1.

Algorithm	Time Complexity	Space Complexity	Complete?	Optimal?
BFS	O(b^d)	O(b^d)	Yes	Yes
UCS	O(b^d)	O(b^d)	Yes	Yes
DFS	O(b^d)	O(b * d)	No	No
DLS	O(b^d)	O(b * d)	No	No
IDS	O(b^d)	O(b * d)	Yes	Yes
A*	O(b^d)	O(b^d)	Yes	Yes

2e.

States Generated

	BFS	DFS	DLS	IDS
Easy	48	958	147	16
Medium	827	1114	372	877
Hard	810	332	252	2234

3c.

	States Generated
A*	61
UCS	64

5.

    Protein folding is difficult because there are over 200 million known proteins and each one is unique and has a complex 3D structure. Figuring out the exact structure of a protein is a very challenging and time-consuming task. There are 20 amino acids but there are endless combinations and interactions that create new proteins. Keeping up with all the proteins is an almost impossible task.

CASP, which stands for Critical Assessment of protein Structure Prediction is a community for researchers to basically compete against each other to make advancements in the field of protein folding. They challenge teams to make predictions about the shape of proteins and the winner is the group that made the most accurate prediction. It is regarded as the 'Olympics of Protein Folding'. In 2018, AlphaFold won the CASP challenge.

AlphaFold is a deep-learning method that predicts protein structure. They use neural networks to predict protein structures based on their amino acids. AlphaFold is discovering new drugs and treatments for neglected diseases such as Chagas disease and leishmaniasis. AlphaFold was also used to discover the protein responsible for COVID-19. AlphaFold has been used to make all sorts of scientific discoveries which help scientists and researchers better understand various diseases and create treatments for them. AlphaFold's ability to predict protein structures is revolutionary for the field of biology and medicine.