

ConGen Data Analysis Course Program

CIBIO, Portugal, 9-14 September, 2008

Track 1	Lecture title
Track 2	Type of lecture
Track 3	Software explanation and use hands on
Track 4	Recommended readings (pdf's) available on course web site for participants
Track 5	Subject

TUESDAY, September 9, 2008

2:00 pm - 6:00 pm	Participants arrive. Registration & computer check for your laptop in the class room. Note: you should have downloaded all computer programs and data sets before class (see http://rastafa.icav.up.pt/congen2008/ & Logon & Password in your emails from ConGen).
6:00 pm - 9:00 pm	Dinner, barbeque, drinks & social time at the pool. Computer set up for your laptop.

WEDNESDAY, September 10, 2008

7:30 am - 8:00 am	Breakfast		
8:00 am - 8:10 am	Welcome address and course overview (Auditorium, ground floor): Albano Beja-Pereira & Gordon Luikart, Univ. of Porto & CIBIO, Portugal, and Univ. of Montana		
8:10 am - 10:00 am	Introduction to conservation genetics, and to data analysis (Auditorium, ground floor)		
8:10 am - 9:00 am	Keynote address: Fred Allendorf, Montana Conservation Genetics Lab, Univ. of Montana		
8:10 am - 9:00 am	The expanding role of genetics in conservation	Concepts / Overview	Chapter 1 from Allendorf & Luikart 2007 Chapter, Avise 2008
9:00 am - 10:00 am	Keynote address: Oscar Gaggiotti, University of Grenoble I, France		
9:00 am - 10:00 am	Frequentist, likelihood, & Bayesian approaches; the coalescent	Concepts / Background	Appendix 1 from Allendorf and Luikart 2007, Beaumont and Rannala 2004, Rosenberg and Nordborg 2002
10:00 am - 10:30 am	6 or 8 student introductions & presentations (2-4 minutes each, 2-4 power point slides)		
10:30 am - 10:45	Coffee/snack break		
10:45 pm - 12:30 pm	Data quality control, non-invasive DNA sampling, & population abundance estimation (classroom)		
10:45 pm - 12:30 pm	Keynote address: Mike Schwartz, US Forest Service, Missoula, USA		
10:45 pm - 12:30 pm	Data quality: Background concepts & overview	Concepts / Background	McKelvey & Schwartz 2004, JWM Schwartz & Monfort, 2008, Book Cptr.
10:45 pm - 12:30 pm	Genotyping errors, individual identification, & Introduction to population abundance estimation with non-invasive samples	Hands on	Drop-out McKelvey and Schwartz 2005, Mol. Ecol.
12:30 pm - 1:15 pm	Lunch		
1:30 pm - 3:00 pm	Effective population size estimation & approximate Bayesian methods		
1:30 pm - 3:00 pm	Keynote Address: David Tallmon, University of Alaska at Juneau, USA		
1:30 pm - 3:00 pm	N_e estimation and approximate Bayesian methods: Background & overview	Concepts / Background	Waples, 2005, Mol. Ecol. Tallmon et al. 2004, Genetics
1:30 pm - 3:00 pm	N_e estimation	Concepts / Hands on	OneSamp, LDNe Tallmon et al. 2008, Mol. Res. Waples & Do 2008, Mol. Res.
3:00 pm - 3:30 pm	Coffee/snack break		
3:30 pm - 4:30 pm	Detecting population bottlenecks		

	Keynote Address: Gordon Luikart			
3:30 pm - 4:30 pm	Bottlenecks: Background concepts & overview	Concepts / Background	Luikart and Cornuet 1998, Con. Biol. Williamson-Natesan 2005, Con. Gen. Beaumont 1999, Genetics	
	Bottleneck tests	Hands on	Bottleneck	Piry et al. 1999, J. Heredity
4:30 pm - 5:15 pm	15 Student introductions & presentations (2-4 minutes each, 2-4 power point slides)			
5:15 pm - 5:30	Robin Waples Introduces Data Analysis Exercises for Day 2 (EASYPop & STRUCTURE)			
5:30 pm - 6:00 pm	Free time to swim etc.			
6:00 pm - 6:45 pm	Dinner			
7:00 pm - 9:30... pm	Hands on data analysis & discussion with Allendorf, Gaggiotti, Luikart, Schwartz, Tallmon, & Waples. Students are encouraged to bring questions on their data, software, and statistical analyses. Students should have their data set formatted for software programs before arriving.			

THURSDAY, September 11, 2008

7:30 am - 8:00 am	Breakfast			
8:00 am - 9:30 am	DNA markers and new sequencing technologies (classroom)			
8:00 am - 9:30 am	Keynote address: Christian Schlotterer, DNA markers & new sequencing technologies			
	DNA markers, massively parallel sequencing, and their influence on population genetics	Concepts/ Background	Schlotterer 2004, Nat. Rev. Gen. Mardis 2008, TREE Ellegren 2008, Mol. Ecol.	
	Identification of SNPs in 454 sequence data	Hands on	PanGEA RC4	PanGEA RC4 Online manual
9:30 am - 11:00 am	Population structure, evolutionary significant units, and management units			
9:30 am - 11:00 am	Keynote Address: Robin Waples, US National Marine Fisheries Service, Seattle			
	Background concepts & overview	Concepts / Background	Waples and Gaggiotti 2006, Mol. Ecol. Evano et al. 2005, Mol. Ecol. Schwartz and McKelvey 2008, Con. Gen.	
	Population identification, detecting clusters	Theoretical & Hands on	Easypop Convert Structure	Pritchard & Wen, STRUCTURE User's Manual
11:00 am - 11:30 am	Coffee/snack break			
11:30 am - 12:30 pm	Landscape genetics, and spatially explicit approaches			
11:30 am - 12:30 pm	Keynote address: Gilles Guillot, French National Institute for Agricultural Research (INRA)			
	Landscape genetics and spatially explicit approaches	Concepts / Background	Guillot et al. 2005 Genetics Fontaine et al. 2007, BMC Biol. Coulon et al. 2006, Mol. Ecol.	
	Assessing substructure - spatilly explicit approaches	Hands on	GENELAND	Guillot et al. 2008, Bioinformatics
12:30 pm - 1:15 pm	Lunch			
1:30 pm - 2:30 pm	Continuation of Geneland with Gilles			
2:30 pm - 3:00 pm	Remaining 5-10 student introductions & presentations (3-4 minutes each)			
3:00 am - 3:15 am	Coffee/snack break			

3:15 pm - 5:00 pm	Hands on data analysis by Schlotterer, Guillot & Waples Students are invited to introduce questions on their data, software, and statistical analyses
5:00 pm - 10:00 pm	Boat cruise on the Douro River with DINNER & Port wine tasting

FRIDAY, September 12, 2008

7:30 am - 8:00 am	Breakfast			
8:30 am - 10:30 am	Combining genetic and demographic information to infer dispersal or colonization			
8:30 am - 10:30 am	Keynote address: Oscar Gaggiotti, University of Grenoble I, France			
	Dispersal & colonization: Background concepts & overview	Concepts / Background	Gaggiotti et al. 2002, Nature Foll and Gaggiotti 2006, Genetics	
	Estimating dispersal & colonization	Hands on	GESTE	Foll and Gaggiotti 2006, Genetics HelpGESTE1.rtf
10:30 am - 11:00 am	Coffee/snack break			
11:00 am - 12:30 pm	Migration rate estimation via direct (assignment test) and indirect (Fst) approaches			
11:00 am - 12:30 pm	Keynote address: Pierre Faubet, University of Grenoble I, France			
	Non-equilibrium approaches to estimate migration rates (Nm)	Concepts / Background	Wilson and Rannala 2003, Genetics Faubet and Gaggiotti 2008, Genetics	
	Estimating Nm	Hands on	BayesAss	Wilson and Rannala 2003, Gen. Faubet and Gaggiotti 2008, Gen.
12:30 pm - 1:15 pm	Lunch			
1:30 pm - 3:30 pm	Detecting selection: Fst-outliers, local adaptation and the genic model of speciation			
	Keynote address: Mark Beaumont University of Reading, UK			
	Selection & Fst outliers	Concepts / Background	Beaumont & Nichols 1996, Proc. Roy. Soc. Beaumont 2005, TREE	
	Detecting Fst outliers	Hands on	Fdist	Beaumont and Balding, 2004, Mol. Ecol.
3:30 pm - 4:00 pm	Coffee/snack break			
4:00 pm - 5:30 pm	Ranking populations for conservation			
4:00 pm - 5:30 pm	Keynote address: Miguel A. Toro, INIA, Madrid, Spain			
	Prioritizing populations/breeds for conservation	Concepts / Background	Toro 2008, Livestock Sci. Toro and Caballero 2005, Proc. Roy. Soc. Bonin et al. 2007, Con. Biol.	
	Ranking populations		METAPOP	In Press
6:00 pm - 7:00 pm	Dinner & final discussion among all instructors and participants Take home messages? Future needs and directions for conservation genetic data analysis?''			
7:30 pm - 9:00... pm	Hands on data analysis by Gaggiotti, Faubet, Beaumont, Toro Students are invited to introduce questions on their data, software, and statistical analyses			

SATURDAY, September 13, 2008

8:00 am - 9:00 am	Breakfast
9:00 pm - 12:00	Final hands on data analysis, review, & reflection with most instructors present
12:00 pm - 5:30 pm	Visit to a wildlife recovery center & LUNCH
6:00 - 6:40 pm	Dinner

SUNDAY, September 14, 2008

8:00 am - 9:00 am	Breakfast
Morning	All depart