

The UNC Charlotte Department of Bioinformatics and Genomics is delighted to host



WINGS

WORKSHOP IN
NEXT GENERATION
SEQUENCING

WHEN

MAY 17-18, 2012

Thursday, May 17
12PM - 6PM

Friday, May 18
8AM - 4:30PM

WHERE

UNC CHARLOTTE

Bioinformatics Building
Robert D. Snyder Road
Charlotte, NC 28223

This workshop is designed to showcase paths to successful utilization of high-seq data while providing a solid understanding as to why specific tools were chosen. It includes a collection of presentations describing the experiments themselves followed by extended hands-on sessions. Our goal is to provide experimentalists both the theory and the experience to be able to institute these pipeline in their own laboratory.

- **ON THURSDAY** the presenters will explain the various experimental design choices from selecting methods and algorithms to other parameters and considerations in order to achieve specific outcomes.
- **ON FRIDAY** there will be three 2-hour sessions with two workshops per session running concurrently. Attendees get hands-on experience in a directed tutorial that takes a preliminary dataset through a pipeline that is properly tuned to the experiment. Attendees select workshop sessions, on a first-come first-serve basis.

Participants will take home the datasets, presentations, and will be able to obtain images of the analysis system for use in their home labs.

Topics include:

- Basic HTS data cleansing with Velvet – the preliminary sorting of raw data to exclude poor quality, adaptors and other artefacts.
 - ChIP-Seq data analysis – the goal of this session is to perform some basic tasks in the analysis of ChIP-Seq data.
 - Amplicon frequency in a forensic experiment
 - Amplicon frequency in a metagenomic experiment
 - RNA-Seq analysis in a Visual analytics framework for splice form recognition
 - Tailoring NGS analysis pipelines using Galaxy
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