RETRATOS de EMPREGABILIDADE

Mestrado em Engenharia Matemática

Seminários temáticos: análise de situações concretas e debate de ideias sobre o enquadramento do perfil de um Engenheiro Matemático nas atuais e inovadoras oportunidades profissionais.

📅 18 de Abril - 17h00 - FC1 0.30

📍 **DEPARTAMENTO DE MATEMÁTICA**

VALIDATING SOFTWARE TO ESTIMATE GENETIC RELATEDNESS – ONE SMALL STEP FOR ALGEBRA, ONE GIANT LEAP FOR FORENSICS

A major share of the forensic genetics practical work is related with kinship evaluation. In fact, from identity (mostly evaluated in criminal context) to very complex genealogies, what is asked of the expert is to evaluate the posterior probability of genetic kinships between samples and/or individuals given a specific phenotype constellation (or the computation of likelihood ratios between the probabilities of alternative pedigrees). Indeed, in forensics the use of likelihood ratios has become globally accepted as the best way to evaluate genetic evidence, comparing the probability of the observations under the claimed kinship with the probability of the same observations under the alternative hypothesis of kinship. These probabilities are formally established for pairs of individuals and depend on both: (a.) the frequency of the alleles in the population, and (b.) the probabilities of the individuals sharing alleles descendent of the same ancestral allele, given the pedigree under assumption.

For this, the use of unlinked autosomal markers is currently the standard practice in forensic laboratories and it should be highlighted that, whatever the mode of transmission considered, there are pedigrees that are theoretically indistinguishable, no matter the amount of genetic information analysed. In previous works of ours we proved which pedigrees belong to each kinship classes for both autosomal and X-chromosomal mode of transmission and pairs of non-inbred individuals.

There are several software programs available (freeware and commercial products) to compute and evaluate the likelihood of disputed kinships but the forensic community, particularly the International Society for Forensic Genetics, claims the need of validating such programs, which, most of them, are nothing more than "black boxes". The development of exact algebraic expressions for any number of individuals and pedigree linking them is, of course, the procedure of excellence for software validation and, the development of a method for its easy attainment is, from our point of view, the next step for the improvement of the state of art.

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Nádia Pinto holds three academic degrees from the Faculty of Sciences of the University of Porto: BSc in Mathematics – Educational branch (2003), MSc in Mathematical Engineering (2006), and PhD in Applied Mathematics (2012). Currently she is a postdoctoral fellow in the Population Genetics and Evolution group at IPATIMUP/i3s and in the Centre of Mathematics of the University of Porto. Her work is mainly focused on the estimation of genetic relatedness among individuals and she is interested in the theoretical and formal perspective, and software development.

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