \] (fuzzy condition)

The departure from the exact condition can then be properly quantified and one can decide whether the analysis upper limits are applicable or not to the model being considered. Concretely, SModelS computes for each condition a number between 0 and 1, where 0 means the condition is exactly satisfied and 1 means it is maximally violated. Allowing for a 20% violation of a condition corresponds approximately to a “condition violation value” (or simply condition value) of 0.2. The condition values are given as an output of SModelS, so the user can decide on the allowed violation.
Efficiency Map Results

Efficiency maps correspond to a grid of simulated acceptance times efficiency ($A \times \varepsilon$) values for a specific signal region for a specific simplified model. In the following we will refer to $A \times \varepsilon$ simply as efficiency and denote it by $\varepsilon$. Furthermore, additional information, such as the luminosity, number of observed and expected events, etc is also stored in a EM-type result.

An important difference between UL-type results and EM-type results is the existence of several signal regions in the latter, which in SModelS are mapped to data sets. While UL-type results contain a single data set, EM results hold several data sets, one for each signal region (see Figure 6). Each data set contains one or more efficiency maps, one for each element or sum of elements. The efficiency map is usually a function of the BSM masses appearing in the element, as shown in Figure 9.

![Efficiency Map](image)

Figure 9: An example of an efficiency map from [37]. The information used by SModelS is indicated by arrows.

The concept of efficiency maps can also be extended to UL-type results. For the latter, the efficiencies for a given element are either 1, if the element appears in the UL constraint, or 0, otherwise. Although trivial, this extension allows us to treat EM-type results and UL-type results in a very similar fashion (see Section 3.3 for more details).

TxName Convention

Since using the bracket notation to describe the simplified models appearing in the upper limit or efficiency maps can be rather lengthy, it is useful to define a shorthand notation for the constraints. SModelS adopts a notation based on the CMS SMS conventions, where each specific constraint is labeled as $T<constraint\ name>$, which we refer to as TxName. For instance, the TxName corresponding to the constraint in Figure 8 is $TSlepSlep$. A complete list of TxNames can be found in [38].
Database Structure

Let us now discuss in more detail how the information about the experimental results are stored in the database. As shown in Figure 6, the basic structure is an ordinary (UNIX) directory hierarchy. A thin Python layer serves as the access to the database.

In the official release, the database is organized according to the center-of-mass energies (‘8TeV’ and ‘13TeV’), followed by the name of the collaboration (e.g. ‘8TeV/ATLAS’). The third level of the directory hierarchy encodes the experimental results:

• 8TeV/ATLAS/ATLAS-SUSY-2013-02
• 8TeV/CMS/CMS-SUS-12-024
• ...

This folder structure is, however, flexible and may be customised by the user. More as well as fewer subdirectories are allowed, making for instance a simple division according to the data’s provenance (‘LHC’, ‘FastLim’, ‘MadAnalysis5’, ...) a viable alternative. One small requirement that is imposed on the database is that the top-level directory contains a version file with a simple version string. The structure of the experimental result folders is as follows. Each experimental result folder contains:

• a folder for each data set (e.g. data)
• a globalInfo.txt file

The globalInfo.txt file contains the meta information about the experimental result. It defines the center-of-mass energy $\sqrt{s}$, the integrated luminosity, the id used to identify the result and additional information about the source of the data. Below we show the content of CMS-SUS-12-024/globalInfo.txt as an example:

```
sqrts: 8.0*TeV
lumi: 19.4(fb
id: CMS-SUS-12-024
url: https://twiki.cern.ch/twiki/bin/view/CMSPublic/
    PhysicsResultsSUS12024
arxiv: http://arxiv.org/abs/1305.2390
publication: http://www.sciencedirect.com/science/article/pii/
   S0370269313005339
implementedBy: Wolfgang Waltenberger
lastUpdate: 2015/5/11
```

Data Set Folder Each data set folder contains:

• the Upper Limit maps for UL-type results or Efficiency maps for EM-type results (TxName.txt files)
• a dataInfo.txt file containing meta information about the Data Set
Data Set Folder: Upper Limit Type  Since UL-type results have a single dataset the info file only holds some trivial information, such as the type of experimental result (UL) and the dataset id (‘None’ for UL-type results). For example, the content of CMS-SUS-12-024/data/dataInfo.txt is

```
dataType: upperLimit
dataId: None
```

Each TxName.txt file contains the UL map for a given simplified model as well as some meta information, including the corresponding constraint and conditions. The first few lines of CMS-SUS-12-024/data/T1tttt.txt read:

```
taxName: T1tttt
cconditionDescription: None
ccondition: None
cconstraint: [[[t',t']],[[t',t']]]
cfigureUrl: https://twiki.cern.ch/twiki/pub/CMSPublic/

    PhysicsResultsSUS12024/T1tttt_exclusions_corrected.pdf
```

The second block contains the upper limits as a function of the BSM masses, according to the mass array convention defined in Section 2.1. It is given as a Python array with the structure `[[masses,upper limit], [masses,upper limit],...]`. Explicitly, continuing the above example:

```
upperLimits: [
    [[400.0*GeV, 0.0*GeV], [400.0*GeV, 0.0*GeV]], 1.815773*pb],
    [[400.0*GeV, 25.0*GeV], [400.0*GeV, 25.0*GeV]], 1.806528*pb],
    [[400.0*GeV, 50.0*GeV], [400.0*GeV, 50.0*GeV]], 2.139336*pb],
    [[400.0*GeV, 75.0*GeV], [400.0*GeV, 75.0*GeV]], 2.472143*pb],
    ...
```

Data Set Folder: Efficiency Map Type  For EM-type results the dataInfo.txt contains an id to identify the data set (signal region), the number of observed and expected background events and the error on the number of background events for this signal region and the respective signal upper limits. Below we list the content of CMS-SUS-13-012-eff/3NJet6_1000HT1250_200MHT300/dataInfo.txt as an example:

```
dataType: efficiencyMap
dataId: 3NJet6_1000HT1250_200MHT300
observedN: 335
expectedBG: 305
bgError: 41
upperLimit: 5.681*fb
expectedUpperLimit: 4.585*fb
```

Each TxName.txt file then contains the efficiency map for a given simplified model as well
as some meta information. Here are the first few lines of CMS-SUS-13-012-eff/3NJet6_1000HT1250_200MHT300/T2.txt:

```
| txName: T2 |
| conditionDescription: None |
| condition: None |
| constraint: [[['jet']], [['jet']]] |
| figureUrl: https://twiki.cern.ch/twiki/pub/CMSPublic/PhysicsResultsSUS13012/Fig_7a.pdf |
```

This first block of data in the T2.txt file contains information about the element ([['jet'],[['jet']]]) in bracket notation for which the efficiencies refers to as well as reference to the original data source and some additional information. The second block of data contains the efficiencies as a function of the BSM masses, given as a Python array with the structure [[masses,efficiency],[masses,efficiency],...]:

```
| efficiencyMap: [ |
| [[312.5*GeV, 12.5*GeV], [312.5*GeV, 12.5*GeV]], 0.00109], |
| [[312.5*GeV, 62.5*GeV], [312.5*GeV, 62.5*GeV]], 0.00118], |
| [[312.5*GeV, 112.5*GeV], [312.5*GeV, 112.5*GeV]], 0.00073], |
| [[312.5*GeV, 162.5*GeV], [312.5*GeV, 162.5*GeV]], 0.00044], |
| ... |
```

**Binary (Pickle) Format**

At the first time of instantiating the Database class, the text files in database-path are loaded and parsed, and the corresponding data objects are built. The efficiency and upper limit maps themselves are subjected to standard preprocessing steps such as a principal component analysis and Delaunay triangulation. The simplices defined during triangulation are then used for linearly interpolating the data grid, thus allowing SModelS to compute efficiencies or upper limits for arbitrary mass values (as long as they fall inside the data grid). This procedure provides an efficient and numerically robust way of dealing with generic data grids, including arbitrary parametrizations of the mass parameter space, irregular data grids and asymmetric branches.

For the sake of efficiency, the entire database – including the Delaunay triangulation – is then serialized into a pickle file, which will be read directly the next time the database is loaded. If any changes in the database folder structure are detected, the Python or the SModelS version has changed, SModelS will automatically re-build the pickle file. This action may take a few minutes, but it is performed only once. If desired, the pickling process can be skipped using the option force_load = ‘txt’ when running SModelS (see Section 4).
3 The SModelS Procedure

In this section we describe in detail the main tasks performed by SModelS: the simplified model decomposition, the computation of the relevant signal cross-sections (“theory predictions”) and how these are confronted with the constraints stored in the database. Finally, we explain how missing topologies are identified. First, however, we need to describe how the information about the full model is given as an input.

3.1 Input Model

The information about the input (full) model can be given as

- an SLHA (SUSY Les Houches Accord [39]) file containing masses, branching ratios and cross sections for the BSM states, or
- an LHE (Les Houches Event [40]) file containing parton level events.

The SLHA format is usually more compact and best suited for supersymmetric models. On the other hand, an LHE file can always be generated for any BSM model (through the use of your favorite MC generator).\(^5\) In this case, however, the precision of the results is limited to the MC statistics used to generate the file.

**In the case of SLHA input**, the production cross sections for the BSM states have to be included in the SLHA file following the format defined in [41]. Figure 10 exemplifies the SLHA cross section format with \(pp \rightarrow \tilde{u}_L^* + \tilde{g}\) at a center-of-mass energy of 8 TeV and at NLO+NLL QCD accuracy. The information used by SModelS are the center-of-mass energy, the outgoing particle PID’s, the cross section value, and the QCD order. If the input file contains two cross sections for the same process but at different QCD orders, only the highest order will be used.

For the MSSM and some of its extensions,\(^6\) the cross sections may be calculated automatically and appended to the SLHA file using the cross-section calculator tool provided by SModelS, see Appendix B.1.

**In the case of LHE input**, the total production cross section as well as the center-of-mass energy should be listed in the \(<\text{init}>/\text{init}>\) block, according to the standard LHE format. Moreover, all the \(\mathbb{Z}_2\)-even particles (see definition in Section 2.1) should be set as stable, since in SModelS they are effectively considered as final states. When generating the events it is also important to ensure that no mass smearing is applied, so the mass values for a given particle are the same throughout the LHE file.

\(^5\)SModelS can easily be used for non-SUSY models as long as they present a \(\mathbb{Z}_2\)-type symmetry. However, as mentioned at the beginning of Section 2 (see also [6]), a few caveats need to be taken into account. It is the responsibility of the user to make sure that the experimental results used actually apply to the model under consideration—if necessary, a subset of results can be selected via the parameters.ini file, see Section 4.2.

\(^6\)Typically extensions by a dark matter candidate other than the neutralino as the lightest SUSY particle (LSP). If the direct production of non-MSSM particles is important, the relevant cross sections have to be computed by external tools and then added by the user to the SLHA file.
New Particles

Besides information about the masses and branching ratios, the user must also define which particles are $\mathbb{Z}_2$-odd states (intermediate states) and which are $\mathbb{Z}_2$-even (final states). These definitions must be given in the `particles.py` file, where some default values (for SM and MSSM particles) are already loaded.

If the user wants to check the SLHA input file for possible errors (see Appendix B.2), it is also necessary to define the particle’s quantum numbers in the `particles.py` file.

3.2 Decomposition into Simplified Models

Given an input model, the first task of SModelS is to decompose it into a sum of simplified models (or ‘elements’ in SModelS language). Based on the input format, SLHA or LHE file, one of two distinct decomposition methods is applied: either the SLHA-based or the LHE-based decomposition.

SLHA-based Decomposition

The SLHA file describing the input model is required to contain the masses of all the BSM states as well as their production cross sections and decay branching ratios. All of this information must follow the SLHA file standard.

Once the production cross sections are read from the input file, all the cross sections for production of two $\mathbb{Z}_2$-odd states are stored and serve as the initial step for the decomposition. (All the other cross sections with a different number of $\mathbb{Z}_2$-odd states are ignored.) Starting from these primary mothers, all the possible decays are generated according to the information contained in the DECAY blocks. This procedure is represented by the first decomposition step shown in Figure 11. Each of the possible cascade decays for each mother corresponds to a branch. In order to finally generate elements, all the branches are combined in pairs according to the branching ratios, as shown by the second step in Figure 11.

Each of the elements generated according to the procedure just described will also store its weight, which equals the element production cross section times all the branching ratios appearing in it. In
Figure 11: SModelS decomposition process: the diagram represents the creation of elements given the primary mother pair production and subsequent branches.

Order to avoid a too large number of elements, only those satisfying a minimum weight requirement are kept. Furthermore, the elements are grouped according to their topologies. The final output of the SLHA decomposition is a list of such topologies, where each topology contains a list of the elements generated during the decomposition.

**Minimum Decomposition Weight** Some models may contain a large number of new states and each may have a large number of possible decays. As a result, long cascade decays are possible and the number of elements generated by the decomposition process may become too large, resulting in excessively long computing times. For most practical purposes, however, elements with very small weights can be discarded, since they will fall well below the experimental limits. Therefore, during the SLHA decomposition, whenever an element is generated with a weight below some minimum value, this element, and all elements which would be derived from it, are ignored. The minimum weight to be considered is set by the \( \text{sigmacut} \) parameter and is easily adjustable, see Section 4.2.

Note that, when computing the theory predictions, the weight of several elements can be combined together. Hence it is recommended to set the value of \( \text{sigmacut} \) approximately one order of magnitude below the minimum signal cross sections the experimental data can constrain.

**LHE-based Decomposition**

More general models can be input through an LHE event file containing parton-level events, including the production of the primary mothers and their cascade decays. Each event can then be directly mapped to an element with the element weight corresponding to the event weight. Finally, identical elements can be combined together (adding their weights). How the information from an LHE event is used to construct a SModelS element is illustrated in Figure 12.
Figure 12: An example of an LHE event. Arrows indicate the information used by SModelS to construct the corresponding element.

Notice that, for the LHE decomposition, the elements generated are restricted to the events in the input file. Hence, the uncertainties on the elements weights (and which elements are actually generated by the model) are fully dependent on the Monte Carlo statistics used to generate the LHE file. Also, when generating the events it is important to ensure that no mass smearing is applied, so the events always contain the same mass value for a given particle.

Compression of Elements

During the decomposition process it is possible to perform several simplifications on the elements generated. In both the LHE and SLHA-based decompositions, two useful simplifications are possible: mass compression and invisible compression. The main advantage of performing these compressions is that the simplified element is always shorter (has fewer cascade decay steps), which makes it more likely to be constrained by experimental results. The details behind the compression methods are as follows:

**Mass Compression**  In case of small mass differences, the decay of an intermediate state to a nearly degenerate one will in most cases produce soft final states, which can not be experimentally detected. Consequently, it is a good approximation to neglect the soft final states and compress the respective decay, as shown in Figure 13.

After the compression, only the lightest of the two near-degenerate masses are kept in the element, as shown in Figure 13. The main parameter which controls the compression is called \texttt{minmassgap} (see Section 4.2), which corresponds to the maximum value of \( \varepsilon \) in Figure 13 up to which the compression is performed:
if $|M_j - M_{j+1}| < \text{minmassgap}$ → the decay is compressed
if $|M_j - M_{j+1}| > \text{minmassgap}$ → the decay is NOT compressed

Note that the compression is an approximation since the final states, depending on the boost of the parent state, may not always be soft. It is recommended to choose values of $\text{minmassgap}$ of 1–10 GeV; the default value is 5 GeV.

**Invisible Compression** Another type of compression is possible when the final states of the last decay are invisible. The most common example is

$$A \rightarrow \nu + B$$

as the last step of the decay chain, where $B$ is an invisible particle leading to a MET signature. Since both the neutrino and $B$ are invisible, for all experimental purposes the effective MET object is $B + \nu = A$. Hence it is possible to omit the last step in the cascade decay, resulting in a compressed element. Note that this compression can be applied consecutively to several steps of the cascade decay if all of them contain only invisible final states, as illustrated in Figure 14.

### 3.3 Computing Theory Predictions

After the decomposition of the input model into simplified models, the next step consists of computing the relevant signal cross sections (or *theory predictions*) for comparison with the experimental limits.

Note that UL and EM-type results each require different theoretical predictions to be compared against experimental limits. While UL-type results constrain the total weight ($\sigma \times \text{BR}$) of a given simplified model, EM-type results constrain the total signal cross-section ($\sum \sigma \times \text{BR} \times \varepsilon$) in a given signal region (data set). We deal with both types of results in an equal footing by defining

$$\text{theory prediction} = \sum_{\text{elements}} (\sigma \times \text{BR} \times \varepsilon)$$

(1)

Figure 13: Schematic representation of ‘mass compression’ performed by SModelS to deal with soft final states.
Figure 14: A schematic representation of ‘invisible compression’ as performed by SModelS to deal with the emission of invisible particles in the final steps of the cascade decay.

where $\epsilon$ is a “generalized efficiency”: for EM-type results it corresponds to the simplified model signal efficiency, while for UL-type results it equals to 1 (0) if the element is (is not) constrained by the experimental result. With this definition the theory prediction value can then be directly compared to the respective 95% CL upper limit on the signal cross-section extracted from the UL map (for UL-type results) or with the signal upper limit for the respective signal region (for EM-type results).

The calculation of the theory prediction can always be divided in two main steps: Element Selection and Element Clustering, as shown schematically in Figure 15. These steps are described in more detail below.

Figure 15: SModelS procedure for computing the signal cross sections. The generated elements undergo selection and clustering procedure before the final theory prediction can be compared with the corresponding experimental limit.

**Element Selection**

Given a specific experimental result (either EM-type or UL-type), the first step for computing the theory predictions is to select the simplified models which are constrained by the corresponding result. For EM-type results this corresponds to selecting all elements which contain non-zero efficiencies ($\epsilon$) for a given signal region, while for UL-type results this step implies selecting all elements which are constrained by the corresponding UL map (see Section 2.2).
During this step, the selected elements have their weights \((\sigma \times BR)\) rescaled by their corresponding efficiencies. As mentioned above, for UL-type results these efficiencies are trivial and equal 1 (0) if the element appears (does not appear) in the UL constraint. On the other hand, for EM-type results, these efficiencies are obtained from the efficiency maps stored in the database for the corresponding experimental result/data set.

At the end of the element selection step only the elements with non-zero (rescaled) weights are relevant for computing the theory prediction for the corresponding experimental result and all the other elements are ignored. The procedure just described is illustrated graphically in Figures 16 and 17 for an UL-type and EM-type result, respectively.

**Element Clustering**

Naively one would expect that after all the elements constrained by the experimental result have been selected and their weights have been rescaled by the corresponding efficiencies, it is trivial to compute the theory prediction. One must simply sum up the weights \((\sigma \times BR \times \epsilon)\) of all the selected elements. This is indeed the case for EM-type results, where the final theory prediction is simply given by the sum of the selected element weights.

For UL-type results, however, the experimental limit on \(\sigma \times BR\) only applies to elements with the same mass\(^7\) (or mass array). As a result, the selected elements must be grouped into *clusters* of equal masses. When grouping the elements, one can allow for small mass differences, since the experimental efficiencies should not be strongly sensitive to them. For instance, assume two elements contain identical mass arrays, except for the parent masses which differ by 1 MeV. In this case it

---

\(^7\)When referring to an element mass, we mean all the intermediate state masses appearing in the element (see Section 2.1 for more details). Two elements are considered to have identical masses if their mass arrays are identical.
is obvious that for all experimental purposes the two elements have identical masses and should contribute to the same theory prediction (e.g., their weights should be added when computing the signal cross section). Unfortunately there is no way to unambiguously define “similar masses” and the definition should depend on the experimental result, since different results will be more or less sensitive to mass differences. SModelS uses an UL map-dependent measure of the distance between two element masses, as described below.

If two of the selected elements have a mass distance smaller than a maximum value (defined by \( \text{maxDist} \)), they are grouped in the same mass cluster, as illustrated in Figure 18. Once all the elements have been clustered, their weights can finally be added together and compared against the experimental upper limit.

\[ \text{Mass Distance} \] As mentioned above, for UL-type results it is necessary to group elements with similar masses. Since an absolute definition of “similar masses” is not possible and the sensitivity to mass differences depends on the experimental result, SModelS uses an “upper limit map-dependent” definition. For each element’s mass array, the upper limit for the corresponding mass values is obtained from the UL map. This way, each mass array is mapped to a single number (the cross section upper limit for the experimental result). Then the distance between the two elements’ masses is simply given by the relative difference between their respective upper limits. More explicitly:

\[
\text{Element } A \ (M_A = [[M_1, M_2, \ldots], [m_1, m_2, \ldots]]) \rightarrow \text{Upper Limit}(M_A) = x \\
\text{Element } B \ (M_B = [[M_1', M_2', \ldots], [m_1', m_2', \ldots]]) \rightarrow \text{Upper Limit}(M_B) = y \\
\Rightarrow \text{mass distance}(A, B) = \frac{2|x - y|}{(x + y)} \quad (2)
\]
where $M_A, M_B (x, y)$ are the mass arrays (upper limits) for the elements A and B, respectively. If the mass distance of two elements is smaller than $\text{maxDist}$, the two masses are considered similar. The default value for $\text{maxDist}$ in SModelS is 0.2.

Notice that the above definition of mass distance quantifies the experimental analysis’ sensitivity to mass differences, which is the relevant parameter when clustering elements. Also, a check is performed to ensure that masses with very distinct values but similar upper limits are not clustered together.

### 3.4 Confronting Predictions with Experimental Limits

#### R-Values

Once the relevant signal cross sections (theory predictions) have been computed for the input model, they must be compared to the respective experimental constraints. SModelS reports the result in the form of $r$-values defined as

$$r = \frac{\text{theory prediction}}{\text{upper limit}}.$$  \hspace{1cm} (3)

In the case of an UL-type result, the theory predictions typically consist of a list of signal cross sections (one for each cluster). Each theory prediction must then be compared to its corresponding upper limit. This limit is simply the cross section upper limit provided by the experimental publication or preliminary result and is extracted from the corresponding UL map (see Section 2.2).

For EM-type results there is a single theory prediction ($\sum \sigma \times BR \times \varepsilon$) for each data set (or signal region). This value must be compared to the upper limit on the number of signal events for the
corresponding signal region. This upper limit is easily computed using the number of observed and expected events for the data set and their uncertainties and is typically stored in the database. Since most EM-type results have several signal regions (data sets), there will be one theory prediction/upper limit for each data set. By default SModelS considers only the best data set, i.e. the one with the largest value for \( r_{\text{exp}} = (\text{theory prediction})/(\text{expected limit}) \). In this case each EM-type result will have a single \( r \)-value, corresponding to the signal region with the best expected limit.

The procedure described above can be applied to all the experimental results in the database, resulting in a list of theory predictions and upper limits for each experimental result. A model can then be considered excluded by the experimental results if, for one or more predictions, we have \( r > 1 \). SModelS can also identify the relevant simplified model topologies which have large cross-sections, but are not constrained by any of the experimental results in the database, see Section 3.5.

**Likelihood Computation** In the case of EM-type results, additional statistical information about the constrained model can be provided by the SModelS output. Following Ref. [42], we construct a simplified likelihood which describes the plausibility of the data \( D \), given a signal strength \( \mu \):

\[
\mathcal{L}(\mu, \theta|D) = P(D|\mu + b + \theta) p(\theta).
\] (4)

Here, \( \theta \) denotes the nuisance parameter that describes the variations in the signal and background contributions due to systematic effects. We assume \( p(\theta) \) to follow a Gaussian distribution centered around zero and with a variance of \( \delta^2 \), whereas \( P(D) \) corresponds to a counting variable and is thus properly described by a Poissonian. The complete likelihood thus reads

\[
\mathcal{L}(\mu, \theta|D) = \frac{(\mu + b + \theta)^{n_{\text{obs}}} e^{-(\mu + b + \theta)}}{n_{\text{obs}}!} \exp \left( -\frac{\theta^2}{2\delta^2} \right),
\] (5)

where \( n_{\text{obs}} \) is the number of observed events in the signal region. A test statistic \( T \) can now be constructed from a likelihood ratio test:

\[
T = -2\ln \frac{H_0}{H_1} = -2\ln \left( \frac{\sup\{\mathcal{L}(\mu, \theta|D) : \mu \in \mathbb{R}^+\}}{\mathcal{L}(\mu = n_{\text{signal}}, \theta|D)} \right).
\] (6)

As the signal hypothesis in the numerator presents a special case of the likelihood in the denominator, the Neyman-Pearson lemma holds, and we can assume \( T \) to be asymptotically distributed according to a \( \chi^2 \) distribution with one degree of freedom. Of course care must taken in deep Poissonian cases where both \( b \) and \( \theta \) are small, as the test statistic in this case cannot be expected to follow a \( \chi^2 \) distribution anymore. Because \( H_0 \) assumes the signal strength of a particular model, \( T = 0 \) corresponds to a perfect match between that model’s prediction and the measured data. \( T \gtrsim 3.84 \) corresponds to a 95% CL upper limit (in the asymptotic case).

---

8The statistical significance of the exclusion statement is difficult to quantify exactly, since the model is being tested by a large number of results simultaneously.
While \( n_{\text{obs}} \), \( b \) and \( \delta_{b} \) are directly extracted from the data set (coined \texttt{observedN}, \texttt{expectedBG} and \texttt{bgError}, respectively), \( n_{\text{signal}} \) is obtained from the calculation of the theory predictions. A default 20\% systematical uncertainty is assumed for \( n_{\text{signal}} \), resulting in \( \delta^{2} = \delta_{b}^{2} + (0.2n_{\text{signal}})^{2} \).

SModelS reports the \( \chi^{2} \) (\( T \) values) and likelihood for each EM-type result, together with the observed and expected \( r \) values. We note that in the general case analyses may be correlated, so summing up the \( T \) values will no longer follow a \( \chi^{2} \) distribution. Therefore, for a conservative interpretation, only the result with the best expected limit should be used. Moreover, for a statistically rigorous usage in scans, it is recommended to check that the analysis giving the best expected limit does not wildly jump within continuous regions of parameter space that give roughly the same phenomenology.

### 3.5 Identifying Missing Topologies

The constraints provided by SModelS are obviously limited by the available set of simplified model interpretations in the database. Therefore it is interesting to identify classes of missing simplified models (termed ‘missing topologies’) which are relevant for a given input model, but are not constrained by the results in the SModelS database. This task is performed as a last step in SModelS, once the decomposition and the theory predictions have been computed.

Using the decomposition output, the elements (see Section 2.1) which are not tested by any of the experimental results in the database are grouped into the following classes:\(^9\)

- \textit{missingTopos}: elements whose final states are not tested by any of the experimental results in the database (independent of the element mass). The missing topologies are further classified as:
  - \textit{longCascade}: elements with long cascade decays (more than one intermediate particle in one of the branches);
  - \textit{asymmetricBranches}: elements with one branch differing from the other (not considering cases of long cascade decays, see above).

- \textit{outsideGrid}: elements which could be tested by one or more experimental results, but are not constrained because the mass array falls outside the experimental mass grids.

Usually the list of \textit{missingTopos} or \textit{outsideGrid} elements is of considerable length. Hence, to compress this list, all elements differing only by their masses (with the same final states) or electric charges are combined into a \textit{missing} or \textit{outsideGrid} topology. Moreover, by default, electrons and muons are combined to light leptons (denoted “l”); gluons and light quarks are combined into jets. The \textit{missing} topologies are then further classified (if applicable) into \textit{longCascade} or \textit{asymmetricBranches} topologies.

The topologies for each of the four categories are then grouped according to the final state (for the \textit{missingTopos} and \textit{outsideGrid} classes) or according to the PID’s of the initially produced mother particles (for the \textit{longCascade} and \textit{asymmetricBranches} classes). For the latter, elements deriving

\(^9\)If mass or invisible compression are turned on, elements which can be compressed are not considered, to avoid double counting.
from different mother particles but with the same final state and mass array cannot be distinguished and are therefore combined. The full list of mother PID’s is provided in the Python output or as a comment in both the ‘stdout’ and ‘summary’ outputs.

The topology coverage tool is normally called from within SModelS (e.g., when running runSModelS.py) by setting testCoverage=True in the parameters file (see Section 4.2). In the output, contributions in each category are ordered by cross section. By default only the ten with the largest cross sections are shown.

4 Using SModelS

SModelS ships with a command-line tool, runSModelS.py, which is deemed configurable enough to cover a large range of applications. The functionalities contained in this tool include detailed checks of input SLHA or LHE files, running the decomposition, evaluating the theory predictions and comparing them to the experimental limits available in the database, determining missing topologies and printing the output in several available formats. Moreover, starting from v1.1.0, runSModelS.py can process a whole folder containing a set of SLHA or LHE files in a parallelized fashion.

The command-line tool and the parameter file are described in detail below. Users familiar with Python and the SModelS basics may however prefer to write their own main routine. A simple example code is provided in Example.py and explained step-by-step in the html manual.

Finally, SModelS can also conveniently be used within micrOMEGAS, as explained in [43].

4.1 Usage of runSModelS.py

runSModelS.py [-h] -f FILENAME [-p PARAMETERFILE] [-o OUTPUTDIR] [-d] [-t] [-V] [-c] [-v VERBOSE] [-T TIMEOUT]

arguments:

-h, --help show this help message and exit.

-f FILENAME, --filename FILENAME name of SLHA or LHE input file or a directory path (required argument). If a directory is given, loop over all files in the directory.

-p PARAMETERFILE, --parameterFile PARAMETERFILE name of the parameter file, where most options are defined (optional argument). If not set, use all parameters from smodels/etc/parameters_default.ini.

-o OUTPUTDIR, --outputDir OUTPUTDIR name of output directory (optional argument). The default folder is ./results/.
-d, --development if set, SModelS will run in development mode and exit if any errors are found
-t, --force_txt force loading the text database.
-V, --version show program’s version number and exit
-c, --run-crashreport parse crash report file and use its contents for a SModelS run. Supply the crash file simply via ‘–filename myfile.crash’.
-v VERBOSE, --verbose VERBOSE sets the verbosity level (debug, info, warning, error). Default value is “info”.
-T TIMEOUT, --timeout TIMEOUT define a limit on the running time (in secs).

A typical usage example is:

```
runSModelS.py -f inputFiles/slha/gluino_squarks.slha
             -p parameters.ini -o ./ -v warning
```

The resulting output will be generated in the current folder, according to the printer options set in the parameter file.

### 4.2 Parameter File

The basic options and parameters used by `runSModelS.py` are defined in the parameter file. An example parameter file, including all available parameters together with a short description, is stored in `parameters.ini`. If no parameter file is specified, the default parameters stored in `smodels/etc/parameters_default.ini` are used. Below we describe each entry in the parameter file.

**options:** main options for turning SModelS features on or off

- **checkInput** (True/False): if True, `runSModelS.py` will run the file check tool on the input file and verify that the input contains all the necessary information.
- **doInvisible** (True/False): turns invisible compression on or off during the decomposition.
- **doCompress** (True/False): turns mass compression on or off during the decomposition.
- **computeStatistics** (True/False): turns the likelihood and $\chi^2$ computation on or off for EM-type results (see Section 3.4).
- **testCoverage** (True/False): set to True to run the coverage tool (see Section 3.5).

**parameters:** basic parameter values for running SModelS

- **sigmacut** (float): minimum value for an element weight (in fb). Elements with a weight below `sigmacut` are neglected during decomposition of SLHA input files (see Section 3.2).
default value is 0.03 fb. Note that, depending on the input model, the running time may increase considerably if sigmacut is too low, while too large values might eliminate relevant elements.

- **minmassgap** (float): maximum value of the mass difference (in GeV) for performing mass compression. The default value is 5 GeV. *Only used if doCompress = True.*

- **maxcond** (float): maximum allowed value (in the [0,1] interval) for the violation of upper limit conditions. A zero value means the conditions are strictly enforced, while 1 means the conditions are never enforced. *Only relevant for printing the output summary.*

- **ncpus** (int): number of CPUs. When processing multiple SLHA/LHE files, SModelS can be run in a parallelized fashion, splitting up the input files in equal chunks. ncpus=-1 uses the total number of CPU cores of the machine.

**database:** allows for selection of a subset of experimental results from the database

- **path:** the absolute or relative path to the database. The user can supply either the directory name of the database, or the path to the pickle file (see Section 2.2).

- **analyses** (list of results): set to *all* to use all available results. If a list of experimental analyses is given, only these will be used. For instance, setting analyses = ATLAS-SUSY-2015-09, CMS-PAS-SUS-15-002 will only use the experimental results from these two analyses.

- **txnames** (list of topologies): set to *all* to use all available simplified model topologies. The topologies are labeled according to the TxName convention. If a list of TxNames are given, only the corresponding topologies will be considered. For instance, setting txnames=T2 will only consider experimental results for $pp \rightarrow \tilde{q} + \tilde{q} \rightarrow (jet + \tilde{\chi}^0_1) + (jet + \tilde{\chi}^0_1)$ and the output will only contain constraints for this topology. A list of all topologies and their corresponding TxNames can be found at [38].

- **dataselector** (list of datasets): set to *all* to use all available data sets. If dataselector = upperLimit (efficiencyMap), only UL-type results (EM-type results) will be used. Furthermore, if a list of signal regions (data sets) is given, only the experimental results containing these datasets will be used. For instance, if dataselector = SRA mCT150, SRA mCT200, only these signal regions will be used.

- **discardZeroes** (True/False): set to True to discard all efficiency maps with zero-only entries.

**printer:** main options for the output format

- **outputType** (list of outputs): use to list all the output formats to be generated. Available output formats are: summary, stdout, log, python, xml and slha.

**stdout-printer:** options for the stdout or log printer

- **printDatabase** (True/False): set to True to print the list of selected experimental results to stdout.

- **addAnaInfo** (True/False): set to True to include detailed information about the TxNames tested by each experimental result. *Only used if printDatabase=True.*
• printDecomp (True/False): set to True to print basic information from the decomposition (topologies, total weights, ...).

• addElementInfo (True/False): set to True to include detailed information about the elements generated by the decomposition. Only used if printDecomp=True.

• printExtendedResults (True/False): set to True to print extended information about the theory predictions, including the PID’s of the particles contributing to the predicted cross section, their masses and the expected upper limit (if available).

• addCoverageID (True/False): set to True to print the list of element IDs contributing to each missing topology (see coverage). Only used if testCoverage = True. This option should be used along with addElementInfo = True so the user can precisely identify which elements were classified as missing.

**summary-printer:** options for the summary printer

- expandedSummary (True/False): set to True to include in the summary output all applicable experimental results, False for only the strongest one.

**python-printer:** options for the Python printer

- addElementList (True/False): set to True to include in the Python output all information about all elements generated in the decomposition. If set to True the output file can be quite large.

**xml-printer:** options for the xml printer

- addElementList (True/False): set to True to include in the xml output all information about all elements generated in the decomposition. If set to True the output file can be quite large.

### 4.3 Output

The results of runSModelS.py are printed in the format(s) specified by the outputType in the parameter file. The following formats are available:

- a human-readable screen output (stdout) or log output. These are intended to provide detailed information about the database, the decomposition, the theory predictions and the missing topologies. The complexity of the output can be controlled through several options in the parameter file. Due to its size, this output is not suitable for storing the results from a large scan; it is more appropriate for a single file input.

- a human-readable text file output containing a summary of the run. This format contains the main SModelS results: the theory predictions and the missing topologies, as described in detail below. It can be used for a large scan, since the output can be made quite compact, using the options in the parameter file.

- a Python dictionary printed to a file containing information about the decomposition, the theory predictions, and the missing topologies. The output can be significantly long, if all options in the parameter file are set to True. However this output can be easily imported to a Python
environment, making it easy to access the desired information. For users familiar with the Python language this is the recommended format.

- an xml file containing information about the decomposition, the theory predictions and the missing topologies. The output can be significantly long, if all options are set to True.
- a .smodelsslha file (outputType=slha) containing a summary of the most constraining results, and the missing topologies in the SLHA-type format described in [43].

Notes:

- The list of elements can be extremely long. Try setting addElementInfo = False and/or printDecomp = False to obtain a smaller output.

- A comment of caution is in order regarding a potentially naive use of the highest r-value reported by SModelS, as this does not necessarily come from the most sensitive analysis. For a rigorous statistical interpretation, one should use the r-value of the result with the highest expected r ($r_{exp}$). Unfortunately, for UL-type results, the expected limits are often not available; $r_{exp}$ is then reported as N/A in the SModelS output.

- We also point out that the r-values do not include systematic uncertainties for the signal prediction. The signal uncertainties may be relevant, in particular in cases where cross sections are computed only at LO.

As an example we explain below the text-type (summary) output obtained from the sample file gluino_squarks.slha in inputFiles/slha/. The output file is written in terms of the following blocks:

- information about the basic input parameters and the status of the run:

```plaintext
Input status: 1
Decomposition output status: 1 #decomposition was successful
# Input File: inputFiles/slha/gluino_squarks.slha
# maxcond = 0.2
# minmassgap = 5.
# ncpus = 1
# sigmacut = 0.03
# Database version: 1.1.1
```

- a list of all the theory predictions obtained and the corresponding experimental result upper limit. If expandedSummary = False only the most constraining experimental result is printed. For each applicable experimental result, the corresponding experimental result ID and the center-of-mass energy ($sqrts$) are printed together with the theory cross section (‘Theory_Value’), the observed upper limit (‘Exp_limit’), the (theory cross section)/(observed upper limit) ratio (r) and, when available, the expected r value (r_expected). Moreover, the condition violation is given for UL-type results; for EM-type results the signal region used is printed. Finally, the TxNames contributing to the signal cross section are listed and, if
computeStatistics = True, the $\chi^2$ and likelihood values are printed for EM-type results:

| Analysis | Sqrts (TeV) | Cond_Violation | Theory_Value(fb) | Exp_limit(fb) | $r$ | $r$_expected |
|----------|-------------|----------------|------------------|--------------|-----|--------------|
| CMS-SUS-13-019 | 8.00E+00 | 0.0 | 1.773E+00 | 3.760E+00 | 4.716E-01 | N/A |
| Signal Region: | (UL) | Txnames: | T2 |
| ATLAS-SUSY-2013-02 | 8.00E+00 | 0.0 | 6.617E+00 | 1.718E+01 | 3.851E-01 | N/A |
| Signal Region: | (UL) | Txnames: | T6WW |
| ATLAS-SUSY-2013-02 | 8.00E+00 | 0.0 | 5.525E-01 | 1.818E+00 | 3.039E-01 | 3.653E-01 |
| Signal Region: | SR2jt | Txnames: | T1, T2 |
| Chi2, Likelihood = | 4.185E-02 | 2.542E-02 |
| ... |

- the maximum value for the (theory cross section)/(observed upper limit) ratio. If this value is higher than 1, the input model is likely excluded by one of the experimental results.

| Total missing topology cross section (fb): | 2.767E+02 |
| Total cross section where we are outside the mass grid (fb): | 1.760E-01 |
| Total cross section in long cascade decays (fb): | 1.096E+02 |
| Total cross section in decays with asymmetric branches (fb): | 1.630E+02 |

- summary information about the missing topologies, if testCoverage = True. The total ‘missing topology’ cross section corresponds to the sum of weights of all elements which are not tested by any experimental result. If an element is constrained by one or more experimental results, but its mass is outside the efficiency or upper limit grids, its cross section is instead included in the “outside the mass grid” category. Finally, the elements which contribute to the total missing topology cross section are subdivided into elements with long decays (cascades with more than one intermediate particle) and with asymmetric branches.

| Missing topologies with the highest cross sections (up to 10): |
| Sqrts (TeV) | Weight (fb) | Element description |
|-------------|--------------|---------------------|
| 8.0 | 1.601E+01 | # | [[[jet],[W]],[[jet,jet],[W]]] |
| 8.0 | 1.395E+01 | # | [[[jet],[jet,jet],[W]],[[jet,jet],[W]]] |
| 8.0 | 9.206E+00 | # | [[[b,t],[W]],[[jet,jet],[W]]] |

- detailed information about the topologies which are outside the experimental results data grid:
5 Conclusions and Outlook

SModelS is an automated tool for interpreting simplified model results from the LHC. It can decompose the signatures of any BSM model containing a $\mathbb{Z}_2$ symmetry into its SMS topologies and compare them to the existing LHC constraints from a large database of experimental results.

Version 1.1 of the code, presented in this paper, includes several new features, most importantly the use of efficiency maps. Efficiency maps allow us to combine the results from different topologies and thus improve the constraining power of the tool. SModelS v1.1 is also equipped with a likelihood and $\chi^2$ calculator useful for a basic statistical interpretation of the results. Moreover, extended information is provided on the topology coverage. Several speed improvements are further included in order to allow for a faster testing of BSM models.

Not counting results marked as ‘superseded by a more recent analysis’, the database v1.1.1 is comprised of 186 results (125 upper limits and 61 efficiency maps) from 21 ATLAS and 23 CMS SUSY searches [44], covering a total of 37 simplified models. From these 44 searches, 11 (4 from ATLAS and 7 from CMS) are based on early 13 TeV Run 2 data, comprising 35 UL-type and 2 EM-type results. FastLim-1.0 efficiency maps converted to SModelS v1.1 format are also available; they cover another 15 simplified models.

A new database browser tool is provided for easy access to the information stored in the database. An update of the database with more 13 TeV results is in preparation and will be released soon, as will be
Figure 19: Fraction of the ATLAS-excluded pMSSM points [45] also excluded by SModelS as a function of the gluino mass. The exclusion using only UL-type results (blue) is contrasted to the exclusion achieved by using also EM-type results (red). Note that this is based on 8 TeV results only; points with long-lived sparticles are not considered.

new ‘home-grown’ efficiency maps for testing topologies currently absent in the SModelS database.

To illustrate the importance of the extension to efficiency maps presented here, we have tested how SModelS v1.1 constrains the publicly available points from the ATLAS pMSSM study [45]. For a direct comparison with ATLAS, we here consider only 8 TeV results in the database. Points with long-lived BSM particles, which currently cannot be treated in SModelS, are discarded. The fraction of points excluded by ATLAS which is also excluded by SModelS is shown in Figure 19 as a function of the gluino mass. As can be seen, the gain from using efficiency maps is quite substantial, in particular for gluinos within LHC reach that exhibit a variety of different decay modes.\textsuperscript{10}

Generally, the improvement achieved by using efficiency maps is particularly relevant for regions of parameter space where the signal cross section is spread over several competing simplified model topologies. We therefore ask the ATLAS and CMS collaborations to provide as much as possible efficiency maps for each (aggregated) signal region in addition to the UL maps—this will considerably enhance the usefulness of their SMS interpretations. The alternative is to produce ‘home-grown’ efficiency maps based on implementations of the experimental analyses in public recast frameworks like MADANALYSIS 5 [14, 15] or CHECKMATE [12, 13] as presented in Appendix C. This is, however, clearly less precise than using ‘official’ efficiency maps.

\textsuperscript{10}A detailed study of the coverage of the pMSSM by simplified model results will be presented elsewhere.
In conclusion, SModelS v1.1 marks an important milestone for the SModelS collaboration, and towards the efforts of using SMS results in a systematic fashion. However, the mission is far from complete: extending the software to non-MET final states is but one out of several major improvements envisaged for future versions of SModelS.

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A Installation and Deployment

A.1 Standard Installation

SModelS is Python code that requires Python version 2.6 or later with the Python packages setuptools, unum, numpy, argparse, docutils (≥ 0.3), scipy (≥ 0.9.0), and pyslha (≥ 3.1.0).

The cross section computer provided by smodelsTools.py makes use of PYTHIA 6.4 [21] or PYTHIA 8.2 [21, 22] together with NLLFAST 1.2 (7 TeV), 2.1 (8 TeV), and 3.1 (13 TeV) [23–29]. These programs need not be downloaded separately: PYTHIA 6.4.27 and NLLFAST are included in the SModelS v1.1 distribution, while PYTHIA 8 will be downloaded and compiled automatically when required. A fortran compiler (preferably gfortran) is needed to compile PYTHIA 6.4 and a C++ compiler for PYTHIA 8. In addition, the database browser in smodelsTools.py requires IPython.

SModelS v1.1 has been tested on Ubuntu, Scientific Linux (CERN) 5 and 6, as well as on Mac OS X 10.11. The SModelS package can be downloaded from [20]. Unpacking the tarball with

```
tar -zxvf smodels-v1.1.x.tgz
```

creates the directory smodels-v1.1.x, where the code (subdirectory smodels) and the results database (subdirectory smodels-database) are located.

For installation, SModelS makes use of Python’s setuptools:
python setup.py install

should install the entire project and compile the internal PYTHIA and NLLFAST versions. It should also resolve the external dependencies, i.e. install the Python libraries listed above using e.g. `pip`. If the Python libraries are installed in a system folder (as is the default behavior), it will be necessary to run the install command with superuser privilege. Alternatively, one can run `setup.py` with the “–user” flag:

```bash
python setup.py install --user
```

In case the compilation of SModelS fails, it is advised to try to compile the tools manually, by issuing “make” in the `lib/` or in `smodels-v1.1.x` directory. In case the installation of the external libraries fails, you can also try to install them manually, then rerun `setup.py`.

To further help with installation and deployment, there is also a diagnostic tool available:

```bash
python smodelsTools.py toolbox
```

lists and checks all internal tools (PYTHIA and NLLFAST) and external (`numpy`, `scipy`, `unum`, ...) dependencies.

More details on the installation procedure, in particular specific instructions for installation on Ubuntu, Scientific Linux, other platforms or without superuser privileges can be found in the README.rst file provided with the code. In case everything fails, please contact the authors at smodels-users@lists.oeaw.ac.at.

The installation procedure also installs the SModelS database of experimental results in the smodels-database subdirectory. As mentioned in Section 5, the v1.1.1 database release contains 186 results (125 upper limits and 61 efficiency maps) from 44 searches; 24 of the EM-type results were ‘home-grown’ using MADANALYSIS 5 [15] and CHECKMATE [12] recasting, see Appendix C. The database also includes 35 preliminary results from 13 ATLAS and 4 CMS notes which were superseded by a subsequent publication; they are kept in the database for historical reasons but are not used in the default settings in SModelS. The complete list of analyses and results included in the database can be consulted at [44]. We certify that all the results in the official database release have been carefully validated and the validation material can be found at [46].

### A.2 Adding Results to the Database

The database can conveniently be updated independently from SModelS code updates. It suffices to unpack any new database tarball and replace the database directory. In the same fashion, one can easily add additional results as explained below.

**Adding FastLim data**

The official SModelS database can be augmented with data from the FastLim [9] database. A tarball with the *properly converted fastlim-1.0* efficiency maps can be downloaded from [20].
Exploding the tarball in the top level directory of the database:

```
mv smodels-v1.1-fastlim-1.0.tgz <smodels-database folder>
cd <smodels-database folder>
tar -xzvf smodels-v1.1-fastlim-1.0.tgz
rm smodels-v1.1-fastlim-1.0.tgz
```

adds the FastLim-1.0 results in the standard directory structure (i.e. in 8TeV/ATLAS/), see Section 2.2.

SModelS auto-detects FastLim results and issues an acknowledgement. When using these results, please properly cite the FastLim paper [9] and the relevant experimental results; for convenience, a bibtex file is provided in the smodels-fastlim tarball.

For completeness we note that FastLim-1.0 contains 264 EM-type results based on 11 ATLAS conference notes, which were recast by the authors. Since in SModelS v1.1 efficiencies with a relative statistical uncertainty greater than 25% are set to zero and, moreover, zero-only EM’s are discarded per default, effectively used in practice are 163 EM-type results from 9 conference notes.

Adding one’s own results

The database is organized as files in an ordinary directory hierarchy. Therefore, adding additional experimental results is a matter of copying and editing text files. Once the new folders and files have been added following the format explained in Section 2.2, SModelS automatically rebuilds the binary (pickle) database file.

B SModelS Tools

SModelS comes with a number of tools that may be convenient for the user:

- a cross section calculator based on PYTHIA and NLLFAST,
- SLHA and LHE file checkers to check your input files for completeness and sanity,
- a database browser to provide easy access to the database of experimental results,

B.1 Cross-Section Calculator

This tool computes LHC production cross sections for MSSM particles and writes them out in an SLHA-type format (see “SLHA Format for Cross-Sections” in Section 3.1) This can be particularly convenient for adding cross sections to SLHA input files. The calculation is done at LO with PYTHIA (optionally PYTHIA 6.4 or PYTHIA 8.2); K-factors for colored particles are computed with NLLFAST.
The usage of the cross section calculator is:

```
smodelsTools.py xseccomputer [-h] -f FILENAME
[-s SQRTS [SQRTS ...]] [-e NEVENTS] [-v VERBOSITY]
[-c NCPUS] [-p] [-q] [-k] [-n] [-N] [-O] [-6] [-8]
```

**arguments:**

- `-h`, `--help`  
  show help message and exit.

- `-s SQRTS`, `--sqrts SQRTS`  (int): LHC center-of-mass energy in TeV for computing the cross sections. Can be more than one value; default is both 8 and 13.

- `-e NEVENTS`, `--nevents NEVENTS`  (int): number of Monte Carlo events to be simulated when running Pythia.

- `-c NCPUS`, `--ncpus NCPUS`  (int): number of CPU cores to be used simultaneously. −1 means ‘all’. This is only used when cross sections are computed for multiple SLHA files.

- `-p`, `--tofile`  
  if set, the cross sections will be written back to the file. If the input file already contains cross sections, only new records will be written. If not set, the cross sections will be written to the screen, only.

- `-q`, `--query`  
  only query whether the input file already contains cross sections.

- `-k`, `--keep`  
  keep the temporary directory containing the Pythia run output. This option is only relevant when checking for errors when running Pythia.

- `-n`, `--NLO`  
  use Pythia and NLLfast to compute NLO cross sections (default is LO). Note that since NLLfast only contains results for production of gluinos and squarks (incl. 3rd generation), only these cross sections will be generated.

- `-N`, `--NLL`  
  use Pythia and NLLfast to compute NLO+NLL cross sections (takes precedence over NLO, default is LO). Note that since NLLfast only contains results for production of gluinos and squarks (incl. 3rd generation), only these cross sections will be generated.

- `-O`, `--LOfromSLHA`  
  if set, SModelS will read the LO cross sections from the input file and use NLLfast to compute the NLO or NLO+NLL cross sections for squarks and gluinos.

- `-f FILENAME`, `--filename FILENAME`  
  SLHA file to compute cross sections for. If a directory is given, compute cross sections for all files in the directory.

- `-v VERBOSITY`, `--verbosity VERBOSITY`  
  Verbosity (‘debug’, ‘info’, ‘warning’, ‘error’. Default is ‘info’).
-6, --pythia6 use PYTHIA 6 for LO cross sections.
-8, --pythia8 use PYTHIA 8 for LO cross sections (default).

Further PYTHIA parameters are defined in smodels/etc/pythia8.cfg (PYTHIA 8) or smodels/etc/pythia.card (PYTHIA 6).

A typical usage example is:

```
smodelsTools.py xseccomputer -s 8 13 -e 50000 -p
   -f inputFiles/slha/compressedSpec.slha -6
```

which will compute 8 TeV and 13 TeV LO cross sections (at the LHC) with PYTHIA 6 for all MSSM processes using 50k MC events. If, after the LO cross sections have been computed, one wants to add the NLO+NLL cross sections for gluinos and squarks (incl. 3rd generation):

```
smodelsTools.py xseccomputer -s 8 13 -p -N -O
   -f inputFiles/slha/compressedSpec.slha
```

The resulting file will then contain LO cross sections for all MSSM processes and NLO+NLL cross sections for the available processes in NLLfast (gluino and squark production).\(^{11}\) When reading the input file, SModelS will then use only the highest-order cross section available for each process.

### B.2 Input File Checks

As discussed in Section 3.1, SModelS accepts both SLHA and LHE input files. It can be convenient to perform certain sanity checks on these files as described below.

#### LHE File Checker

For an LHE input file only very basic checks are performed, namely that

- the file exists,
- it contains at least one event,
- the information on the total cross section and the center of mass energy can be found.

The usage of the LHE checker is simply:

```
smodelsTools.py lhechecker [-h] -f FILENAME
```

**arguments:**

- **-h, --help** show this help message and exit

\(^{11}\)If a higher precision is needed, for instance for electroweak production or for gluino/squark masses outside the NLLFAST grids, this has to be taken care of by the user.
-f FILENAME, --filename FILENAME  name of input LHE file

A typical usage example is:

```
smodelsTools.py lhechecker -f
   inputFiles/slha/gluino_squarks.lhe
```

**SLHA File Checker**

The SLHA file checker allows to perform quite rigorous checks of SLHA input files. Concretely, it verifies that

- the file exists and is given in SLHA format,
- the file contains masses and decay branching ratios in standard SLHA format,
- the file contains cross sections according to the SLHA format for cross sections,
- the lightest $\mathbb{Z}_2$-odd state (the LSP in supersymmetric models) is neutral,
- there are no stable charged particles nor displaced vertices (no non-prompt visible decays), as currently all the analyses considered by SModelS require a prompt MET signature.

In addition, one can ask that

- all decays listed in the DECAY block are kinematically allowed, *i.e.* the sum of masses of the decay products may not exceed the mother mass. *This check for “illegal decays” is turned off by default.*

If any of the above tests fails (returns a negative result), an error message is shown.

Some more comments are in order. In order to check that the lightest $\mathbb{Z}_2$-odd state has zero electric and color charges, the quantum numbers of the BSM particles must be given in the `qNumbers` dictionary in `particles.py`. The format is

```
[2*spin, 3*electric charge, dimension of SU(3) representation]
```

The list of quantum numbers is also required to check for displaced vertices or heavy charged particles. The check for long-lived (or stable) particles first verifies that these appear in one of the cross section blocks and their cross section exceeds the minimum cross section value defined by `sigmacut` in the parameters file, see Section 4.2. If the cross section is larger than `sigmacut` and the particle is stable, the checker checks if it is neutral (both electric and color charges are zero). On the other hand, if the particle is unstable, but its lifetime (times $c$) is larger than a minimum value (`default = 10 mm`), the particle is considered a non-prompt decay. For these cases all channels are then checked for visible decay products. If the branching ratio to visible decays times the maximum production cross section for the particle exceeds `sigmacut`, the particle’s decay is considered a displaced vertex.
The usage of the SLHA checker is:

```
smodelsTools.py slhachecker [-h] [-xS] [-lsp] [-longlived]
    [-m DISPLACEMENT] [-s SIGMACUT] [-illegal]
    [-dB] -f FILENAME
```

**arguments:**

- `-h, --help`  
  show this help message and exit
- `-xS, --xsec`  
  turn off the check for xsection blocks
- `-lsp, --lsp`  
  turn off the check for charged lsp
- `-longlived, --longlived`  
  turn off the check for stable charged particles and visible displaced vertices
- `-m DISPLACEMENT, --displacement DISPLACEMENT`  
  give maximum displacement of secondary vertex in m
- `-s SIGMACUT, --sigmacut SIGMACUT`  
  give sigmacut in fb
- `-illegal, --illegal`  
  turn on check for kinematically forbidden decays
- `-dB, --decayBlocks`  
  turn off the check for missing decay blocks
- `-f FILENAME, --filename FILENAME`  
  name of input SLHA file

A typical usage example is:

```
smodelsTools.py slhachecker -m 0.001 -s 0.01
    -f inputFiles/slha/lightSquarks.slha
```

Running this will print the status flag and a message with potential warnings and error messages.

**B.3 Database Browser**

The database browser is a tool based on IPython which provides an easy way to directly access the SModelS database. It owns several methods to select experimental results or data sets satisfying some user-defined conditions as well as to access the meta data and data inside each experimental result.

The usage of the browser interface is:

```
smodelsTools.py database-browser [-h] -p PATH_TO_DATABASE [-t]
```

**arguments:**

- `-h, --help`  
  show this help message and exit
-p PATH_TO_DATABASE,
--path_to_database PATH_TO_DATABASE  path to SModelS database
-t, --text        load text database, don’t even search for binary database file

A typical usage example is:

```
smodelsTools.py database-browser -p ./smodels-database
```

Loading the database may take a few seconds if the binary database file exists. Otherwise the pickle file will be created. Starting the browser opens an IPython session, which can be used to select specific experimental results (or groups of experimental results), check upper limits and/or efficiencies for specific masses/topologies and access all the available information in the database. A simple example is given below:

```
In [1]: print browser  #Print all experimental results in the browser
['ATLAS-SUSY-2015-09', 'CMS-SUS-PAS-15-002', 'ATLAS-CONF-2012-105', ...

In [2]: browser.selectExpResultsWith(txName = 'T1tttt', dataType =
'upperLimit')  #Select only the UL results with the topology T1tttt

In [3]: print browser  #Print all experimental results in the browser
(after selection)
['ATLAS-SUSY-2015-09', 'CMS-SUS-PAS-15-002', 'ATLAS-CONF-2012-105',
'ATLAS-CONF-2013-007', 'ATLAS-CONF-2013-061', 'ATLAS-SUSY-2013-04',
'ATLAS-SUSY-2013-09', 'ATLAS-SUSY-2013-18', 'CMS-PAS-SUS-12-026',
...

#Define masses for the T1tttt topology:
In [4]: gluinoMass, LSPmass = 800.*GeV, 100.*GeV

#Get UL for a specific experimental result
In [5]: browser.getULFor('CMS-SUS-PAS-15-002','T1tttt',
[[gluinoMass,LSPmass],[gluinoMass,LSPmass]])
Out[5]: 5.03E-02 [pb]

#Get the upper limits for all the selected results for the given
#topology and mass
In [6]: for expResult in browser:
   ...:    print expResult.getValuesFor('id'),'UL = ',
   expResult.getUpperLimitFor(txname='T1tttt',mass=
   [[gluinoMass,LSPmass],[gluinoMass,LSPmass]])
   ...
['ATLAS-SUSY-2015-09'] UL =  None
['CMS-SUS-PAS-15-002'] UL =  5.03E-02 [pb]
['ATLAS-CONF-2012-105'] UL =  6.70E-02 [pb]
['ATLAS-CONF-2013-007'] UL =  2.40E-02 [pb]
```
# Print the luminosities for the selected experimental results
In [7]: for exp in browser:
    ...:     print exp.getValuesFor('id'), exp.getValuesFor('lumi')
    ...:
['ATLAS-SUSY-2015-09'] [3.20E+00 [1/fb]]
['CMS-SUS-PAS-15-002'] [2.20E+00 [1/fb]]
['ATLAS-CONF-2012-105'] [5.80E+00 [1/fb]]
['ATLAS-CONF-2013-007'] [2.07E+01 [1/fb]]
C Home-grown Efficiency Maps

While most efficiency maps included in the SModelS v1.1 database were directly provided by the experimental collaborations as auxiliary material for their publications, we also produced a number of them ourselves in order to improve the coverage of simplified models. Such ‘home-grown’ efficiency maps are particularly relevant for topologies with one or more intermediate particles: here we need several mass planes for the interpolation, but often only one is provided in the official results. The home-grown efficiency maps included in the v1.1.1 database are summarised in Table 1. The TxNames denote the following simplified models:\(^{12}\)

- **T1bbbb**: \(pp \rightarrow \tilde{g}\tilde{g}, \tilde{g} \rightarrow b\bar{b}\tilde{\chi}_1^0;\)
- **T1btbt**: \(pp \rightarrow \tilde{g}\tilde{g}, \tilde{g} \rightarrow b\tilde{\chi}_1^0;\)
- **T2bb**: \(pp \rightarrow \tilde{b}_1\tilde{b}_1^*, \tilde{b}_1 \rightarrow b\tilde{\chi}_1^0;\)
- **T2tt**: \(pp \rightarrow \tilde{\chi}_1^\pm, \tilde{\chi}_1^- \rightarrow t\tilde{\chi}_1^0;\)
- **T5**: \(pp \rightarrow \tilde{g}\tilde{g}, \tilde{g} \rightarrow q\bar{q}, \bar{q} \rightarrow q\tilde{\chi}_1^0;\)
- **T5bbbb**: \(pp \rightarrow \tilde{g}\tilde{g}, \tilde{g} \rightarrow b\tilde{b}_1, \tilde{b}_1 \rightarrow b\tilde{\chi}_1^0;\)
- **T5tttt**: \(pp \rightarrow \tilde{g}\tilde{g}, \tilde{g} \rightarrow t\bar{t}, \bar{t} \rightarrow t\tilde{\chi}_1^0;\)
- **T5WW**: \(pp \rightarrow \tilde{g}\tilde{g}, \tilde{g} \rightarrow q\bar{q}'\tilde{\chi}_1^\pm, \tilde{\chi}_1^\pm \rightarrow W^\pm\tilde{\chi}_1^0;\)
- **T5ZZ**: \(pp \rightarrow \tilde{g}\tilde{g}, \tilde{g} \rightarrow q\bar{q}'\tilde{\chi}_2^0, \tilde{\chi}_2^0 \rightarrow Z\tilde{\chi}_1^0;\)
- **T6bbWW**: \(pp \rightarrow \tilde{\chi}_1^\pm, \tilde{\chi}_1^- \rightarrow b\tilde{\chi}_1^+, \tilde{\chi}_1^+ \rightarrow W^+\tilde{\chi}_1^0;\)
- **TChiWW**: \(pp \rightarrow \tilde{\chi}_1^\pm\tilde{\chi}_1^-, \tilde{\chi}_1^- \rightarrow W^\pm\tilde{\chi}_1^0;\)
- **TChiWZ**: \(pp \rightarrow \tilde{\chi}_1^\pm\tilde{\chi}_2^0, \tilde{\chi}_2^0 \rightarrow W^\pm\tilde{\chi}_1^0, \tilde{\chi}_2^0 \rightarrow Z\tilde{\chi}_1^0;\)
- **TChiZZ**: \(pp \rightarrow \tilde{\chi}_2^0\tilde{\chi}_2^0, \tilde{\chi}_2^0 \rightarrow Z\tilde{\chi}_1^0;\)

Table 1: Summary of the ‘home-grown’ efficiency maps included in the v1.1.1 database.

\(^{12}\)For gluinos decays, charge-conjugated final states are assumed implicitly.
Monte Carlo events for the above processes were generated using MADGRAPH5_aMC@NLO [50] (v.2.3.3) with decay and hadronisation performed via the integrated installation of PYTHIA 6.4 [21]. For recasting analyses sensitive to hadronic final states, events were generated including up to one extra jet, see Table 1. The merging was performed using Matrix Element–Parton Shower (ME-PS) matching according to the $k_T$-jet MLM scheme [51–53] with merging and matching parameters set as $(Qcut, XQcut) = (90, 50)$ GeV, following CMS practice. The hadronised samples were then passed through MADANALYSIS 5 [14, 15] (v1.4.4) or CHECKMATE [12] (v1.2.2) for further processing. Both these codes interface to the DELPHES 3 [54] detector simulation, using FASTJET [55] for jet clustering. Concretely, we used the following recasting codes:

- MADANALYSIS 5 recast code [56] for the ATLAS multi-jet + MET analysis [47];
- MADANALYSIS 5 recast code [57] for the CMS multi-jet + MET analysis [37];
- MADANALYSIS 5 recast code [58] for the ATLAS dilepton plus MET analysis [48];
- CHECKMATE [12] for the ATLAS third generation squark search [49].

In the case of topologies with one-step cascade decays (T5, T5bbbb, T5tttt, T5WW, T5ZZ, T6bbWW, TChipChimSlepSnu) we created at least three different mass planes, so that the mass of the intermediate sparticle assumes a value close to the mother mass, close to the neutralino mass and equally spaced between the two, in order to obtain a good coverage of the parameter space. To this end, a parameterization in terms of relative mass differences, $m_{interm.} = x \cdot m_{Mother} + (1 - x) \cdot m_{\tilde{\chi}_1^0}$ with $x = \text{const.}$, was used. Moreover, where relevant, we produced planes with fixed mass gaps of $\Delta M(A, B) = m_A - m_B$ to improve the accuracy of the interpolation, e.g. for T5tttt near the kinematic boundary for on-shell top quarks, and for the T5WW and T6bbWW models (only for CMS-SUS-13-012) in the region where the chargino decays via an off-shell $W$ boson. For the T1btbt model, the chargino and the LSP were considered mass-degenerate. An overview of the various mass planes is given in Table 2.

In the input SLHA files, we assumed diagonal mixing matrices for both charginos and neutralinos, giving a pure bino $\tilde{\chi}_1^0$ and pure winos $\tilde{\chi}_1^\pm$ and $\tilde{\chi}_2^0$. However, since PYTHIA 6.4 was used for decaying the intermediate particles, any effects in kinematic distributions that might arise from sparticle mixing (due to polarization of the decay products) as well as spin correlations are disregarded. No additional

| TxName                        | mass planes, $x$ parametrization | mass planes, fixed $\Delta M(A, B)$ [GeV] |
|-------------------------------|---------------------------------|---------------------------------------|
| T5                            | $x = 0.05, 0.5, 0.95$           | $\Delta M(\tilde{\chi}_1^\pm, \tilde{\chi}_1^0) = 177$, $\Delta M(\tilde{\chi}_1^-, \tilde{\chi}_1^0) = 177$ |
| T5tttt                        | $x = 0.5$                      |                                       |
| T5bbbb                        | $x = 0.05, 0.5, 0.95$          | $\Delta M(\tilde{\chi}_1^\pm, \tilde{\chi}_1^0) = 10, 75$ |
| T5WW                          | $x = 0.05, 0.5, 0.95$          |                                       |
| T5ZZ                          | $x = 0.05, 0.5, 0.95$          |                                       |
| T6bbWW                        | $x = 0.1, 0.5, 0.9$            | $\Delta M(\tilde{\chi}_1^\pm, \tilde{\chi}_1^0) = 10, 75$ |
| TChipChimSlepSnu               | $x = 0.05, 0.25, 0.50, 0.75, 0.95$ | $\Delta M(\tilde{\chi}_1^\pm, \tilde{\chi}_1^0) = 5, 10, 15$, $\Delta M(\tilde{\chi}_2^\pm) = 5, 10, 15$ |

Table 2: Mass planes produced for topologies with one-step cascade decays.
radiation was produced for ATLAS-SUSY-2013-11 since the signal regions targeting these specific SMS veto the presence of jets. For the TSlepSlep simplified model, we took \( \tilde{l} \equiv \tilde{e}_L, \tilde{e}_R, \tilde{\mu}_L, \tilde{\mu}_R \), with all of them being mass-degenerate. For the TChipChimSlepSnu model, the intermediate left-handed sleptons and sneutrinos are taken mass degenerate for all the three slepton flavours.

We have verified that our procedure reproduces well the official 95% CL exclusion curves whenever provided by the experimental collaborations; the validation plots are available at [46]. For completeness, we also note that detailed validation notes for the MADANALYSIS 5 recast codes are available at [59–61] and for CHECKMATE at [62].
References

[1] N. Arkani-Hamed, P. Schuster, N. Toro, J. Thaler, L.-T. Wang, B. Knuteson, and S. Mrenna, “MARMOSE: The Path from LHC Data to the New Standard Model via On-Shell Effective Theories,” hep-ph/0703088.

[2] J. Alwall, P. Schuster, and N. Toro, “Simplified Models for a First Characterization of New Physics at the LHC,” Phys. Rev. D79 (2009) 075020, 0810.3921.

[3] LHC New Physics Working Group Collaboration, D. Alves, “Simplified Models for LHC New Physics Searches,” J. Phys. G39 (2012) 105005, 1105.2838.

[4] ATLAS Collaboration, H. Okawa, “Interpretations of SUSY Searches in ATLAS with Simplified Models,” in Particles and fields. Proceedings, Meeting of the Division of the American Physical Society, DPF 2011, Providence, USA, August 9-13, 2011. 2011. 1110.0282.

[5] CMS Collaboration, S. Chatrchyan et al., “Interpretation of Searches for Supersymmetry with simplified Models,” Phys. Rev. D88 (2013), no. 5, 052017, 1301.2175.

[6] S. Kraml, S. Kulkarni, U. Laa, A. Lessa, W. Magerl, D. Proschofsky, and W. Waltenberger, “SModelS: a tool for interpreting simplified-model results from the LHC and its application to supersymmetry,” Eur.Phys.J. C74 (2014) 2868, 1312.4175.

[7] S. Kraml, S. Kulkarni, U. Laa, A. Lessa, V. Magerl, W. Magerl, D. Proschofsky-Spindler, M. Traub, and W. Waltenberger, “SModelS v1.0: a short user guide.,” 1412.1745.

[8] J. Heisig, A. Lessa, and L. Quertenmont, “Simplified Models for Exotic BSM Searches,” JHEP 12 (2015) 087, 1509.00473.

[9] M. Papucci, K. Sakurai, A. Weiler, and L. Zeune, “Fastlim: a fast LHC limit calculator,” Eur. Phys. J. C74 (2014), no. 11, 3163, 1402.0492.

[10] D. Barducci, A. Belyaev, M. Buchkremer, J. Marrouche, S. Moretti, and L. Panizzi, “XQCAT: eXtra Quark Combined Analysis Tool,” Comput. Phys. Commun. 197 (2015) 263–275, 1409.3116.

[11] S. Caron, J. S. Kim, K. Rolbiecki, R. Ruiz de Austri, and B. Stienen, “The BSM-AI project: SUSY-AI – generalizing LHC limits on supersymmetry with machine learning,” Eur. Phys. J. C77 (2017), no. 4, 257, 1605.02797.

[12] M. Drees, H. Dreiner, D. Schmeier, J. Tattersall, and J. S. Kim, “CheckMATE: Confronting your Favourite New Physics Model with LHC Data,” Comput. Phys. Commun. 187 (2015) 227–265, 1312.2591.

[13] D. Dercks, N. Desai, J. S. Kim, K. Rolbiecki, J. Tattersall, and T. Weber, “CheckMATE 2: From the model to the limit.,” 1611.09856.

[14] E. Conte, B. Dumont, B. Fuks, and C. Wymant, “Designing and recasting LHC analyses with MadAnalysis 5,” Eur. Phys. J. C74 (2014), no. 10, 3103, 1405.3982.
[15] B. Dumont, B. Fuks, S. Kraml, S. Bein, G. Chalons, E. Conte, S. Kulkarni, D. Sengupta, and C. Wyman, “Toward a public analysis database for LHC new physics searches using MADANALYSIS 5,” *Eur. Phys. J. C* **75** (2015), no. 2, 56, 1407.3278.

[16] A. Buckley, J. Butterworth, L. Lonnblad, D. Grellscheid, H. Hoeth, J. Monk, H. Schulz, and F. Siegert, “Rivet user manual,” *Comput. Phys. Commun.* **184** (2013) 2803–2819, 1003.0694.

[17] The GAMBIT Collaboration, P. Athron et al., “GAMBIT: The Global and Modular Beyond-the-Standard-Model Inference Tool,” 1705.07908.

[18] C. Balazs et al., “ColliderBit: a GAMBIT module for the calculation of high-energy collider observables and likelihoods,” 1705.07919.

[19] J. M. Butterworth, D. Grellscheid, M. Krämer, B. Sarrazin, and D. Yallup, “Constraining new physics with collider measurements of Standard Model signatures,” *JHEP* **03** (2017) 078, 1606.05296.

[20] http://smodels.hephy.at.

[21] T. Sjostrand, S. Mrenna, and P. Z. Skands, “PYTHIA 6.4 Physics and Manual,” *JHEP* **05** (2006) 026, hep-ph/0603175.

[22] T. Sjöstrand, S. Ask, J. R. Christiansen, R. Corke, N. Desai, P. Ilten, S. Mrenna, S. Prestel, C. O. Rasmussen, and P. Z. Skands, “An Introduction to PYTHIA 8.2,” *Comput. Phys. Commun.* **191** (2015) 159–177, 1410.3012.

[23] W. Beenakker, R. Hopker, M. Spira, and P. Zerwas, “Squark and gluino production at hadron colliders,” *Nucl.Phys.* **B492** (1997) 51–103, hep-ph/9610490.

[24] W. Beenakker, M. Krämer, T. Plehn, M. Spira, and P. Zerwas, “Stop production at hadron colliders,” *Nucl.Phys.* **B515** (1998) 3–14, hep-ph/9710451.

[25] A. Kulesza and L. Motyka, “Threshold resummation for squark-antisquark and gluino-pair production at the LHC,” *Phys.Rev.Lett.* **102** (2009) 111802, 0807.2405.

[26] A. Kulesza and L. Motyka, “Soft gluon resummation for the production of gluino-gluino and squark-antisquark pairs at the LHC,” *Phys.Rev.* **D80** (2009) 095004, 0905.4749.

[27] W. Beenakker, S. Brensing, M. Krämer, A. Kulesza, E. Laenen, et al., “Soft-gluon resummation for squark and gluino hadroproduction,” *JHEP* **0912** (2009) 041, 0909.4418.

[28] W. Beenakker, S. Brensing, M. Krämer, A. Kulesza, E. Laenen, et al., “Supersymmetric top and bottom squark production at hadron colliders,” *JHEP* **1008** (2010) 098, 1006.4771.

[29] W. Beenakker, S. Brensing, M. Krämer, A. Kulesza, E. Laenen, et al., “Squark and Gluino Hadroproduction,” *Int.J.Mod.Phys.* **A26** (2011) 2637–2664, 1105.1110.

[30] A. Buckley, “PySLHA: a Pythie interface to SUSY Les Houches Accord data,” 1305.4194.
[31] L. Edelhauser, J. Heisig, M. Krämer, L. Oymanns, and J. Sonneveld, “Constraining supersymmetry at the LHC with simplified models for squark production,” JHEP 12 (2014) 022, 1410.0965.

[32] L. Edelhäuser, M. Krämer, and J. Sonneveld, “Simplified models for same-spin new physics scenarios,” JHEP 04 (2015) 146, 1501.03942.

[33] C. Arina, M. E. C. Catalan, S. Kraml, S. Kulkarni, and U. Laa, “Constraints on sneutrino dark matter from LHC Run 1,” JHEP 05 (2015) 142, 1503.02960.

[34] S. Kraml, U. Laa, L. Panizzi, and H. Prager, “Scalar versus fermionic top partner interpretations of $t\bar{t} + E_T^{miss}$ searches at the LHC,” JHEP 11 (2016) 107, 1607.02050.

[35] CMS Collaboration, S. Chatrchyan et al., “Search for supersymmetry in hadronic final states with missing transverse energy using the variables $\alpha_T$ and b-quark multiplicity in pp collisions at $\sqrt{s} = 8$ TeV,” Eur.Phys.J. C73 (2013), no. 9, 2568, 1303.2985.

[36] ATLAS Collaboration, “Search for direct-slepton and direct-chargino production in final states with two opposite-sign leptons, missing transverse momentum and no jets in 20/fb of pp collisions at $\sqrt{s} = 8$ TeV with the ATLAS detector,” Tech. Rep. ATLAS-CONF-2013-049, CERN, Geneva, May, 2013.

[37] CMS Collaboration, S. Chatrchyan et al., “Search for new physics in the multijet and missing transverse momentum final state in proton-proton collisions at $\sqrt{s}= 8$ TeV,” JHEP 06 (2014) 055, 1402.4770.

[38] http://smodels.hephy.at/wiki/SmsDictionary.

[39] P. Z. Skands, B. Allanach, H. Baer, C. Balazs, G. Belanger, et al., “SUSY Les Houches accord: Interfacing SUSY spectrum calculators, decay packages, and event generators,” JHEP 0407 (2004) 036, hep-ph/0311123.

[40] J. Alwall, A. Ballestrero, P. Bartalini, S. Belov, E. Boos, et al., “A Standard format for Les Houches event files,” Comput.Phys.Commun. 176 (2007) 300–304, hep-ph/0609017.

[41] http://phystev.cnrs.fr/wiki/2013:groups:tools:slha.

[42] CMS Collaboration Collaboration, T. C. Collaboration, “Simplified likelihood for the re-interpretation of public CMS results,” Tech. Rep. CMS-NOTE-2017-001, CERN, Geneva, Jan, 2017.

[43] D. Barducci, G. Belanger, J. Bernon, F. Boudjema, J. Da Silva, S. Kraml, U. Laa, and A. Pukhov, “Collider limits on new physics within micrOMEGAs,” 1606.03834.

[44] http://smodels.hephy.at/wiki/ListOfAnalysesv111.

[45] ATLAS Collaboration, G. Aad et al., “Summary of the ATLAS experiment’s sensitivity to supersymmetry after LHC Run 1 interpreted in the phenomenological MSSM,” JHEP 10 (2015) 134, 1508.06608.

[46] http://smodels.hephy.at/wiki/Validationv111.
[47] **ATLAS** Collaboration, G. Aad *et al.*, “Search for new phenomena in final states with large jet multiplicities and missing transverse momentum at $\sqrt{s} = 8$ TeV proton-proton collisions using the ATLAS experiment,” *JHEP* **10** (2013) 130, [1308.1841]. [Erratum: JHEP01,109(2014)].

[48] **ATLAS** Collaboration, G. Aad *et al.*, “Search for direct production of charginos, neutralinos and sleptons in final states with two leptons and missing transverse momentum in $pp$ collisions at $\sqrt{s} = 8$ TeV with the ATLAS detector,” *JHEP* **05** (2014) 071, [1403.5294].

[49] **ATLAS** Collaboration, G. Aad *et al.*, “Search for direct third-generation squark pair production in final states with missing transverse momentum and two $b$-jets in $\sqrt{s} = 8$ TeV $pp$ collisions with the ATLAS detector,” *JHEP* **1310** (2013) 189, [1308.2631].

[50] J. Alwall, R. Frederix, S. Frixione, V. Hirschi, F. Maltoni, O. Mattelaer, H. S. Shao, T. Stelzer, P. Torrielli, and M. Zaro, “The automated computation of tree-level and next-to-leading order differential cross sections, and their matching to parton shower simulations,” *JHEP* **07** (2014) 079, [1405.0301].

[51] M. Mangano. presentation at the FNAL Matrix Element/Monte Carlo Tuning Working Group, 15 Nov 2002.

[52] S. Hoeche, F. Krauss, N. Lavesson, L. Lonnblad, M. Mangano, A. Schalicke, and S. Schumann, “Matching parton showers and matrix elements,” in *HERA and the LHC: A Workshop on the implications of HERA for LHC physics: Proceedings Part A*, pp. 288–289. 2005. hep-ph/0602031.

[53] J. Alwall *et al.*, “Comparative study of various algorithms for the merging of parton showers and matrix elements in hadronic collisions,” *Eur. Phys. J. C* **53** (2008) 473–500, [0706.2569].

[54] **DELPHES 3** Collaboration, J. de Favereau, C. Delaere, P. Demin, A. Giammanco, V. Lemaître, A. Mertens, and M. Selvaggi, “DELPHES 3, A modular framework for fast simulation of a generic collider experiment,” *JHEP* **02** (2014) 057, [1307.6346].

[55] M. Cacciari, G. P. Salam, and G. Soyez, “FastJet User Manual,” *Eur.Phys.J.* **C72** (2012) 1896, [1111.6097].

[56] B. Fuks, M. Blanke, and I. Galon, “MadAnalysis5 implementation of ATLAS-SUSY-2013-04.” http://doi.org/10.7484/INSPIREHEP.DATA.STLS.SAMT.

[57] S. Bein and D. Sengupta, “MadAnalysis 5 implementation of CMS-SUS-13-012.” http://doi.org/10.7484/INSPIREHEP.DATA.83GG.U5BW.

[58] B. Dumont, “MadAnalysis 5 implementation of ATLAS-SUSY-2013-11: di-leptons plus MET.” http://doi.org/10.7484/INSPIREHEP.DATA.HLMR.T56W.2.

[59] “MadAnalysis5 Public Analysis Database ATLAS-SUSY-2013-04 validation.” http://madanalysis.irmp.ucl.ac.be/raw-attachment/wiki/PublicAnalysisDatabase/GFV.pdf.

[60] “MadAnalysis5 Public Analysis Database CMS-SUS-13-012 validation.” http://madanalysis.irmp.ucl.ac.be/raw-attachment/wiki/PublicAnalysisDatabase/ma5_validation_CMS-SUS-13-012.pdf.
[61] “MadAnalysis5 Public Analysis Database ATLAS-SUSY-2013-11 validation.”
http://madanalysis.irmp.ucl.ac.be/raw-attachment/wiki/PublicAnalysisDatabase/ma5_validation_ATLAS-SUSY-2013-11_v2.pdf.

[62] http://checkmate.hepforge.org/AnalysesList/ATLAS_8TeV.html.