



GENERAL PROGRAM

(final)

PLEASE NOTE THAT

- Venues are indicated using the same 2-letter abbreviation indicated in the map you can find in the last page
- For each symposium, between 2 and 4 bidirectional streaming rooms will be available
- Rooms for the symposia will be indicated in the venues as follow:
 - City Theatre (CT). CT-M: main theatre hall; CT-R: streaming room
 - Polo Adelardi (AD1). AD-M1: main room, first floor; AD-A5, AD-A6, and AD-AP1: streaming rooms
 - Polo Adelardi (AD2). AD-M2: main room, second floor; AD-A9, AD-A10, and AD-AP2: streaming rooms
 - Palazzo Bevilacqua Costabili (BC). BC-M: main room; BC-EC4, BC-EC5, BC-EC6, BC-EC7: streaming rooms
- Plenary lecture will be held in CT, with streaming in AD and BC
- Posters will be on display at the following two venues:
 - San Paolo Cloisters (SP)
 - Estense Castle (EC)
- The society/journal/project events are indicated at the end of the main table (see below)
- All talks and evening events will be available in Gather Town

			PP Palazzo Pendaglia	MP Massari Park	SP San Paolo cloisters	EC Estense Castle	CT City Theater	AD1 Polo Adelardi, first floor	AD2 Polo Adelardi, second floor	BC Palazzo Bevilacqua Costabili
July 23	14:00	20:00				Registration				
	16:45	18:45				Welcome cocktail				
	19:00	20:00					Plenary Philip Donoghue	Plenary available in streaming	Plenary available in streaming	Plenary available in streaming
July 24	09:00	10:00					Plenary - Presidential Address Kateryna D. Makova	Plenary available in streaming	Plenary available in streaming	Plenary available in streaming
	10:00	10:30					Coffee break			
	10:30	12:30					15 - Animal genomics goes wild	6 - Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict	13 - Polygenic Adaptation – Predictability and Pleiotropy	23 - Evolutionary approaches to understand cancer across scales
	12:30	13:30	Lunch break (starting 12:00)					<u>Event</u> : Scientist Rebellion 1 (AD-A1) <u>Event</u> : MBE&GBE Meet the Editors (AD-A2) Commercial talk: Royal Publishing (AD-A11). Tips from the Royal Society for promoting your published work		
	13:30	15:30					15 - Animal genomics goes wild	20 - Evolutionary biology through a functional genomics lens	22 - Experimental evolution of non model species and systems	24 - Indels: computational methods, evolutionary dynamics, and biological applications
	15:30	16:00					Coffee break			
	16:00	18:00					1 - Open symposium	1 - Open symposium	1 - Open symposium	1 - Open symposium

			PP Palazzo Pendaglia	MP Massari Park	SP San Paolo cloisters	EC Estense Castle	CT City Theater	AD1 Polo Adelardi, first floor	AD2 Polo Adelardi, second floor	BC Palazzo Bevilacqua Costabili
	18:00	20:00			Poster session 1 (with refreshment)			Event: ERGA1 (AD-A1). 19:00-20:00		
	20:45	22:15					Round table: Why publishing a scientific paper is becoming so expensive?			
July 25	09:00	10:00					Plenary Emilia Huerta-Sanchez	Plenary available in streaming	Plenary available in streaming	Plenary available in streaming
	10:00	10:30					Coffee break			
	10:30	12:30					Graduate Student Excellence Awards	GSEA in streaming	GSEA in streaming	GSEA in streaming
	12:30	13:30	Lunch break (starting 12:00)					Event: Doing Research in Italy: a field guide (AD-AD1) Commercial talk: IgaTech (AD-A11). All in one: structural, nucleotide, and epigenetic variations via ultra-long nanopore reads with phase information		
	13:30	15:30					7 - Computational evolutionary genomics in the era of machine learning	27 - Regulatory evolution and the emergence of diversity	11 - Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics	21 - Science for everybody: education and outreach in Molecular Biology and Evolution
	15:30	16:00					Coffee break			
	16:00	18:00					7 - Computational evolutionary genomics in the era of machine learning	27 - Regulatory evolution and the emergence of diversity	28 - Host-pathogen co- evolutionary dynamics through the lens of paleogenomics	29 - Leveraging evolution: controlling wild populations using gene drives and pathogens
	18:00	20:00			Poster session 2 (with refreshment)			Event: ERGA2 (AD-A1). 19:00-20:00		

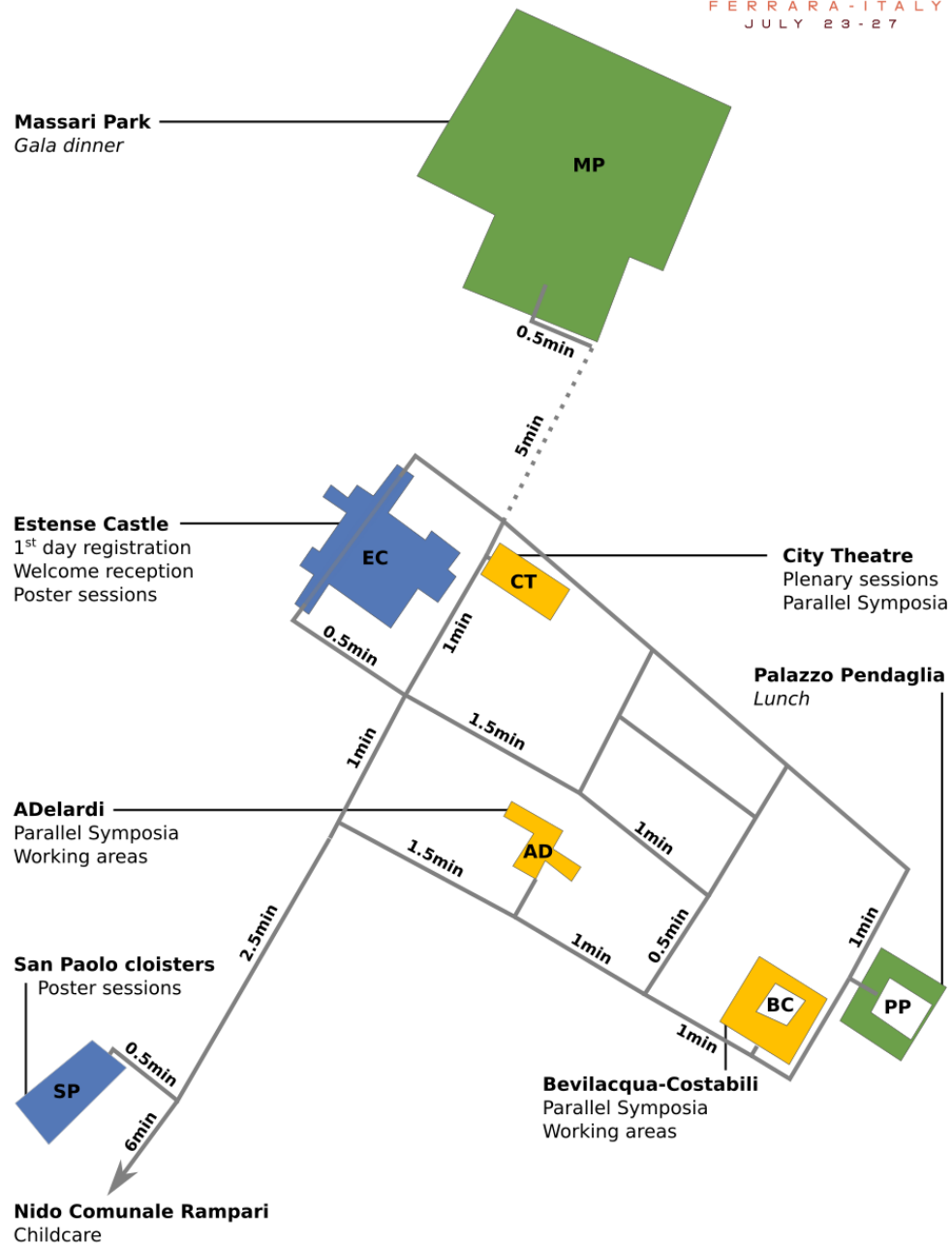
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	20:00	20:30					<u>Refreshment before the celebration</u>			
	20:45	22:15					<u>Celebration: Celebrating Nei life and legacy</u>			
July 26	9:00	11:00					19 - Evolution of structural genomic variation in populations & species	5 - New frontiers in conservation genomics (dedicated to Mike&Bob)	10 - Integrating fossils and molecules to reconstruct the evolution of life in deep time	30 – IDEA symposium
	11:00	11:30					Coffee break			
	11:30	13:30					19 - Evolution of structural genomic variation in populations & species	3 - The dark side of introgression	14 - Novel proteins and their emergence from LUCA until today	30 – IDEA symposium
	13:30	14:30	Lunch break (starting 12:00)					<u>Event: Scientist Rebellion 2 (AD-A1)</u> <u>Event: SMBE Business meeting (AD-A2)</u> <u>Celebration: Bob Wayne and Mike Bruford legacies (AD-A12)</u>		
	14:30	16:30					16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	31 - Causation in protein evolution	18 - Modeling the genomic, social, and ecological drivers of speciation	17 - Roles and evolution of oxygen sensing across kingdoms
	16:30	17:00					Coffee break			

			PP Palazzo Pendaglia	MP Massari Park	SP San Paolo cloisters	EC Estense Castle	CT City Theater	AD1 Polo Adelardi, first floor	AD2 Polo Adelardi, second floor	BC Palazzo Bevilacqua Costabili
	17:00	19:00					16 - From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology	12 - Evolution of sensory systems	4 - Origins, evolution and ecology of microbial hopeful monsters	2 - Editors symposium
	20:00			Gala Dinner						
	9:30	11:30					26 - Genomics of adaptations to extreme environments	9 - Evolution on repeat in the genomics era	8 - Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution	25 - The puzzle of eukaryotic cellular origins
July 27	11:30	12:15					Brunch			
	12:15	13:15					Plenary Michael Lynch	Plenary available in streaming	Plenary available in streaming	Plenary available in streaming
	13:15	14:30					Awards Ceremony and Introduction to SMBE 2024			

SOCIETY/JOURNAL/PROJECT MEETINGS:

- July 23, 8:00-19:00. SMBE Council Meeting. Where: CT-SP1
- July 24, 10:00-11:00. GEVOL-DFG meeting. Where: AD-A3
- July 24, 10:00-13:30. Heredity Editors meeting. Where: AD-AP3
- July 24, 18:00-19:00. GBE Editors meeting. Where: AD-A3
- July 25, 18:00-19:00. MBE Editors meeting. Where: AD-A3

Urban Diffused Meeting





PROGRAM OF TALKS

(final)

PLEASE NOTE THAT

- Five minutes of musical interval will play between talks as you take a moment to relax or move to other venues; the only exception are a few consecutive flash talks in uninterrupted succession.
- A sound will indicate the beginning of the question time (between 2 and 5 minutes depending on the talk duration)
- Time intervals will be strictly enforced by the automatic system and by the chairs

23 July

14:00-18:45 **Registration and Welcome Cocktail**

Plenary Lecture (CT; streaming in AD1, AD2, and BC)

19:00-20:00 Philip Donoghue Telling evolutionary time

24 July

Plenary Lecture - Presidential Address (CT; streaming in AD1, AD2, and BC)

9:00-10:00 Kateryna D. Makova Telomere-to-telomere assemblies uncover secrets of ape sex chromosomes

COFFEE BREAK

15- Animal genomics goes wild (CT)

10:30 - 10:55	Susan Johnston	Sexual dimorphism in recombination rates & landscapes in wild vertebrates.
11:00 - 11:15	Harrison Ostridge	Local genetic adaptation in wild chimpanzees
11:20 - 11:35	Craig Primmer	Beyond GWAS: Complex mechanisms underlie the simple genomic architecture of Atlantic salmon age at maturity
11:40 - 11:55	Angela Fuentes-Pardo	Genomic adaptations in Atlantic herring to past, present, and future climate
12:00 - 12:12	Flávia Fernandes	Late but good: genomic and plastic signals of adaptive mismatch in a long-lived sub-Antarctic species
12:12 - 12:24	Pierre Lesturgie	Size matters: how a chromosomal inversion determining size shaped the demographic history of a chondrichthyan species (<i>Amblyraja radiata</i>)

6- Molecular Evolutionary Patterns under Sex-Dependent Selection and Sexual Conflict (AD1)

10:30 - 10:55	Manyuan Long	Sexual conflict drive in new gene evolution
11:00 - 11:15	Cristina Berenguer Millanes	Effect of inversion size on recombination landscape, and its impact on selection for recombination suppression in the early stages of sex chromosome evolution
11:20 - 11:35	Daniel Shaw	Single-cell gene expression of spermatogenesis reveals evolution of post-meiotic gene repression and activation of amplicons on the threespine stickleback fish Y chromosome
11:40 - 11:55	Iulia Darolti	The genomic architecture of sex-specific adaptation in stick insects
12:00 - 12:25	Max Reuter	Sexually antagonistic genetic variation in <i>Drosophila melanogaster</i>

13- Polygenic Adaptation – Predictability and Pleiotropy (AD2)

10:30 - 10:55	Daniel Ortiz-Barrientos	A systems view of polygenic adaptation in an Australian wildflower
11:00 - 11:15	Frederic Guillaume	Predictability of gene expression evolution during climate adaptation
11:20 - 11:35	Grant Kinsler	Phenotypic and evolutionary properties of large-effect adaptive mutations isolated from a two-step adaptive walk
11:40 - 11:55	Isabela do O	The evolution of genetic covariance and modularity as a result of multigenerational environmental fluctuations
12:00 - 12:25	Jacqueline Sztepanacz	The role of pleiotropy in generating evolutionary limits

23- Evolutionary approaches to understand cancer across scales (BC)

10:30 - 10:55	Ivana Bozic	Evolutionary dynamics of tumor progression
11:00 - 11:15	Brian Johnson	Estimating clonal dynamics in human blood using coalescent theory
11:20 - 11:35	Elisa Scanu	A mathematical model in evolutionary medicine: ecDNA dynamics
11:40 - 11:55	Jorge Alfaro-Murillo	Detecting pairwise and higher-order epistatic effects among somatic cancer mutations across oncogenesis
12:00 - 12:25	Alexander Cagan	The impossibility of whales: somatic mutation across the tree of life

LUNCH BREAK

15- Animal genomics goes wild (CT)

13:30 - 13:55	Michael Westbury	Arctic marine mammals in a changing environment
14:00 - 14:15	Patricia Pecnerova	STAMPEDE: Spatial and Temporal Analysis of Modern and Past Elephant Diversity
14:20 - 14:35	Xenia Wietlisbach	1000 full genomes of Darwin's finches reveal polygenic architecture of both beak morphology and individual fitness
14:40 - 14:55	Lara Urban	A ghost of past selection: the evolution and conservation relevance of colour polymorphism in the critically endangered kākāpō
15:00 - 15:12	Xuejing Wang	Islands of selective sweep in an ocean of genetic drift: genome-wide relaxation of selection of a big insular rodent
15:12 - 15:24	Jonas Oppenheimer	Evolutionary history of bison revealed through ancient DNA

20- Evolutionary biology through a functional genomics lens (AD1)

13:30 - 13:55	Genevieve Housman	Cell culture systems to interrogate primate skeletal functional genomics
14:00 - 14:15	Alessandro Raveane	The influence of ancient ancestries on the immunological landscape of present-day Europeans
14:20 - 14:35	Andres Bendesky	Genetic causes and phenotypic consequences of a newly evolved adrenal cell type
14:40 - 14:55	Malgorzata Gazda	Evolution of the uterine epithelium in model mammals
15:00 - 15:25	Steven Reilley	The functional and evolutionary impacts of human-specific deletions in conserved elements

22- Experimental evolution of non-model species and systems (AD2)

13:30 - 13:55	Vaughn Cooper	Adaptation to overflow metabolism by mutations that impair tRNA modification in experimentally evolved bacteria
14:00 - 14:15	Yu-Ying (Phoebe) Hsieh	Fungal-mediated magnesium competition shapes bacterial fitness and the evolution of antibiotic resistance
14:20 - 14:35	Jan Engelstädter	The impact of natural transformation on adaptation to heterogeneous environments
14:40 - 14:55	William DeWitt	Evolutionary dynamics of antibody affinity maturation in replica germinal centers
15:00 - 15:25	Britt Koskella	Experimental evolution from populations to communities

24- Indels: computational methods, evolutionary dynamics, and biological applications (BC)

13:30 - 13:55	Gerton Lunter	The impact of indels on bioinformatics, health, and evolution
14:00 - 14:15	Jülija Pečerska	Polynomial-time frequentist joint alignment and tree inference
14:20 - 14:35	Ian Holmes	Hidden Markov model generators of indel processes
14:40 - 14:55	Guillaume Beslon	Spontaneous regulation of non-coding sequences in bacteria through border effect duplications neutral bias
15:00 - 15:25	Benjamin Redelings	Indels, rate variation, and heterotachy

COFFEE BREAK

Open symposium (CT)

16:00 - 16:15	Siliang Song	Adaptive tracking generates quasi-neutral molecular evolution
16:20 - 16:35	Jennifer James	Within and between species variation in the distribution of fitness effects
16:40 - 16:55	Alessio Iannucci	Genome size evolution in squamate reptiles is influenced by ecological factors and parity mode
17:00 - 17:15	Karen Siu-Ting	How to become poisonous and avoid dying in the attempt: Investigating molecular adaptations in neotropical poison frogs
17:20 - 17:35	Christopher Wheat	miRNA targets: non-model species, false-positives, and functional coherence
17:40 - 17:55	Andrew Clark	Are expression levels of homologous alleles independent of each other?

Open symposium (AD1)

16:00 - 16:15	Eric Baptiste	Interactomics: dozens of viruses, co-evolving with humans, including the influenza A virus, may actively distort human aging
16:20 - 16:35	Jiansi Gao	Model misspecification misleads inference of the spatial dynamics of disease outbreaks
16:40 - 16:55	Eva Šatović Vukšić	Bivalves disclose novel pattern of satellite DNA organization, highly dispersed and closely connected to Helitron mobile elements
17:00 - 17:15	Esther Betran	Recurrent co-domestication of PIF/Harbinger transposable element proteins in insects
17:20 - 17:35	Alba Marino	Effective population size does not explain transposable elements and genome size variation in animals
17:40 - 17:55	Murillo Rodrigues	Shared evolutionary processes shape landscapes of genomic variation in the great apes

Open symposium (AD2)

16:00 - 16:15	Muthukumaran Panchaksaram	Bayesian clock model selection to distinguish evolutionary rate variation models for divergence time estimation
16:20 - 16:35	Nicolas Galtier	Distinguishing gene flow from incomplete lineage sorting via branch length analysis
16:40 - 16:55	Marta Álvarez-Presas	Assessing the origin of Bilateria with new genomic methods
17:00 - 17:15	Luca Ferretti	Trees grow while you aren't looking: an artefactual correlation of branch lengths with sample size in reconstruction of large phylogenies
17:20 - 17:35	Zachary Szpiech	Scanning for selection in unphased data
17:40 - 17:55	Georgette Femerling	Testing for ancestral population structure in demographic models using linkage disequilibrium statistics

Open symposium (BC)

16:00 - 16:15	Lara R Arauna	Biological relatedness and social structure in an ancient Oceanian population
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16:20 - 16:35	Aida Andrés	The genetics and anatomy of face evolution in humans and other primates
16:40 - 16:55	Parul Johri	Developing an evolutionary baseline model for humans: jointly inferring purifying selection with population history
17:00 - 17:15	Hanaïsa Sant'Anna	History of Sex-Biased Admixture: new method and insights on mating behavior in Brazil
17:20 - 17:35	Flávia Schlichta	How does genetic surfing impact genomic diversity? Predictions and applications to human genomes
17:40 - 17:55	Benjamin Vernot	The Dog in my Data: faunal aDNA that maps to the human genome
18:00-20:00	Poster session 1 (SP and EC)	

25 July

Plenary Lecture (CT; streaming in AD1, AD2, and BC)

9:00-10:00	Emilia Huerta-Sanchez	Archaic and modern humans: an evolutionary history of recurrent introgression and natural selection
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COFFEE BREAK

Graduate Student Excellence Awards (CT; streaming in AD1, AD2, and BC)

10:30 - 10:43	Matteo Sebastianelli	Genome-wide association study reveals the polygenic nature of rhythm in a wild non-passerine bird
10:43 - 10:56	Aurora Alvarez-Buylla	Dealing with a deadly diet: toxin binding proteins in poison frogs
10:56 - 11:09	Harvinder Pawar	Ghost admixture in eastern gorillas
11:09 - 11:22	Carmina Barberena-Jonas	Analyzing IBD segments in the MX Biobank to track the genetic structure of Mexico through time
11:22 - 11:35	Ujani Hazra	Differences in disease burdens across human populations are governed more by neutral evolution than by recent polygenic selection
11:35 - 11:48	Margaux Aubel	Comparing de novo emerged proteins with their unevolved random-sequence counterparts
11:48 - 12:01	Marianne Dehasque	Temporal dynamics of woolly mammoth genome erosion prior to extinction
12:01 - 12:14	Carlos Cortez	Simple mechanisms for the evolution of heterospecificity in the hemoglobin complex
12:14 - 12:27	Kai Yan	Modification of maternally defined H3K4me3 regulates the inviability of interspecific <i>Xenopus</i> hybrids

LUNCH BREAK

7- Computational evolutionary genomics in the era of machine learning (CT)

13:30 - 13:55	Sohini Ramachandran	Interpretable models for complex trait architecture via learning from population genetic datasets
14:00 - 14:15	Santiago Medina-Muñoz	Demographic modeling of admixed latin american populations from whole genomes
14:20 - 14:35	Luca Nesterenko	Phyloformer: towards fast and accurate phylogeny estimation with self-attention networks
14:40 - 14:55	Alex Mas-Sandoval	The genomic footprint of social stratification in admixing American populations
15:00 - 15:12	Cai Li	A generalizable deep learning framework for inferring fine-scale germline mutation rate maps
15:12 - 15:24	Letizia Lamperti	Using transformers to relate DNA sequence composition from eDNA to ecosystem properties

27- Regulatory evolution and the emergence of diversity (AD1)

13:30 - 13:55	Patricia J. Wittkopp	Evolutionary changes in gene regulatory networks inferred from patterns of co-expression
14:00 - 14:15	Thea Rogers	Novel regulatory units underlie the evolution of complex traits in coleoid cephalopods
14:20 - 14:35	Nataša Puzović	Make all the right noises: the evolution of gene expression mean and expression noise in changing environments is constrained by the gene position in the gene regulatory network
14:40 - 14:55	Antoine Fages	A single-cell perspective on the role of gene expression regulation in promoting ecological and dietary adaptations in Lake Tanganyika cichlid fishes
15:00 - 15:08	Riccardo Papa	High level of novelty under the hood of convergent evolution
15:08 - 15:16	Sandra Goutte	Regulatory variation leads to striking color polymorphism in a grass frog
15:16 - 15:24	Amanda Glaser-Schmitt	Population- and developmental stage-specific gene regulation in <i>Drosophila melanogaster</i>

11- Entangled histories: insights into the evolution of humans and their domesticates through paleogenomics (AD2)

13:30 - 13:55	Victoria Mullin	Ten thousand years of cattle human interaction
14:00 - 14:15	Torsten Günther	the impact of human actions and wild introgression in the history of domestic cattle on the Iberian Peninsula
14:20 - 14:35	Elisabetta Canteri	An interdisciplinary analysis of the drivers and consequences of human mobility changes during the West Eurasian Holocene

14:40 - 14:55	Audrey Lin	Integrating genomics and Indigenous knowledge to illuminate the life, history, and loss of Coast Salish woolly dogs
15:00 - 15:25	Anders Bergström	The entangled genomic histories of humans and dogs

21- Science for everybody: education and outreach in Molecular Biology and Evolution (BC)

13:30 - 13:55	Laura MacDonald	Facilitating the inclusive classroom: building meaningful connections with and between students
14:00 - 14:15	Natasha Glover	Bringing science to the public in the light of evolution
14:20 - 14:35	Elaine Guevara	Teaching and outreach to broaden engagement and combat harmful misconceptions in human evolutionary genetics
14:40 - 14:55	Akos Dobay	How to teach computational biology to biologists and biomedical students
15:00 - 15:25	Natalia Pasternak Taschner	Supporting science is not the same as understanding science: teaching critical thinking for science-based policies

COFFEE BREAK

7- Computational evolutionary genomics in the era of machine learning (CT)

16:00 - 16:25	Yun Song	Advances in learning complex evolutionary constraints and predicting variant effects
16:30 - 16:45	M. Elise Lauterbur	Versatile detection of diverse selective sweeps in model and non-model organisms with flex-sweep
16:50 - 17:05	Erin Gilbertson	Using machine learning to predict 3D genome organization across thousands of diverse individuals reveals conservation and population differentiation.
17:10 - 17:25	Elias Dohmen	Resolving deep phylogenetic conflicts with deep learning
17:30 - 17:42	Burak Yelmen	Deep convolutional and conditional neural networks for large-scale genomic data generation
17:42 - 17:54	Ziyi Mo	Domain-adaptive neural networks improve supervised machine learning based on simulated population genetic data

27- Regulatory evolution and the emergence of diversity (AD1)

16:00 - 16:25	Tarang K. Mehta	Regulatory networks evolution underlying the rapid diversification of cichlids fishes in the Great African Lakes
16:30 - 16:45	Quentin Horta-Lacueva	Evolution of canalization: lessons from gene expression in an extreme case of divergence, the Arctic charr of Thingvallavatn.
16:50 - 17:05	Attila Placido Sachslehner	Hoxc13-dependent regulation of keratin genes facilitated the evolution of cornified claws and hair in terrestrial vertebrates
17:10 - 17:25	Fabricio Almeida-Silva	The impact of whole-genome duplications in the topology of angiosperm gene regulatory networks
17:30 - 17:38	Pamela Espíndola Hernandez	Signals of accelerated evolution in regulatory regions are linked to the emergence of diurnality in owls
17:38 - 17:46	Matthew Goulty	Evolution of monoaminergic cell types
17:46 - 17:54	Vincent Castric	Molecular control of dominance/recessivity interactions between self-incompatibility alleles in <i>Arabidopsis</i>

28- Host-pathogen co-evolutionary dynamics through the lens of paleogenomics (AD2)

16:00 - 16:25	Gaspard Kerner	A time-series aDNA approach detects genetic adaptation to pathogens in post-Neolithic Europe
16:30 - 16:45	Iseult Jackson	Contrasting evolutionary and adaptive histories revealed for three oral pathobionts recovered from Bronze Age Irish remains
16:50 - 17:05	Michael Dannemann	Defend and adapt: the evolutionary impact on the genetics of the human immune response
17:10 - 17:25	Onur Özer	Spatio-temporal analysis of ancient HLA data reveals major effects of demography and admixture on immune gene diversity
17:30 - 17:55	Maria A. Spyrou	Investigating the genomic history of plague, from the Neolithic to the present

29- Leveraging evolution: controlling wild populations using gene drives and pathogens (BC)

16:00 - 16:25	Florence Débarre	Spatial structure and demographic feedbacks affect the spread of a gene drive
16:30 - 16:45	Nicky Faber	A two-target gene drive improves suppressive power when drive conversion is inefficient
16:50 - 17:05	Josh Reynolds	Exploring the potential of rare variants to help parameterise models of gene drive in <i>Anopheles gambiae</i> mosquitoes
17:10 - 17:25	Wenfeng Qian	CRISPR-mediated toxin-antidote system subverts mendelian inheritance in <i>Arabidopsis</i>
17:30 - 17:55	Paul Thomas	Using synthetic and natural gene drives for feral rodent population suppression

18:00-20:00 Poster session 2 (SP and EC)

19- Evolution of structural genomic variation in populations & species (CT)

9:00 - 9:25	Scott Edwards	Pangenomes of Scrub-Jays (<i>Apelocoma</i>) reveal abundant structural variation and rapid shifts in the landscape of satellite DNA
9:30 - 9:45	Aurora Ruiz-Herrera	Unveiling patterns of 3D chromatin folding across the mammalian phylogeny - insights into genome evolution
9:50 - 10:05	William Murphy	Single-haplotype comparative genomics resolves the role of structural innovations during cat speciation.
10:10 - 10:25	Carina Mugal	The combination of HiFi and HiC sequencing technologies enables the investigation of structural variants in speciation of <i>Ficedula</i> flycatchers
10:30 - 10:38	Alexander Mackintosh	Have chromosome fusions in <i>Brenthis</i> butterflies evolved by positive natural selection?
10:38 - 10:46	Valentina Peona	Structural variation evolution during hybridisation in wheatears
10:46 - 10:54	Rishi De-Kayne	Evolutionary dynamics of a modular supergene in the African monarch butterfly (<i>Danaus chrysippus</i>)

5- New frontiers in conservation genomics (AD1)

9:00 - 9:25	Katerina Guschanski	Metagenomics of population declines in Scandinavian Brown Bears
9:30 - 9:45	Emily Patterson	Combating illegal trade in animal products by rapid on-site DNA sequencing
9:50 - 10:05	Nicolas Alexandre	The High Stakes of Low Diversity – Predicting population-specific genomic consequences of dispersal barriers and inbreeding in California Mountain Lions
10:10 - 10:25	Christopher Kyriazis	Using computational simulations to model deleterious variation and genetic load in natural populations
10:30 - 10:55	Moises Exposito-Alonso	The population genetics of species range contraction in the Anthropocene

10- Integrating fossils and molecules to reconstruct the evolution of life in deep time (AD2)

9:00 - 9:25	Joanna Wolfe	The challenge and promise of integrating genomics and fossils in deep time phenotypic evolution
9:30 - 9:45	Giulia Campli	Tracing the evolutionary history of moulting genes across arthropod diversity
9:50 - 10:05	Eduard Ocaña-Pallarès	A fungal tree of life dated with fossil and horizontal gene transfer data
10:10 - 10:25	Maria Eleonora Rossi	Independent origins of spicules help disentangle the evolutionary history of sponges (Porifera)
10:30 - 10:55	Jeffrey Thompson	Using fossils, genes, and developmental biology to understand the evolution of Echinozoan body plans

30- IDEA symposium (BC)

9:00 - 9:25	C. Eduardo G. Amorim	SMBE IDEA Taskforce: achievements and future plans for inclusion, diversity, equity, and access
9:30 - 9:45	Sergio González-Mollinedo	The EvoBio Crash Course: a student-led project to bridge the knowledge gaps with the global south in evolutionary biology
9:50 - 10:05	Paula Adams	The inclusion of societally relevant concepts in biology education combats student misconceptions of science
10:10 - 10:25	Melinda Yang	Increasing accessibility to molecular biology and evolutionary concepts in an introductory biology classroom using a collaborative course-based undergraduate research experience through the genomics education partnership
10:30 - 10:55	Sadye Paez	Beyond absolutes: justice, equity, diversity, inclusion in the Earth BioGenome Project

COFFEE BREAK

19- Evolution of structural genomic variation in populations & species (CT)

11:30 - 11:55	Sissel Jentoff	The evolutionary role of genomic architectures in marine fishes
12:00 - 12:15	Tobias Lenz	Evolution of intra-specific copy-number-variation in the MHC and its role in local adaptation
12:20 - 12:35	Wesley Warren	Adaptation to extreme ecological change with structural variation in a cave-dwelling fish
12:40 - 12:55	Tuomas Hämälä	Impact of whole-genome duplications on structural variant evolution
13:00 - 13:08	Bohao Fang	Multiple long-read de novo assemblies of House Finches enable pangenome analysis of structural variants
13:08 - 13:16	Mafalda Sousa Ferreira	Old supergenes underly temperature adaptation in Atlantic herring
13:16 - 13:24	Kimberly Gilbert	Signatures of local adaptation within genomic inversions

3- The dark side of introgression (AD1)

11:30 - 11:55	Molly Schumer	The evolutionary origin of hybrid incompatibilities: insights from swordtail fish
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12:00 - 12:15	Juliette de Meaux	Interspecies introgression in low diversity endangered species: hybrid breakdown or potential for a supergenotype?
12:20 - 12:35	Mozes Blom	The genomic consequences of recurring hybridization between lekking Birds-of-Paradise species
12:40 - 12:55	Arielle Fogel	Assortative mating and offspring viability shape introgression along baboon hybrid genomes
13:00 - 13:25	James Mallet	Extraordinary case of hybrid speciation and ongoing introgression in the Amazon

14- Novel proteins and their emergence from LUCA until today (AD2)

11:30 - 11:55	Klara Hlouchova	Early proteins: could they do without all 20?
12:00 - 12:15	Arianne Babina	Investigating the de novo origins of small protein-coding genes: rescuing an <i>E. coli</i> auxotroph with novel proteins selected from random sequence
12:20 - 12:35	Lars Eicholt	From de novo a beginning - Identifying structures and activities of de novo proteins
12:40 - 12:55	David Rinker	No homologs? No problem! Functional characterization of de novo genes through alignment-free protein structure prediction.
13:00 - 13:25	Richard Goldstein	Principles of protein evolution from a biophysical perspective

30- IDEA symposium (BC)

11:30 - 11:55	Sarah Bay	Approaching diversity, equity, and inclusion as a scientific society: lessons learned at GSA
12:00 - 12:15	Joanna L. Kelley	Making connections across continents: virtual lab meeting training program
12:20 - 13:30	General Discussion	

LUNCH BREAK

16- From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology (CT)

14:30 - 14:55	Vincent Buffalo	The case for conducting a thousand more temporal genomics studies
15:00 - 15:15	Alexis Simon	The contribution of admixture, selection, and genetic drift to four thousand years of human allele frequency change
15:20 - 15:35	Olivia Johnson	The population genetic signatures of temporally fluctuating selection.
15:40 - 15:55	Benjamin Blackman	Sunflower domestication in space and time
16:00 - 16:08	Yilei Huang	Estimating population size trajectories with IBD time transect
16:08 - 16:16	Kwi Young Han	Looking for the smoking gun of fisheries induced selection using temporal genomic data
16:16 - 16:24	Johanna Pieplow	Long-term genomic consequences of thelytokous reproduction in the Cape Honeybee <i>Apis mellifera capensis</i>

31- Causation in protein evolution (AD1)

14:30 - 14:55	Joanna Masel	Birth, death and tinkering: levels of proteome selection at different timescales
15:00 - 15:15	David Liberles	A statistical analysis of clusters of amino acid substitutions to compare compensatory processes with directional selection
15:20 - 15:35	Jia Zheng	Lowered temperature accelerates Darwinian evolution
15:40 - 15:55	Claud��le Lemay-St-Denis	Adventitious catalytic activity promotes the emergence of a thermostable SH3 fold as a powerful antimicrobial resistance mechanism
16:00 - 16:25	Joseph Thornton	The epistatic architecture of proteins is simple, and it facilitates functional evolution

18- Modeling the genomic, social, and ecological drivers of speciation (AD2)

14:30 - 14:55	Guojie Zhang	Incomplete lineage sorting drove the phenotypic evolution in marsupials
15:00 - 15:15	Zhe Xue	Detecting environmental drivers of leopards speciation
15:20 - 15:35	Dabao Lu	Reticulate evolution and rapid development of reproductive barriers upon secondary contact pose challenges for species delineation in a forest fungus
15:40 - 15:55	Nicole Creanza	The interactions between socially learned song and speciation in songbirds
16:00 - 16:25	Tomas Marques-Bonet	A global primate sequencing initiative: lessons from conservation, evolution and speciation

17- Roles and evolution of oxygen sensing across kingdoms (BC)

14:30 - 14:55	Emily Flashman	CysteinyI dioxygenases: a molecular view of their role in oxygen sensing in plants, animals and evolution
15:00 - 15:15	Olivia Gray	Exploring Tibetan adaptations to high altitude hypoxia through functional genomics: insights from iPSC-based approaches
15:20 - 15:35	Noam Shtolz	Hypoxia shifts the mtDNA transcriptional pattern and alters mito-nuclear regulatory coordination

15:40 - 15:55	Laura Dalle Carbonare	Defining the molecular basis for the acquisition of a unique oxygen-sensing mechanism in vascular plants
16:00 - 16:25	Pierdomenico Perata	The many facets of hypoxia in plants

COFFEE BREAK

16- From the ancient to the recent: using temporal genomics to answer questions in evolutionary biology (CT)

17:00 - 17:25	Leo Speidel	Zooming in on the ancient world with genealogy-boosted analyses of ancient DNA
17:30 - 17:45	Adam Andrews	Using ancient genomes to investigate responses to climate and anthropogenic impacts in the Atlantic bluefin tuna
17:50 - 18:05	Jan Laine	Ancient stickleback environmental genomes track adaptation across ecological transitions
18:10 - 18:25	Alexander Salis	Best-practice historical DNA extraction from formalin-fixed museum specimens
18:30 - 18:38	Lucas Anchieri	Assessing ancient DNA sampling strategies for natural selection inference with time-series data
18:38 - 18:46	Leonardo Iasi	The evolution of introgressed Neandertal segments through space and time: Insights from ancient and present-day human genomes
18:46 - 18:54	Xinyi Li	A new model-based method obtains less biased estimates of the selection coefficient while controlling for migration using aDNA

12- Evolution of sensory systems (AD1)

17:00 - 17:25	Marjorie Liénard	The evolution and function of insect visual opsins
17:30 - 17:45	Wendy Andrea Valencia-Montoya	Evolution of sensory receptors in octopus and squid
17:50 - 18:05	Maxime Policarpo	Highly dynamic evolution of chemoreceptor genes in Vertebrates
18:10 - 18:25	Alexander Van Nynatten	Adaptive evolution of Nearctic deepwater fish vision: a novel metabarcoding approach to monitor functional variation for conservation
18:30 - 18:55	Thomas Auer	<i>Drosophila sechellia</i> : a model for chemosensory system evolution

4- Origins, evolution and ecology of microbial hopeful monsters (AD2)

17:00 - 17:25	Gregorio Iraola	<i>Campylobacter fetus</i> : hopefully jumping through hosts and continents
17:30 - 17:45	Talia Karasov	A weaponized phage suppresses competitors in a metapopulation of pathogenic bacteria
17:50 - 18:05	Héloïse Muller	Investigating polyDNAviruses as a route of horizontal transfer from parasitoid wasps to their lepidopteran hosts
18:10 - 18:25	Fanny Mazzamurro	Causes and effects of the evolution of natural transformation in bacteria
18:30 - 18:55	Lucy Weinert	Predicting the emergence of hopeful monsters from the dynamics of genetic elements

2- Editors Symposium (BC)

17:00 - 17:12	Connie Mulligan	Epigenetics, gene expression, and stress in mothers and offspring in the Democratic Republic of Congo: biocultural investigation of the intergenerational effects of stress
17:12 - 17:30	Rebecca Zufall	Amitosis, asexuality, and adaptation: evolutionary effects of genome structure in the ciliate <i>Tetrahymena thermophila</i>
17:30 - 17:50	Irina Arkhipova	Non-canonical base modifications of bacterial origin in a eukaryotic genome
17:50 - 18:10	Angela Hancock	Genetic architectures of complex traits differ between populations with contrasting demographic and selective histories
18:10 - 18:30	Deepa Agashe	Mutation rate and bias jointly determine evolutionary dynamics
18:30 - 18:42	Yuseob Kim	Positive feedback between demographic and fitness fluctuation greatly amplifies population size oscillation and causes long-term, multi-locus oscillation of allele frequencies
18:42 - 18:54	Yoko Satta	A new method for excavating Denisovan segments in unphased diploid sequences of East Eurasians

27 July

26- Genomics of adaptations to extreme environments (CT)

9:30 - 9:55	Joanna Kelley	Fish tales: convergent adaptation to extreme environments
10:00 - 10:15	Khaled Hazzouri	The genome of the mimosoid legume <i>Prosopis cineraria</i> , a desert tree
10:20 - 10:35	Maeva Perez	Evolutionary history of deep-sea clam symbionts
10:40 - 10:55	Juliana Vianna	Adapting to extreme environment: vertebrate genomics from the Atacama Desert to Antarctica
11:00 - 11:25	Andres Moreno Estrada	Latin American genomes tell extreme tales on isolation, adaptation, and migration

9- Evolution on repeat in the genomics era (AD1)

9:30 - 9:55	David Baum	The parallelism-convergence continuum and its implications for homology assessment
10:00 - 10:15	Emily Lau	Predictable genetic recruitment in the convergent evolution of bioluminescent substrate storage in fireflies, sea pansies, and ostracods
10:20 - 10:35	John Allard	Genetic models of convergent evolutionary traits by sparse learning
10:40 - 10:55	Frédéric Delsuc	The fundamental role of historical contingency and evolutionary tinkering in the convergent evolution of ant-eating mammals
11:00 - 11:25	Nathalie Feiner	The genomic basis of a repeatedly evolving sexually-selected syndrome in Mediterranean wall lizards

8- Mitochondria across biodiversity: comparative genomics as a tool to unravel mitochondrial biology and evolution (AD2)

9:30 - 9:55	Daniel Sloan	Contrasting mechanisms of mitochondrial DNA repair and transmission bottlenecks across eukaryotes
10:00 - 10:15	Yongsung Lee	Multipartite mitochondrial genomes in red algae
10:20 - 10:35	Dennis Lavrov	Mitochondrial tRNA gene loss and its consequences for evolution of animal mtDNA.
10:40 - 10:55	Kendra Zwonitzer	Copy number explains extreme evolutionary rate variation of mitochondrial DNA across plants
11:00 - 11:25	Sophie Breton	The mitochondria-derived alternative proteome

25- The puzzle of eukaryotic cellular origins (BC)

9:30 - 9:55	Courtney Stairs	Anoxychlamydiales and the origin of anaerobic metabolism in eukaryotes
10:00 - 10:15	Julian Vosseberg	Genome evolution of Asgard archaea: a window into eukaryogenesis?
10:20 - 10:35	Tara Mahendrarajah	ATP synthase evolution in the light of a cross-braced dated tree of life
10:40 - 10:55	Laura Katz	Foraminifera as a model of eukaryotic genome dynamics
11:00 - 11:25	Robert Robinson	The functional origins of the eukaryotic cytoskeleton

BRUNCH

Plenary Lecture (CT; streaming in AD1, AD2, and BC)

12:15-13:15	Michael Lynch	Principles of evolutionary overdesign and underperformance
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13-15-14:30	Awards Ceremony and Introduction to SMBE 2024
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