from Geo Gamow

"Come, listen, my men, while I tell you again
~~The five~~ A few unmistakable codels
By which you may know, wherever you go,
The genuine RNA models."

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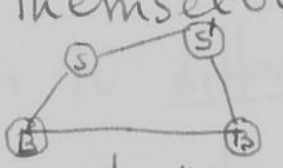
March 8th 1954

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 an others. They have a model of RNA, big and nice looking, but they do not ~~t~~ 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". ~~I have spent however~~ And there are 20 different holes. I have found however that the

BUT 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 ~~which~~ the other 10 only in odd places; ~~which~~ is certainly not true. In particular, dubbling, like GluGlu, or GyGy, is not permited at all!

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

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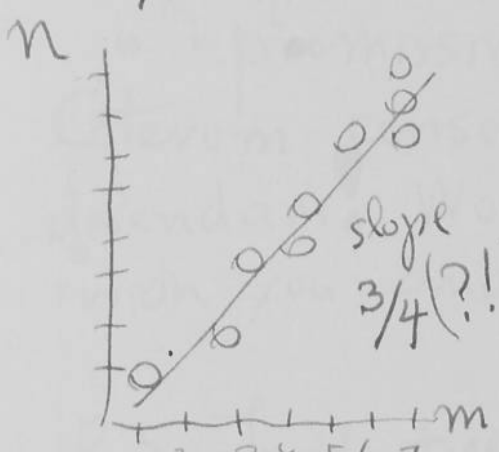
in each corner) with the eye on the monostranded RNA (whatever the model could be!). There are also 20 triangles, but the role of combinations are different: 4 of them can combine with 10 others; 12 with 7 others, and 4 with only 5 others. I didn't yet use this for insulin decoding. Will do soon, (+vasopressin)

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 time 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:

using tables of random numbers. L 3

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: Sellected 60 letters (out of twenty) & arranged at random, and tried to make it up, first in triangles, than in diamonds. In Δ's it does not look at all like a protein: ~~tods~~ udles and undles of dublets, and triplets! In ◇'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 te 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: George

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

*) chemist **) nucl. phys.

Please write air mail to te above adress.