🍃 Spring

# **Spring** Bioinformatics Users Group (BUG)

The Bioinformatics Users Group (BUG) consists of scientists in the life sciences, computing, math, statistics, and other areas who meet to discuss topics related to those fields. Meetings are generally informal, consisting of discussions, interactive talks, or short workshops. **No experience needed to participate.**

## Wednesdays from noon-1pm in Ag. & Life Sciences (ALS) 3006

**Apr 3rd**  **"CERENKOV2: Computational Elucidation of the Regulatory Noncoding Variome, i.e., a machine learning approach to detect the probably most expensive typos in human DNA"** - *Yao Yao (Stephen Ramsey Lab)*

**Apr 17th**  **"Biological Knowledge Graphs, i.e., Finding the unknown knowns and dark data in biology"** - *Anne Thessen and Kent Shefchek (TISLab)*

**May 1st**  **"What is a replicate? Celebrating the 100th dating anniversary of when statistics met biological experimentation, i.e., Common experimental design issues and consulting services at Department of Statistics"** - *Yanming Di (Statistics)*

**May 15th**  **"Genome analysis of off-target CRISPR mutagenesis in poplar and eucalypts, i.e., Damage control: how often does gene editing happen in the wrong place?"** - *Greg Goralogia (Steve Strauss Lab)*

**May 29th**  **"Population genomic variation of North Pacific albacore tuna investigated using ddRAD sequencing, i.e., One fish, two fish… where do albacore tuna come from?"** - *Felix Vaux (Kathleen O'Malley Lab)*

**Jun 12th**  **"Machine learning for phenomics and association testing in genome-wide association studies of regeneration in poplar, i.e., how neural networks help us to see the phenes and the genes"** - *Michael Nagle (Steve Strauss Lab)*

https://cgrb.oregonstate.edu/**bug**

Oregon State University

CENTER FOR GENOME RESEARCH & BIOCOMPUTING

Poster is valid from March 21st, 2019 – June 13th