Computation of relic densities within freeze-out mechanism

Marco Palmiotto

Université Claude Bernard Lyon 1
Institut de Physique des deux infinis

22/10/2021

The ΛCDM model

The standard cosmological model relies on 4 assumptions

- GR describes gravity
- The SM describes the particle content of the universe
- The **cosmological principle**: i.e. the universe is homogeneous and isotropic at large scales
- A parameter Λ is needed in the Einstein equation to obtain a consistent value for the expansion velocity of the universe

The ΛCDM model

and it has two main issues:

- **Dark energy**: Λ can be predicted by the vacuum state energy, but the SM strongly disagrees with the observed value
- **Dark matter**
  - Discrepancies on matter content of the universe
  - Discrepancies on rotational curves of the galaxies
  - Impossibility of explaining structure formation

For these reasons, it's called Λ Cold Dark Matter

The Friedmann equations

Using the cosmological principle and GR we can write the FLRW metric

$$ds^2 = -dt^2 + a(t)^2 \Big(\frac{1}{1 - kr^2} dr^2 + r^2 d\theta^2 + r^2 \sin(\theta)^2 d\phi^2 \Big)$$

Plugging it into the Einstein equations (modified with Λ) we get the *Friedmann equations*

$$\frac{\ddot{a}}{a} = -\frac{4\pi G}{3}(\rho + 3P) + \frac{\Lambda}{3}$$

$$H^2 \equiv \frac{\dot{a}^2}{a^2} = \frac{8\pi G}{3}\rho - \frac{k}{a^2} + \frac{\Lambda}{3}$$

What's a relic?

- A particle X is in equilibrium with $\bar{X}$ while $T > m_X$
- If X is stable, than only the reaction $X\bar{X} \to Y\bar{Y}$ can modify n_X
- If X remains in **equilibrium**, n_X becomes negligible due to **Boltzmann suppression**

$$n_X \sim (m/T)^{3/2} \exp(-m/T)$$

- To make X a DM candidate, its density today has to match the observations (and thus be nonzero)
- A particle that goes out of thermodynamic equilibrium and whose density is nonzero today is called a *relic*

The Boltzmann equation

To study the evolution of a species density we can make the following assumptions:

- **Maxwell-Boltzmann** distribution : very good for temperatures $T < 3m$
- The annihilation **products** are in **thermal equilibrium**
- After decoupling, the species under consideration **remains in kinetical equilibrium**
- The initial chemical potential of the species under consideration is negligible

The Boltzmann equation

Then, called f the distribution function we have

$$\frac{\mathrm{d}f}{\mathrm{d}t} = C[f] \quad \Rightarrow \quad \frac{x}{Y_{\mathrm{eq}}}\frac{\mathrm{d}Y}{\mathrm{d}x} = -\frac{\Gamma_{\mathrm{eq}}}{H}\left[\left(\frac{Y}{Y_{\mathrm{eq}}}\right)^2 - 1\right]$$

where

- $C[f]$ is the number of particles per phase space volume which are lost or gained per unit of time under collisions with other particles
- $x = m/T$
- $Y = n/s$ is a "comoving density"
- $\Gamma_{\mathrm{eq}} = n_{\mathrm{eq}}\langle \sigma v \rangle$ is roughly the interaction rate

The freeze-out

$$\frac{x}{Y_{eq}}\frac{dY}{dx} = -\frac{\Gamma_{eq}}{H}\left[\left(\frac{Y}{Y_{eq}}\right)^2 - 1\right]$$

Note that

- if $\Gamma_{eq}/H \gg 1$ then Y is close to Y_{eq}
- if $\Gamma_{eq}/H \ll 1$ then the RHS is close to 0 and Y is constant

For some value of $x = x_F$ we will have the *freeze-out* i.e.

$$\Gamma_{eq}(x_F) = H(x_F)$$

and from this point Y can be considered constant

The freeze-out

Maybe you're tired of pointless oyster jokes, so I made something pedagogical ...

The freeze-out

Maybe you're tired of pointless oyster jokes, so I made something pedagogical ... It's like storing fresh oysters (according to wikihow)

1. **Don't wash them!** keeping oysters in their shells makes them easier to store and reduces the chance that they'll go bad
2. Fill a bowl with ice
3. Place the oysters
4. Put a towel on
5. Put them in the refrigerator (2 to 4 degrees)

The freeze-out

Maybe you're tired of pointless oyster jokes, so I made something pedagogical . . . It's like storing fresh oysters (according to wikihow)

1. **Don't wash them!** keeping oysters in their shells makes them easier to store and reduces the chance that they'll go bad
2. Fill a bowl with ice
3. Place the oysters
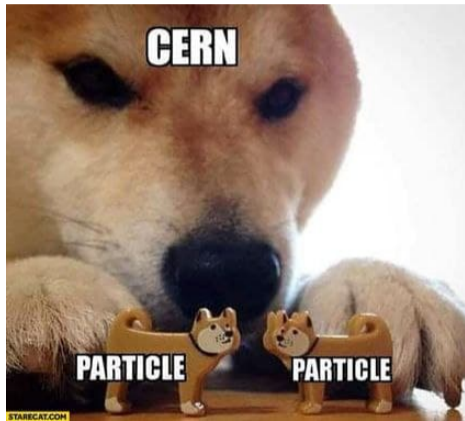4. Put a towel on
5. Put them in the refrigerator (2 to 4 degrees)

. . . and of course, eat them in two days max!
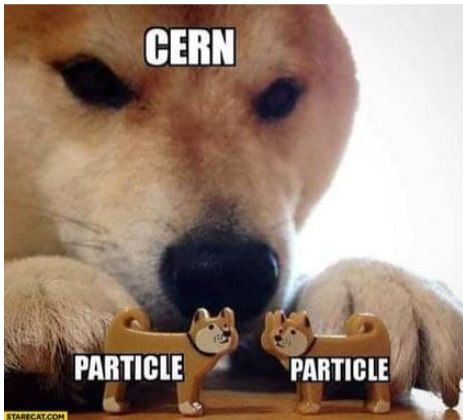
The freeze-out
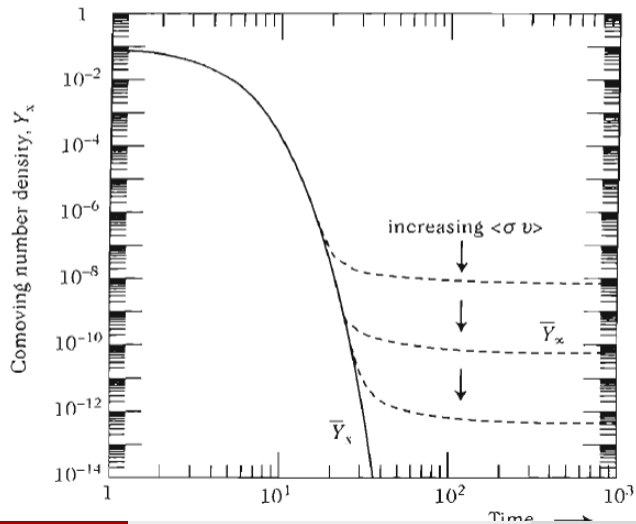
SUSY as a viable framework

- Although SUSY has not still been observed at CERN . . .

SUSY as a viable framework

- Although SUSY has not still been observed at CERN ...
- ... among the possible BSM frameworks SUSY provides a natural candidate for dark matter
- Proton decay is in principle possible, so we impose the so-called R-parity
- Reactions like 1 SUSY $\leftrightarrow$ 1 SM are forbidden
- In this way we can choose the lightest neutralino as the lightest SUSY particle

Current features of SuperIso Relic

As far as freeze-out is concerned, the current version of the software allows the followings

- Considering **non-thermal** production of **DM**
- Considering **entropy injection**
- Considering **variable dark energy**
- Some freedom in the choice of the **QCD equation of state** by modifying the lattice parameters
- Considering MSSM and NMSSM
- Following the evolution of the density of only the LSP

Current features of SuperIso Relic

As example, you can give your inputs in an `.lha` format and execute some predefined programs, or write your own in C thanks to the manual

```
./ testmodeleff .x example .lha
Dependence of the relic density on the calculation of heff and geff
For model_eff =1 ( model A): omega =1.254 e+01
For model_eff =2 ( model B ( default )): omega =1.254 e+01
For model_eff =3 ( model B2 ): omega =1.262 e+01
For model_eff =4 ( model B3 ): omega =1.247 e+01
For model_eff =5 ( model C): omega =1.255 e+01
For model_eff =6 (Bonn model ): omega =1.231 e+01
For model_eff =0 (old model ): omega =1.229 e+01
```

What's next?

- I'm starting from trying to follow the evolution of the densities of **more than one species**
- This will allow to better explore the **parameter space** of each viable model
- A lot of work is required since a new setting to compute $\langle \sigma v \rangle$ is needed
- The current setup relies on self-generated FORMcalc code,
    - Only for pMSSM and pNMSSM
    - Does not allow the separation of different contributions to $\langle \sigma v \rangle$
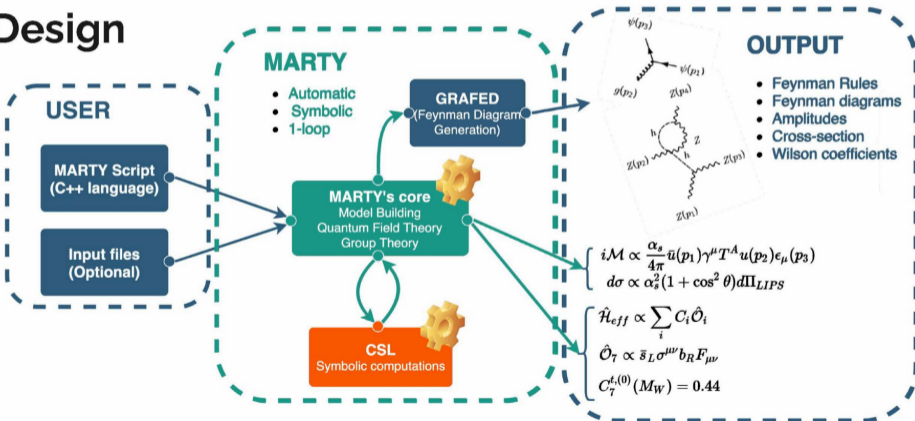
Why these limitations?
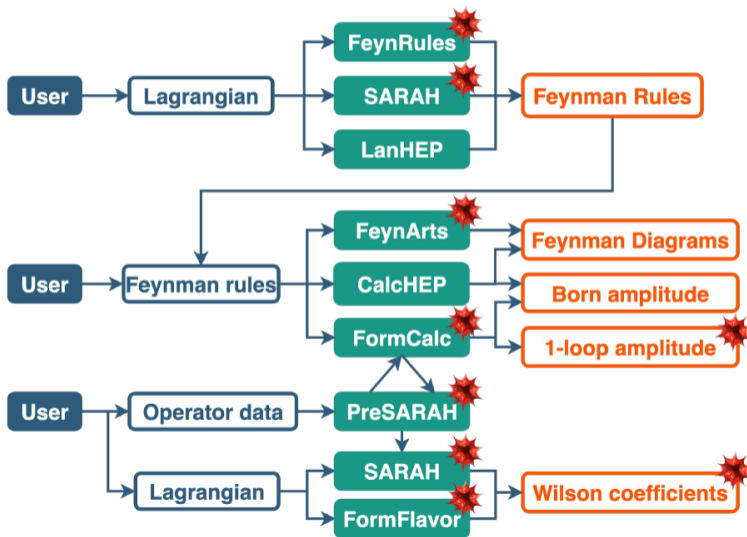
In the current version:

- Many codes are required
- Several passages of inputs
- There are some Mathematica dependencies

MARTY

So, we've chosen to switch to MARTY

The state of art situation

$$\texttt{MSSM.cpp} \rightarrow \texttt{testlib} \rightarrow \sigma(\text{SUSY} \rightarrow \text{anything})$$

- I have a model file (1h to compile + execute)
- Then I have a library with some auxiliary files
  - Sharing inputs with SuperIso
  - Handling running
  - 30m to compile with 8 cores
- Finally I can execute the final program (3m to execute the test file)

As a result only ~ 50 processes on 3400 do not work (still)

$$C_1 + \bar{\bar{s}}_L \rightarrow \bar{s} + H^+$$
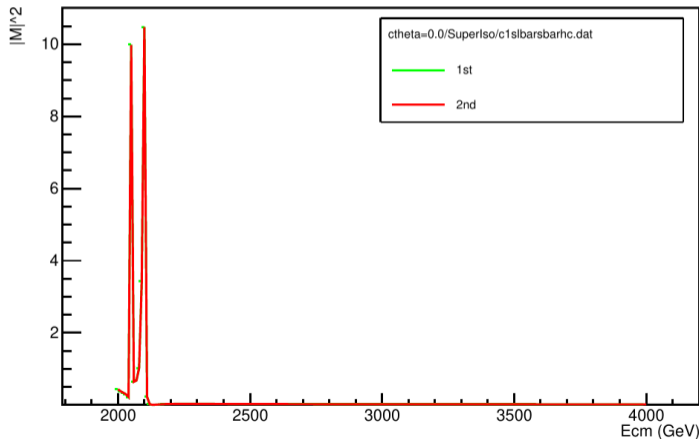
What's next?

- Performances have been an important aspect of my work, but some further improvements may be possible
- Soon I'll implement the pNMSSM and I'll finish the interface among `SuperIso` and this code
- Next, I'll implement the code to have multiple Boltzmann equations
- If MARTY will support new features, some of the things I did could be remade in a more portable way
- Comparison with `DarkSUSY` and `micromega`

Conclusions

- We have lots of BSM theories with a DM candidate
- Having more tools to explore the parameter space of SUSY models is helpful since there are a lot of parameters that come into play
- The simpler the code, the easier it is to do modifications
- In the next versions of the code, different calculation will be made for different species
- MARTY is an useful tool since it allows to chose any lagrangian
- We hope to add more models, and the possibility of studying the freeze-in as well !