



**ISFG**  
**PRAGUE**

# THE 28<sup>th</sup> CONGRESS OF THE INTERNATIONAL SOCIETY FOR FORENSIC GENETICS

9 – 13<sup>th</sup> SEPTEMBER 2019

PRAGUE CONGRESS CENTRE, THE CZECH REPUBLIC

**PROGRAMME  
BOOK**

[www.isfg2019.org](http://www.isfg2019.org)



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# ISFG 2019

## 28<sup>th</sup> Congress of the International Society for Forensic Genetics

9 – 13<sup>th</sup> September 2019

Prague Congress Centre, the Czech Republic

Hosted by

International Society for Forensic Genetics



Czechoslovak Society for Forensic Genetics





# Unlock the Power of DNA Sequencing

CRIMINAL CASEWORK  
MISSING PERSONS  
ANCESTRY ESTIMATION  
PHENOTYPE ESTIMATION  
MIXTURE RESOLUTION  
DNA DATABASING  
MOLECULAR AUTOPSY  
BODY-FLUID ID  
METAGENOMICS  
CGAGAGAG  
CCGCA  
CAATAG  
AAGGAACTGC

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# Welcome Words

## Dear Colleagues,

preparation for the 28<sup>th</sup> International Congress of International Society for Forensic Genetics (ISFG) is approaching its climax. Online registration is running, promising to beat the record from Seoul in number of participants. Program is ready, featuring hands-on and ear-on workshops, meetings of national or topical societies, lectures from renowned and rising scientists, austere and lavish posters, and last but not least, accompanying social programme.



It is possible that for ISFG executive committee and professional congress organiser C-IN it is just another event in the row. However, for me and members of local organizing committee it was so far thrilling experience, different in quantity and quality from our biannual Forensica conference. We hope that congress itself will be not only thrilling, but also congenial and seminal experience for all of you.

What can you expect?

Pre-congress workshop leaders will teach you, how to use software flawlessly, semicontinuously, continuously, FAMILIarly, or STRUCTURally, how to handle mixture, pristine, and canine samples in seamless workflow, how to recognize body fluid or phenotype, how to publish your findings using correct nomenclature, how to do everything while networking, and with high quality and ethics mark.

Keynote speakers Drs. Erlich, Kayser, Metcalf, van Oorschot, Pouyet, Roewer, Šimková will set the pace and roll the canvas out, on which 60+ other speakers will glue their stone to create the final scientific mosaic where topics of Forensic DNA Phenotyping, Probabilistic Reasoning, Genealogy, DNA transfer, Population Genetics, and Microbiome will have chance to shine like gem. For those whom auditory stimulation does not suffice, hundreds of posters will feed and please their eyes.

Sponsoring companies will try to catch your attention to secure future deals, musicians and chefs will try to evoke cordial and cooperative atmosphere. If you will be attentive, you may be rewarded by topics of voodoo or mammoths that sneaked into the program as well.

In epitome, we tried to blend cornucopian cuvée that will make alchemy of Prague memorable and will stay on your palate for long time.

It is my great honour to welcome you in Prague, to greet you all!

## Jiří Drábek

ISFG2019 Congress President

# Committees

## Local Organizing Committee

Jiří Drábek  
Andrea Cignová  
Veronika Gazdová  
Marie Korabečná  
Jana Matoušková  
Martina Novotná  
Tomáš Pexa  
Halina Šimková  
Petra Škapová  
Kateřina Štaffová  
Zuzana Štaffová  
Pavel Tomek

## ISFG Board and Scientific Committee

Walther Parson  
Peter M. Schneider  
John Butler  
Mechthild Prinz  
Leonor Gusmão

## About ISFG

The International Society for Forensic Genetics is an international association promoting scientific knowledge in the field of genetic markers analyzed for forensic purposes. The ISFG has been founded in 1968 and represents more than 1100 members from over 60 countries. Regular meetings are held at a regional and international level. Scientific recommendations on relevant forensic genetic issues are developed and published by expert commissions of the ISFG.

# DEPArray™ NxT

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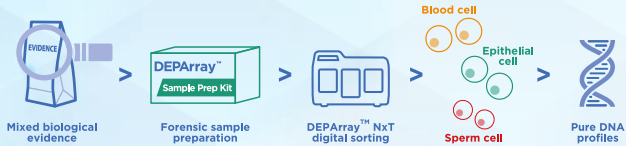
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# Programme at a Glance

	<b>Monday</b>	<b>Tuesday</b>	<b>Wednesday</b>	<b>Thursday</b>	<b>Friday</b>	
	<b>9 September 2019</b>	<b>10 September 2019</b>	<b>11 September 2019</b>	<b>12 September 2019</b>	<b>13 September 2019</b>	
	<b>Pre-Congress Programme</b>		<b>Congress Programme</b>			
8:30						
9:00	Pre-Congress Workshops	Pre-Congress Workshops	Scientific Session 1	Scientific Session 5	Scientific Session 9	
9:30			Coffee Break & Poster Session	Coffee Break & Poster Session	Coffee Break & Poster Session	
10:00						
10:30	Coffee Break	Coffee Break				
11:00	Pre-Congress Workshops	Pre-Congress Workshops	Scientific Session 2	Scientific Session 6	Scientific Session 10	
11:30						
12:00			Company Symposium – Thermo Fisher Scientific (12:30 – 13:20)	Company Symposium – Promega (12:30 – 13:20)		Lunch
12:30						
13:00	Lunch	Lunch	Company Symposium – QIAGEN (13:30 – 14:20)	Lunch		
13:30			Lunch	Lunch		
14:00	Pre-Congress Workshops	Pre-Congress Workshops			Scientific Session 11	
14:30			Scientific Session 3	Scientific Session 7		
15:00						Coffee Break
15:30	Coffee Break	Coffee Break	Coffee Break	Coffee Break		
16:00					Scientific Session 12	
16:30	Pre-Congress Workshops	Pre-Congress Workshops	Scientific Session 4	Scientific Session 8		
17:00						
17:30						
18:00						
18:30		Opening Ceremony & Scientific Prize Lecture	Working Groups Meetings	General Assembly		
19:00						
19:30						
20:00		Welcome Cocktail			Closing Ceremony & Congress Dinner	
20:30						
21:00						
21:30						
22:00						
22:30						
23:00						
23:30						

# Guidelines for Authors

The ISFG board and the local organizing committee have carefully reviewed a lot of abstracts of high quality. All authors of oral and poster presentations are kindly required to follow the instruction as below.

## Oral Presentation Guidelines

Oral presentations are always accompanied by PowerPoint presentations. The speakers are entirely responsible for the presentation content (order, graphics etc. . .). All presentations and questions must be delivered in English. Time reserved for scientific presentation is:

- **Keynote presentation** 40 min + 5 min discussion
- **Presentation** 12 min + 3 min discussion
- **Presentation** 10 min + 2 min discussion

## Presentation format

Please prepare your presentation preferably using up to date version of Microsoft PowerPoint; however older versions are also supported. Screens' aspect ratio will be 16:9.

Please note that Apple Keynote and Prezi presentations are not supported and they have to be converted into PDF files.

When saving your final presentation to the USB stick, do not forget to make sure to include your video files and all links to these multimedia files.

As no presentation template is prepared, you are welcome to use your own. Please restrain inviting to other scientific conferences, if any, to the last slide of your presentation.

## Depositing the File

Presentations must be handed over to the personnel in **the SPEAKERS' PREVIEW ROOM**, with USB stick, as far in advance as possible and **TWO hours before the start of entire session**, where the presentation is to be displayed. The presentation for an early morning session should be handed over the evening before.

SPEAKERS' PREVIEW ROOM will be located in **on 1<sup>st</sup> floor in room 1.1**, clearly marked and will be available in following times:

Monday 9 <sup>th</sup> , September	8:00 – 18:00
Tuesday 10 <sup>th</sup> , September	8:00 – 20:00
Wednesday 11 <sup>th</sup> , September	7:30 – 19:00
Thursday 12 <sup>th</sup> , September	7:30 – 19:00
Friday 13 <sup>th</sup> , September	7:30 – 17:00

## In the Lecture Room

All presentations will be sent directly to the lecture room through the internal computer network. Please, we kindly ask all authors NOT to come at the last minute with their own computer into the lecture room. All presentations must be downloaded in the **SPEAKERS' PREVIEW ROOM** beforehand.

## Poster Dimensions, Mounting & Removing

The presenting authors are entirely responsible for the poster content (order, graphics etc...).

All posters must be delivered in English.

Kindly note the posters **should not exceed the given dimensions, which are 120 × 90 cm, portrait orientation**. Posters will be hanged on a standard poster boards. The organizer will provide suitable fixing material.

## Poster Mounting

**Tuesday, 11<sup>th</sup> September 2019, 17:30 – 21:30**

**Wednesday, 12<sup>th</sup> September 2019, 7:30 – 10:00**

Each poster board was given a specific number. Authors are kindly asked to make sure to mount their poster on the poster board with the number corresponding to the number assigned to their poster presentation (e. g. P 01, P 02 etc...).

## Poster Dismantling

**Friday, 13<sup>th</sup> September 16:30 – 19:00**

Poster shall remain displayed within the whole meeting period and be removed by their authors at the end of the meeting. Posters left behind after 19:00, Friday 13<sup>th</sup> September will be discarded by organizers without notice. Organizing committee is not responsible for any loss or damage to your poster if it is not removed by the notified time. Posters not dismantled by their authors by the end of the Congress will be removed by the organizers and discarded. Storage for poster cases is not available.

## Poster Sessions

Presenting authors should be available at their poster (Poster Area, South Hall 2) to explain and discuss their work to interested participants during the attended poster sessions listed below:

Wednesday 11 <sup>th</sup> , September	10:00 – 11:00
Thursday 12 <sup>th</sup> , September	10:00 – 11:00
Friday 13 <sup>th</sup> , September	10:00 – 11:00

# Pre-Congress Workshops

## FW1 – Interpretation of complex DNA profile mixtures using open-source software including LRmix and EuroForMix

**Organisers:** Peter Gill & Corina Benschop & Oyvind Bleka

**Type:** Full Day Workshop, Hands-on

**Room:** Club B

**Date & Time:** Monday, 9<sup>th</sup> September 2019 (9:00 – 18:00)

**Aim:** To provide participants with necessary skills to carry out probabilistic genotyping of complex mixtures using open-source programs to calculate the strength of evidence of complex mixtures.

**Target Group:** Law enforcement forensic experts – experienced reporting officers who deal routinely with DNA profiling evidence and are required to interpret complex mixtures in casework.

### **General Learning Outcomes:**

- Understand the theory behind using likelihood ratios to interpret evidence
- Discuss the theory used to interpret complex mixtures of two or more contributors where the samples may be compromised - partial, degraded
- Describe best practice in relation to the ISFG DNA commission recommendations
- Be proficient in the use of open source software in order to carry out the calculations (LRmix Studio, EuroForMix)
- Write court going statements
- Describe the limitations of methods
- New developments will be presented, including DNAXs, a new package for reporting officers
- Participants will be provided with necessary tools to carry out cascade training at a national level

### **Organisation of the course:**

The course is practically orientated. The participants must bring their own laptop. Approximately one month before the course, participants will be provided with pre-course material and links that will enable them to download necessary software. Participants are encouraged to view the training videos on the EuroForMix website

### **Software:**

All softwares are open-source and freely available for users. Free support is provided to users via help desks found on the web-sites.

LRmix studio is a commonly used qualitative program that utilises the peak designation only <http://lrmixstudio.org/>.

EuroForMix is a more complicated quantitative program. Its development was supported by a EU-FP7 initiative (EuroForGen-NOE). Peak height, stutter and degradation are incorporated into the model. This package is 'state of the art', and is also used for analysis of massive parallel sequencing data <http://www.euroformix.com/>.

DNAx is a new program under development by the NFI. EuroForMix will be integrated into this package, along with a host of features designed to assist the reporting officer to interpret complex DNA profiles. Corina Benschop will provide feedback and demonstrate program features.

## FW2 – Kinship statistics using Familias and FamLink

**Organisers:** Thore Egeland & Daniel Kling

**Type:** Full Day Workshop, Hands-on

**Room:** Club B

**Date & Time:** Tuesday, 10<sup>th</sup> September (9:00 – 18:00)

The workshop provides the necessary background for relationship inference using autosomal markers. Statistical methods are introduced and the likelihood ratio based approach is emphasized. Models for linked markers are discussed and their relevance for recent forensic applications are illustrated. The freely available softwares Familias and FamLink are exemplified. The former software is restricted to unlinked autosomal markers. However, the functionality goes beyond standard kinship problems and includes modules for simulation, disaster victim identification and familial searching. The program FamLink has recently been extended to deal with any number of linked markers (STR-s or SNP-s). The open software R is introduced, and the relevance for plotting of pedigrees and estimation of haplotype frequencies is demonstrated. The participants should bring a laptop with the mentioned software installed.

## FW3 – Population analysis of forensic DNA data using Snipper and STRUCTURE

**Organisers:** Christopher Phillips & Leonor Gusmao

**Type:** Full Day Workshop, Hands-on

**Room:** Club E

**Date & Time:** Monday, 9<sup>th</sup> September (14:00 – 18:00), Tuesday, 10 September (9:00 – 13:00)

This workshop will cover the preparation of reference population data and forensic profile data for analysis with Snipper-based Bayes likelihood ratio tests and Principal Component Analysis; and STRUCTURE-based genetic cluster analysis. Such tests are gaining increasing interest as a way to estimate the possible bio-geographical ancestry of DNA recovered from forensic samples.

Students will run all three analyses with autosomal STR and SNP genotypes generated from both capillary electrophoresis and massively parallel sequencing assays typing established forensic panels. STRUCTURE tests of medium-scale population data will be run 'overnight' between the pm and am sessions of the workshop, which is divided across two half-days. Students will be required to pre-install STRUCTURE software and allow their laptops to run STRUCTURE in the background overnight. Students are invited to bring their own data, which could be analysed during the workshop.

## HW1 – NGS Workflows for forensic genetics

**Organiser:** Pete Vallone

**Type:** Half Day Workshop, Lecture

**Room:** Club E

**Date & Time:** Monday, 9<sup>th</sup> September (9:00 – 13:00)

This workshop aims to review and explore the details of various NGS/MPS sequencing methods. Common sequencing methods and platforms that may be applied to forensic genetic analyses will be discussed. The laboratory workflow steps involved in library preparation and their specific purposes will be presented. Examples of the process will be illustrated through forensically-relevant workflows for the sequencing of STRs, SNPs and the mitochondrial genome. Examination of the resulting sequence data will be demonstrated by the instructor using open source and commercial software tools.

This workshop is intended as an introduction to those attendees interested in the basic and practical aspects of carrying out sequencing experiments and considerations in adopting this method of genetic analysis in their laboratory. Questions related to the scope of the workshop can be directed to the instructor ([peter.vallone@nist.gov](mailto:peter.vallone@nist.gov))

## HW2 – Y chromosome: YHRD, mixture interpretation, kinship, population differentiation

**Organisers:** Lutz Roewer & Sascha Willuweit

**Type:** Half Day Workshop, Hands-on

**Room:** Club C

**Date & Time:** Monday, 9<sup>th</sup> September (9:00 – 13:00)

### **Program:**

- 09:00 – 09:15 Introduction
- 09:15 – 10:30 Current national and international guidelines on interpretation of Y-STRs and reporting to court (Germany, USA, ISFG)
- 10:30 – 11:30 Use of YHRD to generate match statistics (Augmented counting, Discrete Laplace method, Meta- and Suspect population)
- 11:30 – 11:45 Break
- 11:45 – 13:00 Casework challenge (Match probability, Mixture and Kinship analysis, Ancestry inference using Y-SNPs)  
Note: We will bring casework examples, but please bring your own and enter discussion!

## HW3 – Body fluid identification through mRNA profiling or DNA methylation analysis

**Organisers:** Titia Sijen & Hwan Young Lee

**Type:** Half Day Workshop, Lecture

**Room:** Club H

**Date & Time:** Monday, 9<sup>th</sup> September (9:00 – 13:00)

Human DNA profiling has the potential to present strong evidence for placing a suspect at a crime scene. Increasingly, forensic questions that go beyond the identity of the donor of a sample are asked. Knowledge regarding the cell types residing in an evidentiary trace can facilitate inference of activities. Body fluids such as blood, saliva, semen, vaginal mucosa and menstrual secretion are mostly assessed in both sexual assaults and violent crimes. The inference of organ tissues such as brain, lung, kidney, liver, heart and skeletal muscle can also be useful. Tissue identification may be achieved through various marker types: mRNAs, miRNAs, DNA methylation or microbial markers.

In this workshop, we will focus on mRNA profiling and DNA methylation analysis. mRNA profiling has been studied at the Netherlands Forensic Institute since 2009 and the mRNA assays have been applied to over 250 forensic cases. Around the same time, research on tissue-specific DNA methylation begun in several research groups, and the multiplex assays developed by Lee's group have been validated for practical application in forensic casework samples.

We will explain the foundations of assay design, share how the assays were developed and demonstrate the basic procedures regarding the application of the assays. We will discuss technical issues that may occur with compromised forensic samples and explain how data interpretation is achieved considering an accompanying DNA profile and the context of a case. Through casework examples we will illustrate the forensic possibilities and opportunities. Issues that were raised in court will also be discussed.

Participants will actively work with exemplar results to gain hands-on experience. An interactive format will be used throughout the session to stimulate discussions.

## HW4 – Forensic mitochondrial DNA analysis: Alignment and interpretation using the EMPOP database

**Organiser:** Walther Parson

**Type:** Half Day Workshop, Hands-on

**Room:** Club C

**Date & Time:** Monday, 9<sup>th</sup> September (14:00-18:00)

This is a practical workshop using EMPOP tools to better understand the mitochondrial phylogeny in the context of

- database queries for frequency estimations
- retrieving statistical information on common and rare haplotypes
- forensic reporting of mtDNA data

- searching and interpreting point and length heteroplasmy
- estimating the haplogroup status of an mtDNA sequence
- interpreting geographic distribution of haplotypes and haplogroups

We try to make the workshop as practical as possible and present/discuss forensic examples. You are invited to contribute to the workshop by bringing your own mtDNA sequences. These can involve haplotypes from research projects, from practical forensic work or your own mtDNA. Also feel free to bring challenging haplotypes that you would like to have discussed at the workshop.

You can bring your own laptop but it is not necessary! In case you plan to use your own laptop, please make sure you are a registered EMPOP user (via <https://empop.online>).

Please send questions that you may have also before the meeting to [walther.parson@gmail.com](mailto:walther.parson@gmail.com)

## HW5 – ISO/IEC 17025:2017

**Organiser:** Jiri Drabek

**Type:** Half Day Workshop, Lecture

**Room:** Club H

**Date & Time:** Monday, 9<sup>th</sup> September (14:00 – 18:00)

The basic requirements for a management system for forensic genetics laboratories are based on the international standard ISO/IEC 17025. This standard is used for the assessment and accreditation of laboratories worldwide by Accreditation Bodies in order to enhance the confidence of the clients for the competence, impartiality, and consistently high performance of these laboratories, producing high quality results.

The ISO/IEC 17025 was revised in 2017 in order to reflect the risk-based thinking, the latest version of ISO9001 norm stressing process approach in quality management, changes in IT and other technologies available for laboratories, and changes in client requirements. Laboratories already accredited to ISO/IEC 17025:2005 will need to transition their processes to the new version till November 2020.

Workshop on accreditation according to ISO/IEC 17025:2017 norm in forensic genetics laboratory is aimed at all levels of competent personnel, involved with establishing, implementing and maintaining laboratory quality and technical systems.

Workshop will cover topics of:

- Terminology, scope, definition, and normative references
- Requirements regarding management, training, and laboratory work
- Records, documents and procedures
- Internal Audit Assessment and Proficiency Testing / Interlaboratory Programs
- Method validation and conducting testing.

Upon successful completion of the course, learners will be able to:

- Identify and understand the general requirements of ISO/IEC 17025:2017, its principles and concepts
- Understand processes for controlling risks associated with the laboratory's testing processes
- Plan method validation
- Apply the requirements of ISO/IEC 17025 to their laboratory systems.



## HW6 – Scientific publication: Reading, writing, and reviewing

**Organiser:** John Butler

**Type:** Half Day Workshop, Lecture

**Room:** Club C

**Date & Time:** Tuesday, 10<sup>th</sup> September (9:00 – 13:00)

Science benefits from effective communication of ideas. Research results are shared with others through publications and presentations. Scientific publication involves efforts in reading, writing, and reviewing the literature. Editors of peer-reviewed journals rely on input from scientific colleagues to judge the merits of submitted manuscripts. Knowledgeable reviewers providing timely feedback are important for a successful peer-review process. This workshop will share insights based upon editorial experience with Forensic Science International: Genetics as well as extensive writing practice in preparing five textbooks and over 170 research articles and invited book chapters. Reviewing manuscripts is a chance to provide an important service and to influence the scientific community for good. In addition to discussing approaches to reading, writing, and reviewing relevant literature, some recent articles covering forensic genetics will be considered and examined.

## HW7 – CaDNAP Meeting – Canine DNA Profiling group

**Organisers:** CaDNAP Group

**Type:** Half Day Workshop

**Room:** Club H

**Date & Time:** Tuesday, 10<sup>th</sup> September (9:00 – 13:00)

### **Preliminary Agenda:**

#### CaDNAP - a brief historical sketch

Walther Parson<sup>1,5</sup> on behalf of the CaDNAP group

#### The CaDNAP 13-STR panel: a tool for identification and breed assignment

Burkhard Berger<sup>1</sup>, Cordula Berger<sup>1</sup>, Josephin Heinrich<sup>1</sup>, Andreas Hellmann<sup>3</sup>, Uwe Schleenbecker<sup>3</sup>, Udo Rohleder<sup>3</sup>, Werner Hecht<sup>2</sup>, Nadja V. Morf<sup>4</sup>, Walther Parson<sup>1,5</sup>

#### The CaDNAP proficiency test

Werner Hecht<sup>2</sup>, Burkhard Berger<sup>1</sup>, Cordula Berger<sup>1</sup>, Andreas Hellmann<sup>3</sup>, Uwe Schleenbecker<sup>3</sup>, Udo Rohleder<sup>3</sup>, Nadja V. Morf<sup>4</sup>, Walther Parson<sup>1,5</sup>

#### Population structure, mating strategies and generation interval in dogs: Implications for forensic profiling?

Werner Hecht<sup>2</sup>

#### Detecting the DNA from poached and poachers

Adrian Linacre<sup>6</sup>

#### Forensic genetics and taxonomic identification

Antonio Amorim<sup>7,8</sup>

Dog attacks, voodoo and mammoth cases at Zurich Institute of Forensic Medicine

Nadja V. Morf<sup>1</sup>, Pamela Voegeli<sup>4</sup>, Adelgunde Kratzer<sup>4</sup>

History of origins of the non-human DNA department of the Bundeskriminalamt Wiesbaden (BKA)

Andreas Hellmann<sup>3</sup>, Uwe Schleenbecker<sup>3</sup>, Udo Rohleder<sup>3</sup>

Canine mitochondrial DNA analysis – casework tool of last resort and reference databases

Cordula Berger<sup>1</sup>, Werner Hecht<sup>2</sup>, Walther Parson<sup>1,5</sup>

Genetic drawing of dog identikit pictures – Canine DNA phenotyping for forensic applications

Cordula Berger<sup>1</sup>, Josephin Heinrich<sup>1</sup>, Werner Hecht<sup>2</sup>, Burkhard Berger<sup>1</sup>, Walther Parson<sup>1,5</sup>

#### **Affiliations:**

- <sup>1</sup> Institute of Legal Medicine, Medical University of Innsbruck, Austria
- <sup>2</sup> Institute of Veterinary Pathology, Justus-Liebig-University Giessen, Germany
- <sup>3</sup> Bundeskriminalamt, Kriminaltechnisches Institut, Wiesbaden, Germany
- <sup>4</sup> Zurich Institute of Forensic Medicine, University of Zurich, Switzerland
- <sup>5</sup> Forensic Science Program, The Pennsylvania State University, University Park, PA, USA
- <sup>6</sup> School of Biological Sciences, Flinders University, Adelaide, Australia
- <sup>7</sup> Faculdade de Ciências da Universidade do Porto, Instituto de Investigação, Portugal
- <sup>8</sup> Inovação em Saúde, Universidade do Porto, Portugal

## HW8 – Autosomal STR Genomics 101: Sequence variation and nomenclature

**Organiser:** Katherine Gettings

**Type:** Half Day Workshop, Lecture

**Room:** Club H

**Date & Time:** Tuesday, 10<sup>th</sup> September (14:00 – 18:00)

This workshop will introduce attendees to autosomal STR sequences, with a target audience of students and practitioners having minimal sequencing experience or background knowledge. The workshop will be divided into three modules: 1) Anatomy of an STR Locus, 2) Historical and Modern STR Sequencing, and 3) STR Sequencing Quality Control and Nomenclature.

In the first module, we will begin by dissecting the sequences of autosomal STR loci in the traditional categories of simple, compound, and complex repeat motifs. We will use these example loci to explore the concept of bracketing (e.g. [GATA]8), considering historical precedent, modern guidance, and issues of CE backward compatibility. Then we will venture out into the flanking regions to find examples of SNPs and Indels, exemplifying their role in concordance between both length- and sequence-based assays.

In the second module, we will consider historical STR sequencing challenges and the benefits of modern sequencing platforms. We will review commercial STR sequencing assays and bioinformatic tools designed specifically for the forensic community, as well as bioinformatics geared toward STR analysis in whole genome sequence data. Lastly in this module, we will discuss

the proliferation of STR population sequence data, following an example of how a lab could implement such data to generate match statistics.

Finally, in the third module, we will explore interpretation issues specific to STR sequencing, and additional quality control measures which may be useful. Quality control and guidance initiatives expected to be discussed in the congress session will be described and contextualized so that attendees will have a firm foundation for the coming days. Lastly, we will discuss examples of early adopter casework implementation.

## HW9 – Forensic DNA Phenotyping: basics of data acquisition and interpretation

**Organiser:** Wojciech Branicki

**Type:** Half Day Workshop, Lecture

**Room:** Club E

**Date & Time:** Tuesday, 10<sup>th</sup> September (14:00 – 18:00)

Forensic DNA Phenotyping (FDP) is a relatively new area in the field of forensic genetics that utilizes the potential of DNA to predict ancestry, appearance and age. The obtained predictions can be used for intelligence purposes to track unknown individuals and speed up the investigation. This workshop will introduce the entire concept of FDP including theoretical aspects of marker selection, prediction modelling and practical application. Participants will get acquainted with technologies, assays and mathematical models available for predictive DNA analysis in forensics. They will also learn about the principles of data interpretation, accuracy parameters like AUC and MAE and prediction error related to different FDP methods. Much attention will be placed to the prediction of pigmentation traits and forensic implementation of the new system HirisPlex-S for simultaneous prediction of eye, hair and skin colour. The workshop will also address the issue of epigenetic age prediction in the forensic field. Participants will learn about the current problems of age estimation by DNA methylation analysis including tissue specificity of age markers, sensitivity of the assays and sources of prediction errors. The available methods of age prediction will be reviewed and the concept of biological age and age acceleration will be introduced. Participants will get acquainted with the importance of combining information about gender, ancestry, and age for appearance prediction. The lectures will be illustrated with practical examples and participants will have opportunity to familiarize themselves with the methods currently used in FDP.

## HW10 – Making sense of Ethical, Legal & Social Aspects of forensic genetics

**Organisers:** Matthias Wienroth & Gabrielle Samuel

**Type:** Half Day Workshop, Lecture

**Room:** Club C

**Date & Time:** Tuesday, 10<sup>th</sup> September (14:00 – 18:00)

The aim of the workshop is to make accessible to forensic stakeholders the concept of 'ethical, legal and social aspects' of science and technology. We will not discuss ethics approval procedures or health & safety concerns, but instead look at the type of knowledge that ethical, legal and social aspects represent. The ideas of anticipation and responsibility will guide this workshop. In order to equip participants with the tools to explore how such understanding can be applied in making forensic genetics research and technology uses societally and ethically more robust, participants will be supported in engaging in case study work, exploring two very topical emerging forensic technologies and applications in (1) forensic DNA phenotyping, and (2) the searching of public and private genetic databases for investigative purposes.

### **Methods:**

- Introductory lectures
- Case study work

### **Objectives:**

- To provide participants with tools for understanding and assessing ethical, legal and social aspects of the development and use of forensic genetics technologies.
- To encourage participants to adopt the principles of anticipation and responsibility
- To support the management of dilemmas in researching and applying new technologies.

## HW11 – Bayesian reasoning in the framework of Bayesian Networks

**Organiser:** Tomas Furst

**Type:** Half Day Workshop, Lecture

**Room:** Club D

**Date & Time:** Tuesday, 10<sup>th</sup> September (14:00 – 18:00)

Bayesian networks represent a universal framework for almost any inference tasks.

BN is a network of nodes connected by directed links such that the resulting graph contains no loops. The nodes represent random variables (e.g. an action of a suspect, or the presence of a trace) whose state may be either known or unknown.

The links represent causal relations (e.g. the presence of the suspect causes the occurrence of a trace). In each node, a probability distribution conditional on the parent nodes is given (e.g. the presence of a suspect leads to the occurrence of a particular trace with the probability of 0.7). The network is used for making inference about unobserved nodes (e.g. on the activity level

on hierarchy of propositions) conditional on the values of observed nodes (usually the evidence nodes).

In the workshop, fundamentals of Bayesian inference will be explained and various examples of their usage in forensic context will be given. The examples will be illustrated in freely available software (unbbayes.sourceforge.net), so that the participants may explore the behavior of the network themselves. The examples will go from a really trivial case all the way to a rather involved illustration of BN usage in forensic practice.

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# Scientific Prize Lecture

Prof. Dr. Manfred Kayser

Department of Genetic Identification, Erasmus MC University Medical Center Rotterdam  
ROTTERDAM, THE NETHERLANDS

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*Date & time of the presentation: 10<sup>th</sup> September 2019, 18:45 – 19:30, Forum Hall*

Manfred Kayser is (full) Professor of Forensic Molecular Biology at Erasmus University Rotterdam and (founding) Head of the Department of Genetic Identification at Erasmus University Medical Center. He obtained his diploma in biology with magna cum laude from University of Leipzig, his doctorate degree in biology/genetics with summa cum laude from Humboldt University Berlin, and his habilitation in genetics from University of Leipzig. After postdoctoral research at the Department of Anthropology, Pennsylvania State University, he was staff scientist, later Heisenberg Fellow of the German Research Council, at the Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology Leipzig, before he accepted his professorship appointment in Rotterdam. His research interest is in various aspects of forensic and anthropological genetics. In the forensic field, he is well known for his pioneering work on forensic DNA phenotyping and his contributions to the introduction and further development of forensic Y-chromosome analysis, while also published on various other forensic genetic topics. As of early 2019, he authored 240 articles (60 % as leading author) in peer-reviewed scientific journals that were cited 14,000 times; his h-index is 67. He received the Scientific Prize 1998 of the German Society of Legal Medicine and the Biennial Scientific Prize 2017 of the International Society for Forensic Genetics. He serves/d as editor-in-chief, academic editor, section editor, guest editor, and editorial board member of several forensic and human genetic journals, and is regular ad-hoc reviewer for various scientific journals and research funding agencies in different countries and the EU.

# Keynote Speakers

## Prof. Dr. Lutz Roewer, PhD

Institute of Legal Medicine and Forensic Sciences, Charité -Universitätsmedizin  
BERLIN, GERMANY

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*Date & time of the presentation: 11<sup>th</sup> September 2019, 08:30 – 09:15, Forum Hall*

Lutz Roewer studied biochemistry in Leipzig and received his PhD in molecular biology in 1990 at the Charité in Berlin. His early work encompassed the application of oligonucleotide probes for forensic DNA fingerprinting and the development of PCR-based methods to analyze autosomal and Y-chromosomal microsatellites. Since 2008 he is professor for forensic genetics at the Institute of Legal Medicine and Forensic Sciences, Charité -Universitätsmedizin Berlin, Germany and head of the Department of Forensic Genetics. His laboratory with 14 staff members processes several thousand crime cases per year. Lutz was awarded the scientific price of the DGRM (Deutsche Gesellschaft für Rechtsmedizin) in 1990 and 1998 and the scientific prize of the ISFG (International Society of Forensic Genetics) in 1999 for the development of the Y chromosome STR haplotyping method.

Lutz Roewer is founder and curator of the largest forensic reference database for Y chromosome profiles, the YHRD (<https://yhrd.org>). His major research interest is the molecular and population genetics of the Y chromosome with regard to its forensic application. Another research line is the evolution and demography of world populations. He studied indigenous populations in Europe, Asia and the Americas and authored large multi-centred studies on this topic. He is co-beneficiary of a grant of the European Union to develop autosomal/Y-chromosomal STR prototypes for massive parallel sequencing analysis (MPS) in forensics.

## Mgr. Halina Šimková

Faculty of Science, Charles University  
PRAGUE, THE CZECH REPUBLIC

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*Date & time of the presentation: 11<sup>th</sup> September 2019, 14:30 – 15:15, Forum Hall*

Forensic geneticist, lecturer and science popularizer.

Halina Šimková graduated in Anthropology and Human Genetics at the Faculty of Science at Charles University in Prague and in Scenography at Master School of Art Design in Prague. During her studies at the Faculty of Science, Charles University, she became a civilian intern at the Institute of Criminalistics in Prague, later she started working there as an expert in the field of DNA analysis. She co-founded the Czechoslovak Society for Forensic Genetics, and has been Vice-Chair since 2008. In order to demonstrate her generally declared love of uncertainty, she left her stable position to become freelancer in 2016 and her interest gradually shifted mainly to promote the use of Bayesian inference in the field of forensic expertise and within other disciplines working with probabilistic conclusions.

She enjoys lecturing and popularization very much, emphasizing the use of non-verbal and combined teaching tools. She is the author of the educational book Breviary of Forensic Genetics, in 2016 she won the Neuron Prima ZOOM award for the best popular science video. She regards Bayesian inference as beautiful, brilliant and logical, and it bothers her that the vast majority of people do not know Bayesian inference at all – not even those whose decisions cannot be properly made without it. She wants to change it.

## Dr. Yaniv Erlich

Data Science Institute, Columbia University

NEW YORK, USA

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*Date & time of the presentation: 12<sup>th</sup> September 2019, 08:30 – 09:15, Forum Hall*

Dr. Yaniv Erlich is the Chief Science Officer of MyHeritage.com and an Associate Professor of Computer Science and Computational Biology at Columbia University (leave of absence). Prior to these positions, he was a Fellow at the Whitehead Institute, MIT. Dr. Erlich received his bachelor's degree from Tel-Aviv University, Israel (2006) and a PhD from the Watson School of Biological Sciences at Cold Spring Harbor Laboratory (2010). Dr. Erlich's research interests are computational human genetics. Dr. Erlich is a TEDMED speaker (2018), the recipient of DARPA's Young Faculty Award (2017), the Burroughs Wellcome Career Award (2013), Harold M. Weintraub award (2010), the IEEE/ACM-CS HPC award (2008), and he was selected as one of 2010 Tomorrow's Pls team of Genome Technology.

## Assoc. Prof. Roland van Oorschot

School of Molecular Sciences, La Trobe University

MELBOURNE, AUSTRALIA

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*Date & time of the presentation: 12<sup>th</sup> September, 14:30 – 15:15, Forum Hall*

After acquiring an Agricultural science and engineering degree in the Netherlands, a PhD from Macquarie University in Australia on marsupial genetics, postdoctoral positions at the Southwest Foundation for Biomedical Research in San Antonio, Texas on genemapping and at the Centre for Animal Biotechnology at Melbourne University in Australia on genetics of disease resistance in sheep, Roland started working, in 1992, at the Forensic Services Department of Victoria Police where he is currently a Principal RD&I Specialist. He is also an Adjunct Professor in the School of Molecular Sciences at La Trobe University.

Roland has over 160 publications in scientific journals and books. Including an article in Nature (in 1997) regarding the ability to retrieve directly and indirectly deposited DNA from touched objects that helped revolutionise forensic investigations. Roland has supervised over 90 post-graduate students, examined several theses, sits on University course advisory committees and has reviewed manuscripts for several journals. His current interests include the areas of: 'DNA transfer, persistence prevalence, and recovery', 'contamination minimisation' and 'acquiring more information from available biological samples to assist investigations of criminal activity'.



## Fanny Pouyet, PhD

Institute of Ecology and Evolution, University of Bern

BERN, SWITZERLAND

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*Date & time of the presentation: 13<sup>th</sup> September, 08:30–09:15, Forum Hall*

Fanny Pouyet received a MSc degree in Biology from the Ecole Normale Supérieure de Lyon and a MSc in Bioinformatics from the University of Paris VI. During my PhD in Lyon, I quantified the importance of both adaptive and non-adaptive processes on the evolution of codon usage in genes in Human.

I have currently a postdoctoral position at the University of Bern since October 2016 in the laboratory of Prof. Laurent Excoffier. My research focus on disentangling the impact of evolutionary mechanisms that constrain the genome-wide diversity in humans as a population geneticist. I am particularly interested in understanding the links between such evolutionary processes and recombination across the genome.

## Dr. Jessica Metcalf

Department of Animal Sciences, Colorado State University

FORT COLLINS, COLORADO, USA

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*Date & time of the presentation: 13<sup>th</sup> September, 14:30–15:15, Forum Hall*

Dr. Jessica L. Metcalf is a microbiome scientist who leads highly interdisciplinary, innovative research projects that span the fields of forensics, animal science, and health by combining experimental ecology, large genomic datasets, and bioinformatics tools. Her lab studies the complex suite of microorganisms (bacteria, archaea, fungi, protists, etc) driving decomposition of post-mortem vertebrate animals. Over the past several years, she has been developing a microbial clock to estimate how long vertebrate (including human) remains have been decomposing. Along with several collaborators, she is developing the microbial clock into a new forensic science tool to help investigators estimate the postmortem interval (PMI) for cases with unknown PMIs. She also studies the gastrointestinal tract of vertebrate animals with a focus on the effects of captivity and domestication on animal health. In a similar vein, she also studies the loss of microbial diversity in the human gastrointestinal tract associated with the industrialization/urbanization of human populations.

Metcalf earned a Bachelor of Science in chemistry from University of Georgia and a Ph.D. in ecology and evolution from University of Colorado Boulder. She completed postdoctoral positions in ancient DNA at the University of Adelaide in South Australia and in microbiome science at UC San Diego. She joined Colorado State University in 2016 as part of the Microbiome Systems Cluster Hire Initiative. She is an Associate Professor in the Department of Animal Sciences.

# Detailed Scientific Programme

Tuesday 10<sup>th</sup> September 2019, Forum Hall

18:30

**OPENING CEREMONY**

19:00

**OPENING CEREMONY & SCIENTIFIC PRIZE LECTURE**

**FORENSIC APPEARANCE PREDICTION FROM DNA: A JOURNEY THROUGH 10 YEARS OF SCIENTIFIC CONTRIBUTIONS**

Kayer, Manfred

20:00

**WELCOME COCKTAIL (FOYER)**

Wednesday 11<sup>th</sup> September, Forum Hall

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## Session 1

**Chairs: Walther Parson, Marie Korabečná**

08:30

**KEYNOTE LECTURE**

**THE WHITE ELEPHANT IN THE FIELD – WHAT MEANS “POPULATION” IN FORENSIC GENETICS?**

Roewer, Lutz

09:15

**DEVELOPMENT AND OPTIMIZATION OF THE VISAGE PROTOTYPE TOOLS FOR BIO-GEOGRAPHIC ANCESTRY AND APPEARANCE TRAITS INFERENCE USING TARGETED MPS**

Xavier, Catarina

09:30

**APPROACHES TO EXPLAIN AND POTENTIALLY PREDICT THE COMPLEX ARCHITECTURE OF THE HUMAN FACE**

Walsh, Susan

09:45

**INTRODUCTION OF A PREDICTIVE DNA TEST FOR THE OCCURRENCE OF FRECKLES**

Branicki, Wojciech

10:00

**COFFEE BREAK (FOYER) & POSTER SESSION (SOUTH HALL 2)**

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## Session 2

**Chairs: Walther Parson, Marie Korabečná**

- 11:00 **FORENSIC DNA PHENOTYPING: A SERVICE PROVIDER TRIAL**  
Raymond, Jennifer
- 11:12 **COMPARISON OF CE- AND MPS-BASED ANALYSES OF FORENSIC MARKERS WITH SINGLE CELL AFTER WHOLE GENOME AMPLIFICATION**  
Chen, Man
- 11:24 **PRESENTATION OF THE HUMAN PIGMENTATION (HUPI) AMPLISEQ CUSTOM PANEL**  
Meyer, Olivia Strunge
- 11:36 **PREDICTIVE DNA ANALYSIS OF HUMAN HEAD HAIR GREYING USING WHOLE-EXOME AND TARGETED NGS DATA EXAMINED WITH DEEP LEARNING METHODS**  
Pošpiech, Ewelina
- 11:48 **A COMPARISON OF DNA METHYLATION TECHNOLOGIES AND PERFORMANCE OF AGE PREDICTION MODELS**  
Freire-Aradas, Ana
- 12:00 **A COMING OF AGE TALE**  
Aliferi, Anastasia
- 12:12 **IN SEARCH OF CENTRAL- AND EASTERN EUROPEAN- SPECIFIC ANCESTRY INFORMATIVE MARKERS**  
Woźniak, Marcin
- 12:30 **COMPANY SYMPOSIUM BY THERMO FISHER SCIENTIFIC**
- 13:00 **LUNCH**
- 13:30 **COMPANY SYMPOSIUM BY QIAGEN (SOUTH HALL 1B)**

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## Session 3

**Chairs: John Butler, Manfred Kayser**

- 14:30 **KEYNOTE LECTURE**  
**EXPLAINING BAYESIAN INFERENCE PRINCIPLES NONVERBALLY: HOW TO HELP NON-MATHEMATICIANS UNDERSTANDING THE WEIGHT OF EVIDENCE**  
Šimková, Halina
- 15:15 **HOW TO AVOID DRIVING DNA CASEWORKERS CRAZY: CASESOLVER, AN EXPERT SYSTEM TO INVESTIGATE COMPLEX CRIME SCENES**  
Prieto, Lourdes

15:30

**COMPARISON OF CE AND MPS BASED ANALYSIS FOR THE PROBABILISTIC INTERPRETATION OF MIXED STR PROFILES**

Benschop, Corina

15:45

**USING GENETIC COMPLEXITY TO SOLVE FORENSIC COMPLEXITY: A NEW CLASS OF COMPLEX HYPERVARIABLE STR MARKERS FOR DECONVOLUTION OF COMPLEX DNA MIXTURES**

Ralf, Arwin

16:00

**COFFEE BREAK (FOYER)**

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## Session 4

**Chairs: John Butler, Manfred Kayser**

16:30

**THE FIRST MPS-STR BASED CONVICTION IN A CRIMINAL CASE?**

De Knijff, Peter

16:42

**ENHANCING STR SEQUENCE ALLELE REPRESENTATION FOR PROBABILISTIC GENOTYPING**

Just, Rebecca

16:54

**A MASSIVELY PARALLEL SEQUENCING ASSAY OF MICROHAPLOTYPES FOR MIXTURE DECONVOLUTION**

Oldoni, Fabio

17:06

**A TOP-DOWN APPROACH TO MIXTURE EVALUATION**

Slooten, Klaas

17:18

**FROM REFERENCE TO MIXTURE TO MIXTURE TO MIXTURE AND BEYOND**

Kruijver, Maarten

17:30

**EXPLORING DNA INTERPRETATION SOFTWARE USING THE PROVEDIT DATASET**

Riman, Sarah

17:42

**ARE REPORTED LIKELIHOOD RATIOS WELL CALIBRATED?**

Hannig, Jan

18:00

**WORKING GROUPS MEETINGS**

Thursday 12<sup>th</sup> September 2019, Forum Hall

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## Session 5

**Chairs: Mechthild Prinz, Jiří Drábek**


- 8:30 **KEYNOTE LECTURE**  
**FORENSIC GENETICS AND DTC GENOMICS: FRIEND OR FOE?**  
Erich, Yaniv
- 9:15 **DEVELOPING PRIORITIES FOR DISCUSSION AND OVERSIGHT OF THE RAPIDLY EVOLVING FIELD OF GENETIC GENEALOGY**  
Phillips, Christopher
- 9:30 **THE EFFECTIVENESS OF FORENSIC GENEALOGY TECHNIQUES IN THE UNITED KINGDOM – AN EXPERIMENTAL ASSESSMENT**  
Thomson, Jim
- 9:45 **FORENSIC GENEALOGY – PERFORMANCE OF DENSE SNP DATA TO TRACE DISTANT RELATIVES**  
Kling, Daniel
- 10:00 **COFFEE BREAK (FOYER) & POSTER SESSION (SOUTH HALL 2)**

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## Session 6

**Chairs: Mechthild Prinz, Jiří Drábek**

- 11:00 **AN INTERNATIONAL CONSIDERATION OF A STANDARDS-BASED APPROACH TO FORENSIC GENETIC GENEALOGY**  
Scudder, Nathan
- 11:12 **WHOLE GENOME SEQUENCING OF HUMAN REMAINS TO ENABLE GENEALOGY DNA DATABASE SEARCHES – A CASE REPORT**  
Tillmar, Andreas
- 11:24 **ETHICAL, SOCIAL AND LEGAL ISSUES OF FAMILIAL SEARCHING: NEW AND OLD DEBATES**  
Granja, Rafaela
- 11:36 **THE GENETIC IDENTIFICATION OF DEAD MIGRANTS IN THE MEDITERRANEAN SEA: THE LAMPEDUSA 2013 SHIPWRECK**  
Bertoglio, Barbara
- 11:48 **RE-EVALUATION OF DNA BASED IDENTIFICATION RESULTS OF VICTIMS OF A TERRORIST ATTACK 25 YEARS LATER**  
Corach, Daniel

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- 12:00 **NEW ISO STANDARDS FOR FORENSICS: DNA “FREE” CONSUMABLES AND THE FORENSIC PROCESS**  
Bastisch, Ingo
- 12:12 **REFLECTIONS AND EXAMPLES OF PROBLEMATIC REPORTING IN DNA CASES: THE NEED FOR ACCREDITED FORMATS AND CERTIFIED REPORTING COMPETENCE**  
Hicks, Tacha
- 12:30 **COMPANY SYMPOSIUM BY PROMEGA**
- 13:00 **LUNCH**
- 

## Session 7

**Chairs: Peter Schneider, Titia Sijen**

- 14:30 **KEYNOTE LECTURE**  
**DNA TRANSFER: ASPECTS RELEVANT TO FORENSIC INVESTIGATIONS**  
van Oorschot, Roland
- 15:15 **TRANSFER, PERSISTENCE AND RECOVERY OF EPITHELIAL CELLS ON THE SKIN IN DIRECT AND SECONDARY TRANSFER SCENARIOS**  
Fonneløp, Ane Elida
- 15:30 **MODELLING DNA TRANSFERS IN COMPLEX SCENARIOS**  
Taylor, Duncan
- 15:45 **ASSIGNING FORENSIC BODY FLUIDS TO DNA DONORS IN MIXED SAMPLES BY TARGETED RNA/DNA DEEP SEQUENCING OF CODING REGION SNPS USING ION TORRENT TECHNOLOGY**  
Ballantyne, John
- 16:00 **COFFEE BREAK (FOYER)**
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## Session 8

**Chairs: Peter Schneider, Titia Sijen**

- 16:30 **VISUALISING DNA TRANSFER: LATENT DNA DETECTION USING DIAMOND DYE**  
Champion, Jessica
- 16:42 **IN AND OUT OF TOUCH: RELATIVE ACCUMULATION OF CELLULAR AND ACELLULAR “TOUCH DNA” FROM ENDOGENOUS AND EXOGENOUS SOURCES ON HANDS OVER TIME**  
Burrill, Julie

- 16:54 **CHARACTERIZATION OF TISSUE-SPECIFIC BIOMARKERS WITH THE EXPRESSION OF CIRC RNAs IN FORENSICALLY RELEVANT BODY FLUIDS**  
Yang, Qinrui
- 17:06 **BODY FLUID IDENTIFICATION USING MRNA – BETTER, FASTER, CHEAPER – WHAT METHOD IS BEST OR SHOULD A COMBINATION OF TECHNIQUES BE USED?**  
Harbison, Sallyann
- 17:18 **PREDICTING THE ORIGIN OF FORENSICALLY RELEVANT BIOLOGICAL MATERIAL USING A MACHINE LEARNING APPROACH**  
Iacob, Diana
- 17:30 **DEVELOPMENT OF A MIRNA BODY FLUID PREDICTION SYSTEM USING PROBABILISTIC APPROACHES**  
Li, Zhilong
- 17:42 **PROTEOMIC GENOTYPING: USING MASS SPECTROMETRY TO INFER SNP GENOTYPES IN A FORENSIC CONTEXT**  
Parker, Glendon
- 18:00 **GENERAL ASSEMBLY**

Friday 13<sup>th</sup> October 2019, Forum Hall

## Session 9

**Chairs: Leonor Gusmão, Halina Šimková**

- 8:30 **KEYNOTE LECTURE**  
**BACKGROUND SELECTION AND BIASED GENE CONVERSION AFFECT MORE THAN 95 % OF THE HUMAN GENOME AND BIAS DEMOGRAPHIC INFERENCES**  
Pouyet, Fanny
- 9:15 **Y-PROFILE EVIDENCE: CLOSE PATERNAL RELATIVES AND MIXTURES**  
Andersen, Mikkel Meyer
- 9:30 **INFERENCE OF ADMIXED ANCESTRY WITH ANCESTRY INFORMATIVE MARKERS**  
Tvedebrink, Torben
- 9:45 **THE IMPACT OF IGNORING INBREEDING IN KINSHIP EVALUATIONS**  
Kjelgaard Brustad, Hilde
- 10:00 **COFFEE BREAK (FOYER) & POSTER SESSION (SOUTH HALL 2)**

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## Session 10

**Chairs: Leonor Gusmão, Halina Šimková**

- 11:00 **STR SEQUENCE NOMENCLATURE: PROGRESS REPORT FROM THE STRAND WORKING GROUP**  
Gettings, Katherine
- 11:12 **THE STRIDER REPORT ON QUALITY CONTROL OF AUTOSOMAL STR DATASETS – THE GOOD, THE NOT SO GOOD AND THE UGLY**  
Bodner, Martin
- 11:24 **ADVANCING MITOCHONDRIAL GENOME DATA INTERPRETATION IN MISSING PERSONS CASEWORK**  
Marshall, Charla
- 11:36 **CSY? A PANEL-BASED MPS APPROACH INCLUDING 12,523 Y-CHROMOSOME POLYMORPHISMS**  
Claerhout, Sofie
- 11:48 **ANALYSIS OF RECOMBINATION AND MUTATION EVENTS FOR 12 X-CHR STR LOCI: A COLLABORATIVE FAMILY STUDY OF THE ITALIAN SPEAKING WORKING GROUP GE.F.I.**  
Bini, Carla
- 12:00 **GENETIC PEOPLING OF PAKISTAN AND THE IMPACT OF HISTORICAL MIGRATIONS, ETHNIC CULTURES AND THE PRACTICE OF ENDOGAMY ON THE FORENSIC MATCH PROBABILITIES**  
Anwar, Ijaz
- 12:12 **THE SCOPE AND LIMITATIONS OF THE LIKELIHOOD RATIO METHOD APPLIED TO STR DATA FOR DETERMINING GENETIC KINSHIP IN ANCIENT OR ISOLATED HUMAN POPULATIONS**  
Zvenigorosky, Vincent
- 12:30 **LUNCH**

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## Session 11

**Chairs: Adrian Linacre, Eugenia D'Amato**

- 14:00 **KEYNOTE LECTURE**  
**USING MICROBIOME TOOLS TO ESTIMATE THE POSTMORTEM INTERVAL OF HUMAN REMAINS**  
Metcalf, Jessica
- 14:45 **ENVIRONMENTAL DNA TO ASSIST FORENSIC INVESTIGATIONS, COUNTER-TERRORISM, FRAUDULENT MEDICINES AND DRUG SEIZURES**  
Young, Jennifer



- 15:00 **TAXONOMY-INDEPENDENT DEEP LEARNING MICROBIOME APPROACH FOR ACCURATE CLASSIFICATION OF FORENSICALLY RELEVANT HUMAN BIOMATERIALS USING TARGETED MPS**  
Díez López, Celia
- 15:15 **PERFORMANCE OF ENVIRONMENTAL DNA METABARCODING IN SOIL TRACE MATCHING AND PROVENANCING**  
Frøslev, Tobias Guldberg
- 15:30 **COFFEE BREAK (FOYER)**

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## Session 12

**Chairs: Adrian Linacre, Eugenia D'Amato**

- 16:00 **COLLABORATION ACROSS BORDERS TO IMPLEMENT A EUROPEAN DATABASE FOR CANINE STR IDENTIFICATION MARKERS**  
Giangasparo, Federica
- 16:12 **MULTI-LOCUS DNA METABARCODING FOR AUTHENTICATION OF HIGHLY PROCESSED MEAT PRODUCTS COLLECTED IN SOUTH AFRICA**  
Pietroni, Carlotta
- 16:24 **SPECIES IDENTIFICATION USING MASSIVELY PARALLEL SEQUENCING – DETECTING MULTIPLE SPECIES IN MIXED SOURCES**  
Dellamico, Barbara
- 16:36 **SPECIES IDENTIFICATION IN ROUTINE CASEWORK SAMPLES USING THE SPINDEL KIT**  
Pereira, Filipe
- 16:48 **WHOLE-GENOME SEQUENCING OF NEISSERIA GONORRHOEAE IN A FORENSIC TRANSMISSION CASE**  
Gonzalez-Candelas, Fernando
- 17:00 **WHOLE TRANSCRIPTOME ANALYSIS OF AGED BIOLOGICAL CRIME SCENE TRACES**  
Salzmann, Andrea
- 17:12 **PREVALENCE OF DNA IN VEHICLES: OPTIMIZING SAMPLING STRATEGY AND ACTIVITY LEVEL EVALUATION OF DNA TYPING RESULTS**  
Kokshoorn, Bas
- 19:30 **CLOSING CEREMONY & CONGRESS DINNER (MUNICIPAL HOUSE – SMETANA HALL)**

# Company Symposia

## Thermo Fisher Scientific



**Date:** Wednesday, 11<sup>th</sup> September, 2019

**Time:** 12:30–13:20

**Location:** Forum Hall, 2<sup>nd</sup> floor

### **Validation of the latest forensic genetic technologies for the solution of complex cases**

**Speakers:** Magdalena Marcińska, Instytut Ekspertyz Sądowych, Krakow, Poland

Ten.Col. CC RT inv. sc. Andrea Berti, Reparto Carabinieri Investigazioni Scientifiche di Roma – Sezione di Biologia, Italy

During this symposium the speakers will present their validation work with the newest Applied Biosystems™ systems for forensic genetics: the SeqStudio™ HID Genetic Analyzer and the Rapid HiT™ Rapid DNA system.

## QIAGEN



**Date:** Wednesday, 11<sup>th</sup> September 2019

**Time:** 13:30–14:20

**Location:** South Hall 1B, 1<sup>st</sup> floor

### **Identifying the missing**

**Speakers:** Mrs. Ingrid Gudmundsson, Sweden

Dr. Thomas J. Parsons, Director of Science and Technology, ICMP, The Hague, Netherlands

How a new NGS workflow is enabling missing persons identification and bringing closure to families around the world.

## Promega Corporation



**Date:** Thursday, 12<sup>th</sup> September, 2019

**Time:** 12:30–13:20

**Location:** Forum Hall, 2<sup>nd</sup> floor

### **Streamlined Workflows for Forensic DNA Extraction and Analysis**

**Speakers:** Stefan Kutranov, Promega UK - Gro Bjørnstad, Oslo University Hospital, Norway –

Dr. Richard Zehner, University of Frankfurt, Germany

During this symposium you will hear about the latest advances in STR Analysis and the forensics workflow from Promega, an Evaluation of Promega's Casework Direct Kit, Custom for DNA extraction from various casework samples, including a comparison of its performance to Chelex extraction, and Validation studies with the Maxwell® RSC 48 instrument.

# ISFG Working Groups Meetings

Wednesday 11<sup>th</sup> September, 18:00 – 19:30

	Room
<b>Polish Speaking WG</b>	Club D
<b>French Speaking WG</b>	ISFG Board meeting room (room number 2.3)
<b>English Speaking WG</b>	Forum Hall
<b>Spanish/Portuguese (GHEP)</b>	South Hall 1A (9 <sup>th</sup> – 10 <sup>th</sup> September)
<b>German Speaking WG</b>	Club C
<b>Italian Speaking WG</b>	Club A
<b>Chinese Speaking WG</b>	Club B
<b>Korean Speaking WG</b>	LOC meeting room (room number 241)



# Social Programme



## Opening Ceremony & Scientific Prize Lecture

Tuesday – 10<sup>th</sup> September 2019 (18:30 – 20:00)  
Prague Congress Centre, 2<sup>nd</sup> floor, Forum Hall

*Included in the registration fees for full delegates (all categories) and accompanying persons. NOT INCLUDED in the pre-congress workshop registrations.*

The ISFG 2019 Congress will be officially opened on 10<sup>th</sup> September 2019 with the Opening Ceremony held in the Forum Hall where we will be welcome by our hosts and hosting institution representatives. We sincerely invite all our participants to take part and listen to Prof. Dr. Manfred Kayser (Scientific Prize Lecture) talking about *Forensic appearance prediction from DNA: a journey through 10 years of scientific contributions* as well as enjoy the Light Art show prepared especially for this purpose.



## Welcome Cocktail

Tuesday – 10<sup>th</sup> September 2019 (20:00 – 22:00)  
Prague Congress Centre, 2<sup>nd</sup> floor, exhibition foyer

*Included in the registration fees for full delegates (all categories) and accompanying persons. NOT INCLUDED in the pre-congress workshop registrations.*

The ISFG 2019 Congress will be officially opened with the Opening Ceremony & Scientific Prize Lecture starting at 18:30 in the Forum Hall. Afterward, all participants are kindly invited to take part in the Welcome Cocktail. It is the perfect opportunity to catch up with old acquaintances and network with your colleagues. This is an informal evening prior to the serious scientific discussions. Light cocktail refreshment will be served.

Dress code: smart casual.

Welcome Cocktail is kindly supported by the City of Prague.



## Closing Ceremony & Congress Dinner

Friday – 13<sup>th</sup> September 2019 (19:30 – 23:30)  
Municipal House – Smetana Hall, nam. Republiky  
1090/5, 111 21 Prague 1

*NOT INCLUDED in the delegate registration, pre-booking necessary*

The Municipal House has been one of the most significant public buildings in Prague for over a hundred years. After the city administration had purchased the plots where the Royal Court, the medieval seat of the Bohemian kings, used to be located, they announced an architectural competition for the Municipal House in 1903. Unsatisfied with the results of the competition, the city administration awarded this project to architects Antonín Balšánek and Osvald Polívka.

Enjoy the last evening of the Congress, closing ceremony and an unforgettable cultural event in one. Experience the city of Prague while enjoying dinner and entertainment, showcasing Prague's cuisine and arts.

Dress code: business attire.

Please note that transfers from and back to the venue won't be provided. For transfers from and back to the hotels *Holiday Inn* and *Corinthia Tower*, please stop by at the registration to sign in.

## Prague City Tours

Don't forget to stop by the information kiosk of The Premium City Tours located near the registration area. The staff will be happy to assist and inform you about the wide offer of guided tours that can be purchased separately at discounted prices.



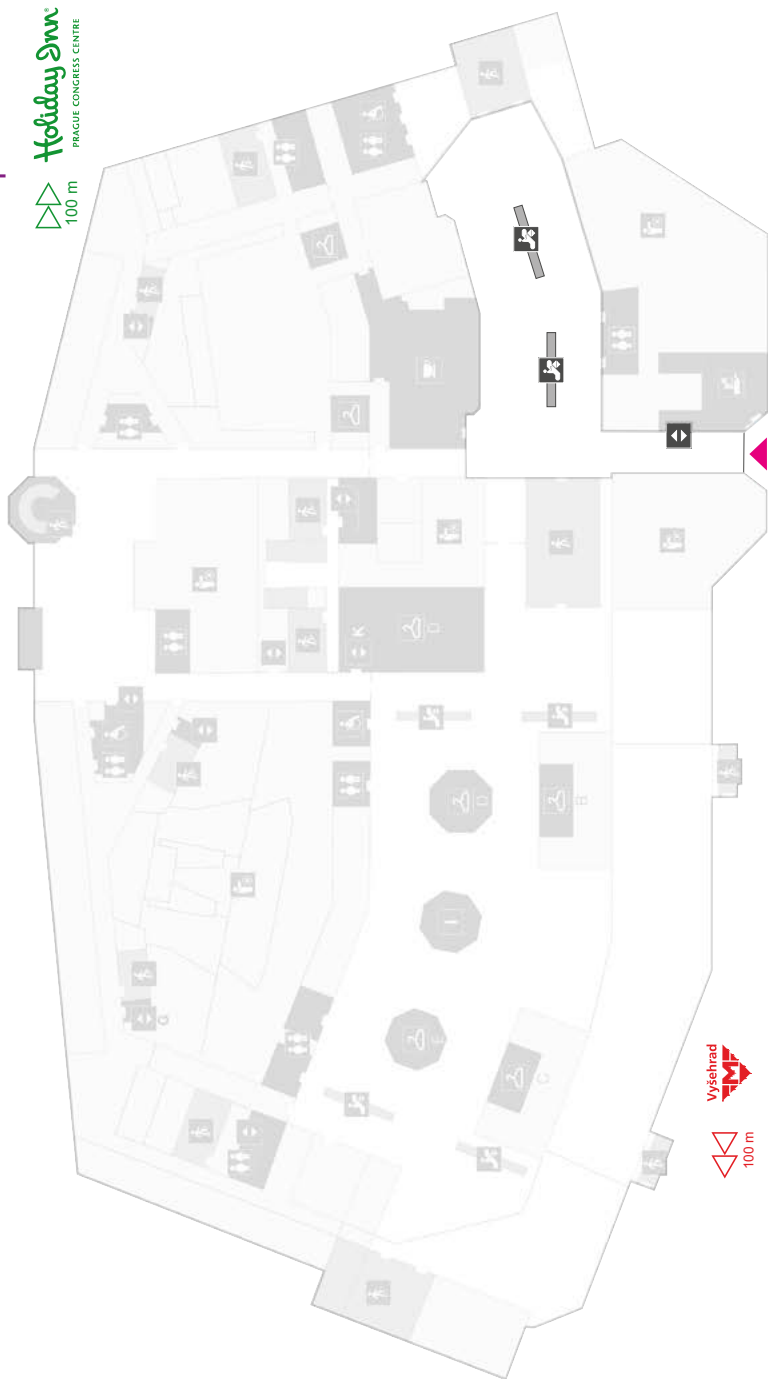
© Ivan Král

### How to get there:

*Metro C+B (15 minutes):*

- ➔ From the Prague Congress Centre take the Metro C (station Vyšehrad)
- ➔ to the station Florenc
- ➔ and change to Metro B (yellow line).
- ➔ Continue one stop to the station Náměstí Republiky.
- 🕒 Walking distance to the Municipal House 150 m, 2 minutes.

# Floorplans



Entrance Nr. 5

Ground Floor

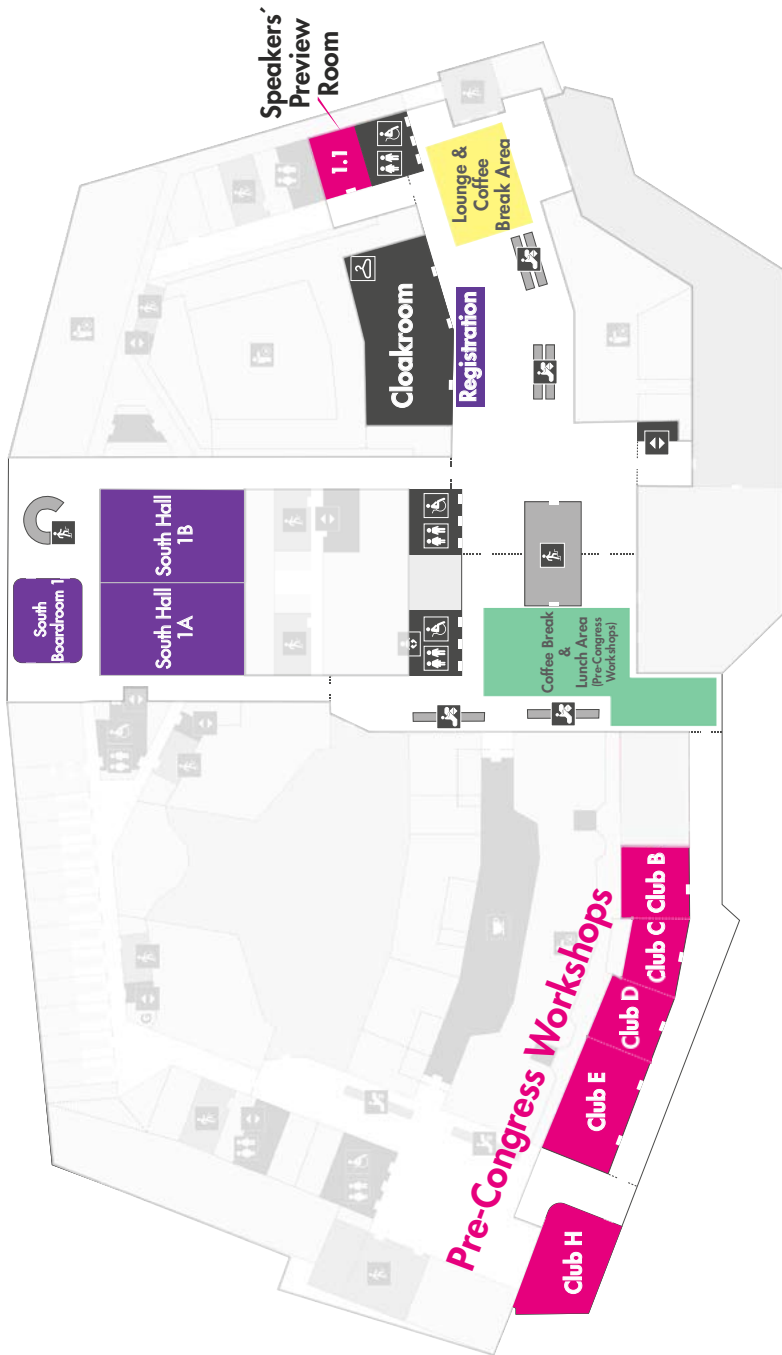
100 m  
Holiday Inn  
PRAGUE CONGRESS CENTRE

Vysehrad  
HOTEL

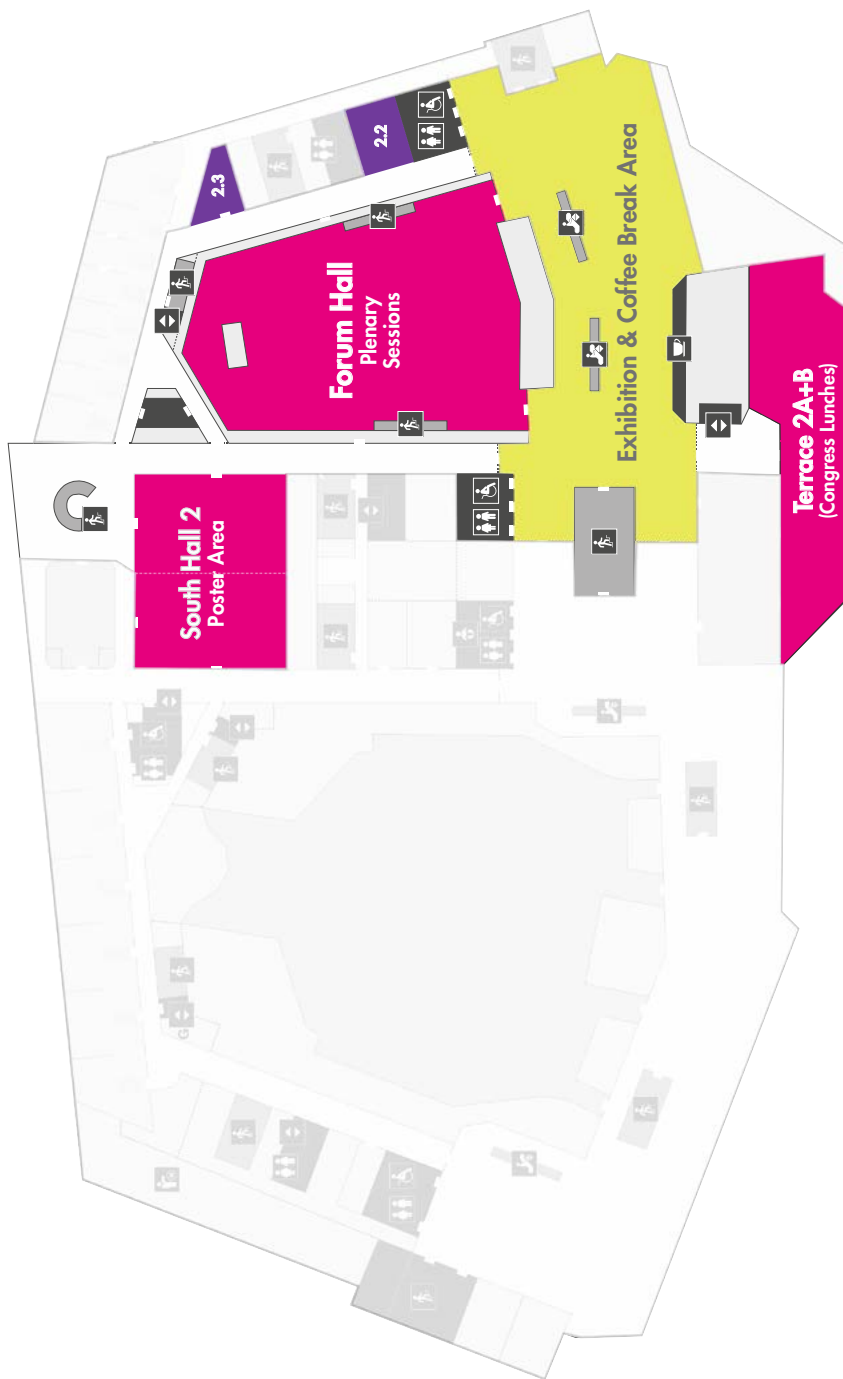
100 m

CORINTHIA  
HOTEL  
PRAGUE

200 m



1st Floor

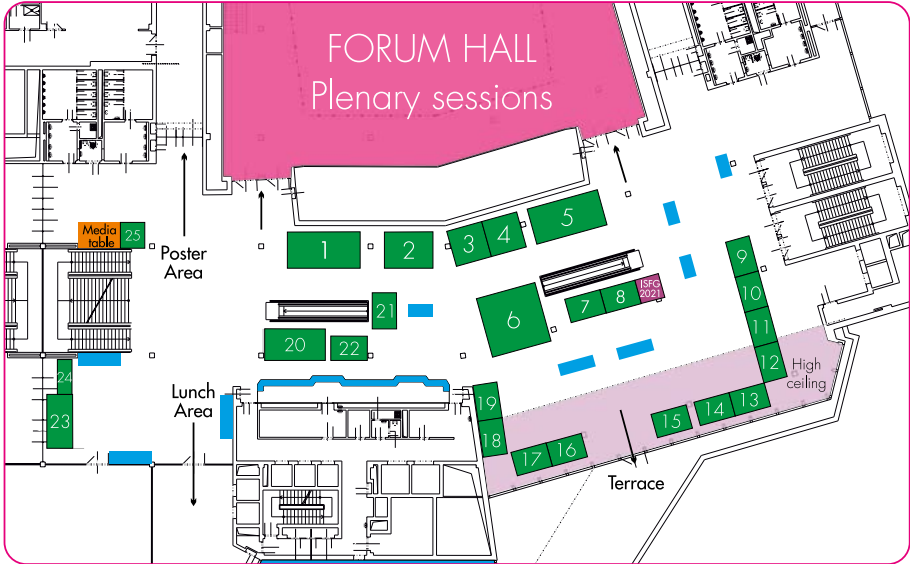


2nd Floor



# Exhibition Floorplan

## 2<sup>nd</sup> Floor



■ Catering / Coffee Stations

## List of Exhibitors

- |    |                             |    |                           |
|----|-----------------------------|----|---------------------------|
| 1  | QIAGEN                      | 14 | SERATEC GmbH              |
| 2  | Verogen                     | 15 | Forensic DNA Service      |
| 3  | Carolina Biosystems         | 16 | STRmix                    |
| 4  | MENARINI SILICON BIOSYSTEMS | 17 | MGI                       |
| 5  | Promega                     | 18 | GORDIZ                    |
| 6  | Thermo Fisher Scientific    | 19 | Independent Forensics     |
| 7  | GENETEK BIOPHARMA           | 20 | Spot On Sciences          |
| 8  | Qualitype GmbH              | 21 | GE Healthcare             |
| 9  | Purdue University Northwest | 22 | CLIMS - VERISIS           |
| 10 | HEALTH Gene Technologies    | 23 | HiMedia Laboratories GmbH |
| 11 | AXO Science                 | 24 | Xceltis                   |
| 12 | Miltenyi Biotec GmbH        | 25 | Bio-Port                  |
| 13 | NicheVision Forensics LLC   |    |                           |

# Acknowledgment

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# Company Profiles

## Booth 1: QIAGEN

**Contact Person:** Inga Gerard

**Telephone:** +33 7 63 43 65 38

**Email:** inga.gerard@qiagen.com

**Website:** www.qiagen.com



QIAGEN is a global leader in Sample to Insight solutions in rapidly growing fields of molecular diagnostics and life sciences. We are at the forefront of human identity and forensic testing, and have actively supported the development of global forensic standards. Our product portfolio offers a full range of forensic DNA grade chemistries combined with high-quality instruments that address the diverse needs and challenges of crime scene investigation and human identification, covering every step in the workflow, from sample to result. QIAGEN quality, efficient solutions, innovative bioinformatics tools and comprehensive validation services help customers unlock valuable molecular insights. This is how we make improvements in life possible.

## Booth 2: Verogen

**Contact Person:** Verogen

**Telephone:** +1 858 285 4101 (Global)  
+44 (20) 399 28411 (United Kingdom)  
+1 833 837 6436 toll-free (North America)

**Email:** info@verogen.com

**Website:** www.verogen.com



Verogen serves those who pursue the truth using genetic tools. Powered by Illumina's gold standard technology and working in partnership with forensic laboratories, we are advancing massively parallel sequencing to help unlock the true potential of forensic genomics.

## Booth 3: Carolina Biosystems

**Contact Person:** Marek Minarik

**Telephone:** +420 226 203 536

**Email:** info@carolinabiosystems.com

**Website:** www.carolinabiosystems.com



We supply original consumables for DNA sequencing and fragment analysis including polymers, kits, size standards, buffers etc. We also provide top-quality service and maintenance for ABI PRISM® line of capillary genetic analyzers. As an exclusive distributor for Softgenetics in Eastern Europe, we offer dedicated bioinformatics solutions for forensics (GeneMarker®HID).

### Booth 4: MENARINI SILICON MENARINI



**Contact Person:** Massimo Scrobogna  
**Telephone:** +39 3703344705  
**Email:** mscrobogna@siliconbiosystems.com  
**Website:** www.siliconbiosystems.com/forensics

Menarini Silicon Biosystems is a biotech company, which developed the DEPAArray™ system. The instrument can work with low input and separates forensic samples composed of epithelial cells, white blood cells, and sperm cells into 100% pure cell type specific preparations, enabling clear-cut genetic profiles through Single Cell Forensics.

### Booth 5: Promega Corporation



**Contact Person:** Nicole Siffling  
**Telephone:** +49 621 8501283  
**Email:** nicole.siffling@promega.com  
**Website:** www.promega.com

Promega Corporation is a global leader in the development, distribution and sale of products for human identification. Promega offers flexible, reliable solutions for all stages in the DNA laboratory workflow, from pre-processing through STR analysis. Joining our workflow kit and reagent solutions are two CE instruments, as well as a new Maxwell instrument, our Maxwell RSC 48, which is capable of processing 48 samples in less than 30 minutes. Also available is the Maxprep Liquid Handler, which comes with all the methods preloaded and offers sample tracking and traceability through each step of the forensics workflow.

### Booth 6: Thermo Fisher Scientific



**Contact Person:** Caroline Reddick  
**Telephone:** +44 7738 312970  
**Email:** caroline.reddick@thermofisher.com  
**Website:** www.thermofisher.com/hid

Thermo Fisher Scientific is the world leader in serving science. Our mission is to enable our customers to make the world healthier, cleaner and safer. Through our Applied Biosystems brand, we offer an unmatched combination of innovative technologies, purchasing convenience and support. As a worldwide leader in forensics, we deliver some of the most comprehensively validated products, expertise, and application support available to the human identification community. From our trusted reagents, through high-performance genetic analyzers and software, to in-depth training and on-site technical assistance, our integrated systems work together to help maximize your productivity and enable your success.

### Booth 7: GENETEK BIOPHARMA



**Contact Person:** Michael Onwuatuegwu  
**Telephone:** +49 30 63927050  
**Email:** onwuatuegwu@genetek.de  
**Website:** www.genetek-biopharma.com

GENETEK Biopharma is located in the Science City of Adlershof in Berlin, Germany. The scope of the company includes Development, Production, Marketing and Distribution of in-vitro diagnostic kits for detection of genetic diseases and chromosomal anomalies, Human DNA profiling kits used in forensics and/or kinship issues and Horse identification kits.

### Booth 8: Qualitype GmbH



**Contact Person:** Dr. Isabell Hilger  
**Telephone:** +49 351 88382812  
**Email:** i.hilger@qualitype.de  
info@qualitype.de  
**Website:** www.qualitype.de/de/start

As an internationally operating software company, we implement customised IT solutions – in use by customers in over 30 countries worldwide. These include classic off-the-shelf software, highly individualised software systems and central- or self-operated database solutions for laboratory and manufacturing applications.

### Booth 9: Purdue University Northwest



**Contact Person:** George F. Kacenga  
**Telephone:** +1-724-454-8734  
**Email:** gkacenga@pnw.edu  
**Website:** www.pnw.edu

As part of the Purdue University system, Purdue University Northwest (PNW) is a fully accredited comprehensive university proud to offer more than 70 areas of study. PNW offers one-of-a-kind proximity to active manufacturing, industry, the relaxing Lake Michigan shoreline, and the nearby opportunities of the third largest city in the United States – Chicago!

### Booth 10: HEALTH Gene Technologies



**Contact Person:** Ausma Bernot  
**Telephone:** +86 (0)574 2797 8799  
**Email:** ausma.b@healthgenetech.com  
**Website:** www.healthgenetech.net

Health Gene Technologies is a developer and manufacturer of proprietary molecular diagnostics products for forensic STR testing. Established in 2011, Health Gene Technologies has taken on the challenge to bring in further options of routine STR testing kits alongside innovative STR analysis reagents to forensic laboratories.

### Booth 11: AXO Science

**Contact Person:** Samuel Serraz

**Telephone:** +33 6 07 44 51 10

**Email:** samuel.serraz@axoscience.com

**Website:** www.axoscience.com

STK Sperm Tracker is the perfect solution for semen screening both in the lab and directly on the crime scene.

STK Lab: specific, sensitive, STK Lab is NOT toxic and is ready to use.

STK Spray: spray the scene directly with and reveal unsuspected semen stains on the field.



### Booth 12: Miltenyi Biotec GmbH

**Contact Person:** Carola Kluefer

**Telephone:** +49 2204 83066619

**Email:** carolak@miltenyibiotec.de

**Website:** www.miltenyibiotec.com



Miltenyi Biotec provides products that advance biomedical research and cellular therapy. Our innovative tools support research from basic research to translational research to clinical application. Our 30 years of expertise includes immunology, stem cell biology, neuroscience, and cancer. Miltenyi Biotec has 2,500 employees in 28 countries.

### Booth 13: NicheVision Forensics, LLC

**Contact Person:** Victor Meles

**Telephone:** +1-330-252-2711

**Email:** vic@nichevision.com

**Website:** www.nichevision.com



NicheVision develops and commercializes software solutions for forensic DNA human identity including tools like STRmix™, ArmedXpert™ and DNAXpress™, and most recent releases including PACE™ using artificial intelligence to automatically determine number of contributors in mixture and MixtureAce™ for typing and resolving MPS mixture data.

### Booth 14: SERATEC GmbH

**Contact Person:** Alexander Griberman

**Telephone:** +49 551 504800

**Email:** contact@seratec.com

**Website:** www.seratec.com



We manufacture tests for the detection of forensically relevant body fluids such as seminal fluid, saliva, blood and menstrual blood. They are rapid, easy in use and compatible with the subsequent DNA extraction and STR typing techniques.

### Booth 15: Forensic DNA Service

**Contact Person:** Dr. Daniel Vanek

**Telephone:** +420 603 979 915

**Email:** daniel.vanek@fdnas.cz

**Website:** www.fdnas.cz



Forensic DNA Service provides the services of paternity and genealogical testing, forensic DNA testing, specie identification of unknown biological material, individual identification of selected species and contracted research. Forensic DNA Service distributes products of the following companies: ZymoResearch, Eppendorf, Biomatrix, Seratec, COPAN, BLOO Scientific, and NZYTech.

### Booth 16: STRmix™

**Contact Person:** Adam McCarthy

**Telephone:** +44(0)7590 405 501

**Email:** adam.mccarthy@esr.cri.nz

**Website:** www.strmix.com



STRmix™ uses a world leading, fully continuous approach for the interpretation of DNA profiles and is now in over 150 laboratories globally. Recently we have released DBLR™ for the rapid calculation of likelihood ratios. Please come and see us for a demonstration of our latest release, STRmix™ v2.7, and DBLR™.

### Booth 17: MGI

**Contact Person:** Xiaoxi Guo

**Telephone:** +86 13428999426

**Email:** shirley.guo@genomics.cn

**Website:** www.en.mgitech.cn



MGI Tech Co., Ltd. (MGI), a subsidiary of BGI Group, is committed to enabling effective and affordable healthcare solutions for all. Based on its proprietary technology, MGI produces sequencing devices, equipment, consumables and reagents to support life science research, medicine and healthcare.

### Booth 18: GORDIZ

**Contact Person:** Vladimir Orekhov

**Telephone:** +7 903 799 38 72

**Email:** orekhov@gordiz.ru

**Website:** www.gordiz.com



GORDIZ Ltd. – biotechnology company that develops and manufactures the reagents for forensics and animal genetics. We developed a unique range of solutions in the field of DNA identification in close cooperation with forensic laboratories covering all the stages of analysis – from DNA extraction to fragment and sequencing.

### Booth 19: Independent Forensics

**Contact Person:** Dina Mattes

**Telephone:** +1 708-234-1200

**Email:** info@ifi-test.com

**Website:** www.ifi-test.com



Solutions for your most difficult forensic DNA cases: touch and sexual assault evidence. Fully accredited ISO17025 facility develops products to increase sensitivity of DNA profiling & accurately identify body fluids to triage cases. Confirmatory tests for human blood, semen, and sperm. The most sensitive/scientifically justified tests for saliva, urine and feces. ONETOUCH kits for obtaining DNA profiles from fingerprints, tape lifts, and touched items designed to fully integrate your latent section. AMPLICON Rx for repairing data from partial profiles. On-site demonstrations/workshops/training/installations/validation/microscope systems for forensic laboratories world-wide.

### Booth 20: Spot On Sciences

**Contact Person:** Nathalie Donche

**Telephone:** +415 347-3402

**Email:** nathalie.donche@spotonsciences.com

**Website:** www.spotonsciences.com



Spot On Sciences is a medical device company offering groundbreaking improvements in bio-specimen sample collection, storage, and transport. Unmatched by any other products on the market, their signature devices are unique in offering innovative sample protection, increased safety, stability, longevity, and speed. With the assistance of industry leaders, Spot On Sciences is moving toward making its devices global standard of care.

### Booth 21: GE Healthcare

**Contact Person:** Olga Bogonina / Inga Gerard

**Email:** olga.bogonina@ge.com

inga.gerard@qiagen.com

**Website:** www.gehealthcare.com



GE Healthcare is excited for QIAGEN to take its Whatman FTA technology to the next level and advance the field of forensic science. Our forensic portfolio is now part of QIAGEN, and you can visit booth #1 to learn more from the experts.



### Booth 22: CLIMS - VERISIS

**Contact Person:** Murat Isik

**Telephone:** +90 5556044010

**Email:** misik@verisis.co

**Website:** www.verisis.co



VERISIS A.S. is a 30 years old company mainly focused on developing solutions, consultancy and training based on Forensic Laboratories. Our main solution CLIMS – Forensic Laboratory Solutions Platform is a Case and Workflow Management solution together with DNA Banking & Matching and Kinship & Paternity Analysis.

### Booth 23: HIMEDIA LABORATORIES PVT LTD

**Contact Person:** Aseem Trehan

**Telephone:** +91 22 6147 1919

**Email:** info@himedialabs.com  
atrehan@himedialabs.com

**Website:** www.himedialabs.com



For Life is Precious

HiMedia possesses excellent hi-tech expertise for manufacturing a complete range of standard microbiological, chromogenic, HiVeg™, animal & plant tissue culture media, Molecular biology, laboratory chemicals & biochemicals products. We are ISO, CE Mark, WHO-GMP certified, US-FDA registered company exporting to over 130 countries, specializing in Automated Instrumentation solutions in Molecular Biology.

### Booth 24: Xceltis GmbH

**Contact Person:** Steffen Roth

**Telephone:** +49-621-872096-0

**Email:** info@xceltis.de

**Website:** www.xceltis.de



Xceltis GmbH is a privately held company founded in 2008 and headquartered in Mannheim, Germany, that markets pioneering products for life science research and routine diagnostics. This includes both laboratory equipment and reagents. One of these innovative products is the "Erase Sperm Isolation Kit", that is used for forensic investigations.

### Booth 25: Bio-Port Europe

**Contact Person:** Eva Mitášová, PhD.

**Telephone:** +420 602 251 901

**Email:** orders@bio-port.cz

**Website:** www.bio-port.cz



Bio-Port Europe is the Czech distributor company of premier brands like Thermo Fisher Scientific, Bio Molecular Systems, Jena Bioscience or Apogee. We provide advancing solutions for life sciences research, medical research and clinical laboratories.

# General Information

## ABSTRACTS



The ISFG 2019 Abstracts USB is given to each delegate upon registration; it contains all Abstracts that were accepted by the Scientific Programme Committee as well as those submitted by keynote speakers and presenters of invited sessions.

## BADGES



Along with your registration, you will receive your name badge, which must be worn when attending all sessions and official congress programme. Participants without a badge will not be allowed to enter sessions.

## CASH POINTS



A Komerční Banka cash point is located right between the venue entrances no. 5 and 6, and there is a Česká spořitelna cashpoint next to the underground station Vyšehrad.

## CERTIFICATE OF ATTENDANCE



The certificates of attendance will be sent to all attending delegates by email after the congress.

## CLOAKROOM

A cloakroom is located on the first floor near the registration area. The service is provided free of charge to all registered participants.

## CURRENCY

The Czech currency is called the Czech crown (CZK). Exchange offices are located all around the city centre (exchange offices, banks, post offices).

## CONFERENCE LANGUAGE



The congress language is English. No simultaneous translation is provided.

## DISCLAIMER



The Congress Organizers have taken all reasonable care in making arrangements for the congress, including accommodation and social events. In the event of unforeseen disruptions, neither ISFG, CSSFG, and C-IN the Conference Organizer nor their agents can be held responsible for any losses or damages incurred by delegates. The programme is accurate at the time of printing, but organizers reserve the right to alter the programme if and when deemed necessary. The Congress Organizers act as agents only in securing hotels, transport and travel services and shall in no event be liable for acts or omissions in the event of injury, damage, loss, accident, delay or irregularity of any kind whatsoever during arrangements organized through contractors or by the employees of such contractors. Hotel and transportation services are subject to the terms and conditions under which they are offered to the general public. Delegates should make their own arrangements with respect to personal insurance. The Congress Organizers reserve the right to make changes as and when deemed necessary without prior notice to the parties concerned. All disputes are subject to resolution under Czech law.

## DOCTOR / FIRST AID / PHARMACY



No first aid is available at the Prague Congress Centre. In case of emergency, please contact the Registration desk or dial 112 to get specialized help.

A Medical Centre (Poliklinika Budějovicka) is located at the station Budějovicka, three underground stations from the station Vyšehrad (the location of the venue).

### MEDICON A.S. – POLIKLINIKA BUDĚJOVICKA

Antala Staška 1670/80  
140 46 Praha 4  
Tel.: +420 261 006 111

### EMERGENCY PHONE NUMBERS

General emergency	112
Police	158
Fire department	150
Emergency medical service	155

### EXHIBITION OPENING HOURS

Tuesday, 10 <sup>th</sup> September	19:30 – 21:30
Wednesday, 11 <sup>th</sup> September	09:30 – 18:00
Thursday, 12 <sup>th</sup> September	09:30 – 18:00
Friday, 13 <sup>th</sup> September	09:30 – 17:30

### FOOD AND BEVERAGES

Coffee breaks and lunches are included in the pre-congress and congress registration fee and will be served at designated times within the coffee break and lunch stations.

### INSURANCE AND LIABILITY

The Congress Organizers will accept no liability for personal injuries sustained by or for loss or damage to property belonging to conference participants, accompanying persons either during or as a result of the conference or during all tours and events. Upon registration participants accept this proviso. Participants are strongly advised to seek insurance coverage for health and accident, lost luggage and trip cancellation.

### INTERNET

Free Wi-Fi internet connection is available throughout the congress premises. Network name: **ISFG2019**  
Password: **ISFG2019**

### LOST & FOUND

A lost and found service is available at the information desk at the registration.

### MESSAGE BOARD / JOBS BOARD

This is located on the ground floor, next to the Registration desk, and is available for all delegates to use.

### MOBILE APPLICATION

#### CONGRESS APP

Stay updated and download the **ISFG 2019** congress app via Apple app store or Google Play Store. Once logged in, you can make use of the app every day, any time...

#### SEARCH THE CONGRESS PROGRAMME

- View individual abstracts
- Create your own agenda
- Search by speaker name
- Search by keyword
- Rate oral presentations (scale 1 – 5 stars) and poster presentations
- See the venue floorplans
- Send messages to other congress participants
- Receive notifications from congress organizers

To use the full range of features, please note you will need to use the password/code upon the first login. The code and login procedure have been emailed to you by the congress secretariat. If you are unable to locate your login information, the registration desk staff will be happy to provide assistance.

## INTERACTIVE SCIENTIFIC PROGRAMME AND INDIVIDUAL PLANNING

Full program details are available in the section: Scientific Program – Create your own personalized schedule for the ISFG 2019 Congress:

- Add session to My program
- Add the presentation to My program

To view your personalized program, use the My Program button at the bottom right corner of your screen within the Scientific Program section.

## ATTENDEE PROFILES

Each pre-registered delegate is featured within the Attendee list. If you wish you can customize and update your own delegate profile by adding a website, a profile picture and short bio. To do so, click the blue “hamburger” button at the top left corner of your main screen and click the account email address (first item in the list). Speakers can also edit or delete biographies (submitted during abstract submission and published automatically from the database) as desired.

## SEND MESSAGES TO OTHER PARTICIPANTS

Take advantage of networking with ISFG 2019 participants – search within the attendees and speakers list and send messages within the app to selected contacts. To send a message to selected attendee, click his name in the list and then click the blue envelope button (✉) at the top right corner of the screen. Note: Attendees who are available and logged-in are highlighted with a blue dot beside their name in the Attendee List and are available for messaging. No contact information is visible to delegates and communications are all carried out in a closed environment only available to those with password access.

## OFFLINE OPTIONS

The ISFG 2019 app is available offline except the following features:

- in-app messaging
- all external links (marked with a link icon)
- updating content
- receiving announcements

## UPDATING THE APPLICATION CONTENT

The application updates the content automatically in the background upon each app restart (static meeting poster appears on the screen). Alternatively, you can force the application to update the content by pressing the last button in the list on the main screen – “Refresh event data”. Each menu item containing updated data will be labelled automatically.

## MOBILE PHONES



Participants are kindly requested to keep their mobile phones turned off/muted in all meeting rooms while sessions are being held.

## POSTERS



The Poster Area is placed on the second floor (South Hall). For more information about Poster Sessions please check respective pages in this Programme book (page number 9).

## SPEAKERS' PREVIEW ROOM – UPLOADING YOUR PRESENTATION ONSITE



Your presentation must be handed over to the technicians in the SPEAKERS' PREVIEW ROOM (located on the first floor near the registration area) as much in advance as possible, but no later than TWO HOURS BEFORE the beginning of the corresponding session. The presentation for an early morning session must be handed over the day before.

## SPEAKERS' PREVIEW OPENING HOURS:

Monday 9 <sup>th</sup> September	8:00 – 18:00
Tuesday 10 <sup>th</sup> September	8:00 – 20:00
Wednesday 11 <sup>th</sup> September	7:30 – 19:00
Thursday 12 <sup>th</sup> September	7:30 – 19:00
Friday 13 <sup>th</sup> September	7:30 – 17:00

## PROGRAMME CHANGES



The Congress Organizers cannot assume liability for any changes in the programme due to external or unforeseen circumstances.

## REGISTRATION OPENING HOURS



Monday 9 <sup>th</sup> September	8:00 – 18:00
Tuesday 10 <sup>th</sup> September	8:00 – 20:00
Wednesday 11 <sup>th</sup> September	7:30 – 19:00
Thursday 12 <sup>th</sup> September	7:30 – 19:00
Friday 13 <sup>th</sup> September	7:30 – 18:00

**Registration hotline: +420 724 566 445**

## REGISTRATION DESK



The Registration Desk is located on the first floor.

## CONGRESS FEE INCLUDES:

- Admission to all scientific sessions, exhibition and poster area
- Congress bag with all materials incl. programme book, abstract book (USB)
- Admission to Welcome Cocktail
- Coffee breaks and lunches during main congress days
- Prague public transport ticket valid throughout the congress dates

## WORKSHOP REGISTRATION FEE INCLUDES:

- Admission to pre-congress workshops
- Coffee breaks and lunches during pre-congress day(s)

## SHOPPING HOURS



Most shops in Prague are open from 09:00 to 18:00, Monday through Saturday. Shops in the city centre are usually open from 09:00 – 20:00, Monday through Sunday.

## SMOKING POLICY

Please note that smoking is not permitted in the venue.

## TAXI



The most comfortable option is to use one of many taxi services mobile applications. Czech app "Liftago" connects several taxi providers in one application. Install and use it as it is safe and reliable. [www.liftago.com](http://www.liftago.com).

Uber works in Prague properly as well.

Other: AAA (+ 420 14 014),

City Taxi (+420 257 257 257) or

Speed Cars (+420 224 234 234).

Boarding charge: approximately 40 CZK.

## TRANSPORTATION



With your free ISFG transport ticket you can travel where ever you want around Prague using metro, tram, bus, train, funicular to Petrin or our nice little ferries. [www.dpp.cz/en](http://www.dpp.cz/en)

## VENUE



Prague Congress Centre

5. kvetna 65

140 21 Prague 4

Czech Republic

# List of Orals

- O001 **FORENSIC APPEARANCE PREDICTION FROM DNA: A JOURNEY THROUGH 10 YEARS OF SCIENTIFIC CONTRIBUTIONS**  
Kayser, Manfred
- O002 **THE WHITE ELEPHANT IN THE FIELD – WHAT MEANS “POPULATION” IN FORENSIC GENETICS?**  
Roewer, Lutz
- O003 **DEVELOPMENT AND OPTIMIZATION OF THE VISAGE PROTOTYPE TOOLS FOR BIO-GEOGRAPHIC ANCESTRY AND APPEARANCE TRAITS INFERENCE USING TARGETED MPS**  
Xavier, Catarina
- O004 **APPROACHES TO EXPLAIN AND POTENTIALLY PREDICT THE COMPLEX ARCHITECTURE OF THE HUMAN FACE**  
Walsh, Susan
- O005 **INTRODUCTION OF A PREDICTIVE DNA TEST FOR THE OCCURRENCE OF FRECKLES**  
Branicki, Wojciech
- O006 **FORENSIC DNA PHENOTYPING: A SERVICE PROVIDER TRIAL**  
Raymond, Jennifer
- O007 **COMPARISON OF CE- AND MPS-BASED ANALYSES OF FORENSIC MARKERS WITH SINGLE CELL AFTER WHOLE GENOME AMPLIFICATION**  
Chen, Man
- O008 **PRESENTATION OF THE HUMAN PIGMENTATION (HUPI) AMPLISEQ CUSTOM PANEL**  
Meyer, Olivia Strunge
- O009 **PREDICTIVE DNA ANALYSIS OF HUMAN HEAD HAIR GREYING USING WHOLE-EXOME AND TARGETED NGS DATA EXAMINED WITH DEEP LEARNING METHODS**  
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- O010 **A COMPARISON OF DNA METHYLATION TECHNOLOGIES AND PERFORMANCE OF AGE PREDICTION MODELS**  
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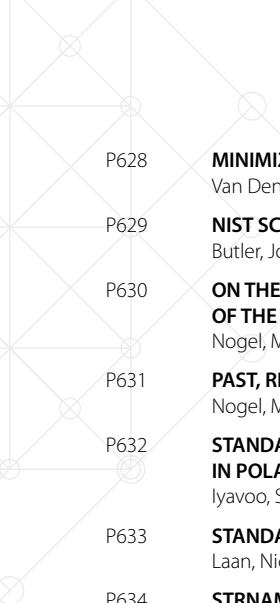
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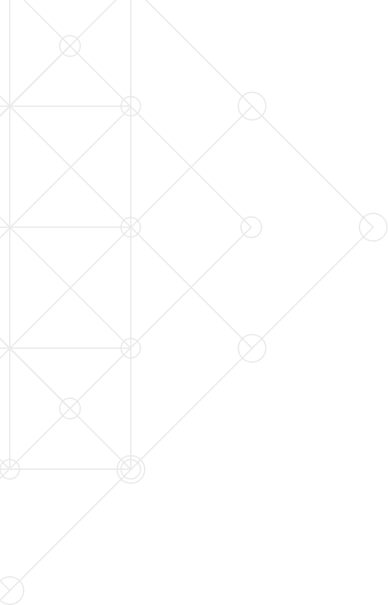
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# Identifying the missing

Join our symposium at the  
2019 ISFG Congress, Prague:

**Date:** Wednesday, September 11, 2019

**Time:** 13:30–14:20

**Location:** South Hall 1B, 1st floor,  
Prague Congress Centre

## Agenda

- 13:30 – 13:35 **Welcome**
- 13:35 – 13:45 **How missing persons identification enables the families of the missing to move on. A personal story.**  
Speaker: Mrs. Ingrid Gudmundsson, Sweden
- 13:45 – 14:15 **Development of a large, massively parallel sequencing SNP panel for missing persons identification**  
Speaker: Dr. Thomas J. Parsons, Director of Science and Technology, International Commission on Missing Persons (ICMP), The Hague, Netherlands
- 14:15 – 14:20 **Wrap up**

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