NORMALIZATION AND MIXED-MODEL ANALYSIS OF NOVEL MULTI-SPECIES MICROARRAYS TO MEASURE THE EVOLUTION OF GENE EXPRESSION IN PRIMATES

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A number of recent studies have used microarrays to compare patterns of gene expression between closely related primate species. One flaw with previous studies is the use of microarrays with probes based on human sequences to characterise general trends in gene expression between species. In this study we use novel microarrays which contain species specific probes for four primate species to compare expression between primates. For the first time we are able to identify specific genes whose regulation has been evolving under natural selection. I will present new normalization procedures which take into account the reduced binding affinities caused by sequence mismatches between target of one species and probes of another species. I will discuss how the previous use of human specific microarrays biased previous results and I will discuss the linear mixed model used to fit both fixed and random effects in this data.