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Evolution of sparsity and modularity in a model of living matter MATHIEU HEMERY, Laboratoire Interdisciplinaire de Physique (Grenoble), OLIVIER RIVOIRE, CNRS & Université Grenoble Alpes — How much of the sequence of a protein accounts for its current function and how much is the result of its past evolutionary history? Being the product of a long evolutionary process in an ever changing environment, the sequence of current natural proteins may retain the trace of prior selected functions. Or more simply, it may contain elements that are not – or no more – subject to selection. Using a simple physical model previously analysed to study the folding problem, we probe the influence of past evolutionary environments on protein sequences. Simulations of evolutionary dynamics generically lead to non-trivial correlations between temporal fluctuations and geometrical structure, illuminating the link between history, geometry and function.

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