

“Nature and Nurture” - Program

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| 9.00 | Registration |
| 9.30 | Welcome - Isabelle Devos |
| 9.45 | Historical Demography for Dummies - Paul Puschmann |
| 10.00 | Genetics for Dummies - Sofie Claerhout |
| 10.15 | Keynote: The Genetic Genealogy Revolution - Debbie Kennett |
| 11.00 - 11.10 COFFEE | |
| FAMILY HISTORY AND DNA // chair: Paul Puschmann | |
| 11.10 | Does DNA confirm the chaotic 'Jan Steen household' in the 17th century? - Biological relatedness in extended genealogies from the Low Countries (Maarten Larmuseau) |
| 11.30 | Using 21st century DNA to identify fathers in the 18th and 19th centuries (Cathy Day) |
| 11.50 | Expanding your family tree with DNA tests: why genealogists, historical demographers and geneticists should collaborate (Martine Zoeterman van Pelt) |
| 12.10 | Ascendant Genealogies as a Source for Demographic and Genetic Studies: some estimates of bias (Jim Oeppen) |
| 12.30 - 13.30 LUNCH | |
| POPULATION HISTORY AND GENETICS // chair: Sofie Claerhout | |
| 13.30 | Genetic connectedness between medieval and modern populations of Europe (Toomas Kivisild) |
| 13.50 | The Dutch Y-chromosome from the Early Middle Ages to present day (Eveline Altena) |
| 14.10 | The Genetic Diversity in Västerbotten, Sweden (Erling Häggström Lundevaller) |
| 14.30 | Longevity genetics in the Netherlands: from quantitative trait definition to gene discovery (Marian Beekman) |
| 14.50 | Does Ashkenazic DNA refer to the Biblical Israelites? (Jits Van Straten) |
| 15.10 - 15.30 COFFEE | |
| HISTORICAL DEMOGRAPHY AND GENETICS // chair: Isabelle Devos | |
| 15.30 | Contextualising skeletal analyses: combining burial context and paleodemographic data to study the social composition on St.Rombout's cemetery, Mechelen (10th-18th centuries AD) (Katrien Van de Vijver) |
| 15.50 | Twins in the Calvinist Parish Registers in Eastern Croatia in the Second Half of the 18th and the First Half of the 19th Century (Denis Njari) |
| 16.10 | Paper Trails of Everyday Lives in the Austrian Military Frontier (Alexander Buczynski) |
| 16.30 | Genetic and shared-environment effects on stature and lifespan, a pedigree study of Dutch birth cohorts, 1785-1922 (Jan Kok) |
| 16.50 | Trading social status for genetics in marriage markets: evidence from UK Biobank (David Hugh-Jones) |
| 17.10 | CONCLUSIONS, DISCUSSION, Q & A Ronny Decorte |
| 17.30 - 18.30 DRINKS | |

“Nature and Nurture” - Oral presentations

1. KEYNOTE: Debbie Kennett

*Honorary Research Associate
Department of Genetics, Evolution and Environment
University College London*

The Genetic Genealogy Revolution

Genealogical research has been transformed in the last two decades by the mass digitisation and indexing of core genealogical records. During this same period the direct-to-consumer DNA testing market has grown exponentially. Over 40 million people have now taken a DNA test and are being matched with their genetic cousins from around the world. Genetic genealogy – the combination of DNA testing with genealogical and historical records – is proving to be a powerful and revolutionary tool. As well as helping family historians to solve long-standing family history mysteries, DNA testing is also being used by adoptees and donor-conceived individuals to bypass legislative restrictions and identify their biological parents. DNA testing can also throw up surprises. Some people find that they are not who they thought they were, while others discover unknown siblings or branches of the family that they did not know existed. More controversially, some genetic genealogy databases are now being used by law enforcement agencies to generate investigative leads to solve homicides and other serious crimes. Genetic genealogy has had a transformative effect on society but the technology has advanced faster than our ability to put in place the necessary support networks, regulatory oversight and legislative frameworks.



2. Maarten Larmuseau

*Laboratory of Human Genetic Genealogy, Department of Human Genetics, KU Leuven, Belgium
ARCHES, Antwerp Cultural Heritage Sciences, Faculty of Design Sciences, KU Leuven, Belgium
Histories vzw, Gent, Belgium*

Does DNA confirm the chaotic 'Jan Steen household' in the 17th century? - Biological relatedness in extended genealogies from the Low Countries

Familial relatedness refers to three distinct aspects: legal, social, and biological kinship. These three aspects often go together, but that does not have to be the case. For example, in the case of an adopted child or a stepfather, there is no biological relatedness, but the familial connection is clear. In any case, there is discussion today about the importance of each of these aspects, and it stays an overly sensitive subject for many people. Although, even genealogists who consider the biological aspect to be completely subordinate to the legal or social origin, will acknowledge that information about genetic parents and biological relatives is relevant to describing the family history. Figuring out the relationships between the three aspects of relatedness provides insight into the relationships between people within families. That is why the current genetic revolution in genealogy will be a lasting one, not just a short-lived hype. Moreover, this revolution gives us a new perspective on family trees that was previously hidden. We can evaluate to what extent the legal sources correspond to the biological ties between family members, even from the distant past. This also applies to the seventeenth century of painter Jan Havickszoon Steen (c.1626-1679). In his paintings, Jan Steen often depicted quite chaotic households where the bond between the three aspects of kinship is not always clear. In this talk, I will present the

genetic genealogical method to assess deep family trees in order to investigate the relationship between legal, social, and biological kinship in the Low Countries in past centuries. This will also allow us to decide to what extent the 'household of Jan Steen' corresponded to general trends in the seventeenth century.

3. Cathy Day

*National Centre for Epidemiology and Population Health
Australian National University*

Using 21st century DNA to identify fathers in the 18th and 19th centuries

This paper describes a method of identifying fathers of illegitimate children who lived in the 18th and 19th century from the DNA of their 21st century descendants. It focuses on fathers of children born in England, but the descendants can live anywhere in the world and the techniques can be applied in any country in which consumer DNA testing is common, such as those in Europe and North America.

It describes the process of identification using the results of consumer DNA tests, consumer-generated family trees and historical documentation. Through examples, the paper demonstrates how DNA can supplement documentary sources and validate, or disprove, assumptions about paternity.

4. Martine Zoeteman van Pelt

Center for Family History, The Netherlands

Expanding your family tree with DNA tests: why genealogists, historical demographers and geneticists should collaborate

As a researcher at the CBG|Center for Family History, Martine Zoeteman-van Pelt noticed a great change over the past decade. Written documents were the only source for genealogists for a long time. Because of new techniques you can now trace your family tree centuries and even thousands of years further back in time. Also searching for biological relatives, without knowing their names, became a possibility.

Genealogical DNA tests became more affordable and popular, including those who pretend to give genetic insight ("health test"). This presentation will show the possibilities of an autosomal-, Y- or mitochondrial test, including test strategies and tools for interpretation of the results.

A good collaboration will benefit all. Genealogists can provide familytree case studies, but the interpretation of the DNA results is (too) difficult for many of them. It would be great if geneticists and historical demographers could help and share their knowledge.

Biography: Martine Zoeteman-van Pelt is a genealogist and historian. She obtained her PhD in 2011 at Leiden University. Her research concerned the Leiden student population between 1575-1812. She works at the CBG|Center for Family History and is a genealogical DNA specialist. She also supervises historical crowdsourcing projects.

5. Jim Oeppen

*Interdisciplinary Center on Population Dynamics,
University of Southern Denmark*

Ascendant Genealogies as a Source for Demographic and Genetic Studies: some estimates of bias.

Demography has a 'descending' perspective, whereas most genealogies are 'ascending'. Failure to recognise this difference has led to inappropriate analyses of genealogical data. Demographers argue that ascendant genealogies are biased towards high levels of nuptiality, survival and fertility, and that the incidence of missing data is not random. This presentation addresses the first element: bias in perfectly recorded ascendant genealogies. I use both analytic and microsimulation methods from demography to estimate these biases. Where analytic methods are not available, microsimulation is used to create ascending genealogies, with descendant branches. The known demographic input parameters are then contrasted with what would be calculated from the ascending perspective. To illustrate the analysis I show some results for nineteenth century France.

6. Toomas Kivisild

Laboratory for Human Evolutionary Genetics, Department of Human Genetics, KU Leuven

Genetic connectedness between medieval and modern populations of Europe

Genetic ancestry and relatedness refer to different levels of population structure at which we can identify our common origins with others within and outside our own community. While mitochondrial DNA and Y chromosome analyses have been useful in allowing us to trace deep in time connections between uniparentally related individuals they cover only tiny fraction of the genetic links to our ancestors and living relatives. With whole genome analyses we can identify wide spectrum of ancestries and relationships not only between us and other living individuals but also with those from past populations. We need to proceed with caution as the identification of relatedness can be influenced by demographic events and mating customs in population histories. Advances in ancient DNA methods have enabled us to explore the genetic ancestries and relationships with past communities in ever increasing detail. In this presentation specific focus will be on approaches that link community structures extracted from large biobank-scale data from present-day populations of Estonia, the UK and Belgium with ancient genomes from Iron Age, Roman and Medieval periods

7. Eveline Altena, Risha Smeding, Kristiaan J van der Gaag, Rick H de Leeuw, Eileen Vaske, Paul Reusink, Yoan Diekmann, Mark G Thomas, Peter de Knijff

*Department Human Genetics
Leiden University Medical Center
The Netherlands*

The Dutch Y-chromosome from the Early Middle Ages to present day

In the last decade many large-scale DNA studies on prehistoric human skeletal remains have become available, but genetic data from historical European populations is still sparse while our knowledge of prehistoric processes is currently insufficient to explain the modern European genetic landscape. Here we present historical Y-chromosomal data from nearly 350 early medieval to Early Modern Period (450-1850 CE) individuals from 13 locations across the Netherlands. In combination with data from the present-day population of the Netherlands [1], we explore spatiotemporal patterns of genetic variation and test for population continuity, with which we contribute to the reconstruction of the male population history of the Netherlands over the past 1.5k years.

We observed statistically significant differences in the distribution of Y chromosome haplogroups over time and across space, indicating that their modern distributions formed only recently. We could not, however, reject population continuity, suggesting that drift needs to be considered as a key factor in these differences. We therefore caution against attributing frequency differences of genetic variants over time to specific historical events. However, we do observe Y-chromosomal haplogroup T at relatively high frequencies in late medieval Eindhoven, despite being very rare in the Netherlands and Europe

overall both in the past and today. This haplogroup has been hypothesized to have been brought to Europe along with the medieval Jewish diaspora. We may therefore have identified genetic signatures of a Jewish community in medieval Eindhoven; something that had not been inferred from the archaeological record.

8. Erling Häggström Lundevaller, Lotta Vikström

*Centre for Demographic and Ageing Research
Umeå University
Sweden*

The genetic diversity in Västerbotten, Sweden

Several studies have highlighted the low genetic diversity in Västerbotten and at the same time the pronounced genetic difference between the population of Västerbotten County in northern Sweden and the population in southern Sweden. This causes rare genetic variants to be more common which has medical relevance in several ways. The effect of these rare variants can be more easily studied under these conditions and knowledge of occurring genetic variants can help in diagnosing medical conditions. This makes it important to understand the development and geography of the population from a genetic perspective.

At least three possible explanations of the low genetic diversity and genetic difference, alone or in combination, can be suggested:

1. The population is a unique mix of different migration waves that might be relatively recent.
2. The population stems from a small founding population that might be relatively recent and since lived in relative isolation.
3. The population stems from quite old migrations that since remained in the area.

The use of gene tests to shed light on these matters is possible due to the rapid development of gene testing technology making mass testing of whole genomes possible. DNA tests give unique insight to the development of populations long before written sources. This can be used as an important complement to history, linguistics and archaeology in understanding how populations evolved. In this project we will focus

on using this developing DNA technology in combination with parish registers to shed light on the question:

How did the population of Västerbotten come to be?

1. Is the low genetic variability due to a small population base or cousin marriages 19:century. This can be answered combining analysis of DNA and parish registers.
2. How has demographics and migration shaped the population during the period with recorded sources, from 1700 onwards.
3. What can the Y chromosome and mitochondrial lineages as well as autosomal tests can tell us about the origin of the population before written sources. Can for example the population be divided in coastal, inland and settler groups?

Methods

A common method for analyzing the origin of a population is to take DNA samples from skeletons from historical sites such as graves. This approach has not been possible to use in northern Sweden as most remains has degraded so much that DNA testing is impossible. This calls for another approach to analyze the origin of the population of Västerbotten. Instead we will use three other sources to answer the questions stated:

- DDB: Parish registers from Västerbotten
- ACpop: modern DNA results from Västerbotten and
- SweGen DNA results from Sweden

9. Marian Beekman, Niels van den Berg

LUMC, Leiden University Medical Center

Longevity genetics: from quantitative trait definition to gene discovery

Longevity loci represent key mechanisms of a life-long decreased mortality, decreased morbidity, and compression of morbidity towards the end of life. However, identifying such loci has shown to be challenging. One of the most plausible reasons is the uncertainty in defining long-lived cases with the heritable longevity trait amongst long-living phenocopies, for example due to the epidemiological transition. This brought us to further investigate the transmission of the trait and the definition that separates cases expressing heritable longevity from phenocopies. We use three-generational mortality data from large datasets, UPDB (US), LINKS and HSN (both Netherlands). In data from the first two databases we studied 20,360 unselected families containing index persons, their parents, siblings, spouses, and children, comprising 314,819 individuals. Our analyses provide strong evidence that longevity is transmitted as a quantitative genetic trait among survivors up to the top 10% of their birth cohort. We subsequently showed a survival advantage, mounting to 31%, for individuals with top 10% surviving first and second-degree relatives in both databases and across generations, even in the presence of non-long-lived parents. To guide future genetic studies we subsequently used the third database where we constructed and explored a novel score (LRC score) that summarizes familial longevity. Currently we applied the novel longevity definitions to the Leiden Longevity Study and obtained promising results by conducting a genetic linkage analysis and prospectively investigating over 20 years of disease incidence.

10. Jits Van Straten

Independent researcher

Does Ashkenazic DNA refer to the Biblical Israelites?

Genetic research of Ashkenazic Jews cannot disregard the patrilineal system of the Biblical Israelites, the establishment of Ashkenazic Jews according to descent and according to religious rites, and the modern theory of population growth in Europe before 1800.

Investigation of mitochondrial DNA has shown that Ashkenazic Jews are mostly Europeans, and that there is a genetic difference between West and East European Ashkenazim.

Y chromosomes of Ashkenazic lay- Jews show that the Biblical Israelites cannot be descendants of an arch-father (Abraham) who lived between 3000 and 4000 years ago. A similar conclusion can be drawn regarding Aaron being the common ancestor of the Jewish priests.

11. Katrien Van de Vijver

*Royal Belgian Institute of Natural Sciences
Center for Archaeological Sciences
KU Leuven*

Contextualising skeletal analyses: Combining burial context and paleodemographic data to study the social composition on St. Rombout's cemetery, Mechelen (10th-18th centuries AD).

St. Rombout's churchyard in Mechelen was partially excavated between 2009 and 2011 and yielded over 4000 individual depositions, resulting in a large collection of skeletal human remains with a huge potential for the study of past populations. The cemetery goes back as far as the 10th century AD and it was used continuously until the end of the 18th century, offering a wide chronological overview. Four hundred individuals have so far been analysed in detail, which included the study of paleodemography and paleopathology to reconstruct the social composition and lifestyle of the population buried in this churchyard.

Skeletal data included age-at-death, sex and pathological changes which were compared and associated with variations in the burial context, such as the presence or absence of a coffin or multiple burial. Such contextual analyses, combining skeletal and archaeological data and interpreting the results within the historical context, allow the exploration of 'who' was buried in the churchyard and to observe different social groups with potential differences in life-style and physical health.

The cemetery was mainly used as the burial ground for inhabitants of St. Rombout's parish, but the contextual study suggests a change in the composition of the buried population over time and the presence of different groups. One of the main observations was the appearance of a large group of young individuals, adolescents (12-17 years of age) and mostly male, young adults (18-25 years of age), from the 15th-16th century layer onwards. The skeletal data differed from historical archival data, which may suggest the assemblage contains particular demographic groups. This large group of young individuals in the skeletal assemblage was more commonly associated with less expensive plain earth graves, plural burials and unusual body positions, suggesting a poorer socio-economic background. They often showed higher prevalences of growth disturbances, physical stress and disease. This group may be associated with servants, apprentices and possibly immigrants, and since many of the young adults were determined as male it may also reflect the 'extended male adolescence' known from medieval historical studies. However, a Spanish military hospital which was located near the cemetery between 1585 and 1715 AD may also have affected the composition of the buried population.

Like most skeletal collections, the assemblage excavated at St. Rombout's cemetery is not a direct representation of the living parish population. The study indicated that the excavated assemblage includes different social groups from likely the lower and middle classes, as well the possible presence of non-parishioners.

12. Denis Njari, Dubravka Božić Bogović, Eldina Lovaš

*University of Rijeka
Croatian Institute of History
University of Osijek*

Twins in the Calvinist Parish Registers in Eastern Croatia in the Second Half of the 18th and the First Half of the 19th Century

The research aimed to analyse the possibilities of applying the genealogical method in order to establish the hereditary aspects of the twin births, recorded in the oldest surviving registers of the Calvinist Hungarian population in the regions of Eastern Slavonia and Southern Baranya. The analysis included the data for the Calvinist Hungarian population of four villages in Eastern Slavonia (Hrastin, Laslovo, Korod and Retfala) and ten villages in Southern Baranya (Bilje, Kamenac, Karanac, Kneževi Vinogradi, Kopačevo, Kotlina, Lug, Vardarac, Suza and Zmajevac). The analysed register entries cover the period of one hundred years, the earliest being from the mid-18th century. However, the time scope of the analysis varies for the aforesaid settlements due to discontinuities regarding the preservation of the records and the way the books were kept. The results for these villages were compared with the results of other researches relevant to the mentioned time and period.

The characteristics of the register books as a source for the historical demography of the, so called, pre-statistical period, significantly limit the application of the genealogical method, and, as a result, they also limit the possibilities of determining of the hereditary aspects of the twin births in certain families. Besides the physical damage and illegibility, which do not present a significant obstacle for the analysis of the registers, the limited possibilities of the genealogical method applied in this case are the result of the

discontinuity of entries and, even more, the inability to achieve a completely ambiguous identification of individuals, who, during the pre-statistical period, were not assigned a unique identifier, as in the practice of the present-day registries. This problematic fact is even more aggravated by orthographic inconsistencies in writing first and family names, as well as the pronounced onomastic entropy, because of which we find a number of individuals with identical first and family names in different villages. Furthermore, the data which could enable a more certain identification (such as the names of parents, place of origin, age, house number, occupation etc.) were recorded unsystematically or not at all. Although, it is necessary to approach the historical sources, due to their limitations regarding the content and applicable methodology, with adequate caution, bearing in mind that the results should not be regarded as absolute and accurate figures, the received results of the register data analysis still are a valuable, and sometimes the only, source that provides insights in certain demographic facts, trends and enables case-studies for the pre-statistical period.

In the analysed register books of baptisms, the births of twins were explicitly noted by using adequate terminology, depending on whether the registers were kept in Latin or Hungarian (gemini, kettős gyermek, kettős, kettősök, két ep hassal). For all four analysed Slavonian villages, 220 out of 5304 children were registered as twins (4.15% of all entries), that is, 110 twin couples were born between 1758 and 1831, in the settlements for which preserved sources are available. As for the villages in Southern Baranya, from the mid-18th to the mid-19th century, the birth of 538 twins was registered (3.29% of 16356 births registered in the aforesaid period), that is 264 twin couples. Also, in the villages of Southern Baranya there were for cases of triplets. Besides the trends in the number of twin births during the analysed period, their share in the total number of births and their sex structure, within the framework of limited possibilities of applying the genealogical method in this case, repeated twin pregnancies were identified and the genetic predisposition for the twin pregnancies was confirmed both in the male and female lineage. Furthermore, there were several cases the twin couples born of the same parents.

13. Alexander Buczynski

Croatian Institute of History

Paper Trails of Everyday Lives in the Austrian Military Frontier

The Austrian Military Frontier (Militärgrenze, Vojna krajina) represents a borderland adjacent to the Ottoman Empire that stretched approximately 1,900 km from the Adriatic coast across the Balkans to the Carpathian Mountains. At its greatest extent in the mid 19th century this part of the Habsburg Monarchy comprised about 39,000 sq km of land and had a total of 1.3 million residents. From its establishment, in the 1520s, the Military Frontier, primarily served a defensive purpose, similar to that of the Great Wall of China and Roman Limes. Originally its purpose was to protect the Habsburg dominions against Ottoman attacks that passed through poorly defended Croatian highlands and Hungarian plains. Following the immense territorial expansion of the Habsburg Monarchy along its southeastern border after the second unsuccessful Ottoman siege of Vienna in 1683, this initial *raison d'être* of the Military Frontier changed and it primarily became a source of cheap and reliable military manpower for the Habsburgs.

The Frontier was almost exclusively governed by military authorities following direct orders given by the Court and highest military circles in Vienna: The Court War Council (Hofkriegsrat) prior to, and Ministry of War (Kriegsministerium) after 1848. This essentially unique military institution with a special structure and singular character, consisted of six main frontier regions, that were divided into 16 infantry and one hussar regiments. These frontier regiments (Grenzregimenter) and the companies they were composed of did not serve merely as tactical army units, but also as administrative districts.

The Frontier population consisted overwhelmingly of peasant-soldiers or Grenzer (krajišnici, graničari, grāniceri), as they were officially called. All men between 16 and 60 years of age, capable of bearing arms, served in the army. Town dwellers, craftsmen and merchants accounted for only 7% of the total population. The collective group identity shared by the Grenzer and produced by the Austrian imperial bureaucracy did not supersede divisions based on and driven by family, communal household, village and religious belief.

In 2019 a group of scholars from the Croatian Institute of History and the Institute for Anthropological Research teamed up to work out a multidisciplinary project proposal that will contribute to the understanding of everyday life of the Military Frontier population. To that end the project addresses three specific research fields – core issues – based on defining who these inhabitants were and what they

did, how they behaved and what they believed in: 1. Demography, organization and social order. 2. Health and wealth of the population, 3. Social and cultural identity in everyday life. The project aims to use data on the Grenzer population from three different sources: archival material, archaeological finds and skeletal remains, and methodologically combine various approaches, knowledges and skills of scholars with different expertise to assess these sources.

Research will specifically deal with the Karlovac Generalcy (Karlstädter Generalat) that was the oldest and best-organized part of the Military Frontier, covering 24% (9,500 sq km) of the entire area and containing 21% of the total population. Its territory roughly corresponds to today's Croatia's geographical regions of Lika, Kordun and part of its Littoral. The Karlovac Generalcy was divided into four regiments: Lika, Otočac, Ogulin and Slunj.

Historical analysis and demography will not concentrate primarily on the quantitative study of the Grenzer population but aims to present – prosopographically – actual, concrete individuals and families that lived in the Military Frontier. This will be done through constructing databases that include every soldier and officer mentioned in muster rolls (Musterlisten, Monatsakten, Standestabellen, Verpfleglisten) of the regiments and similar lists (so-called Conduite-Listen of officers refer to their special skills, character traits, behaviour, etc.), and through composing (if possible) complete biographies of them. Names, surnames, birth origin, religion, military rank and position, marital status, children, mobility (transfer from one unit to another), as well as different personal data (height, physical condition, age, hair color etc.) make a personal, direct and concrete approach possible.

Sociocultural analysis will focus on identities, images, stereotypes and representations of the Grenzer, as well as the civilian inhabitants of the Karlovac Generalcy, combining data from a variety of historical sources (reports, testimonies, public and personal documents, official and private correspondence), narrative sources (oral legends), literary sources (memoirs, biographies, travel writings) and visual sources (pictures, drawings, maps, newspapers, postcards).

Human biology and archeological analysis will examine the influences and interplay of bioanthropology data (body size parameters) and epidemiology data (distribution and the determinants of health-related states and events) with environmental influences (climatological natural hazards, war-related stress), nutrition (diet composition, interchange of periods of hunger and satiety), and sociocultural influences on the Frontier population. Applied biostatistical (biometrical) methods will utilize the basic elements of epidemiology, biology and computing science, to statistically explore characteristics in biological and biomedical phenomena.

Whenever possible results from each analysis will be compared to and/or combined with those of the other analyses. For instance, medical data of the Frontier military personnel were collected annually because the authorities wanted to assess the physical readiness of the enlisted Grenzer. Regular medical examination included measuring height, control of sight, diagnosis or description of illnesses and injuries, if present, and the overall assessment of combat readiness. Historical analysis of archival records along with human biology analysis of archaeological finds and skeletal remains can provide information about the history of medicine and health care, occurrence of specific diseases (particularly contagious), availability of health care as well as the environmental conditions that could have influenced individuals' health.

This paper will discuss the first-mentioned analysis, that is the paper trail leading to the reconstruction of the "historical population" and its possibilities for a multidisciplinary approach.

14. Jan Kok

*Radboud Universiteit Nijmegen
The Netherlands*

Genetic and shared-environment effects on stature and lifespan, a pedigree study of Dutch birth cohorts, 1785-1922

Historical demography is generally concerned with the changing economic, social and normative contexts of human behaviour and health outcomes. To most historical demographers, the 'genetic' component of behaviour and health is either unknown or assumed to be constant. However, several studies (e.g. Kohler et al 2002) point at the shift over time in the relative importance of environment and genes: in periods and social groups with strong normative or economic constraints on behaviour, the 'genetic potential' is often not realized. Therefore, to some extent, the waning of environmental constraints on heritability plays a role in changes in demographic outcomes over time.

Determining relative importance of heritability versus shared environment is the goal of twin studies, which have been applied to many psychological, behavioural and health outcomes. In historical demography, twin studies are quite rare relative to pedigree designs (Van den Berg et al. 2017). However, assessing the role of 'shared environment' is quite a challenge, as kin may live in different periods, and in different cultural and social settings. This may explain why research in this direction tends to focus on relatively closed and non-dynamic groups, as the Old Order Amish (Sorkina et al., 2005). Shared environment can also be approached by controlling for the age difference between, e.g. siblings. This method has been applied in the form of an 'extended DeFries-Fulker' model to fertility outcomes in 19th century Zeeland (a Dutch province) (Bras, Van Bavel & Mandemakers, 2013).

In the proposed paper, I experiment with their approach by looking at three different indicators of health: height at age 19, height at age 25, and life span after age 19. I use the genetic distance between (full, half and twin) brothers as well as cousins to answer the question in what socio-economic settings and periods the role of shared genes/heritability becomes more or less important relative to environmental factors. My data consists of about 3000 men culled from Texel island genealogies, which also include descendants of families who had left the island. These genealogies have been linked to the well-preserved records of the medical examinations of the military draft (age 19) as well as the civil guards (age 25).

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15. David Hugh-Jones, Abdel Abdellaoui, Oana Borcan, Pierre Chiappori

University of East Anglia

Trading social status for genetics in marriage markets: evidence from UK Biobank

If social status and genetic variants are both assets in marriage markets, then the two will become associated in spouse pairs, and will be passed on to subsequent generations together. This process provides a new explanation for the surprising persistence of inequality across generations, and for observed genetic differences across the distribution of socio-economic status. We model Social-Genetic Assortative Mating (SGAM) and test for its existence in a large genetically-informed survey. We compare spouses of individuals with different birth order, which is known to affect socio-economic status and which is exogenous to own genetic endowments among siblings. Spouses of earlier-born siblings have more genetic variants that predict educational attainment. We provide evidence that this effect is mediated by individuals' own educational attainment and income. Thus, environmental shocks to socio-economic status are reflected in the DNA of subsequent generations. SGAM reveals a new aspect of the inheritance of inequality in contemporary and historical societies.