Genetics& Society
Garriga lecture notes 4/15/09

We finished the lecture on Eugenics. See the 4/1 lecture notes for a discussion of this topic.

Forensics
DNA technology has developed into the new gold standard for forensic identification. Before DNA evidence, fingerprint analysis of crime scenes was often the best information that implicated a perpetrator in the crime. Often called DNA fingerprinting, analysis of DNA left at the scene of a crime is a powerful addition to the types of evidence used to prosecute criminals.

How does it work? It turns out that 99.9% of the DNA sequences are identical among individuals, so the analysis focuses on the sequences that differ. Investigators isolate DNA from suspects, usually from a cheek swab, and these DNA sequences are compared with those from the crime scene.

What type of analysis is used? By now you should be able to predict that PCR is the basis for current DNA analysis because it is so sensitive. A single molecule of DNA can be amplified by PCR to generate amounts that are easily analyzed. PCR can be used to detect Single Nucleotide Polymorphisms (SNPs), which then are analyzed after cutting with a restriction enzyme if an enzyme site differs between two sequences. Alternatively the SNP can be detected by DNA sequencing. Most analysis uses Short Tandem Repeats (STRs), which are a repeats in tandem of short sequences only a few base pairs long. The number of repeats can be quite variable in the population making these sites good for identifying unique individuals in the population. The differences are easily detected by observing the different sizes of the PCR products.

Often, you will hear that a particular DNA analysis identifies How are probabilities ?

We have a DNA sample from a crime scene, and it matches the suspect's DNA for a single STR. What is the likelihood of this happening by chance?

Let's say that there are 7-44 repeats at this STR locus or 38 possible alleles.

Both the DNA sample and the suspect have 22 and 31 repeats at this locus. In other words, one chromosome has 22 copies of the repeat; the other 31.

If we spin the roulette wheel twice, the probability of getting a 22 and a 31 is:
2 x 1/38 x 1/38 = 1/722
We can now say "the chance of obtaining this DNA profile if the DNA in the forensic sample came from an individual other than the defendant is 1 in a 722."

If there was a second STR locus with a match, and it also contained 38 alleles, the likelihood of this happening by chance is 1/722 x 1/722 = 1/521,284

With more STR loci, we can be more confident that we have the right person. The lack of a match means the suspect cannot be the person that left the DNA sample.
Not all alleles have an equal probability, so the frequencies of each allele is estimated by measuring its frequency in a sample of the population. Different groups will have different allele frequencies, and this is also incorporated into the calculations.

CODIS is forensic science and computer technology tool that is now used by the FBI. CODIS began as a pilot project in 1990 serving 14 state and local laboratories, and in 1994, the DNA Identification Act formalized the FBI's authority to establish a national DNA index for law enforcement. The National DNA Index System (NDIS) became operational in 1998. CODIS is now used for: the identification of criminals, the identification of family members, and the identification in certain fatality cases.