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APh/BE 161

Poster Session Title and Abstract

Title: Proofreading in tRNA-amino acid coupling

Abstract:

Before translation from mRNA to protein can occur, animoacyl-tRNA synthetase covalently couples a tRNA molecule with its corresponding amino acid. Without a consistently accurate mechanism for doing this, the downstream mechanisms of tRNA-mRNA codon matching are of no use. According to Alberts, the overall accuracy of tRNA charging is approximately one mistake in 40,000 couplings. Because a number of amino acids are very similar (e.g. isoleucine and valine), this level of accuracy can probably not be accounted for by thermodynamics alone.

To examine the impact of the proofreading mechanism in tRNA synthetase, I plan to first estimate what the error rate would be without this mechanism, based on a thermodynamic argument. After reading up some more on how the editing mechanism works, I hope to be able to model the system well enough mathematically to verify that the mechanism is indeed capable of having a ~39999 in 40000 chance of getting it right.

I would appreciate any advice you have on how I should proceed in this project. Right now, one problem I can see is that finding binding energies and reaction energies for these molecules might be difficult.