

## **Information research workshop 2015**

### **Ancestry, ethnicity, race and DNA 1990-2015**

The technological revolution in genetic research during the last couple of decades has led to a boom in research on human genetic variation, including research on the genetic makeup, ancestry, and prehistory of ethnically, linguistically, or geographically defined human populations. As a result, historians and philosophers of science, social scientists, biological anthropologists, and geneticists have once again engaged into discussions about the reality, reemergence, or even the non-disappearance of race. This workshop turns the attention towards the notions of 'ethnicity', 'race', and 'ancestry' associated with the production of knowledge about human genetic variation, and will engage with questions such as: How are these concepts defined and used within diverse research areas such as human evolution, population movements and prehistory, biomedicine, and forensics; to what extent do they reflect social, cultural, or political ideas about ancestry, ethnicity, race and nationhood; and what are the social, cultural and/or political implications of their use?

The workshop is part of the research project "From Racial typology to DNA sequencing" (<http://www.ethnicityandrace.com/>), and includes only invited participants. All participants are asked to contribute with a paper based on their ongoing research. Each participant will get 30 minutes for presentation followed by another 30 minutes for discussion. All papers should be submitted two weeks before the workshop and all participants are expected to read the papers in advance.

As part of the workshop the museum will arrange a public discussion meeting, which includes a lecture by Jon Marks: *Tales of the ex-Apes: How We Think About Race*.

**Deadline for submitting manuscripts: 20. August**

**Please send your manuscript to**

[workshoprace@tekniskmuseum.no](mailto:workshoprace@tekniskmuseum.no)

After submitting your manuscript you will receive a link to a Dropbox folder where you can find the submitted manuscripts of all workshop participants (to be read in advance).

- Workshop begins at 2 p.m., on Thursday, September 3., and ends 4 p.m. on Saturday, September 5.
- Venue: Norsk Teknisk Museum:  
<http://www.tekniskmuseum.no/besok-oss/information-in-english>
- Accommodation: Thon Hotel Oslo Panorama  
<http://www.thonhotels.com/hotels/countrys/norway/oslo/thon-hotel-oslo-panorama/>

## Participants (*alphabetically*)

---

Yulia Egorova

<https://durham.academia.edu/YuliaEgorova>

Hallvard Fossheim

<http://www.ethnicityandrace.com/researchers.html>

Joan Fujimura

[http://www.ssc.wisc.edu/soc/faculty/show-person.php?person\\_id=16](http://www.ssc.wisc.edu/soc/faculty/show-person.php?person_id=16)

Erika Hagelberg

<http://www.ethnicityandrace.com/researchers.html>

<http://www.mn.uio.no/ibv/english/people/aca/erikaha/>

Jon Røyne Kyllingstad

<http://www.ethnicityandrace.com/researchers.html>

Åsa Larsson

<https://uppsala.academia.edu/AsaMLarsson>

Ageliki Lefkaditou

<http://www.ethnicityandrace.com/researchers.html>

Jonathan Marks

<http://anthropology.uncc.edu/marks-jonathan>

Amade M'charek

<http://www.uva.nl/over-de-uva/organisatie/medewerkers/content/m/-/a.a.mcharek/a.a.m-charek.html>

Catherine Nash

<http://www.geog.qmul.ac.uk/staff/nashc.html>

Ramya Rajagopalan

<http://biotechhistory.org/staff/ramya-rajagopalan/>

Marianne Sommer

<https://www.unilu.ch/fakultaeten/ksf/institute/seminar-fuer-kulturwissenschaften-und-wissenschaftsforschung/kulturwissenschaften/mitarbeitende/marianne-sommer/>

## Abstracts (*alphabetically*)

---

**Yulia Egorova**

### **Genomic sovereignty and genetic research on Jewish populations**

Past two decades witnessed an intensification of genetic research which attempted to engage with different aspects of Jewish history – DNA analysis was thus employed to cast light on the formation history of different Jewish communities around the world, from ‘mainstream’ to those who declared their affiliation to the Jewish people only in the past century. The aim of this paper is to consider the naturalizing tendencies of what became to be known as 'Jewish genetics' in a new analytical light by putting academic scholarship that has explored the sociocultural significance of DNA research conducted among Jewish communities, in dialogue with postcolonial theory and recent STS research on the concept of genomic sovereignty. More specifically, I will focus on genetic studies of Jewish history conducted in the period from 1990 to 2014 and will employ social theory research that has focused on the development of biotechnology in the context of the Global South to highlight new theoretical avenues for scholars looking for explanation of the interest that 'genetic history' seems to have attracted in Israeli society and among some members of the Jewish communities around the world.

**Hallvard Fossheim**

### **Past responsibility? Research, ethnicity, and the ethical relevance of history**

It is a common tenet of research ethics that the researcher has a set of responsibilities. Furthermore, it seems that certain breeches of the responsibilities attendant on the researcher can affect not only the standing of the individual researcher, but that of her discipline as well.

Perhaps less obviously, past actions of researchers might be said to have a corresponding effect on the activities of later-day research related activities, in extreme cases affecting even the standing of the results by somehow “tainting” them for future use or further research.

To the extent that it is correctly deemed a morally relevant relation, this tendency will be a general feature of most, if not all, research. What is particular about research producing results affecting our understanding of ethnicity, is that the research activity in this case contributes to defining a group of human beings. Such co-definition will by various mechanisms tend to modify not only the understanding of the group within the discipline, but among wider groups as well and, ultimately, the population at large. Not least, a partial result to be expected is that the research comes to co-define—directly and indirectly—how the group in question views itself. As such results are rarely unproblematically and purely non-normative, the effect will in practice include an evaluative dimension.

I will suggest that this state of affairs engenders a responsibility, on the part of the researcher investigating such issues, to familiarize herself not only with the history and identity of the group in question, but also with the history of interaction between the group in question and the discipline the researcher herself represents.

*Joan Fujimura*

### **Big Biology, infrastructures, and race: How genomics is being used to misrepresent race**

Do the new genomics undo our understandings of races as social constructions? This talk analyzes the latest statistical genomics technologies and data to demonstrate that genetic differences are clinal and therefore do not map onto racial categories. Why then are some geneticists, sociologists, and news media interpreting the new genomic data to say that race categories are biological and genetic categories? In the 1990s, geneticists began to build infrastructures as “short-cuts” to quickly find genomic markers that would lead them to the many genes they suspected were involved in common complex diseases. But each infrastructure was not enough, so they built another. At this time, we have layers of infrastructures, each supporting the other, each based on the previous. Genetics is now in a time of “big science,” “big data.” But infrastructures are not innocent. They carry with them practices, some of which have become embedded in the infrastructure. The Hapmap is one such infrastructure that incorporated notions of population differences that some have read as ancestral differences that some downstream users have read as racial differences. In a situation of uncertainty, ambiguity, and many folk assumptions about social differences, some geneticists, sociologists, media members, and members of various publics have read race into the differences that were constructed using algorithmic technologies of difference. We conduct an archaeology of the assumptions and practices built into the layers of infrastructure, which we use to argue against the reading of race into DNA clusters.

*Erika Hagelberg*

### **The biological origins of the Rapanui: past and present research**

Easter Island is the most remote inhabited island in the world. The origins of the Rapanui, the inhabitants of Easter Island, are of significant interest to historians, archaeologists and anthropologists. The Rapanui have probably been studied more than any other population worldwide, from blood group surveys to genome-wide analyses. The Norwegian explorer Thor Heyerdahl suggested an ultimate South American origin for the earliest Rapanui, but this view was not supported by the finding of Polynesian genetic markers in bones of the prehistoric inhabitants. Genetic studies on the living population have been hampered by the extreme depopulation of the island during the nineteenth century, and high levels of admixture with newcomers from South America in the past decades. High-resolution genetic analyses of DNA from the present-day population support the idea of Polynesian origins, but the Rapanui also carry a large proportion of European genes as the result of admixture since European contacts. They also carry genes which suggest that trans-Pacific contacts happened in prehistory, before the arrival of the Europeans. In this paper, I will outline the history of genetic research on Easter Island since the early decades of the twentieth century and discuss the implications of the findings for our understanding of the origins of the islanders. More importantly, I will present an ongoing study on Easter Island, and the perception and reactions of the Rapanui to current genetic research.

*Jon Røyne Kyllingstad*

### **Ethnicity and genes in North-Scandinavian prehistory**

In the 1980s, in parallel with a political and cultural revival among the Sami (the indigenous people in Northern Scandinavia) questions about ethnic groups and boundaries became an important issue among Norwegian archaeologists involved in the study of North-Scandinavian prehistory. Since the 1980s there has also been an increase in the genetic research on Scandinavian populations, focusing on questions about the prehistoric origins, migrations and settlement of ethnic groups, such as the Sami. Thus, archaeologists and geneticists have approached the same general issue about the history and

origin of ethnic groups in Northern Scandinavia, but they have often had diverging views on the concept of ethnicity. Archaeologists have been inspired by notions of ethnicity developed within social anthropology, in particular by Fredrik Barth. They have seen ethnic groups and boundaries as socio-cultural entities, and have used the archaeological evidence to explore the social and cultural processes that have given rise to these entities. The geneticists, on the other hand, have been studying the ethnic groups as genetically distinct populations, and have addressed questions about the genetic characteristics of these groups, their genetic relatedness to other ethnic groups and their histories of migrations and settlement. This paper discusses the relationship between archaeological concepts of culture and ethnicity and biological concepts of population and ancestry, and how these conceptualizations are related to public imaginations about identity and roots.

*Åsa Larsson*

### **Return of the ancestors. Ancient DNA, archaeology and the public**

Post WW2 archaeology underwent a strong reaction against the search for ancestors and national identities which had been an important part of the discipline up until that point. In the late 20<sup>th</sup> century culture and society were mainly seen as social constructions, and biology was kept out of prehistoric research. However, at the same time the study of ancient DNA was growing rapidly as a field within evolutionary biology. The study of the genetic makeup of prehistoric populations has captured the public's and media's interest in an unprecedented way, even catching geneticists off guard. In Sweden a huge project, "Atlas", is now underway to map the DNA of several hundred prehistoric individuals from the Stone Age to historic times. I will discuss how the new field of ancient DNA challenges what archaeology can and should study, and how it has altered the relationship between archaeologists on the one hand, and the public and the media on the other. How are Swedish researchers in the Atlas project tackling the sensitive subject with possible political ramifications? Are genetics replacing the role history used to play in people's lives? If so, should archaeologists join in, dig in, or try to find a path in between?

*Ageliki Lefkadiou*

### **One to fit them all: biological reconstructions of a Greek past**

This paper takes its inspiration from the publication of the first semi-popular book on the genetic history of the Greeks to ask how our conceptions of collective identities such as nation, ethnic group, or population are challenged, reshaped or completely altered by genetic studies. In the absence of an established research tradition on human genetic variation and genetic diversity within Greece, such publications seem to perpetuate the sensational appeal of science, and especially genetics. At the same time, however, they are part of debates over the categories of race and ethnicity both within and outside academia. By focusing on this recent publication and how it has been featured in public press, public fora, and scholarly discussions, my aim is twofold: a) to examine how the Greeks have been constructed as a subject of genetic research, and b) to assess how this kind of research deals with older categorizations and understand how it gains its legitimacy.

*Jonathan Marks*

### **Race, botanical metaphors, and the bio-politics of human ancestry**

A narrative that explains who we are and how we got this way is generally known as an origin myth, and these universally are value-laden narratives. The reason scientific narratives of human evolution and human variation are publicly contested (by creationists and racists, respectively) is that these scientific narratives have cultural valence that transcends their status as scientific knowledge. I will argue that when the first generation of Darwinians connected Europeans to apes through the non-

European races in order to counter the absence (in the 1860s) of a fossil record linking humans to apes, they incurred a debt that evolutionary biologists will forever continue to repay. From the beginning, then, one crucial aspect of any narrative of human evolution is the relationship between human diversity and human evolution. This distinction in turn hinges critically on identifying species in the human fossil record – this, itself, a bio-cultural endeavor. Present-day human populations today are genetically connected in complex ways, and it is likely that they were connected in the distant past as well. This implies that the relationships among human populations tens or hundreds of thousands of years ago are being poorly served by the metaphor of a branching evolutionary tree.

*Amade M'Charek*

#### **Doing Time: DNA and the dis/continuous city**

DNA has become part of everyday contemporary life. Its role in medical and scientific practices is ever growing and it increasingly features as technology for the identification of individuals and populations. Recently we even see DNA getting involved in the enactment of city identities.

This paper attends to a remarkable collaboration between geneticists, archaeologists and a city archivist and analyses the reshaping of identity of the city of Vlaardingen, situated in the southwest of the Netherlands. We follow the quest for the 'Oer-Vlaardinger' and examine how a DNA match helps to undo a 1000 year distance while simultaneously recreating it through a chronological timeline. DNA thus helps to fold and unfold time.

By situating DNA and following it in practices it becomes clear how DNA in this case is not so much figured as a biological 'essence' but rather as a technology that is able to create temporal distance and proximity.

*Catherine Nash*

#### **From race to geography: geographical perspectives on accounts of genetic distance and difference**

Human population geneticists have recently begun to use the term 'genography' to describe the geographical patterning or 'structure' of human genetic variation and its study. This paper brings a critical geographical perspective on scale and spatial designations and categorisations to bear on accounts of the genetic structure of human populations. While there has been considerable critical attention paid to the ways in which accounts of human genetic variation at the global scale reproduce continental categories of genetic difference that bear striking similarity to conventional racial categories, I argue here for the importance of considering the making of ideas of difference and belonging through shared ancestry at other scales, across Europe for example, or within countries, regions or localities. I do so by considering both the implications of the idea of foundational geography of gradients of genetic distance in relation to the politics of identity and nationhood, and geneticists' efforts to produce accounts of the structure of that graded variation through the use of geographical identifiers – countries, regions, localities - or though the ethnic or national designation of their inhabitants. Geographical labels have been figured as neutral alternatives to more controversial racial or ethnic categories in human population genetics. However, though these 'genographies' are not a matter of visible difference or hierarchical races they are about ideas of locally rooted and ancestrally bound groups that can suggest 'natural', and sometimes more overtly racialised, ideas of belonging and non-belonging. In this paper I focus on recent accounts of the genography of Europe as a whole, and the United Kingdom more specifically, to explore the nature and implications of these genetic geographies of human ancestral relatedness.

**Ramya Rajagopalan**

### **Variations on a chip: SNPs and the making of populations in human genetic variation studies**

In the aftermath of the Human Genome Project, geneticists have focused intensively on DNA variation to try to locate and explain common complex diseases. Geneticists now routinely scan thousands of human genomes and examine millions of points of difference in human DNA, known as single nucleotide polymorphisms, or “SNPs.” Using new statistical tools and large sample sizes, SNPs have become the foundation of a set of tools used to produce, bound, and circumscribe “population” groups. Genetic variation has thus become a potent lever for conceptualizing and reconfiguring notions of difference that produce and often reproduce sociocultural categories of difference.

This paper traces the technological, methodological and conceptual developments in the 1990s that established SNPs as key focal points for locating human difference in the genome. It does so by examining the production of SNPs and the “SNP chip,” a high-throughput technology for assessing SNP variations among individuals and groups. How did SNP chips become instruments for measuring genetic difference? How did their design, production and use serve to reinforce ideas and assumptions about the boundaries and limits of certain population groups? Tracking the development of the SNP chip reveals how notions of human difference and genetic diversity have become encoded and embedded within the new technologies of genomics. By examining how SNP chips are used to operationalize population genetic theories about ancestry, DNA variation, and race, this paper illuminates the historical roots of the contemporary ways in which human groups have come to be viewed in terms of differences at the level of their DNA.

**Marianne Sommer**

### **"What's in a tree? On the geneticization of an icon"**

From the 1960s, mathematical and computational tools have been developed to arrive at human population-trees from various kinds of serological and molecular data. In my talk, I discuss aspects of the history of such tree building. In order to better understand the issues involved in recent genomic tree building, I have to look back at their precedents from the early blood-group studies onward. Tree iconography has been abundant throughout the history of molecular and genetic anthropology, and in integrative efforts, also trees based on other than molecular data, for example linguistic diagrams, appear in conjunction with particular approaches and interpretations of human origins and diversity. At the basis of the population-tree are technologies to analyze distributions, movements, series, combinations, as well as instruments to render visible, to register, to differentiate and to compare. Tree building is one among other disciplinary technologies that ensure the ordering of human diversity. Population-trees are condensations of elaborate theories and scenarios, although they in themselves do not lay bare the decisions on which their particular way of branching and systematization is based. But despite the highly specialized knowledge, theoretical assumptions, and algorithms and computer programs that may inform such diagrams, due to the icon's situatedness in cultural history, they seem readily understandable. Among the processes behind the surface of the genetic tree-diagram are population identification, sampling, and labeling. On the other hand, very conspicuous but no less burdened with problems are the separate branches that may render isolated groups of people who have in reality been interacting and converging.

## Preliminary schedule research workshop 2015

### Thursday, 3 September

---

**13.00 – 14.00** *Arrival at the museum (welcome coffee/tea)*

**14.00 – 16.15** *Session 1*

*Moderator:* Jon Røyne Kyllingstad (also: short presentation of the background of the project and the workshop)

Paper 1: **Catherine Nash**, *“From race to genography: geographical perspectives on accounts of genetic distance and difference”*, commentator: Hallvard Fosshem

Paper 2: **Ageliki Lefkadiou**, *“One to fit them all: biological reconstructions of a Greek past”*, commentator: Yulia Egorova

**16.15 – 16.30** *Coffee/tea break*

**16.30 – 18.30** *Session 2*

Paper 3: **Amade M’Charek**,  
*“Doing Time: DNA and the dis/continuous city”*, commentator: Åsa Larsson

Paper 4: **Erika Hagelberg**,  
*“The biological origins of the Rapanui: past and present research”*, commentator: Jon Marks

**19.30 – 21.00** *Dinner in central Oslo*

### Friday, 4 September

---

**09.00 – 11.00** *Session 3*

*Moderator:* Amade M’Charek

Paper 5: **Jon Røyne Kyllingstad**, *“Ethnicity and genes in North-Scandinavian prehistory”*, commentator: Catherine Nash

Paper 6: **Yulia Egorova**, *“Genomic sovereignty and genetic research on Jewish populations”*, commentator: Ramya Rajagopalan

**11.00 – 12.00** *Lunch and brief introduction to the Museum*

**12.00 – 14.00 Session 4**

*Moderator: Ageliki Lefkadiou*

Paper 7: **Hallvard Fossheim**, *“Past responsibility? Research, ethnicity, and the ethical relevance of history”*, commentator: Amade M’Charek

Paper 8: **Åsa Larsson**, *“Return of the Ancestors. Ancient DNA, Archaeology and the Public”*, commentator: Erika Hagelberg

**14.00 – 14.30 Coffee/tea break**

**14.30 – 16.30 Session 5**

*Moderator: Åsa Larsson*

Paper 9: **Joan Fujimura**, *“Big Biology, Infrastructures, and Race: How genomics is being used to misrepresent race”*, commentator: Ageliki Lefkadiou

Paper 10: **Ramya Rajagopalan**, *“Variations on a Chip: SNPs and the Making of Populations in Human Genetic Variation Studies”*, commentator: Marianne Sommer

**17.00 – 18.30 Dinner at the museum**

**19.00 – 21:00 Public lecture at the museum by Jon Marks**

**Saturday, 5 September**

---

**10:00 – 12.00 Session 6**

*Moderator: Hallvard Fossheim*

Paper 11: **Marianne Sommer**, *“What's in a tree? On the geneticization of an icon”*, commentator: Joan Fujimura

Paper 12: **Jon Marks**, *“Race, botanical metaphors, and the bio-politics of human ancestry”*, commentator: Jon Røyne Kyllingstad

**12.00 – 13.00 Lunch**

**13.00 – 15.00 Session 7**

Summing up by **Alan Goodman** and general discussion

Funded by: Research Council of Norway -  
Cultural Conditions Underlying Social Change (SAMKUL).

