Jacob Urquidi

Research Interests: Current research interests involve:

- The development of new radiation protocols for the sterilization of insects using mobile, self-deployable platforms.
- The use of backscattering interferometry to look at changes in polarizability at the molecular level to develop a predictive model that can be applied to protein folding.
- Understanding the source of degradation of formants for the French Horn and Euphonium as a predictive measure of instrument quality.

Grant Submissions:

- Partnered with The University of Texas at El Paso's (UTEP) submission to the Minority Serving Institutions Partnership Program (MSIPP) with Dr. Jorge Lopez titled, "Southwest Consortium on Nuclear Security". Submitted

Research Personnel

Grad students: Josh Amburgey; matriculated with a Ph.D. Summer of 2018, Greggory McPhearson; matriculated with a Ph.D. Fall 2018. No current graduate students.

Research highlight:

The forces responsible for a protein's higher order conformations vary considerably in an aqueous environment compared to the crystalline state. Changes in pH, pressure, temperature, or ionic concentration can induce a protein to fold from its native state to a denatured state. The structure of water at the interface between bulk water and a protein molecule profoundly impacts a protein's conformation in the transition from its native, compact state to its unfolded, denatured state. Water molecules have different arrangements near both the polar and nonpolar groups of a protein molecule compared to bulk water. As a protein unfolds, the ratio of nonpolar to polar groups exposed to water changes, affecting a protein's thermodynamic properties. My group's interest lies in understanding the structural pathway during the unfolding process. Our approach involves isolating intermediate structures of unfolding proteins and resolving them using small angle scattering. Because the systems being studied have been characterized using differential scanning calorimetry we should be able to make a thermodynamic correlation with particular structural motifs as the protein progresses from its compact state to its denatured state. An exciting development has been our ability to employ backscattering interferometry to make very precise measurements of changes in the polarizability of the protein as it proceeds along the changing structural pathway during unfolding. Currently we can measure changes of 1 part in 10^{10}. This will hopefully allow us to develop predictive models by measuring how the electron density redistributes itself during the process.

Service: Recruiting/retention committee - chair; Department Safety Officer; Lab oversight committee