



**Oral Session III-1**

**Friday, September 18 (14:00 – 16:00)**

- O 27 14:00 X-chromosomal markers in relationship testing: The effects of linkage and linkage disequilibrium on computed likelihood ratios**  
*Andreas Tillmar<sup>1</sup>, Thore Egeland<sup>2</sup>, Bertil Lindblom<sup>1</sup>, Gunilla Holmlund<sup>1</sup>, Petter Mostad<sup>3</sup>, <sup>1</sup>National Board of Forensic Medicine, Department of Forensic Genetics and Forensic Toxicology, Linköping, Sweden, <sup>2</sup>University of Oslo, Institute of Forensic Medicine, Oslo, Norway, <sup>3</sup>Mathematical Sciences, Chalmers University of Technology, and Mathematical Sciences Göteborg University, Göteborg, Sweden*
- O 28 14:12 Distinguishing kinship from genealogical likelihoods**  
*Nádia Pinto<sup>1,2</sup>, Leonor Gusmão<sup>1</sup>, António Amorim<sup>1,2</sup>, <sup>1</sup>IPATIMUP, Instituto de Patologia e Imunologia Molecular da Universidade do Porto, Porto, Portugal, <sup>2</sup>Faculdade de Ciências da Universidade do Porto, Porto, Portugal*
- O 29 14:24 Evaluating the usage of *Fst* to correct for population stratification when estimating PI values**  
*Ulises Toscanini<sup>1</sup>, Antonio Salas<sup>2</sup>, Manuel García-Magariños<sup>2</sup>, Eduardo Raimondi<sup>1</sup>, <sup>1</sup>PRICAI-FUNDACIÓN FAVALORO, Buenos Aires, Argentina, <sup>2</sup>Unidad de Xenética, Inst. Med. Leg., Univ. de Santiago de Compostela, Santiago de Compostela, Spain*
- O 30 14:36 Overdispersion in allelic counts and  $\theta$ -correction in forensic genetics**  
*Torben Tvedebrink<sup>1</sup>, <sup>1</sup>Department of Mathematical Sciences, Aalborg University, Aalborg, Denmark*
- O 31 14:48 More for the same? Enhancing the investigative potential of forensic DNA databases**  
*Tim Clayton<sup>1</sup>, Sue Pope<sup>1</sup>, Jonathan Whitaker<sup>1</sup>, Roberto Puch-Solis<sup>1</sup>, John Lowe<sup>1</sup>, <sup>1</sup>Forensic Science Service, Birmingham, United Kingdom*
- O 32 15:00 Development of a quantitative method for taking account of the sizes of peaks when interpreting STR mixtures for court purposes**  
*Roberto Puch-Solis<sup>1</sup>, Ian Evett<sup>1</sup>, Lauren Rodgers<sup>1</sup>, <sup>1</sup>Forensic Science Service, Birmingham, United Kingdom*
- O 33 15:12 Dropout for dummies -- modular methods for dropout analysis**  
*Charles Brenner<sup>1</sup>, <sup>1</sup>UC Berkeley, Berkeley, CA, United States*



**O 34 15:24 RMNE probability of forensic DNA profiles with allelic drop-out**

Filip Van Nieuwerburgh<sup>1</sup>, Els Goetghebeur<sup>2</sup>, Mado Vandewoestyne<sup>1</sup>, Dieter Deforce<sup>1</sup>, <sup>1</sup>*Laboratory for Pharmaceutical Biotechnology, Ghent University, Ghent, Belgium*, <sup>2</sup>*Department of Applied Mathematics and Computer Science, Ghent University, Ghent, Belgium*

**O 35 15:48 Interpretation of low-copy-number DNA profile after post-PCR purification.**

Sabine Michel<sup>1</sup>, Anne De Bast<sup>1</sup>, Olivier Froment<sup>1</sup>, <sup>1</sup>*Bio.be SA - CRI, 6041 Gosselies, Belgium*