

from Gobarnow

"Come, listen, my men, while I tell you again

~~The five~~ unmistakable codes

A few

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By which you may know,

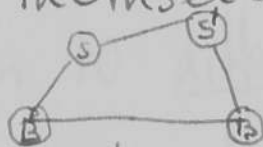
where soever you go,

March 8th 1954

The genuine RNA models."

Dear Francis,

Your letter just arrived forwarded from Washington, and, having recently a lot of practice in decoding proteins, I have decoded your handwriting almost completely. I drove to Pasadena a fortnight ago, and spent two days with Jim, Max Delbrück and others. They have a model of RNA, big and nice looking, but they do not believe in it very much themselves. (except of Alex Rich who conceived it). It has trapezoidal holes



formed by two bases, and two different "sugar-edges". ~~There are 20 different holes.~~ And there are 20 different holes.

BUT

I have found (however) that the combination rules do not work at all. According to that model, 10 amino acids can occur only at even places in the protein sequence, ~~with~~ ^{with} the other 10 only in odd places, ~~which~~ ^{which} is certainly not true.

In particular, doubling, like GluGlu, or GlyGly, is not permitted at all!

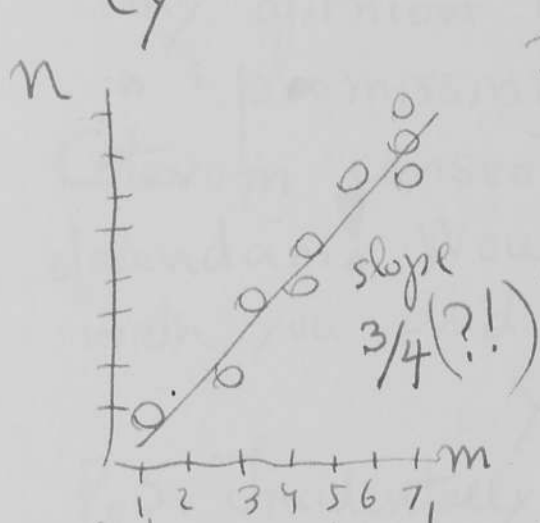
After I came back, I have tried a new code of Triangles (with three independent bases

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in each corner) with the eye on the monostranded RNA (whatever the model could be!); There are also 20 triangles, but the role of combinations are different: 4 of them can combine with 10 others; 12 with 7 others, and 4 with only 5 others. I didn't yet use this for insulin decoding. Will do soon, + vassopresin

But what I did was to take the insulin data and to make statistics: how often (m) each amino acid occurs, and how many (n) different neighbours it has. Thus, for example, Cy occurs 7 times and has 10 different neighbours.



Plotting n against m one gets something like that

← Amusing, isn't it!? why slope $3/4$!? I have tried to derive theoretical formula,

but couldn't, and the people from statistical Lab. here told me it is a full time work for at least a month. Thus I tried another way:

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using tables
of random numbers. 3

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Selected 60 letters (out of twenty) & arranged at random, and tried to make it up, first in triangles, then in diamonds. In Δ 's it does not look at all like a protein: ~~lots~~ ^{lots} of duples and undles of dublets, and triplets! In \diamond 's it looks much better, but I did not finish it yest.

Jim comes here on Thursday, and will stay for several days. So I hope that he will join me, Calvin^{*}, and McMillan^{**} in building the Fisher-model of DNA since my strained rings cast-in-plastic just arrived.

Well, as you see from all said above, my opinion about all this "decoding stuff" is: promissing, but not yet quite right. Ceterum censeo Cartagenem DNA-PROTEIN esse delendam! Would love to have a joint article with you and Jim on that subject.

Yours as ever: Geo

P.S. Incidentally, due to a spontaneous mutation, my longer article will appear not in the Nat. Acad. of Sc. of U.S.A. but in Royal Danish Acad. of Sc.

*) chemist **) nucl. phys.

Please write air mail to
the above adress.