1003-92-1531   **Manolis Dermitzakis** (`md4@sanger.ac.uk`) and **Lior Pachter***
(`lpachter@math.berkeley.edu`), Department of Mathematics, U.C. Berkeley, Berkeley, CA 94708.
Identifying functional elements in the human genome.

This two-part talk will begin with an introduction to functional genomics, with an emphasis on the role of non-coding conserved DNA in the human genome. In particular, we will discuss the importance of comparing multiple primate species for identifying functional elements in the genome. We will then describe the related mathematics of "phylogenetic shadowing" which has been successfully applied to infer functional regions within multiple primate alignments. (Received October 05, 2004)