

A High Throughput Bioinformatics Method for Analyzing Nucleotide Polymers Demonstrating Physiological Effects within Eukaryotic Cells

1. **Research Title:** A High Throughput Bioinformatics Method For Analyzing Nucleotide Polymers Demonstrating Physiological Effects Within Eukaryotic Cells
2. **Individual Sponsor:**

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3. **Academic Area/Field and Education Level:** Biology/biochemistry plus computer science, mathematics, physics, and/or engineering (BA/BS, MS or PhD)
4. **Objectives:** The proposed project applies inexpensive software to fold intracellular parasite genomes, select sequence candidates using patterns of human-centric attenuation and significant evolutionary conservation, and then compare resultant structures to the human transcriptome to identify sequences and structures of potential benefit to the warfighter.
5. **Description:** Given that the process of folding the entire human genome *in-silico* remains an intractable problem, this project will utilize viral genomes to reduce the problem domain associated with identifying higher-order (secondary and tertiary) nucleotide structures demonstrating a potential to interact with human physiology. Since the technology required to complete project goals is novel, much of it must be fabricated within the lab. Potential contributions for DAGSI interns are many and varied, thus providing appeal to a wide range of scholastic interests. Students interested in combining biology or chemistry with mathematics, engineering, physics, or computer science will have a rich, rewarding research-oriented experience and leave the lab with the lucrative and high-demand bioinformatics skills requisite to education as an inter-disciplinary scientist/engineer. Possible project contributions include smart device app development, relational database development, supercomputer script development, R/MatLab add-in development, C++/Java/Objective-C core algorithm development, GUI design, and more. Ideally, each contribution will result in one or more peer-reviewed publications with associated patent applications, where feasible.
6. **Research Classification/Restrictions:** None
7. **Eligible Research Institutions:**

DAGSI