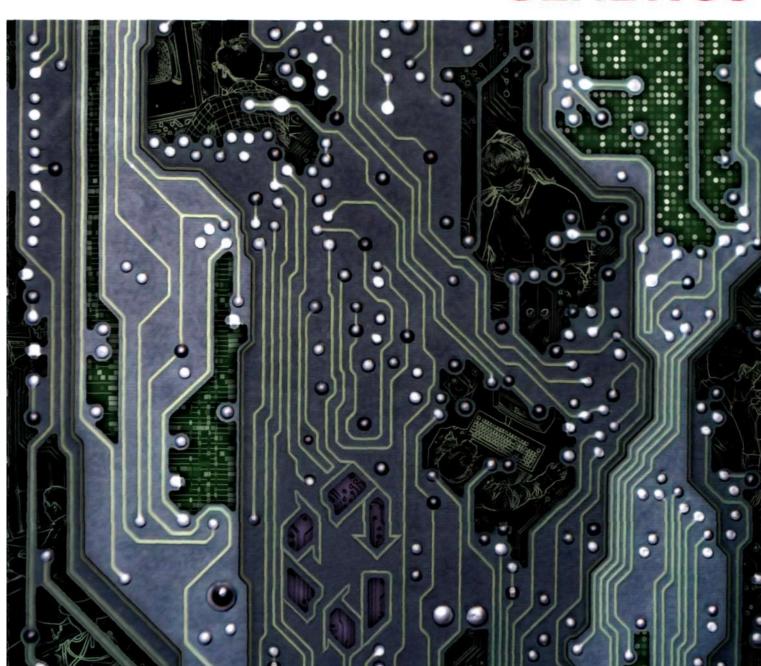


february 2013 volume 14 no. 2 www.nature.com/reviews

# **GENETICS**



REUSING GENE EXPRESSION DATA

Opportunities and nitfalls

Genomic structural variation

Implication for



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# REVIEWS

Reuse of public genome-wide gene expression data

Johan Rung and Alvis Brazma

A wealth of microarray gene expression data and a growing volume of RNA sequencing data are now available in public databases. The authors look at how these data are being used and discuss considerations for how such data should be analysed and deposited and how data reuse could be improved.

100 FEATURED ARTICLE RNA interference in the nucleus: roles for small RNAs in transcription, epigenetics and beyond

Stephane E. Castel and Robert A. Martienssen
In addition to well-known roles in the cytoplasm, a
growing number of functions for small RNAs in the
nucleus are being discovered. These include roles in
transcriptional repression, epigenetic modifications
and genome stability. This Review considers examples
from animals, plants and fungi.

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Y-chromosome evolution: emerging insights into processes of Y-chromosome degeneration

Doris Bachtroa

The Y chromosomes of many species, including humans, are gene-poor and degenerate. The recent application of genome-wide technologies to evolutionarily old and young Y chromosomes has provided insight into the processes that have shaped them and their future.

Phenotypic impact of genomic structural variation: insights from and for human disease

Joachim Weischenfeldt, Orsolya Symmons, François Spitz and Jan O. Korbel

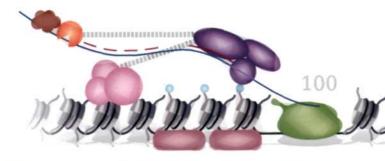
With the increased cataloguing of human structural variants, our understanding of their influence on phenotype is ever improving. Here, the influence of structural variants on phenotypes including disease is discussed, and strategies for further characterization are presented.

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The heritability of human disease: estimation, uses and abuses

Albert Tenesa and Chris S. Haley

Heritability estimates provide a useful means of understanding the genetic and environmental contributions to phenotypic variance. The authors define heritability, discuss how to estimate and interpret it in the context of disease and examine how biases in heritability estimates arise.



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Sequence assembly demystified

Niranjan Nagarajan and Mihai Pop

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DNA methylation: rdies in mammalian development

Zachary D. Smith and Alexander Meissner

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## RESEARCH HIGHLIGHTS

Selections from the recent scientific literature

#### PROGRESS

The evolutionary causes and consequences of sex-biased gene expression

John Parsch and Hans Ellegren

The authors discuss recent advances - mainly gained through genomic methods such as RNA sequencing — in our understanding of the causes and consequences of differences in gene expression between females and males. Areas of progress include our understanding of the roles of sexual antagonism and dosage compensation,







COVER: 'Data-based' by Patrick Morgan, inspired by the Review on p89.



Microbiome variants get personal p80

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