

Computational Exploration of the Chemical Space Surrounding the Molecules of Life

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How the transition of disorganized, inanimate matter to organized, living systems took place on our planet and might have occurred on other bodies of our solar system or elsewhere in the universe is one of the fundamental questions studied in the field of astrobiology. The only instance of life known so far is the terrestrial one, and all living organisms on Earth share many of the same biochemical foundations with respect to reproduction and metabolism.

These biochemical foundations rely on a small pool of biomolecules, which represent a minute subset of plausible structural analogs, which themselves form only a very small fraction of all possible chemical compounds in chemical space. We believe that one key to understanding the origins of life is to study biomolecules in context of their surrounding neighborhood in chemical space.

Using unique software tools, so-called structure generators, we are able to construct well defined subsets of chemical space exhaustively. These virtual compound libraries are then computationally analyzed with respect to physico-chemical properties of their constituents.

In this talk some basic mathematical models and computational aspects of generating molecular structures are presented,¹ results concerning the amino acid alphabet,^{2,3,4} nucleotide analogs^{5,6} and the core of intermediary metabolism⁷ are summarized, and perspectives of ongoing studies related to astrobiology exploration missions are outlined.⁸

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