



cordially invites you to an

Interdisciplinary Seminar

with

Dr. Sarah Flanagan

on

“Identifying signatures of selection on the genome: Case studies using pipefish”

Tuesday, September 20, 2016

3:30-5 p.m.

Reception & refreshments at 3 p.m.

Hallam Auditorium, Room 206

1122 Volunteer Boulevard



Sarah Flanagan (Biology, Texas A&M Univ., 2016) is developing different approaches to generate better a priori predictions for next-generation sequencing population genetics studies.

Abstract: Understanding the genetic basis of complex traits is one of the major goals of evolutionary biology. Population genetics, which focuses on genetic variation within and among populations, is one way to approach understanding the genetic basis of evolutionarily relevant traits by differentiating between signatures of neutral processes (e.g. migration and drift) and selective pressures. In this talk, I will discuss various approaches to identifying signatures of selection in the context of next-generation sequencing studies, as well as some of their challenges and constraints when applied to actual datasets. Specifically, I will focus on traditional population genetics approaches to identifying signatures of selection among populations, such as F_{ST} outlier scans, as well as selection components analysis, a method that compares allele frequencies among individuals within a single population to identify signatures of selection. Throughout the talk, I will include results from empirical studies of natural populations of the Gulf pipefish, a marine fish characterized by male pregnancy and sex-role-reversal.