Abstract:

Accurate RNA structural prediction remains challenging, despite its increasing biomedical importance. Sampling secondary structures from the Gibbs distribution yields a strong signal of high probability base pairs. However, identifying higher order substructures requires further analysis. Profiling (Rogers & Heitsch, NAR, 2014) is a novel method which identifies the most probable combinations of base pairs across the Boltzmann ensemble. This combinatorial approach is straightforward, stable, and clearly separates structural signal from thermodynamic noise.

Special Note:
Powell-Focht Bioengineering Hall, Room 191

Host: Glenn Tesler

Thursday, April 4, 2019
12:00 PM
Fung Auditorium (PFBH 191)