Article

Image and exposure: Envisioning genetics as a forensic-surveillance matrix

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Abstract

This paper takes the ‘visual’ as the primary subject to engage in a dialogue about surveillance by drawing upon the specific case of the genetic image. Specifically, the genetic image has shifted from the ‘one gene for one identification’ model used in criminal law to what are now categorical, contextual and pattern-based configurations of DNA profiling that are able to compare multiple genetic samples in a singular image. The ability to profile genetics for law and security purposes is, thus, protracting well beyond the confines of the criminal legal domain (i.e. the crime scene, forensic laboratory, courtroom) and into the realm of surveillance: national security, defence, immigration, military and even humanitarian domains. Such a notable transition in visual profiling has also been met with a synonymous reformation in the status of genetic data as it converts from evidence in the realm of criminal law to, now, intelligence in the surveillance-based contexts noted above. This visual reclassification of genetic data reorients DNA to an informing, as opposed to an identifying, role. Finally, how experts, scientists, legalists and other relevant practitioners conceive and represent ‘truth’ and ‘trust’ in light of an increasingly diverse range of genetic imagery is subject to discussion.

I. Introduction

This paper analyses the ways by which the DNA profile, or genetic image, is conceived and represented. Over time, DNA profiling has moved from the ‘one gene for one identification’ model used in criminal law, where an unknown sample (i.e. crime scene) is compared to a known sample (i.e. suspect) in order to determine if a match exists (Figure 1). Rather, in the post-9/11 security environment and, most notably in the past few years, novel alterations and reconfigurations of genetic imaging systems have started to emerge. These include, for instance, categorical, contextual and pattern-based display systems of genetic data, such as the microarray, the lattice and the ‘cluster’ (Figures 2, 3, 4), that are able to compare multiple genetic samples and forms in a singular image. The ability to profile DNA is thus protracting well beyond the confines of the criminal legal domain (i.e. the crime scene, forensic laboratory, courtroom) into the realms of surveillance: national security, defence, immigration, humanitarian, army and military operations. Similar to the ways that ‘surveillance creep’ has occurred in relation to expanding DNA databases (Nelkin and Andrews 1999), the ability to reclassify genetic imagery has justified new profiling strategies for agencies involved in diverse jurisdictions and across multiple domains. Such agencies include national and international security (i.e. immigration, customs, border patrol), military (i.e. war zones), humanitarian efforts (i.e. mass disasters), genealogical and kinship analysis (i.e. familial DNA testing, external visible characteristic extrapolations from genetic data), and multimodal, robotic and biometric applications (i.e. rapid and combined DNA analysis, and the enhanced portability and mobility expected through portable laboratories with ‘on-the-spot’ testing capabilities). Consequently, new ways of representing genetic information are increasingly applied to *populations*, mass levels, as opposed to *individuals*, as witnessed in examples such as war victims in mass graves, missing soldiers and military personnel from past wars (i.e. military ‘dog tags’ or IDs), or the remains from mass disasters due to

natural catastrophes or terrorism attacks (i.e. airplane crashes, the World Trade Centre tragedy and the southeast Asia tsunami) (Ge et al. 2010). Such a notable transition in visual profiling has also been met with a synonymous reformation in the status of genetic data as it converts from *evidence* in the realm of criminal law to *intelligence* in the surveillance-based contexts noted above (see, for instance, Machado et al. 2011). While such a distinction may appear trivial, reclassifying genetic data from evidence to intelligence is significant in the sense that it reorients DNA to an *informing*, as opposed to *identifying*, role.

For the purpose of this discussion, four genetic profile-types will be evaluated as a source of comparison and contrast: the electropherogram (Figure 1), the microarray (Figure 2), the lattice (kinship or genealogical modes of analysis) (Figure 3) and the bacterial cluster (microbial forensics) (Figure 4), with additional reference to biometric and multimodal applications (conjoined bodily identifiers, such as those used at border crossings or other points of entry into a given country, or in war-zones). Drawing from these examples, the key questions this argument seeks to open, identify and clarify relate to the authentication and legitimation of each image-type. For instance, how do we know what we see? How accurate is knowledge about DNA when the genetic display itself is undergoing ongoing states of transition? Who are the experts responsible for interpreting genetic-based information, and do these individuals or systems vary when DNA is classified as evidence as opposed to intelligence? Along the same lines, are different modes of expertise required for different genetic image-types, series and classifications?

This is not to say that the idea of genetic-based surveillance is entirely novel to the surveillance literature. To date, the most theoretically-informed definition appears to be that of bio-surveillance (and/or biopolitical surveillance) as it derives from Foucault's (1977) notion of bio-power: the idea that natural life (the material or physical body) is included in, or inseparable from, the mechanisms and calculations of politics and law. Contemporary notions of bio-surveillance are not restricted to the human body, however, with the exact meaning of what constitutes the 'body' or 'bodily' having undergone radical changes. Now, there are unprecedented ways in which bodily matters and functions can be monitored, assessed, analysed and categorised (Van der Ploeg 2012: 177). For instance, the recent mission statement of the Department of Homeland Security's National Biosurveillance Integration Center (2012) contends that its primary objectives include biological tracking to rapidly identify, characterise, and localise a biological event of national concern; integrate and analyse data relating to human health, animal, plant, food, water and environmental domains; as well as disseminate alerts and other pertinent information. Importantly, the definition of biology is not restricted to the human body, but extends to non-human and even environmental sources. Moreover, it is noteworthy to acknowledge the crucial role of the image to any type of genetic-based surveillance, since DNA in its natural state is imperceptible to the 'naked eye'. Only once DNA data is rendered visible may any kind of surveillance (monitoring, observation, exposing) take effect. Therefore, the genetic profile is forefront in shaping surveillance strategies as each image is a necessary starting point to predict what sorts of monitoring, detecting, framing or exposing may be initiated.

The expansion of genetic data through imaging and profiling technologies can also be understood through Latour's (1994: 30-5) notion of 'technical mediation' which, he argues, is a phenomenon composed of four key qualities: a programme of action (institutional and infrastructural agendas), translation (drift, displacement and invention), hybridity (the human-machine coupling), and symmetry (what is conserved through ongoing transformations). In line with this notion, emerging and in-effect genetic-based surveillance directives align with national and international security agendas (i.e. including immigration, military, war-zones and bioterrorism), humanitarian operations (i.e. mass fatality incidents) and kinship modes of analysis that seek to infer familial genetic similarities and/or external visible characteristics (EVCs) based on genetic data. The multitude of emerging DNA profiles are also 'hybrid' in that any image produced requires expert, or at least an informed, opinion to read, interpret and communicate the

meanings of, more often than not, highly specialised and technical information (see Edmond and San Roque, this issue). The notion of symmetry also applies to genetic-derived surveillance in that, regardless of the particular profile at stake, all images are associated to one another in the common nomenclature and concept of DNA as the key point of reference.

Overall, this paper seeks to identify and clarify the types of images available and emerging at the forensic-surveillance nexus by inquiring how and why such data has been deemed necessary from a surveillance standpoint. The rest of this paper is ordered into four subsequent sections. The second section provides a detailed pictorial analysis that pinpoints the ways in which genetic data is classified and reclassified at the visual level (i.e. the shift from individual to categorical, contextual and indirect profiling) as well as in status, from evidence to intelligence. The third section theoretically attends to the complexity of the notion of the image in both surveillance and scientific discourses. The fourth and fifth sections deal with larger epistemological questions regarding how genetic knowledge acts as a source of ‘truth’. Here, questions are posed in terms of what images are deemed valid, how accuracy is defined, and how information is collected, interpreted, portrayed, categorised and disseminated—whether to experts, practitioners, the public, or any other.

II. Technique: The visual reclassification of genetic data

This section traces DNA profiling from its original forensic location as *evidence* in the criminal justice system (Figure 1) to the current use of genetic imaging as a tracking, monitoring and exposing device inherent to surveillance practices (Figures 2, 3, 4). This shift, I contend, is most evident in the *image*: from the individual identification that the electropherogram affords, to the less-precise combinatory, contextual and pluralised display patterns that DNA as a source of intelligence affords. Evidence, in common-law jurisdictions, refers to any number of witness testimonies, documents, photographs and other images, scientific and/or visual data as they ascertain facts for law enforcement and fact-finders (i.e. judges, lawyers, jurors). Scientific evidence, such as DNA profiling, requires mediation via expert testimony for judges and/or juries to be able to determine the relevance, as well as the validity, reliability and credibility of the evidence and the science at hand. The admissibility and presentation of expert evidence is often a contentious exercise in the adversarial setting of the courtroom (Edmond 2003; see also Edmond and San Roque, this issue). Intelligence, on the other hand, refers to strategically informing and identifying patterns and relationships between genetic (or other crime) data, in response to evolving risks or threats, as these strategically identified risks dictate, shape and prioritise investigative activities and objectives (Cope 2004; Gill 2000). Walsh (2007) points to how the establishment of what is now a universally recognised, standardised and uniform platform to conduct forensic DNA profiling in legal systems has been the stabilising force that has paradoxically allowed new rationales, initiatives and applications relating to genetic-based investigations to emerge and proliferate into wider institutional contexts. In contrast, and unlike the evidentiary standards in place for DNA profiling (NFSTC 2011), there are no clearly defined criteria or quality controls in place for genetic profiling as an intelligence tool. Thus, there is no guarantee that data will not be misused or misinterpreted. The following examples highlight the radically different ways DNA can be visualised in a forensic-surveillance matrix, including the electropherogram, the microarray, the lattice model (or family-tree), and the (bacterial) cluster.

Figure 1. Example of individual genetic profile, the Electropherogram. Image courtesy of Nature Review Genetics (Source: Jobling and Gill 2004)

The first image for consideration, the electropherogram, is the current forensic profile used in criminal proceedings to determine whether a match exists at the individual level between an unknown (crime scene) sample and suspect (known) DNA sample (Figure 1). This peak-based graph is highly regulated and standardised within the international forensic community to ensure consistency within and between profiles (NFSTC 2011). With the exception of visual anomalies that are associated with low-quality and low-quantity DNA samples, the electropherogram is an internationally validated system of profiling that determines, compares and regulates human identification in a forensic legal context.

The electropherogram's legitimacy as a human identification mechanism has allowed for its transformation into the specifically surveillance-oriented methods of biometric, robotic, multi-modal and even impending lab-on-a-chip (LOC) technologies as they are deemed essential for highly secure spaces including borders, airports or other points of entry into a given country.

In particular, multimodal applications provide the speed and efficiency to conjoin genetics with other human identification systems, including human anatomy, physiology, physics, mathematics, engineering and computer science. The ability to orchestrate rapid identifications and/or authentications of individuals quickly, and with ease, renders these tracking systems particularly attractive to national and international security (Van der Ploeg 2012: 179-80). For example, the Ion Personal Genome Machine (PGM), a product of the Department of Homeland Security, directly translates genetic sequencing information into digital form by using semi-conductor technology to enable high throughput analysis of up to ninety-six samples simultaneously. The emphasis on achieving rapidity, mobility and portability by security specialists and surveillance operators justifies the implementation of biometric and multimodal techniques as necessary to counter potential risks and/or threats, such as terrorism.

The shift from individual to categorical profiling, and evidence to intelligence, is mirrored in the shift from the electropherogram to the microarray (see Figure 2). Both image-profiles are similar in that they compare human DNA samples, albeit in very different ways. This particular microarray compares thousands of forensically relevant human DNA samples to determine varying bodily and environmental contexts.

The microarray is a comparative or 'indirect' profile of human DNA in the sense that there is very little precise detail regarding the individual sample, although it elucidates a broader picture in terms of how sample-contexts relate to one another, making it useful as a research and intelligence tool. This particular pattern highlights the differences between human genetic sample-types, including semen (SE), saliva (SA), vaginal (VS), menstrual blood (MS) and whole venous blood (WB). The goal here is to elucidate three key features as they vary between sample-types: cellular origin, timing-sample placement (i.e. the age, deposition and degradation features) and environmental contexts (i.e. indoors, outdoors, heat, cold, thawing) (Kayser and De Kniff 2011).

Figure 2. Example of categorical genetic profiling, the Microarray. Image courtesy of Nature Review Genetics (Source: Kayser and DeKniff 2011).

Figure 3. Example of genetic lineage when there are many possibilities. A Lattice of identification. Image courtesy of Charles Brenner. Available online at: <http://dna-view.com/lattice.htm>, Date accessed February 2, 2012.

While the microarray was originally designed for epidemiology and disease research, its incorporation into the forensic-surveillance matrix is justified on the basis of its diagnostic capacity to illuminate visual comparisons within and between sample-types. Yet these same capacities that allow the comparison of thousands of forensically relevant human bodily fluids synonymously, and in a single frame of reference, render it unable to provide unique and individual identifications.

The third image for consideration is the lattice structure, which derives from forensic mathematics and is likened to a ‘family-tree’ model (Figure 3). This profile relates to the aforementioned electropherogram and microarray in that it refers to human DNA—albeit, another ‘type’ of human DNA known as familial DNA that includes either maternal [mitochondrial or mtDNA] or paternal [Y-STR or Y-chromosomal] information.

The use of familial DNA (either maternal or paternal) is relatively new and to date has been restricted to cases deemed exceptional to investigators in law enforcement or security contexts, such as major case crimes (i.e. serial killer cases and other violent and sexual offences) (Miller 2010; Keiper 2011). The goal of familial DNA profiling is to trace suspects through potential maternal or paternal DNA profiles already stored in law enforcement or security databases.

Tracing an unknown or suspect genetic sample through ancestral lineage involves a much more labour-intensive search process, since a familial-based search may result in many matches to many different individuals within a family-type (Williams 2010). Due to the privacy implications, procedural leeway is typically granted for investigators to search familial DNA databases in a specific case if all other leads have ‘grown cold’. To date, perhaps the most famous example of familial DNA as an investigative tool was the Los Angeles serial killer case, the Grim Sleeper, which was lauded as a success story in that authorities traced the killer by collecting and comparing an unknown (crime scene) genetic sample to what was determined to be his father’s DNA profile that was already stored in a relevant criminal database.

The second form of familial or genealogical-based genetic testing that is equally controversial is called forensic DNA phenotyping (FDP). This method seeks to infer external visible characteristics (EVCs) (i.e. eye, skin and hair colour) directly from a familial (maternal or paternal) genetic sample (Kayser and De Kniff 2011: 182). In line with surveillance logics, FDP seeks to reduce a pool of suspects and guide law enforcement and security agents by predicting the physical appearance of suspects through EVC data that stems from unknown genetic material recovered at a crime scene. Genetic testing mechanisms such as *Retinome* or *DNA Witness* are already available and marketed in the United States to deduce such outward features from genetic information—in this case, predicting human iris colour and other EVCs from ancestry-based genetic samples. The sociological consequences associated with familial-based genetic profiling are prolific as they introduce new forms of genetic ‘social sorting’ (Lyon 2006) that recast genetic profiling along multiple lines, including ethnic background, socio-economic status, geographical positioning and, now, family ancestry.

Figure 4. Example of bacterial genetic, cluster-based profiling. *Bacillus anthracis*, Anthrax. Image for public viewing. Date accessed, February 18, 2013. Available online at: https://en.wikipedia.org/wiki/Bacillus_anthraxis

The final image deviates from the previous three in that it is non-human genetic material at stake. Rather, Figure 4 reveals an image of the pathogenic mould, *Anthrax*, a strain of bacterial DNA used as a weapon in bioterrorism. Bacterial microorganisms are used in terrorist plots and attacks since they are easily grown from a single organism or cell (unlike other nuclear weapons that require sophisticated instrumentation or skilled labour). Deadly forms of bacteria, which may include other viruses and toxic agents, contain the potential to induce death or serious health concerns to food supplies and environments (Pattnaik and Jana 2005).

This particular profile is meant to depict the growth and evolution of bacterial strains through environmentally based branch of forensics: microbial forensics. Establishing standards for evidence collection, analysis and interpretation, will depend on the bacterial outlook for a given strain.

Unlike other genetic-based images and investigations, bacterial formations are collected from the site of the attack as a way of detecting the *route of exposure* for an infectious microbe. The investigative focus, therefore, is on collecting environmental samples as a way to establish the essential background, ambient materials and geographic origin. Measuring the genetic variations between microbial strains is necessary to infer the origin, relationship or transmission route to link causative agents to specific bacterial

formations. Uniquely, the investigator (usually an investigatory team) then obtains samples from both victims and the environment to precisely identify the microorganism that led to the attack, and preserve such evidence for an impending trial or for further experimentation.

Taken together, these four image-types reflect how categorical, contextual and clustered genetic profiles diverge from the longstanding individual profile, the electropherogram. The move from standardised forensic profiling techniques that work at a ‘one gene for one identification’ basis (Figure 1) to categorical, contextual and cluster-based imaging (Figures 2, 3, 4) indicate emerging trends that demand attention, especially in the uncertain terrain involving the use of genetics as an intelligence source. At the same time, the diversification of genetic imaging suggests a potentially endless future for DNA profiling as the sources are no longer restricted to the human body but now include, or make reference to, the genetic material of animals, plants, bacteria and other living organisms. The precise detail afforded at the individual level in the electropherogram continues to render genetic information attractive to law and security alike. This ‘original’ DNA profile has been the impetus that has inspired what are now ongoing technological innovations (i.e. rapid testing devices, the enhanced mobility and portability of laboratories, and higher throughput capacities) that stretch far beyond what was initially imagined for DNA as a law enforcement tool in the 1980s (Lynch et al. 2008). Now, advances in genetic testing are being designed to register profile data ‘on the spot’, or in the field, as this is deemed necessary in situations where a quick result is needed (e.g. deciding to hold or release a suspect in a terrorism investigation), to provide initial screening (e.g. at an airport or point of entry), or when getting to a forensic laboratory is difficult (e.g. in a war zone) (Messmer 2011, 2012; Quick 2010). The genetic image, categorised variably in the four image-types presented above, is thus paradoxical in the ability to synonymously sustain, transform and overlap forensics with surveillance as witnessed in the increasingly wide range of genetic visualisation tactics and procedures. New imaging possibilities bring with them new inconsistencies, difficulties and controversies, however, such complexities associated with the image are considered next.

III. The complexity of the image

The previous section reorients theoretical and analytic attention to the visual as the centrepiece and exemplar to comprehend the genetic image in a forensic-surveillance context, elucidated in the shift from individual to categorical modes of profiling and mirrored by the change in status from evidence to intelligence. This ‘visual turn’ towards categorical and contextual modes of DNA profiling methods (Figures 2, 3, 4) derives from the longstanding DNA profile inherent to the criminal legal domain (Figure 1). Yet, what are not acknowledged in governmental discourses that parade the benefits of such novel DNA profiling techniques (Miller 2010; Quick 2010; Randerson 2013; Daw and Finkelstein 2006) are the many complexities associated with scientific visualisation. This section outlines how the scientific image is theorised along multiple lines, including how it is produced, selected, and engaged. Decisions regarding how to select one image at the expense of others are significant and often the subject of great debate in determining what constitutes the ‘best picture’ to convey an idea, all the while preserving the validity and accuracy of the knowledge portrayed. As Lynch (1991: 2) states, ‘although they strive for representational realism when they assemble and analyze micrographs, chart recordings and intensity maps, scientists can achieve this realism only by means of complex textual and instrumental mediations’. That is, the genetic image is not to be viewed simply as a discrete or isolated ‘surface indicator’, but is a multifaceted creation and collaboration that is inseparable from the technologies, techniques, histories, researchers, investigators and institutional agendas that coalesce to render its visibility in the first place. As such, certain key features pertaining to the image itself will be elaborated further in this section as they relate to the formulating, analysing and the general provision of genetic knowledge as an information source to the forensic-surveillance matrix (institutions, logics, strategies).

The notion of the image is a complex topic that has been the subject of historical, sociological and philosophical insights and debates, especially as it relates to scientific knowledge and an idealisation of

objectivity. To begin, how visualisation is presented in the surveillance literature aligns most frequently with Bogard's (2006) use of Baudrillard's (1994) simulation notion. Here, the image is likened to a captured moment or activity that occurs as a, 'metamorphosis of reality into hyper-reality', and is framed within computerised and digitised networks. The picture is a surface indicator, utilised and stylised to show, 'what the viewer needs to know', at the expense of providing in-depth and contextualised insight. Both Baudrillard and Bogard emphasise the digital quality of simulation, as these notions align with Deleuze's (1992) data double, where data is virtual and located in computerised networks. Here, the image is inseparable from the fluid, mobile and digitised environment where electronic data is assessed and retrieved. The genetic, in line with Bogard's (2006: 66) schema, is one of many 'elementary particles of social strata', that may include other body parts, fragments, partial movements, skin colours, scars, vocal sounds or any other bodily substance. Larger-scale classifications and frames of reference such as race, class and gender are rearranged by Bogard's (2006: 66) 'sorting of particles' approach as the mechanised manipulation of data creates new formulations, assemblages and matrices of data in novel, emerging and tentative formations. Surveillance in such simulated and visual terms is rendered mobile as it adheres to an electronic logic that encapsulates bodies and bodily presences in the flows of digital movements, actions, and engagements.

The conceptual interplay Bogard (2006) articulates reveals the simulated image as one where there is no reality outside of imitation and replication. For surveillance, this means 'what you see is what you get' as it applies to material and immaterial contexts. On the other hand, from a scientific viewpoint, the image is thought of as inextricably linked to a host of detailed and complex scientific processes. Whether diagrams, graphs, photographs, maps, charts or other related visual representations, decisions about what is the best way to represent and communicate scientific information visually are the fundamental goals, yet equally problematic concerns of contemporary scientific practitioners. Moreover, those responsible for producing, interpreting and communicating imagery must also account for a cultural context in terms of how seeing and recognition is historically and affectively shaped (Jones and Galison 1998; Foucault 1970). Social studies of experimental and laboratory science have elucidated the complex ways that visual outputs are not restricted to a singular stage of analysis but originate from the methodologies, procedures, techniques and instrumentation (i.e. microscopes, telescopes) that render otherwise undetectable matter into observable and intelligible objects (Lynch and Woolgar 1990). The further dimensions of engagement and deployment of scientific knowledge through images reflects the instrumental role of picturing science in the production of knowledge, as well as the dissemination of this information into various milieus (Burri and Dumit 2008: 300). The image is not a discrete or bound aspect of science or surveillance for that matter, but indivisible from the historical, theoretical, analytic and experimental applications that expedite the production and dissemination of these results. Here, surveillance intersects with science along the lines of, 'to see is to know' or, in the case of surveillance, 'to see is to expose, detect and capture'.

Selecting an image is one of the key components for scientists to determine what are the best images, or 'working objects'. This decision-making is crucial in the sense that it instils visual reference points that erect boundaries around what domains of phenomena are deemed worthy of study and, thus, standardising certain images and/or objects for generalisation and comparison purposes (Daston and Galison 1992: 82-5). The process of selection thus requires deducing, simplifying and presenting findings as they reflect in the 'fine edge and final stage' of an entire process of theoretical precepts, data gathering, analysis and experimental procedure (including accidents, errors or any other features of the knowledge-producing process). Nancy (2005) in his work, *The Ground of the Image*, posits the image as both distinct and indistinct, where distinction relates to the surface quality of the image, what he calls the 'site of concentration'. However, this same image is also indistinct in the sense that it contains a relational capacity that engages the viewer or audience in any number of ways (i.e. evoking a reaction, interpretation or judgment). This engagement may also be forceful, as in a surveillance context, where the consequence of DNA profiling has potentially severe consequences, such as restricting entry to a given country or sentencing to punishment in the case of a criminal conviction.

Another key perspective that relates to the scientific image is that of layering. Rose (2011), from a critical methodological standpoint, assesses the image as a layering process in articulating the production aspects (i.e. the technological apparatus used to envision), composition and design (i.e. image classification and content, colour, spatial organisation, symbols and relations to other images) and communications (i.e. the extension of information provided for evidential or intelligential forecasting). Likewise, Pinch (1995) argues that each image is likened to a compilation of ‘building-blocks’ that intertwine historical and theoretical knowledge, individuals, instruments and laboratory facilities. Beneath the visual conclusion of the image surface, he argues, are ‘cascades of information’ that relay diverse knowledge systems, sources and practices, instilling a sense of preservation by retaining the historical, theoretical, instrumental, experimental and technical lineages. Accordingly, Daston and Galison (1992: 82) point to this layering-effect in terms of making sense of and, granting weight to, the historical, theoretical and philosophical accounts of scientific knowledge. In relation to the image, they contend this:

...accounts for the hopelessly, but interestingly, confused present usage of the term objectivity, which can be applied to everything from empirical reliability to procedural correctness... As historians of objectivity, we will not be concerned with recent controversies over whether objectivity exists and, if so, which disciplines have it. We believe, however, that a history of scientific objectivity may clarify these debates by revealing both the contingency and diversity of the components that make up the current concept. Without knowing what we mean and why we mean it in asking such questions as ‘is scientific knowledge objective?’ it is hard to imagine what a sensible answer would look like.

In accordance with this outlook, each scientific image has its own history of research, theory, experimentation and techniques that culminates in a singular display. The scientific image, in this sense, reflects and preserves all of the diverse processes that have rendered it visible and knowable in the first place through the integration of ‘disparate components, which are historically and conceptually distinct’ (Daston and Galison 1992: 82). Along these same lines, a longstanding concern in scientific domains has been to delineate what are the most successful visualisations. Those most successful have been deemed ‘master images’—for example, the solar system, periodic table and, even the DNA double helix—as they have each achieved a type of iconic status due to their universal recognition, conceptual significance, and ability to translate complex ideas into simplistic terms. Notwithstanding the knowledge foundations provided through such master images, the innovating and refining nature of contemporary science and technology has created a ‘pluralizing effect’ on portrayals of science such as those depicted in the previous section. Now, advanced technologies are able to diversify the number and types of images associated with a singular scientific object/concept. Consequently, the idea of the singular image preserving historical knowledge is at odds with the transient nature of modern pictorial representations to change form through the contemporary technological advancements and integrated networks, witnessed in such movements as e-science and/or ‘big science’ (Carusi 2008). Here, computers and databases facilitate the instantaneous movement, manipulation and collaboration of scientific illustration and information at a pace previously unheard of.

The final feature is transformation, a process that addresses the capacity and mobility of the (scientific) image to displace, transport, and depart from its initial rendering (Latour 1986). The case of the genetic image highlights this transition from singular to pluralised image-types as set out in shift from individual to categorical profiles listed above (see also Nancy 2001, on the notion of singular-plural). Encapsulated under the rubric of DNA, the genetic profile acts both as a source of ‘shared seeing’ in its electropherogram form, but is also as a visually-heterogeneous entity contingent upon the application and interaction of potentially innumerable circumstantial aspects and dynamics, such as spatial context (i.e. laboratory, courtroom, war-zone), discipline (i.e. biology, epidemiology, robotics), examining technology

and the consequent image-type (i.e. electropherogram, microarray, lattice, cluster). The ability for the genetic image to ‘change but stay the same,’ resonates with Rheinberger’s (2010) conception of ‘epistemic things’ as tentative scientific formations that emerge and are contingent upon the technical conditions embedded in experimental systems. Specifically, he argues that scientific ‘things’ are malleable, varying by the technical conditions of experimental systems, as well as between the material and conceptual frameworks from which they are understood. The multi-dimensional genetic profile adheres to this adaptable and transformative quality identified by Rheinberger (1997) as evidenced in the visual contingency that accompanies each pictorial representation. The question, then, is how this visual reformation impacts ideas of scientific ‘truth’ and/or ‘trust’ as they are rendered intelligible under these changing and emerging parameters that the forensic-surveillance nexus draws attention to. These questions are discussed next.

IV. Looking ahead: Genetic imaging, truth and trust

What constitutes the greatest degree of legitimacy and trust in a scientific image has traditionally been located in the ability to convey information and shape understandings to the greatest number of people by instituting ‘shared modes of seeing’ (Carusi 2008). Depictions such as the solar system, the periodic table and the DNA double helix are all universally recognised models that have acted as substantial guideposts to translate significant, complex and specialised knowledge to both scientific and non-specialist audiences in ways to make sense of science. The venerable success of these visuals has been attributed not only to their perceived assembling qualities, but also to the incorporation of ‘less is more’ approach that works to unify and simplify scientific ideas through overarching, comprehensive and symmetrical structures that reveal a proclivity towards the classification and comparison of layers of information as the formation of scientific knowledge. What has typically been a ‘singularity of vision’ style in science has produced what are arguably the most convincing versions of ‘truth’ as set out in classic and enduringly popular images and diagrams like the solar system that appeal to experts and amateurs alike.

In contrast, this paper has demonstrated the complex ways that genetic imagery has proliferated away from a ‘singularity of vision’ style to a pluralised set of depictions. Each image-type corresponds to a specific methodology, procedure, technique, series of instrumentations and institutions. The four images exemplified in this argument—the electropherogram, microarray, lattice and cluster—indicate and exemplify the visual plurality and diversity that accompanies a singular scientific concept: DNA. In this sense, truth is no longer associated with a ‘singularity of vision’ but a complex series of processes that render the genetic image into a multiplicity through the varying modes of extraction, representation, transformation, engagement and deployment that coexist with each depiction. This shift from ‘singular’ to ‘plural’ imagery as it associates to a single concept, DNA, renders novel and significant questions where notions of truth and trust, authenticity and legitimacy, are concerned. Most evidently, how do we know, interpret and understand what we see? How do we trust a singular depiction of DNA when the frames of reference are constantly shifting? How are decisions made about what images ‘count’? As well, what knowledge or alternative ways of seeing are left out?

The extension of DNA profiling beyond the criminal legal sphere and into the domain of surveillance necessarily reframes ideas of ‘truth’ and ‘trust’ or, at the very least, challenges the longstanding assumption that DNA is the ‘gold standard’ of forensic science (Lynch 2003). One way to grapple with such questions is to look to the traditional criminal legal sphere from which DNA profiling originated as a forensic identification technique. What has been an implicit trust in forensic genetic profiling has been tied to, what Lynch et al. (2008) identifies as the influence of science and technology on contemporary society. Specifically, why scientific evidence such as DNA profiling has achieved a greater degree of legitimacy depends on:

...the hope of transcending 'subjective' (often prejudicial) judgments with 'objective' facts, so that court decisions can rest upon a secure, scientific foundation. Yet, the history of Western concepts and practices shows us the trend towards shifting 'truth' and 'trust' from the sovereign individual and emplacing it in material and bureaucratic mechanisms. 'Mechanical' or 'technological' objectivity trumps personal judgment, such as the advent of DNA technologies and processes of visualization.

(Lynch et al. 2008: 245)

The significance of this statement is that it associates our modern understanding of truth and trust in genetic evidence as inextricably bound to science, technology, and the visualisation thereof. In a like manner, Latour (1986: 12) contends that truth is not in a 'new vision' but in the 'same old vision applying itself to new visible objects, that mobilise space and time differently'. For Latour, then, truth is inherently visual, and may be discerned by tracing backwards in time as opposed to forwards—back-peddling, so to speak—to the historical, theoretical and visual foundations from which modern genetic depictions are sustained and developed.

A third view, and perhaps the most relevant to this argument, is the idea of the image as interpreted through the lens of the surveillant assemblage. This notion, put forth by Haggerty and Ericson (2000), draws from Deleuze and Guattari's (1987) more abstract idea of the assemblage: a process of arranging, organising and fitting together a collection of heterogeneous elements, including things and relations that coincide as they elicit novel reactions, interpretations and responses. More specifically, the surveillant assemblage refers to a collection of previously discrete tracking systems contained within an overarching assemblage or synthesis. It operates to extract human bodies from their geographical settings and translate them into electronic flows or data doubles that can be observed and targeted for intervention. The genetic image translates into this theorisation in two key ways. First, the image itself may be thought of as a tentative and contingent pictorial synthesis—an assemblage—that foregrounds complex layers of genetic knowledge into a singular display. Along these lines, a graphic image such as the electropherogram (Figure 1) is not simply a *representation* of a person's genetic make-up, but an *integration* of logics, empirical practices (i.e. observation, measurement, analysis, description and visualisation) and institutional configurations that coalesce in the overall profile, which then serves as evidence or intelligence for a slated institutional response or intervention. The image, in this case, is convergent in the sense that it provides a foundation to stabilise, diffuse and render genetic data into a mutually comprehensible form with the goal of instituting multiple, targeted interventions whether in the courtroom, the database, border-points or war-zones.

The idea of the surveillant assemblage as a tentative formation also attends to the *supplementary* quality of the genetic image in the capacity to transform from one profile type to the next (i.e. the electropherogram to the microarray to the lattice). This malleability is due to digital and computational processes, which facilitates relationships and collaborations between institutions, researchers, technologies, and other relevant fields of knowledge (i.e. disease, medical, biochemistry, engineering, mathematics, statistics). Different DNA profiles are thus subject to different modes of intervention. The potential to target genetic data as part of intelligence gathering and information sharing is now much easier with big data genomics databases and research capabilities that enable the combination of advanced genetics, comparative genomics, as well as high throughput biochemistry and bioinformatics that are able to process multiple samples simultaneously. Relatedly, the 'big science' or e-science movement has facilitated the integration of cyber-infrastructural resources in novel ways to enable high-performance computational collaborations between knowledge fields and data sources (Carusi 2008; Collins et al. 2003). As discussed, the consequence of such innovative technologies and resources has been the integration and adaptability of visual outputs. Now, each image or profile of DNA is both context-specific as well as subject to replacement, revision or innovation. The image is thus inseparable from the ongoing interchange of

techno-analytic methods, forensic, regulatory and surveillance agendas, operational discretion and disciplinary frameworks.

Overall, the collaborative interchange of genetic data specifically, and biological data more generally, is integrating and transmitting imagery in increasingly rapid and synthesised ways. This has radically reconfigured or, at least challenged, how and what it means to accurately represent, identify, interpret and 'know' genetic information. For surveillance, the genetic image is the key site from which interpretation, judgment, reflection and negotiation are articulated and decided, whether in the criminal justice sphere or the larger intelligence framework that genetic data is increasingly deemed relevant (i.e. national security frameworks, mass disasters, and so on). In the multiple images that exist for a singular concept such as DNA (i.e. the microarray, lattice, cluster), issues of truth and trust become increasingly complex: they are necessarily bound, contextualised and localised to a given image-type, all the while containing the capacity to transform and change form, whether between human and non-human genetic samples, individual and categorical displays, or between the status of evidence and intelligence.

V. Image and exposure

This article has sought to 'expose', or bring attention to, the complexity of the genetic image as it transcends forensic and surveillance networks in both theoretical and empirical terms. As a final point, this section considers what exactly the genetic image is capable of exposing. On the one hand, regardless of the image-type, each genetic profile has the potential to reveal ambiguities, errors, and other non-conformities. Contrary to the longstanding view of DNA as the gold standard of forensic science (Lynch 2003), the same advances that have led to advanced technologies pertaining to genetic imaging (i.e. rapid sample detection capabilities, mobile laboratories and higher throughput capabilities) bring with them a whole new series of 'troubles' evident only at the pictorial level. In the forensic context, where the electropherogram is the main profiling technique, recent technological advances designed to increase the sensitivity and detection of low-quality and low-quantity samples have, paradoxically, rendered numerous visual anomalies apparent. Such anomalies may include the presentation of extra peaks, misshapen or all together missing peaks, and typically indicate either an error with the sample or the analysing technology. Nonetheless, these consequent imperfect, partial and incomplete profiles are increasingly being used as intelligence and, in some cases, evidence in the courtroom. As Thompson (2008: 8) notes, the consequence is serious when partial or incomplete profiles are in the balance:

Greater risks of false matches arise when the government chooses to search databases for matches to incomplete or mixed DNA profiles. There is no published research from which one could estimate the average coincidental match probability, or the range of such probabilities, in cold hit cases.

This statement draws attention to how the decision to use imperfect or incomplete profiles as evidence heightens the risk of false matches with the consequence of obtaining false acquittals or even false convictions. Moreover, the shift to categorical and contextual profiling is even less certain about how this data will be used to monitor, assess and regulate genetics and, consequently, the individuals that are implicated through these emerging profiling strategies. The microarray, the lattice, and what I have called the bacterial 'cluster' have all been subject to associated and ongoing reassessments and readjustments that have the potential to redefine scientific meanings, technologies and the images that emerge with each new system of representation as it relates to genetic data collection, observation, comprehension and exposure (see, for example, Courts and Burkhard 2010; Bieber et al. 2006; Hartman et al. 2011; Holobinko 2012; Enserink 2003). How exactly categorical, as opposed to 'one-to-one' genetic profiling systems, will be used in the future is still uncertain. At the same time, the speed by which such technologies are developing novel images geared towards identifying genetics along multiple and diverse lines is unprecedented.

Forensic-genetic surveillance, outlined in this article through the medium of the image, is increasingly diverse in the ways that it tracks, watches, regulates and exposes DNA in range of spaces, modes and designations. The multi-faceted characteristics of genetic imaging are evident not only in its evidentiary context in the criminal law, but increasingly in the emerging sphere of intelligence across security and surveillance thresholds, and in national and international domains. In a productive sense, new ways of envisioning DNA opens the possibilities to ask different questions and challenge long-standing assumptions as they relate to 'truth' and 'trust'. For instance, how do we know what we see and, more significantly, how do we *trust* what we see? With what degrees of accuracy can one ensure that genetic profiles are legitimate when the visual configurations are undergoing states of transition? Who are the experts responsible for interpreting genetic data, and do these individuals or systems vary when DNA is classified as evidence as opposed to intelligence? Along the same lines, are different modes of expertise required per profile-type, series and/or classification?

As a final point, although technological achievements, such as the enhanced rapidity, mobility and portability of robotic, biometric and multimodal forensic identifiers have been prioritised, the proliferation of genetic data in its plurality and visual complexity brings with it serious concerns. While governmental discourses 'parade' the benefits of emerging technologies (see, for example, Keiper 2011; Messmer 2012, 2011), there has much less attention granted to discerning what systems of expertise are in place to interpret and judge genetic visual profiling in its increasingly diverse formations. While there is a designated role for expert witnesses to evaluate and contest genetic and other forms of scientific evidence in the courtroom (see for instance Edmond and San Roque 2012), it remains unclear and uncertain who or what systems of expertise are in place to interpret, monitor and decipher genetic data in its intelligential role as this informs and guides investigative efforts. The lack of standardised systems of expertise and interpretation guidelines are of particular significance in the context of war zones, mass disasters or terrorism investigations where a 'quick' detection is required to detain individuals as prisoners of war or as terrorist suspects. Of special concern are recent American initiatives to deploy rapid testing through portable laboratories in war zones, where soldiers and other officers will be taught to interpret DNA profiles 'on the spot' (Messmer 2012). Equally troubling is the phenomenon Aas (2011) has coined the 'crimmigrant,' where biometric and multimodal forensic identifiers operate at airports and other border regions as 'gate-closing' and 'gate-opening' techniques. The role of trained experts with the ability to interpret complex genetic data, regardless of whether genetic information is parcelled as evidence or (the less restrictive) intelligence, is vital to the identification efforts of law and surveillance alike. In all, each novel and emerging image and technique brings with it new challenges, insights, controversies and debates that this argument has only begun to indicate, pinpoint and clarify as they exist both within and beyond the forensic sphere of the criminal legal domain.

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