Title: Genomics of Disease in Wildlife: A Workshop
Course Host: Jill Pecon-Slattery, Ph.D.
Venue Host: Sue VandeWoude, DVM.
Location: Lory Conference Center, Colorado State University, Fort Collins, CO
Dates: June 3-11, 2017

Abstract: Wildlife biodiversity can be drastically affected by the outbreak and transmission of disease pathogens in both natural habitats and *ex situ* populations. Recent technological advances in genomic sciences and increasingly affordable Next Generation Sequencing (NGS) assay costs have coalesced to result in powerful tools to monitor, detect, and reconstruct the past, present and future role of pathogens within wildlife biodiversity. This short course will provide hands-on training for graduate level and above researchers in wildlife disease related disciplines seeking to incorporate genomic data into their projects. The course will be taught by a core group of experts in genome data analyses with invited faculty comprised of pre-eminent scientists performing cutting edge of research in host-pathogen genomics in wildlife.

Rationale:

(a) **Why is the course needed?** Advances in genomic technology now provide extraordinary opportunities to rapidly assess the impact of disease in wildlife biodiversity, management, and conservation. Wildlife researchers are uniquely positioned to merge ecological, biological, and evolutionary studies with genomic technologies to generate unprecedented 'Big Data' tools in disease research. The workshop will provide a venue to accomplish this goal, will provide networking opportunities for colleagues from intersecting interests, and will advance genomic tools in wildlife disease investigations.

(b) **How will the course address the need?** The course will provide essential training to wildlife biologists, veterinarians, conservation managers, and related experts to successfully incorporate NGS data in wildlife research. Attendees will conduct hands-on analyses of 'real world' genomic data of both host and pathogen. The course will provide: (1) an overview of current bioinformatics developments and approaches; (2) guidance to implement genomic tools in study design; (3) NGS data analysis and interpretation; and, (4) opportunities for interaction with peers, core faculty, and invited experts.

Workshop Description

The venue for the inaugural Genomics of Disease in Wildlife Workshop will be Colorado State University (CSU) in Fort Collins Colorado situated in the foothills of the majestic Rocky Mountains an hour north of Denver. Core leaders, organizers and instructors for the workshop will include CSU faculty with expertise in genomics and wildlife diseases as well as a panel of international experts. The workshop curriculum will include segments on wildlife diseases in iconic species of the North American west including wild felids, canids, elk, bison, and bighorn sheep, as well as fauna that have experienced precipitous declines in population and biodiversity in recent years such as amphibians, bats and primates.

Participant Selection

We will invite applications from researchers involved in wildlife disease through four major fields of inquiry: wildlife biology, veterinary medicine, conservation managers, and genome scientists. Participants will be comprised of senior level graduate students, post-doctoral fellows, and faculty from academia as well as managers of wildlife and conservation programs from government agencies and non-profit organizations. As the workshop is limited to 24 attendees, applicants will be prioritized by level of technical experience, ongoing funded research project topic, affiliation, academic/agency rank, and potential for a direct impact of the workshop experience on wildlife survival.

We anticipate a diverse group of participants, including minorities, women and international researchers. Our goal is to generate a new network of colleagues focused on using the most advanced tools targeting animal health and survival in the wild and in managed populations worldwide.

Workshop Syllabus

The workshop will cover a typical workflow commonly used in NGS analyses starting with the initial raw sequence through final stages of identifying variants linked to disease phenotypes. The workshop will consist of eight days of intensive instruction, with each day covering an essential component of the NGS workflow. Morning sessions will be a series of instructional lectures and demonstrations that will concisely present the purpose, justification and implementation of the specific workflow unit. Afternoon sessions will be conducted in a computer lab. Evening plenary lectures from invited faculty will conclude each day's activities.

Table 1. Tentative Schedule and Daily Topics (06/03/2017-06/11/2017)

Saturday:	Arrival, Evening welcome reception, 12 students-3 minute presentation
Sunday:	12 students-3 minute presentation, Overview of NGS Methods
Monday:	NGS Data Assessment, Databases, Browsers, and Genome Mining Tools
Tuesday:	Alignments
Wednesday:	Phylogenomics
Thursday:	Signals of Selection and Adaptation in Genome
Friday:	Population Genomics
Saturday:	Variant Discovery and Interpretation
Sunday:	Wrap-up, Workshop Evaluation, Departure

Each attendee will be provided with a MacBook Pro computer and peripheral equipment, and prepared genome datasets from several host species and associated pathogens. These datasets will be organized into various files and formats prior to the course, demonstrate key concepts, and be the foundation for computer exercises and teaching tools. Participants will be able to select a specific host-pathogen system suited to their own interests, and use this system for the duration of the course exercises.

Table 2. Potential host-pathogen whole genome sequence for teaching tools

Host Whole Genome	Pathogen Whole Genome	Rationale
Domestic and wild felids	Feline immunodeficiency Virus, Foamy Virus, Feline Leukemia Virus	Domestic and nondomestic felids harbor species-specific strains that have varying levels of pathogenicity.
Domestic and wild carnivores	Parvoviruses, rabies	Domestic dog, related canids and ferret represent an expanding number of species infected in the wild.
Domestic and wild ungulates	Brucellosis/Tuberculosis/Blue Tongue virus	Elk, bison, bighorn sheep show pathogen interchange between domestic and wild herds and influence wildlife management decisions.
Amphibians	Batrachochytrium dendrobatidis	The chytridiomycosis epidemic in frogs has rapidly decimated populations worldwide.
Rodent	Yersinia pestis	Black-tailed prairie dog represents one of several species affected by sylvan plague in the western USA.
Bat	Pseudogymnoascus destructans	The white-nose epidemic of USA has rapidly spread throughout bat colonies with high morbidity and mortality
Domestic and wild birds	Avian influenza	Bird flu continues to pose a chronic threat to both domestic and wild species worldwide.
Cetaceans	Morbillivirus	Episodic outbreaks of morbillivirus in dolphins and other marine mammals affect species survival and remain unpredictable.
Primates	T-Cell Leukemia Virus	Diverse species are naturally infected in the wild with episodes of interspecies transmission driving viral evolution and global expansion.

Potential outcome to include peer-reviewed publications: Given the increasing scope of genomic tools in wildlife disease research, we envision the workshop will result in the publication of a special issue in journals such as Journal of Heredity or Frontiers in Ecology and Evolution. The workshop will help to address a current need for journals focused on the ecology, evolution and genomics of disease in wildlife.

Sponsors

Confirmed sponsors include Morris Animal Foundation, Biomatters (Geneious Software license for 30 workshop participants), Center for Species Survival-Smithsonian Conservation Biology Institute (Travel awards TBD), and CSU College of Veterinary Medicine and Biomedical Sciences.
Additional sponsorships are under development.