Docket #: S13-178

RFMix: A fast, discriminative method for inferring local ancestry and correcting phase errors

Stanford researchers have discovered a fast, discriminative method for inferring local ancestry and correcting phase errors. This local ancestry inference method is both faster and more accurate than the previous state-of-the-art. It has been demonstrated to have high accuracy when inferring sub-continental ancestries, as well as when reference information is sparse. It has also been demonstrated to improve phase estimates.

Applications

- In medical genetics and trait mapping studies, where local ancestry information can be used to increase statistical power
- In demography, where local ancestry information can be used to infer the histories of populations

Advantages

- Fast, accurate, easy to use
- Simultaneously corrects phase errors in the input data
- Speed can be increased through parallelization
- Can use dense whole genome sequencing data
- Highly accurate in scenarios where other methods do poorly, such as small, low quality, or nonexistent reference panels

Publications

- Maples BK, Gravel S, Kenny EE, Bustamante CD, "RFMix: A Discriminative Modeling Approach for Rapid and Robust Local-Ancestry Inference". *Am J Hum Genet*, Jul 30, 2013.
- The 1000 Genomes Project Consortium, "An integrated map of genetic variation from 1,092 human genomes," *Nature* 491, 56-65 (2012).

Innovators

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