Symposium runs from 09.30-17.30 BST on the 26th of April

to see what time that is where you are, visit:
https://www.timeanddate.com/worldclock/fixedtime.html?msg=Advancing+Genetic+Genealogy+Symposium%3A+April+26+2025&iso=20250426T0930&p1=3903&ah=8

09.15 – Begin allowing people in from the Zoom waiting room.

09.30 – Welcome and housekeeping

09.35-10.35 – Keynote talk by Prof. dr. Maarten H.D. Larmuseau

"Mommy's baby, daddy's maybe": Genetic genealogical reconstruction of extra-pair paternity behaviour

Paternity has long been a subject of cultural, legal, political, and scientific debate. While a mother's identity is evident at birth, the biological father's identity has historically remained uncertain—captured in the adage *Mater certa, pater semper incertus* ("Mommy's baby, daddy's maybe"). Until recently, this uncertainty could only be speculated upon but advances in genetic genealogy now allow for a detailed reconstruction of extra-pair paternity (EPP) patterns over centuries, shedding new light on the biological, social, and historical dimensions of fatherhood.

This keynote presents a population-level genetic genealogy approach to reconstruct the spatiotemporal dynamics of EPP in Western Europe over the past 500 years. By combining extensive patrilineal and matrilineal genealogies from the Low Countries with Y chromosome and mitochondrial genome sequencing, we reveal historical EPP rates—generally low, averaging around 1.5% per generation—yet significantly influenced by socioeconomic and demographic factors. Among married couples, rates ranged from 0.4% to 5.9%, with peaks observed in lower socioeconomic classes in densely populated urban centers during the late 19th century. These findings demonstrate that historical EPP rates fluctuated over time and across social contexts.

By integrating contemporary genomic data with historical research, we illustrate how sexual behaviour and perceptions of fatherhood have evolved. This interdisciplinary approach underscores the power of genetic genealogy in exploring human reproductive behaviour and kinship, bridging the gap between historical records and biological reality.

Biographical note

Prof. dr. Maarten H.D. Larmuseau is a genetic genealogist at KU Leuven (University of Leuven, Belgium) and head of the Laboratory of Human Genetic Genealogy. His team combines family history with DNA analysis—both from living individuals and ancient remains—to study the evolution of biological kinship. He works closely with citizen scientists, fostering participatory research that connects the public with academia. Larmuseau also directs the KU Leuven Institute of Genetics in Society (LIGAS), which explores the ethical, legal, and social dimensions of human genetics.

10.35-10.45 – break

10.45-11.50 – breakout sessions A & B

Breakout session A

10.45 – 11.15 – Matthew Waterfield

IGG in the UK: Prospective Advantages, Potential Challenges and Proven Solutions

In contrast to many of its counterparts in the Anglosphere and in mainland Europe, the UK has been slow to adopt investigative genetic genealogy (IGG). Although the UK has hundreds of UHR cases on its books - not to mention an indeterminate number of potential suspect cases - IGG has not yet been tried, which means that the efficacy of the technique for UK cases remains unknown.

However, this does not mean that British genealogical research falls outside the realm of existing IGG work. There have been multiple examples of cases solved using IGG where the perpetrator/Doe was of recent British heritage, and these cases can give us an indication of how effective IGG will be when applied to cases in the UK.

In order to illustrate the potential of IGG to solve UK cases, this presentation will look at three UHR cases where the Doe was of recent British heritage, all of which were solved by the DNA Doe Project. These cases are Annie Doe (Annie Lehman), whose mother was British, Carson City Jane Doe (Joyce Rodgers), whose paternal grandmother was British, and Downtown Phoenix John Doe (Frank Beck), whose maternal grandparents were British.

The research processes that led to identifications in these three cases serve as an example of some of the advantages and disadvantages of using IGG on cases where the person of interest has recent British heritage. As a result, the pros and cons of using IGG in the UK will be discussed in the context of real-world examples, as will the solutions that IGG practitioners can employ in order to overcome UK-specific drawbacks.

Biographical note

Matthew Waterfield is a Team Leader and an investigative genetic genealogist with the DNA Doe Project. He has led and/or worked on over 20 unidentified human remains cases, including Brad Doe (John Brandenburg, Jr.), Matilda Doe (Shelly Rae Kephart) and Carson City Jane Doe (Joyce Rodgers). Matthew is passionate about the UK embracing the usage of IGG and has participated in various forms of media to promote this technique in the UK. He is also registered with the Association of Professional Genealogists and specialises in genetic genealogy. A graduate of the University of Leeds, Matthew is originally from London.

11.20-11.50 – Taner Kuru

EU legal framework and FIGG

Investigative genetic genealogy has emerged as an effective investigation tool in the last few years, gaining popularity, especially after the arrest of the Golden State Killer. Since then, hundreds of cases have been reported to be solved thanks to this novel and promising technique. Unsurprisingly, this success also led law enforcement authorities in the EU to experiment with it. So far, countries such as Sweden, Norway, and France have successfully used this technique, the Netherlands is currently experimenting with it in a pilot project, and the feasibility of using investigative genetic genealogy has been under consideration in the United Kingdom. Meanwhile, Denmark has passed a law permitting its use under certain conditions.

However, there appears to be an ambiguity on which legal basis in the EU data protection framework should be used to access the personal data of genetic genealogy database users for investigative purposes. For example, while the Swedish pilot case relied on Article 10(c) of the Law Enforcement Directive (2016/810), which allows sensitive personal data processing if the data is manifestly made public by the data subject, it appears that the Dutch and Danish cases rely on other legal bases. However, this ambiguity and reliance on an improper legal basis could put the legality and legitimacy of investigative genetic genealogy at stake.

Accordingly, this presentation will examine whether the “manifestly made public by the data subject” legal basis enshrined in Article 10(c) of the Law Enforcement Directive could be used for accessing the personal data of genetic genealogy database users for investigative purposes and suggest a way forward to ensure the lawfulness and legitimacy of investigative genetic genealogy in the EU legal framework from the data protection perspective.

Biographical note

Taner Kuru is a PhD researcher at Tilburg Institute for Law, Technology and Society (TILT) of Tilburg University, focusing on the ethical and legal implications of investigative genetic genealogy. He holds an Advanced LL.M. degree in Law and Digital Technologies from Leiden University (cum laude distinction) as an awardee of the Jean Monnet Scholarship. In 2021, he received the European Data Protection Law Review’s “Young Scholar Award” for his article titled “Genetic Data: The Achilles’ Heel of the GDPR?” based on his master’s thesis. He also interned at the United Nations Interregional Crime and Justice Institute (UNICRI) Centre for Artificial Intelligence and Robotics.

Breakout session B

10.45-11.15 - Dr. Martine Zoeteman-van Pelt

Genetic Genealogy at the CBG: Tools, Ethics, and Historical Cases

How can DNA testing enhance genealogical research, and what ethical challenges does it bring? The CBG|Centre for Family History (established 1945) in the Netherlands serves as a hub for genetic genealogy, providing essential tools such as the *WieWasWie (“WhoWasWho”)* online civil registry database and the *National Register of Deceased Persons* to help identify DNA matches from DTC tests who lack family trees. We are also developing *PiCo* (Persons in Context), an advanced system for automated family reconstructions based on civil registry data, making it even easier to recognize DNA matches.

Beyond technology, we emphasize public education on DNA testing, including its benefits, limitations, and ethical implications. While DNA can unlock family histories, it also raises concerns about privacy and unexpected discoveries. Our workshops explore these topics through renowned international case studies, as well as Dutch cases like the question of painter Vincent van Gogh’s possible illegitimate child.

A key focus is the history of slavery. For many descendants of enslaved individuals from the former Dutch colonies of Suriname and the Antilles, DNA testing is the only way to reconnect with their African roots. This talk will highlight how genetic genealogy can bridge historical gaps and open new avenues for research.

Biographical note

Dr. Martine Zoeteman-van Pelt began researching her family tree at the age of 11, inspired by her grandfather's captivating stories about an ancestor who served in Napoleon's army. She earned her doctorate in history with a thesis (2011) focusing on the student population of Leiden University between 1575 and 1812. In 2022–2023, she obtained a microcredential in genetic genealogy from the University of Antwerp in Belgium.

Currently, Martine works as a senior researcher and DNA expert at the CBG|Centre for Family History in The Hague. The CBG serves as the Netherlands' leading centre for genealogical expertise and information, housing several government collections.

11.20-11.50 – Dr Maurice Gleeson

Slavery, Reparations & DNA.

Both the Caribbean Reparations Commission and the National African American Reparations Commission have each produced a 10 point Action Plan to help achieve reparations for slavery. Several of the items on each of the Action Plans could potentially be achieved with the help of commercial DNA testing. These include Right of Repatriation, Building of Cultural Institutions, African Knowledge Programme, Public Health Improvement, Psychological Rehabilitation, and Indigenous People's Development Programme. How commercial DNA testing could help achieve these objectives will be discussed, highlighting various initiatives that have already been undertaken.

Biographical note

Maurice Gleeson is a medical doctor as well as a genetic genealogist. He is an Honorary Research Fellow at the University of Strathclyde, and organiser of the DNA Lectures for "Genetic Genealogy Ireland" in Dublin/Belfast and "Who Do You Think You Are" in England. He also works with people of unknown parentage and has appeared on Irish TV as a consultant for the TV series Adoption Stories. His YouTube videos on genetic genealogy are very popular.

11.50-12.00 – break

12.00-13.00 - Keynote talk by Dr Pille Hallast

Insights from long-read genome assemblies into autosomal and Y-chromosomal diversity and mutation rates in complex genomic regions.

Recent advances in long-read sequencing and de novo assembly tools now allow for near telomere-to-telomere resolution of entire human genomes, enabling unprecedented insights into genetic diversity and mutational processes. The Y chromosome, with its repetitive and ampliconic structure, has long posed challenges for genomic analysis, resulting in its systematic omission from reference assemblies. Despite being one of the smallest human chromosomes, over 50% of its ~57 Mb sequence is not resolved in the GRCh38 reference genome. To better characterize human Y-chromosomal diversity, we assembled and analysed Y chromosomes from 44 individuals across 21 populations, revealing an extraordinary level of structural and sequence variation spanning 183,000 years of human evolution (Rhie et al., 2023; Hallast et al., 2023 Nature).

In addition to the Y chromosome, we applied long-read sequencing to a four-generation, 28-member pedigree (CEPH 1463) to phase and assemble over 95% of each diploid genome. This dataset provides base-pair resolution insights into de novo mutation rates and processes, particularly in complex and repetitive regions across both the autosomes as well as the sex chromosomes. By fully resolving these genomes, we can study fundamental aspects of human genetic variation, inheritance and disease, offering new opportunities to explore mutation patterns and structural changes at a level of detail previously unattainable.

Biographical note

Dr. Pille Hallast is a Research Scientist at The Jackson Laboratory for Genomic Medicine, USA, specializing in genome diversity and population genetics, with a primary focus on the Y chromosome. Her research explores human population history, Y-chromosomal variation and mutation rates, and male fertility genetics. Currently, she utilizes long-read sequencing to uncover the full extent of genetic variation in complex genomic regions, enhancing our understanding of their evolution and

functional impact. Her work has important implications for human migration, genetic history and reproductive health.

13.00-13.45 – Lunch break

13.45-14.45 – Keynote talk by Andrew Hochreiter and Eryk Jan Grzeszkowiak

Introduction to the Investigative Genetic Genealogy Accreditation Examination

The application of Investigative Genetic Genealogy (IGG) in law enforcement and unidentified human remains cases has increased rapidly in recent times. The Investigative Genetic Genealogy Accreditation Board (IGGAB) was formed in 2022 to address the need for standards and accreditation in the field. The Board has produced a set of IGG Professional Standards, Code of Ethics, and an IGG Accreditation Examination. The Professional Standards and Code of Ethics were published in December 2023 with an update to the Standards in April 2024. The Accreditation Exam involved a professional exam development cycle that utilized the expertise of experienced IGG practitioners.

This presentation will describe the effort to ensure the professional integrity and validity of the exam with the use of subject matter experts, selection of a specialized secure exam software platform, rigorous beta testing, and meticulous revisions. Emphasis will be given to describing the fifteen IGGAB "core competencies" that represent the foundational knowledge, practical skills, and ethical standards required to perform IGG work effectively and responsibly. These competencies encompass both theoretical understanding and real-world application, ensuring practitioners can contribute to criminal investigations and unidentified human remains identifications while adhering to legal and ethical guidelines. Exam application, preparation, retest, and recertification policies will be explained. The exam topics and questions will test the expertise of these competencies. The demonstration of IGG knowledge, experience and proficiency will be required to pass the exam.

This talk will provide information on the IGG accreditation requirements to be designated an "Accredited Investigative Genetic Genealogist" (AIGG).

Biographical notes

Andrew Hochreiter

Andrew Hochreiter, MEd, MIS, is an avid genetic genealogist and founding member of the Investigative Genetic Genealogy Accreditation Board (IGGAB), promoting IGG standards, code of conduct, and accreditation. He is a graduate of UNH Forensic Genetic Genealogy and Ramapo College IGG Certificate Programs. He is chairman of East Coast Genetic Genealogy Conference, board member at mitoYDNA.org and Association of Professional Genealogists Forensic Genealogy SIG, and a DNA Doe Project investigator. He is a genetic genealogy instructor at a Maryland community college and leads the DNA Special Interest Group at the Washington DC Family Research Center.

Eryk Jan Grzeszkowiak

Eryk Jan Grzeszkowiak is a genetic genealogy lecturer who has taught at four universities across Europe. He is currently teaching at the University College Cork and the University of Limerick and previously lectured at the University of Strathclyde. In 2021, he developed and taught Poland's first academic course in Genetic Genealogy.

As the Exam Director at the Investigative Genetic Genealogy Accreditation Board (IGGAB), Eryk plays a key role in setting professional standards in the field. He is also an investigative genetic genealogist

with the DNA Doe Project, where he co-leads the Education Team as a Research and Curriculum Development Specialist, conducting research and training the next generation of investigative genetic genealogists. His work is backed by over a decade of experience in genetic genealogy and a formal background in human genetics (University of Edinburgh).

In 2015, Eryk launched Poland's first genetic genealogy blog (genealogiagenetyczna.com). He has worked with clients worldwide, presented his research at numerous national and international genetic and genealogical conferences, and been featured in TVN, Esquire, Newsweek, and other media outlets.

14.45-15.00 - break

15.00 – 16.05 – breakout sessions C & D

Breakout session C

15.00-15.30 – Kate Penney Howard

Untangling Complex DNA: Advanced Tools for Challenging Genealogical Research

Consumer DNA testing has revolutionized genealogical research, but standard genetic genealogical methods do not work for all individuals. This session explores methodologies for navigating three interrelated phenomena in genetic genealogy: pedigree collapse (when cousins marry, causing their ancestors to appear multiple times in a family tree), endogamy (when pedigree collapse happens numerous times within communities that are isolated by cultural norms or by geography), and high runs of homozygosity (when parents are closely related). Traditional relationship predictions often fail in these populations due to inflated amounts of shared DNA and multiple relationship paths with matches.

When the Leeds Method doesn't lead to answers, there are other techniques to untangle difficult DNA. We will explore the SMARTTA (Shared Match Analysis on Rows with Top Tier Averages) method, a structured approach for analyzing DNA results in endogamous populations. This methodology employs tiered classification of matches based on average segment sizes and provides systematic documentation procedures for complex cases.

While these cases require more patience and careful documentation, they are not unsolvable. By focusing on larger segments, organizing matches into tiers, and maintaining thorough documentation of your analysis process, you can successfully navigate even the most challenging genetic genealogy cases.

Biographical note

Kate Penney Howard is a genetic genealogist, specializing in brick wall work, HighRoH, and endogamy. During a bout with cancer, she discovered that she loves sharing her knowledge with other genealogists. She is intentional about addressing injustice and myths in her presentations.

Kate has presented at Rootstech, East Coast Genetic Genealogy Conference, the International Congress on Medieval Studies, NAAP/RTK's Untangling Our Roots, and the General Assembly of the Christian Church (Disciples of Christ). 2025 speaking engagements include Rootstech, Ohio Genealogical Society 2025, and Ontario Ancestors Webinar Series, as well as local library and genealogical society gatherings.

Kate studied vocal music and earned a Master of Divinity from Christian Theological Seminary in Indianapolis in 2011 and has been pastor of North Christian Church since her ordination in 2012.

15.35-16.05 – Caleb Anderson

Reconstructing a Family Tree with Multiple Consecutive NPEs

One of the commonly accepted benefits of the use of DNA in genealogy is its ability to expose where an individual's genetic tree does not match their family tree of record. However, this process becomes immensely more complicated when the research makes it evident that the initial NPE (non-paternal event) was preceded by another (or even multiple) NPEs. This presentation will explore strategies for identifying, analyzing, and resolving NPEs through chromosome mapping and advanced clustering techniques.

The presentation will begin with an overview of NPEs, distinguishing between "expected" and "unexpected" cases, and discussing methods for identification, including key indicators of potential NPEs and approaches to resolving them. Specific techniques for addressing NPEs such as clustering, triangulation, and chromosome mapping, (alongside the use of traditional genealogical methods) will be discussed in depth. Special emphasis will be placed on the use of tools like What Are the Odds? (WATO) and the Shared cM Project in support of these techniques.

The complexities of working with multiple NPEs will then be examined in conversation with a case study containing multiple ancestral and collateral NPEs, demonstrating practical approaches for analyzing NPEs and building out an accurate genetic family tree.

Biographical note

Caleb Anderson is a genetic genealogist based in Rocklin, California (just northeast of Sacramento). With over ten years of experience working with genealogy cases of various kinds, his particular interests include unknown parentage cases (particularly those several generations removed from the tester), medieval genealogy, the West Yorkshire and West Virginia regions, and the usage of Y-DNA, mtDNA, and even atDNA to answer historical questions.

He is a current MSc student at the University of Strathclyde in the process of finishing a dissertation on the genealogical value of the Eastern Cherokee Guion Miller Roll applications.

Breakout session D

15.00-15.30 – Laura House

Methodology and Applications of Visual Phasing

Visual phasing is a chromosome mapping technique that uses crossover points in the autosomal DNA of three full siblings to identify which sections of a chromosome were inherited from which of the siblings' four grandparents. The process will someday be automated, but until then, genetic genealogists must perform it manually.

We will outline the methodology, and then we will discuss a case study in which three siblings descend from three known grandparents and one unknown grandparent. The unknown grandparent is Canarian and possibly Madeiran, so he belongs to communities that are underrepresented in the DNA databases. For this reason, it is challenging to identify him using traditional genetic genealogical

methods. We will explore the insights obtained from visual phasing about the documented grandparents, and we will use our phased data to learn about the unknown grandfather. Our case study uses GEDmatch to compare the DNA of the siblings and utilises autosomal DNA databases that offer a chromosome browser and segment data.

In addition to the practical genealogical applications of visual phasing, we can cross-reference the siblings' phased data with their biogeographical ancestry estimates, health and traits results, and we can discover which of their grandparents made the largest contribution to their genetic makeup.

Visual phasing is time consuming and labour intensive, but fascinating and gratifying. The methodology can be carried out using the DNA of any three full siblings in a family, enabling a researcher to learn more about the grandparents of those siblings and immediately identify which grandparent connects the siblings to matches in any databases with a chromosome browser.

Biographical note:

Laura House is an Ancestry spokesperson and the primary genetic genealogist on AncestryProGenealogist's International team. She has an MSc. degree in Genealogical, Palaeographic and Heraldic Studies from the University of Strathclyde, and her dissertation focuses on the limitations of Y and autosomal DNA when applied to the investigation of surname changes. Her specialisms are genetic genealogy and unknown parentage, and she has written articles and delivered talks on DNA testing for genealogy. Laura is an onscreen expert for several documentaries on the BBC, ITV, and SBS, and she has spoken about her work on television, radio, and podcasts, including *Channel 4 News*, BBC Radio, *BBC Breakfast*, and *Woman's Hour*.

15.35-16.05 – Kathryn Johnston

Visually phased DNA crossover zones on chromosomes determine genetic networks – the demonstration of a simplified method for genetic genealogists.

Over a century ago Thomas Hunt Morgan demonstrated the basics of crossover recombination of chromosomes through research on the fruit fly. He won the Nobel Prize in Physiology or Medicine in 1933 by establishing the chromosome theory of heredity. Genetic genealogists continue to build on this research using centimorgan (cM) values, but instead of the identification of traits, crossover recombination zones can now be established through the segment matching between relatives. Shared matches (i.e. groups of genetic networks and clusters of matching cousins) depend on borders created through crossover recombination. Unknown parentage cases rely on shared matches, but few genealogists understand the scientific basis for their groups of DNA segments in common.

A case report will demonstrate the use of crossover zones through a combined modified Leeds Method and the practical use of Jonny Perl's DNA Painter tool. Visual phasing is now possible without the need for siblings or grandparent matches if there are specific cousins willing to share (at GEDmatch and/or some of the direct-to-consumer DNA companies).

In this presentation, recommendations involving four grandparent-defined groups will be provided to create an individualized browser of crossover zones. Genealogists are known to home in on individual families with precision and without the need for gene mapping. The scientific basis for the success of shared matches will be discussed. Educators will be interested in seeing how genetic networks really work at the molecular (chromosome) level.

Biographical note:

Kathryn (Kathy) Johnston MD, a retired dermatologist has been engaged in genetic genealogy for over 20 years. She has given numerous presentations on DNA at genealogy conferences including the Southern California Genealogical Society Jamboree and Institute for Genetic Genealogy. She has been with Firebird Forensics for the past five years. A recent publication by T. Whit Athey, PhD and Kathryn Johnston, MD entitled "Recombination and phasing for a group of three or four (or more) siblings – two practical approaches", *Journal of Genetic Genealogy*, Volume 12 Number 1 (Spring 2024) pp, 1-45 is available in PDF format online, https://jogg.info/wp-content/uploads/2024/03/JoGG-121-Issue-1.pdf.

16.05-16.15 – break

16.15-17.15 – Keynote talk by Dave Vance

Advancing Genetic Genealogy Through Long-Read WGS Sequencing: Enhanced Phasing and Ancestral Pattern Detection

Long-read DNA sequencing technology represents a significant advancement in genetic genealogy, offering unprecedented capabilities in analyzing inherited genetic patterns. This presentation explores how long-read will revolutionize our approach to ancestral tracking and relationship determination. A key advantage lies in its capacity to accurately phase homozygous Single Nucleotide Polymorphisms (SNPs) across maternal and paternal chromosomes, providing clear distinction between parental genetic contributions. This enhanced phasing capability reveals previously undetectable patterns of novel SNPs, enabling the identification of smaller shared segments between DNA testers and their ancestors with greater precision than traditional short-read sequencing methods.

The technology's application in genetic genealogy extends beyond basic relationship determination. By analyzing the distribution and frequency of novel SNPs across matched segments, we can develop more accurate grouping and ranking for in-common matches, providing genealogists not only with an estimate of their degree of relationship with matches but also with automated sorting, grouping and generational order of their matches around common ancestral lines. Furthermore, the identification of shared and divergent novel SNPs would enable more precise estimation of the temporal distance to common ancestors, offering genealogists a powerful tool for validating documentary research and identifying potential relationship paths. This presentation demonstrates how these capabilities combine to create a more robust framework for genetic genealogy research, particularly in cases where traditional documentary evidence is limited or conflicting.

To support this framework, companies will need to implement matching databases of whole genome sequencing data which can store and detect detailed patterns of individual autosomal SNP mutations across family branches, and simplify the user interfaces of analysis tools like clustering, triangulation and segment analysis to mask the increasing analytic complexity. The presentation reviews these and other steps that commercial companies will need to implement before the full advantage of long-read data will be realized.

The implications of this technology extend to improving the accuracy of family tree reconstruction and enhancing our understanding of genetic inheritance patterns across multiple generations. The advent of long-read sequencing will eventually allow family trees to be reconstructed in their entirety from DNA alone, even if the ancestors involved may never be named. This presentation will include practical examples demonstrating how these advances translate into tangible benefits for all genetic genealogists.

Biographical note

Dave Vance has been a genealogist for more than 35 years and active in genetic genealogy since 2005. He is the author of “The Genealogist’s Guide to Y-DNA Testing for Genetic Genealogy: Second Edition” published in 2024. Dave is also the author of the SAPP tool for Y-DNA phylogenetic trees and until recently was the editor for the Journal of Genetic Genealogy.

In October 2024, Dave was hired as General Manager responsible for FamilyTreeDNA, a genetic genealogy division within the Gene By Gene/MyDNA companies.

Dave is also the administrator for the Vance surname project and co-admin for the R1b-L513 haplogroup project as well as the president and DNA advisor for the Vance Family Association, a traditional genealogy surname association.

17.15-17.30 – Symposium wrap up and thanks