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► **COVER:** 'Untangling the web' by Manuel Enriquez, inspired by the review on p23.



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There is no doubt that human biology, and consequently cancer biology, is complex, and the birth of the 'omics' era reinforces this view. Fortunately, tools are being developed to help cope with the complexity and more effectively apply Occam's razor.

Data from expression profiling and genetic screens are accumulating quickly, and although these data can be informative on their own, there is a need to determine biological functions of previously uncharacterized cancer genes pulled from these profiles and screens. In this issue (page 23), Andrew Emili and colleagues review computational methods for predicting cancer-gene function, emphasizing tools and resources that are accessible to cancer biologists.

On page 35, Kevin Zbuk and Charis Eng discuss cancer phenomics, the study of phenotypic variation that results from the influences of genetic and environmental variation, using two cancer predisposition syndromes as examples. Phenomics goes beyond traditional genotype–phenotype correlations and integrates systematically collected clinical, molecular and cellular phenotypes, which should help us better understand genomic and proteomic data in the context of cancer.

Justin Lamb also gives his perspective on the Connectivity Map tool that he and his colleagues developed (page 54) to help systematize and centralize screening. This tool uses gene-expression signatures to draw connections among diseases, the genes that cause them and drugs that might be able to treat them, and it has already been used to make interesting connections in cancer biology. He discusses the principles that guided the design of the Connectivity Map, limitations and future content. The tool is freely available, and it is hoped that the scientific community will use it to make other meaningful connections in cancer and other diseases.

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