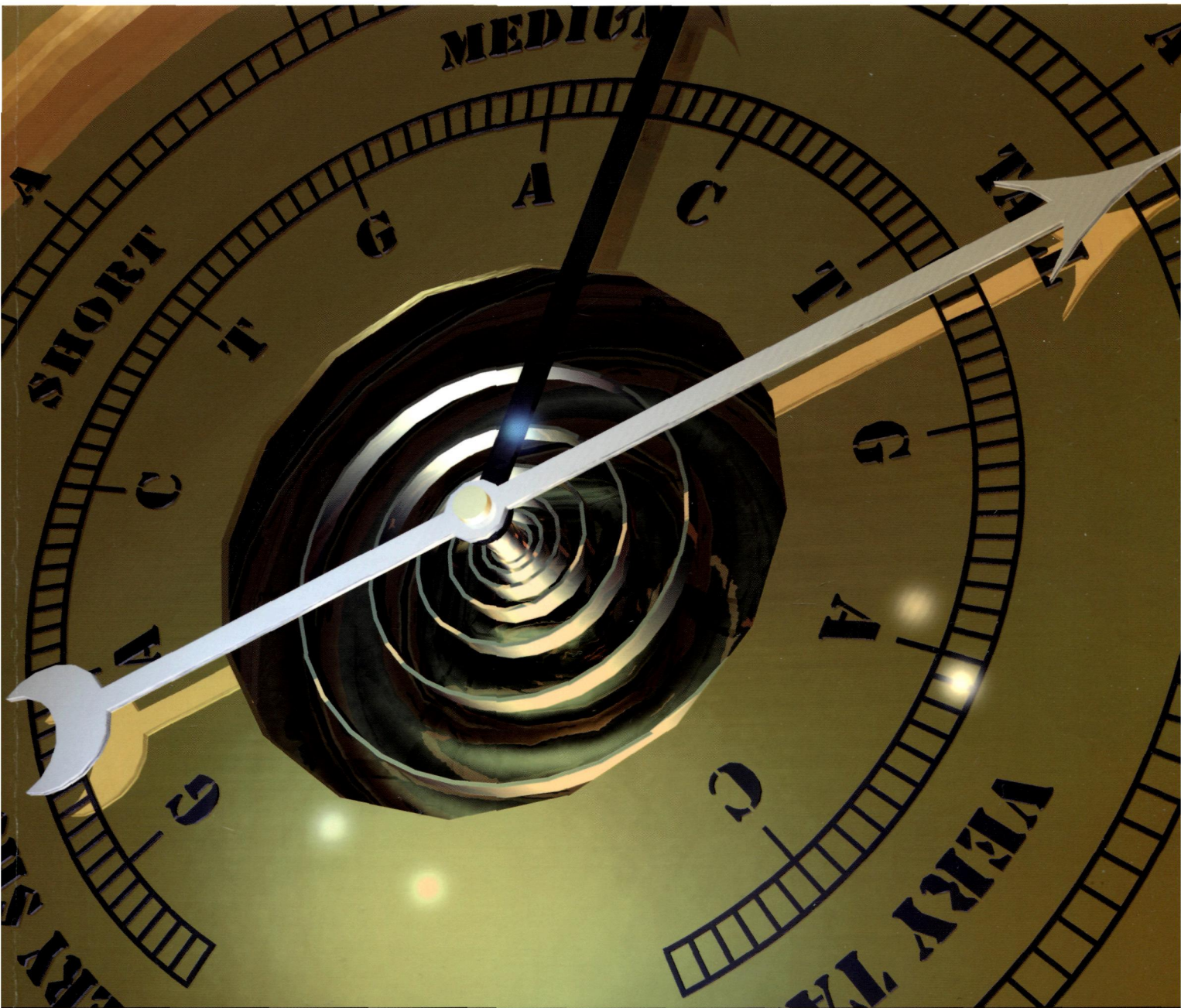


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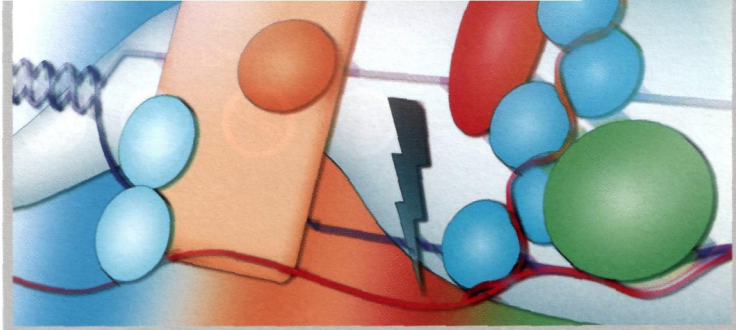


PREDICTIVE POWER?

From SNP genotypes to complex trait phenotypes

Sequencing-based studies for disease-gene discovery

Optimizing design and interpretation



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Gunter Meister

Argonaute proteins are vital components of small-RNA-guided modes of gene regulation. Recent studies have provided important details about classical modes of Argonaute function, such as their structure and loading with small RNAs, and have also revealed unexpected roles in other cellular functions.

460 Sequencing studies in human genetics: design and interpretation



David B. Goldstein, Andrew Allen, Jonathan Keebler, Elliott H. Margulies, Steven Petrou, Slavé Petrovski and Shamil Sunyaev

Next-generation sequencing is now poised for the discovery of genetic variants involved in common and rare diseases. Here, the authors present considerations for the workflow of these studies in order to identify true associations of disease and mutation.

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Nadia Solovieff, Chris Cotsapas, Phil H. Lee, Shaun M. Purcell and Jordan W. Smoller

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FEATURED ARTICLE

Ran Elkon, Alejandro P. Ugalde and Reuven Agami

Recent advances have allowed the genomic characterization of the extent and regulation of alternative polyadenylation. Here, the biological processes with which alternative polyadenylation has been associated, the mechanisms of its regulation and its involvement in disease are discussed.



M. Miller and D. K. Ko

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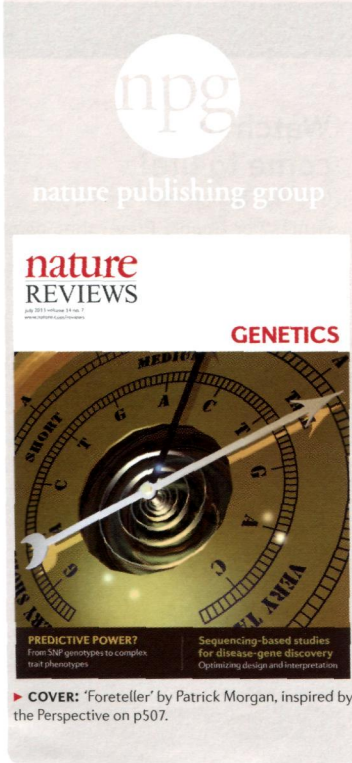
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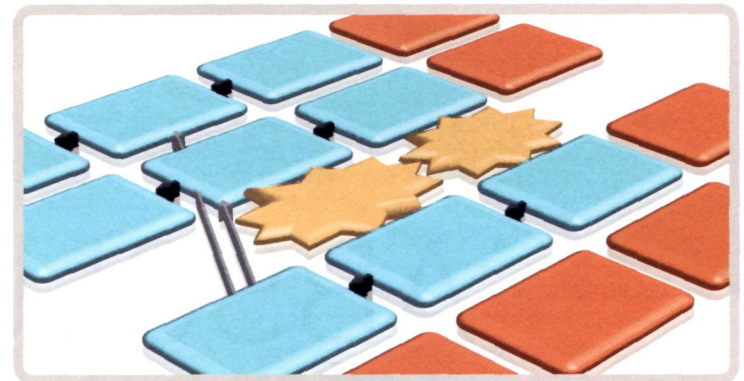
OPINION

507 Pitfalls of predicting complex traits from SNPs



Naomi R. Wray, Jian Yang, Ben J. Hayes, Alkes L. Price, Michael E. Goddard and Peter M. Visscher

The data from genome-wide association studies can be applied to genotype data to predict the phenotype of a complex trait. Here the authors discuss the potential pitfalls of such analyses and the inherent limitations of the method.



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