Introduction:
The DNA of an organism contains the genes that are the instructions for the development and behavior of organisms. The genome of an organism is the entire collection of their genes. Since the beginning of the human genome project in the mid-1980s the sequencing of whole genomes has become a powerful technique to better understand the development, evolution, physiology and behavior of organisms.

I am proposing a project in collaboration with Dr. Nipam Patel at the University of California at Berkeley that will generate two genomic DNA libraries that contain the DNA from the genome and a set of gene sequences from the brine shrimp, *Artemia*. Knowledge of the genome of the crustacean *Artemia* will provide further insight into the unique nature of this remarkable organism. It is an animal extremophile found in severely stressful environments worldwide, including Great Salt Lake (GSL). *Artemia* has evolved the ability to thrive in extremely hypersaline habitats in which no other animal can complete its life cycle. Survival under these and other harsh conditions is achieved in large part by the production of encysted embryos that tolerate intense UV exposure, years without oxygen, thermal extremes, severe desiccation and repeated cycles of hydration-dehydration. Animal extremophiles with the capabilities of *Artemia* are rare and this, in my view, provides a compelling reason to describe its genome.

*Artemia* is also used extensively as an important food source in aquaculture, in some cases being a critical nutritional component. There is an extensive brine shrimp harvest every fall from GSL and most of this material is used in fish and shrimp farming. In addition, a wide variety of environmental toxicology experiments use *Artemia* as an indicator species, and it is a very popular animal for science projects in middle and high schools around the world. In addition to these uses, *Artemia* is a popular model for research in biochemistry and molecular biology, ecology, population genetics, evolution and developmental biology and has even been included in space shuttle payloads.

I currently have several undergraduate research projects that involve *Artemia* and the goals of the merit leave project would aid those projects, inspire new research work, and stimulate further course development in the biology program as discussed below.

**Project goals and outcomes:**

**Material goals:**
The main goal of the proposed project is to use a molecular biology technique called Cot cloning to make an *Artemia* genomic DNA library that is enriched for single copy genes. Single copy
genes represent the majority of information contained in the genome, however, many organisms also contain repetitive DNA that is information poor. The Cot cloning technique has been developed for studying the genomes of various crop plants, which are notorious for having large genomes with large regions that are highly repetitive and gene poor. Since the single copy genes direct most of the functions of organisms, separating out the gene rich regions for more intense analysis has been a successful strategy for maximizing the amount of information obtained from DNA sequencing projects with limited funding. *Artemia* also has a very large genome that contains a high amount of repetitive DNA sequences. This makes it an excellent candidate for adapting this technique to animals for the first time. If the technique is successful it will provide us with genomic DNA libraries and sequences that have not yet been available anywhere in the scientific community, as well as providing us with a resource for additional undergraduate research projects and curriculum development in the areas of molecular genetics, genomics, and bioinformatics.