Prevalence-knowledge and the changing store of molecular biology

Pierre-Luc Germain[*2,1]

[2]Università degli studi di Milano (UniMi) – Italy
[1]European School of Molecular Medicine (SEMM) – Italy

Abstract

One can distinguish two kinds of generalizations in biology (Shaffner 1994; Waters 1998): the first concerns causal regularities (same cause, same effect), while the second, which I will call "prevalence-knowledge", has been described as the scope of kinds over which such regularities are valid. The contemporary focus on mechanisms deals with causal regularities, but leaves prevalence-knowledge largely unanalysed: with the exception of evolutionary studies, knowledge about the prevalence of mechanisms is not perceived as relevant. I object to this, and argue that prevalence-knowledge is the object of major scientific transformations and plays an important role in scientific inference and discovery. Prevalence-knowledge has mostly been discussed in terms of inter-species generalizations, which however constitute only a subset of it. My paper therefore focuses on intra-species/organism generalizations, or prevalence-knowledge concerning schemata, abstract entities and their mapping to activites. Such knowledge is critical in bioinformatics and "-*omics*", where generalization of basic organizational schemes is methodologically necessary. Indeed, as I show through a discussion of the ENCODE project, this knowledge is now explicitly sought in and for itself. However, I argue that it has played the same role, albeit more implicitly, throughout the history of molecular biology. Elaborating on Darden's (2006) notion of the "store" of a scientific field, I propose a way of integrating prevalence knowledge in a mechanism-based understanding of molecular biology.

[*]Speaker