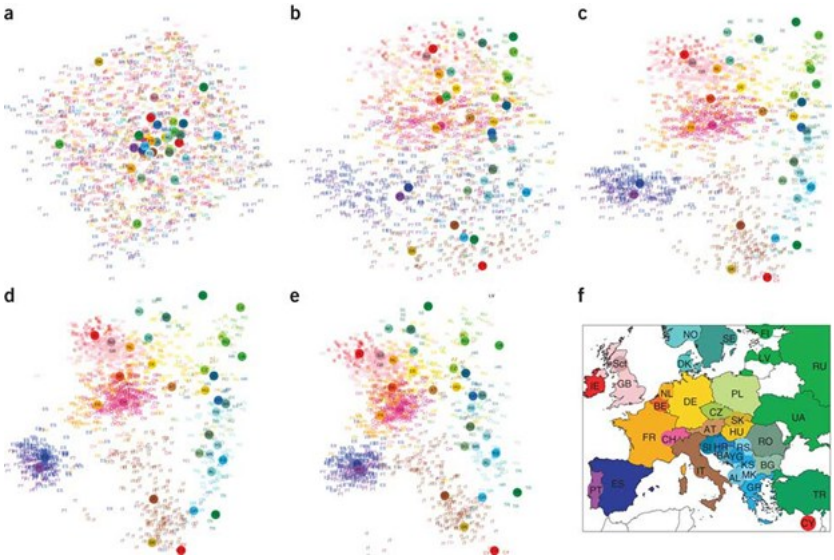
Genetic mapping pinpoints parents' origins to within a few hundred kilometres

By Liat Clark (/search/author/Liat+Clark) | 20 August 12 (Mon, 20 Aug 2012 17:00:00 +01:00)



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A team of computer scientists and geneticists has published a paper detailing a novel approach to genetic mapping that uses a probability algorithm and DNA data to accurately pinpoint the geographical origins of a subject's parents.

The study, published (http://www.nature.com/ng/journal/v44/n6/full/ng.2285.html#/abstract) in *Nature Genetics*, explains how the Tel-Aviv University and University of California team created a genetic map (http://www.wired.co.uk/news/archive/2012-07/04/genetic-mapping-britain) by identifying populations that share subtle genetic mutations. An algorithm was then used to compare those genetic geographical sites against a subject's DNA. After studying 1,157 samples from people across Europe the method was shown to successfully identify the geographical origins of a subject's parents to within a few hundred kilometres.

"If the location of an individual is unknown, our model can actually infer geographic origins for each individual using only their genetic data with surprising accuracy," said Wen-Yun Yang, a UCLA computer scientist involved in the study.

Mutations of the single-nucleotide sequence that makes up our DNA were used to generate the map. There are four types of single nucleotide, adenine (A), cytosine (C), guanine (G) and thymine (T). Instances where one appears where another should be is classed as a mutation, and these tend to be shared by those individuals closely related by blood. These shared variations, that make one group of people subtly genetically distinct from another, are known as single-nucleotide polymorphism (SNP). The team studied about 500,000 genomic sites to help develop a SNP spatial distribution model of where these variations frequently occur geographically -- a 3D world map where every geographical location has a genetic marker (for instance, in one city a mutation might occur 80 percent of the time, while in another it may only occur 10 percent of the time). A probabilistic algorithm using this world map could then be used to identify the exact origins of specific genome mutation.

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"If we know from where each individual in our study originated, what we observe is that some variation is more common in one part of the world and less common in another part of the world," said Eleazar Eskin, a UCLA computer scientist. "How common these variants are in a specific location changes gradually as the location changes."

"In this study, we think of the frequency of variation as being defined by a specific location. This gives us a different way to think about populations, which are usually thought of as being discrete. Instead, we think about the variant frequencies changing in different locations. If you think about a person's ancestry, it is no longer about being from a specific population -- but instead, each person's ancestry is defined by the location they're from. Now ancestry is a continuum."

The probability algorithm has also been adjusted to take into account whether one parent hails from a different geographical location from the other -- for instance, old models would come back saying a subject hails from a middle point, C, rather than recognising that one parent was from A and another from B.

"The combined genetic fingerprint of the mother and father is manifested in the child," said Eran Halperin of Tel-Aviv University's Blavatnik School of Computer Science and Department of Molecular Microbiology and Biotechnology, who specialises in disease genetics. "We are able to 'reverse engineer' this information to detect the parents' origins without ever observing their genetic fingerprints directly. In principle our approach could be extended to grandparents, great grandparents."

The way the system functions means that as populations continue to migrate and the team attempt to look back further into ancestry, the accuracy of the results can be hampered.

"Analyses of populations such as North Americans or Jews are more complicated, because they have been mixing with other populations or mixing among themselves regardless of their geographic origins," said Halperin.

The new methodology could open up plenty of applications in genetic mapping, including the study of historic migration patterns, genetic diseases and even the migration of animal populations. The study revealed that the most extreme genetic variations (between one individual and another) were present when selection had recently occurred -- it therefore also presents a new methodology for identifying human genetic selection.

Story
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