ᛚᚨᚤᛈᚻᚤᛚᚨᛒᛁᚤᚲ ᚢᚨᛏᚤᚲ᜔ᚨᛈ

ConGenOmics workshop

Uppsala Sweden 2014

Academic exercise or transition with real-world implications?

ᛈᚢᚱᚴᛈᚴᛟᚴᛋᚷᛟᚷᛈᛈᚴ

ConGenOmics workshop, Uppsala Sweden 2014

Welcome!

It is our pleasure to welcome you to the workshop *ConGenOmics: Academic Exercise or Transition with Real-World Implications.* Our venue in the beautiful Wiks slott and we hope that you will take full advantage of the history and nature offered here during the workshop.

In this packet you will find the schedule, list of participants, the PLoS Biology pre-proposal and a list of solicited propositions. We have an impressive list of invited speakers that will form the foundation for discussion in the working groups. The general themes we want to explore with this workshop are *scaling up* with genomic data — what have we / can we learn?, *what is possible* with new technology and methods, and *what is useful* in todays conservation climate. With any luck, we will produce a near complete manuscript by the end of the workshop that we are all coauthors on!

Again, we welcome you to Uppsala, Wiks slott, and the ConGenOmics workshop and look forward to three days of active discussion and developing new friendships and collaborations.

Your workshop organizers,

Jochen Wolf

Aaron Shafer

Start time	Monday	Tuesday	Wednesday		Thursday		Friday
09:00:00 AM		Bus to destination (pick up at CityStay Uppsala Hotel); check in at Wiks slott	**Session 2** Emerging and alternative approaches	J. Krause	**Session 4** Real world applications	M. Schwartz	**Bus return to Uppsala (~9:30 arrival time back in Uppsala with drop off at Uppsala Konsert & Kongress – Storgatan)**
				L. Dahlén		M. Bruford	
				J. McKay		R. Ogden	
				-		-	
10:00:00 AM		Fika (30 min)	Fika (30 min)		Fika (30 min)		
10:30:00 AM		Welcome to ConGenOmics	**Session 3** Emerging and alternative approaches	M. Hajibabaei	Working groups		
				C. Primmer			
				F. Reed			
				-			
12:00:00 PM	Arrivals in Uppsala	LUNCH	LUNCH		LUNCH		
01:00:00 PM		**Session 1** Extending conservation genetics	J. Hoglund	Nature walk / working groups	Working groups		
			R. Hoezel				
			J. Ouborg				
		Group and proposition selection					
03:00:00 PM		Fika (30 min)	Fika (30 min)		Fika (30 min)		
03:30:00 PM		Working groups	Working groups		<u>Final</u> working groups session		
05:00:00 PM		Plenary – progress and discussion	Plenary – progress and discussion		Wrap up & plenary discussion		
06:00:00 PM	Optional dinner at Katalin restaurant (Roslagsgatan 1)	**Dinner**	**Dinner**		**Dinner & live music**		
		Get to know your working group (social)	Working groups				
	Contacts: Aaron Shafer (+46 76 057 8013) Jochen Wolf (+46 70 478 8093)						
	***All events take place in the castle and breakfast is from 7:00 – 9:00						

I: Scaling-up: What have we learned / can we learn?
(GROUP 1 and 2)

The field of conservation genetics embraced the genomic revolution with the hope that the more traditional problems would be better resolved with genome-scale data. Now, more than a decade since the human genome was sequenced, genome-scale data is readily generated in non-model organisms of conservation relevance. Groups 1 and 2 will explore what genomic data has done for addressing the traditional conservation genetic problems that had been tackled with small-scale genetic approaches before (sensu Allendorf et al. 2010).

Problems:

- Estimation of effective population size, migration and selection
- Past demographic reconstruction
- Census population size estimation
- Neutral genetic variation vs. locally adaptive variation: predict ability of populations to react to environmental perturbation / assess adaptive potential
- Evolutionary Significant Units / management units / taxonomic delineation
- Predict viability of local populations: inbreeding depression / outbreeding depression / relatedness
- Assess admixture
- Minimize adaptation to captivity
- Marker assisted breeding / population restoration

Propositions:

"When does "conservation genetics" become "conservation genomics", and does it even matter?"

"How do we weigh the information from each gene in making management recommendations such as identification of management units?

"Landscape genetic structure is often likely strongly influenced by founder effects, serial colonization and isolation-by-adaptation. How does that influence our view on how to use population genomics data in conservation?"

"When defining units of conservation, we should consider two patterns of structure, and recognize that they may not coincide (neutral vs. Selective loci)"

"Can estimates of genome-wide heterozygosity, obtained through genomics, replace pedigrees in endangered populations?"

"How can we use genomics to asses whether losses in neutral genetic variation observed in small endangered populations also reflect the amount of selectively important variation that has been lost?"

"How can quantitative genetics be linked to conservation genomics?"

"Is local adaptation predictable and do we expect the frequency of alleles under local selection to differ from the genome-wide average?"

"Is adaptation due to an infinitesimal number of loci?"

"Haplotype information will signficantly help demographic reconstruction".

"Can domestication of wildlife lead to conservation? What are the genetic considerations?"

"Can we discovering how species are adapting to environmental change and should this be encouraged or discouraged in conservation application?"

II: Novel approaches: What are the possibilities?
(GROUP 3 and 4)

Next-generation technology and the expansion of 'omics' hold great potential for conservation. These developments also have created novel analytical approaches and relevant databases that can possibly inform conservation initiatives. Groups 3 and 4 will focus on identifying and evaluating what these novel approaches hold for conservation.

Technologies with potential:

- Ancient DNA to help in reconstruction of past demography (e.g. Bayesian skyline plots)
- Use of gene expression / proteomic studies
- Admixture and release of transposable elements
- Genetic engineering
- Epigenetic inheritance and variation
- Environmental DNA
- Metagenomics vs. barcoding to assess microbial biodiversity
- Conservation genetic / genomic databanks
- Metabolomics
- use of bioinformatic resources: conservation genomic databases

Propositions:

"Can we deduce anything on population viability from comparing past population size (estimates) to current population sizes?"

"Can we use genomic data to screen for deleterious or disease susceptible alleles and employ that in captive breeding programs?"

"Genomic technologies will still not answer all of the questions – conservation geneticists must be prepared to take risks."

"Do we need to account for epigenetic variation and parental effects"

"Can we genetically modify wild populations for conservation purposes?"

III. What is useful? Outreach, communication with stakeholders and cost-benefit considerations (GROUP 5 and 6)

Effective conservation requires an interdisciplinary effort along with collaboration among multiple stakeholders and organizations. The possibility of a *growing gap* between conservation genomics and conservation practitioners appears on the horizon: it is therefore important to be pragmatic and honest when genomics enters into real-world conservation. With the fields intended goal of conserving biodiversity, groups 5 and 6 will identify the most pressing conservation issues that can benefit from genomic data and discuss the general utility of genomic data for conservation.

Problems:

- Impact on conservation decisions
- Communication with stakeholders / pedagogics / outreach
- Cost-benefit considerations
- Legal considerations

"A road map for conservation – when do we need genomics?"

"With projected human population growth and continued loss of habitat, can genomics play a role with reserve design?"

"How much of conservation genomics is merely an academic exercise? And are we actively engaging with lawmakers and on the ground conservationists both before and after such studies?

"Given ever-growing issues over genome quality (and inferences), and the increasingly specialized training required to handle such data - how can the insights from genomics be put into conservation practice?"

"Genome sequencing of highly endangered species/populations: is it really money well spent?"

"Are there examples of genomics approaches being overkill, and can we come up with general guidelines about this point?"

"How much are we beyond "proof of principle" in linking genomes to adaptive evolution"

"There is a need for concerted efforts that integrate variation at different spatial scales"

"Is genomics being vastly oversold to the management community, and will there be backlash to this over-promising?"

"Will the ability to identify genes with known function, tempt or lead scientists and managers to make poor decisions in that they will sacrifice overall genetic diversity for a single gene that confers a specific advantage?"

"How would we use genomics to assist us when having to resort to assisted migration to protect organisms that are at the brink of extinction because of climate change?"

"Cost-benefit evaluation: Would it not often be justified to use funds going into genomic approaches for other purposes?"

"In analogy to ethical and biomedical problems (cloning, pre-natal diagnostic) can current laws accomodate findings from genomic studies appropriately?"

"Law enforcement: If we protect 'genes' instead of (sub-)species how can that be enforced? Field-based test would be necessary."

ᛕᛚ ᛉᛈᚻᚤᛚᛒᛁᛎᚳ ᚢᛚ ᛏᛉᚳᛝᛚᛈ

ConGenOmics workshop, Uppsala Sweden 2014

Notes: