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**Department of Marine Sciences
Presents a Seminar By**

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Insights into the Composition and Function of Microbial Communities through Next-Generation Sequencing

The study of microorganisms and microbial communities has been impacted dramatically by advances in DNA sequencing technologies. Next-generation sequencing has provided researchers with new opportunities to determine the composition of microbial communities by sequencing PCR-amplified regions of the 16S rRNA gene, determine their functional potential through sequencing the DNA from the community (metagenomics) and their function by sequencing cDNA generated from RNA isolated from these communities (metatranscriptomics). Using the gut microbiota of local termites as an examples approaches for determining the composition of the microbiota and identifying the members of the community that comprise the core will be described. Using the medicinal leech as an example metagenomics and metatranscriptomics will be used to determine the nutrient utilization by digestive-tract symbionts in the host. These sequencing approaches enable researchers to develop new hypotheses that can be evaluated in experimentally tractable systems.

Host: Evan Ward

Time & Date: 11:00 am, Friday, October 23, 2015

Place: Marine Sciences Building, Seminar Room 103

Please see this [page](#) for cancelations and additional seminar information, email marinesciences@uconn.edu, or call 860-405-9152 or 860-405-9151