# Galactic Phylogenetics

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**Abstract.** Phylogenetics is a widely used concept in evolutionary biology. It is the reconstruction of evolutionary history by building trees that represent branching patterns and sequences. These trees represent shared history, and it is our contention that this approach can be employed in the analysis of Galactic history. In Galactic archaeology the shared environment is the interstellar medium in which stars form and provides the basis for tree-building as a methodological tool.

Using elemental abundances of solar-type stars as a proxy for DNA, we built such an evolutionary tree to study the chemical evolution of the solar neighbourhood and published in Jofré *et al.* (2017). In this proceeding we summarise these results and discuss future prospects.

**Keywords.** Keyword1, keyword2, keyword3, etc.

## 1. Introduction

### 1.1. *Stellar DNAs*

In the widely-read review of Freeman & (2002) a very important concept was discussed: chemical tagging. Unlike the kinematical memory of long-lived low-mass stars, the chemical pattern imprinted in their atmospheres remain intact, reflecting the chemical composition of the gas from which they formed. Hence, the chemical abundances of stars can be used to identify their building blocks. By doing this for stars at different locations and of different ages, and complementing this information with their kinematical properties, one can constrain chemodynamical models of the Galaxy.

This idea, combined with the arrival of Gaia data, is motivating the development of very large high resolution spectroscopic surveys, able to provide with chemical information of about 20 elements for thousands of stars. This is further leading to the development of sophisticated clustering techniques which are able to classify different stellar populations in chemical space, and hence, identify the building blocks of different stellar populations.

### 1.2. *Chemical continuity*

It is already well known that there is a continuity in the change of chemical pattern from one stellar generation to the next. Massive stars pollute the interstellar medium with more metals enabling the formation of new stars that are more metal-rich. This implies that the building blocks of stars identified with chemical tagging are related to each other, and understanding their relationship is what reveals the chemical evolution of the Milky Way.

## 2. Evolutionary tree of solar neighborhood stars

If we can identify the building blocks of stars using the concept of chemical tagging, phylogenetics offers a powerful way to complement chemical tagging and study the

chemical evolution Milky Way. We can use the chemical pattern of stars as DNA and build evolutionary trees, in which every branch represents a different stellar population. At a first stage, this is doing the same as chemical tagging as we are essentially classifying stars in their chemical space. But at a second stage, the branches can be used to study their relationships and like this reconstruct their shared history.

In Jofré *et al.* (2017) we took the sample of solar twins of Nissen (2016), which comprises of accurate chemical abundances of 17 different elements, ages and kinematical properties. With these abundances we constructed an evolutionary tree and found 3 different branches. By analysing the ages and kinematics of the stars in these branches we could attribute these branches to be stars of the thick disk, thin disk and an intermediate population.

By further analysing their branch lengths, we could estimate a total chemical enrichment rate for each of the populations, finding that the thick disk had a faster star formation rate than the thin disk, confirming, in a purely empirical manner, previous findings. We finally identified nodes in the tree which ramified in multiple branches, discussing possible extreme events in the past which might drive independent evolutionary paths for different populations. Although our sample of stars was very small, we showed that this approach has great potential to disentangle the different physical processes that formed our Galaxy.

## 3. Future

Phylogenetic tools exist for over a century and are based on using evolutionary trees to understand the evolution of systems. These can be biological, but also sociological (languages, religions). While the mechanisms of evolution for these different systems are different, the way of how phylogenetic trees are interpreted is remarkably similar. Why then not apply theories of Evolution to the Milky Way? As long as we believe chemical tagging can work, we can do "Galactic Phylogenetics" and reconstruct the history of our Galaxy.

## References

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