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SPECIAL TOPIC

Next generation sequencing

Challenges for science and society

Next generation sequencing has led to major knowledge gains in the molecular life sciences. But the new technology provides data that pose new challenges to both science and society. New fields of research are emerging and questions of identity on the basis of genetic analyses are being negotiated.

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INTRODUCTION

New sequencing methods

New data and new challenges

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Abstract • Today, DNA sequencing is part of the standard repertoire of biological and medical research. Next generation sequencing (NGS), established around the mid-2000s, was the main catalyst for this development. NGS has led to major knowledge gains in the molecular life sciences. However, the new technology provides data that pose new challenges that both science and society still must learn to deal with. A technology-driven dynamic can already be observed in this field, leading to transformation processes in science, where new fields of research are emerging, but also in society, where questions of identity are increasingly being negotiated based on genetic analyses.

Neue Sequenzierungsmethoden. *Neue Daten und neue Herausforderungen*

Zusammenfassung • *Die Sequenzierung von DNA gehört heute zum Standardrepertoire der biologischen und medizinischen Forschung. Das um die Mitte der 2000er-Jahre etablierte Next Generation Sequencing (NGS) war der wichtigste Auslöser für diese Entwicklung. NGS führte zu großen Erkenntnisgewinnen in den molekularen Biowissenschaften. Die neue Technologie liefert allerdings Daten, die Wissenschaft und Gesellschaft vor neue Herausforderungen stellen. Schon jetzt lässt sich in diesem Feld eine technikgetriebene Eigendynamik feststellen, die zu Transformationsprozessen in der Wissenschaft führt, wo sich neue Forschungsfelder herausbilden, aber auch in der Gesellschaft, in der Fragen von Identität zunehmend anhand von genetischen Analysen verhandelt werden.*

Keywords • *NGS, technoscience, transformation processes, archaeogenetics*

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Introduction

These days, everyone is talking about genomes, mutants, variants, DNA, and sequencing. Most people, at least here in Germany, are now familiar with cryptic rows of letters and numbers such as B.1.1.7, B.1.351, and P1 – these are three variants of the SARS-CoV-2 coronavirus, which has been running rampant worldwide since 2020. In January 2021, as many other countries had already done, the German government and the Robert Koch Institute (RKI) decided to carry out more extensive genome sequencing of SARS-CoV-2 in order to discover new virus variants and to track their frequency and spread. This expansion of what is known as "molecular surveillance" in Germany is linked to the goal of increasing the rate of genome sequencing and ensuring that approximately five percent of positive samples are sequenced (Robert Koch Institut 2021, p. 1). The current success of rapid and, above all, mass sequencing of SARS-CoV-2 is in part due to the methods of next generation sequencing (NGS), which have been "adapted to the SARS-CoV-2 paradigm" and have been "shown to be applicable to a wide variety of associated biological questions. The rate of data production and analysis has been unprecedented and would have been inconceivable only a few years ago." (Chiara et al. 2021, p. 626)

Without any doubt and as this example illustrates well, DNA sequencing has become part of the common toolkit of biological and medical research. NGS, which emerged in the mid-2000s, was the most important catalyst for this development. NGS procedures allow for the sequencing of many DNA molecules simultaneously and cost-effectively. This new procedure and the rapidly decreasing costs of sequencing generated significant impacts. The rate of knowledge generation expanded rapidly in molecular-based biosciences, particularly evolutionary research but also pharmacogenomics, oncology, reproductive medicine, and epigenetics.

When this TATuP special topic was conceived in the winter of 2019/20, SARS-CoV-2 had not yet reached Central Europe. Our focus was on the social, cultural, economic, and political

consequences of the "molecularization of science and society" (Bösl 2017, p. 339, our translation) that accompanied the emergence of NGS. Thus, even then, we had less in mind the 'classical' sectors for the application of gene sequencing such as medicine, pharmacology, and forensics. On the contrary, from the interdisciplinary perspective of technology assessment (TA) we were specifically looking for contributions relating to fields of application that defy disciplinary classification and cross traditional boundaries, as well as papers dealing with the consequences for these fields.

Consequently, the focus of the published papers is not on NGS per se or conflicts relating to its implementation. Rather, the authors deal with the data obtained by means of NGS and the associated scientific, social, and ethical impacts and challenges. Ultimately, the new technology provides new data that science and society still have to learn to deal with. The impact of the technology becomes apparent indirectly – both through the data obtained and the way we deal with it. In terms of science and technology studies, NGS can be considered a new 'actor' that has emerged, that is 'getting involved' in many fields – some of which are far removed from medicine – and that has changed "the way different groups imagine human identities, such as race, gender, kinship, citizenship and disease risk" (McGonigle and Benjamin 2016, p. 1). The papers published in this TATuP special topic engage with debates of this kind.

Next generation sequencing provides new data that science and society still have to learn to deal with.

New cross-cutting fields

NGS is used in many fields today. The medical sector is undoubtedly central, but there are, in addition, several research areas and cross-cutting fields that first emerged as a result of NGS. Thanks to technological innovation, these new interdisciplinary fields have acquired a place in academia in just a few years. The field alternately known as archaeogenetics or palaeogenetics, which traces the historical biological development of not only humans but also animals and other fossil organisms through the changes in their DNA, is part of this development. Research based on sampling and sequencing ancient DNA (aDNA) has triggered a great deal of "hype" (Jones and Bösl 2021) within and outside the academic world in the last ten years. Archaeogenetics, with its "combination of enticing cultural imagery and the authority of genetics" is proving to be a successful formula for drawing attention to the new field (Källén et al. 2019, p. 83; see also Samida 2020, 2021, pp. 86–111).

Archaeogenetics thus challenges the established historical sciences on two accounts: first, by claiming to conduct historical research and second, by producing provoking headlines about historical issues. One of its most prominent representatives, David Reich (2018, p. xxiii), emphasized predictively that the "ancient DNA revolution is rapidly disrupting our assumptions of the past". However, the extent to which these "assumptions" are actually 'blown up' is currently the subject of intensive debates. These debates are accompanied by discussions on disciplinary self-conceptions and epistemological issues, including discussions of a fundamental nature, e. g., the relationship between the 'two cultures' – the sciences and the humanities – in terms of C. P. Snow (Bösl 2017; Meier and Patzold 2021; Samida 2021). As a laboratory science, archaeogenetics also makes claims to objectivity and credibility, which in turn provokes criticism from well-established disciplines such as history and (prehistoric) archaeology (see, for example, debates in special issues of Medieval Worlds 2016, NTM 2018 and 2019, World Archaeology 2019, and recently Journal of Social Archaeology 2021).

Struggles over the interpretation of findings and disciplinary boundaries as well as heated debates about terms and concepts are evident. Moreover, the fabrication of ethnicities by archaeogeneticists as immediately disseminated in the media, whether intentionally or not, creates not only a false impression of stable and collective identities from prehistoric times to the present day, but is also increasingly misused in debates over identity politics (Maran, in press). Recently, Catherine J. Frieman and Daniela Hofmann (2019) impressively analyzed how right-wing and racist activists make use of the results of archaeogenetic studies. In the context of contemporary debates on migration, these activists simultaneously propagate an invasion from the east while also promoting "a narrative of (biological and social) domination by pale, blue-eyed men" (ibid. p. 529). Arguments that rest on ethnic essentialism and biological determinism are increasingly prominent (Furholt 2020). This is a matter of concern not only for scientific discussions but also for social and political debates.

Lab technologies and established disciplines

In practical terms, NGS is just a new technology that is being put to use in fields with long research traditions. It is being used to approach questions and hypotheses that, in many cases, have long been part of these fields. In archaeogenetics, for example, the techniques of taking and processing samples were developed in the late 1980s and the 1990s and have not undergone much modification since then. Moreover, the methodol-

ogy associated with stratigraphy, dating, prospection, i. e. the entire field of archaeology, is not new either, nor has it been revised or altered because of or to better suit NGS. Sequencing also relies on samples being collected, stored, and processed, as archaeogenetic studies are inconceivable without archaeological context information. While archaeological methodology is obviously also subject to historical change in general, there is much more of the old than the new in NGS-based archaeogenetics. The importance of substantial context information is by no means diminished by NGS. On the contrary, the whole business of archaeogenetics is coming to rely even more on 'old', established methodologies, precisely because new sequencing techniques are producing new source material in hitherto unknown quantities. The incorporation of the new into the old in this way is a phenomenon widely known to historians of technology, even though historiography itself has long been so focused on innovation that it has ignored old, tried-and-trusted approaches (Edgerton 2006; Möser 2010).

As much as geneticists would like to, they cannot solve the paramount problem of archaeology and historiography – no technological advance or ingenuity can overcome the lack of source material and its characteristic selectivity, fragmentariness, and perspectivity. Neither NGS nor any other technoscience can eliminate such fundamental limitations, which are as old as the disciplines themselves. In most cases, the problems to which geneticists are applying their state-of-the-art technology have been there for a long time. And while high-end technology can often offer alternative ways to look at them, the basic problem remains. Moreover, just like the technologies that preceded it, NGS has limits. One of these limits, or rather a characteristic of lab technology in general, is that it can only help to produce proxy data which, later on, has to be interpreted using a different set of methods.

The importance of substantial context information is by no means diminished by next generation sequencing.

Technology-driven processes

The example of archaeogenetics stands pars pro toto for other, very similar developments that to a certain extent are all manifestations of the same technology-driven momentum. What do we mean by this? TA proposes the "systematic identification and evaluation of technical, environmental, economic, social, cultural, and psychological effects associated with the production, use, and exploitation of technologies" (Renn 2011, pp. 64, our translation). However, TA's promise to assess technological effects in advance is hardly feasible. This applies equally to methods such as NGS, in particular, and to the "uncanny development of genomic investigations" (Hagner 2012, p. 49, our translation) in general. Ambivalence, complexity, and uncertainty, as Ortwin Renn (2011, p. 65) has put it, are part of the attendant circumstances of TA, because opportunities and risks become apparent only gradually over time. In terms of NGS, this means that every new technical procedure is *ambivalent* – there are never only positive aspects, but also always negative ones. At first glance, the current sequencing of the coronavirus to uncover potential mutants falls into the 'positive' category and is rarely questioned. However, police investigations using DNA to identify the skin color of a suspect are sensitive and trigger critical questions. *Complexity* and *uncertainty*, in turn, are reflected in, among other things, computational operations, statistical procedures, and modeling of new data sets.

An example from the arts illustrates this quite impressively. Heather Dewey-Hagborg's 2017 installation "Probably Chelsea" presents thirty different possible portraits of the famous whistleblower Chelsea E. Manning. These portraits, however, were algorithmically modeled based on an analysis of Manning's DNA before being 3D printed. This example shows not only "how subjective the act of reading DNA really is" (Dewey-Hagborg 2017, p. 11) but also that "there exists an array of possible identities that are all simultaneously correct" (Schrock 2017, p. 7).

The novel methods of NGS, which were developed in molecular biology, do not only matter for medical research and diagnostics and for archaeogenetics. NGS makes the use of DNA analysis possible in numerous fields and has led to increasing commercialization in the private sector. This includes the hobbyist arena of genealogical research, which – once considered dusty and outdated – has become a rapidly growing market. Private genetic analyses (*direct-to-consumer genetic testing*) – including medical services – are in great demand and have become everyday commodities. Enterprises such as "MyHeritage" and "Ancestry DNA" not only act as large-scale collectors of genetic data, but also create specific concepts of ancestry and heredity in their marketing activities. This sort of 'entertainment genetics' is closely connected to questions of identity, which undoubtedly both draw from and impact on current identity discourses. This concerns individual as well as collective dimensions of identity formation (Sommer and Krüger 2011). Accordingly, 'biogeographical narratives' certainly create and convey forms of evidence but often remain unquestioned and unreflective.

Recently, quite a few empirical studies have made an effort to research how individuals deal with this information and incorporate it into their identity work. A new cultural studies paper (Strand and Källèn 2021) studied how genetic ancestry testing (GAT) clients from the UK, USA, and Sweden interpreted their

test results. The interviewees, including some accomplished genealogists, all had at least vaguely imagined a priori that they were testing for genetic traces of their 'Scandinavian' origin. As it turned out, they dealt selectively and quite differently with the genetic data they obtained, which suggests that identity work is an individual and rather ambivalent process, one that depends on an individual's preconceptions, interests, and very specific goals. Interestingly, however, most brought up the concept of the 'Viking' and attributed traits of their own character and behavior and aspects of their own biographies to their concept of a typical 'Viking'. Those concepts varied, however, between an image of Vikings as brutal conquerors and plunderers, and one that sees them as ingenious inventors, seafarers, and skilled traders. Some attributed family violence to what they thought of as their Viking ancestry. The contrasting popular concepts and images of the Viking reproduced here have, in fact, no empirical basis in archaeology or history. The image of Vikings as an ethnic group of violent, brave, adventurous conquerors was created in the 19th century in Northern Europe under the influence of Romantic nationalism. There is however no evidence from archaeological and historical sources that an ethnically cohesive group of this kind ever existed in Northern Europe. The groups that did live there did not even usually see themselves as forming a socio-cultural unity. And it is not possible to define 'the Viking' in genetic terms. Although the interviews had fairly varied ideas about the characteristics of Vikings, they all regarded these as determined by genetics. The test results were used to reinforce preexisting identity constructs. Another remarkable result of the study is that some participants described feeling physically close to the Vikings – even though the latter never actually existed in the way the interviewees perceived them (Strand and Källèn 2021).

Technoscience and transformation processes

The example of genetic ancestry testing also sheds light on how we experience the world around us through technoscience. Not only are our lives completely saturated with technology, we also make sense of the world via technologies (Nye 2006; Böhme 2007; Nordmann 2008). While this may be obvious when we consider a phenomenon such as surfing the web, it is also true for technologies such as NGS. NGS appears to give us access to the molecular dimension of the world, which would otherwise be out of reach. The world of molecules is becoming tangible for many now, as molecular genetic data is being communicated to the public via a growing variety of channels.

As the above clearly shows, DNA sequencing methods developed in molecular genetics have triggered transformation processes for both the general public, and in established fields of research. Nevertheless, one has to ask how much old there really is in all the new. As several authors in this TATuP special topic suggest, NGS has brought about a change of perspectives: from the taxonomic or phylogenetic dimension, i. e. the genetic relationships among various biological species, to the (meta-) genomic dimension of organisms in microbial ecology and from a symptoms-based clinical stance to a molecular-genetic-virological-epidemiological perspective in the research and management of a pandemic. NGS provides a genomic view of organisms. Such shifts in perspective change what we think a certain phenomenon consists of and also determine how researchers and practitioners deal with it. Obviously, NGS has made sequencing fast and cheap and has given access to a new level – the genome. Whether one needs to regard this as revolutionary, as Frieman and Brück do in their contribution to this issue, is certainly debatable.

Contributions to this TATuP special topic

Since DNA sequencing is significant for numerous fields, this special topic of TATuP brings together a broad range of perspectives from a variety of disciplines and cross-cutting fields. The authors discuss discourses and practices, actors and their networks, as well as concepts and specific (research) interests. In doing so, all address the various benefits, limitations, and inherent ambivalences of technoscience as manifested in NGS. They analyze how new technological options bring new social challenges and commitments as well as unintended effects.

Karen Kastenhofer addresses the molecular-genetic dimension of the Covid-19 pandemic from the perspective of TA and the sociology of science and technology. In our everyday experience of the pandemic, Polymerase chain reaction (PCR) is on everyone's lips and features prominently in the media. The PCR test, in particular, may become an icon of our time. NGS-based practices are far less present in everyday life but are of special importance to virology and epidemiology, as they capture the entire viral genome and thus enable scientists to detect variants and mutations. Geneticists and virologists are constantly trying to analyze the virus at the genetic level, to track its mutations, and to chart its genetic evolution. This molecular genetic knowledge is being used to develop not just test methods and novel vaccines but also new risk management concepts. NGS plays an essential role in this, as only it allows genome-wide study of the virus and the investigation of mutations. NGS leads to enormous increases in knowledge in a short time as well as to huge amounts of data made available in international databases. This happens within a new and potentially limitless network of actors, instruments, practices, rules, ontologies, and objects where SARS-CoV-2 is processed and as a knowledge artifact co-produced. Kastenhofer uses the idea of the "seamless web" to classify this phenomenon. The weak point of this highly efficient network, she points out, is the exclusion of clinical practice. Kastenhofer argues that while the new virus is thus conceptualized and stabilized as a molecular-genetic-virological-epidemiological event and the molecular genetic dimension of the pan-

demic is central to our understanding and management of the pandemic, other dimensions take a back seat.

Historians of science may find this an interesting parallel to the shift in focus that occurred after Alexandre Yersin, a Swiss and French physician, identified the causal agent of plague in 1896, a bacillus that was later named *Yersinia pestis*. In the case of plague, the diagnosis of the disease shifted from the clinical symptoms towards the bacteriological evidence. What plague is and what it means has been largely considered on the bacteriological level ever since. In the meantime, in the last 30 years, the focus in plague research and practice has again shifted: towards the perspective of molecular genetics.

Metagenomics, i. e., the analysis of the collective genomic content of a certain sample containing a variety of organisms (microbial communities), has only become feasible because of NGS. Robert Meunier and Saliha Bayır discuss the transformation processes that have affected microbial ecology (the study of microorganisms in relation to their environment and to one another) and especially agricultural soil research as a consequence. From their philosophy-of-science perspective, they argue that metagenomcis is greatly impacting agricultural research and practice because it gives access to other aspects of microbial life than the earlier culture-based or PCR methodologies. Metagenomics has changed both basic science and, consequently, design science, i. e., the type of science that produces recommendations for interventions in, in this case, agricultural practice. While culture-based approaches focused on taxonomies and physiology and PCR sequencing produced data on the phylogeny of single organisms, metagenomic approaches allow the focus to move onto interacting microbial communities, the microbiome, and their genetic structures and functions. NGS made possible a systems approach and a shift from studying structure to studying the integrated functional units of microbial communities, which were now understood to a large extent through the lens of their collective genome. These were then transferred to and adopted by agricultural science, whose focus now is on the genomic dimension of microbes rather than their taxonomy or phylogeny. This change of perspectives shaped the perception of ecosystems and thus the interventions devised by agricultural science and the technical norms proposed to farmers, politics, and businesses. While many of these intervention concepts are still to be put into real-world practice, situation assessment including, e. g., soil quality indicators has already been changed by the metagenomic approach, as have the goals and values of agricultural studies.

The sociologists Alexander Lang and Florian Winkler explore aspects of direct-to-consumer genetic testing, while focusing particularly on elements of co-construction and the process by which ancestry is 'produced'. Their analysis of this kind of 'doing ancestry' is based, on the one hand, on a review of existing empirical studies and, on the other, on an explorative qualitative inquiry that includes analysis of relevant websites of popular companies (e. g. "MyHeritage"), qualitative expert interviews, and auto-ethnographic self-observation. Using this mix of methods, the authors present interesting results concerning the companies and their users. In their self-portrayal, the companies seek to present themselves as apolitical and promote their products as tools that produce objective facts. The users, in turn, (re)interpret the test results in an open and playful manner, while incorporating them into their genealogies and lives.

Using the example of 'Jewishness', Noa Sophie Kohler points to ways in which genetic ancestry testing is used for political and religious purposes. A large number of immigrants from the former Soviet Union are seeking to legally 'prove' their 'Jewishness' to the State of Israel, as this has consequences for their civil rights. However, most of them do not have any evidence about their maternal ancestors, which, in accordance with traditional law, the Chief Rabbinate considers to be the main determining factor. Here, genetic testing not only comes to the fore as a central method, but also becomes an important tool for re-claiming Jewish identity. In this respect, DNA is an important actor in this process of negotiation.

From an archaeological point of view, Stefan Burmeister deals with the concept of genetic ancestry. Instead of the concept of race that has been problematized in biology and the social sciences for decades, the term "genetic ancestry" seems at first glance as a harmless alternative. However, Burmeister observes its increasing influence on public discourse, particularly when it comes to identity politics. Archaeogenetics is not entirely innocent in this process, because the careless and often largely unreflecting use of archaeological, ethnic, and genetic categories and concepts opens the door for xenophobic and racist discourses.

Next generation sequencing poses massive challenges to science and society.

Catherine J. Frieman and Joanna Brück discuss archaeogenetic approaches to both horizontal and vertical aspects of kinship. NGS has accelerated the process of generating data on genetic relations and has provided geneticists with an abundance of high-resolution data for a growing number of individuals, a fact that Frieman and Brück call revolutionary. However, as they point out, NGS does not mean that kinship research is now a closed book, but rather that a new class of evidence is available. Genetic evidence of purely genetic relationships between individuals and groups has to be put into relation with other kinds of evidence, such as those generated by archaeology, ethnogra-

phy, and social anthropology. The authors highlight the fact that genetic data alone cannot contribute anything to the understanding of non-genetic relations between people. This data may, however, form part of an integrated, multi-perspective approach to kinship. Kinship, they argue, is likely to be composed by a variety of factors such as care, obligations, beliefs, dependencies, and genetics. The relative importance of these components may vary by period and culture. So neither should genetic relations be equated with kinship in general nor can kinship itself be considered universal. Frieman and Brück also stress that studies on genetic relations inevitably rely on heterosexual reproduction and thus have an inevitable heteronormative tendency. Geneticists working on lineages and ancestry cannot address anything but biological reproduction. And this is a very limited perspective. That is problematic, because as social anthropology and ethnography suggest, there have been many other forms of kinship in past and present societies in which heterosexual reproduction is not the most significant factor at all. So, the authors dig in their heels to protest against reductionism and promote a more complex concept of kinship instead, one that encompasses both genetic and non-genetic relations. Frieman and Brück make another important point: Genetic research into kinship, recently refined and accelerated by NGS, means that archaeologists need to become more active. They should take recent advances in genetics as an incentive to put more effort into researching kinship themselves. Studies should be set up that analyze housing, hoards, food-sharing, burials and other practices to see what these may tell us about how kinship was perceived and practiced. The authors present recent examples of archaeological papers that consider such social practices as part of making kin. From their article it is obvious that the combined efforts of archaeology and genetics may produce complex pictures of kinmaking and thus overcome the concept of people simply being kin by birth.

All the contributors to this special edition point, at least implicitly, to the vital role of bioinformatics. NGS is unthinkable without close collaboration with expert bioinformaticians, not least because of the enormous amounts of data that it generates. NGS technologies result in proxy data – which is pretty meaningless in itself. It is only made significant by means of tools from the computational sciences, statistics, and the modeling expertise of population genetics. While this was also true for PCR-based studies, the sheer amount of data being produced by NGS has increased the importance of bioinformatics. In archaeogenetics, the ongoing refinement of approaches and scenarios is in a way more due to bioinformatics and statistics than to advances in molecular biology, or, to put it another way, advances in molecular biology and population genetics are due at least as much to bioinformatics as they are to new sequencing techniques.

To sum up, NGS influences a huge range of fields and applications and it certainly shows enormous potential. However, as we have seen, it also poses massive challenges to science and society. Continuous reflection from various perspectives therefore remains an important task and many more debates – particularly public debates – on NGS and its (social) implications in the future remain to be carried out.

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RESEARCH ARTICLE

The seamless web of next generation sequencing and Covid-19

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Abstract • "When is Covid Covid?" is the title of a discussion paper published by the Centre for Evidence-Based Medicine at Oxford University on 11 September 2020. Amid the multinational struggle for an appropriate social and political approach to the crisis triggered by Covid-19, a recognized panel of medical experts alerts us that Covid-19 is defined very differently in different contexts. One definition focuses on symptoms, another one on RNA sequences of the virus. In the present contribution, this debate is taken up to discuss the extent to which new sequencing practices and their "seamless webs" become socially effective as instances of interpretation and design. At the same time, the limitations of such webs become noticeable as ruptures, seams, and scars.

Next Generation Sequencing und Covid-19 als nahtloses Netz

Zusammenfassung • *„Wann ist Covid Covid?" titelt ein Diskussionsbeitrag des Centre for Evidence-Based Medicine der Universität Oxford vom 11. September 2020. Inmitten des multinationalen Ringens um einen geeigneten gesellschaftlichen wie politischen Umgang mit der durch Covid-19 ausgelösten Krisensituation weist ein anerkanntes medizinisches Expert*innengremium darauf hin, dass Covid-19 in unterschiedlichen Kontexten sehr unterschiedlich definiert wird. Bei einer Definition geht es um klinische Symptome am Menschen, bei einer anderen um RNA-Sequenzen des Virus. In dem Beitrag wird diese Frage aufgegriffen und diskutiert, inwiefern neue Sequenzierungspraktiken und deren „nahtlose Netze" als Deutungs- und Gestaltungsinstanzen gesellschaftlich wirkmächtig werden. Dabei zeigen sich auch die Grenzen solcher Netze in Form von Brüchen, Nähten und Narben.*

Keywords • *seamless web, next generation sequencing, Covid-19*

Introduction

The recent history of Covid-19 is closely linked to Next Generation Sequencing (NGS). Taking a closer look at this link between an emerging pandemic and NGS as a technique, practice, paradigm and network allows for addressing potential ramifications not of NGS 'per se', but of technoscience-in-context. The following article is dedicated to this ambition.

From its very beginning, a central role in identifying, observing, and processing the current pandemic was assigned to the molecular-genetic virological dimension of the disease, that is, the SARS-CoV-2 viral ribonucleic acid (RNA). The local spread of a previously unknown respiratory syndrome in the Chinese province of Wuhan was linked to the emergence of a novel virus in the Chinese population in autumn 2019 and confirmed as a new disease (coronavirus disease 2019 or Covid-19) at the end of December. The first complete sequences of the viral genome were submitted about eight weeks later, in early March 2020. Whole-genome sequencing of the virus was achieved via the use of Next Generation Sequencing methods (Zhou et al 2020; Wu et al 2020) and led to the characterization, categorization and naming of the virus. Based on this, hypotheses were formulated about the origin of the virus from specific animal populations. NGS has contributed and continues to contribute to describing and differentiating different populations of the novel virus and monitoring the virus' further genetic evolution. Knowledge of the complete genome informs the development of effective vaccines as well as the development of appropriate testing methods that can detect and quantify the respective viral load. Recently, even clinical testing methods based on whole-genome sequencing via NGS techniques have been approved. In contrast to the common real-time PCR tests, which only react to the presence of small but characteristic sections of the viral genome in a sample (sections that had previously been established by whole-genome sequencing), NGS-based tests sequence the entire viral genome present in the sample and allow for the detection of variants and mutations.

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NGS in the seamless web of techno-science

NGS is presented in expert literature and in mass media as a new tool, simply adding to the existing techno-scientific toolbox, opening up for new possibilities via faster and cheaper genome sequencing and bringing about some limitations (such as decreasing reliability with increasing sequence length). As early as 1986, however, the historian of technology Thomas Hughes pointed to an alternative view of technology that does not focus on new techniques in isolation, refraining from a categorical separation of objects, techniques and actors, or actor fields such as science, technology or society. Along with this conception, technology and technological change are realized through "seamless webs", their heterogeneous professionals and organizations: "Heterogeneous professionals – such as engineers, scientists and managers – and heterogeneous organizations – such as manufacturing firms, utilities, and banks – become interacting entities in systems or networks. […] Technology and science, pure and applied, internal and external, and technical and social, are some of the dichotomies foreign to the integrating inventors, engineers, and managers of the system- and network-building era." (Hughes 1986, p. 282, 286). Similar perspectives have been brought to bear by other science and technology researchers such as Michel Callon, Bruno Latour, John Law and Annemarie Mol. But these approaches, roughly summarized as actor-network theory, mostly lack the historical diagnosis that seamless webs -like networks – are a phenomenon linked to a certain era.

A closer look at the practices, instruments and actors involved in NGS promotes the diagnosis of a seamless web: NGS is carried out via specially developed sequencing equipment provided by a few market leaders in this field. The results of the genetic sequencing itself are of very limited informational value. Only in comparison with other genomic sequences and relating metadata deposited and archived in sequence databases do they become interpretable in different directions. Sequence databases, in turn, require consortia that define uniform annotation standards and access options; they must be maintained and checked for legal and ethical aspects. Since the costly creation and maintenance of sequence databases is currently the real brake on high-scale viral whole-genome sequencing, NGS methods are being adapted to best support existing databases (Gohl et al. 2020). Thus, an almost endless network of actors, practices, rules, ontologies and objects is constructed. Whether this endless network also represents a seamless web, whether it comes with no loose ends at all, is another question addressed later in this text.

Remarkably, very useful, high-quality explanatory videos on NGS are being provided via internet platforms. These videos combine scientific-technical explanations from "What is DNA?" to "How does genome sequencing work?" (Chow 2019), infotainment and promotion of sequencing equipment. They explain that NGS encompasses several different sequencing approaches, that all share significant differences from traditional (i. e., Sanger) sequencing. They present relevant differences between the various NGS approaches and relating next generation sequencing machines and discuss appropriate fields of application. It can be assumed that these didactically sophisticated videos are also used in academic education. Some of them feature recognized professors from renowned universities. It is not always easy to see whether a private company and/or a public university is behind these videos; an interesting example of a public-private partnership at the level of scientific didactics as well as another part of the seamless web of which NGS is part!

The implementation of next generation sequencing requires the active construction and expansion of a seamless web of actors, practices, ontologies and objects.

Conversely, the implementation of NGS requires the active construction and expansion of a seamless web of actors, practices, ontologies and objects. This task is incumbent on "heterogeneous engineers": "The technologist [heterogeneous engineer] has to be seen as attempting to build a world where bits and pieces, social, natural, physical or economic, are interrelated", as Hughes (1986, p. 289) quotes his colleague Law[1]. Simultaneously, the importance of categorical differences fades: the heterogeneous engineer is as much an inventor as a scientist or entrepreneur. NGS is thus not just another element in the techno-scientific repertoire; it requires the practice of heterogeneous engineering attributed to the figure of the heterogeneous engineer; it entails the consolidation of existing and/or the construction of new networks of actors, practices, rules, ontologies and objects. Any action or innovation that affects one element of the network will impact on the whole system and its components.

Such a connection has already been drawn in many examples in the history of science and technology, for example in Bruno Latour's account of the "Pasteurisation of France" (Latour 1988). The disciplining aspect of socio-technical innovation is a central theme in Foucault's work on health care or prisons (Foucault 1976). However, the world has continued to change since Latour's and Foucault's empirical case studies and so has the scientific realm. Shapin (2008) depicts this change for the

1 However, the quotation could not be found in the referenced text.

life sciences, he devises the figure of the heterogeneous engineer under the label scientific entrepreneur. Digitally supported platforms connecting network nodes are themselves becoming lucrative business models. They are being critically discussed, for example, under the general catchword network capitalism (Srnicek 2016) or in relation to distinct contexts and issues such as "seamless webs of surveillance" established by the Internet of Things (Sadowski and Pasquale 2015).

The seamless web of Covid-19

With the detection of a new pandemic, its molecular-genetic characterization as SARS-CoV-2 and the (further) development of corresponding networks, the new disease has been successfully established as a molecular-genetic-virological-epidemiological event, a seamless picture of the current situation has emerged and is continuously being stabilized.

Not every subjective feeling of illness, not every clinically observed and medically characterized clinical symptom, is primarily investigated at the molecular genetic level, either because a causal relationship is not (yet) assumed or because it could not (yet) be determined. A robust causal connection between the genetic level and the phenomenological level of a clinical symptom is drawn in our understanding and treatment of hereditary diseases, mutation-based syndromes and genetic predispositions, but also for viral diseases. In the former cases, it is the genome of the diseased; in the latter case, the virus' genome plays the central role. In both cases, the connection between clinical symptoms and genetic characteristics is more complex than simple cause-and-effect models would suggest: the causal relationship between genetic risk factors and the risk of disease is not always clear. The categorization of a disease as a viral disease is sometimes ambiguous: the presence of the virus, its quantitative load and other factors on the part of the patient, such as lifestyle-associated or genetic factors, play a role.

Nevertheless, viral diseases, their treatment and containment are often successfully based on the viral factor alone. This may be partly because such treatments show substantial efficacy, partly because other factors are beyond immediate reach for various reasons. Lifestyle changes, for example, will only have an impact in the medium to long term. Moreover, the choice of lifestyle is (essentially) still considered a personal, free decision. Access to the human genome is neither legally permissible nor is it (currently) technically feasible in a precise, controlled manner. Access to the viral (or microbial) component, on the other hand, is socially rehearsed and established – one could also say seamlessly compatible with established networks of actors, practices, rules, ontologies and objects. New feasibilities, as opened up by NGS procedures, support such an approach from the techno-scientific side. They essentially allow for more genetic material to be sequenced in less time at a lower cost.[2] Thus, science, politics, and the public increasingly focus on the virological properties, molecular genetic characteristics, and epidemiological events in the current crisis.

The witnessed short-term change of focus from clinical symptoms to molecular genetics, virology and epidemiology attends to an obvious rationale: it is paramount to bring a rapidly developing epidemiological event resulting in quickly increasing death rates worldwide under control as effectively as possible. New possibilities of molecular genetic characterization are being exploited and further developed to better understand this side of the pandemic. This gives rise to hopes for a better understanding of the origin of the pandemic and the further development and diversification of the virus, for the development of adequate test kits, for better prevention through appropriate behavioral rules and – last but not least – for effective vaccines. Besides the demand for utmost accuracy of sequencing, there is also the need for maximum throughput to enable the characterization of as many virus samples as quickly and as detailed as possible.

When all societal efforts focus on one perspective – in this case, linking molecular genetics, virology and epidemiology – it is not long before visible successes are being achieved. Enormous knowledge about the new virus has been gathered. The virus has been named and categorized. The genome has been completely sequenced several times. Internationally accessible archives with extensive data material on locally emerging mutations have been created and continuously expanded. The virus' origin from animal populations and its transmission through intermediate hosts to humans is being researched. In an incredibly short time, highly effective vaccines have been developed, approved and put into use. Last but not least, we have all learned to move and behave risk-consciously in public spaces, from keeping distances the size of baby elephants (an expression that became famous in the Austrian primary education context) to hand hygiene and face masks. Public space has been rapidly trans-

The connection between clinical symptoms and genetic characteristics is more complex than simple cause-and-effect models would suggest.

2 The extent to which this leads to losses in the accuracy or reliability of sequencing in comparison to classical sequencing technology cannot be discussed here; however, such a trade-off is to be assumed to a certain extent.

formed into a laboratory to a level that even Bruno Latour could not have anticipated more accurately. An entire generation will no longer associate face masks with safety labs or operating theatres, but with the weekly family trip to the grocery store and an on-off attendance at school.

So much for the enormous success story of the focus on SARS-Cov-2 and its genetic sequence in the current pandemic. The sudden and exclusive molecular-genetic focus, however, obfuscates other relevant factors (such as lifestyle or income level), rendered previously established practices (such as medical diagnostics) incompatible and banished alternative horizons of perception and concern – such as those of curative treatments of symptoms or of addressing long-term societal and ecological impacts. In the short term, these may be unintended side effects that we as a society consciously or unconsciously accept. But what if they stand in the way of dealing productively with the pandemic in the medium and long term? In the following, the unintended side effects of our highly successful short-term molecular-genetic-virological view will be taken into account to discuss why we may have to broaden our horizon again to ensure long-term success.

How to infuse a broader horizon and a tolerance of diversity in these times of crisis?

"When is Covid Covid?": on seams and fractures

Evidence-based medicine propagates placing clinical action on the best available factual basis. Its rather pragmatic take on addressing everyday practical challenges of clinical decision making rarely results in extensive terminological treatises. And yet, the Centre for Evidence-Based Medicine at Oxford University posed an almost philosophical question on 11 September 2020: "When is Covid Covid?" (Spencer et al. 2020). The practical relevance of this question is quickly explained: Covid-19, according to the authors' research, is defined very differently in different national contexts. The contribution contrasts the diagnostic guidelines of the WHO, the European Centre for Disease Prevention and Control (ECDC) of the European Union, the Centers for Disease Control of the USA, the British and the Italian governments. The most significant consensus concerns the detection of confirmed cases. It is almost always based on positive laboratory tests. But even in this case, the technical details often remain unclear, and further incongruences abound.

Moreover, some definitions focus on confirmed cases, others on probable cases or suspected cases. One time, a definition is based solely on the prevalence of specific viral RNA sequences in a sample; another time, it encompasses clinical symptoms. Sequence-based definitions differ in test method, detecting either viral sequences or antibodies. These comprise essentially real-time PCR methods, based on the amplification of genetic material by polymerase chain reactions and subsequent detection of this material in the sample. NGS only provides the reference frame by providing data on the complete viral genome.

And finally, test results are interpreted in different ways, e. g., regarding the minimum threshold of viral load in the sample that would result in a positive test. Treatment and prevention practices based on such diagnostic methods can either focus on case-based clinical decision-making, or on adapting individual behavior, or on population-wide management strategy. Practices thus focus either on the clinical symptoms and their improvement, or on assessing and minimizing the probability that the virus will continue to be transmitted in epidemiologically relevant quantities, or on predicting and responding correctly to the pandemic development as a whole. Spencer and colleagues (2020) call for the harmonization of lower limits of the viral load and for the complimentary recording of clinical symptoms (the recording of lung CTs and serological findings in hospitals) to allow for transnational comparability and a more comprehensive definitory approach.

The web of actors, practices, rules, ontologies and objects thus obviously features seams and fractures along the national borders of regulatory regimes that need to be attended to by a kind of sewing work. Transnational evidence-based medicine is taking on this critical task, as are other relevant actors. Further seams or fractures result from different orientations of action within scientific research, clinical practice and pandemic management. Gathering new and robust insights, treating individual patients and getting a pandemic under control do not always go hand in hand without frictions.

Webs, seams and loose ends

When we speak of seamless webs, seams and fractures in the context of NGS and Covid-19, we are essentially talking about the characterization of a context of action in which NGS can be seen as an element or – in the language of actor-network theory – as an actant. Along with such a conception, NGS is not a passive cog in a superordinate wheel but an active part that co-defines an entire network of actors, practices, ontologies, rules and objects. Conversely, we can also assume that NGS, and techno-science more generally, are being shaped by their role in the pandemic. Thus, the rules that govern techno-science can change in times of crisis. Well-known examples include pre-review publi-

cations and fast-track approvals, which impinge on established routines of quality assurance. At the same time, there are calls for additional techniques of quality assurance to re-stabilize the network. Established funding and ownership models are also being re-discussed (Ravi Srinivas 2020).

The individual elements of this web not only communicate with each other, they condition and constitute each other. Thereby, coordination does not predominantly occur on a meta-level (e. g., through formulating explicit rules and implementing them via regulatory agencies), but rather in a mechanical manner[3]. The fewer seams, fractures and loose ends a web holds, the more ubiquitous and far-reaching such almost mechanical coordination effects can become. In the present context of Covid-19, fractures, seams and loose ends become apparent that resist and sometimes sabotage such coordination. Given the rather frightening idea of ubiquitous coordination by a seamless techno-scientific web (reminiscent of science fiction prose that paints dystopian pictures about machines or the mechanical principle taking over our lifeworld), such ruptures indeed open up for welcome interference.

However, another extreme is also worrying: what if ruptures, seams and loose ends become so dominant that socio-political coordination is no longer possible at all? Fractures at the level of national regulatory regimes and divergent fields of practice have already been mentioned above. They seem workable when acknowledged and addressed. If we recognize that good clinical practice is based on different objectives, success criteria and quality standards than the epistemic practice of virological and epidemiological research or the governmental practice of pandemic management, much can be gained.

native; the (semiotic) web appears seamless for the time being. The advantage of such alleged seamlessness is a maximum of coordination and thus the ability to react quickly and effectively. But with time elapsing, we have to address the question of how long our societies can tolerate such a mechanical state, ignoring existing ruptures, postponing necessary sewing work and drying out alternative networks.

Moreover, a first phase of maximum coordination seems to have been followed by a second phase, marked by increasing resistance (passive as motivational Corona fatigue and active as public protest), infodemias and urban legends. All this points towards the fractures and loose ends of the dominating network to which NGS belongs. This does not mean that it is an ineffective, dysfunctional or even morally bad network. But it shows us that we as a society still have a lot more to look at and work on; or in other words, we cannot and must not be wholly absorbed in this – or any other – single web.

Discussion: the diagnosis of a (not so) seamless web

An end to the current pandemic is currently not in sight: vaccination alone may not terminate the current crises; further pandemics of similar magnitude cannot be ruled out. The network to which NGS essentially belongs (including its heterogeneous engineers, practices, rules, ontologies and objects) seems to have been the only network that could provide practical answers to the life-threatening situation in the short term. Therefore, there can be no question of abandoning it; on the contrary, demand – further promoted by an increasing technology push – will probably continue to rise. Questions nevertheless accrue: in the short and medium-term, concerning the maintenance work that is in any case necessary to ensure the coordination within the network (for example, further developing and maintaining broadly accessible genome databases), concerning the sewing work to promote a robust alignment of relevant actors and actor fields.

Lasting pandemic prevention needs complementary approaches, especially those dedicated to preserving near-natural ecosystems.

But what about our collective, *public* understanding of the pandemic and its mitigation in contemporary societies at large? How to navigate between a worrying picture of total coordination by a seamless web of aligned actors and similarly dangerous fundamental fragmentation based on divergent interests, ontologies or values? How to infuse a broader horizon and a tolerance of diversity in these times of crisis? It is striking that this first year of the pandemic has been characterized by a relative impoverishment of narratives, perspectives and approaches. In public discourse, too, a single, narrative seems to prevail without alter-

In the long run, the question arises whether the existing biomedical web (for a critical analysis of this term and its use, see Cambrosio and Keating 2003; Bruchhausen 2010) of which NGS is a part can address all possibilities for pandemic prevention and management. For example, whole-genome sequencing has pointed to the origin of the virus from animal populations. Ecologists have already spoken out in this regard: lasting pandemic prevention needs complementary approaches, especially

3 An interesting aspect in this respect is that the pandemic's central figure – the virus – is depicted in contemporary culture as "a kind of missing link", "a necessary interface between viralism and mechanism" (Ristow 2021, translation by the author).

those dedicated to preserving near-natural ecosystems and, thus, bio-ecological resilience (Daszak et al. 2020). However, to integrate corresponding actors, practices, rules, ontologies and objects into the existing biomedical web, the currently prevailing heterogeneous engineers do not seem to be heterogeneous enough by far. This concerns not only the elements of the seamless web, but also the attitude of its engineers, which in the best case should also enable curative work and acknowledge diversity and inevitable loose ends.

The concept of the seamless web as put forward by sociologist-historians of science and technology allows for discussing and comparing alternative kinds of networks, with or without seams, with strong or weak ties, endless or finite. It allows for addressing seams (Žižek 2001), fractures, scars (reminiscent of Mary Shelley's figure of Frankenstein) and loose ends from a broader, socio-cultural perspective. NGS and Covid-19 mitigation are certainly not the only context in which such discussions might be favorable (see also Schubert 2019 for the application of the concept to the analysis of Covid-19 vaccination), but they can serve as a worth-while and timely exemplary case.

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RESEARCH ARTICLE

Metagenomics approaches in microbial ecology and research for sustainable agriculture

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Abstract • Technologies such as next generation sequencing (NGS) are transforming research fields at the methodological, conceptual, and organizational level. They open up new possibilities and bring with them new commitments and inherent limitations. We show from a philosophy of science perspective how NGS-based metagenomics has transformed microbial ecology and, with it, parts of agricultural soil science, which integrate ecological approaches with the aim to inform agricultural practices. We reconstruct agricultural science as design science (*sensu* Niiniluoto) and describe how the possibilities, commitments, and limitations of metagenomics approaches in microbial ecology shape values, situation assessments, and recommendations for interventions of soil microbiology in the context of sustainable agriculture.

Metagenomische Ansätze in der mikrobiellen Ökologie und Forschung für nachhaltige Landwirtschaft

Zusammenfassung • *Technologien wie Next Generation Sequencing (NGS) transformieren Forschungsfelder auf der methodischen, konzeptionellen und organisatorischen Ebene. Sie eröffnen neue Möglichkeiten, bringen aber auch neue Festlegungen und inhärente Beschränkungen mit sich. Wir zeigen aus wissenschaftsphilosophischer Perspektive wie NGS-basierte Metagenomik die mikrobielle Ökologie und damit auch Teile der agrarwissenschaftlichen Bodenforschung transformiert hat, die ökologische Ansätze integrieren, um landwirtschaftliche Praktiken zu verändern. Wir rekonstruieren die Agrarwissenschaft als Designwissenschaft (*sensu *Niiniluoto) und beschreiben, wie die Möglichkeiten, Festlegungen und Beschränkungen der metagenomischen Ansätze in der mikrobiellen Ökologie die Werte, Situationsbewertungen und Empfehlungen für Eingriffe der Bodenmikrobiologie im Kontext nachhaltiger Landwirtschaft beeinflussen.*

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Introduction

A metagenomics approach consist in the sampling of genomic material directly from a selected environment. It can capture a whole ecological community in a given environment such as a patch of soil by means of its collective genomic content. This approach, which became possible through next generation sequencing (NGS), is now widely applied in agricultural soil research. The latter is generally viewed as an applied science, aiming to improve agricultural practice. The common distinction between basic and applied science is as useful as it is problematic. Much of the difficulty results from the ambiguity of the notion of science involved, as it can refer to institutionalized disciplines as much as to research practices or results. Furthermore, applied science needs to be distinguished from the scientifically informed contexts of application.

In this paper, we adopt a framework suggested by Ilkka Niiniluoto (1993) and construe individual projects within a given science, in our case soil microbial ecology, as basic or design science, respectively, depending on whether the *outcome* is descriptive or consists in recommendations for interventions, regardless of the disciplinary affiliations of researchers involved. Basic science projects can be motivated by or funded for their potential to produce knowledge relevant for other fields of human practice. But this alone does not turn them into design science if they do not deliver recommendations. In such cases, one might want to speak of 'use-inspired basic research' (Stokes 1997). Basic and design science projects can be pursued in classical university research settings as well as in non-academic or combined 'Mode 2' science settings (Gibbons et al. 1994). Niiniluoto's classificatory schema allows us to track how metagenomics approaches in basic science projects, aimed at developing novel descriptions and

theoretical perspectives regarding soil microbial communities, re-orients the outlook of the respective design science projects delivering recommendations informing agricultural contexts.

The translation of approaches from basic to design science projects

Niiniluoto defines design science as "research aiming at knowledge that is useful for the activity of design", where design "in the broad sense includes all 'artificial' human activities, i. e., the production, preparation, or manipulation of natural systems […] or artefacts" (Niiniluoto 1993, p. 8). Agricultural science is among Niiniluoto's examples of design science. The relevant profession is the farmer, the practice is agriculture, the skill involved is the art of farming. Such human practices underwent processes of mechanization, i. e., the development of tools, as well as scientification, i. e., the development systematic bodies of rules. Design science supports both these developments and results in what Niiniluoto calls 'technical norms' (not to be confused with technical standards), defined as statements relating means and ends of the form 'If you want A, and you believe that you are in a situation B, then you ought to do X'. Such statements, unlike the descriptive statements of basic science, are clearly normative. Whether or not one adopts Niiniluoto's view that their truth value "is an 'objective' and general feature of the world" (Niiniluoto 1993, p. 12), it is clear that agents can agree on the validity of the statement even if they disagree whether the recommendation should be followed. As Niiniluoto points out, there can be disagreement regarding the values and associated goals, the actual state of the current situation, or the causal relations underlying an intervention. While the latter two issues can be addressed by empirical research, the former is subject to political debate. In any case, design science is justified when it is relevant, i. e., the situations expressed in its technical norms do obtain and the values inscribed in the goal in its antecedent are held by at least some group. Values and associated goals can result from public policy planning or attitudes of segments of civil society.

Regarding basic science, Niiniluoto holds a realist view. On his account, basic research delivers descriptive knowledge of causal regularities governing the relation of A, B and X underlying the technical norms of design science. In the following, we will go beyond this analysis, by showing how basic science approaches make phenomena accessible in the first place, thereby establishing new ontologies, and thus pre-configuring the discursive universe in which design science recommendations are formulated. Alternative approaches could make the phenomena in question accessible in a different manner, thus resulting in different recommendations. We thus depart from Niiniluoto's view by emphasizing the pluralistic and perspectival nature of the results of basic science. Such a view, however, is not incompatible with realism and the notion that science delivers true statements about the world (Massimi 2018).

As the purpose of applying Niiniluoto's framework is to distinguish projects with descriptive and normative outcomes in order to reconstruct their interrelation, and to analyze the aspects of values and goals, situation assessments, and interventions characterizing design science projects, issues of realism need not be further discussed here. While we take these aspects on board, we complement Niiniluoto's account in a way that allows us to move beyond the focus on theoretical results emphasized by Niiniluoto as much as by perspectivists. According to these views, knowledge about phenomena in form of the respective representations constitutes a perspective or is transferred from basic to design science. We focus, instead, on the ways that research practices themselves are directional and selective in the way suggested by the metaphor of perspective for theoretical representations. The actor's category of an approach seems to express this fact: to approach an object implies to move towards it from a given direction and to access it in a particular way. On our account, an approach is embodied in an experimental system enabling specific and selective material and cognitive access to epistemic objects (Rheinberger 1997). Approaches are translated from basic to design science projects and with them theoretical perspectives. Pluralism then results from the co-existence of approaches.

We will show how basic science pre-configures the discursive universe in which design science recommendations are formulated.

To return to our case, metagenomics approaches were integrated in experimental systems in microbial ecology and provided access to different aspects of microbial life than earlier culture-based approaches and made them available for basic science descriptions in ecological and genomic terms. In addition to the descriptive knowledge, the approach that enabled such knowledge itself was translated by adapting it to design science projects in agricultural soil science. In this way, the latter inherited the new possibilities and inherent limitations for material access and cognitive and symbolic representation, which then shaped its technical norms.

In the next section, we will show how accessing microbial communities through their collective genomic material (metage-

nome) re-oriented the conceptual representation of microbial life, from a focus on taxonomic groups (microbiota) and their phylogeny (i. e., evolutionary relationships) and physiology (i. e., their functions as a living system), to the study of integrated and interacting communities (microbiomes) and their structure and function, which were then mainly characterized on the level of genes and gene functions.[1] Subsequently, we will indicate how agricultural soil science adopted these metagenomics approaches and with them the genome-centered representation of microbial life. This shaped the conceptualization of goals, situations, and interventions in terms of soil quality in relation to agricultural practices and thus the resulting technical norms that potentially inform policy makers, actors in agribusiness, and farmers.

From microbial cultures to an ecology of genomes in microbial ecology

Microbial ecology emerged from environmental microbiology as the study of the relationships of microorganisms with their environment and among each other. Due to the need for developing procedures for examining microbial life in its natural context and bringing to light life forms which are otherwise invisible, environmental microbiology was a technology-driven field since its inception at the beginning of the twentieth century. Soil and marine microbiology were crucial in the development of microbial ecology. The outlook of these fields differed significantly from those of medical microbiology and food production, which conceived of specific microbes as pathogens to be removed from bodies, or as reagents, respectively (O'Malley 2014). Soil microbiologists, instead, considered the diversity of microbial components of soil as fundamental and as contributing to the richness of soil as substrate for plants. Therefore, the methods of soil microbiologists were developed in the context of or applied by agricultural sciences early on (Ackert 2007).

Environmental microbiologists were aware of a discrepancy between the types of viable cells in the cultured samples and the range of diversity observed with microscopes. In the late 1970s it became apparent that only 0,1–1 % of microbial life from samples could be retrieved with available culturing techniques, a fact referred to as the "great plate count anomaly" (Staley and Konopka 1985; for recent criticism, see Martiny 2019). To overcome the shortcomings of culturing techniques and characterize the biodiversity of environmental samples, researchers began to integrate molecular biology techniques. Following Frederick Sanger's development of a sequencing technique in 1977 and using the insight of Carl Woese and colleagues that highly conserved ribosomal ribonucleic acid (rRNA) subunits can be employed for phylogenetic characterization (Woese 1983), Norman Pace and colleagues began to adjust this molecular technique as a culture-independent approach for studying the biodiversity of naturally-occurring microbial communities, using environmental samples (Pace et al. 1986).

The early development of sequencing techniques thus offered a new way to access the complexity of microbial life. Molecular phylogenetic analysis and the conclusions drawn about species richness and abundance prompted the beginning of environmental metagenomics approaches. As a result of this change of research culture and ensuing possibilities of environmental microbiology to become more ecology-oriented and address microorganisms at the community level, microbial ecology established itself as a hybrid between ecology and microbiology (O'Malley 2014).[2] As the field pushed the advancement and integration of sequencing methods, the development of NGS platforms around 2005 had a strong impact on microbial ecology. NGS allowed for massive parallel sequencing of millions of short reads (i. e., sequences of DNA or RNA strings of several hundred base pairs), as it decreased the time and costs of sequencing significantly (Slatko et al. 2018).

This had several consequences as researchers were now able to a) detect also viral particles and free DNA sequences; b) improve the description of community composition and phylogenetic relations (Pereira et al. 2017); and c) analyze and predict community functions such as nitrogen or sulfur metabolism, respiration, motility, etc. (Fierer et al., 2012). Especially the latter point implies a new, systems-based understanding of microbial communities based on the analysis of the whole DNA content of a sample as it characterizes the new NGS-based metagenomics approaches. Analyzing the genes present in a community, the proteins they potentially encode, and the gene-transfer networks and metabolic pathways they form, gradually became more central to research agendas than identifying individual species, community structure, and phylogenetic relations (Gupta et al. 2019). The shift of emphasis from community structure to community functions resulted in a view of microbial communities as integrated functional units themselves rather than a

Metagenomics approaches generate a selective, genome-centered theoretical perspective on soil ecology.

1 While the term 'microbiota' refers to all microbes in a given environment, 'microbiome' denotes microbial communities in a given habitat, their internal and external interactions, as well as their genomic content (Berg et al. 2020).

2 Ecological communities are composed of various species, which interact with each other in a given habitat.

sum of individual organisms (Konopka 2009). But as indicated by the concept of the microbiome, these units are now mainly understood through their collective genome (Berg et al. 2020).

While we showed how NGS technologies enabled access to previously inaccessible dimensions of microbial life, we conclude that metagenomics approaches generated a genome-centered theoretical perspective on soil ecology. Despite our emphasis on the selective nature of these approaches and the resulting perspective on the *biological* dimension of soil, it is important to note that microbial ecologists typically employ different complementary strategies in addition to NGS. For instance, soil is submitted to chemical and physical characterizations (Fierer, 2017). Furthermore, microbial ecologists are aware of and address limitations of the approach: 1) Predicted community functions reflect only potential activity as many genes may originate from dormant cells or DNA debris and as genes are transcribed and translated into proteins only under certain environmental conditions (Prosser 2020). 2) Testing sequence-based predictions and gaining knowledge about cell-level anatomy and physiology, as well as modes of interaction among microbes and between microbes and plants would require culturing microorganisms in the lab. However, even though new culturing techniques are developed, various factors such as dormancy, symbiotic interdependency, low abundance, and competition still constitute difficulties for cultivation under lab conditions (Lewis et al. 2021). 3) Metagenomics results in massive amounts of data and the 'bioinformatics bottleneck' diagnosed for other fields employing NGS applies here as well (Desai et al. 2012). Filtering out information irrelevant for the pursued research question and analyzing and interpreting data requires special expertise (Kulkarni and Frommolt 2017). Therefore, collaboration with bioinformaticians becomes a necessary organizational feature of microbial ecology.

The next section addresses the fate of metagenomics approaches to soil microbiology in the context of agricultural science.

The constituents of technical norms in research for sustainable agriculture

Agricultural science is a multidisciplinary field producing knowledge about elements of agricultural practice on various levels, including soil, plants and pests, chemical and mechanical production technologies, and crop management strategies, as well as economic and political dimensions (Noll 2016). Many projects deliver descriptive knowledge on these aspects and can be categorized as use-inspired basic research. However, large parts of agricultural science aim at technical norms, i. e., recommendations about how to treat soil, choose or improve crops, handle pests, use technologies or design and implement policies. Such recommendations typically involve (methods for) the assessment of situations and are delivered under the assumption of a set of values and goals. Technical norms are derived by applying knowledge and approaches of basic science to the assessment of situations and the identification of causal regularities suitable for interventions. The study of the microbial dimension of soil in agricultural science has been strongly enhanced by NGS technologies. In the following, we will briefly indicate how the adoption of metagenomics approaches from microbial ecology has shaped the articulation of values and goals, the assessment of situations, as well as the recommended interventions in the technical norms delivered by agricultural soil research.

Values and Goals

Since agricultural research became institutionalized in various national contexts in the latter half of the nineteenth century, increasing productivity was a central goal (Noll 2016). With an ever-increasing demand for food, feed, fiber, fuel and pharmaceuticals, many depict this goal as more urgent than ever. This goal is derived from the underlying, albeit promissory values of (global) prosperity and well-being. Detrimental effects of agricultural intensification such as ecosystem degradation and biodiversity loss led to a new agenda aimed at halting these processes, resulting in calls for sustainable agriculture (Thompson 2016). The role of science is then seen as mitigating these processes, either by developing alternative strategies, or by delivering technological fixes (Puig de la Bellacasa 2015). In some of these contexts, design science projects could be perceived as 'post-normal science' (Funtowicz and Ravetz 1993), which provides advice under conditions of uncertain facts and diverging values.

In the context of agricultural science and policies informing its goals, the maintenance of ecosystems and biodiversity is typically not presented as an intrinsic value, but in a rather utilitarian way with respect to the overarching values of prosperity and well-being (Haines-Young and Potschin 2010). The latter are described as depending on ecosystem services which are provided by intact and diverse ecosystems. The notion of ecosystem services implies an anthropocentric understanding of ecosystem function. Without these, it is feared, not only will productivity eventually break down, but other negative consequences, for instance regarding climate change, will ensue. In the context of these externally set values and goals, agricultural science aims to deliver technical norms that are hoped to mediate the demands of productivity and sustainability. With metagenomics approaches, ecosystem functions of soils become re-interpreted in terms of networks of genes available in the ecosystem and the metabolic pathways they sustain (Schloter et al. 2018). This then has consequences in turn for the way specific goals are formulated regarding possible achievements or fixes, and ultimately determines the kinds of interventions suggested.

Situation assessment

The assessment of situations in which the goals are relevant and that can be changed through intervention happens on a global and a local level. The growing demands for agricultural products and the degree of ecosystem degradation and biodiversity loss need to be determined on a global or national level such that

recommendations can inform policies. Also, on the local level of the individual field, farmers need to make decisions regarding soil and crop management. Much research is thus focused on developing soil quality indicators. Metagenomics approaches are increasingly utilized for this purpose. Microbial indicators can be used to monitor the state of soils on larger scales or report on the state of a specific field, and it is hoped that degradation or biodiversity loss can not only be measured, but detected at early stages, allowing for mitigating actions (Schloter et al. 2018). While physical and chemical indicators are seen as equally valuable, microbial indicators are envisioned to replace other indicators where they are cheaper or easier to apply. Furthermore, such indicators could be highly specific such that they can measure the availability of specific ecosystem services in a given agroecosystem.

Metagenomics approaches are increasingly utilized for developing soil quality indicators.

Intervention

Technologies developed in basic research projects are sometimes developed further in design science projects as handles for interventions (e. g., DNA specific enzymes were developed into biotechnologies). Knowledge about microbiomes and metagenomics approaches qua indicators, instead, are mainly developed to evaluate practices and plan interventions involving other, often well-established technologies such as soil and crop management and the use of fertilizers and pesticides. For instance, much research has focused on how tillage and cropping regimes shape the microbiome and this line of design science has delivered specific technical norms concerning these practices (Bowles et al. 2016). Especially if reliable microbial indicators were turned into easy-to-use testing kits, farmers could make specific interventions based on these technologies, but concerning the use of other technologies. For instance, farmers could apply chemical amendments only when certain metagenomically defined microbial metabolic functions were found missing. Additionally, however, metagenomics knowledge and approaches can be a pre-condition for using microbes as technologies in microbial community engineering (Ke et al. 2020). Even if commercially produced microorganisms are available today for coating seeds before planting, much of the research remains promissory at this stage (Oviatt 2020).

Conclusion

We have shown how the introduction of NGS-based metagenomics has transformed the way microbial ecology describes ecosystems such as soil and how this in turn influences recommendations delivered by agricultural soil research regarding the assessment of situations and possible interventions. We are not suggesting that these fields are limited to a metagenomics approach and the associated theoretical perspective. Physical and chemical technologies for soil analysis are also used and further developed. Nonetheless, metagenomics approaches have oriented the outlook of agricultural soil microbiology strongly on a genome-centered notion of ecosystem services.

Our analysis suggests that this perspective tends to support instrumental attitudes towards sustainability. In extension to Niiniluoto's advice that in order to avoid short term "instrumental reason", focusing solely on economic or technical efficiency, "a technical norm should include among its antecedent A all the relevant valuations that concern the direct and indirect consequences of the recommended action X" (Niiniluoto 1993, p. 16), it would be possible to suggest another meta-technical norm, i. e., a recommendation as to how to construct technical norms, based on our analysis: When developing or adopting technical norms, the directed and selective nature of approaches underlying the assessment of situations and delineation of causal relations should be taken into account and they should be considered and framed against the background of alternative approaches.

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RESEARCH ARTICLE

Co-constructing ancestry through direct-to-consumer genetic testing

Challenges and implications

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Abstract • Direct-to-consumer (DTC) genetic ancestry tests offered via the internet supposedly uncover the ancestry of those tested. While these tests might be seen as a means to find a biologically inscribed and fixed genealogy, this paper explores how companies and customers co-construct ancestry through genetic ancestry testing. The study draws on a review of relevant literature, qualitative interviews with experts and stakeholders, a website analysis, and an autoethnographic self-observation. It shows how DTC genetic testing companies create specific concepts of ancestry in their marketing, development of specific databases, and presentation of results, but also how users interpret and incorporate their results into their own genealogies and lives. Looking at the potential social impact of DTC ancestry testing, the paper questions its categorization as recreational activity or entertainment.

Die Ko-Konstruktion von Herkunft mittels Direct-to-Consumer-Gentests. *Herausforderungen und Implikationen*

Zusammenfassung • *Direkt an Konsument*innen (direct-to-consumer, DTC) über das Internet vermarktete genealogische Gentests sollen die Abstammung der Getesteten aufzeigen. Während diese Gentests als Mittel verstanden werden können, die biologisch fixierte Herkunft zu bestimmen, untersucht der vorliegende Artikel, wie Unternehmen und Kund*innen die Abstammung mittels dieser Gentests ko-konstruieren. Die Studie stützt sich auf eine Analyse relevanter Literatur, qualitative Interviews mit Expert*innen und Stakeholder*innen, Webseitenanalysen und eine autoethnographische Selbstbeobachtung. Es wird gezeigt, wie DTC-Gentestunternehmen durch ihr Marketing, die Entwicklung spezifischer Datenbanken und die Präsentation der Testresultate bestimmte Konzepte von Herkunft kreieren, aber auch, wie die Kund*innen ihre Testergebnisse interpretieren und in ihre Biographien und ihr Leben einbauen. Mit Blick auf die möglichen sozialen Auswirkungen von DTC-Gentests wird ihre Einstufung als Unterhaltung hinterfragt.*

Keywords • *direct-to-consumer (DTC) genetic testing, ancestry, genealogy, co-construction*

Introduction

Since 2000, companies have been selling direct-to-consumer (DTC) genetic ancestry tests over the internet. Customers receive a test kit allowing them to take their own DNA sample in the form of a saliva sample or buccal swab. Having sent the sample to the companies who perform the DNA analysis, they then receive the results via the companies' online platform, by email, or by post. Depending on the service, the results identify different types of ancestry, following either a maternal or paternal lineage thousands of years into the past, or indicating a more recent and broader pattern of composite ancestry. In addition, customers are able to use the companies' services and databases to search for, and allow themselves to be found by genetic relatives also using this service (Shriver and Kittles 2004). In this paper we do not discuss the latter in detail, but focus on the ancestry testing features of these services.

Companies offer genetic ancestry tests for somewhere between 100 € and more than 1.000 €. It has been estimated that, by early 2019, the four largest companies in question had sold more than 26 million of these tests (Regalado 2019). Some companies sell them in conjunction with lifestyle- or health-related

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genetic tests, not all of which are available in Europe. The companies advertise genetic ancestry testing as a form of entertainment and a tool for recreational genealogy, and as a means of widening one's social network and finding out more about oneself. Some of their customers may also be motivated by the desire to contribute to biomedical research with their genetic and personal data (Mählmann et al. 2016).

In DTC genetic testing, ancestors are determined in biological terms as people in the lineage of the tested person. However, the process of identifying ancestors through DNA testing is complex and involves a range of scientific, technical, and social factors (Royal et al. 2010). In addition, customers interpret their results in various ways (Panofsky and Donovan 2019; Roth and Ivemark 2018). This *social co-construction of ancestry* is the focus of our paper. The concept of *social construction of technology* is based on the fundamental insight established in science and technology studies that technologies are shaped by the social circumstance in which social actors make use of them, or for that matter, choose not to (Bijker et al. 1987). By using the concept of *co-construction* (Oudshoorn and Pinch 2003), we furthermore highlight how social and technical practices jointly create ancestry against the backdrop of broader socio-historical ideas of ancestry. Reviewing existing empirical insights as well as exploring the field of DTC genetic ancestry testing ourselves, on the one hand, we examine how the companies in question determine ancestry in marketing and conducting these tests. On the other hand, we investigate the customers' role in the creation of ancestry through their uses of the test results. Our paper further develops ideas from a technology assessment study on new applications of DNA analysis (Lang et al. 2020).

Methodology and data

This paper is predominantly based on reviewing existing empirical studies complemented by explorative qualitative inquiry. We conducted a literature review covering foremost peer-reviewed academic publications gathered via Scopus, PubMed, and Google Scholar. In addition, we carried out, transcribed, and analyzed semi-structured interviews with a molecular geneticist, a population geneticist, a genealogist, a user of DTC ancestry tests, and a manager of a DTC genetic testing company. Furthermore, we analyzed the websites of the four most popular DTC genetic testing companies (23andMe, Ancestry, FamilyTreeDNA, MyHeritage). These websites frame the process, meaning, and outcome of genetic testing in specific ways, and therefore play a crucial role in the social construction of DTC genetic testing. Additional data was drawn from an autoethnographic self-observation: The two researchers involved in our study conducted product research and reflected on their own decision-making process towards voluntarily taking or not taking a DTC genetic test. In the course of the study, we continuously documented, reflected upon, analyzed, and discussed our personal experiences with one another. In the end, one researcher ordered a genetic ancestry test, while the other stepped back from doing so. This reflective self-observation gave us the opportunity to directly experience (non-)customers' perspectives and to access specific information firsthand, e. g., on interaction with customer services or information provided in the course of ordering and conducting a test. The Institute for Advanced Studies' ethics committee approved the self-testing. Results from this self-observation have been estranged for privacy reasons.

Direct-to-consumer genetic ancestry tests are embedded in broader socio-historical conditions and address existing social desires with new technological means.

Co-constructing ancestry in genetic testing

Social context of DTC genetic ancestry tests

Throughout history, the ability to demonstrate one's ancestry has been of social, political, or economic significance. For centuries, ruling elites justified their grip on power on the basis of their noble descent. The rights enjoyed and duties owed in society may be linked to proven group membership (e. g. citizenship). The verification of a biological relationship (e. g. paternity) may lead to financial obligations or entitlements. For many individuals, their belonging by birth to a nation, ethnic group or family is a crucial facet of their personal identity. On the other hand, sociologists have pointed to the flexibility and processual nature of identity in modernity (Abels 2010). The functions and meanings assigned to *genealogy* – as a recreational activity, an ancillary or fully-fledged discipline in its own right, and/or sociopolitical tool – also vary (Teicher 2014). Thereby, the curiosity in one's family ancestry might reflect a general societal interest in the past and history (Tutton 2004, p. 106). Genealogy as historic research uses a variety of approaches including archival research or interviews with relatives to reconstruct or verify family trees. In the recent decades, online archives and various digital tools facilitating the collation and sharing of genealogical information have become increasingly important.

Dtc genetic ancestry tests are embedded in broader socio-historical conditions and address existing social desires with new technological means. Nordgren and Juengst (2009) have argued that these tests offer an opportunity to negotiate the individualism and uniqueness required of every person in modern societies, but also appeal to other desires. They suggest that the tests address "a pre-modern interest in elaborating a naturalistic account of personal identity, a modern enthusiasm for science, and a post-modern emphasis on radical individual self-determination" (Nordgren and Juengst 2009, p. 161). It is this social context in which DTC genetic ancestry tests are co-constructed, in which they receive and support social meaning and practices.

Dtc genetic testing companies constructing ancestry

The marketed genetic ancestry tests are designed to determine one's ethnic background and/or where one's ancestors lived. Lineage testing identifies maternal or paternal ancestry, by analyzing the mitochondrial (mtDNA) or y-chromosomal DNA (Y-DNA) respectively, and assigns those tested to specific temporally more distant ancestry (haplogroups). Both mtDNA and Y-DNA maintain their distinctive features in the process of reproduction and can therefore be used to identify geographically localized groups of people with the same female/male ancestor. "Ancestry Composition" (23andMe) or "myOrigins" (FamilyTreeDNA) admixture tests analyze so-called ancestry informative markers in the autosomal DNA (atDNA) to determine the extent to which various geographically localized ancestral groups have fed into the lineage of those tested (Shriver and Kittles 2004). For example, the tested researcher in our self-observation received both a written and a graphical overview of his ancestry graded by different levels of detail. At the top level, he was classified as being entirely of European ancestry. At the next level, this European ancestry was broken down by current nation states, making him partly French (41,1 percent), German (20,9 percent), Spanish (14,2 percent), and so on, all the way to Dutch (0,6 percent) and Swedish (0,1 percent). These shares were then broken down further by regions (e. g., Normandy or Bavaria). Not least by combining these various levels of detail, the test results construe ancestry as a *singular and plural entity at the same time*. Also, in line with the possibilities of the testing approaches, a single, temporally more distant ancestry (haplogroup) and more recent multiple ancestries (ancestry admixture) are presented. This sense of ancestry as singular and plural is present throughout the companies' advertisement: „Discover when different ancestries were introduced into your DNA. Learn how many generations ago you had an ancestor that was descended from a single population or ethnicity" (23andMe 2020 b).

In this, the companies use an essentialist language. Ancestry is presented as an *objective fact that merely needs to be exposed*. The companies regularly use notions such as "uncovering" or "discovering" ancestry inscribed in the DNA: "Uncover your ethnic origins and find new relatives with our simple DNA test" (MyHeritage 2020). At the same time, their marketing strategies emphasize the constantly evolving nature of the test results. Companies are forthright about the fact that their test results rest on estimates whose precision and reach is likely to increase: "Explore your ancestry's breakdown by region […] with results becoming more refined as our database continues to grow" (23andMe 2020 b). Despite acknowledging some limitations, this optimization of the analysis was also emphasized by the manager from a DTC genetic testing company who we interviewed. The results of the ancestry tests are dependent on the quality of reference databases. In most cases, the reference data for specific regions comes from present-day individuals who are assumed to have ancestors in the regions in question; ancient DNA from archaeological finds often does not have sufficient quality for a thorough analysis. Companies are not always transparent about the ways in which they create reference panels using their own customer-based databases and existing scientific data. However, some companies outline that, e. g., customers are considered for a reference panel if "they have four grandparents all born in the same country – and that the population of that country didn't experience massive migration" (23andMe 2020 a). Yet, even candidates who meet such criteria may still be excluded based on statistical calculations, as described by Ball et al. (2020). The companies present problems of this approach, such as the inadequate consideration of genetic diversity within certain regions/populations or the impact of migration (Bardill and Garrison 2015), rather as manageable challenge for research than as inherent limitations of their approach. While such accounts relativize the significance of the testing results (Ball et al. 2020), they do not question the genetic determination of ancestry per se but reinforce the *identification of an objective, genetically fixed ancestry by continuously improved technological and scientific means*.

Direct-to-consumer genetic testing companies use an essentialist language through which ancestry is presented as an objective fact.

In this, ancestry is not only presented as purely geographical localization. Rather, DTC genetic ancestry tests are advertised

as a *means of empowering oneself by strengthening one's sense of identity* (Lee 2013; Wagner et al. 2012), or as a company puts it: "More ways to discover what makes you, you" (23andMe 2020b). The notion that ancestry can help people make sense of their current lives hinges on the companies' conflation of regions of origin and cultural heritage and the claim that customers could effectively tap into this heritage once they know their test results (Walajahi et al. 2019). In some cases, companies even provide means of ostensible direct access to this heritage, e. g., by providing personalized music playlists (Ancestry 2020) or helping with travel arrangements (23andMe 2020c). Several companies carrying out DTC genetic ancestry tests also cross over into traditional genealogy, offering complementary online genealogy services such as digital access to historical records or family tree applications: „We recommend that anyone who takes a DNA test create a family tree, to make the most of DNA results and uncover the full story behind them" (MyHeritage 2020). However, in their marketing, the genetic makeup of an individual is described as definitive evidence of ancestry. Classical genealogy only contextualizes the genetic information and supports its interpretation.

Users co-constructing ancestry

The DTC genetic testing companies' websites tend to imply that the test results they provide will have nothing short of "an instantly transformative effect on [the] identity" (Scully et al. 2016, p. 178) of their customers. However, research points to a more ambivalent picture and shows that users actively co-construct the meaning of their genetic ancestry test results.

In their study on white nationalists' discussion of their test results in an online forum, Panofsky and Donovan (2019) showed that within one and the same community, users interpret and thus construct the meaning of genetic ancestry test results in varying ways. On the one hand, test results categorizing individuals as being entirely of European ancestry were given credence as evidence of racial "purity" (Panofsky and Donovan 2019, p. 675). On the other hand, of those who received less clear-cut results, many simply denied the validity of the test altogether. Others did not go this far, instead reinterpreting the results, e. g., by "dismiss[ing] low levels of anomalous ancestry as 'statistical error'" (Panofsky and Donovan 2019, p. 667). Further scholars too have highlighted that users do not just "swallow whatever the tests say" (Roth and Ivemark 2018, p. 176). Instead, they adapt the test results to match their identity-related aspirations. People hoping to establish their 'pure' ancestry are more likely to experience a disruption of some parts of their identity; others who embrace the idea of plural identities may welcome results indicating a diverse range of ancestors (Roth and Ivemark 2018). In some cases, even customers who indicated that their genetic ancestry test result was "just information" (Shim et al. 2018, p. 56), concurrently described how it was significant for themselves as proof of their identities (Shim et al. 2018).

The interpretation of genetic ancestry tests can also be in line with broader social and/or political aims. Genetic research and testing have been interlinked with the (re-)definition of indigeneity and the ensuing political claims (TallBear 2013). Genetic ancestry tests may in some cases fragment and in others strengthen social groups. Johnston (2003) outlines how in the USA, the tribal membership of the Black Seminoles, descendants of black slaves who became members of the Seminole Nation under specific historic circumstances, was questioned based upon genetic testing. Analyzing another case, Leroux (2018) describes how a group of descendants from European settlers used genetic ancestry tests to "regularly portray […] its members as the only authentic Indigenous people in 'their' territory" (Leroux 2018, p. 88). Through identifying some (tiny) shares of Native American DNA they genetically supported their political claims to indigenous land. Another case in point has been discussed by Sommer (2010): Pointing to their genetically identified Macedon ancestry, people from the (back then) Republic of Macedonia (since 2019: Republic of North Macedonia) substantiated their entitlement to name their native country Macedonia against demands of Greece that has a region of the same name. At the same time, the genetic testing company repeatedly dismissed these claims as mere propaganda and insisted that genetics were apolitical.

While these examples illustrate that the results of genetic ancestry tests can have consequences for those who receive them, in other cases they may have little impacts. For the researcher who took the test in the context of our autoethnographic study, the results were not particular noteworthy. Most striking about them was ultimately how difficult it was to interpret them in any meaningful way. In part, they simply confirmed what the researcher already knew about his family history. In part, the results did little more than confirm the insight that, not least due to migration, most people's ancestry is more diverse than they might think. Given the high number of potential origins, engaging with all these different regions the tested researcher otherwise does not have any affiliation with, did not evoke curiosity but rather overload. Cases of such *meaningless ancestry test results* have been reported elsewhere too (Horowitz et al. 2019; Shim et al. 2018).

Since DTC genetic ancestry tests often comprise a variety of different functionalities to find more or less deep ancestry but also living relatives, the customers' assessment of these products in total may be rather ambivalent. The interviewed genealogist and lay user were rather critical about identifying their links to specific ancestral tribes or people, but embraced other modes of use (especially finding relatives) as starting point for further genealogical research – in line with the company's assessment that genetics and classical genealogy complement each other (see above). Thus, they deemed these services to be *partially meaningful and partially useless*. In addition, the customer's option to retrieve the genetic raw data as digital file enables users to transform these DTC genetic ancestry tests into means of obtaining genetic data which then can be reanalyzed for other, even health-related purposes on third-party platforms (Nelson et al. 2019).

Discussion

Examining genetic ancestry tests through the lens of co-construction directs our attention towards the various ways in which they can be understood and used. In most cases, DTC genetic testing companies try to promote an objectivistic understanding of genetic ancestry tests and insist on being apolitical. However, users have repeatedly tried and often succeeded in subverting this understanding of genetic ancestry tests by using them in ways that transgress the intended use as conveyed by the DTC genetic ancestry companies.

Genetic ancestry tests may support genetic determinism, racism, and social discrimination.

Our study of genetic ancestry tests calls into question their framing as a simple form of recreational activity or entertainment as others have done before. Scholars have highlighted the risk of genetic ancestry tests supporting genetic determinism, racism, and social discrimination. Emphasis on the genetic identification of ancestry could weaken or undermine various social, political, or cultural modes of integrating social groups (TallBear 2013). The ways in which the reference panels are formed carry the risk of defining ancestry in terms of current populations rather than genuine historical communities and of side-lining or ignoring the diversity and distinctiveness of historical populations (Blell and Hunter 2019). This has the potential to reproduce racial categories and prioritize differences between rather than similarities within populations (Duster 2014). Moreover, on an individual level, the tests may well achieve the exact opposite of their ostensible purpose and create "genealogical disorientation" (Nelson 2008).

Our investigation has several limitations that mirror broader desiderata. Some research has been undertaken on the ways in which customers belonging to specific groups interpret and use genetic ancestry tests, as we have outlined in the section on users co-constructing ancestry tests. Larger studies on the impact of DTC genetic testing on customers in general have mainly focused on the rather specific context of the USA as immigration society with a history of slavery that continues to have a social effect on present day society (Horowitz et al. 2019; Roth and Ivemark 2018; Rubanovich et al. 2021; Shim et al. 2018; Wagner and Weiss 2012). In the European context, larger surveys have explored the attitude towards ancestry tests amongst other DTC genetic tests, such as a recent study amongst Danish citizens (Gerdes et al. 2021), but these rather focus on lifestyle- or health-related impacts of the respective tests. Single qualitative studies have analyzed how in England (Scully et al. 2016) or Switzerland (Sommer 2010) specific groups of users make sense of their test results. However, to the best of our knowledge, we still lack empirical insights about the overall dimension of genetic ancestry testing ordered by a variety of European customers including its impact on those using the tests and their wider social environment.

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RESEARCH ARTICLE

Negotiating Jewishness through genetic testing in the State of Israel

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Abstract • In Israel, several hundred thousand citizens form a minority group that wishes to be acknowledged as Jewish by the state authorities. Most of them immigrated from the former Soviet Union and cannot provide sufficient evidence of their maternal ancestors' affiliation with a Jewish community. This has a direct impact on their civil rights. Based on a scientific research article on matrilineal genetic markers among Eastern and Central European Jews, the rabbinical dean of an institute for advanced Jewish studies in Jerusalem proposed to accept, under certain conditions, the presence of specific genetic markers as legal proof of "Jewishness." Genetic testing here is meant to become a tool for empowerment and (re)claiming Jewish status. This case raises many questions concerning a biological understanding of Judaism and shows how genetic ancestry testing could be used to uphold the religious orthodox narrative.

Die Diskussion um Gentests als Nachweis jüdischer Identität in Israel

Zusammenfassung • *In Israel gehören mehrere hunderttausend Bürger einer Minderheit an, die von den staatlichen Behörden als jüdisch anerkannt werden möchte. Die meisten von ihnen stammen aus der ehemaligen Sowjetunion und können keine ausreichenden Beweise für die Zugehörigkeit ihrer Vorfahren mütterlicherseits zu einer jüdischen Gemeinde vorlegen. Das hat direkte Auswirkungen auf ihre Bürgerrechte. Auf der Grundlage eines wissenschaftlichen Forschungsartikels über matrilineare genetische Marker bei ost- und mitteleuropäischen Juden schlug der rabbinische Dekan eines Instituts für jüdische Studien in Jerusalem vor, unter bestimmten Bedingungen das Vorhandensein spezifischer genetischer Marker als rechtlichen Beweis für „Jüdischsein" zu akzeptieren. Gentests sollen hier als Instrument für Empowerment und die (Wieder-)Erlangung des jüdischen Status dienen. Dieser Fall wirft viele Fragen bezüglich eines biologischen Verständnisses von Judentum auf und zeigt, wie genetische Abstammungstests eingesetzt werden könnten, um das religiös-orthodoxe Narrativ aufrechtzuerhalten.*

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Keywords • *genetic ancestry testing, Jewishness, essentialism, citizenship*

Introduction

Next generation sequencing (NGS) technologies, which significantly lowered the cost and time requirement for DNA sequencing, facilitated research in the field of population genetics as it made possible the identification of genetic markers over entire genomes, and enabled comparisons on a much larger scale between more population groups and with bigger sample sizes. Genetic anthropology is one of the many subfields of human population stratification and concentrates on genetic studies of ethnic groups to shed light on their migrations and genealogic history. At least since the beginning of the Zionist movement, and especially since the establishment of the State of Israel, studies on the genetic proximity among Jews assumed that Jews shared a common biological identity (Efron 1994; Kirsh 2003; Lipphardt 2008, 2012; Egorova 2014; Falk 2015). NGS impacted the growing body of research papers also in the field of "Jewish genetics", which -among others – includes two genome-wide-association studies on the interrelatedness of the world Jewry (Atzmon et al. 2010; Behar et al. 2010) that have received a lot of media and academic attention. Historians and anthropologists, as well as geneticists, have pointed out the pitfalls of such studies, as they are informed by pre-existing notions and narratives about group identity, (national) history, and origins, and assign genetic markers to supposedly clear-cut ethnic population groups so that "Jewishness" is embedded in the biological rather than in the cultural or social realm (Glenn 2002; Gibel-Azoulay 2003; Abu El-Haj 2012; Egorova 2014; Falk 2015; Elhaik 2016).

One related question keeps reappearing in academic and in popular discourse, and that is whether genetic testing can constitute a concrete tool for validating the "Jewishness" of individuals. This question is mainly discussed with regard to ethnic groups that have an oral tradition of being of Jewish descent, the so-called "Judaizing communities" (Devir 2020, p. 73) like the Lemba from South Africa or the Bene Ephraim from

India (Brodwin 2002; Gibel-Azoulay 2003; Parfit and Egorova 2006; Prainsack and Hashiloni-Dolev 2009; Egorova 2014; Devir 2020). However, under discussion here is a question that is thematically related but concerns specifically a group of Israeli citizens who immigrated on the basis of the Law of Return (see below) mainly from the former Soviet Union. The question is whether members of this group could use genetic tests to prove maternal Jewish ancestry by carrying a certain genetic marker.

The scientific DNA study at the center of the debate, which received media coverage around the world, used complete sequences of mitochondrial DNA (which is inherited maternally and can be used to track maternal ancestry) to compare samples of hundreds of Ashkenazi (Central and Eastern European) Jews to those from non-Ashkenazi Jews and to non-Jews, in order to identify and evaluate common ancestry markers (Behar et al 2006). This genetic study was referenced almost eight years after its publication in a quest for helping immigrants to prove their "Jewishness". This is a special case of "Jewish genetics" because it concentrates on maternal ancestry, which is also traditionally seen as the main determining factor of Jewishness. Therefore, there is room to argue that in this case, genetics do not outweigh other, cultural, or religious considerations. On the contrary, as will be shown further down, an attempt is made at integrating genetic evidence with evidence from the cultural realm. But all this is due to the particular political situation in Israel, which makes individuals with maternal Jewish ancestry eligible to citizenship and civil status changes (i. e., marriage, burial, see below), and thus links ancestry with privilege.

Can genetic tests prove maternal Jewish ancestry through a certain genetic marker?

Background: Immigrants and Israeli Law

It is important to note that there is no strict separation between religion and state in Israel. Certain areas of life, like marriages, burials, or conversions fall under the authority of the religious courts of one of the religious groups recognized by the state, like the Bahai, various Christian denominations, Druze, Jews, or Muslims (Edelman 1994, p. 51). Civil marriage does not exist, and therefore also no possibility for interfaith marriages. Jews fall under the jurisdiction of Israel's (orthodox) Chief Rabbinate, an official state body. Against this background, it makes a practical difference for immigrants to Israel and their descendants whether they are officially registered as Jews or not. In case of immigration, the Chief Rabbinate decides whether a person is registered as Jewish based on the traditional, orthodox rule that the person's mother must be (considered) Jewish. Immigrants to Israel prove this by providing evidence like certificates or testimonies, which demonstrate their – or their mother's, or close maternal relatives' – membership in the Jewish community. In order to become a safe haven also for those who suffered antisemitism although they are not considered Jewish according to orthodox religious law, for example, those with only a Jewish father or grandfather, Israel implemented the (secular) Israeli Law of Return with an amendment in 1970. It extends the right to Israeli citizenship likewise to non-Jewish descendants of Jews. With the help of the Jewish Agency, in the years between 1989 and 2001, almost one million people from the former Soviet Union (FSU) immigrated to Israel, including approximately three hundred thousand who were not considered Jewish by the Israeli Chief Rabbinate, either because they have Jewish ancestry on the paternal side, or they were unable to convincingly prove maternal Jewish descent (Lustick 1999; Yakobson 2010; Kravel-Tovi 2012 and 2017; Amit 2018). These immigrants are in large parts socially assimilated citizens with Jewish family background. It has been shown that "considerable segments of FSU non-Jewish olim [new immigrants] subvert the halakhic [Jewish religious law] definition of their identity. Many of those whom the state defines as non-Jews do in fact define themselves as Jewish – in terms of origin and identity. This self-definition is premised to a large extent on the logic of Soviet bureaucracy." (Kravel-Tovi 2017, p. 59). In fact, a recent in-depth study on "First and 1.5 Generation FSU […] Immigrants in Israel" linked the significantly higher rate of emigration among the younger age group (25–40 years old) of FSU immigrants (compared to Israeli born emigrants) to feelings of frustration and estrangement caused by the demand of the religious authorities to prove their "Jewishness" – especially when they want to register for marriage (Amit 2018).

DNA testing for establishing descent

In March 2019, several Israeli newspapers reported that the Chief Rabbinate admitted demanding DNA testing from immigrants from the former Soviet Union "in some cases" in order to establish Jewish ancestry (Maltz 2019; Sharon 2019; Azoulay 2019). According to the Chief Rabbinate, applicants were asked to undergo testing to prove they are biological descendants of a person who was already officially accepted as being Jewish. The use of DNA tests drew criticism from politicians as well as from opinion leaders, although it was not based on the idea that "Jewishness" could be proven biologically, but that descent can be established. Some years earlier, in 2013, Israeli newspapers

had reported on a somewhat similar case where a young woman was refused participation on a "birthright"[1] trip to Israel unless proving by DNA test to be the biological daughter of her father (Eli 2013; Times of Israel Staff 2013). Still, this kind of DNA test was judged by anthropologist McGonigle to "suggest a policy decision to enshrine Jewishness at the level of DNA, render 'Jewish genes' legally legible by the State, and make DNA signatures a basis for basic rights and citizenship" and as raising "concern over a reinscription of ethnic essentialisms, entailing a 'biopolitical' project that could foster a new regime of 'biopower'" (McGonigle 2015, pp. 90, 99).

Genetic Ancestry Markers and "Jewishness"

A new aspect of DNA use was added in 2014, when Rabbi Yosef Carmel from the Eretz Hemdah Institute for Advanced Jewish Studies in Jerusalem, which trains religious judges and teachers, came up with an idea to help those individuals who have a family history of being Jewish, but cannot provide sufficient evidence for their claim to the religious authorities (Carmel 2014). He published a responsum, i. e. a reply made by rabbinic scholars in answer to submitted questions about Jewish law, to the question of whether the "Jewishness" of a person could be established based on a DNA ancestry test result, which shows that the applicant carries a certain genetic marker prevalent among Jews (for an abbreviated English language summary of the responsum see Carmel 2016). Here, the circumstances are different from the cases described above: it is not the Chief Rabbinate casting doubt on the biological descent of an applicant from a specific person who is already accepted as Jewish and thus forces this individual to identify by DNA test. It is rather meant to empower an applicant who does not have a relative to refer to or enough other documentary evidence – like letters or register entries – to prove maternal Jewish ancestry. In his answer, Carmel explicitly distinguishes between DNA evidence that is used to identify a person, as in forensics or paternity tests – and which qualifies for the theological concept of "unambiguous marker" on the one hand, and genetic ancestry testing on the other (Carmel 2014, p. 96; Devir 2020, p. 75).

The result and significance of genetic ancestry testing are, also in the theological sense, different from forensic DNA identification: genetic ancestry testing does not ultimately determine anything, it offers merely a statistical value of probability for ancestry. Concerning the specific case of self-identified Jews from the Eastern Bloc, Carmel relies on the findings from the above-mentioned peer-reviewed scientific research article by Doron Behar and co-authors that was published in a renowned journal in the field of human genetics (Behar et al. 2006). This study, which was made possible through NGS techniques, compared ancestry specific markers in mtDNA samples from 583 Ashkenazi Jews, 1,111 non-Ashkenazi (of North African, Caucasian, Near Eastern, and Spanish-exile ancestry) Jews, and 11,665 samples of non-Jews from across the world (Behar et al. 2006, p. 494 and Table 5).

The study found that 40 % of the Ashkenazi Jews can be traced back to four female founding lineages (mitochondrial haplogroups). The result stands for the world-wide Ashkenazi Jewry and is presented in a way that is appealing to the public, who associates the four female lines with the biblical matriarchs: "we show that close to one-half of Ashkenazi Jews, estimated at 8,000,000 people, can be traced back to only 4 women carrying distinct mtDNAs that are virtually absent in other populations" (Behar et al. 2006, p. 487). This association with the biblical matriarchs was picked up by media outlets from around the world: the German magazine Der Spiegel headlined for example "Vier Urmütter haben 3,5 Millionen Nachkommen" (Four matriarchs have 3.5 million descendants) (Der Spiegel 2006).

In his ruling, Carmel argues thus: As these four Ashkenazi mitochondrial haplotypes were not found among non-Jewish Europeans, and as the sample sizes are so big thanks to the latest sequencing technologies, it is statistically highly likely that a person who carries one of these markers, has maternal Jewish ancestry. The presence of a genetic marker will not conclusively identify a person as Jewish, nor will its absence label an individual as non-Jewish. But, Carmel argues, if someone struggles to provide sufficient supporting documents or testimonies for her or his maternal Jewish ancestry, then the specific genetic signature should be considered as one additional piece of evidence so that taken together, there might be reason enough to declare this person Jewish. He even calls upon Israel's Chief Rabbinate to accept genetic markers as one piece of evidence among others for consideration (Carmel 2014, pp. 98).

Genetic ancestry testing does not ultimately determine anything, it offers merely a statistical value of probability for ancestry.

Carmel's suggestion was not adopted by the Chief Rabbinate. This means that individuals cannot claim a right that genetic ancestry tests should be counted as evidence by the authorities. But on the other hand, the responsum was also not denounced

1 "Birthright Israel" is an educational tourism organization that offers a free educational trip to Israel for young adults from all over the world, who have at least one Jewish birth parent or have converted to Judaism. The goal is to strengthen Jewish identity, Jewish communities, and connection with Israel. It is funded by various sources, including the State of Israel, several Jewish foundations, and private donors.

by the Chief Rabbinate – although it could have argued for example that one year earlier, a different DNA study on maternal Ashkenazi ancestry (Costa et al. 2013) casts doubt on the interpretation of the four haplogroups given by Behar and co-authors. It could also have argued theologically that an ancestry marker does not show whether the individuals of the maternal line indeed stayed within the Jewish faith. In a personal communication (phone conversation on January 17, 2021), Carmel explained the silence by the Chief Rabbinate at least in part with a general and understandable uneasiness to associate genetics with Judaism.

Can we continue to speak about DNA as seemingly "hard evidence", when it becomes re-interpreted and (possibly) used as "soft evidence"?

But even though Carmel's proposal was not implemented, the matter still raises interesting questions concerning the use of genetic ancestry tests for identity politics which in the future need to be discussed in greater detail. Anthropologist Yulia Egorova made a beginning when she wrote that "the ruling thus contains the promise of social empowerment", but "it also appears that both the case of the Eretz Hemdah proposal and of the tests conducted among the 'emerging' Jewish groups point to the oppressive nature of genetic test usage in matters of identity arbitration even in those cases when such tests are commissioned by the disenfranchised groups or individuals themselves" (Egorova 2018, p. 549). We also need to ask how much can we rely on the results of one scientific study – even though it was published in a high-ranking scientific journal – given the current discussion on irreproducibility of scientific studies and the consequences which are entailed for personal lives? Can we continue to speak about DNA as seemingly "hard evidence", when it becomes re-interpreted and (possibly) used as "soft evidence"? If there was a practice of using DNA tests as additional, "soft" evidence in a cultural context, would this not weaken the perception of DNA as decisive or determinative, rather than strengthen this notion? Can we speak about the danger of "biologization" in the Jewish context, when the "biological" is one component of its culture from the outset? In our specific case, the DNA test does not change the "conventional understanding of identity" (Brodwin 2002, p. 326), which is maternal Jewish descent. Equating the "new genetics" with essentialism does not reflect the subject in its complexity. In our context here, DNA-testing reinforces the conventional understanding of Jewishness as inherited maternally. This is especially the case given that the individuals already perceive themselves as part of a secular Jewish society, where most other members likewise identify by ancestry rather than by belonging to a religious group (Amit 2018). On the other hand, the use of genetic testing was criticized as a sign for Israel "increasingly embracing ethno-nationalist policies" (Ungar-Sargon 2019). But can a "racialization" of "Jewishness" be avoided, when DNA tests are meant to support the individual's endeavor to "prove" her/his identity, especially vis-à-vis government officials?

Conclusion

The civil status situation of a group of Israeli citizens, against the current political and legal background, brings to fore the complexity of "Jewish genetics". It highlights the overlap of the biological and religious narrative of Judaism. In the present constellation, a Jewish identity needs to be legally "proven" and "Jewishness" is legally defined according to traditional law by the Chief Rabbinate as maternal ancestry. This creates a situation in which DNA becomes an object of negotiation. Consequently, the narrative of biological determinism (the maternal descent) is maintained, and even enforced, although the criteria for "Jewishness" are in fact subordinated to the freedom of decision by the rabbinical authorities.

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RESEARCH ARTICLE

Does the concept of genetic ancestry reinforce racism?

A commentary on the discourse practice of archaeogenetics

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Abstract • Genetic ancestry is seen as an alternative to the problematic concept of race and is positioned against abusive racist and nationalist perspectives. The concept of genetic ancestry is nevertheless not free of racial categorizations. Increasingly, it is becoming an integral part of identity politics. Genetic ancestry is promoted as a way to give identity and visibility to marginalized groups but is also rejected as a form of biocolonialism. In xenophobic and racist discourses of right-wing groups, the concept has found fertile ground. The field of genetics is partly to blame for this since it opens the door to problematic identity discourses through a careless use of archaeological, ethnic, and genetic categories.

Fördert das Konzept der genetischen Abstammung Rassismus?
Kommentar zur Diskurspraxis der Archäogenetik

Zusammenfassung • *Genetische Abstammung wird als Gegenentwurf zum überkommenen Konzept der Rasse gesehen und gegen missbräuchliche rassistische und nationalistische Perspektiven in Stellung gebracht. Das genetische Abstammungskonzept ist dennoch nicht frei von rassischen Kategorisierungen. Zunehmend wird es zum integralen Bestandteil von Identitätspolitik. Genetische Abstammung wird als Möglichkeit propagiert, marginalisierten Gruppen Identität und Sichtbarkeit zu verschaffen, wird aber auch als eine Form des Biokolonialismus zurückgewiesen. In den xenophoben und rassistischen Diskursen rechter Gruppen hat das Konzept Konjunktur. Daran trägt die Genetik eine Mitschuld, da sie durch leichtfertigen Umgang mit archäologischen, ethnischen und genetischen Kategorien problematischen Identitätsdiskursen die Tür öffnet.*

Keywords • *ancestry, genetics, migration, race, racism*

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The new technical possibilities of genome sequencing and decoding of ancient DNA (aDNA) have led to an avalanche of palaeogenetic studies, which have received great attention not only in scientific debates but also in the public media. Next generation sequencing (NGS) exponentially increases the throughput of genome analyses compared to previously common methods. For the first time, complete genome analyses can be performed comparatively inexpensively in a relatively short time. Initial assessments of the new methods were euphorically optimistic about their potential for further research (Mardis 2008; Knapp and Hofreiter 2010). Although later judgements have already become slightly overcast, the positive assessment generally remains unbroken (Goodwin et al. 2016; Orlando et al. 2021). The new possibilities are appreciated as a genome revolution; in archaeology, a scientific revolution has been proclaimed (Kristiansen 2014). Revolutions are a promise of a better, in science a more enlightened and knowledgeable future. Although only the future itself will show what it is really like, it is already possible to see the beginnings of where the journey is heading.

The technical problems of genome analysis are becoming increasingly manageable, so that it is now possible to analyze sample material that has so far eluded investigation. Instead, new challenges are now emerging at points that were not previously seen as problematic. The new high-frequency throughput of analyses generates an unprecedented data stream that seems almost unmanageable. The control of the data is usually carried out neither by the disciplines that provide the sample material nor by the geneticists who generate the data, but rather by computer scientists and statisticians whose task it is to process the data and ultimately to make them interpretable in the first place. This represents a shift in the epistemic basis of the disciplines involved (Jones 2019). The problem area has shifted from data generation to data interpretation, and at the same time the locus of interpretation is moving increasingly away from the fields that were the sources of the data – as has already been criticized (Meier and Patzold 2021). This shift leads to a number of 'undead' creeping into scientific discourse (Burmeister 2019,

pp. 356–357). One of these 'undead' is the concept of race and its ideological implementation in racism. In the remainder of the paper, the issue of race, racism and genetic ancestry will be the subject of scrutiny.

Geneticists such as David Reich (2018 a) aim to answer fundamental issues in the history of humankind. One of his core statements is that all people have a shared history, that we are all hybrid beings who are related to each other to different degrees. Against the background of human evolution and the exodus from Africa together with the subsequent colonization of the planet, our differences are trivial. In recent studies, the processes of genetic mixing of populations over the last 100,000 years have gained a hitherto unknown historical depth of focus and detail, which opens new perspectives on the history of humankind. For Reich, his research is also a rejection of racist and nationalist instrumentalization of population history. But is DNA analysis a weapon against racism and nationalistic interpretive abuses?

Is DNA analysis a weapon against racism and nationalistic interpretive abuses?

Ancestry as an alternative to the problematic concept of race

The concept of race has been problematized in biology and in the social sciences, where it was long ago exposed as a cultural construct. In genetics its place has now been taken by ancestry, which no longer focuses on individual traits of human appearance – however certain or insinuated they may be – but on individual and collective relationships. In their plea to take race out of human genetics, Yudell et al. (2016) differentiate between race and ancestry as follows: While race is a "pattern-based concept" with which individuals can be assigned to preconceived groups, ancestry is a "process-based concept" that makes statements about genetic kinship.

But genetic kinship means more than mere relationship of familial descent. Genome-wide association studies identify and define ancestry groups based on specific gene variations. Certain allele expressions are part of the individual biological machine code and thus become characteristic features of individual ancestry groups. They are an individual and collective trait that has the potential for labeling and group assignment. It is not surprising that studies are not limited to identifying ancestral groups but, for example, aim also to detect typical dispositions for specific diseases. Nor are intellectual capacities taboo. Even David Reich (2018 a, pp. 254–258) demands an open mind, albeit stating that our understanding of the genome is still too immature to draw far-reaching conclusions. He therefore rejects those studies that aim at behavioral traits, but this is only a provisional situation due to the current state of research. So, it is not surprising that for the period between 1998 and 2007, Chow-White and Green (2013) note a clear increase in racial discourse within genetics that suggests that race has a genetic foundation.

In a *New York Times* column, Reich (2018 b) published a slightly modified version of his book chapter on "The Genomics of Race and Identity", in which he explicitly emphasized that the "average genetic differences among 'races'" could no longer be ignored and that "differences in genetic ancestry that happen to correlate to many of today's racial constructs are real". One of his most prominent examples is the genetically higher disposition for prostate cancer in African Americans, the majority of whom are descendants of slaves deported from West Africa. The same genetic characteristics can also be found in members of today's West African population. So, does this observation permit the statement that West Africans as an ancestry group on their own confirm the social construct of race as real? Are West Africans in this sense a "race of their own" at all? Reich overlooks the conditions of formation of racial constructs, which do not argue with an origin from West Africa, but rather with the outer appearance of black people and their status in a white slaveholder society. Accordingly, black people, not West Africans, were constructed as a race. Reich mixes categories of different contexts of formation and different levels of integration that cannot be reduced to a common denominator. Studies that could support Reich's postulate would have to be designed completely differently. Only recently has the missing diversity in human genetic studies been criticized (Sirugo et al. 2019). Even when the authors expressly problematize the predominance of studies on groups with European ancestry, it is clear that an over focus on a selected group out of populations with shared ancestry results in a bias that diminishes the meaningfulness of the scientific outcome.

Criticism of the concept of ancestry

The aim here is not to criticize the formation of categories in general, which are a fundamental part of any scientific work, but rather the obvious myopia facing the social context of these categories and the careless use of racial terminology (BuzzFeed Opinion 2018). It is remarkable that geneticists almost obsessively and without scientific necessity bring race into play to express the apparently inexpressible. The social sciences have been monitoring genomic science for a long time and have often criticized the fact that the concept of genetic ancestry is permeated by problematic racial categorizations that have ultimately not lost their compatibility with racist perspectives of past cen-

turies and instead even reinforce them (Gannett 2014; Morning 2014; Nash 2015; Panofsky and Bliss 2017).

Nevertheless, genomic studies cannot all be lumped together, and a clear distinction must be made between different approaches of ancestry analysis. While admixture mapping and ancestry information markers still include racial categorizations, the genetic ancestry made possible by genome-wide association studies is free of a priori settings and therefore actually manages without racial categorizations. This approach has been co-developed by Reich and has now become standard in palaeogenetic studies (Patterson et al. 2006; Price et al. 2006). However, it should be borne in mind that due to statistical dispersion of the data, the analysis does not always lead to clear distribution patterns, and groups may only be represented as tendencies of their statistical means – a matter that is usually neglected when reaching conclusions. Depending on the data, ancestry groups so defined are influenced by subjective interpretations. But we can agree with Fujimura and Rajagopalan (2011, p. 22) that this is a viable methodological approach that works without the problem of racial or ethnic categorization. So, it is all the more surprising that geneticists are still playing the race card.

Genetic ancestry is increasingly becoming an integral part of identity politics.

And the spiral of problems keeps growing. Genetic ancestry is increasingly becoming an integral part of identity politics. It is propagated as a way of assigning identity and visibility to marginalized groups (Guglielmi 2019), but it is also rejected as a form of biocolonialism (TallBear 2013). White nationalists reify their racist worldview by analyzing their own genetic ancestry, whereby their pride results not only from genetic "purity" but also from the awareness that they are part of a specific history (Panofsky and Donovan 2017). The extreme right-wing Greek political party, Golden Dawn, saw the results of a palaeogenetic study (Lazaridis et al. 2017) as confirming a racial continuity of the Greeks from the Bronze Age to the present day. Surely, the best scientific study is not immune from abusive misinterpretations, but here the authors of the study have contributed their part through awkward wording and the problematic combination of archaeological, ethnic and genetic categories (Hamilakis 2017; Maran in press). Fujimura and Rajagopalan (2011, p. 20) already warned that the "subtlety of the difference between race and ancestry may get *lost in translation*".

Ancestry as biocultural artefact

It is an established method in the analysis of genetic differences between modern populations to refer to individuals whose grandparents were born in the same region or country (Novembre et al. 2008). By comparing aDNA and recent DNA, statements on prehistoric migrations and population-genetic continuities can be made. Today's English population is genetically closely related to populations from Denmark, northern Germany and the Netherlands (Leslie et al. 2015; Schiffels et al. 2016). Continental European ancestry was inscribed into the genomic profile of the British population via the Anglo-Saxon migration around 1,500 years ago. By collecting data from individuals whose families have lived in a region for several generations, recent migration events are excluded, while earlier demographic processes can be identified. The population of the Netherlands as a postulated ancestral home of the English has, however, been shaped to a considerable extent by numerous later migrations over the last 1,000 years (Abdellaoui et al. 2013; Altena et al. 2020; Lao et al. 2013). A genetic identity of the Dutch population around AD 500 with that of 1900 can therefore hardly be assumed.

Genetic similarities can be explained with genetic ancestry, but no direct statement can be made about historical population identities. Moreover, this approach is problematic in that it mixes ethnic and genetic categories, thus opening the door to problematic identity discourses (Lipphardt 2019). Thus, it is not the ethnic self-attribution or citizenship that determines who is German, Danish or British, but the birthplace of the grandparents. In studies on the genetics of national or regional groups, individuals whose ancestors immigrated only one or two generations ago are excluded. Are British citizens with Pakistani roots not British, children of Turkish immigrants not Germans? By comparing aDNA with modern DNA, statements are made about prehistoric migrations and genetic continuities. Here the argumentation of right-wing groups is served unintentionally, and indeed, they increasingly refer less to race and more to ancestry. "Biological Germans", e. g., is their rhetoric to exclude all German citizens whose families have not already lived in Germany for several generations.

For the reconstruction of past migration processes, this approach may be methodologically adequate, but it is problematic because the results of these studies and the postulated ancestry become part of national identity discourses. Reich (2018 a, p. 253) sees 'ancestry' as a necessary term to discuss genetic differences between people. However, Mathieson and Scally (2020) show that ancestry is neither clearly defined nor does it have a consistent meaning. Ultimately, it captures genetic similarity and not genetic ancestry in the strict sense. While genetic similarities can be traced back to heredity and thus to a common ancestry, genetic ancestry does not map all ancestral relationships. Only some of the ancestors have passed on their genetic material, so that genetic similarity does not permit a statement

about all ancestors. Consequently, genetic ancestry has numerous blind spots and is only an excerpt of our genealogical ancestry. The concept of ancestry has a much broader semantic field than genetic similarity is able to cover. It includes some people and excludes others. It is part of cultural practice, and even the hard facts of genetics do not change this: as "biocultural artefacts" (Abel and Schroeder 2020, p. 200) they are part of "genealogical imaginaries" (Nash 2017) and have a social life (Pálsson 2002).

Ancestry as door opener for a new racism

Let us come back to the question posed in the title, whether ancestry reinforces racism. The conclusion must be that it does not necessarily do so, but it can. Geneticists themselves repeatedly draw the race card, without always making a clear distinction between social and biological categories. Furthermore, they seem to ignore the historical and often ideological ties of social categories or to be unaware of them. Geneticists have for the most part a critical awareness of the biological concept of race – and beyond all doubt do not have a racist agenda. On September 11, 2019, the Jena Declaration was published, co-authored by the geneticist Johannes Krause. It clarifies that the concept of race is the result of racism and not its prerequisite (Jena declaration 2019). But to state again that racism has no scientific basis is to miss the real problem. Racism as an ideological orientation is a social practice that does not need a scientific foundation. That is why the emancipative approach, which David Reich, for example, never tires of emphasizing, fizzles out in social reality. geneticists oppose their concept of ancestry to the traditional concept of race in an enlightened way, they do not consider current right-wing discourses. In the face of political reality, the emancipative approach goes up in smoke.

It goes without saying that geneticists cannot be blamed that their studies are misused by third parties, but part of the problem lies in the geneticists' lack of awareness of the social and discursive conditions of categorizations and knowledge. A general problem arises when genetic data leave the laboratory and are linked to phenomena in the world outside. This necessarily leads to the confrontation of genomic classifications, for example of genetically defined ancestry groups, with classifications of other epistemic systems. This is particularly evident when genomic ancestry is associated with archaeological cultures. Archaeological cultures are technical classifications for ordering the archaeological record; they do not reflect the material remains of ethnic groups or populations. A correlation between common ancestry and culture would at least have to be proven first and should not anticipate the result of a study by assigning labels beforehand. Problems arising from the need to name groups can be minimized by using neutral, technical terms (Eisenmann et al. 2018).

But even this is not a definite solution against political misuse. As modern populations are used as reference groups, geneticists fling the gates wide open for political identity discourses. Genetic reference to contemporary national populations correlates neither with individual self-attributions nor with the legal criteria of citizenship. The national or regional label is not a scientific classification of a genomic fact, but a terminologically problematic construct that pretends to objectively identify and

Are British citizens with Pakistani roots not British, children of Turkish immigrants not Germans?

Stuart Hall (1989) and Etienne Balibar (1991) diagnosed racism without races 30 years ago. There is no need for a pronounced race theory to exclude groups identified as "other" from postulated communities. Ancestry fulfills all the requirements for a practice of social exclusion. Today, xenophobic discourses among the European Right argue less with race and instead draw on cultural descriptors and genetic ancestry. Thus, politicians of the right-wing populist party Alternative for Germany (AFD) demand that the so-called bio-Germans with two German parents and four German grandparents (!) must prevent the "Great Exchange" caused by immigration. The Nazi "Aryan certificate" was also based on this genealogical approach. The AFD follows the ethnopluralist concept of the European New Right, which promotes the ethnocultural unity – and purity – of peoples in a conscious departure from classical racism (Bundesamt für Verfassungsschutz 2019). Peoples, genes, culture and land are seen – at least in the political vision – as a unity. When name ancestry. The groups thus defined become exclusive ones that disguise who is excluded from them. This unintentionally leads to identity discourses that provide arguments for racist politics, especially in the right-wing political spectrum.

Geneticists not only provide impressive and important research results but also produce narratives of cultural and national belonging that reveal their political impact in society. These narratives become independent, solidify into ways of thinking and worldviews, and in the end leave the realm of purely scientific discourse to affect society. In right-wing discourse, they become toxic narratives (Baldauf et al. 2017). Ancestry has the potential for a new racism. A change in labeling practice is one solution. But the calls to reflect on one's vocabulary, to avoid biological essentialism and racial, nationalistic or simplistic narratives (Orlando et al. 2021, p. 4) trail off. What is needed is a closer cooperation with the social sciences as a necessary contribution to technology assessment.

Genetic sequencing methods generate raw data, not history (Bösl 2017, p. 25). The data and statistics alone do not provide historical knowledge; this can only be achieved within the framework of historical sciences. As data can always be read in different ways, this requires an open and comprehensive discussion with the participating scholarly disciplines, which takes into account the epistemic potential of the respective evidence as well as the controversies within the disciplines. Reich and many other geneticists do not achieve all this – nor can they be expected to, given the complexity of the research problems of all the fields involved. Instead, one sees a practice that makes affirmative use of a wide range of relevant sciences and ignores everything that does not seem to fit its own results. The geneticist Mark Jobling (2012, p. 797) already diagnosed cherry-picking as a problem that could only be circumvented if the disciplines involved entered into a dialogue and tried to understand the others. But there is still a long way to go; much is still in conflict and many things seem incompatible.

Ancestry has the potential for a new racism.

Reference has already been made to the different cultures of publication, which are diametrically opposed to a debate that does justice to the different scientific discourses (Jones and Bösl 2021, p. 13; Meier and Patzold 2021, p. 36). Jones and Bösl (2021) see that genetics is driven by the quest for attention, celebrity and impact. A hype is created to promote the financing of further research, which continues to be cost-intensive. The high-impact journals such as *Science* or *Nature*, with their relatively short articles in which the complexity of research problems is either relegated to an appendix or suppressed altogether, fuel this process. There are no deliberative publications that address controversies – and are permitted to do so with appropriate length – of the kind that are common in the social and cultural sciences. Neglecting complexity inevitably leads to simplistic narratives. As long as genetics determine the style and content of the debate, this will not change – and the calls not to serve racist or similar narratives remain unfulfilled appeals.

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RESEARCH ARTICLE

Making kin

The archaeology and genetics of human relationships

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Abstract • Thanks to next generation sequencing (NGS), we can now access ancient biological relationships, including ancestry and parentage, with a startling level of clarity. This has led to recentering of kinship within archaeological discourse. In this paper, we argue that blood and biology are key elements of kin-making only in so far as they are contextualized and made sense of through social relations. We argue that the conceptions of kinship that underpin archaeogenetic studies are the product of a particular historical and political context. Archaeology, with its focus on the material remains of the past, provides opportunities to examine how other forms of material and technological intervention (including ritual, exchange, and the sharing of food) facilitated the creation of kinship links not solely rooted in the human body. Here, we consider the extent to which the social salience of biological relationships identified through ancient DNA analysis can be addressed without imposing contemporary forms of familial structure and gender ideology onto the past.

Herstellung von Verwandtschaft. *Die Archäologie und Genetik menschlicher Beziehungen*

Zusammenfassung • *Dank Next Generation Sequencing (NGS – Sequenzierung der nächsten Generation) haben wir jetzt erstaunlich klaren Zugang zu alten biologischen Beziehungen, einschließlich Abstammung und Elternschaft. Verwandtschaft ist dadurch wieder in den Mittelpunkt des archäologischen Diskurses gerückt. In diesem Aufsatz argumentieren wir, dass Blut und Biologie nur insofern Schlüsselelemente der Verwandtschaftsherstellung sind, als sie durch soziale Beziehungen kontextualisiert und mit Sinn gefüllt werden. Wir argumentieren, dass die Vorstellungen von Verwandtschaft, die archäogenetischen Studien zugrunde liegen, das Produkt eines bestimmten historischen und politischen Kontextes sind. Die Archäologie mit ihrem Fokus auf die materiellen Überreste der Vergangenheit bietet die Möglichkeit zu untersuchen, wie andere Formen der materiellen und technologischen Intervention (einschließlich Rituale, Austausch und das Teilen von Nahrung) die Herstellung von Verwandtschaftsbeziehungen ermöglicht haben, die nicht nur im menschlichen Körper verwurzelt waren. Wir betrachten hier, inwieweit die soziale Bedeutung biologischer Beziehungen, die durch Analysen alter DNA identifiziert wurden, adressiert werden kann, ohne der Vergangenheit heutige Formen der Familienstruktur und Geschlechterideologie aufzupressen.*

Keywords • *archaeogenetics, kinship, biogenetic determinism, relations, identity*

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Introduction

Kin-making is a key part of how humans structure their relations with each other, with their wider community and with the non-human world. Kin relations are constituted by shared values and shared experience, as well as by shared cultural or biological lineage. Yet some of the most prominent narratives of kinship in the present moment concern themselves only, or largely, with biological relatedness as discoverable by DNA testing, as critiqued by, among others, TallBear (2013). Archaeological collaboration with geneticists has led to an explosion of new and more refined methods for studying ancient DNA (aDNA) and, thanks to the methodological refinements of next generation sequencing (NGS), we are now able to ask specific questions about genetic ancestry in our studies of the past. Biomolecular data have also begun to be applied to the reconstruction of past kinship organization and social structure through marriage and mobility patterns extrapolated from aDNA research, requiring a new attention to kinship studies by archaeologists so that the biological data can be put in dialogue with more complex, social models or approaches (Brück 2021 with comments).

At this crucial moment for our discipline, when archaeogenetic studies are being heralded as offering extraordinary insights into past communities, it is imperative that archaeologists attend to the work of colleagues elsewhere in the social sciences (TallBear 2018) in order to retain a critical stance on the assumptions that so often underpin interpretations of archaeogenetic data. Here, we present the models of kinship afforded

by archaeogenetic research and compare these to social conceptions of kinship developed by anthropologists and Indigenous scholars in order to develop a more complex approach to making kin in the past that encompasses a range of archaeological data.

Genetics, biology and relatedness

Archaeogenetic research has been part of the discipline in one form or another for several decades (Hofreiter et al. 2001; Willerslev and Cooper 2005) but the ability to reliably and rapidly sequence the whole genome of archaeological modern humans is a more recent development, and one which has allowed aDNA to have a major impact on our understanding of past people and their world. Thanks to NGS, we now have access to an ever-increasing wealth of high definition genetic data for thousands of prehistoric individuals, offering us unprecedented information about the biology, pathology, and lineage of ancient people (Skoglund and Mathieson 2018). Using sophisticated modelling it is now possible, on the one hand, to define the genetic characteristics of whole populations past and present, and on the other, to speak with extraordinary detail about the lives and relationships of individual people. Here, we divide this research into lineage somewhat arbitrarily into two general groups: 1) research into vertical patterns of relatedness, that is between ancient and modern populations in order to study, for example, hominin evolution or the population structure of Eurasia, and 2) horizontal patterns of relatedness, that is between populations or individuals in the past.

Schiffles et al. (2016) provide us one example of vertical research. They set out to investigate the impact of Iron Age, Roman and early medieval mobility, including migrations, on the genetic structure of the current British population by comparing ten archaeological whole-genome sequences with 30 modern British and over 500 modern European ones. They then applied statistical modeling to determine the shared lineage between these different samples and found that early medieval ancestry makes up less than 40 % of the genetic profile of the modern British population with notable regional variation. At the time, this study presented novel methods applied to whole genomes. That said, drawing connections between past and present populations through mitochondrial DNA (mtDNA) transmitted maternally and y-haplogroup lineages transmitted paternally is an established area of research, applied by the public in various ways, both laudable (Abel and Schroeder 2020) and dangerous (Hakenbeck 2019).

By contrast, Knipper and colleagues (2017) and Mittnik and colleagues (2019) offer two well-developed articles examining the horizontal relatedness among individuals in a series of approximately 4000-year-old cemeteries in southern Germany. Through a mixture of genomic and isotopic methods combined with fine-grained archaeological data, they are able to reconstruct biological family trees, link these with spatial patterns in cemeteries and specific grave goods, and combine them with mobility data suggesting some members of the cemetery community – typically female-bodied – were born elsewhere. They use this to argue for a social structure predicated on female exogamy and patrilocality. These two papers are part of an emerging trend (Reich 2019; Sjögren et al. 2020) of archaeologists and geneticists arguing that biomolecular data offer special insight into past social practices, including kinship and mobility, at least in part through these patterns of relatedness revealed by NGS.

Both vertical and horizontal studies of relatedness, being based in genetic data, necessarily equate kinship and lineage with biological relatedness, with blood relations forming the building blocks of their social and population models.

Relations and relatedness

Social scientists (especially anthropologists) have long grappled with the tension between biology and society when seeking to understand kinship. Since the 1980s, biologized models of relations have been critiqued for their eurocentrism and for reifying a false opposition between nature and culture (MacCormack and Strathern 1980; Schneider 1984).

Subsequent research has expanded our understanding of kinship beyond biological relatedness to include affiliative and adoptive relationships as well as relations with other-than-human kin (Sahlins 2013). In many cultural contexts, kinship is not conferred by birth but is a product of social practices such as co-residence or the sharing of food (Carsten 2004); kin, in other words, are made. Feminist and queer approaches to kinship have decentered the heteronormative assumptions of consanguinity and descent in favor of relations of care (Weston 2013), and recent research has pushed us to consider its materiality (Goldfarb and Schuster 2016). From a standpoint in disability studies, Wolf-Meyer (2020) proposes that technology can also be kin in that we develop intimacy and mutuality with technological things as they mediate our engagement with the wider world, as with the use of a walking stick or a prosthetic. Webs of obligation encompass more than the living world.

In many cultural contexts, kinship is not conferred by birth but is a product of social practices.

Indeed, following the lead of First Nations and Indigenous scholars (TallBear 2018; Todd 2017; Watts 2013), kin-making is not cross-culturally generalizable, and the line we tend to draw between human and non-human substance is an artefact of our own society rather than a universal experience. Dwelling in the world creates and sustains kinship (Andrade 2014). Relations may be plants, animals, and places; and we are obliged to the non-human world, just as we are to our human kin (Kimmerer 2013, pp. 233–239).

Biological concerns, of course, remain present, as demonstrated by vibrant ongoing research around in vitro fertilization, post-humanist 'biohacking' and the public's engagement with personal genetic testing (Carsten 2004; Haraway 2016). But, even here, the definition of biological kin is expanded (Franklin 2001). Although some anthropologists reject biological definitions of kinship (Sahlins 2013), genomic data and genetic webs of relations remain part of the Euro-American definition and experience of kinship (Reardon 2017; Stallard and de Groot 2020).

The development of whole genome sequencing and the 'new genetics' it spawned also birthed a new and complex discourse around genetics and kinship that has only accelerated with the advent of NGS. Marks (2001), for example, delineates the racist legacy of human population genetics which influenced and shaped the long-running vertical relatedness study the Human Genome Diversity Project with its promise to tell (an unspecified) us '*who* and *what*' we are. Indeed, the intersection of ancestry, personal identity, and race remains a dominant concern, with more recent work investigating how, for example, contemporary people use home DNA tests to construct ancestral lineages tying them to imagined past populations (Strand and Källén 2021). TallBear (2013), while rejecting a genetic definition of Indianness as an imposition of colonialism, outlines the complex relationship between 'gene talk' and 'blood talk' for describing lineage in First Nations communities and, perhaps more importantly to her argument, making genealogies legible within the racist framework of a settler state. Indeed, Wolf-Meyer (2020) argues that genetic tests do not so much expose kin relations as invent them, by creating ties between bodies through substance. This echoes earlier work by Haraway (1997, pp. 56) who sees genes creating new intimacies between humans and between us and non-humans, since we share genes amongst us despite our difference of species.

TallBear (2013, pp. 60) describes how technical choices and technological knowledge in DNA and aDNA research shape perceived patterns of relatedness. Y-chromosome and mtDNA analyses reveal only a tiny percentage of an individual's ancestry, for example, while the patterns of relatedness that emerge depend on which genetic markers are analyzed. Moreover, studies of population genetics construct Indigeneity in a particular way. The drive to collect DNA samples from living representatives of Indigenous groups in order to understand human evolutionary history is underlined by the assumption that such groups are pristine, uncontaminated by complex historical processes of interaction with their neighbors, and that they are in danger of disappearing (Marks 2001). Thus, as TallBear (2013) argues, they are rendered relics of earlier stages of human evolution whose DNA is essential to understanding the history of humanity – here construed primarily as the history of the modern European/white subject. By representing Indigenous DNA as part of 'modern' humans' inheritance, such studies promote new forms of colonialism.

By representing Indigenous DNA as part of 'modern' humans' inheritance, such studies promote new forms of colonialism.

Science, in other words, does not reveal hidden truths but generates, orders, and evaluates data to create a particular vision of the world. But, the critiques of Indigenous scholars, anthropologists and others have yet to be adequately addressed in the recent flood of archaeogenetic studies. The research questions at the heart of NGS analyses presuppose the existence of distinct groups – groups that are then created through the application of statistical methods. Such results bolster essentialist, biogenetic formulations of identity that do not fit people's lived experience and that are too easily weaponized in political debates around rights, roots, and belonging.

Kinship in archaeology

Although archaeology and anthropology have been entwined for generations, archaeological data has rarely been fine-grained or abundant enough to afford insight into the kinship structures our social anthropologist colleagues have delineated. Instead, individual bodies of the dead have been a primary focus for studies of relations. For example, the identification of non-metric traits in human bone assemblages (that is, morphological features that may have been inherited) has been argued to indicate biological relatedness, as at the megalithic tomb at La Chausée-Tirancourt in northern France (Leclerc and Masset 2006), where each chamber was interpreted as the burial-place for a different family group. Elsewhere, close spatial relationships between different individuals in the grave have been interpreted as indicating kinship among the deceased. MtDNA analysis indicated that the woman buried together with two children in a Corded Ware grave at Eulau in northern Germany was not their biological mother, but the excavators argue that she is likely to have been their stepmother (Haak et al. 2008). This example fore-

grounds possible points of disjunction between biological and social kinship and highlights the modern, Eurocentric assumptions regarding the character of the family unit that underlie such interpretations.

Archaeologists have occasionally attempted to identify more specific forms of kinship organization. It has been observed that the primary burials in British Bronze Age barrows were frequently male, while women and children were often buried in satellite positions; and it has therefore been suggested that these communities were patrilineal (Parker Pearson 1999, pp. 90). However, such interpretations ignore the many barrows in which women or children were the primary burials, and essentialize a binary gender system based on archaeological methods of sexing human remains and interpreting grave goods (Frieman et al. 2019). Inferences regarding kinship structure have been made using other types of archaeological data also. Ensor (2017), for example, has employed cross-cultural analysis to identify regular associations between house size, settlement layout and kinship organization, distinguishing a variety of different descent and residence patterns among Maya and Hohokam groups.

The evidence of biogenetic relatedness offered in increasing quantity and detail since the adaption of NGS methods for the study of ancient DNA has both challenged and enriched this patchy research history into kinship. Horizontal kinship studies in particular have been extended beyond groups of already associated human remains to explore patterns of relatedness across whole cemeteries or even regions. However, this wealth of scientific data is not matched by the equivalent development of social models, unlike elsewhere in the human sciences where whole genome data has been rapidly assimilated into a rich ongoing discourse into social structure and kinship.

Making kin

As a direct result of the ancient genetic revolution of the last decade, archaeologists are now grappling with kinship, both horizontally between ancient individuals and vertically as it connects past and present populations, with more depth, rigor and complexity than at any time in the discipline's past. We are, to some extent, playing catch up as we try concomitantly to assimilate an ever widening pool of scientific data about biological relatedness; to explore how kin were *made* through social practices such as ritual, exchange, and the sharing of food; and to push back against uncritical constructions of lineage and identity that reinforce narratives of race and ethnicity in the present (Frieman and Hofmann 2019; Furholt 2019).

We ground our own work in the need to balance ideas of relation that are discoverable by genetic research with those whose form is less tangible. This applies both to what we have termed vertical and horizontal kinship. Hence, Frieman and colleagues (Frieman et al 2019) have been exploring the ways that biologized kinship discourse about past individuals has the potential to impact and shape contemporary worldviews due to the sense of connection or vertical lineage that forms part of the DNA discourse. We delineate how social models drawn from genetic data necessarily foreground heterosexually reproductive individuals, meaning genetic-led narratives of affiliation and social reproduction make central unions between two individuals of opposite binary gender, even though this conformation is far from universal in global human society past and present. In this way, social models predicated on genetic lineage inadvertently reinforce contemporary inequalities and render harder to parse those aspects of gender, relation, and identity that do not materialize biologically.

Social models predicated on genetic lineage inadvertently reinforce contemporary inequalities.

Brück and colleagues (Booth et al 2021) have called into question generalized models that uncritically impose contemporary gender relations onto the past by demonstrating variability in kinship structures among Chalcolithic groups in Britain – groups that have elsewhere been modelled as patrilineal and patriarchal (Sjögren et al 2020). Instead, we drew on archaeological and genetic evidence to elucidate the importance of matrilineal links and of kinship between those who were not genetically related. We argue that, even where patrilineal relations were foregrounded, this did not mean that women lacked social and political power. We noted, for example, that no genetic links could be discerned amongst the small group of near-contemporary burials from Windmill Fields, Ingleby Barwick, North Yorkshire; here, kinship may have been based not on biological links but on co-residence or other shared social practice. On Amesbury Down in Wiltshire, paternal links were sometimes emphasized (for example, in the neighboring graves of two adult men, identified genetically as father and son). Yet, evidence for the reopening of the nearby grave of an adult woman in order to retrieve some of her bones, possibly for curation, suggests that she may have been viewed as a venerated ancestor.

Indeed, archaeology is particularly well positioned to consider how kin relations are generated through social practice and are not solely located in the human body. Johnston (2020), for example, argues that Bronze Age hoards in Britain and Ireland gave material form to the inter-personal and inter-group exchanges central to the maintenance of kin relations, a task he describes as *kinwork*. He also addresses the role of non-human kin, exploring how Bronze Age kin relations were rooted

in places invested with animate and ancestral powers. These relations can be traced in material interventions in the landscape, such as the deposition of bronze objects at striking landmarks. One of us has interpreted the child-sized shale bracelets from British Bronze Age settlements, deliberately snapped into halves or quarters, as the residues of age-grade ceremonies in which fragments of socially-significant artefacts were gifted to important kin (Brück and Davies 2018). Such practices can be viewed as technologies that make kin, just as DNA testing is used to make kin in the present. Archaeology's focus on materiality, in other words, provides us with a unique perspective on kin-making that calls into question essentializing narratives, allowing us more scope to explore how kinship transcends the boundaries of the body and taking account of relations of obligation and care between humans and non-human others.

Conclusion

Although genetic models currently dominate archaeological discourse about kinship, we reject the proposition that they offer special insight into social structures or interpersonal relations. Genetic data offer one class of evidence which must be weighed alongside many others and carefully integrated into archaeological models so as not to reproduce our own unequal world in the past. The affordances of genetic research artificially limit the extent of kin modelling. Because genetic analysis defines relatedness as the outcome of sexual reproduction, it can only ever identify kin in a narrow and reductive sense that elides webs of obligation, mutuality, and interdependence. As an approach, it is inherently heteronormative and lacks tools to encompass the richness and complexity of social life. Too often, archaeogenetics offer an impoverished conception of kinship that biologizes social relations in immutable and irrevocable, natural patterns.

In contrast, as we have discussed, Indigenous scholars and feminist anthropologists exhort us to resist biological supremacy and move beyond models of kinship rooted in the heteronormative, patriarchal, and anthropocentric structures of settler sexuality (Kimmerer 2013; TallBear 2018). They consider what it means to be in relation with others and they develop a more expansive and inclusive definition of kinship as the outcome of ongoing acts of mutual care. This perspective makes space for forms of kinship that are not predicated on sexual reproduction. It allows for alternative visions of gender and sexuality, and is open to including other-than-humans as kin – a key prerequisite to imagining better ways of living in a world scarred by extractive capitalism.

The advent of rapid, increasingly affordable whole genome analysis for ancient samples has, for the first time, created an impetus for archaeologists to develop our own models of kinship that engage both with biological relatedness and with the social patterns discoverable in our other, fragmented datasets. In fact, we argue that the archaeological data can challenge and extend biologized narratives of kinship. Moreover, archaeologists, we suggest, are particularly well-placed to contribute to wider debates about identity, kinship and biology for we reconstruct the varied social practices – for example building houses, burying the dead, or giving gifts – central to the creation of diverse forms of relations and relating in the past and the present.

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