AST 309L
Genomic perspective on convergence of intelligence
(based on 11/20 lecture)

This is a summary of the lecture on genomic aspects of "intelligence," material that is not in the textbook. We began with a clarification about the similarity of the pygmy chimp and human genome—98% similarity still leaves a *huge* number of base pairs different, enough for thousands of genes. It is a myth that there intelligence or any human distinction must be expressed in a tiny part of the genome *based on this similarity.* Instead we emphasized that the similarity (or the 64% similarity with the mouse genome) strongly supports the idea that we had a common ancestor.

On the other hand, I *did* present lots of evidence that the basis for human-like intelligence *does* reside on an even smaller part of the genome than anyone previously thought. That is the main subject here.

We expected to find the "complexity" of "higher" animals and the "intelligence" of humans and perhaps a few other animals, to be reflected as a longer genome, with more DNA base pairs, or more genes to code for complex functions.

However our conclusions point us in another direction:

- Complexity of humans and other apparently "complex" organisms is *not* reflected in the number of base pairs in the genome, the "size" or "length" of the genome, nor is it reflected in the number of coding genes, which are the units of production of function (by coding for proteins).

An implication we must take seriously for later is that we may be naïve to think that a big brain suggests high intelligence, just as we thought we thought high complexity would be reflected in a large genome.

- The other conclusion is a puzzle: If not genome size, then where are the "instructions" for the complexity stored? What part of the genome codes for bipedal posture, big brains, opposable thumbs, complex neural circuitry, … intelligence? One possibility is that most of the complex "action" in the genome is taken by the "mobilome" of transposable elements and other dynamical processes, not in coding genes.

- We also gave several examples that show that a complex trait can be carried by a small number of mutations, or even a single mutation, in a single gene. The examples included a number of diseases, but also camera eyes (PAX-6 gene), the development of plants that all animals require (through the symbiosis of plants with bacteria to utilize the nitrogen cycle), and size of cerebral cortex (ASPM gene) and skull (MYH16 gene mutation, disabling large and powerful jaw muscles). Actually this is a bit of a simplification—there are over a hundred genes that have been tentatively implicated as related to cognition, but ASPM and MYH16 are the most important by far.

This seems to imply that factors leading to complexity, and intelligence, are contingent, since they depend on single mutations, and mutations are chance events.

From one perspective, this is true, because out of the astronomical number of mutations that have occurred during the history of life, we have no way to say whether any *particular* mutation would occur again. (We could go further with this but it would require too much math.)

However it is *not* true that these single mutations mean there has been no convergence. There are theoretical (and experimental) reasons for thinking that a rare but advantageous mutation *will* spread throughout a population, and **it is a fundamental mistake to think that the same mutation had to occur independently in several creatures (e.g. the eight species with camera eyes), which is part of what suggested contingency to us. Instead, all that is required is that the mutation occurred in a distant (in time) enough *common ancestor*.** Now recall the statement at the beginning, that this is what is implied by the genomic similarities of humans, chimps, mice, and other creatures.

This *was* the case for the eyeball example, and for the plant-bacteria symbiosis example.

What we have not answered (yet) is whether the mutation(s) for big brain, etc. leading to our kind of intelligence arose far back in our lineage (say a common ancestor like prosimians). If so, why don't all the members of this lineage share these features that lead to intelligence?

If instead, the mutation occurred recently, say five million years ago (e.g. giving rise to bipedality in only one line of creatures *so far*), why did it take so long? In this case humans could be the only creatures with intelligence on Earth at present. (Discounting crows and other cognitively-able organisms.) But now we can see that this does *not* suggest that extraterrestrial intelligence is improbable—it only shows that we neglected to even consider that humans are probably not the end of the line for the development of life on Earth. In particular, if our "lineage" continues, with branchings to other distinctive (and unimaginable) creatures in the future, they will indeed inherit those genes with the particular mutations that gave us all those traits we have discussed, *and more*.

The "and more" is the most fascinating part, because we have no way to even guess what these future evolutionary changes may be, only that they will probably build on what exists here and now. Whatever they are, we only have to imagine a time in the distant future, after many more "branchings" have occurred in this lineage, to see that at that time "our kind of intelligence" will appear common, ***unless*** **some other mutation or genome process eliminates it!**

→ Remember the loss of the powerful jaws due to the MYH16 gene mutation!

We concluded long ago, from the Drake equation, that *if* extraterrestrial civilizations are numerous enough so that the nearest average one is within a few hundred light years, their average time spent already as an "advanced civilization" must be very long, much longer than we have been a technological civilization. Our lowest estimates were about 100 thousand years.

Putting these two results together, this shows how intelligence "like ours" could be convergent, even if humans are the only animals that possess it on Earth, and even if it depends on a few choice mutations, ***as long as we allow for the possibility that there is a lot of evolution yet to occur.*** Isn't it peculiar that this "future evolution" is so rarely discussed? [See a book on the subject by Peter Ward if interested.] The major uncertainties in this seem to be:

● How long does it take the necessary first mutations to occur at random, on average? It took nearly four billion years here. That does not bode well for finding other intelligent life forms capable of communication ***unless*** **we (Earth life) were late bloomers compared to the average development time for organisms on other planets.** Maybe the prerequisites for intelligence most commonly arise in only a billion years on Earth-like planets orbiting other stars. Or maybe it takes much longer than 4 Gyr, in which case…. [please fill in the blank to be sure that you understand the argument here].

● Will the attributes we value so highly in humans remain adaptive when they need to co-exist with whatever new features eventually evolve?

● A related question is whether the mutations giving rise to the "smart" features (big head say) were adaptive in the first place. Many evolutionary biologists think *most* of the mutations that spread through a species ("fix") are *neutral* (see notes for previous exam) in the sense of having no beneficial or detrimental effects—in more technical terms, their "selection coefficients" would be near zero.

There are tests to determine the probability that a certain altered sequence in a genome was adaptive or neutral. The methods are uncertain and are in a state of flux (the best known is called the Kreitman test), but they may have already been attempted for the ASPM and MYH15 gene mutations. I have a list of about 100 follow-up papers on this subject in case anyone is interested…