BYU MOLECULAR GENEALOGY

ABSTRACT DNA Analysis Techniques for Molecular Genealogy Luke Hutchison (lukeh@email.byu.edu); Project leader: Dr. Scott Woodward

The BYU Molecular Genealogy Project is creating a database of DNA patterns that are found throughout the world and that are being passed down through families. Using this database, people will one day be able to have questions answered about the origins or possible identity of unknown ancestors in their genealogy, based on their own DNA.

The initial goals of the project are to collect at least 100,000 blood samples from people around the world, along with the pedigree chart for each person who gives a blood sample. The association of ancestral data with the DNA sequence data will produce the first database of its kind and scale in the world. Opportunities have opened for the analysis of DNA, particularly in the genealogical context, in ways which have not been possible until this time.

Because this type of analysis has not been done before, many new computer algorithms must be developed to process the data that is being collected in this project. Examples include fitting the DNA to pedigree charts to produce a "genetic map" of the world, both topologically and back through time; searching for common ancestors based on descendants' shared DNA; inferring the correct alignment of unordered fragments of DNA data; and inferring the geographical origins of ancestors using population genetics.

Once the database is built and the analysis software is developed, the aim is to be able to have individuals come to us with specific questions about their ancestors, which will then often be answerable by looking at the living individual's own DNA. Examples of questions we hope to be able to answer are questions concerning adoptions vs. blood lineages, and origins in space and time of a specific ancestor (based on the DNA sample, and the rest of the known parts of the pedigree chart).

Some of the algorithms and techniques which have been developed successfully so far for data analysis are discussed, along with problems faced and future research directions.

[Please see http://molecular-genealogy.byu.edu for more information.]