Interview with Jeff Bond

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Dr. Jeffrey P. Bond received a Ph.D. in biophysics from the University of Rochester and had postdoctoral training at Cornell University and the University of Wisconsin-Madison. He joined the University of Vermont faculty in 1995 and is currently conducting research in the field of bioinformatics. Bioinformatics, the combined study of biology and informatics, involves a great deal of statistical mathematics. It also involves two data types: sequence and expression.

The largest project on which Dr. Bond is currently working is compromised of enzymes and how they work. He is conducting this research alongside Dr. Susan Wallace to determine how DNA repair enzymes recognize damaged DNA. Failure to recognize damaged DNA may lead to the development of cancer. Repair enzymes may lead to cancer diagnosis and treatment, as well. The presence of broken repair enzymes indicates an increased risk of developing cancer, so a patient may require closer monitoring. Also, if repair enzymes are functioning within the cells of a tumor, they may need to be disabled in order to kill the tumor.

Dr. Bond is also researching how enzymes interact with the sequence and structural features of DNA, particularly with amino acids involved in specificity. For example, he may compare the sequences of two proteins that have different functions to determine which amino acids control those functions. Once properly aligned, it becomes easy to be seen which amino acids differ among various sequences for that protein in different species. If an amino

acid is the same (or similar) throughout all sequences of a protein, and especially in both proteins, it is known as "functional residue" and it is likely safe to assume that that amino acid is important to the structure of the protein, but not necessarily to its function. Along those same lines, if there is a wide variety of amino acids in a particular location in every sequence, it is may also be safe to assume that that location does not have any bearing on the function on the protein. However, if there is an apparent mutation that affects the function of the protein, it warrants further investigation.

There are two types of these mutations: Type I, which involves the evolutionary variation rate, and Type II, which involves the properties of the protein. If the amino acid at a particular location is consistent throughout the sequences of the same protein, but differs across proteins, it is likely a Type II mutation that affects the function of the protein. If there are mutations across sequences of the same protein that are not present in another protein, they are likely of Type I. This latter case means that although there has been mutation among similar species at that location that has not changed the function of the protein, there may have once been a mutation in the evolutionary chain at that location that did change the function of the protein.

So, Dr. Bond's work involves automating the process of comparing sequences, determining which of these amino acid locations have changed recently in the evolutionary chain and which locations have an effect on the function of the protein. During the comparison of sequences, it is important to remember that the selection of each amino acid is not a random choice among 20 options. Rather, it is a random event that mutates the amino acid from a previously established choice.