Preface

Because high-throughput biology produces molecular data, the new scientific context of biological research suggests emphasizing the constructive approaches, starting from molecules up while incorporating top-down constraints when available. In the case of (post-) genomic data, the first constructive step is the description and dynamical analysis of molecular networks. However, several scientists, including some of the speakers at the Paris/Evry meetings held in July 2002, have emphasized the need to replace the commonplace genetic determinism by an epigenetic one and have urged us to face up to this more realistic challenge. As a tribute to these pioneers of the epigenetics of molecular networks, we would like to coin here the term 'epigenomics' which, by analogy to epigenetics, alludes to the construction of biological objects positioned at increasing levels of integration, albeit with the genome as reference instead of the gene¹. In a remotely related fashion, epigenomics also encompasses the analysis of how multiple layers of information are superimposed on a single physical substrate, the DNA.

While the Paris Symposium covered a wide spectrum of research activities, the Evry Workshop was devoted to two key problems that reduce our ability to interpret transcriptomic data and to model the dynamics of genetic networks. One is the control of macromolecular traffic on DNA, and the other is the interplay between regulating proteins acting on the same target gene. A detailed account of both meetings has appeared elsewhere [1].

Some of the Workshop speakers accepted to submit an original manuscript to *ComPlexUs*. Following a regular editorial process, four of these manuscripts are published in the present issue. Each in a different manner, they testify to the benefit of tackling epigenomics. The undersigned editors of this thematic issue wish to thank the authors for their contribution.

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Reference

- 1 Képès F, Carbone A: Modelling macromolecular networks: Two meetings in Paris, July 2002. *Bioessays* 2002;24: 1188–1190.

¹ Two existing words are semantically close to 'epigenomics'. 'Post-genomics' refers to a field of investigation that follows genomics from a mostly chronological viewpoint, but it does not have a precise scientific content. It includes high-throughput bench work (except sequencing) and an unspecified portion of bioinformatics. 'Integrative biology' refers to a project that is quite similar in spirit to the one described here, but with a more physiological and less molecular connotation. Due to its ancient roots, integrative biology does not refer to the genome.