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**Marc Allen Harper\*** (marcharper@ucla.edu). *Phenotype Sequencing*.

Phenotype sequencing is a mathematical and statistical approach to the identification of mutations and genes causing and contributing to phenotypes resulting from the evolution of organisms subject to natural or artificial mutagenesis, as well as to the detection of rare-variants associated to particular phenotypes, through next-generation high-throughput DNA sequencing. This technique can significantly reduce the cost of identifying such genes in some cases. In this talk I present explicit results from experiments on biofuel-tolerant bacterial strains independently created through random chemical mutagenesis (effectively screening through background mutations and identifying the mutations and genes that confer tolerance), results from an analysis identifying a gene associated to a rare disease in six Korean subjects, other experimental results and information-theoretic evaluation metrics for these methods and experiment designs if time permits. This is joint work with Chris Lee of UCLA. (Received September 21, 2011)