

Re: How are genes counted in Human Genome Project?

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- *From:* "Perplexed in Peoria" <jimmenegay@xxxxxxxxxxxxxxx>
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"John Edser" <edser@xxxxxxxxxxxxxxx> wrote in message
[news:eggknn\\$2m1d\\$1@xxxxxxxxxxxxxxx](mailto:news:eggknn$2m1d$1@xxxxxxxxxxxxxxx)

"ErikW" bryophyta@xxxxxxxxxxxx wrote

Perplexed in Peoria wrote:

<drosen0000@xxxxxxxxxxxx> wrote in message

...However, the word "gene" in popular use is ambiguous. It refers to any one of several different units of hereditary. It sometimes refers to the triplet of nucleotides designating an amino acid,

I've never heard that one. That is usually called a 'codon', not a 'gene'.

it sometimes refers to a sequence of DNA designating an enzyme (e.g., Sean Carroll),

The usual definition is a sequence designating a *protein*. Not all proteins are enzymes. Some have a more structural or

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regulatory role.

it sometimes refers to a portion of a chromosome that particularly resists crossover (e.g., Dawkins),

You have misread Dawkins. He meant a segment small enough so that crossing over within it is rare. There are no particularly resistant regions. Dawkins's definition is not an unambiguous one, but it is useful in thinking about evolution.

and there are other "genes." Each definition of gene would correspond to a different size gene and therefore a number of genes in the genome. What type of gene is being counted in these references to the "Human Genome Project."?

It is the 'Sean Carroll' one that is used. The reason for the uncertainty in the count is that a segment may 'look like' it codes for a protein, but no one has ever seen that protein. Perhaps it is only produced in the knee-cap (to take a silly example) and no one has ever studied knee-caps carefully enough. Yet.

JE:–

To be CORRECT any segment that is deemed "one gene" has to code for one polypeptide and NOT one protein.

I stand corrected. Nice catch.

Almost all proteins are complex combinations of MORE than just one polypeptide which means that at the very least MORE than one gene is almost always required to code for ONE protein.

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Almost all? I don't think so. I doubt that it is even a majority.
Nevertheless, it is true that many of the most important proteins do
involve more than one gene and one polypeptide.

In biological terms, the enormous difference between a polypeptide and a
protein (which remains glossed over within gene centric theory only because
it is inconvenient) places genetic epistasis at the forefront of SYNTHETIC
genetics and not on just the backburner where it has been languishing ever
since Fisher et al.

And a big majority of proteins must interact with other proteins to do
their job. So your point about epistasis is valid. (A first?)