

Introduction to Evolutionary biology for Infection biologists

12-13 May 2016

Leibniz-Institut für Zoo- und Wildtierforschung (IZW)
Alfred-Kowalke-Straße 17, 10315 Berlin



12 May 2016 morning : Evolutionary Ecology (Block 1)

9:00-10:05	1.Principles of evolutionary biology & population biology	Heribert Hofer direktor@izw-berlin.de
10:15-11:20	2.(theoretical) principles of host-pathogen interactions: co-evolution, virulence, ecological impact, evolutionary impact	Justyna Wolinska wolinska@igb-berlin.de
11:30-12:00	Practical link lead by a student	
	<i>Key insight: How do organismal and cellular perspectives differ, why are they both necessary for each other? The importance of variation.</i>	

12 May 2016 afternoon : Evolution & Phylogeny (Block 2)

13:00-14:00	1.Phylogeny and evolutionary trees	Joerns Fickel fickel@izw-berlin.de
14:10-15:10	2.Models for evolutionary trees & phylogenies: Maximum likelihood, maximum parsimony, Bayesian probabilities, phylodynamics...	Dino McMahon dino.mcmahon@fu-berlin.de
15:20-16:20	3.Bayesian phylogeography: A tutorial	Sibelle Vilaça vilaca@izw-berlin.de
16:20-16:40	Practical link lead by a student	
	<i>Key insight: How to better understand the classification methods and their interests, and how these methods can help us to better understand our pathogens of interest, their relationships with others, etc.</i>	

13 May 2016 morning : Population genetics and genomics, and evolution (Block 3)

9:00-10:00	1.Population genetics & its relevance to understand evolution	January Weiner january.weiner@mpiib-berlin.mpg.de
10:10-11:10	2.Neutral theory of evolution, signatures of selection, etc.	January Weiner
11:20-12:20	3.Genome evolution & Human genome evolution	January Weiner
12:20-12:40	Practical link lead by a student	
	<i>Key insights: Modeling populations underlying selection and genetic drift - is "beanbag" genetics still relevant? How do genomes evolve? Evolution as a tinkerer: innovation through duplication and sub-functionalization; 2R genome duplications. Why do we have such a large genome? Do humans evolve? Junk DNA & it is true that 80% of our genomes are under selection?</i>	

13 May 2016 afternoon : Technical issues on genomics & evolutionary theory (Block 4)

13:40-14:40	1.Technologies and bioinformatics method that enable biological conclusion to be drawn from large genome wide datasets	Emanuel Heitlinger emanuel.heitlinger@hu-berlin.de
14:50-15:50	2.Identification of episodes of positive selection in genome wide studies	Emanuel Heitlinger
16:00-16:20	Practical link lead by a student	
16:30-17:30	3.Perspective : Evolutionary theories in the concept of wildlife conservation	Bettina Wachter wachter@izw-berlin.de
	<i>Key insights: Which are the key challenges, and how can they be successfully overcome, to answering insightful research problems within an evolutionary genomics context?</i>	

Each part would be 45min lecture + 15min discussion + 10min coffee break
For more precise information, please send an email to: alice.balard@fu-berlin.de
For registration, please send an email to Silke Ehle at: ehle@izw-berlin.de