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Race, Time and Folded Objects: The HeLa Error

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Given their commitment to practices science studies have bestowed considerable attention upon objects. We have the boundary object, the standardized package, the network object, the immutable mobile, the fluid object, even a fire object has entered the scene. However, these objects do not provide us with a way of understanding their historicity. They are timeless, motionless pictures rather than things that change over time, and while enacting 'historical moments' they do not make visible the histories they contain within them.

What kind of object could embody history and make that history visible? We might learn from Michel Serres about objects and time, and about the way that histories cannot be left behind. The image of a dog cadaver, constantly orbiting a projectile in space, might turn out helpful here. Inspired by Serres, I suggest the *folded object* is a way to attend to the temporality and spatiality of objects.

In this paper, I explore this new object by unravelling the history of a DNA reference sequence. I show how, ever since it was produced in the early 1980s, attempts have been made to filter race out of the sequence. That effort has failed due to what one could call 'political noise'. Making and remaking the sequence have left traces that cannot be erased.

Keywords: race, topological time, objects and history, folded objects, mtDNA genome.

Objects are made at particular places and times. Objects have agency. This much we know from Science and Technology Studies (STS). How these aspects are related, that is, how the history of an object might have political effects has not been well explored. This paper focuses on the making and remaking of an object and its relation to race. I show that rather than leaving its history behind, this objects indexes and enacts its history. My argument is that granting objects history and attending to temporality is crucial for understanding the politics they articulate.

What is an object?

If object-ness is not a stable state, then what is an object? Rather than answering this question head on, let me start with a story borrowed from Jules Verne's *From the Earth to the Moon* (1865) or rather, from Michel Serres' rendering of it in his *L'Obus, Le Canon: Deuxième Fondation*:

Propelled by the Columbiad, a giant cannon, a bullet-shaped projectile carrying three astronauts and two dogs strikes off to the moon. On the journey one of the dogs, Satellite, dies. Since it is impossible to keep the dead dog's body on board, and notwithstanding the laws of physics, the astronauts decide to open a hatch and dispose of the dog and some other waste out into space. Then, after a long discussion on algebra and ballistics, one of the travellers observes an object passing by. It is Satellite's cadaver, circling around them at a constant distance, appearing now in view and then disappearing out of sight again (based on Serres 1989: 35-38).

Michel Serres uses this story to think about the object-ness of objects and about how objects make the collective, that is, the 'social' that consists of humans and non-humans. Death is immediately followed by the radical exclusion of the dog from the social.¹ In this process, the cadaver is placed 'out there', or so the astronauts hope. On the face of it, this is the well-known mechanism of *objects*. Once made, they appear to be independent of human action, 'thrown at us' and assuming an allegedly stable state (Daston 2000). However, in Serres' universe there is no given exteriority (the object out there) or interiority (the subject 'in here'). In this universe objects get back to us. Rather than mute entities, dependant on humans to reanimate them, objects are actively involved in the social. In fact, the ongoing circulation of objects is what makes and holds the collective together.²

Objects make us! But they do so in intricate ways.

Our relationships, social bonds, would be as airy as clouds were they only contracts between subjects. In fact, the object, specific to Hominidae, stabilizes our relationships, it slows down the time of our revolutions. For an unstable band of baboons, social changes are flaring up every minute. One could characterize their

history as unbound, insanely so. The object, for us, makes our history slow (Serres [1982] 1995a: 87, quoted in Brown, p. 22).

Objects not only give a material basis to social relations, they also capture history and make it slow down. Time no longer flows linearly, but 'passes [in a] turbulent and chaotic manner, it percolates' (Serres and Latour 1995: 58-59). Serres' notion of time is linked to a topological notion of space.

If you take a handkerchief and spread it out in order to iron it, you can see in it certain fixed distances and proximities. If you sketch a circle in one area, you can mark out nearby points and measure far off distances. Then take the same handkerchief and crumple it, by putting it in your pocket. Two distant points are suddenly close, even superimposed. [...] The science of nearness and rifts is called topology. (Serres and Latour 1995: 60)

In contrast to linear time which is related to geometry, topological time is crumpled and folded in multiple ways. Time is gathered together and folded in objects (Serres and Latour 1995). 'An object, a circumstance, is thus polychronic, multi-temporal, and reveals a time that is gathered together, with multiple pleats' (ibid: 60). An effect of folding time is that history can be *recalled* in objects. History is never left behind. The dead dog keeps coming back. But how can we recall the history that objects carry with them? How do objects do time? I want to use these insights about time and objects to think about histories that are not linear, chained, or well-ordered since history can strike back capriciously. More precisely, I want to attend to the relation between race and time and how both are gathered together in an object.³

Objects in Science Studies

Science Studies have long been concerned with objects.⁴ Various metaphors have been invented to highlight the different realities of objects. The *boundary object* emphasizes the simultaneous robustness and plasticity of objects. A boundary object is plastic enough to adapt to the local needs of the various actors that employ it yet robust enough to maintain a common identity. Such objects assume different meanings in different work practices, and as Leigh Star and James Griesemer (1989) have argued, they facilitate collaborations between diverse social worlds. The *standardized package* developed by Joan Fujimura comments, as it were, on the infinite flexibility of boundary objects. It highlights the ways scientific practice stabilizes facts. Similar to the boundary object, the standardized package focuses on collective work across different social worlds. Yet it differs, not only in its emphasis on stabilizing facts, but in how such an object affects and changes the world it operates in (Fujimura 1992).

The *network object* invented in actor network theory (ANT) emphasizes the spatial aspect of objects. Network objects, such as an electric car, a scallop, a vessel and so on, have been conceptualized as 'stable networks of associations'. It is vital to note that whereas the boundary object and the standardized package are bounded objects *interpreted* by human actors, network objects are less clearly delineated, and they are *done* (or enacted). They are enacted in practice as specific relations (networks of associations) in which, famously, both human and non-human actors participate. Network objects keep their shape as long as the relations between the entities that constitute them are stable and as long as the identities of these entities do not change.⁵ They are what Bruno Latour (1990) calls 'immutable mobiles', heterogeneous practices made flat. Interested in the power of science Latour argues that this power is based on the circulation of immutable mobiles. The flattened worlds embodied by these devices enable their mobility *and* immutability while they move between different practices.⁶

This rigidity of networks and the tendency to make invisible the work required to make them hold is what inspired a related object in ANT, namely the *fluid object*. Far from being immutable, a fluid object is a set of relations that changes from one practice to another while keeping its shape (Mol and Law 1994). Fluid objects help us to attend to a variety of adjustments that need making for an object to maintain its integrity. The changes between different versions of a fluid object are best characterized as 'gentle flows' (Law and Singleton 2005). A fluid object changes yet stays the same.

My final example is the *fire object* (Law and Singleton 2005). Just as fluid objects, fire objects shift and change, not in gentle flows but in jumps and discontinuities. Fire objects are untamed, difficult to apprehend, tend to change shape rapidly and thus escape from view.⁷ John Law and Vicky Singleton argue that the fire object is a pattern of presences and absences. This is based on the idea that to make things present is to make other things absent. These 'othered' things neither go away nor cease to exist. They become absent presences. Fire objects are 'energetic entities or processes that juxtapose, distinguish, make and transform absences and presences' (Law and Singleton 2005: 343-344). They produce difference but also depend on difference since what is othered does not vanish. Instead it is generative of that which is made manifestly present.⁸ Think of the cadaver in space! The fire object helps us to think about difference and the *vital* role of what is othered.

This insight into absent presences is particularly helpful when thinking about race, and I will draw on it in my analysis. My main concern in this paper is not with race in general but with how a specific object in genetics carries its history along with itself and enacts its history

of making and remaking. I suggest that this object is best understood as a *folded object*. Like Serres' handkerchief, it gathers many places and times in itself. Although the actor network and after approach has taught us about objects as spatial enactments, little attention has been paid to the temporality of objects and more specifically, to how objects enact time. It seems that the ANT focus on enacting objects in the here and now has made absent the layered temporalities of objects (see also Asdal 2012).

After the spatial turn the temporal turn is yet to arrive, even if theoretically and conceptually the temporality of objects has been anticipated. Notably Latour (2002), following Serres, as I do here, addresses the spatiality and temporality of technology. Technology, he argues, will betray (*trahir*) and translate both itself and its users in the interaction. Once put to use, technology will modify not just the user but also the times and places it gathers together. Crucially, technology is not a repository of places and times. The specific times and places that are drawn together are an effect of the specific practice in which a technology is put to use.⁹ Although the temporality of objects has been anticipated at the theoretical and conceptual level there is little ANT research that substantiates these claims systematically and empirically.¹⁰ Here I will go into the details of one object and the ways it keeps histories folded in itself. The essence of the folded object that I propose lies in the intricate ways in which it gathers heterogeneous spaces and temporalities together. As will become clear the making and remaking of this object, a DNA sequence, is connected to a history of race.

In this paper I examine race and its politics of difference as an absent presence. To grasp this notion better, I shall borrow from Serres' metaphor of Satellite, although my use and concerns differ somewhat. I think the image of the circling dog coming round and around, in and out of sight is both powerful and helpful to understand how race plays out in this case. The cadaver of the dog does not disappear or vanish entirely. It becomes something that haunts us. In the words of Kevin Heatherington, it is as if '[w]e encounter the unexpected presence of absence as a ghost' (Heatherington 2004: 170).

To order my story about the DNA reference sequence and its entanglement with time and race, I will present three visual metaphors that capture specific moments in its history.¹¹ The first image, 'Small is Beautiful', presents the reference sequence as a *portrait*. Here I tell the heroic story of the reference sequence coming into being. The portrait helps us to see the attempts to represent nature as it is. The second metaphor, 'Once Upon a Time in the Lab', presents the sequence as a *collage*. This story is about the messiness of scientific practices, the dense layers of realities that the sequence carries in itself. The third metaphor, 'The HeLa

Error', presents the sequence as a *montage*. It talks about a history that refuses to be rewritten or be left behind. It is about 'nature' carrying and displaying its technically mediated character. Through a simple letter, a C, the sequence has the potential to reveal an ongoing history. A history in which race is othered. In the concluding part I will argue that these different images do not connote a sequential trajectory but instead enact a *folded object*.

The Portrait: Small is Beautiful

[figure Small is Beautiful]

In the 1990s geneticists embarked on a prestigious Big Science project (Kevles and Hood 1991) aimed at unravelling the first genetic map of the human genome. The international multibillion Human Genome Project (HGP) dramatically changed the field of genetics, not merely by facilitating novel knowledge, but especially by its emphasis and contribution to novel technologies¹² that nowadays populate our laboratories and clinics. Right from the start the HGP released large sums of money (5% of its budget) to educate the public about genes and promote the benefit of the genome project (e.g. Kevles and Hood 1991; Nelkin and Lindee 1995). In June 2000 the draft of the human genome was presented to the world by Bill Clinton, former president of the United States and Tony Blair, former prime minister of the United Kingdom (through video conferencing), Francis Collins, director of the Human Genome Project and Craig Venter, CEO of Celera Genomics (published in Venter et al. 2001).¹³ Completion of the draft map was framed as a major historic event. On the occasion President Clinton stated the following:

Today, the world is joining us here in the East Room to behold a map of even greater significance [than the map of the American Frontier of 200 years earlier, AM]. We are here to celebrate the completion of the first survey of the entire human genome. Without a doubt, this is the most important, most wondrous map ever produced by humankind. [...] Today's announcement represents more than just an epic-making triumph of science and reason. [...] Today, we are learning the language in which God created life.¹⁴

Along this line, Francis Collins added:

Today, we celebrate the revelation of the first draft of the human book of life. [...] What more powerful form of study of humanity could there be than to read our own instruction book? [...] It is humbling for me and awe-inspiring to realize that we have caught the first glimpse of our own instruction book, previously known only to God.¹⁵

The human genome is obviously a major achievement of state-of-the-art technology and internationally organized science. Its transformative power has been widely acknowledged. However, 20 years earlier another human genome was completed, not of nuclear DNA (the 46 chromosomes located in the nucleus), but of mitochondrial DNA (mtDNA).

Mitochondrial DNA is located in cytoplasm, on the mitochondria, the suppliers of energy to the cell. To be sure, mtDNA consists of the same basic chemical substance as nuclear DNA. An important difference, though, is that mtDNA is inherited by offspring from the mother's side only; fathers cannot pass their mtDNA on to the next generation. This is

why mtDNA is deemed interesting in population studies of genetic lineages, that is, maternal genetic lineages (M'charek 2005, Nash 2005). The complete sequence of the mtDNA genome was published in 1981 in the scientific journal *Nature* in a paper co-authored by 14 scientists (Anderson et al. 1981). Underlining the significance of this publication were three accompanying articles on the mitochondrial genome, one of which was a short introductory paper by Piet Borst and Leslie Grivell entitled 'Small is Beautiful: Portrait of a Mitochondrial Genome' (Borst and Grivell 1981). Borst and Grivell's paper celebrates the major achievement of their colleagues and expresses the relevance of the genetic map for the field in more than scientific terms. The poetry of the title is chosen well, for 'small is beautiful' is an oft-heard expression to describe mtDNA in review articles or at conferences (e.g. Casane et al. 1997). For my argument, this interesting title is relevant because the mtDNA genome was not staged as a *map* or *book*, metaphors that are often used to qualify the nuclear human genome, but as a *portrait*.¹⁶ One could say that the metaphor mobilized by Borst and Grivell underlines the creative qualities of the makers of the sequence, the artistic qualities of the geneticists. When linked to the reference sequence itself, the metaphor seems to suggest that at issue is a genuine representation of a person, whose nature and essence is captured in the portrait.

In addition, the portrait qualities, namely the representation of the essence of a person, draws in and at the same time underlines two specific qualities of the genome, namely *small* and *beautiful*. Small, because in contrast to nuclear DNA, which consists of 3 billion base pairs (DNA building blocks), the mitochondrial genome consists of only 16.5 thousand base pairs. This is obviously one of the major reasons why they could sequence it back in 1981. Size, however, is not merely a technical advantage but a quality of beauty. Size is appreciated, and linked to the organization of the genome and the location of its various genes. Papers by Anderson et al. (1981) and Borst and Grivell (1981) both appreciate the *efficiency* of this organization. Again, in contrast to nuclear DNA where genes are scattered about in a landscape of 'junk DNA', the genes of mtDNA are positioned tightly next to one another. Non-coding DNA (the D-Loop) can be found together in one cluster.¹⁷ Thus the small size of the mtDNA genome seems to generate *organizational elegance and efficiency*.¹⁸ On top of this all, and contributing to its beauty, its DNA is not composed of loose fragments (as found on nuclear chromosomes), but is organized in a circular form, a highly appreciated form in various aesthetic traditions.

The paper by Anderson and his colleagues presents the full sequence, taking up no more than three and a half pages of text containing various permutations of the letters ACGT, the

four building blocks of DNA.¹⁹ This textual representation of DNA has come to stand for the thing itself, as if the work of technology and scientists was merely a medium and not an intervention. The sequence thus seems to give a glimpse of the architecture of nature, out there, untouched. Ever since its publication, the Anderson sequence has gained the status of a reference genome for those working with mitochondrial DNA. In laboratories it is referred to as the Anderson sequence, or simply Anderson.²⁰

The Collage: Once Upon a Time in the Lab

[figure Once Upon a Time in the Lab]

In the late 1990s I became interested in the Human Genome Diversity Project. This project had several goals, of which the most central was 'preserving the current human genetic diversity for future generations'. In terms of advancing our knowledge it aimed at mapping genetic similarities and differences between populations to learn about the migration history of humanity. The Diversity Project became controversial, almost overnight, because of a special interest paid in exotic DNA, that is, DNA taken from 'indigenous peoples', or 'isolated populations'. The initial interest of diversity researchers in indigenous peoples and isolated populations was based on the presupposition that they allegedly did not move around or mingle with other people very much and that therefore, their DNA was much better conserved (compared to the Western melting pot) and thus provided a better source, or recourse, to study our migration history.²¹ Obviously the Diversity Project found itself in a fuelled debate about its goals and purposes. It was not hard to criticize it, to side with anti-racist and anti-colonialist politics. Yet why was this project bad, I asked myself? Why was it bad science, compared to the far more powerful and influential Human Genome Project? I grew interested in the politics of the Diversity Project, but the debate surrounding it seemed too strident. I looked for a calm place to study it and thus entered the laboratory. Instead of controversy, I focused on routine technology, instead of merely analyzing what geneticists were saying, I looked at what they were doing. In short, I studied practices where nothing spectacular seemed to be going on. In the laboratory I hit upon the Anderson sequence, in the form of an offprint of the original paper that had specific parts of the sequence, of interest to the population geneticists I was working with, highlighted by marker pen.

The reference sequence functions as a road map for geneticists interested in genetic diversity. Whenever geneticists try to sequence a fragment of DNA they cannot possibly know whether they have sequenced the targeted fragment. Only by aligning and comparing such fragments to a reference genome can geneticists locate the beginning and the end of the targeted fragment and thus identify them on the map. Sequencing is rarely straightforward. The end result often contains mistakes or ambiguities, because of technical handling and procedures. In such cases the reference sequence is used to correct or *edit*, as it is called in the lab, the targeted fragments of DNA. So, if the geneticists do not expect any mutation at loci where such ambiguities occur, they can assume those loci to be similar to Anderson, and edit the target sequence accordingly.

The reference genome plays a key role because of the importance of mtDNA research in diversity studies. The relevance of such research was shown back in 1987 in the classic paper

by Rebecca Cann, Mark Stoneking and Alan Wilson entitled 'Mitochondrial DNA and Human Evolution'. This paper, often referred to as 'the Mitochondrial Eve paper', provided genetic evidence for the Out of Africa theory by showing that genetic diversity is higher in Africa and lower in populations elsewhere in the world. Based on mtDNA diversity in relation to the mutation rate, the authors estimated modern humans to be some 200,000 years old.

The central role the reference sequence played in the everyday practice of laboratories intrigued me, and I began raising questions on how and where it was produced, about its normative content and the self-evident nature it has gained in labs today. In an interview with Svante Pääbo, the head of one of the laboratories that I studied, I asked him to tell me more about Anderson and how it was proposed to the scientific community. In response, he started laughing:

It wasn't *proposed*. It was *determined*. Now, that's a difference between constructionists and geneticists. I mean, it was the sequence that was sequenced, right? It was the first complete human sequence ever determined. It was done in Cambridge and the first author's name on that paper is Anderson. [hence, the Anderson sequence]. This was in 1981. It is a composite though, because different parts of that 16.5 Kb [kilo base pair] count for different individuals, they are not from one person! [...] It became the reference because when people determined sequence number two, they of course compared that to the first one since it was already there. And now four thousand sequences later, we still compare to that [first] one. It is of course totally arbitrary. We could take any other sequence as the reference. Anderson is just a convenient convention. Everybody knows what you're referring to. It is of course a British sequence, or, certainly European, but probably British, because it was done in England.²²

On other occasion Pääbo recounted:

It's a shame that people forget about the origin of the sequence. They tend to *naturalize* it. They'd speak of mutations *from* Anderson, but one could also reason the other way round.

This quote indicates that while aligning (comparing) sequences to Anderson, geneticists are not simply interested in *reference*, but especially in *difference*. As I have just indicated *reference* is important for it helps to determine whether the DNA fragment sequenced was actually the target fragment. But the real interest is difference; any difference between target sequences and Anderson. These differences, mutations (*from* Anderson) are the units of study in population genetics. They are the basis for what comes to count as lineage, as members (sharing mutations) or non-members (not sharing mutations) of a population.

The interview excerpt not only underlines the *convenience* of Anderson to the scientific community, but also *its fabricated nature*. The sequence is European or British if only

because it was made in England, as Pääbo indicates. It was produced at a certain time and place, and it was not 'from one person' but based on cell material from several individuals, as Pääbo explains. At this point I would like to draw briefly on the art metaphor suggested in the first story. There we encountered the sequence as a *portrait*, an object that represents a singular, one whole. In the metaphor pertaining to this story, because of its composite qualities, the sequence is better regarded as a *collage* that brings DNA fragments from various origins together through technical interventions, not to represent but to produce a new (visual) object. In what follows we will look at the collage quality of the sequence by focusing on the various layered practices that went into sequencing Anderson, and the various temporalities that the sequence keeps folded.

First I was struck by the virtual lack of awareness in the scientific community that Anderson was actually a composite, and with that, the lack of knowledge about the cell material used to produce it.²³ Even the scientists actually involved in making the sequence—for example, I spoke to Alan Bankier, the second author of the Anderson paper—could not tell me much about the material. They had not kept detailed records when they sequenced Anderson, so I was told. In our telephone conversation, Bankier said, 'At the time this issue [whose tissue] wasn't addressed that much, we weren't after an *individualized* sequence. Our aim was a *consensus* sequence that everyone could work with.'²⁴

This disinterest in the material used, and lack of knowledge about what went into the applied technology may be more or less common practice in laboratories. Certainly, my aim here is not to discredit scientists, but rather to point at what various STS scholars have come to term the work of *tinkering* (e.g. Mol, Moser and Pols 2010). The idea is that science is often about constructing doable problems and taking the material at hand to solve everyday problems, rather than deliberate selection. In my quest to discover more about the production of the reference sequence ultimately I had to turn to scientific papers to find out more about the bodily material used as the basis for the sequence. The results of my quest were in many ways surprising.

The legend in the original paper (Anderson et al. 1981) gave some clues. It indicated that Anderson is based on three different individuals. Some DNA was derived from placental tissue, some DNA came from an HeLa cell line, and interestingly enough the sequence also consisted of DNA stemming from a bovine. The Cambridge (UK) laboratory that produced Anderson had at that time just produced the complete bovine mtDNA genome. In the absence of a human reference, the bovine genome was used as a reference sequence to produce Anderson.

Parts of the bovine genome were used to correct ambiguous loci in the human sequence. Ambiguous is a technical term referring to loci that have not been sequenced properly, or where the visualizing technology fails to determine which nucleotide (DNA-building block) it has to be. As indicated above, such ambiguities occur often in laboratories. There are always ambiguities. Sequences therefore have to be edited based on the reference. So, in this case a bovine sequence was used for that purpose, working on the assumption that for those specific loci, human and bovine are the same.

The largest part of Anderson was based on placental DNA that was already available in the lab. It had been cloned and studied for another purpose by Jacques Drouin, a co-author of the Anderson paper based in the same laboratory. Drouin 'described' the placenta and although his paper does not include details about the 'origin' of this placenta, clearly it was retrieved from a hospital or a clinic. The paper states: 'Human placentae were obtained at term from normal or caesarean section deliveries and put on ice within 30 min.' It also indicates that one placenta was the source for Anderson. 'A collection of recombinant clones has thus been obtained using mtDNA isolated from a single placenta and is now being used to obtain a complete nucleotide sequence of human mtDNA' (Drouin 1980: 15-6).²⁵ Again, this material was easily accessible for the makers of Anderson.

Some parts of the sequence used DNA from the HeLa cell line, made available by colleagues from the United States. I will return to this cell line shortly. But first I would like to address the 'Britishness' of Anderson. Above, Svante Pääbo referred to Anderson as British. However, given the collection of material that went into producing Anderson, one could say that its Britishness is not so much *in the DNA* as *in where* it was produced, namely a British laboratory. Furthermore, the HeLa DNA adds to the complexity of the alleged European-ness of the sequence. When I was researching Anderson as a student in 1998, it was a real puzzle to learn where the HeLa line actually came from. After touring through colleague geneticists, via Medline, I decided to try my *Penguin Dictionary of Biology* and there it was, 'HeLa cell: Cell from human cell line widely used in study of cancer. Original source was Helen Lane, a carcinoma patient, in 1952' (Thain and Hickman). But this was not the end of the story, as I soon found out. A colleague who had read my paper asked whether HeLa was a cell line from a black America woman. He had seen a documentary about a woman whose cancer cells became the source of a cell line. This question prompted me to contact Allan Bankier, the second author of the Anderson paper, but as indicated, without my learning anything about the origin of the material used in Anderson.

After that I contacted Piet Borst, the head of the Cancer Research Institute in Amsterdam, because I had learned from Medline that HeLa cells were frequently used in cancer research. Professor Borst kindly sent me a paper authored by Howard Jones, a physician who had examined a patient named Henrietta Lacks. 'Helen Lane' appeared to be one of the pseudonyms used for Henrietta Lacks. Jones' paper was published in 1997 under the title, 'Record of the first physician to see Henrietta Lacks at the Johns Hopkins Hospital: History of the beginning of the HeLa cell line'. In this paper Jones recounts the difficulties that cell biologists met trying to grow a cell line successfully in the early 1950s. 'The project [making a cell line] appeared to be a failure until Henrietta Lacks walked onto the stage' (Jones 1997: 227). Mrs Lacks suffered from a cancer of the cervix that grew fast enough to facilitate the cell line, Jones explains. Although the paper gives information about the age of Henrietta Lacks, the number of children she had had and her clinical diagnosis, there is no reference to her colour. She died six months later and, Jones reminds us, '[i]n terms of [her] birth date, the tumour is some 75 years of age and probably immortal' (Jones 1997: 227).

Finally, I found the HeLa cell line addressed in terms of colour and origin in the field of population genetics, in the classic paper by Rebecca Cann, Mark Stoneking and Allan Wilson on the subject of Mitochondrial Eve, the Out of Africa paper briefly mentioned above. Here the HeLa cell line is described as 'derived from a Black American.' This study compared 148 samples from several geographical regions. Anderson and Henrietta Lacks figure as individuals on the genetic tree produced in this paper. While Anderson remains indeterminate in terms of descent or race, Henrietta Lacks and 17 other black Americans in this study were not only qualified as such but were also regarded as 'a reliable source of African mtDNA' (Cann et al. 1987: 32).

This quest for the cell materials used in the sequencing of Anderson and the difficulties of uncovering such histories has a more general relevance. The narrative is in fact indicative of the working of standards, such as Anderson. Standards not only make themselves *self-evident* to those who use them daily, the scientists in this case, their normative content tends to be inaccessible, also to analysts (e.g. Star and Bowker 1999). Moreover, the story about HeLa also suggests a separation of worlds (even networked and globalized ones). While the dense racial history of the cell line was hotly debated in the United States, here, on the European side of the ocean, this debate is virtually non-existent (see e.g. Landecker 2000).

In her 'Immortality, In Vitro', the historian of science Hannah Landecker (2000) analyzes the racialization of the cell line in the 1960s. While the HeLa cell line started out as a major achievement of science, an achievement through which life could be studied in vitro, its

racialization went hand-in-hand with the very cell line becoming a problem in scientific practice. HeLa cells grew so rapidly they started to contaminate laboratory spaces. Because of this, the origin of the cell line, namely a black American woman, was soon placed centre stage, and the reproductive capacity of the cells in laboratory spaces was linked to a discourse on promiscuity, pollution and race. Thus the capacities of the cell line were conveniently equated with alleged (promiscuous and polluting) characteristics of the black other.

The inconvenience of the HeLa cells became part of the 'one drop of blood/HeLa' discourse among geneticists. As *Science* journalist Barbara J Culliton had put: 'If a *non*-HeLa culture is contaminated by even a single HeLa cell, that cell culture is *doomed*. In no time at all, usually unnoticed, HeLa cells will proliferate and take over the culture' (quoted in Landecker 2000: 65). The language of threat to the self by the other is obvious. The enemy is among us. As Landecker shows, discussions about this cell line took place both in scientific journals and the popular media, contributing to fuelled race, if not racist debates.

As a part of the Anderson sequence, however, the HeLa cell line went unmarked to become part of a standardized, naturalized technology. But not for all geneticists!

The Montage: The HeLa Error

[figure: The HeLa Error]

Anderson did not stay unchanged. Especially in the field of *medical* genetics, it had become a ‘talkative thing’ (Daston 2008). Practitioners over the years had reported possible mistakes in the reference sequence. The reason they did so is because of their special interest in functional genes. In contrast to population geneticists whose particular interest lies in difference, medical geneticists are especially interested in reference, in that what is normal. Mutations in genes may suggest the cause of a disease.

In the late 90s Anderson had changed from a routine device into an ‘epistemic thing’, and object of research (Rheinberger 1997).²⁶ In 1999, the placental DNA used to produce Anderson (1981) was re-sequenced. This resulted in a remarkable revision of the original Anderson sequence (Andrews et al. 1999). In another paper published in 2002, scientists reported to have sequenced the mtDNA genomes of six HeLa sublines (Hernstadt et al. 2002), including the HeLa cell line used for the Anderson sequencing of 1981. Echoing questions I had raised in my research, namely, what is the composition of Anderson and which part is

based on which tissue, the researchers were trying to 'resolve uncertainties' related to the composite nature of Anderson (Andrews et al. 1999). As a result of these re-sequencing-efforts, Anderson has been corrected in interesting ways. It has ceased being a *consensus* sequence to become an *individual* reference sequence, now called the revised Cambridge reference sequence (rCRS). No longer a composite, it is based on placental mtDNA only. The re-sequencing of the placenta (in 1999) allowed scientists to revise the 'errors' that had occurred in 1981. It appeared that all the corrections made to the ambiguities, based on the bovine mtDNA sequence, were wrong. Contrary to the assumption held at the time, bovine DNA loci did not correspond with the human DNA sequence. In addition, the re-sequencing of 1999 and 2002 also eliminated named errors introduced by the use of HeLa DNA. One error is particularly interesting in terms of race. Referring to the fragment based on HeLa mtDNA, the 1999 paper states the following:

The only *error* that we were able to explain using the HeLa sequence was that at nt [nucleotide] 14,766 (T versus C, respectively). The revised CRS mtDNA belongs to the *European haplogroup H* on the basis of the cytosine at 14,766 (instead of the thymine in the original CRS) and the cytosine at nt 7028. The assignment of the revised CRS to haplogroup H is confirmed by the absence of any of the predicted restriction site changes that characterize the other European mtDNA haplogroups. (Andrews et al. 1999: 147, emphasis added).

This indicates that the HeLa DNA was mostly similar to the placental mtDNA. Only at one locus was there a difference. One T in the HeLa sequence had to be 'corrected', replaced by a C in accord with the placental DNA. As the quote indicates, by correcting this so-called error the sequence ceased being a consensus sequence and became an individual sequence. However replacing the T with a C changed it from an African into a European sequence and it thus became the rCRS. One could say that the sequence produced in 1981 was *assumed* to be European as a result of the quotidian *deleting* work of science (see, e.g. Latour and Woolgar 1979). The new Anderson is *made* European through the *editing* work of science. It is this work that turned the HeLa mtDNA into an error.

The very correction is made even more striking if we take a further look at the placental mtDNA, the basis for the current reference sequence. The issue is that the very belonging of this mtDNA and therefore the rCRS to a particular *group* (such as European) is problematic. Andrews and his colleagues argue the following about these peculiarities.

There are an additional seven nucleotide positions at which the original sequence is correct and which represent rare (or even private) polymorphic alleles. Six of these polymorphisms are single base pair substitutions, although one involves the simple repeat of cytosine residues at nt 311–315. The CRS has five residues in this repeat, whereas most other human mtDNAs have six (Andrews et al. 1999: 147).

This means that the rCRS contains polymorphisms that are uncommon among Europeans or any other population, and some are even said to be *private*, that is, not yet found in any other human individual. These specificities, the scientists thus urge their colleagues, should be maintained in the revised sequence. They go on to state:

The rare polymorphic alleles should be retained, that is, the revised sequence should be a *true reference sequence* and not a consensus sequence (Andrews et al. 1999: 147, emphasis added).²⁷

Whereas these ‘rare polymorphisms’ are preserved and contribute to Anderson’s individuality, the ‘HeLa error’ is corrected so as to make the sequence fall into a European population. This combined individuality and European-ness contributes to the further naturalization of Anderson, in terms of a real, existing individual sequence. Replacing the composite by an individual sequence contributes to the notion of an mtDNA sequence that exists out there, detached from the work of science, functioning as the natural origin from which all other sequences diverge (mutate), as ‘the Mitochondrial Eve of human genetics’.

This individualized, naturalized aspect of Anderson seems to take us back to the sequence as a still object captured in a *portrait*. As a portrait, which captures the essence of a nature out there, the sequence could stop to raise questions that might refer researchers back to its capricious history, full of unexpected practicalities and decisions.

There is, however, another peculiarity that today might still generate such questions, that might invite us to think of the sequence in terms of a *folded object* rather than a *portrait*. Whereas scientists had decided to correct the so-called HeLa error to produce a ‘true reference’, that is, a European individual sequence, they preserved one technical error in the revised reference sequence. At one particular locus, the makers of Anderson in 1981 had reported two Cs, a so-called ‘CC doublet at positions 3106 and 3107’. The re-sequencing of placental mtDNA in 1999 showed up the mistake. There is actually only one C, meaning that the extra C is a technical artefact. Yet the revised sequence of 1999 continues to encompass that error. It still contains two Cs instead of one.

The last suggestion represents a compromise between accuracy (correcting the numbering to account for the single C residue at nt 3106 and 3107) and consistency with the previous literature. We believe that renumbering all of the previously identified sequence changes beyond nt 3106 would create an unacceptable level of confusion (Andrews et al. 1999: 147).

Rather than deleting one C from the revised reference the scientists plead for 'a compromise between accuracy and consistency.' Removing the extra C, the artefact, would consequently demand the renumbering all previously produced sequences (in the past 30 years) that were numbered according to the initial reference and that 'would create an unacceptable level of confusion.' This decision is fully understandable but obviously contradicts the scientists' wish to deliver 'a true reference sequence.' The sequence contains an extra C, which technically might as well have stemmed from any other individual (a bovine, HeLa herself or any other species). In addition, one could say that the fact that this extra C cannot be found in any human being is unremarkable if one takes 'the private polymorphisms of the rCRS' into account. Nonetheless, the decision to retain the extra C makes the elimination of the HeLa error even more striking. There is no practical reason whatsoever to correct or replace it with placental mtDNA. Technically speaking, given the extra C, the sequence cannot be said to be individual either. It was and still is a consensus sequence. What has changed, however, is that the sequence has switched race. The very correction of the HeLa error has changed the sequence from an African into a European one. The rCRS is not a 'true reference sequence' because it is now based on the mtDNA of *one individual* only but especially because it falls within *one population* group, namely European.

However, given the practicalities of scientific work, maintaining the extra C may function as 'political noise',²⁸ reminding users of the reference sequence that it is a *made object*, with a history. This C is nothing less than the orbiting cadaver of the dog Satellite, now appearing in sight and then disappearing again. This C points to the complex racial history of the reference sequence. Since the second C will not be found in any other human sequence, the void that inevitably will appear on any computer screen may become an index of the history of the sequence, an index of the times and places that are gathered in it.²⁹

Whereas the makers of Anderson aimed at capturing nature, as it is, a *portrait of the genome*, the extra C helps to enact it as a *montage*. Just like a collage, a montage is about making rather than representing nature out there. But a montage is somewhat different too. Firstly, montages are often politically motivated, in the sense that they aspire to create a political effect.³⁰ Secondly, for example in film montage, the aim is to narrate a story without relying on spatial or temporal continuity. With a technique of rapid cuts juxtaposing different

times and places, film montage does not hide temporal ellipses but rather draws attention to them. As a montage the sequence draws attention to its history of making and that draws us in. That extra C is political. It invites us to engage with the sequence, to wonder about it, to raise questions. That extra C invites us to confront a history that refuses to be erased.

Discussion: The Folded Object

[figure 4 the folded object]

The theme of this paper, namely race impelled me to take time and history as part of a material object into account. Race provoked a change in method that attended to spatiality *and* temporality. With this spacio-temporal analysis I aim to contribute to a growing body of literature on race and the new genetics (e.g. Reardon 2005, M'charek 2005, Nash 2005, Skinner 2006, Abu El-Haj 2007, Fullwiley 2007, M'charek 2010, 2013).³¹ But not without shifting the focus somewhat. For the on-going debate on race and biology gives little attention to objects. Much of the work is centred on controversies in genetics, or is based on human accounts of similarities and differences. Here I have focused on one object and its history to show that normativity and race politics are not articulated exclusively by human actors. In this case, race is shown to be entangled in technology. Since race and racial differences are neither

biological givens (out there, in the body, or in nature), nor ideological layers that can be removed surgically, we need to pay attention to the objects and practices that enact race. My object-oriented temporal approach thus helped set the stage for a topological account of race. Race becomes an irreducible, spacio-temporal thing, one that moves and changes shape depending on the times and places that are drawn together. This indicates a complex politics of difference, one that is distributed and more surprising than e.g. suggested by much of the critique voiced against the Human Genome Diversity Project. Understanding the politics of this changing and untamed character of race, an absent presence par excellence, will benefit from detailed object-oriented studies. In addition, as indicated above, 'objects slow down our revolutions'. They not only make relations, they also make them stick (however temporarily). Objects deserve more attention.

This paper aims to contribute to the rich literature within STS and ANT in particular in which spatial topology has been embraced as to decentre the object (and the subject) in western (knowledge) practices. Inspired by Michel Serres' notion of topological time, I have suggested the *folded object* as a way to include the temporal in this spatial rendering of objects. Attending to how objects enact time, how their folds keep it, may help us to understand the relation between the history of an object and the potential of its politics in the here and now. The above case incorporates different versions of time. One version had to do with narrative. It is a linear account of (chronometric) historic time. Attending to linear time is practical and insightful for it can help us order the various events related to the reference sequence. It helped me to order my story.

I mobilized three art metaphors to narrate specific versions of the history of the reference sequence. Although they emerged from the empirical material of this case I have stakes in using art metaphors. The added value of art metaphors is that they are both material objects and 'representations' of time and history in the here and now. I contend that they facilitate a multi-temporal approach. Not only do art-objects invite us to tell a story about what is seen, and to narrate a linear time. Art-objects, if we take these as unfinished and in the making, if not only to invoke a response, cannot but be anachronistic (see also Serres & Latour 1995, Latour 2008). Art-objects are time machines that represent things within different temporal orders simultaneously.³² Art metaphors have proved to be methodologically helpful in this case, but other cases might invite and need other metaphors.

Thus the metaphors of the portrait, the collage and the montage helped to underline particular versions of time. The *portrait* highlighted the aim of science to present nature as it is. As the first human DNA genome ever sequenced, it seemed to give a glimpse of the

architecture of the nature that can be found out there, untouched. This story attends to the story of scientific discovery and is narrated more or less in linear time. The sequence was produced in the 1980s and it is the mtDNA portrait of a human being, a species that has been around for some 150,000 years or so. In contrast, the *collage* underlines the construction of the object. It helps us to attend to the everyday practice of science wherein various entities (DNA material, sequencing technologies, etc.) from various times and places can be included in a single object. I have shown how the 'quotidian mess' tends to be deleted, to become virtually inaccessible. The collage underlines the folding of several temporalities, such as the growing interest in diversity research in the 1990s, the ability to make a cell line in the 1950s, a history of slavery and (scientific) racism, a sequencing technology developed in the 1970s, a modern-day lab in Cambridge where bovine and human mtDNA have become objects of research. This folding was partially the effect of the author, in the identity of a participant observer, who asked questions and engaged with the sequence. This engagement drew together a variety of histories that were usually kept apart. However, as we have seen the participant observer was not the only one engaging with the reference sequence in the late nineties. Medical geneticists were asking similar questions and drawing separate times and places together as well. The *montage* hinted at the fact that an object such as the reference sequence is not a smooth whole, but incorporates frictions and demonstrates time ellipses. Whereas the history of the sequence went unnoticed in population genetics, it raised serious questions in medical genetics. Yet the re-analyzing and re-sequencing did not replace its past. They did not make it timeless. Rather, they added complexity and layers of time to the sequence. I have shown that due to the 'symptomatic C', the history of the sequence refused to be rewritten. This C points to the history of its making, which is also a history of race.

I would like to emphasise that the three metaphors of portrait, collage and montage are not aimed at narrating a linear (meta) history of the sequence but that all three are encompassed in the folded object. To be sure, the goal of my narrative was not to tell a story about an object that has been optimized over time, or a story about how controversies surrounding this object have reached closure. My point is that this history and controversy cannot be left behind. They can be enacted and made relevant in the future to come. There is no end to history, no end to politics. That is not to say that the future of objects is pre-given or that it inheres in the essence of the object. The mtDNA sequence is Serres' folded handkerchief (Serres and Latour 1995). We cannot know beforehand which of its points will be distant or proximate. The consequence of the handkerchief is that it can be ironed producing desperate points and making histories inaccessible (see also Latour 2000: 263).

My talk of *political noise* was also purposeful. '[N]oise gives rise to a new system, an order that is more complex than the simple chain' (Serres [1980] 2007: 14). Noise is productive. It *interferes* with the actual signal (whatever that may be) and produces surprising patterns of interference (see also Rheinberger 1997). These mechanisms are indicative of topological time. Time is crumpled. This pleating produces *multiplicity*, where *pli* stands literally for 'fold' (Serres [1980] 2007: 245). Time materializes in spatially foldable objects. Folded objects are not political because of *what* is put into them, but because of *how* they are folded.

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¹ Michel Serres makes a distinction between the thing and the object. The act of throwing out the dead body of the dog constitutes the collective but it is also a passage from thing (the cadaver) to object (the cadaver orbiting at a constant distance). The cadaver becomes an object because it has become a marker of relations between subjects (Serres 1980 [2007]). On the vital role of getting rid of things for performing the social, see the classic paper by Mary Douglas ([1966] 1984). For a critique of Mary Douglas' notion of 'matter out of place' and a very good exploration of the notion of absent presence in the sociology of consumption, see Hetherington (2004). Hetherington argues that waste never really goes away and that it plays an ongoing role in social relations. 'Social relations are performed not only around what is there but sometimes also around the presence of what is not' (Hetherington 2004: 159).

² Steven Brown gives the following example for how the circulation of objects among humans makes collectives. 'Consider a game of rugby. The players are oriented around the ball, the token. They act in relation to the token, which is like a little sun around which the players orbit. The players become almost extensions of the token – its attributes. They are the means by which it passes, their movements have the sole aim of maintaining the play, of passing the token between one another. In so doing the token weaves the collective' (Brown 2002: 21). For an elaboration on the example of ball play, differences in speed of circulation and interest, see Serres (1980 [2007]): 224 -234).

³ My interest is in ways in which we can grasp the politics of an object without rehearsing a version of technological determinism. A classic, albeit much debated study in STS on the politics of artefacts is the Long Island Bridge mentioned by Langdon Winner (1986). In contrast to Winner I do not contend that objects embody a political script (as an effect e.g. of the intention of its maker). The politics of objects is not just in what is in them, nor is it merely in how they will be put to use. See also Latour (2002).

⁴ See e.g. the special issue in this journal 'The Status of the Object: Performances, Mediations, and Techniques', edited by Pels, Hetherington and Vandenberghe in 2002.

⁵ See Callon (1986) and the effect of a change in the identity of one of the actors in the network.

⁶ As has been observed, *networks* tend to be seen as rigid and tend to be about immutability (e.g. Law and Hassard 1999). For a critique of immutable mobiles, see e.g., Joan Fujimura (1992), Mol and Law (1994), Law and Singleton (2005).

⁷ Race could be one such difficult and fuzzy object. It is slippery and often escapes language. Its articulations are not straightforward and if you tackle it head on it appears to be another object instead. I think it is vital to explore this fuzzy aspect of race. Alas, there is no space for that in this paper.

⁸ One could say that both postcolonial studies and science studies have been engaged in modes of decentring the unmarked subject (of science) but there also differences between them. Science studies have provincialized universal claims of knowledge by studying science as a practice and culture, situating what counts as rationality and as scientific facts, and demonstrating the technologies applied to make facts 'universal'. Yet whereas postcolonial studies have been engaged in unravelling processes of othering and attending to the subaltern, postcolonial approaches to science studies are still marginal or confined to specific topics, such as medical and genetic research (for an excellent review, see Anderson 2002). Finally the turn to practice as well as the material semiotic methods developed in ANT have barely been explored within postcolonial studies and scholarship on race and science studies (M'charek 2013).

⁹ See also Rheinberger (1997) for whom time is not a line along which things occur, but an operator that manipulates and helps to reproduce various functions in an experimental system in a way that

these functions survive. Such functions, such as generating the unknown which is vital for experimental systems to renew themselves, have their own intrinsic time and together account for a multiplicity of time within an experimental setting. Time is then not external to entities but rather co-shapes and becomes a characteristic thereof.

¹⁰ Historians and anthropologists have dealt with time in more systematic ways than STS-scholars, and are far more engaged with the biographies of their objects, see e.g. Appadurai (1986), Anderson (2000), Daston (2000, 2008), Roque (2010).

¹¹ For a similar rapprochement between art and science, see Rheinberger (1997).

¹² See for an official overview of the history of the project:
http://www.ornl.gov/sci/techresources/Human_Genome/home.shtml (last accessed 25 August 2011).

¹³ On the notion of 'the human genome' and the problematics of the collaborations between these actors, see Bostanci 2006.

¹⁴ The White House Office of the Press Secretary (26 June 2000). This press release can be accessed at <http://www.genome.gov/10001356> (last accessed 25 August 2011). Haraway (1997) critically discusses the notion of maps in the context of genetics and calls them 'non-tropic maps' for they represent reality allegedly as it is (1997, Chapter 4).

¹⁵ The White House Office of the Press Secretary (26 June 2000).

¹⁶ The metaphors of maps and books and their use to qualify the human genome were around long before the presentation of the draft genome in June 2000. See e.g. Kevles and Hood 1992. See Kay 2000 for a historical account and the transformation of genetics in terms of cybernetics and communication systems. They did not fully supersede art metaphors such as the portrait. On this point, and on how the appropriation of art metaphors by current day speedy science has made oblique the modern division between the copy and the original, see Haraway 1997.

¹⁷ The full genome is the small circular structure represented in the 'Small is Beautiful' diagram. The genes are well ordered and comprise almost the whole genome, except for the upper part, depicted by a thin line, which represents the non-coding region (D-Loop) of this genome.

¹⁸ The genes are clustered nice and orderly, adjacent to one another, contributing to an Aristotelian ideal of beauty.

¹⁹ These letters stand for the nucleotides adenine (A), cytosine (C), guanine (G), and thymine (T).

²⁰ It seems to me that this name for the sequence (Anderson) was used frequently up until the turn of the millennium. Nowadays it is more often referred to as the Cambridge reference sequence.

²¹ On the Human Genome Diversity Project, see e.g. Cunningham 1998, Hayden 1998, Lock 2001, Marks 2003, Reardon 2005, M'charek 2005.

²² Interview held by the author in February 1997.

²³ I refer in particular to the population geneticists I encountered in the laboratories I studied. The situation might look slightly different in laboratories that study mtDNA in the context of diseases.

²⁴ Allan Bankier, telephone conversation on November 17 1998.

²⁵ I thank the second author of the Anderson paper, Dr Allan Bankier (at the MRC Laboratory of Molecular Biology, Cambridge) for pointing out to me that they had received the mtDNA clones from Dr Jacques Drouin, and for providing other information about the sequencing of Anderson.

²⁶ Epistemic thing-ness is not a stable state. An epistemic thing may switch between being an object of research and a technical object or routine device. A non-technical use of a routine device might turn it into an epistemic thing, a thing that generates the unknown. Rheinberger argues that epistemic things 'present themselves in a characteristic vagueness [for they necessarily] embody what one does not yet know (1997: 29). Vagueness and non-singularity is a virtue for the advancement of knowledge, but they also draw the future in the present.

²⁷ The fact that the makers of the original sequence in 1981 were uninterested in an individual sequence, as the quote by Allan Bankier demonstrates, should make us think. Where does the interest in personal, or individualized genomes come from? Perhaps, through the possibility of individualisation, our current day technology is contributing even more to processes of naturalisation. Perhaps we should call the rCRS the *Mitochondrial Eve of modern genetics*.

²⁸ On the unavoidability and importance of noise in communication, see Brown 2002.

²⁹ In the words of Lorraine Daston (2008) one could say, this C makes the sequence into 'a thing that talks.'

³⁰ Think of the photomontages by the DADA artists and Eisenstein's USSR film montages in the 1920s and 1930s.

³¹ Race is becoming a matter of growing concern, also for scholars who study the new genetics. There are many examples but for some edited volumes, see Wade (2007) Koenig, Lee and Richardson (2008), Whitmarsh and Jones (2010).

³² On different versions of time that can be at work at the same time (so to speak), and particularly on the naturalization of linear time, see Bowker (2006); Mirmalek (2009).