The chemical formula of DNA is well known and established. It consists of a long fibrous molecule containing purine and pyrimidine bases, nucleotides linked together by phosphodiester linkages at the 3' and 5' positions. The back bone of the molecule thus consists of a regular alternation of sugar and phosphate groups as shown in Figure 1. For different types of nucleotides bases are possible, and in fact, it is known the sequence of bases is biologic. The set of possible bases, adenine and guanine are purine, and the other two - thymine and cytosine - are pyrimidines.

Our studies reveal considerable of the structure of DNA. Since the chemical formula of DNA contains at one very long polynucleotide chain, it was generally assumed that its structure would also consist of one chain. However, studies have shown that the mesostructural structure must consist of two than one chain. We have shown that two linear, helical structures of our structure molecule consists of not one but two polynucleotide chains joined by cross waves of common fibro and cis close arrangement in Figure 2. The two chains are held together by hydrogen bonds between the bases.
There was only one chain in.

It has been assumed that since the chemical formula
the chemical formula is correct there would only be one in the
and only one chain. This would also be true for the
However the

structural unit. The x-ray evidence and the density show the density,

4.5 suggests

with the x-ray evidence, indicates very strongly that the structural
there can be more

unit consists of more than one decahydrocyclopentane chain. These
are probably two.
We should emphasize that while the sequence of bases is indeterminate, the necessity for specific pairing demands a complementary relationship between the sequence of bases on the opposite chain. If the sequence on one chain is given, then the sequence on the other is automatically determined. The one chain is, or it may be, the complement of the other. Our model, consists, in effect, of a pair of chains, either of which can be regarded as the complement of each other. This feature appears to be most important as can be seen by replacing the previous sentence to read: our model consists of a pair of templates, either of which can be regarded as the negative of the other. Thus if a single chain could act as a template (or model) for the formation of its complement, the mechanism of DNA self-replication would in principle be understood.

The idea that a single chain could act as a template for the formation of its complement seems reasonable. Our model suggests that this could be done most simply if the single chain in the relevant portion of it takes up the helical configuration of our structure.
of cell structure we imagine. Given the hypothesis we would imagine that
and at this stage in the life of cell free nucleation (strictly polymeroidic
precursors) become available and join up by hydrogen bonds to one of the
bases on the far already formed chain. We would postulate that the
polymerization of the free nucleation to form a new chain is only possible
is the resulting chain can form the proposed structure. This is
plausible...

Naturally for this process to work be important, at some stage in
the cell division, the two complementary strands must separate from
themselves, that is, they must unravel themselves. As the number of
two are two of our belief occurs every 34 A, a very large
number number of extremely large not occur (e.g., 100 times for
every give helix weight of 10^6). The postulation of such a large
amount of unrolling already now. But then it is an inescapable objection
to our scheme of correspondence and especially in view of the situation
above that unrolling of chromosomal occurs easy mitosis. While this
microscope easily it on a scale may feel there are no microscopic rivalry it does
not seem unlikely that the early can be based on a process
in the molecular level.
It is of interest to consider what would happen if a base occurred in one of its less likely tautomeric forms at the moment when the complementary chain is being formed. For example, while adenine, for example, will usually pair with thymine, if there is a tautomeric shift of one of its hydrogen atoms it can pair with cytosine. The new base pairing occurs, the adenine (having returned to its more usual tautomeric form) will pair with thymine, but the cytosine will pair with guanine, and thus a mistake will have occurred in the copying process. It seems possible that this may be the explanation of the spontaneous mutation. The difference in energy of between tautomers under physiological conditions is not known, but making a biological assumption a difference as above 10 kcal/mole would be necessary to obtain the right order of magnitude for the observed rate of spontaneous mutation.
It is not improbable that one chain of a pair, perhaps under the strain of twisting, might occasionally break. The polynucleotide chain remaining intact could then relax the accumulated twist by rotation about single bonds. Following this, the broken ends, being still in close proximity, might rejoin. Such a process obviously bears it is not possible to judge no foundation for the suggestion it entered at the last, but others who have it was able to point to the theory doubtless, having seen and may have been a clue to this phenomenon. 

If this process occurs, however, the breaks do not begin always again.
Legends & Figures

1. The chemical formula of a single chain of DNA.
2. This figure is purely diagrammatic. The two ribbons symbolize the two phosphate-sugar chains, and the horizontal rods the two phosphate-sugar chains, and the horizontal rods the two phosphate-sugar chains, and the horizontal rods the two phosphate-sugar chains, and the horizontal rods the two phosphate-sugar chains, and the horizontal rods the two phosphate-sugar chains, and the horizontal rods the two phosphate-sugar chains, and the horizontal rods the two phosphate-sugar chains, and the horizontal rods the two phosphate-sugar chains, and the horizontal rods the two phosphate-sugar chains, and the horizontal rods the two phosphate-sugar chains, and the horizontal rods
   - The vertical line marks the fibre axis.
   - Pairs of bases holding the chains together. The vertical line marks the fibre axis.
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   - Pairs of bases holding the chains together. The vertical line marks the fibre axis.
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3. The chemical formula of a pair of chains. The hydrogens bonding in pair symbolized by dotted lines.