

Whole Genome Sequencing, Comparative Genomics, and Systems Biology

Eugene Myers

University of California, Berkeley

Abstract

The whole-genome shotgun sequencing method with paired end-reads has proven rapid and economical, producing high-quality reconstructions of *Drosophila* (2000), Human (2001) and Mouse (2001), in quick succession. We discuss the overall algorithmic strategy, the results one can expect by comparing the whole genome assembly of *Drosophila* against the recently finished sequence, and advances such as high-density solid state sequencing and single molecule detection systems.

We anticipate having the euchromatic portions of the

genomes of twelve species of *Drosophila* in the next year. We discuss the current state of the art in comparative gene finding, cis-control module finding, and possible improvements. The hope of these approaches is that we will be able to accurately identify the “parts lists” of the *D. melanogaster* genome, a basic prerequisite for systems biology.

We conclude with a segment on the possibility of a program of high-throughput *in-situ* image analysis in *Drosophila* embryos. We describe what information we might collect and what we might be able to infer from it. It is our contention that this may be the best way to understand development from a systems perspective.