

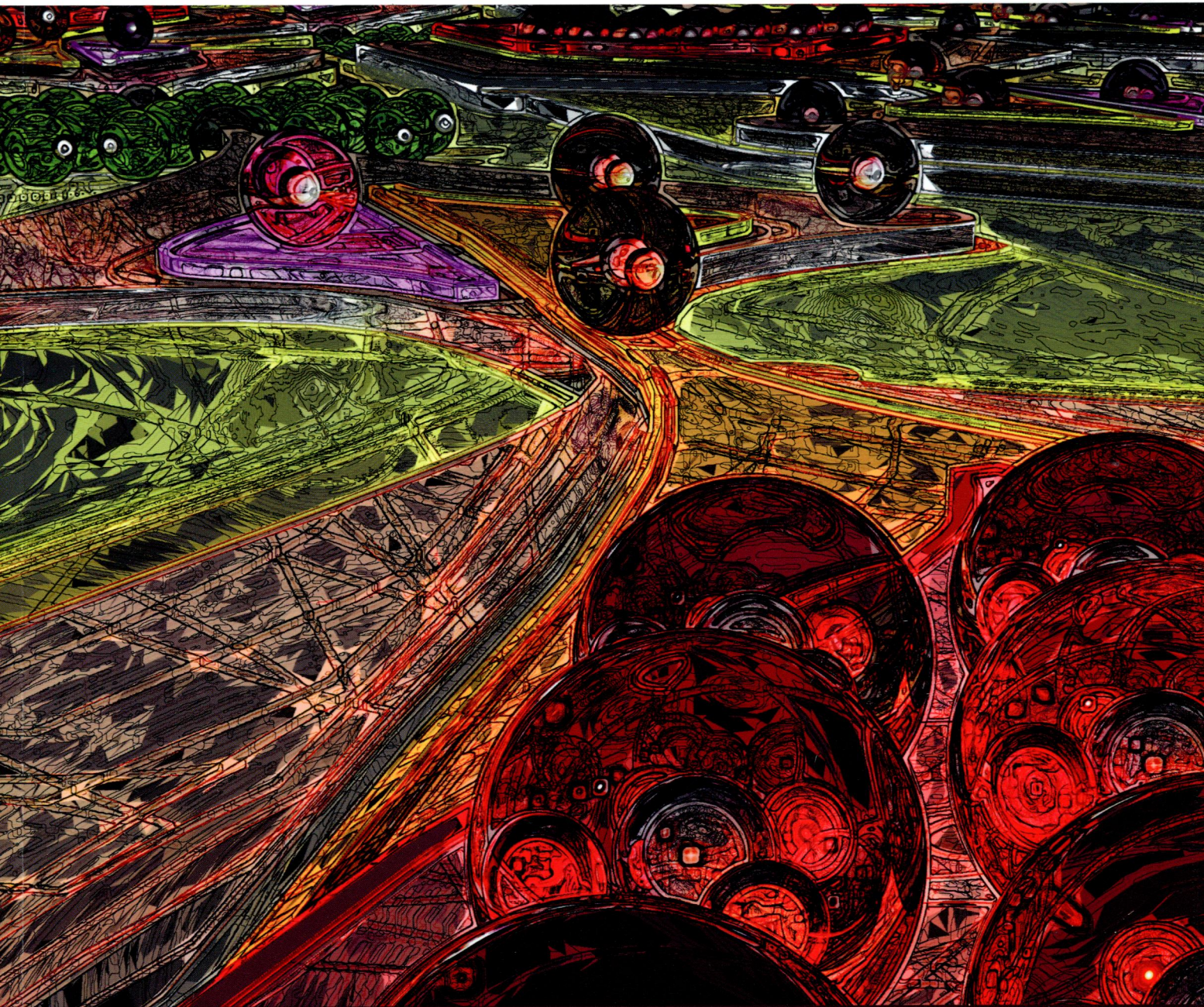
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REVIEWS

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GENETICS

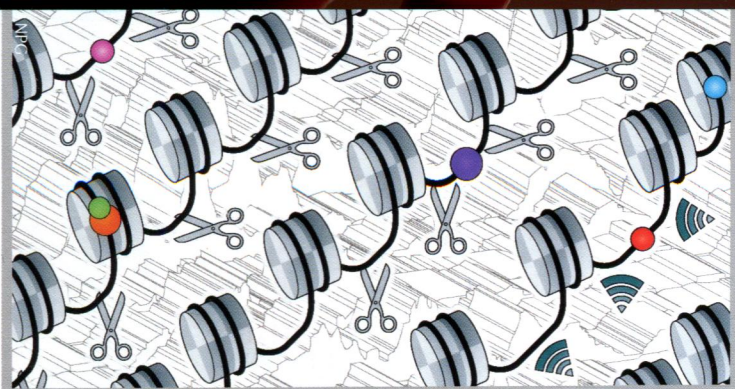


DIPPING INTO THE POOL

Characterizing population diversity by sequencing pools of individuals

Genetic interactions

Identifying and quantifying epistasis in complex traits



Mitigating bias in chromatin profiling methods p709

CONTENTS

November 2014
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REVIEWS

709 Identifying and mitigating bias in next-generation sequencing methods for chromatin biology



Clifford A. Meyer and X. Shirley Liu

Next-generation sequencing methods can be used to examine features of chromatin biology, although the outputs of these methods can be subject to various potential biases. This Review describes the ways in which biases can be introduced to such experiments and outlines methods to detect and mitigate their effect.

722 Detecting epistasis in human complex traits

Wen-Hua Wei, Gibran Hemani and Chris S. Haley

Genome-wide association studies have been extensively used to uncover genetic variants that independently influence complex traits, including diseases. This Review describes advances in computational approaches to detect interactions (epistasis) between genetic variants underlying complex traits, including the different promises and pitfalls of the methods. Additionally, the authors summarize current empirical evidence on how pervasive epistasis is in complex traits and its wider biological implications.

734 Evolutionary dynamics of coding and non-coding transcriptomes

FEATURED ARTICLE



Anamaria Necșulea and Henrik Kaessmann

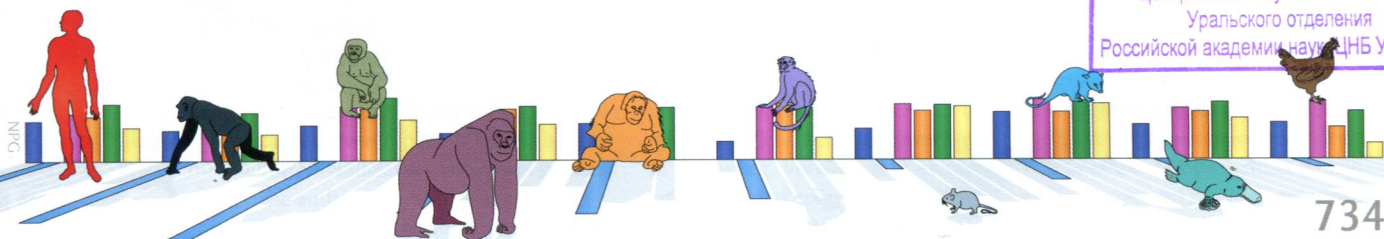
This Review provides insights obtained from comparative transcriptomic studies of mammalian species. The dynamics of gene expression evolution in coding and non-coding genes, as well as the regulatory basis of transcriptome evolution and future research avenues, are discussed.

749 Sequencing pools of individuals — mining genome-wide polymorphism data without big funding



Christian Schlötterer, Raymond Tobler, Robert Kofler and Viola Nolte

This Review describes how whole-genome sequencing of pooled DNA from many individuals (Pool-seq) is an economical alternative to sequencing the genomes of individuals separately. The authors outline the strengths and pitfalls of Pool-seq, and provide example applications across diverse species and biological questions.



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High-resolution digital profiling of the epigenome
Gabriel E. Zentner and Steven Henikoff

Microbial genome-enabled insights into plant-microorganism interactions
David Guttman, Alice C. McHardy and Paul Schulze-Lefert

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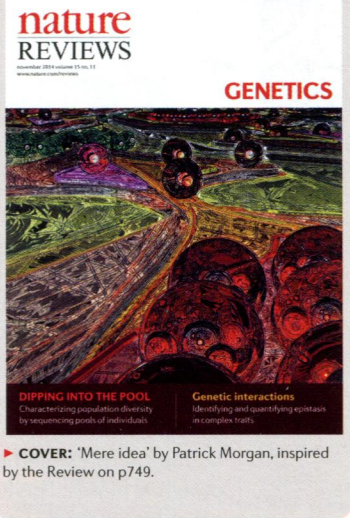
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► COVER: 'Mere idea' by Patrick Morgan, inspired by the Review on p749.

RESEARCH HIGHLIGHTS

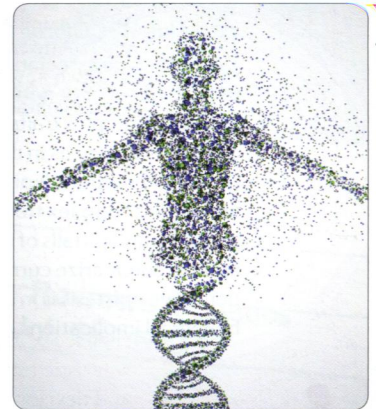
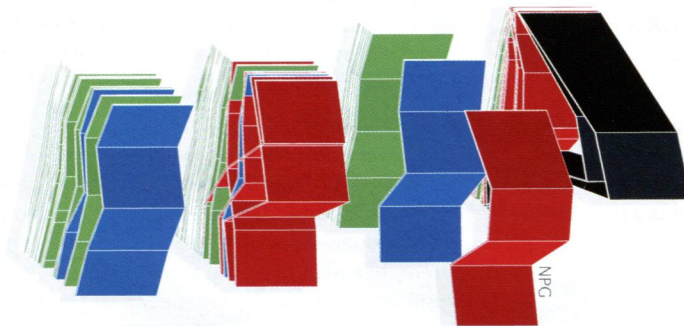
703 Selections from the recent scientific literature

ANALYSIS

765 The contribution of genetic variants to disease depends on the ruler

John S. Witte, Peter M. Visscher and Naomi R. Wray

There are various measures to quantify the contribution of genetic variants to disease risk, but differing terminology and assumptions obfuscate their use and interpretation. In this Analysis, the authors consider and contrast six commonly used measures that assess disease risk of individual variants, and provide numerical examples in breast cancer, Crohn's disease, rheumatoid arthritis and schizophrenia.



Web collection on 'Clinical applications of next-generation sequencing' now online at www.nature.com/nrg/collection/clinical-application-next-gen-seq

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