

//Equity (8 Mar 2019)

If someone is intent on disdaining a sex or race it may be too difficult to undo this intersectional propaganda using a coherent argument.

With respect to sex, historic power differences have been inherited from our ancestors (whom we owe our existence) due to a combination of factors;

- a) innate differences in reproductive motivation: evolutionary programming discourages men from acting specifically feminine as they would either be expelled or not granted access to high genetic quality females in the environment of evolutionary adaptedness. There has been greater evolutionary pressure for the development of male (versus female) reproductive psychology as their decisions had a greater impact on their reproductive fitness. Fertile females were selected for reproduction in their environment of evolutionary adaptedness (100000-100000000 years ago) regardless of the possession of specific psychological traits (an exception perhaps being nurturing behaviours), due to the high value of their gametes. They bore extraordinarily high reproductive opportunity sacrifice per child (> 9 months) compared to that of a male (< 1 hour). Thus contrary to feminist theory, gender is not interchangeable. Their experience of the fluidity of their sexual psychology (including orientation; cf bisexuality) leads them to believe males can and should adopt traditional feminine roles in society - which in reality is untenable due to the strong influence of testosterone in the development of male reproductive psychology. There exists an asymmetry in social status drive; for females competence is optional, while for males competence is necessary.
- b) innate differences in (at least physical) competence: likewise evolutionary programming encourages different forms of competition in the sexes as it is unfavourable for any population/species to risk its high value female gametes. This is primarily exhibited in physiological differences (e.g. strength), although it might also be seen in some personality (e.g. agreeableness, linked to socially protective conformity) and information processing differences (e.g. object/spatial transformation). The most prominent psychological difference observed is that of a disparate focus on people and things - empathising/systemising (although I would argue much of this is likely attributable to differences in reproductive motivation, and its interaction with the social environment).
- c) We also find that males exhibit greater genetic variance, which has been hypothesised to be linked to risk taking. Risk taking was selected for in their natural history as it often led to an extraordinarily large number of offspring for a few males. In the early anthropocene (< 10000 years ago), the ratio of females to males who successfully reproduced was often as high as 10:1, and over the evolutionary timeline of our species (100000+ years ago), the ratio of females to males who successfully reproduced was on average 2:1. This also implies that we are not a naturally monogamous species. Ignoring here opportunism (rape), we have both short-term (ie comparatively low genetic quality fertile female coupled with comparatively high genetic quality/alpha male) and long-term (ie matched genetic quality partnership) mating strategies. One might argue our novel reproductive complementarity enables the re-enactment of such strategies, as it would have been evolutionarily favourable for high genetic quality males to ignore the faces of comparatively lower genetic quality females when engaging in short-term relationships, yet not so in the case of long-term relationships.
- d) limited resources and technology imply it was inefficient and therefore suicidal for a population (nation) not to adopt sex roles beyond that of [more specific than simply] respecting and taking responsibility for the well being of the opposite sex. Known examples of efficient practices have been selected for as all human civilisations which did not adopt these practices appear to have died out (proprietary/clothing, marriage, male warfare, etc).

With respect to race, historic power differences have been inherited from our ancestors (whom we owe our existence) due to a combination of factors;

- a) cultural differences: including religion (although I would argue religion is primarily an evolutionary byproduct rather than being especially adaptive for a group)
- b) environmental differences: including resources, climate, occupational constraints, etc - placing pressure on the development/elimination of traits.
- c) intergroup competition: warfare, interbreeding. While the native African genome is considered pure Homo sapiens, native European/Asian populations contain on average 1-4% of the Neanderthal genome, and native Australian aborigines contain on average 1-10% of the Denisovan genome. Besides these more recent crossings (~50000ya), our last common ancestor with Neanderthals/Denisovans existed 600000ya.

I theorise however that there is an underlying animosity against males which is not entirely due to (ignorance regarding the nature of) these historic power differences. I argue this animosity is product of the break down of cultural structures used to guarantee the fairness of genetic distribution (in matched partnerships). Due to a combination of factors (including technology, education, experimentation, etc), social changes have disrupted the historic cultural systems used to suppress short-term mating strategies in favour of long-term mating strategies. Such were required for a civilisation to compete with its neighbours; both in terms of maintaining the fertility rate and reducing the number of single mothers whose offspring no one (bar the generally absent father) is genetically inclined to care for. What is perceived as social injustice between sexes is actually a byproduct of the corruption of the systems ("patriarchy") and not the systems themselves.

Furthermore, I don't actually conform to the tribalism thesis of the IDW (e.g. JBP). It is in our nature to form tribes; these create intergroup competition. Without tribalism we wouldn't have high intelligence populations (eg Ashkenazi Jews) or races at all, let alone international, interstate or regional/demographic competitiveness. There would be less genetic diversity (limited to additive genetic effects; single nucleotide polymorphisms/mutations). Population level traits/adaptations which rely on the interaction of multiple mutations (at different points in the genome) would cease to emerge after x generations of non-discriminatory coupling. Such biodiversity may have an effect on our species' survival in the face of pathogens (e.g. retroviruses are known to have played a major role in evolution - 50% of our genome has formed from HIV like viruses), although these could likely be combated by advanced medicine (including genetic editing and cloning). With regards to natural minorities (e.g. disability, sexual orientation, gender dysphoria etc), it is the nature of the biological universe to suppress traits (genetically or environmentally disposed) which endanger the population - including deleterious mutations or short-sighted behaviours. The problem is not tribalism per se (e.g. what some might call sexism/etc) but tribal supremacism (e.g. radical feminism/etc). Tribes can still behave like human beings and treat others with respect. Tribalism presents a more serious problem in a modern world which faces species level extinction due to nuclear war however, where the elimination of natural tribes could reduce the genetic incentive to engage in such actions. Yet war itself (in a high tech state) is an unnecessary artefact of ignorance and poor communication. The pro-anti tribalism debate appears to be exercise in risk management, and it is a discussion worth having. Personally however, I fear the consequences of interfering with natural tribalism (the rapid development of tribal extremism/supremacism) may outweigh the risks associated with tribal friction (the acceptance of differences).

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//Group differences (12 May 2019)

Here are some important 2019 findings in population genetics; both from high quality journals (Dunkel et al 2019, Piffer 2019). Methodology: examining the distribution of mutations associated with trait x (here, general intelligence as inferred by IQ and/or EA; educational attainment) across populations*.

Dunkel, C. S., Pallesen, J., & Kirkegaard, E. O. (2019). Polygenic scores mediate the Jewish phenotypic advantage in educational attainment and cognitive ability compared with Catholics and Lutherans. *Evolutionary Behavioral Sciences*. [https://psycnet.apa.org/record/2019-03287-001]

Piffer, D. (2019). Evidence for recent polygenic selection on educational attainment and intelligence inferred from GWAS hits. *Psych*, 1(1), 55-75. [https://www.mdpi.com/2624-8611/1/1/5]

Prior to the current era/full genome analysis, genetic determination of complex traits (ie traits influenced by large portions of the genome) had to be inferred by twin studies, looking at the correlation between the emergence of the trait and twins (separated at birth)**. It was difficult to extrapolate/apply these findings to observed group differences (which might instead have an environmental origin). Critically, considering that even though a trait might be measured to be genetically/environmentally determined as x/y% in one environment, there is often high a 'gene-environment interaction' effect, and so this measurement may not necessarily hold in another environment. In the case of general intelligence for example, genetic determination measurements in low socio-economic environments typically produce relatively low genetic determination measurements (20-30%) as compared to average environments (50-80%), as the majority of the differences observed between low socio-economic individuals appear product of family/peer group (basic school/health prerequisites; confounded also by experimental task engagement/familiarity). Group differences affect how individuals are treated by their environment/society, and so their genetic basis cannot be easily quantified. Even in cases where twins/siblings are separated at birth and raised in different (foster) parental group environments, greater societal influences cannot be partialled out. For this reason psychometric analyses (like IQ tests) of traits (like general/fluid intelligence) are often only considered valid within a given population; the results should be normalised with respect to this population (this is already done for sex).

Enter the era of full scale genetic analysis. In order to conduct such analyses, (i) alleles/mutations (e.g. SNPs; single nucleotide polymorphisms) associated with a trait x are first identified. Next, (ii) the distribution of these alleles/mutations across populations is measured; "polygenic score"/PGS are produced. Finally, (iii) these distributions in polygenic scores are compared to the distributions of the observed trait across populations (simple correlation; i.e. graph of PGS vs trait intensity, each datapoint representing a given population). There are interdependent confounds which must be accounted for in such analysis; 1. even though an allele might be associated with a trait, it doesn't necessarily imply that the trait is caused by the allele, 2. as populations evolutionarily diverge, they tend to accumulate different sets of mutations (even if these mutations serve no adaptive/detrimental effect; ie genetic drift), 3. the polygenic calibration procedure (i) may be biased towards a reference population. Therefore, the more genetically distant two populations are, the less robust the analysis. Various techniques have been applied in Piffer (2019) to cross-examine these confounds; for example seeing if the identified allele distributions (PGS) across populations are also associated with the population distributions of another/arbitrary trait (e.g. height). If the calculated population differences in the original analysis (iii) are purely resultant of the above confounds, then we would expect such an association to be both present and dominant.

* For a background on genetic determination using genome wide analysis methodology (with respect to general intelligence), I am also attaching the most recent Nature review article (Lee et al 2018);

Lee, J. J., Wedow, R., Okbay, A., Kong, E., Maghziyan, O., Zacher, M., ... & Fontana, M. A. (2018). Gene discovery and polygenic prediction from a 1.1-million-person GWAS of educational attainment. *Nature genetics*, 50(8), 1112. (https://www.nature.com/articles/s41588-018-0147-3 / https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6393768).

** For a background on genetic determination using traditional twin studies methodology, I am attaching a summary; twinStudiesSummary-RBB2015-18.txt. Note, this summary assumes 'additive effects' only; genetic determination of a trait is measured using a sample of separated at birth twins using a simple "ACE" model. Note, 'non-additive effects' include recessive/dominant genetic components, gene-gene interaction (ie a more complex dependency of alleles in determinacy of the trait other than a simple addition of their individual effects), etc.

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Civilisation maintenance is a complex subject, especially for a rapidly evolving society; technology included (I would argue pretty much all changes we see are a byproduct of technological changes). I don't have a background in social science, but first became concerned with the topic when mapping out a series of social changes, particularly in the 'purity [sub]domain' (...). It doesn't help when certain countries stop publishing their data however, and moreover, after implementing a series of massive changes to their society (...). I have therefore become increasingly reliant on theory rather than large scale data collection in the analysis of civilisation risk management:

The freedoms we take for granted are dependent on the sustained functioning of our society (e.g. including but not limited cohesion/order). For any civilisation to be maintained, long-term reproductive strategies must be emphasised over short-term reproductive strategies. This arguably is the cornerstone function (goal) of every civilisation. A prototypical example of such emphasis includes the introduction of proprietary norms (e.g. clothing) to suppress short-term mating strategy in favour of long term mating strategy. Short term mating strategies in mammals include a) males seeking relatively (comparatively with respect to themselves) low quality but fertile females, or b) females seeking relatively (comparatively with respect to themselves) high quality males. An asymmetry exists here because of sexual dimorphism; female bodies typically have a higher median value than male bodies due to the sparsity of their gametes/cost of pregnancy. c) (in-group) rape is also a short-term mating strategy of which any tribe/community (not just large scale civilisations) will seek to suppress. Long term mating strategies comprise the identification of partners of equivalent evolutionary value (genetic fitness), and the subsequent sharing of resources (for females; primarily their reproductive/natal/nurture system, for males; primarily their work/protection/wealth) across long periods of time in order to rear and educate children.

The long-term reproductive strategy must be activated because a civilisation's survival depends on a variety of conditions. Critically;

1. The birth rate of the native population and culture must be above ~ 2.0 . Else mass immigration is required; yet if they successfully integrate/assimilate their birth rates too will drop (requiring indefinite immigration), or if not they will replace the existing culture. In either case the host population/culture will be decimated in time, and there is no guarantee of the nature of the replacement population/culture (e.g. is it capable of competing with more efficient or genetically motivated nations?)
2. Families must be able to raise children without financially draining future generations. Else the government will reach the point where either a) war or b) mass automation (AI economy) will be required to lift the debt burden.

In the modern west, both of these conditions are currently unmet, yet there is reason to believe that while technology may have ultimately caused their loss, with sufficient critique/understanding/exploration we can reclaim them. In order for both these conditions to be restored, barring artificial solutions, some level of traditionalism (fidelity) might be required, as a) marital success is positively correlated with a female's number of prior sexual partners, and b) (1) birth rate and (2) child outcomes are positively correlated with traditional family environment (active parents). Yet (1) female sexual promiscuity (typically manifested as hypergamy) and (2) male sexual promiscuity are dependent on societal (moral) standards;

1. If males are 'employing' virtual prostitutes and male short term mating strategy activation/stimulus is primarily a function of perceived presentation/availability of a fertile female body, there is little reason to expect females not to seek their evolutionarily equivalent mating goal in generating similar such fantasies (sexual contact with high-quality males, irrespective of whether the male wishes to support their children - hence for reference, the intentional termination of developing humans). Especially if the virtual stimuli are causing a major attention and/or competition deficit in the mating arena. What benefit is there for a female to invest in their long term mating strategy (fidelity) when a) there is no guarantee of a male seeking such a long-term partnership with them once they are unable to compete with a surplus of ambient short-term mating stimuli and/or b) they can gain the same resources through other means (e.g. government welfare).
2. Male sexual fidelity (including willingness to raise a family) likewise is dependent on female sexual fidelity (societal moral standards). It is difficult for males to maintain focus on their long term reproductive goal when they are constantly primed by signals generated by (imaginary) females (ostensibly) seeking short term reproductive goals.

In order for a civilisation to reprioritise the long-term strategy, it must appreciate the nature of both short term and long term reproductive strategies and their associated stimuli. There is reason to believe they also exhibit associated sexual activity, as it would be adaptive (in the environment of evolutionary adaptedness) for a high quality male when voluntarily engaged in the short-term mating strategy (a/b) to ignore the face of the female (to focus on her fertility). But discrimination of these strategies is becoming increasingly difficult (nigh) impossible where civilisation has reached a point in which it has confounded the correct (and adaptive) evolutionary response to short term reproductive opportunity with long-term necessity. The object of sex has become the emulation of short-term stimuli - an addiction to a fantasy wherein their partner's long-term goals are ignored. Basically, it is believed that the modern west has become inadvertently dependent, and is unable to recognise this or have any hope of freeing itself before it crashes out to its more conservative competition. It has lost all witness of an alternate explanation of human nature, one in which desire is integrated..

//Evolutionary Biology Research question #0 - species risk management (20 November 2018)

I am interested in obtaining a review on species risk management (taking into account cost-benefit of population divergence)...

1. Say that a species becomes distributed across multiple environments, populations of which develop adaptive mutations specific to their own environment (over 1000 generations), others of which die out completely, failing to adapt to their new environment (including pathogens).
2. Now assume that some of these adaptations comprise complex traits; adaptations that are dependent on alleles found at multiple loci on their genome (e.g. polygenic inheritance, as opposed to variation at a single locus/genetic marker, e.g. single nucleotide polymorphism).
3. Now assume that the populations are then mixed; what is the probability that any one of these complex traits will survive after 10 generations of reproduction (in which there is no discriminatory partner preference across breed, and assuming there is no advantage to maintaining these adaptations in their new environment)?
4. What will occur if a pathogen or environmental stressor is then reintroduced to the population, only a tiny fraction of which are adapted to endure (requiring such a previously evolved complex trait)?

Assuming that one wishes to maximise the probability of the species surviving, wouldn't the survival rate to cross-breeding function be non-linear and concave? Has someone already calculated/modelled this?

//Evolutionary Biology Research question #1 - mechanism of extended kin detection (23 July 2020)

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What is the evolved mechanism facilitating lineage (extended kin) detection in Homo sapiens? I hypothesise that facial detection coevolved with kin/lineage detection, but perhaps there is existent ideas/research concerning this?

//Evolutionary Biology Research question #2 - interpopulation aggression and mating preference (14 February 2021)

The following outlines research question I would like investigated, perhaps there is existing literature concerning this?

Hypothesis: a) interpopulation conflict and b) intrapopulation reproductive preference support kin selection, genetic differentiation (polygenic/epistatic adaptation) and divergence/speciation.

Given that;

- The interpopulation F_{ST} s between European (EUR), East-Asian (EAS), and Sub-Saharan Africans (SSA) humans are approximately 0.15 (Nelis ea 2007/Fischer ea 2006; see Table 1 below).
- The interpopulation F_{ST} s between Central (CEN), Western (WES), Nigeria-Cameroon (NIG), and Eastern (EAS) chimpanzees are approximately 0.2 (Schmidt ea 2019/Bowden ea 2012/Fischer ea 2006,Becquet ea 2007; see Table 2 below).
- The interpopulation F_{ST} s between Rottweiler (ROT), Bernese mountain (BMD), flat-coated retriever (FCR), and golden retriever (GR) dogs are approximately 0.35 (Quignon ea 2007; see Table 3 below).

Research hypothesis/question: Do untrained chimpanzees/dogs display differing amounts of a) aggression and b) mating preferences (e.g. sexual attraction) depending on the genetic distance (subspecies/breed) of chimpanzee/dog they encounter?

Data:

Table 1. H. sapiens interpopulation genetic distances (F_{ST}) - sources: Nelis ea 2007/Fischer ea 2006 (Measurement samples: EUR: CEU/Italians, EAS: Chinese, SSA: Yoruba/Hausa)

	EUR	EAS
EUR		
EAS	0.110/0.09	
SSA	0.153/0.14	0.192/0.15

Table 2. P. troglodytes interpopulation genetic distances (F_{ST}) - sources: Schmidt ea 2019/Bowden ea 2012/Fischer ea 2006 (Measurement samples: CEN: Pan troglodytes troglodytes, WES: Pan troglodytes, NIG: Pan troglodytes ellioti/vellerosus, EAS: Pan troglodytes schweinfurthii)

	CEN	WES	NIG
CEN			
WES	0.3497/0.177/0.29		
NIG	0.19914/0.134/NA	0.3931/0.190/NA	
EAS	0.09771/NA/0.09	0.39381/NA/0.32	0.24221/NA/NA

Table 3. C. lupus interpopulation genetic distances (F_{ST}) - source: Quignon ea 2007

	BMD	FCR	GR
BMD			
FCR	0.398 (0.359-0.429)		
GR	0.343 (0.309-0.376)	0.237 (0.211-0.260)	
ROT	0.387 (0.357-0.421)	0.346 (0.310-0.371)	0.271 (0.245-0.299)

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//Evolutionary Biology Research question #3 - the evolutionary unit of selection and relatedness (r) dependence on genetic distance (03 April 2021)

I have identified a problem in the formulation of Relatedness (r) in Hamilton's rule of kin selection

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"f_{st} is a better measurement of genetic distance; an exponential assumption here is spurious because it assumes all the non-common ancestrally transmitted variation will be discordant".

Pinker (and presumably Dawkins et al) claim r detection has evolved with respect to the probability of retaining/sharing identical genes...

1. There is no obvious reason nature would have optimised a Hamiltonian/nepotistic kin selection function with relatedness r being the probability of sharing identical copies of genes, as: a) genetic function is not constrained to genes, b) is often unaltered by minor changes to genes (alleles), and c) sexual reproduction involves crossing within genes (not just between genes).
2. the probability (x) of sharing an identical version of a gene with a sibling is not in principle 50%, it will depend upon how genetically distance the parents were conceiving the offspring. The only reason it happens to be 50% in humans is because genes of individuals within a population (even just their exons) typically contain at least one basepair variation (SNP). This is a byproduct of the fact the human genome contains ~3 billion basepairs, only ~30000 genes, and the minimum/equivalent within population F_{st} distance is approximately 0.001. $30k/3b = 0.00001$, which is < 0.001 . (Or alternatively: avg num base pairs per gene = $3b/30k = 100000$, which if experiencing discordance at a rate of ~0.001 would result in ~100 discordant basepairs/SNPs per gene).
3. if one takes a smaller (sufficiently small) unit of selection than a gene then the probability of sharing an identical version of that unit of selection with a sibling is $> x\%$.
4. relatedness r would therefore have evolved to take into account the percentage of shared genetic material (ie concordant basepairs) within those genes, which varies depending on the overall population/subspecies genetic distance of the individuals (or their parents in the case of siblings r calculations).
5. the precise definition of relatedness r as encoded by evolutionary kin selection remains open to empirical exploration. Most likely we have developed heuristics (e.g. facial recognition) that estimate genetic distance as a function of gene identity (ie traditional relatedness as defined by Hamilton) and the actual % of shared genetic material.

//Evolutionary Biology Research question #4 - gene identity preservation as a natural selection explorer mode (04 April 2021)

Based on previous argumentation (RQ#3) there is no obvious reason natural selection would have exclusively optimised kin selection to be a function of gene identity relatedness (over basepair identity relatedness, or another unit of selection). Why is it then that we (cross species) observe such strong preference for near kin over other members of our population whom we share the vast majority of genetic material with? Apart from proximity heuristics (genetic distance assurance) and reciprocal altruism, it could be that some approximation of traditional Hamiltonian relatedness (as measured by gene identity) has been encoded as a natural selection explorer mode to encourage individuals to diverge unique populations (based on themselves) for the purposes of exploring the evolutionary landscape. That is, natural selection favoured the development of a tendency for relatively large evolutionarily successful portions of a genome to be conserved in the short term (before generations of sexual reproduction/crossing eventually merge these alleles, or the species diverges).