A statistical framework for expression quantitative trait loci mapping, pp. 761–771
Meng Chen and Christina Kendziorski

In 2001, Sen and Churchill reported a powerful statistical framework that unified almost every method for quantitative trait loci (QTL) mapping in inbred line crosses. We have extended that framework to accommodate high dimensional phenotypes, such as expression traits measured via microarrays. This facilitates the understanding, evaluation, and precise comparison of expression QTL (eQTL) mapping methods by revealing their specific characteristics in the context of a common notation, which in turn provides an improved environment for addressing open questions and developing ideas for future methods. As one example, we show how the extension leads to the development of an eQTL mapping approach that improves eQTL localization.

Evolution can favor antagonistic epistasis, pp. 1001–1010
Michael M. Desai, Daniel Weissman and Marcus W. Feldman

The nature of the interactions (epistasis) between deleterious mutations affects a variety of things in evolution—most notably the evolution of sex, which is favored by synergistic epistasis. We show that when epistasis is allowed to evolve, antagonistic epistasis is favored over synergistic, by an amount that increases with recombination rate. Thus, although synergistic epistasis favors the evolution of recombinant, recombination favors the evolution of less synergistic or more antagonistic epistasis.

Estimating meiotic gene conversion rates from population genetic data, pp. 881–894
J. Gay, S. Myers and G. McVean

Estimating the rate at which gene conversion occurs is difficult because of the short lengths of DNA involved. The authors have developed a new statistical approach to estimate gene conversion rates from genetic variation by extending an existing model for haplotype data in the presence of crossover events. Simulations show that the method works well when the rate of gene conversion events is at least comparable to the rate of crossover events. Application of the method to data from the low recombining tip of the X chromosome of Drosophila melanogaster indicates that gene conversion occurs ~400 times more often than crossover events. Human chromosome 1, by contrast, shows a rate of gene conversion ~1.5 times higher than the crossover rate in a region with known recombination hotspots.

B chromosome polymorphism in maize landraces: Adaptive evolution, demographic hypothesis of clinal variation, pp. 895–904
Verónica V. Liá, Viviana A. Confalonieri and Lidia Poggio

Plant B chromosomes have long been regarded as selfish elements that persist in natural populations by means of different accumulation mechanisms. Under this scenario, the altitudinal and longitudinal clines of B’s observed in maize landraces suggest nonneutral processes at play. By analyzing the patterns of variation at selectively neutral markers along an altitudinal cline of B’s, the authors conclude that differences in the mean number of B’s among populations cannot be explained by demographic processes and suggest a local interaction between maize A and B chromosomes.

The roles of mutation accumulation and selection in loss of sporulation in experimental populations of Bacillus subtilis, pp. 937–948
Heather Maughan, Joanna Masel, C. William Birkby, Jr. and Wayne L. Nicholson

Phenotypic loss is prevalent in all groups of organisms. In this article we focus on the loss of a particular phenotype, sporulation ability, in populations of bacteria that were evolved in the laboratory for 6000 generations. We use a combination of experimental and computational approaches to determine whether selection played a role in the loss of sporulation or whether the observed losses were due to the accumulation of mutations alone. We found that, in most of the populations, mutation accumulation was sufficient to explain the loss of sporulation. However, in one population, selection facilitated sporulation loss. This is one of the first examples of evidence that selection plays a role in phenotypic loss.

A selective sweep in the chloroplast DNA of dioecious Silene (section Elisanthe), pp. 1239–1247
Graham Muir and Dmitry Filatov

We report the putative spread of an advantageous allele across the range of two hybridizing plant species. The sweep resulted in a significant loss of DNA diversity and species and population differentiation in the chloroplast DNA. Our results also illustrate that recovery of population structure after the sweep occurs quickly at the local scale, but much slower at the continental scale, resulting in a counterclockwise pattern of high population structuring at the level of demes and very little structure at higher population/species levels.

A genomewide study of reproductive barriers between allopatric populations of a homosporous fern, Ceratopteris richardii, pp. 1141–1150
Takuya Nakazato, Min-Kyung Jung, Elizabeth A. Housworth, Loren H. Rieseberg and Gerald J. Gastony

Although ferns are the second most diverse group of vascular plants after seed plants, their modes of genome evolution and speciation are largely unknown. The authors investigate the genetics of reproductive barriers between divergent allopatric populations of a homosporous fern, Ceratopteris richardii, and show that reproductive barriers have likely accumulated gradually since their divergence and that a surprisingly small proportion of the genome is likely responsible for the strong reproductive isolation.

Genomewide identification of genes under directional selection: Gene transcription Q, scan in diverging Atlantic salmon subpopulations, pp. 1011–1022
C. Robarge, H. Guderley and L. Bernatchez

Identifying genes important for the adaptation of species to newly colonized environments is a central goal of evolutionary biology. We propose a method to identify genes whose transcription levels have most likely evolved through the effect of directional selection. This is achieved by analyzing familial genomewide transcription profiles in a combination of the Q, and genome scan frameworks. We identified 16 such genes in two Atlantic salmon subpopulations that started diverging 30 years ago when a fish ladder was installed at the site of an impassable waterfall on their native river. We postulate that these genes evolved different transcription levels as an adaptive response to different environmental conditions.

Adaptive evolution of recently duplicated accessory gland protein genes in desert Drosophila, pp. 1021–1030
Bradley J. Wagstaff and David J. Begun

Compared to the Drosophila melanogaster subgroup species, the repleta group species have higher remating rates, delayed sexual maturity, and several other interesting differences. Accessory gland protein genes (Acps) of D. mojavensis and D. arizonae evolve more rapidly than Acps in the D. melanogaster subgroup. The D. mojavensis and D. arizonae genomes contain several young duplicated Acps and these Acps have experienced rapid, adaptive protein divergence. Rapid remating of female desert Drosophila generates selection for continuous diversification of the male Acp complement to improve male fertilization potential. Thus, mating system variation may be associated with adaptive protein divergence as well as duplication of Acps in Drosophila.