Cologne Evolution Colloquium

CRC 1310 Predictability in Evolution

Andreas Tiffeau-Mayer
University College London

Statistical Insights into the Immune Receptor Code

Biological systems explore vast spaces of possibility, yet their function is often robust to certain variations while remaining exquisitely sensitive to others. A striking example is the hypervariable repertoire of T cell receptors, which underlies the specificity of the cellular immune response. Can we construct principled coarse-grained descriptions of this diversity that retain functionally relevant variation? In this talk, I will discuss our recent progress on this question. First, I will show how we can quantify, in bits, the information that different receptor regions provide about antigen specificity. Second, I will describe our initial attempts to train protein language models to predict which receptors recognise common targets. Finally, I will reflect on how principled coarse-graining approaches might help us uncover statistical structure in biological complexity across scales.

Tuesday, 17 June 2025, 17:00
Institute for Biological Physics, Zülpicher Str. 77a
Seminar Room S0.02
Hosted by Roberto Morán-Tovar