



Cass Business School
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A new algorithm for finding maximum likelihood pedigrees
New research will help reconstruct pedigrees in mass grave situations

A new algorithm has been formulated which helps to reconstruct pedigrees of individuals, for example in wild animal or plant populations, or in a group of related people. The algorithm uses genotypic data to find the pedigree having the maximum likelihood for a sample which is complete.

The research*, from Dr Robert Cowell at Cass Business School, London, means that searching for the maximum likelihood pedigree with 20 individuals takes around one second, and if the number of individuals rises to 29 individuals it takes just over eight minutes. Previously, an exhaustive search over all pedigrees using earlier algorithms on more than a dozen or so individuals would have been computationally prohibitive.

Such an efficient method is important to scientists trying to establish the familial relationships, if any, of several deceased individuals whose remains are recovered, for example, from mass graves or in multiple fatality disasters. It is particularly applicable to scenarios where it is suspected that there are many individuals that may be closely related to each other, such as the famous case of the Russian Royal family who went missing during the Russian revolution of 1917. In July 1991, nine skeletons were found in a shallow grave which were believed to be the remains of Tsar Nicholas II, his wife, three of their five children, some of their servants and the Royal Physician.

When the new algorithm is applied to DNA evidence available from the nine skeletons, it quickly reconstructs the correct relationships of the five members of the Royal family.

The algorithm can utilize age and sex information, but does not require either. Further research is underway to extend the algorithm for greater applicability, for example to samples that are not complete.

Dr Cowell says: "This algorithm is effective in that it works on building family trees from the available DNA information, efficiently discarding low likelihood scenarios to build up the most likely family structure. While this is useful in identifying human remains, it is also applicable for biologists who are interested in preserving endangered species as pedigree reconstruction could help in gauging the amount of inbreeding and genetic diversity within species."

**Efficient maximum likelihood pedigree reconstruction. Published in Theoretical Population Biology, Volume 76 (2009). Dr Robert G. Cowell, Cass Business School, London..*

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Notes to editors:

Cass Business School

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