Commentary and Review

Review

Microbial community profiling for human microbiome projects: Tools, techniques, and challenges
Micah Hamady and Rob Knight

Research

Letters

Ride the wavelet: A multiscale analysis of genomic contexts flanking small insertions and deletions
Erika M. Kvikstad, Francesca Chiaromonte, and Kateryna D. Makova

Lineage-specific DNA methylation in T cells correlates with histone methylation and enhancer activity
Christian Schmidl, Maja Klug, Tina J. Boeld, Reinhard Andreesen, Petra Hoffmann, Matthias Edinger, and Michael Rehli

New class of microRNA targets containing simultaneous 5'-UTR and 3'-UTR interaction sites
Inhan Lee, Subramanian S. Ajay, Jong In Yook, Hyun Sil Kim, Su Hyung Hong, Nam Hee Kim, Saravana M. Dhanasekaran, Arul M. Chinnaiyan, and Brian D. Athey

Lack of bystander activation shows that localization exterior to chromosome territories is not sufficient to up-regulate gene expression
Céline Morey, Clémence Kress, and Wendy A. Bickmore

Analysis of the genome sequences of three Drosophila melanogaster spontaneous mutation accumulation lines
Peter D. Keightley, Urmil Trivedi, Marian Thomson, Fiona Oliver, Sujaí Kumar, and Mark L. Blaxter

The origins of apicomplexan sequence innovation
James Wasmuth, Jennifer Daub, José Manuel Peregrín-Alvarez, Constance A.M. Finney, and John Parkinson

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Genome sequencing of linezolid-resistant *Streptococcus pneumoniae* mutants reveals novel mechanisms of resistance
Jie Feng, Andréanne Lupien, Hélène Gingras, Jessica Wasserscheid, Ken Dewar, Danielle Légaré, and Marc Ouellette

Pervasive, genome-wide positive selection leading to functional divergence in the bacterial genus *Campylobacter*
Tristan Lefebure and Michael J. Stanhope

The polyadenylation site of Mimivirus transcripts obeys a stringent ‘hairpin rule’
Deborah Byrne, Renata Grzela, Audrey Lartigue, Stéphane Audic, Sabine Chenivesse, Stéphanie Encinas, Jean-Michel Claverie, and Chantal Abergel

**Methods and Resources**

*Methods*

DNA Sudoku—harnessing high-throughput sequencing for multiplexed specimen analysis
Yaniv Erlich, Kenneth Chang, Assaf Gordon, Roy Ronen, Oron Navon, Michelle Rooks, and Gregory J. Hannon

Overlapping pools for high-throughput targeted resequencing
Snehit Prabhu and Itsik Pe’er

Shifted Transversal Design smart-pooling for high coverage interactome mapping
Xiaofeng Xin, Jean-François Rual, Tomoko Hirozane-Kishikawa, David E. Hill, Marc Vidal, Charles Boone, and Nicolas Thierry-Mieg

Combinatorial algorithms for structural variation detection in high-throughput sequenced genomes
Fereydoun Hormozdiari, Can Alkan, Evan E. Eichler, and S. Cenk Sahinalp

Targeted genome editing in human cells with zinc finger nucleases constructed via modular assembly
Hye Joo Kim, Hyung Joo Lee, Hyojin Kim, Seung Woo Cho, and Jin-Soo Kim

Conserved introns reveal novel transcripts in *Drosophila melanogaster*
Michael Hiller, Sven Findeiß, Sandro Lein, Manja Marz, Claudia Nickel, Dominic Rose, Christine Schulz, Rolf Backofen, Sonja J. Prohaska, Gunter Reuter, and Peter F. Stadler

*(continued)*
Dissecting transcription regulatory pathways through a new bacterial one-hybrid reporter system
Manman Guo, Hui Feng, Jun Zhang, Wenqin Wang, Yi Wang, Yuqing Li, Chunhui Gao, Huanchun Chen, Ying Feng, and Zheng-Guo He

Resources

Efficient frequency-based de novo short-read clustering for error trimming in next-generation sequencing
Wei Qu, Shin-ichi Hashimoto, and Shinichi Morishita

The consensus coding sequence (CCDS) project: Identifying a common protein-coding gene set for the human and mouse genomes

Cover

While next-generation sequencing technologies have greatly increased sequencing capacity, genotyping libraries composed of a large number of specimens is still challenging. Combinatorial pooling designs offer a method to harness next-generation sequencers for that task. This solution has deep mathematical connections to concepts in information theory and combinatorics and is reminiscent of the solving of Sudoku puzzles. DNA Sudoku exploits a combinatorial design to genotype thousands of specimens in a single sequencing run. (Cover design by Beni Zaks and Yaniv Erlich. Photo: Ronit Zaks-Erlich. [For details, see Erlich et al., pp. 1243–1253, and related papers by Prabhu and Pe’er, pp. 1254–1261, and Xin et al., pp. 1262–1269.]}