

Omics analysis of marine mammal stress responses and tissue energy usage

Chronic stress is difficult to define and diagnose in free-ranging vertebrates because molecular mechanisms regulating tissue energy utilization and stress responses are poorly understood at the cellular level. The northern elephant seal is an ideal marine mammal model system for investigating downstream consequences of stress due to ease of accessibility, amenability to physiological manipulation under anesthesia, and a wealth of studies on metabolic adaptations. We are examining muscle and blubber transcriptome responses to neuroendocrine stimulation in elephant seals. We recently sequenced the first elephant seal muscle and adipose transcriptomes collected during an acute stress challenge experiment and developed a computational pipeline for de novo transcriptome assembly and analysis in the cloud (Amazon EC2). We are now conducting in-depth analysis of acute stress transcriptomes (annotation using BLAST), examining transcriptome responses to chronic stress (de novo assembly using Trinity), and comparing gene expression between tissues and endocrine manipulations, which require more powerful computing resources. Due to the lack of research computing resources at Sonoma State University and cost limitation of cloud computing, we are requesting access to XSEDE high-performance parallel computing and data storage services to conduct the proposed studies.