3 ARTICLE

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5 **Archaeogenetics and human evolution: the ontogeny of a biological discipline**

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16 **ABSTRACT**

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18 Genomics and ancient DNA methods have revolutionised many areas of biology,
19 including human evolution. Recently we have seen significant advances in
20 archaeogenetics including the use of large-scale genomic datasets to track human
21 movements globally. In addition, advances in ancient and modern genomics have
22 enabled researchers to resolve a range of issues of importance to indigenous people.
23 Most notable among these is the repatriation of ancient remains to their kin i.e. to what
24 Aboriginal Australians refer to as their 'Place and Country'. From an historical
25 perspective, new fields of science can be characterised as moving through three stages
26 beginning with description, followed by a focus on mechanisms / functions and finally
27 the formulation of experiments and hypothesis testing. The new science of
28 archaeogenetics is currently in the descriptive stage. It involves large-scale genome
29 sequencing and the use of explanatory narratives. Our analysis suggests that a mature
30 formulation lies in the future.
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34 **KEYWORDS**

35 Ancient DNA; Aboriginal Australians; hypothesis testing; information and knowledge.
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Introduction

We provide an evolutionary and genetic perspective on the study of human evolution. We have spent the last 10 years working with archaeologists and Australia's First People to better understand some of the important issues facing Indigenous people. Our research has been designed and conducted with the involvement and the participation of Aboriginal Australians. Furthermore, an important goal of our research program is to train the next generation of Indigenous researchers to participate in, and lead, genomic research in the future. We are part of the Australian Research Centre for Human Evolution (<https://www.griffith.edu.au/environmental-futures-research-institute/research-centre-human-evolution>) that was established to promote and improve our scientific understanding of the evolution of Australia's First People and the people of the Asia Pacific region.

Australia as a nation is in the midst of a fundamental debate about the rights of its First People and their recognition under the Constitution. As part of a wider discussion it has been suggested there is a need for a treaty between Aboriginal Australians and Governments at all levels. In addition to the voices expressing the need for legislative changes, there are others who have deeply held concerns of a more personal nature. For example, there is a desire for a much-improved understanding of how people dispersed across the Australian continent and how different language groups are related to each other. At a personal level, many Aboriginal Australians have also lost their connection with 'kin'. This is because many are still suffering the effects of the 'Stolen Generation' (Reid 2006). This term refers to Aboriginal and Torres Strait Islander children who were taken from their families and communities by Governments, churches and welfare bodies and raised in institutions. Children were also fostered out or adopted by European families.

In addition to the grievances resulting from these practices, there is widespread disquiet among Aboriginal Australian communities about the slow progress in returning ancient remains. Large numbers of these remains are still held in museums and other institutions. Slow progress is in part because many of these remains are not accompanied by any collection details. Archaeogenetics has much to contribute to the problem of repatriation. In a social context, we need to work in partnership with Aboriginal Australians, specifically we need to ensure that Indigenous people's DNA is safely stored and that it is not given to others. Also, Indigenous communities need to be the first to be informed of the results and their implications, this needs to be done in everyday language.

Until recent developments in ancient genomics, studies of skeletal morphology, and specifically craniometrics (Pardoe 1991; 2012) was the only method to investigate the geographic origin of ancient Aboriginal Australians. Craniometrics of robust forms of early Aboriginal Australians, suggested to some a link to Javan *Homo erectus* (Thorne 1977; Hawks et al. 2000; Webb 2006). And more recently, robust early Australians have been linked to archaic groups from across China (Webb 2018). However, gross morphological differences among Aboriginal Australian populations have not proved widely applicable for the identification of the geographic origin.

In contrast, it has been suggested that DNA methods can be used to facilitate the accurate identification of the geographic origin of ancient human remains (Kiesslich et al. 2004, Blow et al. 2008). This approach was successful in the case of Kennewick Man (Rasmussen et al. 2015). This ancient male human skeleton was discovered in Washington State (USA) in 1996 and was radiocarbon dated to $8,358 \pm 21$ ^{14}C years BP. Based on a number of craniometric studies it was suggested that Kennewick Man was not a Native American. In order to resolve Kennewick Man's ancestry and affiliations, Rasmussen et al. (2015) sequenced his genome to $\sim 1\times$ coverage. Comparison of this genome to worldwide genomic data showed that Kennewick Man was more closely related to modern Native Americans than to any other population worldwide. Rasmussen et al. (2015) concluded that Kennewick Man showed continuity with Native North Americans over at least the last eight millennia.

The study of Kennewick Man was possible, at least in part, due to the well-preserved nature of these remains from a temperate environment. The environment in Australia is not generally conducive to the preservation of ancient DNA (aDNA) being, at least in many regions, hot and humid (Heupink et al. 2016; Hofreiter et al. 2015). Nevertheless, using whole genome enrichment methods, our studies of Aboriginal Australian remains from the Holocene period, have enabled us to recover 27 mitochondrial genomes, many with high coverage (16x – 332x). We have also been

able to recover 10 nuclear genomes from ancient Aboriginal Australian remains, and the majority of those genomes had more than 1x coverage. To increase the endogenous sequences, first our team has focused on improving the DNA extraction methods for ultra-short DNA fragments (Heupink et al. 2016). Second, we used in-solution target enrichment methods, for both the mitochondrial (Wasef et al. 2018) and the nuclear genome (Heupink et al. 2016; McColl et al. 2018; Wright et al. 2018).

The development of a scientific discipline

We need to consider archaeogenetics in the context of the ontogeny of scientific disciplines generally. We suggest that a common pattern in science is that disciplines begin with a process of description, then progress over time to identify potential mechanisms and functions, and finally move to experimentation and hypothesis testing. However, this is a general pattern and the stages are not necessarily discrete and can be overlapping. In addition, it is important to appreciate that science is conducted within a social context and that this context typically determines what is studied (Figure 1).

Both technology and theory can contribute to significant advances in science. However, today technology is regarded as the ‘driver of scientific advances’ and that it is uniquely responsible for these advances (Botstein 2010). Perhaps this is not surprising given the impact that technology has had on our everyday lives through advances in communication, education and medicine. Furthermore, new technologies can emerge extremely rapidly and can have disruptive consequences, displacing established ways of doing things. For example in recent years, Uber has revolutionised the taxi industry worldwide. In the study of human evolution, the introduction of genomic analyses and aDNA methods has resulted in the production of an unprecedented volume of genomic data (e.g. Posth et al. 2018). These data have been used by researchers to describe patterns of human movement and changes in these patterns over time in enormous detail.

Just as technologies can advance rapidly, theories can also progress quickly (Kuhn, 1962). These ‘jumps’ or paradigm shifts are fundamental to understanding how disciplines develop. Periods of what Kuhn called ‘normal science’ revolve around a consensus of prevailing scientific perceptions. These periods are characterized by approaches that largely involve the implicit use of accepted ideas and ways of doing things. In contrast, paradigm shifts involve innovative events that result in new understandings and theoretical approaches that are incommensurable with the older views. For example, Kuhn asked the rhetorical question: why were Aristotle’s ideas about matter and motion so different from those of Newton? He concluded Aristotle was not a ‘bad Newton’, he was just different (Horgan 2012). This was because he saw the world in a different way, as John Berger (1972) famously described it years later.

Technology and description - stage 1

In 1555 an early biologist Piere Belon recognized and described in detail the homologies between all the skeletal elements of a bird and those of a human. The technology used was a simple comparative sketch of these two skeletons (Figure 2). Interestingly, Belon provided an explanation of this that was consistent with the thinking at the time. He suggested that these fundamental similarities were essentially because God worked in accordance with a plan. Bainbridge (2018) remarked that “The anatomists and artists of the time were fascinated by the creeping realization that each creature is not, it turns out, created anew, an entirely novel design formed without reference to any other. Instead, it was revealed that animal life is not a cataloger’s inventory of discrete unrelated forms, but rather consists of variations on a basic theme. The bird and the man are shown as essentially the same, human separated from fowl by a few minor skeletal tweaks and distortions” (Bainbridge 2018: 94). He also remarked that “The idea that the same structures could be modified and adapted to serve the purposes of a human, a bat, a dove, a serpent, and a halibut spoke of far more profound evidence of the Creator’s plan than the inventoried animal sermons of the Middle Ages” (Bainbridge 2018: 95). Today of course, evolutionary biologists would still recognize the accuracy of Belon’s description but, from a scientific perspective, they would attribute the fundamental ‘sameness’ he identified, to the evolutionary process *sensu* common ancestry. Evolutionary biologists attribute ‘differences’ to the functional properties of a wing (flying) versus the human forelimb (grasping objects etc.). The underlying assumption is that these structures have been ‘shaped’ or ‘fashioned’ by natural selection for the function they perform.

A century later, technology drove another descriptive phase in biology, this time in the form of drawings of biological material using early microscopes. Robert Hooke's volume entitled '*Micrographia*' was the first important work published using microscopy. First published in 1665, it contains large-scale, finely detailed illustrations of some of the specimens he viewed under the microscopes he designed (Hooke 1665). They were of course characterized by extraordinary detail, literally every hair.

Microscope technology was also used to describe the early embryological stages of life. There were two broad preconceptions underlying these descriptions: preformationism and epigenesis (Pinto-Correia 1997). These were distinct ways of describing and attempting to explain the growth of individual organic forms. Epigenetics proposed that the embryological development of individuals starts from material that was undifferentiated and that biological form emerges gradually over time (Maienschein 2017). In contrast, preformationism was the idea that the body of the developing individual was complete in the 'parental seed', so that during development the embryo only increased in size. The 'ovists' were preformationists who argued that the new organism was present in the egg. In contrast, 'animalists' or 'spermists' believed that offspring develop from a tiny fully-formed fetus contained within the head of a sperm cell. This idea gave rise to the well-known 'little man in the sperm', the homunculus (Maienschein 2017) (Figure 3A, B).

Function and mechanism - stage 2

As all biologists know, Darwin's place in history is assured because he was the first to propose a credible mechanism for evolutionary change, not because he was the first to suggest the idea of evolution. In fact, prior to the publication of '*On the Origin of Species by Means of Natural Selection or The Preservation of Favourable Races in the Struggle for Life*' (Darwin 1859), many authors had proposed the phenomenon of evolution, including Jean Baptiste Lamarck (1809), as well Charles Darwin's grandfather, Erasmus Darwin. The first test of evolution was reported decades before 1859 when George Cuvier (1831) compared the skeletal structure of ancient ibis mummies from Egyptian catacombs with the skeletons of individuals of the same species living at the time. He recorded no differences between these specimens. Cuvier used this result to argue against evolution. In so doing, he set back the acceptance of evolution in Europe by decades (Curtis et al. 2018).

Later, Ernst Haeckel, a populariser of Darwin's work, reasoned that there must be intermediates between apes and humans. He argued that humans originated in South Asia, a theory that enjoyed considerable support for the first half of the nineteenth century. In 1866 his chief work appeared - entitled '*A General Morphology of Organisms*' (Haeckel 1866). This work was intended by the author to bring all morphology under "the sway and domination of evolution", as E.S. Russell (1916: 247) later described it. Haeckel's work had strong overtones of description and was interpreted in terms of Darwin's proposed mechanism of evolution.

Hypothesis and experimentation - stage 3

During the 1800s, ideas relating to functional properties of organisms appeared. For example, in relation to human evolution, Samuel George Morton, one of the great 'data-gatherers of American science' (Gould 1981: 51) published three major works on the size and function of the human brain (Morton 1839; 1844; 1851). He gathered a large collection of skulls, to test the idea that different racial groups were characterised by differences in brain volume. His implicit assumption was that brain volume was a proxy of intelligence, and that Europeans would have a larger volume than any other racial group. His studies supported his preconceptions and showed that 'modern Caucasians' had the greatest volume, while members of the so-called 'negro group', which included Aboriginal Australians, had the smallest volume.

One of the great evolutionary biologists of our time, Stephen Jay Gould, provided a careful re-analysis of Morton's findings (Gould 1981). He showed that, without conscious effort, Morton arrived at the answer that supported his preconceptions. After repeating Morton's experimental procedure with unbiased methods, Gould showed that there were no differences in brain size. Despite these problems, Morton's research marked the beginning of the last stage in the scientific

1 ontogeny of the study of human evolution, namely that involving experimentation and theory testing.
2 Although the three stages overlap, the general pattern of scientific progression is clear.

3 4 **The beginnings of archaeogenetics – a famous year**

5
6 The emergence of new technologies quickly results in new fields of study. For example, 1966, a
7 date that all geneticists know, marked the beginning of molecular population genetics. In that year
8 Richard Lewontin and John Hubby reported the application of enzyme gel electrophoresis to the
9 study of genetic variation in natural populations of the fruit fly *Drosophila pseudoobscura* (Hubby
10 and Lewontin 1966; Lewontin and Hubby, 1966). The loci that the authors used were chosen purely
11 for technical convenience, without any prior knowledge of the levels of variability. Together with an
12 independent study of human populations by Harry Harris (1966), these seminal publications
13 provided the first relatively unbiased picture of protein sequence variability within populations. This
14 work revealed that many proteins have surprisingly high levels of diversity. The papers stimulated
15 a worldwide research program that found similarly high electrophoretic variability in many different
16 species (Charlesworth et al. 2016). This led to the development of statistical tools for interpreting
17 such data in terms of genetic drift, balancing and purifying selection, and the effects of selection on
18 linked variants. The current use of whole-genome sequencing and aDNA studies of variation is the
19 direct descendant of these pioneering publications.

20 21 **Ancient DNA data and discovery science**

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23 The field of aDNA began with Allan Wilson's 1984 paper on quagga (Higuchi et al. 1984). Wilson's
24 research team was able to recover short DNA sequences from a museum skin of this extinct
25 species. However, the authors were limited to cloning fragments and to manual DNA sequencing.
26 Subsequently, the field of aDNA has grown with a series of technological advances. These include
27 the development of the Polymerase Chain Reaction by Kary Mullis (Saiki et al. 1985, 1986),
28 automated capillary sequencing, and the invention of massively parallel DNA sequencing by
29 Jonathan Rothberg (Rothberg et al. 2011). These combined developments resulted in a dramatic
30 increase in the number of aDNA studies, although they generally remained limited to short DNA
31 fragments. Subsequent developments in high resolution optics and glass-slide sequencing allowed
32 the reconstruction of substantial regions of many genomes, and finally of 'complete' ancient
33 genomes. The full potential of the field of aDNA was realized with the publication of Svante Paabo's
34 landmark paper (Green et al. 2006) which used the latter technology to sequence the complete
35 Neanderthal genome. Together with the recent developments in DNA capture methods, these
36 technologies laid the foundations for the discipline of archaeogenetics.

37
38 Studies in archaeogenetics have described the relationships among human populations using
39 complete genomes. The description and analysis of these genomes can be characterised as a
40 process of 'discovery science' / 'data mining' (Bergeron 2003) (Figure 4). Discovery science is
41 concerned with extracting patterns in the data using a variety of pre-determined methods. This is a
42 largely descriptive approach without a specific underlying theory or hypothesis under test. For
43 example, principle components analysis (PCA) which is extensively used in archaeogenetics
44 partitions the genetic diversity based on similarity. Although this is useful in many cases it cannot
45 provide direct information about evolutionary processes. This is because it is not possible to identify
46 primitive versus advanced states and therefore cannot be used (directly at least) for the
47 reconstruction of evolutionary history.

48
49 Bioinformatics is an interdisciplinary approach involving biology, computer science,
50 mathematics, and statistics to analyse biological sequence data, genome content, and
51 arrangement (Mount 2001). It is at the heart of archaeogenetics. These analyses are often
52 conducted *post hoc* after decisions about the subject matter and the issue under study have already
53 been made. This is then, essentially, the descriptive science of old, albeit using a new technology
54 (Figure 4). Reference to 'discovery' and 'mining' is the language of 'exploration'. It refers to
55 knowledge as something that is awaiting discovery or of 'industries' in which valuables (like
56 diamonds or coal) simply lie beneath the surface and need only to be uncovered. DNA sequence
57 data are a series of nucleotides that can be represented by four letters. These 'identifiers' are not,
58 in themselves, information. Information is data in context. That is a collection of data and associated
59 explanations, interpretations and other material concerning a particular event or process (Bergeron,

2003). Knowledge is different again. It results from making information intelligible in accordance with some general theory or principles (Figure 4).

Aboriginal Australian archaeogenomics and hypothesis testing

Over recent years, we have worked with colleagues to conduct a series of studies in partnership with Aboriginal Australians. The first of these studies recovered a complete genome from a hair sample collected in the late 1800s from a person living in the desert region of central Australia (Rasmussen et al. 2011). From a technical perspective this was an important development and suggested that larger scale genomic studies in Australia were possible. Our second study recovered aDNA from skeletal remains of another Aboriginal Australian (Heupink et al. 2016). That paper reported the complete mitochondrial genome of a man buried in the Willandra Lakes region of New South Wales. Our study refuted previous findings (Adcock et al. 2001) that Mungo Man, the oldest known Australian, was a member of an archaic group that preceded Aboriginal Australians living today. The third was a comprehensive study of high coverage nuclear genomes of modern Aboriginal Australians from across the continent (Malaspina et al. 2016). That study enabled us to time many of the events in the history of Australia's First People. All three of these studies were generally descriptive in nature.

In contrast, our latest study (Wright et al. 2018) was aimed at testing the hypothesis that DNA sequences from ancient Aboriginal Australian remains could be used to identify their closest living relatives and thereby facilitate their return to 'Place and Country'. We first asked whether complete mitochondrial sequences alone are sufficiently accurate to facilitate repatriation. Because the recovery of complete mitochondrial genomes is technically less challenging than nuclear genomes and would be less expensive, this would be an ideal approach. Unfortunately, it was clear from our findings that mitochondrial genomes do not provide a sufficient level of variation for accurate repatriation. Of 27 complete ancient Aboriginal Australian mitogenomes we recovered, 18 (62.1%) had the closest contemporary match to an individual from the same geographic region (within 235 km). However, for the remaining 11 ancient individuals (37.9%), the results were inconclusive, due to either a lack of contemporary matches, or because some mitochondrial haplotypes were geographically widespread. Hence, unfortunately, the suggestion of Tobler et al. (2017) that mitochondrial genomes can be reliably used for repatriation is unfounded.

As a result, we performed a series of analyses of ancient Aboriginal Australian nuclear genomes that we recovered from pre-European remains. We compared these with 100 complete modern high coverage (typically 60x) nuclear genomes that we had previously sequenced. In addition, we used a reference panel including 2117 modern individuals from worldwide populations genotyped for 593,610 single nucleotide polymorphisms. A principal components analysis revealed high levels of admixture in some samples. In contrast, individuals from the Western Central Desert (WCD) were almost completely unadmixed and were therefore subsequently used as a reference group to identify Aboriginal Australian ancestry. Importantly, all the ancient Aboriginal Australian samples were found to cluster close to the unadmixed WCD individuals.

We also investigated the genetic relationships among the ancient genomes using both PCA and outgroup f3 statistics. We showed that modern Aboriginal Australians projected onto a PCA inferred from the five highest coverage ancient individuals exhibited substantial genetic variation between people from different regions. Three distinct clades were observed (Wright et al. 2018). We next sought to determine whether the ancient Aboriginal Australian individuals were most closely related to those with known traditional connection to the same region. These analyses suggested a higher genetic affinity of ancient individuals to modern groups from the same region, compared to modern individuals from other geographic regions. Again, in both analyses, modern individuals show closest affinities to ancient individuals from the same geographic region.

We also investigated these patterns using f4 statistics with a masked dataset (in which for example DNA sequences indicating European ancestry were removed). These analyses measured the amount of excess allele sharing between each ancient Aboriginal Australian individual with a given modern population, compared to genomes of Papuan people from New Guinea as an outgroup. For each ancient Aboriginal Australian sample, the highest level of allele sharing was with their respective local contemporary group (Wright et al. 2018).

Put together these results highlight the considerable genetic structure of both modern and ancient Aboriginal Australian populations and suggest that this structure is similar in both time periods. If this was not the case, the method described here would not have been successful in identifying kin populations. Also, this stability of genetic structure over time suggests an ongoing connection to country of ancient and modern populations.

In summary, using in-solution DNA capture methods (in which DNA baits are used to selectively recover target sequences) and second-generation sequencing, we successfully recovered 10 ancient nuclear genomes from Aboriginal Australians. Each of these was from the period before European contact and the skeletal remains were dated up to 1,540 years before present (Figure 5A, B). This research shows that it is possible to identify the closest living relatives of ancient people that are known only from their remains (Wright et al. 2018).

Repatriation of ancient remains is a significant problem. For example, there are estimated to be 3,644 unprovenanced post-cranial remains in Australian museums, in addition to 89 unprovenanced crania. Furthermore, there are extremely large numbers of unprovenanced skeletal remains in overseas institutions (S. Webb, personal communication). In Australia there are 995 provenanced crania which will be useful because they will provide additional data points for the 'map of aboriginal genome diversity'.

Science as a social and ethical activity

Science is a social activity, whether we are conscious of it or not (Figure 1). With new technologies new social challenges emerge. An example in relation to archaeogenetics is the controversy regarding access by scientists to genomic data from Indigenous people. Kowal et al. (2017) recently argued against any restrictions to full access to genomic data collected from Indigenous people. These authors cited our 2016 study of Aboriginal Australians as a case in point (Malaspinas et al. 2016). The collection of these samples was fully in accordance with Australia's National Statement on Ethical Conduct in Human Research (National Statement on Ethical Conduct in Human Research 2007 (Updated 2018)). Moreover, we worked with Aboriginal donors to develop the conditions for data sharing. Kowal et al. (2017) mischaracterize this ethical framework as a perceived series of 'hurdles' that interfered with the pursuit of scientific goals.

Many researchers hold the view that journals have a moral obligation to make genomic data publicly available. In reality a journal's only responsibility is to ensure that the work was ethically conducted and that the findings are reproducible. In our view, the implication that scientific goals should take priority over the rights and wishes of Indigenous participants smacks of a paternalism that has dogged this research field since its early days. This paternalism is further evidence of the gulf between some research groups and Indigenous people and is evidenced by the fact that, even today, many recent genomic studies have been conducted without any involvement with Indigenous people. A similar form of paternalism is manifested in the assertion that the ancient remains of Indigenous people must always be available for scientific study, notwithstanding any reluctance of Indigenous communities to agree to such research.

Conclusions

Many archaeogenetic studies continue to focus on recovering large amounts of DNA sequence data and to using such data to describe the relationships among populations. Furthermore, many researchers continue to collect genomic data and then, *post hoc*, compose narratives typically about migration routes and their timing (Landau 1984) and suggest that such narratives explain the data. However, we suggest that there is a need for researchers to look towards mechanisms / functions, and to test specific evolutionary hypotheses. Importantly, we are not waiting for what might be considered 'The Darwin of archaeogenetics' to appear. Many credible evolutionary mechanisms have already been developed e.g. hypotheses about the molecular clock (Zuckerkandl and Pauling 1962; Kumar 2005), neutral theory (Kimura 1968; 1983) and molecular drive (Dover 1982). Furthermore, there is a large body of evolutionary theory on which to base hypotheses and experiments. For example, theories about the nature of species have been widely debated (e.g. Paterson 1981) and a large body of theory has developed. These theories can be applied to genomic data from anatomically modern and archaic humans to clarify the taxonomy and species status. We suggest that this would provide fertile ground for future research.

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List of figure legends

Figure 1. A generalised schema for the ontogeny of biological disciplines. The relative importance of technology decreases as the discipline advances from the descriptive stage 1 to stage 2 in which function and mechanism become more important and stage 3 in which experimental testing of hypotheses tends to dominate. These stages are not mutually exclusive. In contrast to technology, the importance of theories tends to dominate as a discipline matures. Scientific activity occurs within a social context.

Figure 2. Pierre Belon was a French naturalist and writer. In his *L'Histoire de la nature des oyseaux* (1555) he included figures of the skeletons of a human and a bird in which he identified the homologous bones. This image is widely thought of as one of the earliest representations of comparative anatomy.

Figure 3. In contrast to the well-known conception of the homunculus (A) the 'little man in the sperm', the 'ovists' (B) argued for the presence of a 'little man' in the egg. Both these conceptions are preformationist views. They differ only with respect to the relative importance of the egg and the sperm.

Figure 4. The scientific field of bioinformatics includes data gathering, for example DNA or amino acid sequences, understanding these data in a particular context (which is 'information') and finally understanding the relationship between information and knowledge.

Figure 5. A Principal Components Analysis (PCA) and the geographic distribution of ancient and contemporary Aboriginal Australian nuclear genomes. (A) The PCA analysis of the genome data from 10 ancient Aboriginal Australians (squares) shows that, in each case, their closest modern relative (circles) lives geographically very close to where each ancient sample was collected. (B) Other modern samples (small grey circles) were found to be not closely related to any of the 10 sets of ancient remains. This strongly suggests that the origin of un-provenanced ancient samples can be identified to Indigenous communities to whom they are most closely related.

Social context

Paradigm shifts

que la tête seroit peut-être plus grande à proportion du reste du corps, qu'on ne l'a destinée icy.

ART. XC.
Ce que c'est
que l'œuf de
la femme, &
comment un
enfant vient
ordinairement
au monde.

Au reste, l'œuf n'est à proprement parler que ce qu'on appelle *placenta*, dont l'enfant, après y avoir demeuré un certain temps tout courbé & comme en peloton, brise en s'étendant & en s'allongeant le plus qu'il peut, les membranes qui le couvroient, & posant ses pieds contre le *placenta*, qui reste attaché au fond de la matrice, se pousse ainsi avec la tête hors de sa prison; en quoi il est aidé par la mere, qui agitée par la douleur qu'elle en sent, pousse le fond de la matrice en bas, & donne par conséquent d'autant plus d'occasion à cet enfant de se pousser dehors & de venir ainsi au monde.

L'expérience nous apprend que beaucoup d'animaux sortent à peu près de cette maniere des œufs qui les renferment.

L'on peut pousser bien plus loin cette nouvelle pensée de la generation, & dire que chacun de ces animaux mâles, renferme lui-même une infinité d'autres

Bioinformatics