1023-92-1429    **Peter M Huggins\*** (`phuggins@math.berkeley.edu`), Department of Mathematics, University Of California at Berkeley, Berkeley, CA 94720, and **Lior Pachter** and **Bernd Sturmfels**. *Towards the Human Genotope.* Preliminary report.

Given a collection of genotypes, their genotope is the polytope defined as the convex hull of all allele frequency vectors that can arise from populations over the collection of genotypes. On the theoretical front, Beerenwinkel et al have shown that regular subdivisions of genotopes encode shapes of fitness landscapes and generalize the concept of epistasis to arbitrary numbers of genes. Now on the practical side we aim to show that it is computationally feasible to compute certain projections of genotopes for real-world data sets. Using the HapMap data set, we compute projections of sub-polytopes of the human genotope. We report on three classes of low-dimensional projections: projections specified by principal component analysis, by restriction to few SNPs, and by archetypal analysis. (Joint work with L Pachter and B Sturmfels) (Received September 26, 2006)