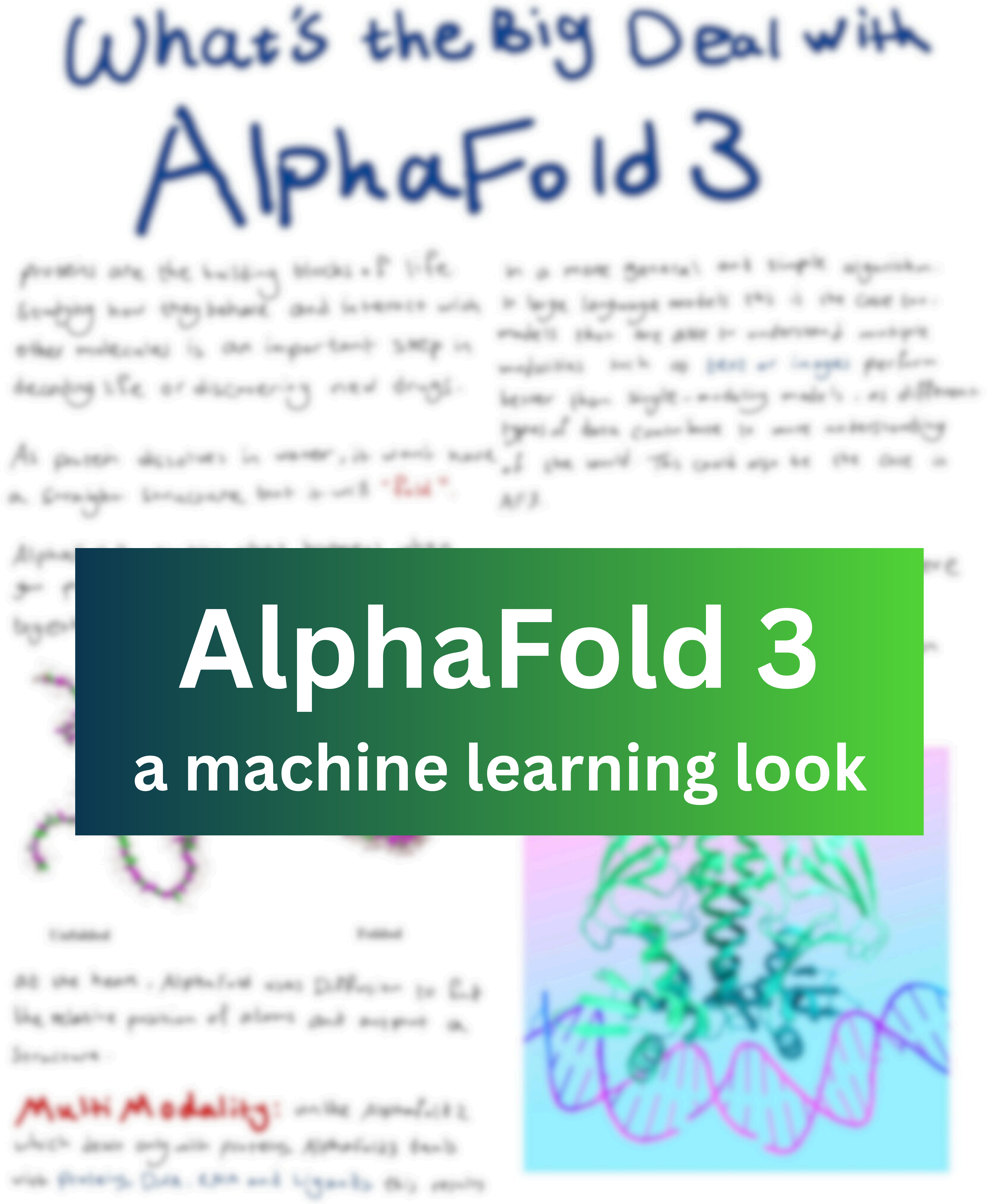


What's the Big Deal with AlphaFold 3

AlphaFold 3

a machine learning look

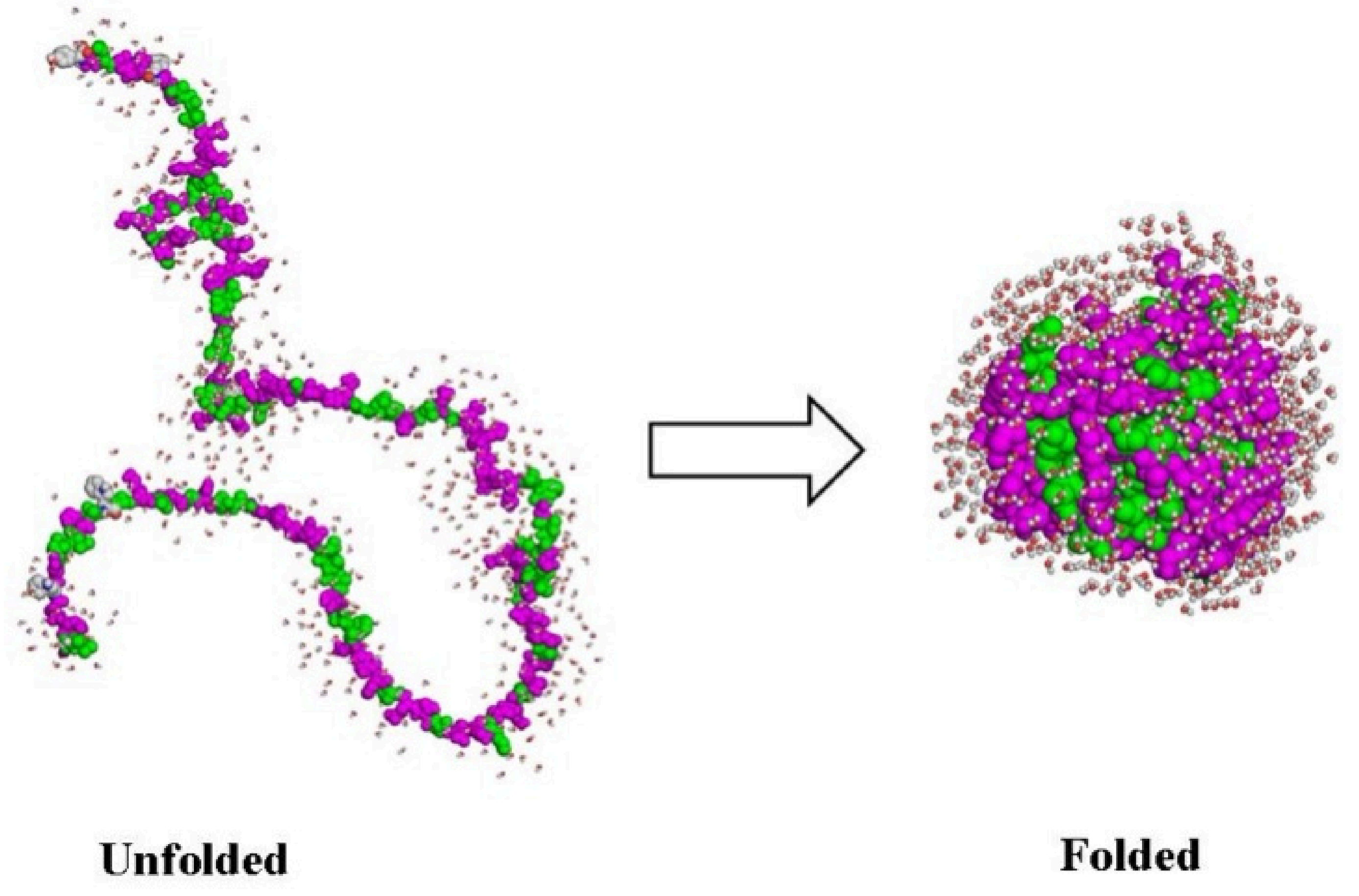
GitHub repo: ml-retreat

What's the Big Deal with AlphaFold 3

proteins are the building blocks of life. Studying how they behave and interact with other molecules is an important step in decoding life or discovering new drugs.

As protein dissolves in water, it won't have a straight structure but it will "fold".

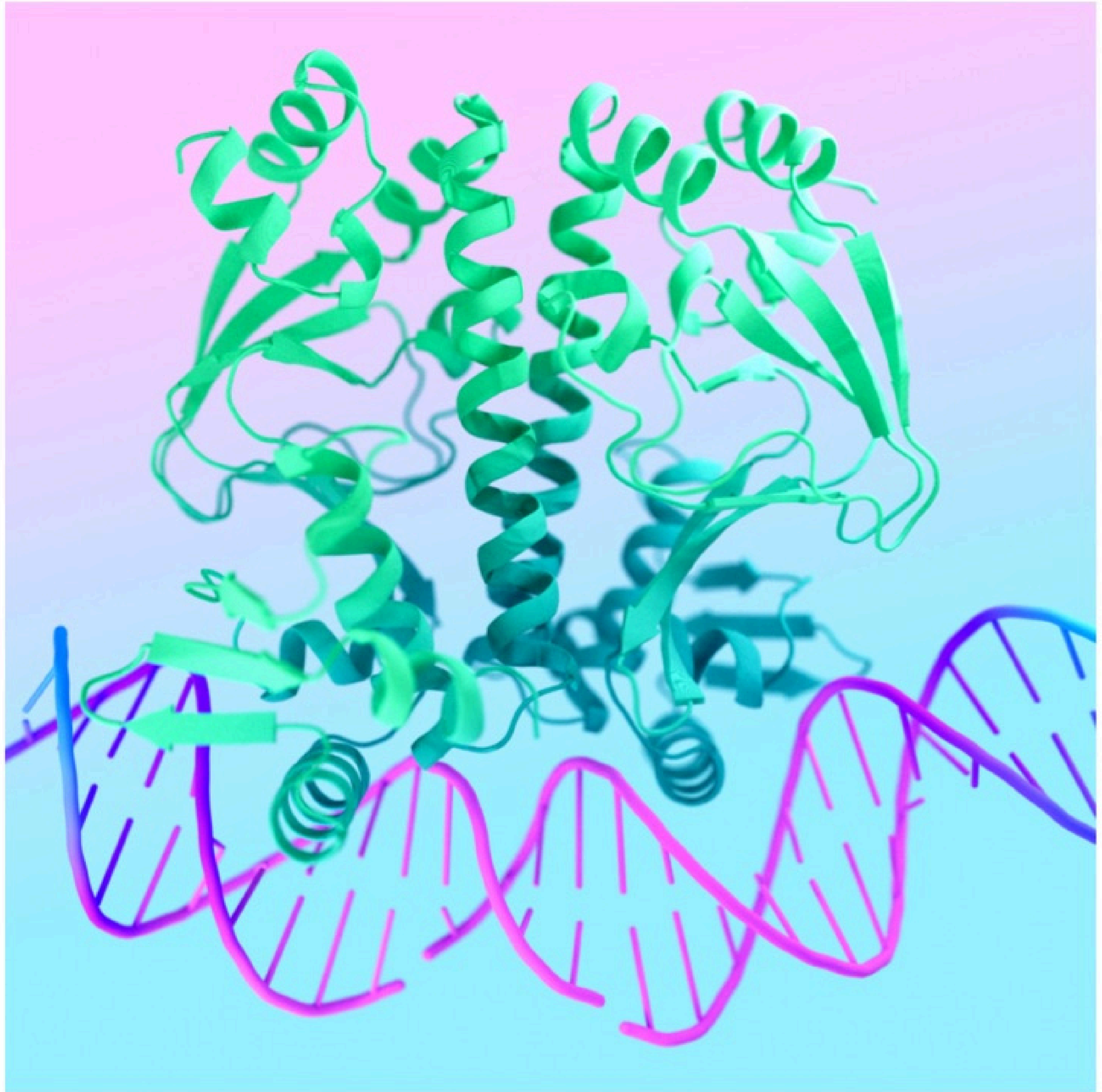
AlphaFold 3 studies what happens when you put proteins, RNA, DNA and ligands together.



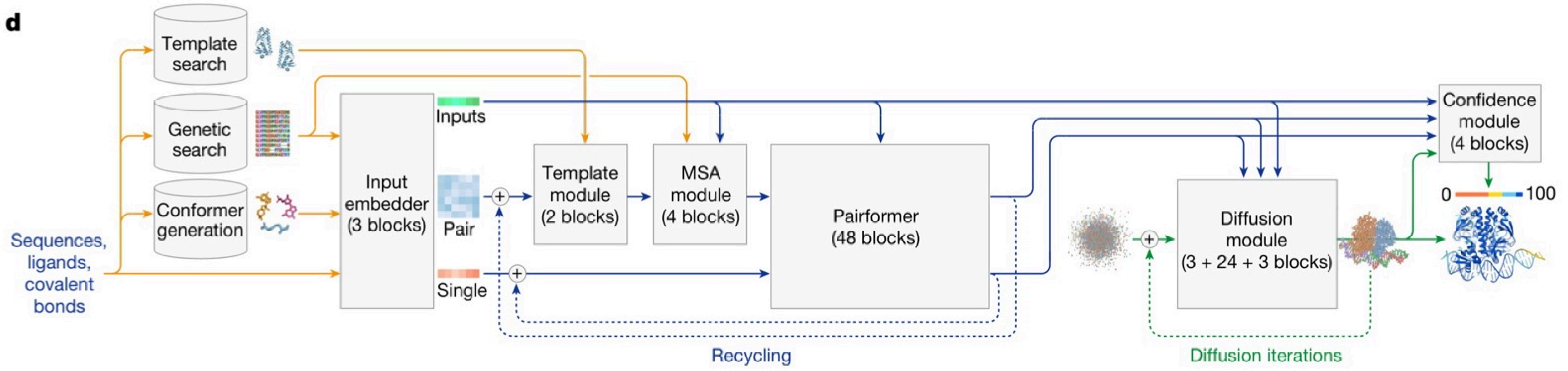
at the heart, AlphaFold uses Diffusion to find the relative position of atoms and output a Structure.

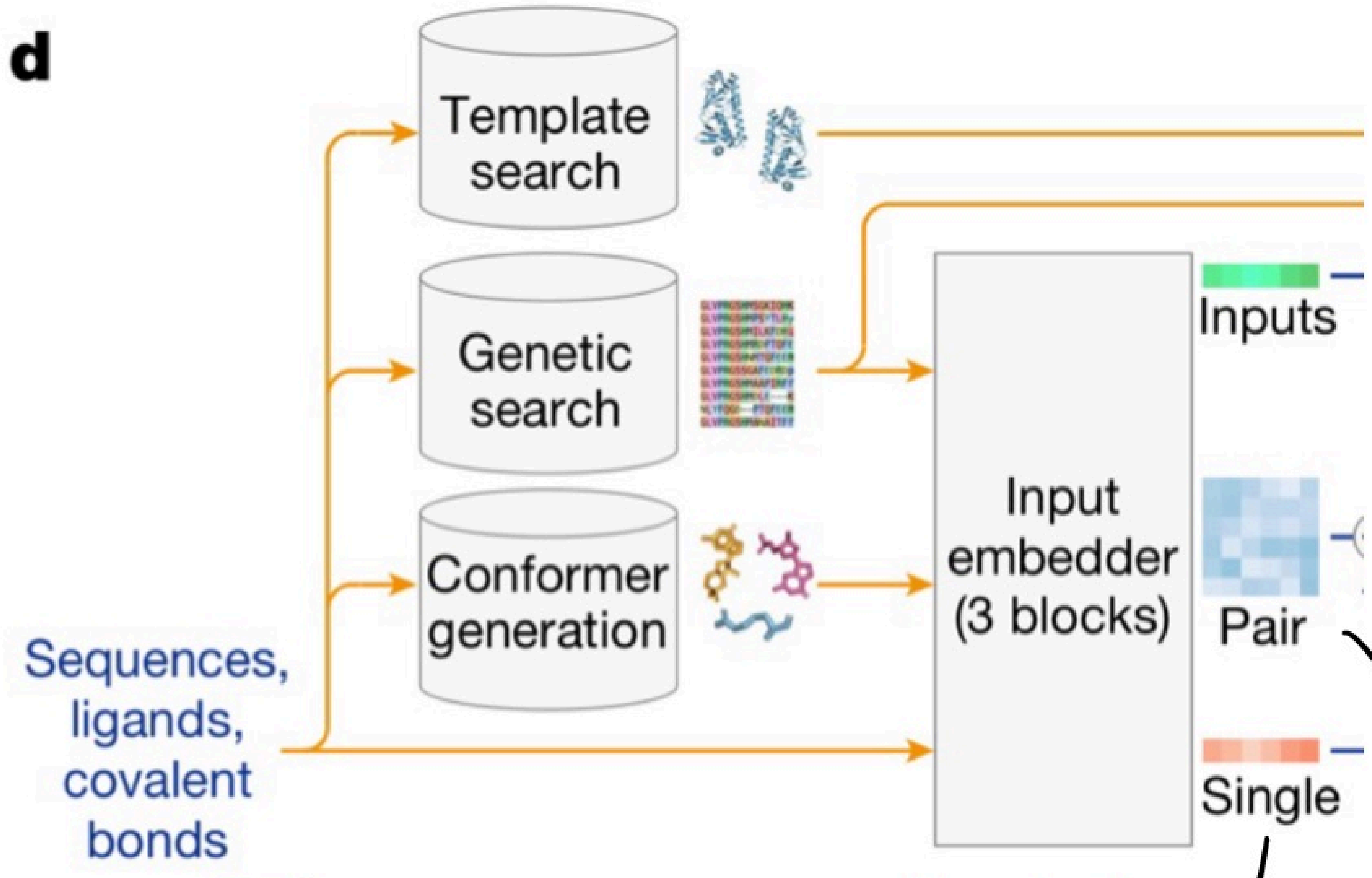
Multi Modality: unlike Alphafold 2 which dealt only with proteins. AlphaFold3 deals with Proteins, DNA, RNA and Ligands. this results in a more general and simple algorithm. In large language models this is the case too, models that are able to understand multiple modalities such as text or images perform better than single-modality models, as different types of data contribute to more understanding of the world. This could also be the case in AF3.

AF3 relies on a diffusion model where the conditioning takes the major Computation and is mostly based on the architecture of AlphaFold 2.



AlphaFold3 Architecture





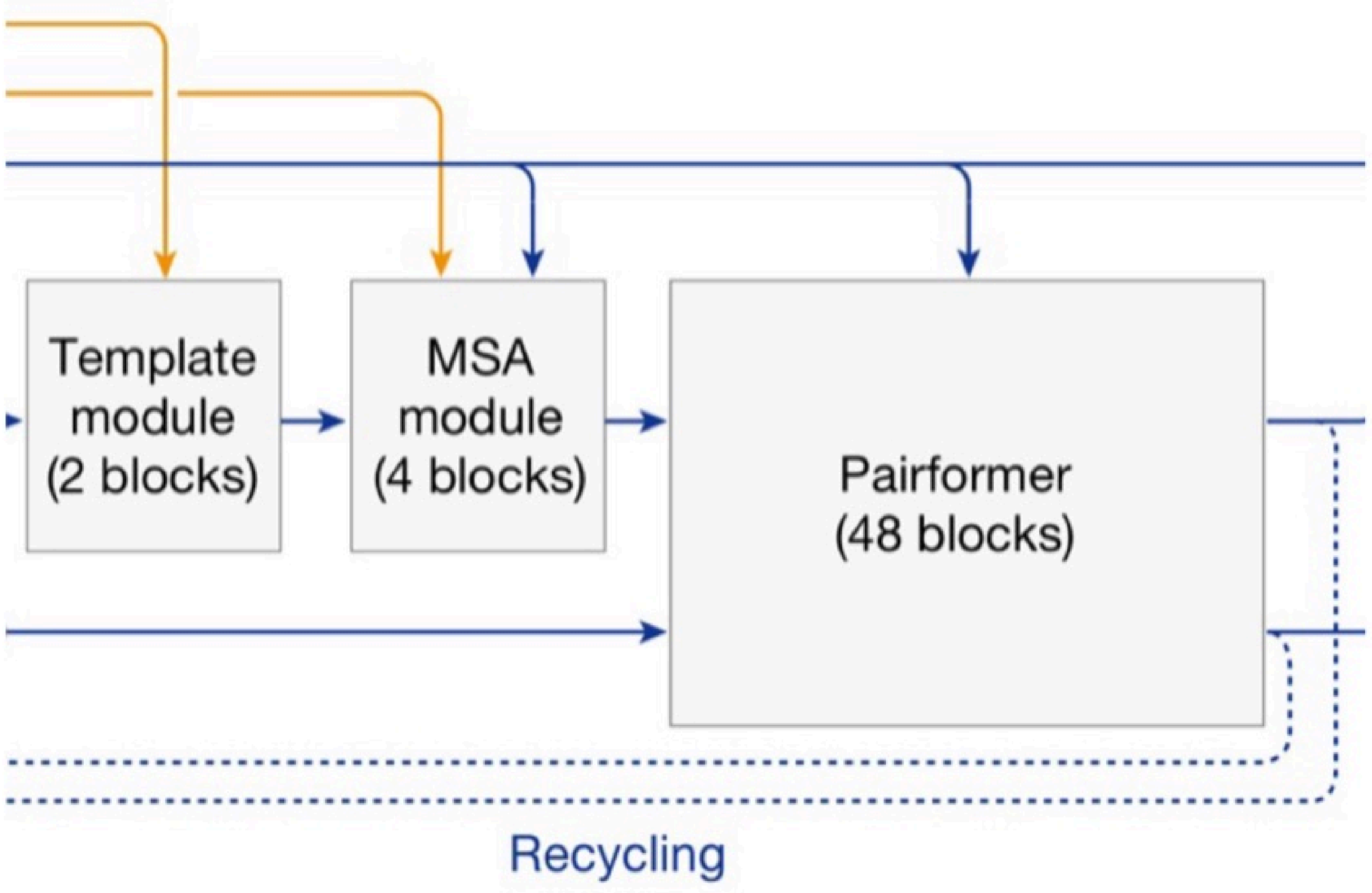
PART I: the input seq we give the mask whether or not this is protein, DNA, etc. and also what that token is.

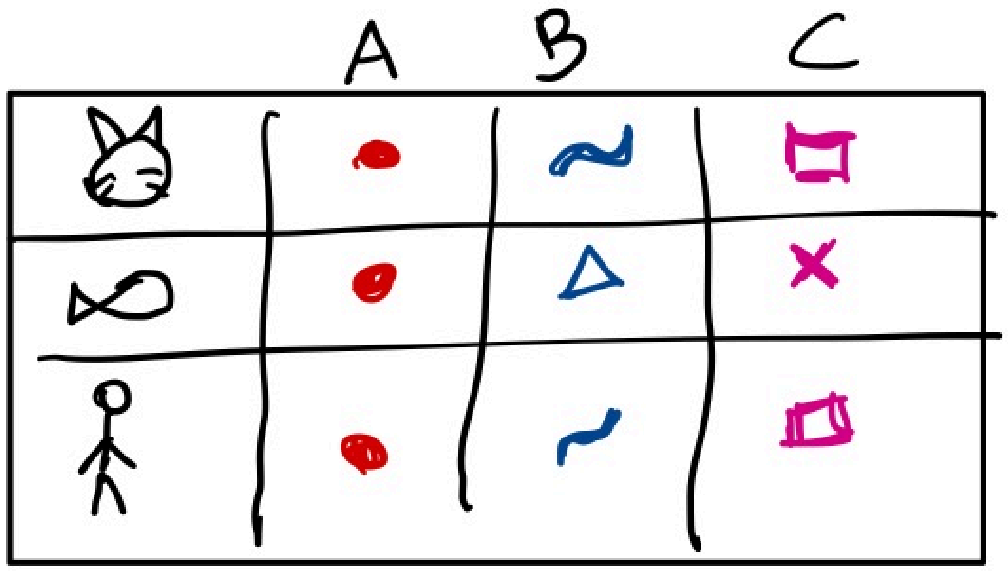
Then some of the features come from the searches. The conformer tells us for a given token, what the standard positions of its atoms are. Genetic Search helps finding how a protein might fold given its evolutionary background. Template Search looks for similar structures between input molecules and the dataset.

the single embedding captures token-level features.

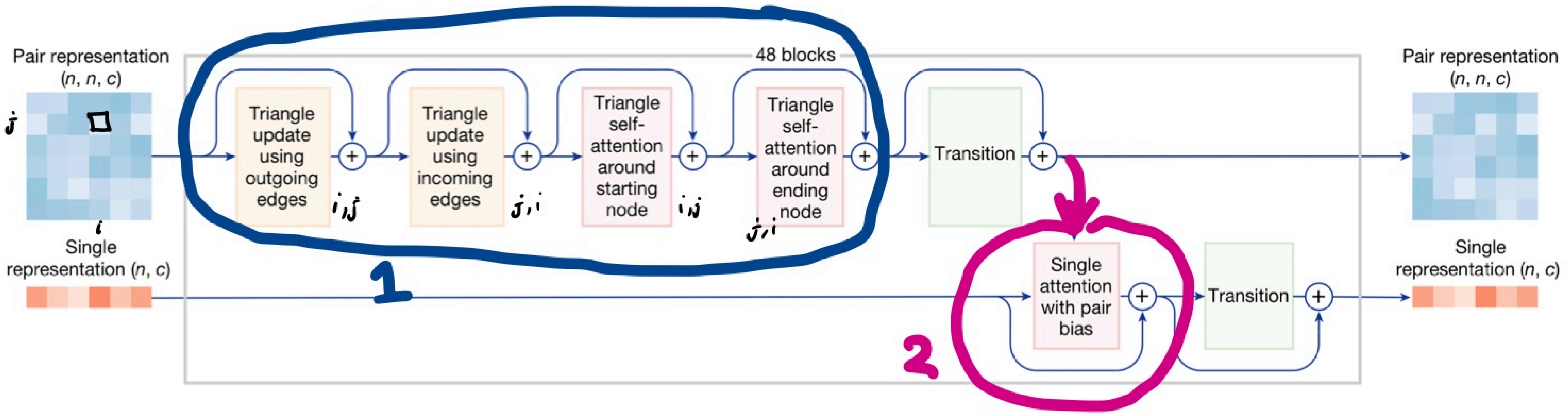
the pair embedding captures the relation between tokens.

PART II: the main computation body. The majority of the Genetic Search is used here. The Template Search found a close template to the input and uses it to fill the pair repr. initially, and when pair repr. is updated in Pairformer, the new pair repr. is merged with the template in Template Module. The MSA module uses the evolution of proteins through species to identify which parts of the proteins are more or less important and thus, how the protein is structured.

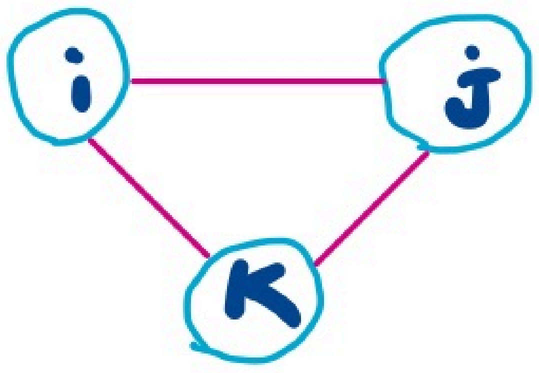




the analysis of protein from different species can tell us a lot of things. For example when amino acid A is preserved through most of them, then it has to be crucial for the protein to be functional. or if B and C get changed with a correlation, then they must have a relation.

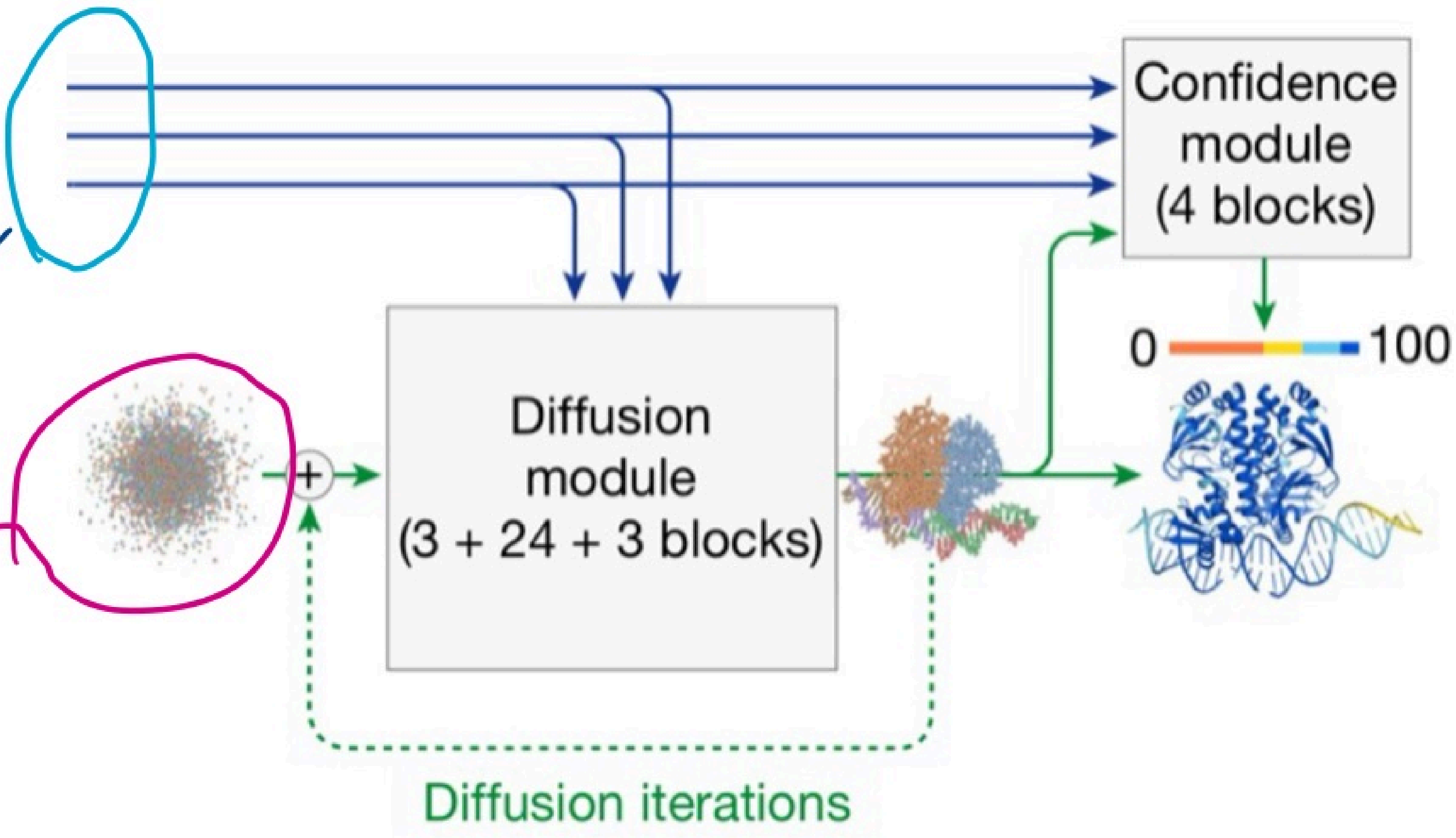


the most compute goes into pairformer module and into part 1 of processing the pair representation. while a normal transformer would look up the relation of two pairs with every other pair, here the transformer attends to the relations between i,j with any K that forms a triangle with them.



if the distance between i and j are estimated so long that the triangle would not form, there would be problems, So when updating i,j the block also update i,k and j,k. Since the relation between i,j is not symmetrical, we have two seperate blocks for i,j and j,i. when pair representation is processed, it's used to process the single repr. as two pairs can have influence on each other via bond, opposite charges, etc.

PART III: takes a description and outputs the atom positions.



the descriptions of the molecules

prone to hallucination

Some noisy position of atoms