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Week 7

Denisovan Discovery

doi:10.1038/nature08976

Background

- ▷ What was known about the existence, age, and geographic extent of hominins in Eurasia before this paper was published?
 - The first evidence of humans leaving Africa was about 1.9 mya.
 - There were at least two groups after initial event: Neanderthals (500 kya and 300 kya, *Homo heidelbergensis* and *Homo rhodesiensis*), and modern humans about 50 kya.
 - DNA from other pleistocene hominins have not been recovered.
 - Archaeological evidence suggests that archaic hominins (*erectus*, *heidelbergensis*, and Neanderthals) lived at higher altitudes and potentially together.

Methods

- ▷ Where does the fossil hominin sequenced for this study come from, and what was the date for when the individual lived?
 - Distal manual phalanx of the fifth digit (tip of pinky?) was found in a Denisova Cave.
 - Was found in stratum layer dated 48-30 kya.
- ▷ What region of DNA was sequenced for this study? Why were the authors so careful to describe their sequencing and analysis methods?
 - Mitochondrial DNA (mtDNA) was sequenced.
 - The method they used took into account the frequent sequence errors associated with base damage in ancient DNA.
 - Also, it was only taken from one individual, so any errors could have large impacts when comparing mtDNA.
- ▷ Sequences from which taxa were used in this study to infer the genetic relatedness of the sampled hominin from Siberia to other hominins, and why were these taxa selected?
 - 54 present-day, with one pleistocene modern human mtDNA from Russia, and 6 complete Neanderthals mtDNA.

- The tree was rooted with chimpanzee and bonobo mtDNA, as they are the two closest related species to *Homo* species.
- Neanderthals differ on average of 202 nucleotide positions, while chimpanzee has 1,462 positions; difference in Denisova would indicate how close to us, Neanderthals, and chimpanzees.

Results

- ▷ What is the phylogenetic relationship of the Siberian Denisovan hominin to other taxa?
 - Denisova mtDNA carries twice as many differences to mtDNA of present day Humans compared to Neanderthal mtDNA.
 - Phylogenetic analysis shows Denisova mtDNA lineage branches well before modern human and Neanderthal lineages.
- ▷ When did the most recent common ancestor of all these human (genus *Homo*) sequences live?
 - Estimated to be approximately 1 mya, which is twice as deep as the most recent ancestor of modern humans and Neanderthals (465,700 ya).

Conclusions

- ▷ Does the Denisovan represent a newly found species of hominin? Why or why not?
 - The d_N/d_S ratio suggest strong purifying selection.
 - The divergence over a 1 mya also suggests that it was distinct from the initial radiation of *Homo erectus* 1.9.
 - Also the different from *Homo heidelbergensis* if it is a direct ancestor of Neanderthals.
- ▷ Based on the data presented, is it likely that different species of humans (genus *Homo*) formerly coexisted in northern Eurasia? Explain.
 - Yes, this individual is presumed to have lived 30-50kya, 100km away from the Altai mountains, where evidence of anatomically modern humans have been shown to be around 40kya.
 - Suggests that there have been three distinct lineages may have been present at same time.

Week 7

Education

What is the current *ultimate* cause for education? Why does it exist as an institution?

- ▷ Education provides a means to teach and transfer knowledge, allowing for individuals to learn and acquire skills that they might need.
 - This seems like what **ought** to be the ultimate cause, and maybe it was true in the environment during its genesis. But I specified what the *current* reasoning for it being might be.
 - Predictions of this hypothesis:
 - Education, and universities, would be end up being more of a social utility—one that should be widely available and one that maximizes the amount people as attending.
 - Any society that adopted such practices should tend to grow and become more productive/influential.
 - A decreases of inequality and an increases of social mobility.
 - Observational evidence:
 - A rise of longer periods of education, such as highschools, particularly after the industrial revolution eliminated a large quantity of jobs due an increase of far too many children that were spending all their time doing cheap manual labour required by the factories. Or doing nothing at all.
 - This resulted in them to grow to be adults that lacked the skills needed to be in a productive society, which lead to the demand for education for *as many people as possible*.
 - Societies that have had the abundance and ability to provide such education have seen great increases in global influence. For example, the United States' early emphasis on education lead to leap in technology, relative to other countries, which started a positive feedback loop of that lead to high rate of immigration of the smartest people across the globe to our universities.
 - Societies that have greater degrees of education tend to have higher social mobility, which tends to increase equality.
- ▷ I'd argue that **current** ultimate reason for education is to provide *credentials* to students and assign *merit* to individuals.
 - Predictions of this hypothesis:

- A rise in competition to get into most successful universities, rather than a goal to educate as many as possible.
- People assigning worth to individuals based on where they went to school.
- An increase for emphasis on merit based on a society's ability to be choosy, i.e., a way to distinguish quality/ability (merit) of individuals.
- An increase of inequality.
- Observational evidence:
 - Many jobs won't let you even apply if you don't have a degree.
 - Degree holders tend to look down on those that do not have one.
 - Letters of recommendation, grade point averages, and standardized test scores becoming overly emphasized metrics.
 - I.e., "knowing" is emphasized, while "understanding" (harder to measure) is de-emphasized.
 - More frequent cheating by individuals in order to enter elite colleges and get good grades.
 - A decrease in social mobility and a major increase in inequality, causing immense social unrest.
- To elaborate: college currently doesn't really provide deep understanding and expertise, rather it currently serves as a means to prove that one is capable and can do something hard.
- The problem is that there is extreme competition, which leads to evolution in social behavior. Like we all know, evolution doesn't mean better, just better in the current environment. And under the current society, which I'd argue values merit to a very high degree, then it appears that any way to establish such merit is strongly selected for, hence why I think the merit-based hypothesis is dominating.

So why am asking you this question and making this distinction?

- ▷ Before I answer that, I do have to acknowledge that it is certainly not a strong dichotomy between the two hypotheses I presented. I'd argue they both exist simultaneously, however, they are in competition for the same niche (institution of education/universities) that WE are currently in.
- ▷ I definitely want one to succeed over the other. I want to increase the quality of my own, and my peers, education. I want to decrease inequality globally. I want to increase our societies understanding and I want to venture past the edge knowledge and into the unknown. I want understanding to be selected for, not merit.
- ▷ Furthermore, I ABSOLUTELY LOVE, evolutionary biology.
 - Richard Dawkins', *The Selfish Gene*, is among my top 3 most influential books. I hope the following statement does not make me sound boastful, but that's is a tremendous statement, because over the past 2 years I've read over 70+ books, a nearly all non-fiction and science/technology related (including entire textbooks)—many of which have had an impact on my personality and view of the world that is hard to accurately describe.
 - Dawkins helped me develop a system-like, evolutionary oriented, mode of thinking that I apply to almost everything.
 - The concept that ideas and culture itself are alive, reproducing themselves via transfer to the minds of others, which allows for the application of the unifying theory of biology, that is evolution, on the analysis of culture itself is absolutely and literally wonderful.
 - I mean, even the word meme, which he coined, is a *mutation* on the word gene! One single letter, just like our DNA. What better way to connect evolutionary thinking with the young minds of today then by showing them the origin of such a popular word is rooted in evolutionary biology.
 - Essentially, his meme makes my mind express a phenotype that allows me to see the world through the lens of system-like thinking. This change in thinking allows me see new hypotheses, novel solutions, and a drive to explore the system I find myself in, which I argue is at the core of science itself.
- ▷ Now, I am not here to persuade you to do anything. I did not start with a thesis today because it required some nuance and a distinction between competing hypotheses—understanding vs. merit. What I want to do is start a conversation on how to change the system we find ourselves in, because unlike most teachers, I think you are willing to try. Also, I'm painfully

concerned with the impact of this class on me, and my peers' motivation/eagerness towards evolutionary thinking.

- Despite my love for this subject, this class has generated a ridiculous level of frustration and self-doubt, more so than any class so far—and it feels fucking awful.
- ▷ Now, there might be several proximate causes for this frustration, but I don't think talking about such causes is the most productive thing to talk about and changing the parameters on an ultimately broken system is frankly, useless.
 - Rather, I'd just wanted to express my concern, and maybe prompt you to seek alternatives for future classes. Because if an evolutionary biology class can't see what's being selected for needs to be changed, then we're doomed.

Ideas for change:

- ▷ I think about possible solutions constantly, and it's major goal of mine, to at least attempt, to drive a major evolution in society in regards to education—hopefully for the better.
- ▷ Maybe I will pursue other goals and drop this one. But I really think this the the most important goal of mine. I'm putting up with this broken system because it's the system I am apart of. Education is like the generation of better enzymes that take the ideas (memes) floating around in society and allows them to be expressed at an increased rate.
 - We will change, or we will fail. I think the best way to make a lasting change in the world is empower as many people as possible in order to create as much diversity in thought as possible—idea-diversity is the bio-diversity of culture.
 - Education is also like the genetic recombination of memes, allowing for the linkage disequilibrium of bad memes to be decreased, and good memes that otherwise would be lost by chance, to be recovered and expressed more often.
- ▷ What I really hope, if I am successful, is to be able to look back at classes like this one and cite it catalyst for change, rather than an example for what is terrible wrong with the system.

Week 6

Whale Menopause

Background

- ▷ Why is the evolution of postreproductive survival in females (menopause) unusual from an evolutionary perspective?
 - Limits ability to reproduce directly and pass on genes, despite being alive still.
- ▷ What is meant by the term “inclusive fitness”?
 - Fitness increased via indirect benefits due to increasing fitness of kin, thus their own fitness.
- ▷ What hypothesis did this study address?
 - The hypothesis that menopause evolved via inclusive fitness benefits gained by helping kin.

Methods

- ▷ What data did the authors’ gather to test their hypothesis?
 - Analysis of 751 hrs of video footage to determine who leads the pod.
 - Multigenerational demographic records used to determine relatedness.
 - Total of 102 individuals, ranging from 0 to 91 years of age.

Results

- ▷ What do Figures 1C and 1D depict?
 - 1C counts of leadership between male and female.
 - 1D counts of leadership between postreproductive and reproductive.
 - Show that both female and postreproductive females lead more often.
- ▷ What does Figure 2 depict?
 - Depicts leadership score relative to salmon abundance.
 - Postreproductive had higher probability to lead in low salmon abundance.
- ▷ What does Figure 3 depict?
 - Shows rate of following of males and female relative to non-mother and mother leaders, and reproductive and post-reproductive leaders.
 - Shows males were more likely to follow and postreproductive leaders had higher rates of following.

- No overall difference in rate at which males followed their mothers compared to non-mothers.
- ▷ What were the 3 major findings of the study?
 - Female and postreproductive females lead more often.
 - Postreproductive had higher probability to lead in low salmon abundance.
 - Shows males were more likely to follow both mothers and non-mothers, and postreproductive leaders had higher rates of following in both sexes.

Conclusions

- ▷ What was the major conclusion of this study?
 - That long live whales, even postreproduction, can act as repositories of ecological knowledge.
 - Postreproductive aged female killer whales tended to lead groups to sources of food in times when pressure to locate food was the highest.
 - Supports hypothesis that menopause may actually be a adaptive trait.
- ▷ Why do the authors' hypothesize that male and female offspring differ in the benefits they receive from following their mother?
 - Due to observed differences in offspring survivorship after deaths of mothers. Males tended to die faster and more often, suggesting the inclusive benefit of following mothers were greater than in females.

Week 5

Heritability Exercise

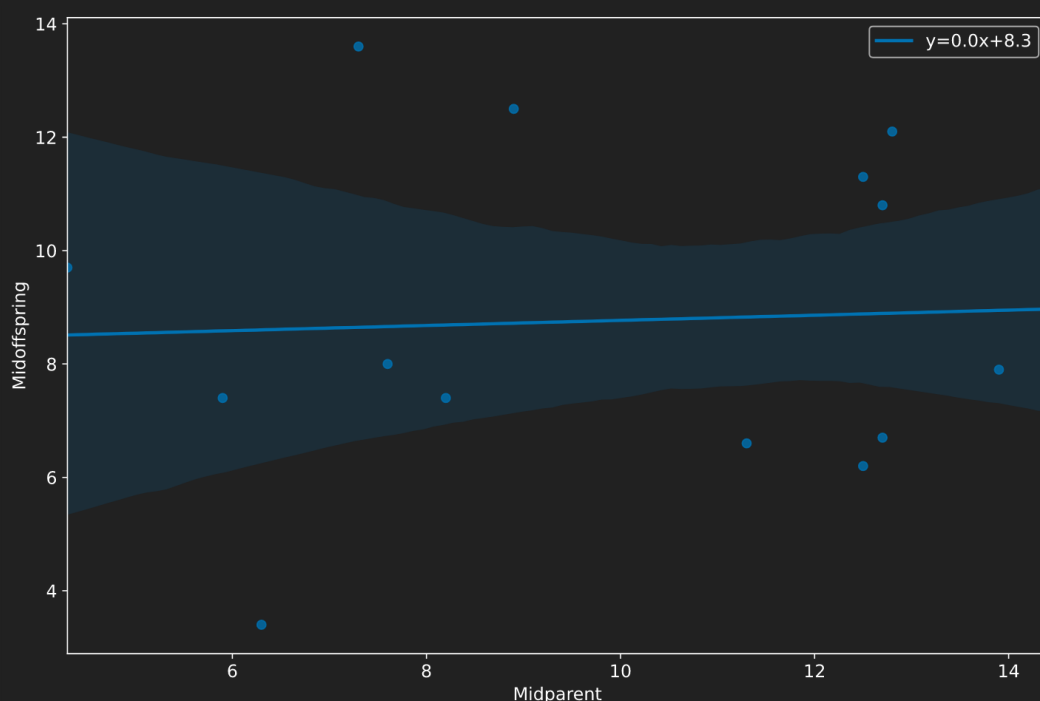
1. Approximately, what is the heritability of running speed in the breeder's dog population?

```
# data given used to create dataframe
d = {
  'Midoffspring':[10.8, 8, 8, 9.7, 6.6, 6.2, 12.5, 7.4,
3.4, 6.7, 7.9, 13.6, 7.4, 12.1, 11.3],
  'Midparent':[12.7, 7.6, 14.4, 4.3, 11.3, 12.5, 8.9,
8.2, 6.3, 12.7, 13.9, 7.3, 5.9, 12.8, 12.5]
}
df = pd.DataFrame(data=d)

# get coefficients of linear fit
slope, intercept, r_value, p_value, std_err =
stats.linregress(df['Midparent'], df['Midoffspring'])

# plot graph, make label for
ax = sns.regplot(df['Midparent'], df['Midoffspring'],
line_kws={'label':
"y={0:.1f}x+{1:.1f}".format(slope, intercept)})

# plot legend
ax.legend()
plt.show()
```



2. If she selectively breeds her dogs, will the next generation run substantially faster than the dogs she has now?
 - ▷ No, very low heritability, nearly 0. ($y=0.0x+8.3$)
3. What else would you suggest the breeder try if she wants to win more races?
 - ▷ Continue to track the midoffspring and midparent speeds, selectively breeding those who tend have a higher heritability ratio in regards to speed
 - ▷ Such a low slope could indicate low heritability of speed, so might be more useful to pursue environmental factors.

Week 4

Molecular Clock

CHEETA EXAMPLE:

Divergence: 5.2% per 1mya, Diversity for this locus: 0.182% per [x=time]

$$\frac{0.182}{x} = \frac{5.2\%}{1 \times 10^6}$$

$$1.82 \times 10^5 = 5.2x$$

$$x = \frac{1.82 \times 10^5}{5.2} = 35\,000 \text{ yrs}$$

Divergence: 6.5% per 1mya, Diversity for this locus: 0.182% per [x=time]

$$\frac{0.182}{x} = \frac{6.5\%}{1 \times 10^6}$$

$$1.82 \times 10^5 = 6.5x$$

$$x = \frac{1.82 \times 10^5}{6.5} = 28\,000 \text{ yrs}$$

DOGS EXAMPLE:

Divergence: 7.5% per 1mya, Diversity for this locus: 1% per [x=time]

Note: 0.075, and 0.01 converted to %

$$\frac{1}{x} = \frac{7.5\%}{1 \times 10^6}$$

$$1 \times 10^6 = 7.5x$$

$$x = \frac{1 \times 10^6}{7.5} = 133\,333 \text{ yrs}$$

Zika Evolution

Metsky HC et al. 2017. Zika virus evolution and spread in the Americas. *Nature* 546: 411-415. ⇨

Background

- ▷ What was known about Zika virus evolution before this paper was written?
 - Fewer than 100 ZIKV genomes were previously sequenced directly from clinical samples, providing little information about its epidemiology and evolution.
 - The virus had a link to birth defects and other neurological complications.
- ▷ What were the goals of the authors of this paper?
 - "to gain a deeper understanding of the viral populations underpinning the ZIKV epidemic by extensive genome sequencing."
 - Understand how sequences are changing and how selection might be acting on the virus.
 - Where the virus originated.

Methods

- ▷ What taxa were sampled for this study and where specifically were they from?
 - Samples were collected from United States, Guatemala/ El Salvador, Haiti, Dominican Republic, Honduras, Puerto Rico, Martinique, Jamaica, Brazil, and Columbia.
 - Puerto Rico, Honduras, Columbia, and the Caribbean (includes USA) were the four well supported clades.
- ▷ Why was this sampling strategy important to address their goals?
 - Unbiased metagenomic sequencing of 38 samples proved to have insufficient ZIKV RNA for genome assembly, so PCR amplification (110/229 genomes) and hybrid capture (37/66 genomes) had to be used for enrichment.
 - They had a short sampling period, so deleterious mutations were hard to catch, as well as other changes. They needed a large and diverse set of samples to establish a molecular clock and a substitution rate.
- ▷ How was evidence of selection on the Zika virus genome determined?
 - Total of 110 genomes, plus 64 previous published genomes were used in a reconstructed phylogenetic tree based on a molecular clock.

- Each lineage was then traced back to root and used to estimate the substitution rate, which would provide evidence of selection.
- Aimed to compare ratio between synonomys and nonsynonymous mutations.

Results

- ▷ Looking at the results shown in Figure 2, explain how the authors arrived at the conclusion that the Zika virus outbreak originated in Brazil.
 - The Brazil ZIKV genomes appear on all deep branches of the tree, and the most recent common ancestor is the root of the tree.
- ▷ When did the authors determine the Zika virus outbreak(s) occurred?
 - Early 2014, 95% confidence interval from August 2013 to July 2014.
- ▷ What was the substitution rate for the Zika virus since the outbreak in the Americas?
 - Within-outbreak substitution rate of 1.15×10^{-3} , 95% confidence interval of 9.78×10^{-4} to 1.33×10^{-3}
 - A 1.3–5 times higher rate than other flaviviruses.
 - May be higher than expected as samples did not have time for purifying selection produce an effect.
- ▷ Why did the authors search for whether there was an excess of nonsynonymous mutations in the Zika virus envelope glycoprotein (nicknamed E)?
 - "Viral surface glycoproteins are known targets for positive selection; mutations in these proteins can confer adaption to new vectors or aid immune escape."
 - If there was an increased substitution rate it would indicate for selection.
- ▷ Was evidence of selection found anywhere in the Zika virus genome? Explain.
 - Adaptive mutations are more likely to be found at high frequency among the nonsynonymous mutations.
 - Strong evidence for unrestrained diversifying selection was not found due to similar nonsynonymous substitution rates compared to other coding regions.
 - So no, no strong evidence for selection was found.

Week 3

Populus Stimulations

Exercise 1: Stimulating Strong Selection

1. Describe how the frequency of the A allele changes due to strong selection.
 - ▷ The frequency of the A allele **increases rapidly** due to strong selection.
2. How many generations passed before the A allele was fixed or lost?
 - ▷ Roughly **60–70** generations.
3. How many generations passed before the a allele was fixed or lost?
 - ▷ Roughly **60–70** generations.

Exercise 2: Simulating Modereate Selection

4. Describe how the frequency of the A allele changes due to slightly weaker selection.
 - ▷ Moderate sigmodal increases in frequency.
5. How many generations passed before the A allele was fixed or lost?
 - ▷ Roughly **120–130** generations.
6. How many generations passed before the a allele was fixed or lost?
 - ▷ Roughly **120–130** generations.

Exercise 3: Simulating Weak Selection

7. Describe how the frequency of the A allele changes due to weak selection.
 - ▷ **Slightly increasing** exponential curve.
8. How many generations passed before the A allele was fixed or lost?
 - ▷ Was not fixed or lost after 1000 generations.
9. How many generations passed before the a allele was fixed or lost?
 - ▷ Same, neither allele was not fixed or lost.
10. If a generation was equal to 10 years, how many years would it take for the frequency of the A allele to double in frequency (from 10% to 20%)
 - ▷ About 550 generations, so approximately **5,500** years.

Week 2

Dog Domestication

▷ Background and Goals

- What hypotheses about dog domestication are examined in this paper?
 - The origin of domestic dogs was the main focus; genetic data suggests East Asia, but other data suggests Europe and Siberia.
- What predictions do these hypotheses make? What would the expected phylogenetic trees look like under each of these hypotheses (i.e. what are the expected topologies)?
 - The most recent common ancestor would indicate origin and genetic data would help confirm time frame.

▷ Methods

- What taxa were sampled for this study?
 - Hypothesis was tested using DNA extracted to trace mitochondrial genomes from 18 prehistoric canids and 20 modern wolves from Eurasian and American origin.
- What gene sequences were used for this study?
 - Wolves, dogs, including divergent breeds, recently published Chinese indigenous dogs, and coyotes. (148 mitochondrial genomes)
- What phylogenetic methods were used to reconstruct the phylogenetic tree in Figure 1?
 - Maximum likelihood, coalescence, and Bayesian.

▷ Results and Discussion

- In Figure 1, which wolf sequence is most closely related to the extant dog clade A, and what geographic region is it from?
 - Wolves: Switzerland 214,500.
 - Dogs: Argentina, USA (8,500, 1,000)
- In Figure 1, which clade of modern dog sequences has the oldest origin? Approximately how old is this clade?
 - Dog clade A, Russia, 18,000 years ago.
- Based upon Figure 1, how many times does it appear that modern extant dogs could possibly have been domesticated?

- Figure 1 suggests 4, but the authors state, "the inferred recent divergence of clade B from wolves now found in Sweden and Ukraine implies that it might represent a mitochondrial genome introgressed from wolves rather than one established by domestication."
- What was the topology of the phylogenetic tree that was recovered, and therefore, which hypothesis was supported?
 - The findings support the conclusion that legacy of dogs derives from wolves of European origin.
 - Analysis of coalescence times support divergence time of >15,000 years ago.
 - Past mitochondrial and Y chromosome analysis suggested non-European, but had less supported data than these findings.
- ▷ Conclusions
 - What are the major conclusions of the paper?
 - Three of four modern dog clades are more closely related to sequences from ancient European rather than extant wolves with divergence times >15,000 years ago.
 - Was the taxonomic sampling sufficient to rule out alternative hypotheses?
 - Ancient panel did not contain specimens from Middle East or China. No, no ancient dog remains older than 13,000 years are known from those regions.
 - The mtDNA sequence tree is well supported, but represents a single genetic locus. Independent loci could offer more power to resolve phylogenetic relations.

How Farming Reshaped Our Smiles and Our Speech

▷ Gibbons A 2019; doi: 10.1126/science.363.6432.113

1. What is this news article about?

▷ How farming may have reshaped our jaws and thus indirectly influencing how we speak.

2. How could diet change the structure of the jaw?

▷ Less wear and tear changed how jaws and teeth developed, creating an overbite with the now less worn down teeth.

3. How could jaw structure change speech patterns of humans?

▷ Jaw and teeth placement changes how easy it is to make certain sounds, and overbites made "f" and "v" easier to make.

4. Are these changes in jaw structure permanent? Why or why not?

▷ Not likely, if you ate diets similar to early humans your teeth would wear down more and impact from wisdom teeth would minimize overbite. Though, there may have been some lasting selection pressure for a natural overbite.

5. Did natural selection shape these changes in jaw structure? Explain.

▷ Not likely, mostly likely from behavior change due to mostly diet change.

6. Can natural selection shape speech patterns? Explain.

▷ Yes, sexual selection could be a significant. Or if the change in speech pattern could confer a advantage in communication.

7. Can you think of any parallels with other animals where diet influenced feeding structures?

▷ Lots of animals, birds (finches!!), dogs, snakes. Huge impact.