Strange view of catalysis,enzymes, transporters, and channels

Bob Eisenberg <bob.eisenberg@gmail.com> Tue, Sep 29, 2015 at 5:25 AM
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Dear Fred

As I have been thinking of our work on NCX, I have been worrying about the conformation change that seems central to its function (the same as in other transporters).

I realized that WHEN MODELLING THE PROTEIN ITSELF there is a STRONG constraint because the protein is a catalyst.

A catalyst is in the same state at the end of its action as at the beginning, so IT IS CHARACTERIZED BY A SINGLE FREE ENERGY (for the protein itself).

Of course, the entire system, and the transport process does NOT have a single free energy. Rather, its whole point is to convert some free energies into others.

But the protein itself has multiple 'states' and conformations (of its free energy landscape) WHILE HAVING THE SAME FREE ENERGY AT THE BEGINNING AND END OF THE PROCESS.

This is (almost) the definition of an UNSTABLE system. (If the protein had the same free energy through the transport process, it would be the definition of an unstable process).

This insight (a) will help a great deal in our modelling of NCX. It suggests that we will be able to estimate the energetics OF THE CONFORMATION CHANGE OF THE PROTEIN easily (the ions etc we know how to do, although computing the dissipation will be an adventure, which we may avoid to beginwith).

The insight (b) suggests that viewing ALL enzymes, transporters, and channels as UNSTABLE proteins may provide a general framework that is useful. Of course, I know absolutely nothing about the theory of stability of such systems. Fortunately, this is an area of great knowledge in math (even pure math) because it is closely related to the existence, AND UNIQUENESS properties that love to study.

What do YOU think? Do you think this will be useful?

As ever
Bob

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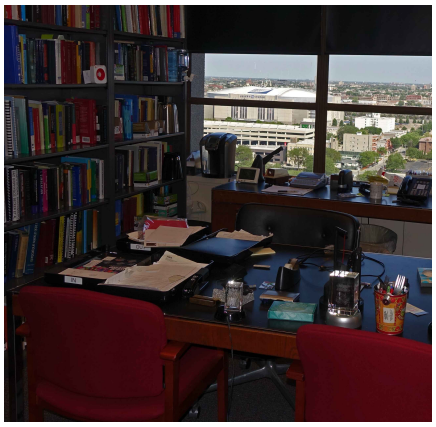
View from New Office



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