“How to plan an effective and efficient population genetics sampling strategy: Markers, samples, and spatial considerations”

Genetic biodiversity contributes to species’ evolutionary potential, ecosystem function, and human prosperity (e.g., agriculture). Preserving genetic resources during rapid environmental change is a pressing scientific and societal challenge. To meet this challenge, it is important to ensure that conservation researchers utilize well-designed and robust analytical methods and sampling/monitoring protocols. Unfortunately, many genetic studies are undertaken without knowledge of how many populations, genetic markers or individuals are needed. With colleagues, I developed software (Hoban et al 2013, Methods in Ecology and Evolution) that calculates power of proposed sampling strategies for five study goals, including performing genetic assignment tests, using ancient DNA, and detecting genetic differentiation. I will explain how I used the software to highlight several concerns seldom considered during study planning: (a) power is rarely a linear function of adding markers/samples; (b) power is situation (species and history) specific; (c) some signals are too weak to detect. I will also explain my current interests in planning ex situ conservation collections (e.g., seed banks). At NIMBioS, I plan to optimize seed sampling from plant populations under local and range-wide population structure, while considering various strategies including those that are spatially biased or otherwise restricted. This project will result in general guidelines as well as software for customizing collections to particular species.

New Location: Room 205 at NIMBioS, Claxton Education Bldg, 1122 Volunteer Blvd.
*Join us for refreshments in the Visitor Breakroom at 3 p.m.

For more information about this and other NIMBioS Seminars, visit http://www.nimbios.org/seminars

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