

Investigator Forum — Workshops

Tuesday, April 1, 2014

Agenda:

10:00 am – 5:00 pm

From Sample to Result: QIAGEN workflow solutions with the QIASymphony SP/AS instrument

Carole Peel, QIAGEN

All-day

Sample purification and qPCR assay set up

- Introduction to QIASymphony SP/AS, consumables, and reagents
- Sample preparation and lysis
- Load and run samples using an integrated run protocol (Casework ADV HE and Quantiplex).
- Quantification transfer data and samples to the RGQ and start Quantiplex assay run; normalization & PCR set-up
- Analyse quant results and transfer samples and data to the QS for normalization and STR set-up
- Run normalization and STR set-up on QIASymphony, then transfer to thermal cycler for STR amplification
- CE and analysis
- Prepare plate and start 3,500 CE instrument run for electrophoresis
- Analyse and review data with discussion time

Please note: This workshop is limited to 8 places

10:00 am – 4:00 pm

Mixture interpretation

Dr. Susan Pope, DNA Principal Forensics Ltd

Morning

- DNA interpretation methods
- Manual interpretation and cognitive bias
- Guidelines and propositions

Afternoon

- Population genetics
- LR formulae
- Low template DNA issues

Please note: This workshop is limited to 30 places

If you are attending the **Mixture interpretation workshop**, or the **Population genetics and statistics workshop** it may be possible to arrange a tour of the QIAGEN production facilities directly after the workshop. Please contact dora.quest@qiagen.com if you are interested. Unfortunately, we cannot offer this option to QIASymphony workshop attendees as QIAGEN does not allow entry to the production buildings after spending time in the laboratory.



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Population Genetics and Statistics

Dr. Chris Phillips, Forensic Genetics Unit, University of Santiago de Compostela

Dr. Andreas Tillmar, National Board of Forensic Medicine, Linköping

Morning

Part 1: Criminal Profiling, Dr. Chris Phillips

- Basics of human population genetics
- Considerations for preparing and using STR allele frequency data
- The profile frequency. Linkage issues with syntenic STRs. The 'ceiling RMP' (e.g. UK's adoption of 1 in 1 billion)
- Non-recombining Y-STR sets - Using YHRD data
- Population sub-structure and using the theta correction factor
- Anticipating brother pleas
- On the horizon: Familial searching, expanded STR sets, STR typing with NGS

Afternoon

Part 2: Relationship testing*, Dr. Andreas Tillmar

A. Theoretical

- Basic paternity issues
- Complex pedigree testing
- Mutations & silent alleles
- Linkage and linkage disequilibrium
- Introduction to the biostatistical softwares Familias & FamLink

B. Practical

- Tutorial Familias version 3 (download via <http://familias.no/english/download>)
- Case examples covering simple paternity issues, complex pedigree issues, and examples of how to account for mutation and silent alleles
- Tutorial FamLink (download via http://www.famlink.se/f_download.html)
- Case examples of how to account for linkage

*The session will include a theoretical part and practical part. The participants are advised to bring their laptops and download the softwares Familias and FamLink before the workshop. Case examples for the practical part will be available for downloading before the workshop.

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