



**BIOINFORMATICS 2016 SPRING SEMINAR SERIES**

Hosted by: Department of Computer and Information Sciences,  
Department of Electrical and Computer Engineering &  
Center for Bioinformatics and Computational Biology  
<http://bioinformatics.udel.edu/Seminars/Current>

**MONDAY, March 7, 2016**

**3:30pm**

**DBI Room 102**

**Comparative analysis of reproductive 21-nt phased  
siRNAs (*phasiRNAs*) in rice**

***Saleh Tamim***

***PhD Student; Bioinformatics and Systems Biology***

**ABSTRACT:** Rice is a model plant studies of monocots, and the variety of sequenced genomes from wild species estimated to be millions of years apart makes it suitable for plant evolutionary analysis. Prior studies of rice domestication have indicated that cultivated Asian rice (*Oryza sativa*) evolved from the wild species *Oryza rufipogon*, while cultivated African rice (*Oryza glabberima*) evolved independently from *Oryza barthii*. Most studies have focused on protein-coding genes associated with domestication traits such as shattering, flowering, and fragrance. Less well-examined are the 21-nt phased, secondary small interfering RNAs (*phasiRNAs*) that are abundant in reproductive development. Using the published genome of the most-diverged wild rice species *Oryza brachyantha*, together with the above mentioned four genomes, we are examining the evolution of *phasiRNA* precursor loci (*PHAS* loci).

**Multiscale Investigation of Histone Modifications:  
Spatiotemporal Dynamics and Epigenetic Memory  
Levels**

***Irem Celen***

***PhD Student; Bioinformatics and Systems Biology***

**ABSTRACT:** Living organisms are exposed to continuous environmental alterations every day and instant genome-wide responses are pivotal for adaptation and survival. Epigenetics in the context of histone modifications (HMs) plays a critical role in gene regulation and has strong relevance to animal adaptation in rapidly changing environments. Uncovering the short and long term kinetics of HMs are essential to understand their individual functions in the genome. In this talk, first, we will present our findings about the transgenerational stable and dynamic epigenetic properties of five HMs. Second, we will discuss about our approach which reveals co-occupancy of HMs on single gene promoters by correlating bioinformatics analyses with super-resolution microscopy techniques. Finally, we will describe the putative pathways that are potentially regulated by distinct HMs under varying environmental conditions.