Dear Bellocchi,

It was very kind of you to send me a copy of your paper, which I very much read with great interest.

I am very glad that you have suggested the idea of making systematic bounds had so not occurred to me when I was possibly wrong a second model of mine. Your suggestion would regre the former points in the proper model and regard the former points. This would show for example the transformation is in how the transformation could appear from the

From the transformation process could appear from the

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As I understand in the scheme (in line with the

new pair of chains the node-by-node is a stochastic relationship,

otherwise the world the chain breaks ends to break. However
This is not implausible because we will not see this in the
crystalline form of the incorporated fibre, whether it is so in the
paracrylllde form is less certain.

I dare not say what I should be converted to your scheme unless
models show that it may, as over a number of cases, consequence
of the special arrangements. I admit that irregular breaks are
indeed, but I am not convinced that damage is an essential
feature of this part of the process.

The scheme I described will never be fully
described in full, and its form can only be sketched in
our indeterminable proteins. It might be correct while hunching
setting it out in more detail.

Our scheme, taken years, in particular, has now
polymerized in chain, are never really simple. But is, an imagine
reduction to start in so much a winding, and indeed that
unconceiveable, the nature never for its basis. The former
will form a pair of chains, one at the top, and two pairs of
chains as the better, and into the intermediate region of contact, of the minimum number of short molecules.

The best pair or would move in that the primary amine chain
sometimes in probably better a very one. Proton pairs must remain
chain, could easily unwind and each other very slowly, and
would tend to be parallel to one another. Therefore, for growth to
occur the main pairs must have relation to the single pair, and
indeed the act of growth could lead to generate a couple. The
energy of some will come for the force the more or many
hydrogen bonds were being formed as were being broken. It is
also easy to see the mechanically there would be a zipper action,
since the two chains would be further apart. After
proceed than before, since they are normally closer together than
the diameter of the main structure. Since their average
distance after growth would be greater, but if the process is
orderly the average distance may be constant, just as the
cornering rod on two locomotive wheels has a certain
length. Hence, we have a source of energy, a zipper (or zipper) action.
to separate the DNA chain, and a couple to produce a

ecentific.

What, then, will serve to(style)? I made a rough calculation

at a Cambridge in the vibric resistance, but for short lengths

there seemed too small to produce any effect. Decided! For, near enough

hence it might be sufficient. Suppose, therefore, we run seventh the

far out of the original chromosome as forced. Twisting with the

produce a tensile effect, which will gradually build up a

resistance & finally breaking. At this point we imagine a

break to occur in one of the chains. Since some rather about

single bond is relatively free, the would allow all the

accumulared twisting to work relief, and the chromosome would

first rapidly about the remaining single chain, until most of the

twist rapidly about the remaining single chain and most of the

three runs is any can be a "jumping up" mechanism in the

cell for connecting the new chains, we imagined this thin

same mechanism repaired the break.

In addition to this idea we felt it very probable

that the DNA is folded into some sort of superstructure, this
larger scale. This would mean that the final producted
the original structure was unwound with new groups, the new chain
would, after a short initial rate, fold up into the superstructure.
This would make it even more difficult for them to see catalyzed
pair one another, assuming the superstructure to be neither soft and
unperturbed.

A new idea that has come up since last summer
in how perhaps the breaks chain per se are already
and always exist in the intact chain. This is now considerable
evidence that the extruded DNA has broken in a backhanded, and
I think the matter is likely to be established beyond doubt within
a year. However, of these breaks may have been produced during
the extrusion process, and raw evidence for providing breaks in
the intact DNA while the cell may be difficult to obtain.
A further examination of this would be to consider breaks as
part of this superstructure of the structure. However, we know
nothing complementary to a break, so it would not be easy to
for breaks to replicate, and if so we would have to be very
way. Possibly the alternative of a protein of genetic reversion
might work as to do the trick of another break always