Commentary and Review

A new way to explore the world of extracellular protein interactions
Christopher M. Sanderson

Research

Letters

Using ChIP-chip technology to reveal common principles of transcriptional repression in normal and cancer cells
Vitalina M. Komashko, Luis G. Acevedo, Sharon L. Squazzo,
Sushma S. Iyengar, Alina Rabinovich, Henriette O’Geen,
Roland Green, and Peggy J. Farnham

Positive selection acting on splicing motifs reflects compensatory evolution
Shengdong Ke, Xiang H.-F. Zhang, and Lawrence A. Chasin

No effect of recombination on the efficacy of natural selection in primates
Kevin Bullaughey, Molly Przeworski, and Graham Coop

A survey of allelic imbalance in F1 mice
Catarina D. Campbell, Andrew Kirby, James Nemesh, Mark J. Daly,
and Joel N. Hirschhorn

Quantitative evidence for conserved longevity pathways between divergent eukaryotic species
Erica D. Smith, Mitsuhiro Tsuchiya, Lindsay A. Fox, Nick Dang,
Di Hu, Emily O. Kerr, Elijah D. Johnston, Bie N. Tchao,
Diana N. Pak, K. Linnea Welton, Daniel E.L. Promislow,
James H. Thomas, Matt Kaeberlein, and Brian K. Kennedy

Comparative analysis of the small RNA transcriptomes of Pinus contorta and Oryza sativa
Ryan D. Morin, Gozde Aksay, Elena Dolgosheina,
H. Alexander Ebhardt, Vincent Magrini, Elaine R. Mardis,
S. Cenk Sahinalp, and Peter J. Unrau

Analysis of sequence variability in the macronuclear DNA of Paramecium tetraurelia: A somatic view of the germline
Laurent Duret, Jean Cohen, Claire Jubin, Philippe Dessen,
Jean-François Goût, Sylvain Mousset, Jean-Marc Aury, Olivier Jaillon,
Benjamin Noël, Olivier Arnaiz, Mireille Bétermier, Patrick Wincker,
Eric Meyer, and Linda Sperling

(continued)
An infectious progenitor for the murine IAP retrotransposon: Emergence of an intracellular genetic parasite from an ancient retrovirus

David Ribet, Francis Harper, Anne Dupressoir, Marie Dewannieux, Gérard Pierron, and Thierry Heidmann

Methods and Resources

Methods

Application of massively parallel sequencing to microRNA profiling and discovery in human embryonic stem cells

Ryan D. Morin, Michael D. O’Connor, Malachi Griffith, Florian Kuchenbauer, Allen Delaney, Anna-Liisa Prabhu, Yongjun Zhao, Helen McDonald, Thomas Zeng, Martin Hirst, Connie J. Eaves, and Marco A. Marra

Large-scale screening for novel low-affinity extracellular protein interactions

K. Mark Bushell, Christian Söllner, Benjamin Schuster-Boeckler, Alex Bateman, and Gavin J. Wright

High-throughput biochemical analysis of in vivo location data reveals novel distinct classes of POUSF1(Oct4)/DNA complexes

Dean Tantin, Matthew Gemberling, Catherine Callister, and William Fairbrother

Resource

WGAViewer: Software for genomic annotation of whole genome association studies

Dongliang Ge, Kunlin Zhang, Anna C. Need, Olivier Martin, Jacques Fellay, Thomas J. Urban, Amalio Telenti, and David B. Goldstein

RECOMB Special Section

[The following Methods papers were accepted for publication by Genome Research in parallel with the 12th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2008).]

Commentary and Review

Review

Protein networks in disease

Trey Ideker and Roded Sharan

Methods and Resources

Methods

Increasing power in association studies by using linkage disequilibrium structure and molecular function as prior information

Eleazar Eskin

Panel construction for mapping in admixed populations via expected mutual information

Sivan Bercovici, Dan Geiger, Liran Shlush, Karl Skorecki, and Alan Templeton

(continued)
On the inference of ancestries in admixed populations
Sriram Sankararaman, Gad Kimmel, Eran Halperin,
and Michael I. Jordan

Effect of genetic divergence in identifying ancestral origin
using HAPAA
Andreas Sundquist, Eugene Fratkin, Chuong B. Do,
and Serafim Batzoglou

Open Access paper.

Cover  A circular representation of small RNA alignment frequency for 21-nt and 24-nt small RNAs along the length of each of the 12 nuclear *Oryza sativa* chromosomes (green), starting with the first chromosome at 12 o’clock. The yellow and orange consecutive rings represent degenerate alignments of 21-nt and 24-nt small RNAs, respectively, to the corresponding chromosomes. Small RNA alignments are nonuniform with hot spots of 24-nt sequences aligning to the heterochromatic regions, including most centromeres and some clusters of ribosomal RNA genes. The fractal trees conceptually represent our use of sequence-based hierarchical clustering and graph theory algorithms to identify novel microRNA families in *Pinus contorta*. (Cover illustration by Ryan Morin using Circos, fractal image created by Maia. [For details, see Morin et al., pp. 571–584.])