natureinsight

FRONTIERS IN BIOLOGY

19 January 2017 / Vol 541 / Issue No 7637



Cover illustration 'Patterning' by Nik Spencer

Editor, Nature Philip Campbell

Publishing Richard Hughes

Insights Editor Ursula Weiss

Production Editor Elizabeth Batty

Art Editor

Nik Spencer **Sponsorship**

Reya Silao

Production Ian Pope

Marketing Steven Hurst

Editorial Assistant Rosalind Metcalfe

The Campus 4 Crinan Street London N1 9XW, UK Tel: +44 (0) 20 7833 4000 e: nature@nature.com

SPRINGER NATURE

he *Nature* Insight 'Frontiers in Biology' aims to cover timely and important developments across biology, ranging from molecular mechanisms to whole-organism physiology and biomedicine.

Improvements in sequencing and in methods for enriching and extracting ancient DNA have furthered the temporal and geographic reach of ancient genomic studies, which have progressed from the analysis of single genomes to population genomics. Rasmus Nielsen and colleagues highlight how analysing the genomes of both modern and ancient individuals has provided deep insights into human history, adaptation and evolution, and compare these findings to theories previously supported by palaeontological and archaeological evidence.

Advances in molecular perturbations, coupled with those in imaging analysis and force measurements, have informed how morphogens — the products of genes that control cell-fate decisions — influence the cellular machineries that direct morphogenesis during development. Darren Gilmour, Martina Rembold and Maria Leptin explore how these approaches have enabled mechanisms of cross-talk to be uncovered, through which changes in shape can, in turn, influence fate decisions at various points in development.

Daniel Chen and Ira Mellman survey the elements that govern interactions between tumour cells and the host immune system, incorporating cell-intrinsic properties and external factors such as environmental exposure and the microbiota. On this basis, they suggest a framework that aims to predict the outcome of endogenous and therapy-induced anti-tumour immune responses.

Amos Tanay and Aviv Regev discuss how analysis of gene expression using single-cell approaches is changing our definitions of cell identities and fate acquisition during development and disease. They also outline how temporally and spatially resolved information is essential for overcoming the complexity of such data sets.

Recent studies have found that base modifications in messenger RNA, known collectively as the epitranscriptome, are pervasive. Emily Harcourt, Anna Kietrys and Eric Kool describe the chemistry behind these modifications and how they influence RNA folding, interactions and function.

Orli Bahcall, Angela K. Eggleston, Nathalie Le Bot & **Ursula Weiss**

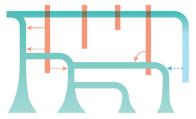
Senior Editors

CONTENTS

REVIEWS

302 Tracing the peopling of the world through genomics

> Rasmus Nielsen, Joshua M. Akey, Mattias Jakobsson, Jonathan K. Pritchard, Sarah Tishkoff & Eske Willerslev



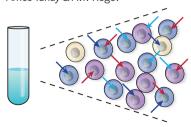
311 From morphogen to morphogenesis

Darren Gilmour, Martina Rembold & Maria Leptin



- 321 Elements of cancer immunity and the cancer-immune set point Daniel S. Chen & Ira Mellman
- 331 Scaling single-cell genomics from phenomenology to mechanism

Amos Tanay & Aviv Regev



339 Chemical and structural effects of base modifications in messenger

> Emily M. Harcourt, Anna M. Kietrys & Eric T. Kool