SMBEv2021 Symposia

Symposium Title: Coevolution of viruses with their microbial hosts: insights from the lab and the wild

Organizers: Carolin Wendling, Anne Kupczok

Overview: Viruses that infect microbes (bacteria, archaea, and unicellular eukaryotes) are the most abundant and diverse biological entities. They contribute significantly to microbial ecology and evolution, where differential virus predation modulates microbial population structure. To defend against virus infections, microbes have evolved a diverse range of resistance mechanisms. Viruses, in turn, are under selection pressure to increase infectivity and respond to these resistance mechanisms by a multitude of counter-strategies, such as, modification of binding proteins or a diversity of anti-CRISPR proteins. Additionally, viruses in natural communities might respond by infecting sub-optimal hosts and even adapt their host range. The outcome of the virus-microbe coevolutionary dynamics is influenced by the supply of genomic variation of both players in the presence of fitness trade-offs in a particular environment. Coevolution experiments and the analysis of natural populations have contributed to our current understanding of these dynamics and it is of outstanding interest to use the strengths of both approaches to disentangle the factors and mechanisms that underlie virus-microbe antagonistic coevolution. This symposium will bring together researchers with different approaches - such as experimental evolution, analysis of natural populations, and mathematical modelling - to understand the coevolutionary dynamics between microbes and their viruses, its genomic basis, and the various factors that influence it. We will take advantage of the up to date genome sequencing technologies and will foster discussions beyond the descriptive analysis of genomic variation towards a detailed understanding of the underlying coevolutionary processes.

Time Zone: EU/Africa

Symposium Title: Mitochondrial Biology and Evolution

Organizers: Sophie Breton, Liliana Milani, Fabrizio Ghiselli

Overview: In the current climate change situation, it is becoming of general interest to understand the mechanisms by which organisms face a changing environment. Organisms respond to environmental factors over time in two ways: (i) short-term changes during their lifetime (e.g. epigenetic modifications and gene expression changes) and (ii) long-term changes across generations, i.e. heritable evolutionary responses, resulting in genetically distinct populations – potentially even new species. While empirical examples of rapid responses and evolutionary adaptations involving nuclear genes exist from a range of animals and plants, the importance of mitochondria and their genomes in promoting adaptation to both short- and long-term environmental changes is still largely unexplored. This major knowledge gap is surprising given the pivotal role of mitochondria in cell survival and functions, ageing and human health. Indeed, mitochondria are on the frontline of the cellular response to the environment and emerging data suggest that mitochondrial epigenetic and genetic systems can fuel phenotypic variation and evolutionary innovations. This symposium aims at reviewing advances in our understanding of how mitochondrial function, structure, expression, evolution, inheritance, and interactions with the nuclear genome contribute to organism adaptation to environmental conditions.

Time Zone: EU/Africa

Symposium Title: The evolution of regulatory elements and its role in phenotypic variability and speciation

Organizers: Isabel Alves, Frédéric Fyon

Overview: The genetic basis of gene expression regulation, its effect on phenotypic variation, and how together they influence evolutionary patterns within and between species, are central topics in evolutionary biology. Technological advances in recent years have allowed researchers to uncover some of these patterns. We now know that: 1) gene expression levels appear to be under stabilizing selection, and 2) whilecis-regulatory variation (DNA sequences located on the same chromosome and often nearby the regulated gene) mostly contributes to gene expression divergence between species, trans-regulatory variation (DNA sequences producing diffusible molecules that act on the expression of genes located anywhere in the genome) mostly influences gene expression variation within species. However, there still

remain questions to explore, and apparently conflicting patterns need to be resolved. For instance, it has been proposed thatcis-regulatory divergence may be driven by positive selection, but recent results in humans suggest thatcis-regulatory variation is under pervasive purifying selection. Theoretical work has shown that somecis-regulatory sequences should behave similarly to self-promoting elements, but this theory lacks empirical attempts to verify it. Finally, the extent to which interactions between cis- and trans-regulatory variation contribute to speciation is not yet understood. This symposium will feature theoretical and empirical efforts to understand the role of evolutionary forces in shaping regulatory variation, the interplay between regulatory variation, gene expression and phenotypic variation, and the importance of gene expression evolution in population divergence and speciation.

Time Zone: EU/Africa

Symposium Title: Genomic forecasting

Organizers: Rebekah Oomen, Sissel Jentoft

Overview: Predicting the responses of populations, species, and ecosystems to environmental change is a major challenge of our time. Building on the concept of 'ecological forecasting', which leverages an abundance of environmental and ecological data to predict demographic responses to environmental change, 'genomic forecasting' integrates an evolutionary perspective using increasingly available genome sequence data. This eco-evolutionary approach acknowledges that evolution occurs on contemporary timescales. Therefore, genomic forecasting is highly relevant for biodiversity conservation, management of harvested populations, and agriculture and breeding programs because it can inform short- and long-term responses of populations to a variety of selection pressures, such as climate change, harvesting, and domestication. Current global efforts to establish high quality genomic resources for all eukaryotic life on Earth make this emerging field poised to contribute to solving global challenges. This symposium aims to highlight studies that use genomic approaches with the aim of predicting population and species responses to selection. Such studies might include the spatial distribution and abundance of adaptive/deleterious alleles, genetic and genomic architecture, and phenotypic plasticity to draw inferences regarding trait evolution and/or future population dynamics and distributions. Spanning empirical and theoretical, studies might incorporate population genomics, genetic simulations, or mathematical modelling, to understand the evolutionary consequences of genomic and environmental variation. Studies on non-model taxa in both wild and domesticated contexts are particularly encouraged. By bringing together genomicists, evolutionary ecologists, and the mathematical and modelling community, we aim to build bridges between genotypes, phenotypes, and the dynamics of populations, species, and ecosystems.

Time Zone: EU/Africa

Symposium Title: Characterizing natural selection and uncovering the genetic basis of complex traits with ancient DNA and time-series data

Organizers: C. Eduardo Guerra Amorim, Anna-Sapfo Malaspinas

Overview: In recent years, novel technology for obtaining DNA molecules from archeological material and sediments has opened up new horizons in the development of the field of paleogenomics. Compared to traditional present-day datasets composed of a single time point, ancient DNA enables the direct assessment of allele frequencies in different time transects and the recovery of lost genetic diversity. Despite the wide range of possible applications of ancient DNA in genomics, this type of data has mostly been used for the reconstruction of demographic history and the phylogenetic placement of extinct taxa. In contrast, most evolutionary studies seeking to uncover targets of natural selection have relied solely on present-day data. This symposium will address how ancient DNA – and, more generally, time-series data – can be used to better understand evolutionary processes such as natural selection, while highlighting new methods that leverage information from time-series genetic datasets to understand processes such as adaptive introgression, selective sweeps, polygenic adaptation, and background selection, and also to uncover the genetic basis of complex traits. In this symposium, we welcome both methodological and empirical studies.

Time Zone: EU/Africa

Symposium Title: New approaches in reconstructing complex trait evolution

Organizers: Liisa Loog

Overview: Recent years have seen parallel advances in understanding the genetic basis of complex traits, inferring evolutionary histories from large numbers of present-day genomes, and obtaining genetic data from archaeological and historical specimens. These advances open up new opportunities to investigate genetic adaptations in non-model organisms and have the potential to vastly improve our understanding of the evolution of complex traits through time. However, taking advantage of these new developments also raises a number of statistical, bioinformatic and interpretational challenges. This session will be a forum for discussing how statistical, bioinformatic and data-driven approaches can be combined with ancient or present-day genetic data for inference of past adaptations and complex trait evolution. It will also provide an opportunity to discuss the potential pitfalls, interpretative challenges, and approaches to overcome them. We welcome contributions on methods and novel application of quantitative genetics to past or present-day populations, both human and non-human, using present-day or ancient genetic data.

Time Zone: EU/Africa

Symposium Title: Machine-learning applications in population genetics and phylogenomics

Organizers: Aurélien Tellier, Matteo Fumagalli, Tal Pupko, and Daniel Schrider

Overview: Machine learning algorithms applied to full genome data have shown promising results in the inference of population genetic parameters with or without the calculation of summary statistics. It opens new avenues for inference of past demographic history, hybridization/admixture events, spatial structure, and life history traits as well as to search for genes under positive or balancing selection. In addition, machine-learning algorithms can be used to accurately and efficiently reconstruct phylogenetic trees and to infer divergence dates. The symposium will include several talks from researchers that combine machine-learning (including deep learning and reinforcement learning) with population genetics as well as with molecular phylogenetics to infer neutral and selective forces at various time and spatial scales.

Time Zone: Asia/Oceania

Symposium Title: Evolution and regulation of gene expression at the translational level

Organizers: Jian Lu, Xuhua Xia

Overview: Evolution proceeds not just by changing protein sequences, but also by adjusting the levels of gene products. mRNA translation is a fundamental stage of gene expression and is highly regulated to control cellular protein homeostasis. Recent studies have significantly advanced our understanding of the role gene regulation plays in organismal environmental adaptations, whereas most of these studies were pursued at the transcriptional level, but our knowledge of the mechanisms and function of mRNA translational regulation is still very limited. Although the molecular mechanisms underlying translational control are well understood for a few genes, we still do not know the full suite of cis-elements or trans-factors that are important for translational regulation at the genome-wide level. The advent of high-throughput sequencing, functional genomic technologies, and comparative genomics has provided us with an unprecedented opportunity to pursue this task at the genome-wide level. In this symposium, studies that aim to advance our understanding of the functions and evolutionary driving forces of mRNA translational regulation will be presented. We encourage topics that explore translational regulation in the context of evolutionary biology from different time scales and of different research systems.

Time Zone: Asia/Oceania

Symposium Title: Genome assembly, spatiotemporal variation, and genetic admixture in Asia

Organizers: Shuhua Xu, Qiaomei Fu

Overview: With its 4.5 billion people constituting around 60% of the total population on the earth, Asia is the world's most populated area and harbors substantial cultural and linguistic diversity. However, human genomics research has long been over-concentrated on populations of European ancestry. Asian scientists have been active in the fields of molecular evolutionary biology and population genetics, in particular, they maderemarkable progress in novel genome assembly, structural variation analysis, and spatiotemporal evolution of both humans and non-human species.

In this session, we carefully select and invite speakers from diverse and representative research fields of genetics and genomics. The speakers will present their latest studies on applying the new generation sequencing technology for genome assembly, applying ancient DNA approach for reconstructing human evolution, as well as developing sophisticated computational methods for genetic admixture analysis. This session will also highlight the importance of coordinating progress between computational and experimental strategies for current and future evolutionary studies.

Time Zone: Asia/Oceania

Symposium Title: Evolutionary and Functional Genomics of Primates

Organizers: Zhijin Liu, Christian Roos

Overview: With more than 500 species, primates represent a diverse group of mammals. While humans have colonized all of earth's extreme environments, non-human primates are mainly found in tropical, sub-tropical, and temperate regions. However, non-human primates also are highly adaptable and inhabit a broad range of environments including forests, savannahs, mangroves, and semi-deserts. Adaptations of humans and non-human primates (NHPs) to severe ecological conditions have been increasingly investigated in recent years. Overall, knowledge of the patterns and processes underlying the evolution and adaptation of humans and non-human primates is critical for understanding hominin origins, physiological ecology, morphological evolution, and applications in biomedicine. In particular, NHPs offer great promise as models for many aspects of human health and disease. These are NHP species exhibiting substantial levels of genetic variation, providing a substantial opportunity to investigate the interactions between naturally occurring functional variation and the changing environments. However, understanding of the contribution of this kind of variations to phenotypes is lagging behind in NHPs. Now, advances in genome sequencing technologies have created new opportunities for comparative primate genomics. Genome assemblies and whole-genome resequencing data are available for various primate species now, and provide remarkable new information about the biology and evolution of humans and NHPs. In this symposium, we are attempting to bring together the body of scientific work about how changes in genome architecture have shaped the evolution of primates, and address the biomedical implications of the new advances in primate genomics.

Time Zone: Asia/Oceania

Symposium Title: Intrinsic molecular drivers of biodiversity evolution

Organizers: Huabin Zhao, Liliana Dávalos

Overview: How some clades diversify their phenotypes whereas others do not is a central question in evolutionary biology. The traditional models of diversification focus on evolutionary responses to ecological and environmental factors, which are external drivers of biodiversity evolution. By contrast, the evidence for intrinsic molecular drivers of biodiversity evolution, including chromosomal evolution, transposable elements, new syntenies, and endogenous viral elements, has been limited. Advances in genome sequencing allow addressing these intrinsic molecular drivers of biodiversity evolution beyond the traditional model organisms that were formerly confined to. In this symposium, we will bring together the body of scientific work addressing how changes in genome architecture, i.e., intrinsic molecular drivers, have shaped the evolution of biodiversity across many non-model organisms.

Time Zone: Asia/Oceania

Symposium Title: Evolutionary Genetics in Natural Microbial Populations

Organizers: Nandita Garud, Will Shoemaker, Mike McDonald

Overview: Our knowledge of the evolutionary dynamics of microbial populations has rapidly advanced in recent years. This is primarily due to scientific progress on two fronts: microbial experimental evolution and sequence-based observations of natural microbial populations. Experimental evolution has allowed researchers to leverage the power of controlled laboratory conditions and model organisms to answer open questions in evolutionary biology, as well as provide insights into adaptive dynamics. Concurrently, sequence-based studies of microbial communities have revealed that microbes often evolve in the context of rampant horizontal gene exchange and multiple species interactions. These observational studies have highlighted key variables to manipulate in evolution experiments, such as the exchange of DNA or competition for shared resources, variables that alter the molecular dynamics of evolution as well as adaptation. In turn, such experiments ground and refine observational studies of natural communities. Ultimately, communication between these two seemingly disparate empirical approaches allows researchers to gain a more complete understanding of the microbial molecular evolutionary dynamics and contributors of adaptation in natural communities. This symposium will focus on research that synthesizes both approaches as well as highlighting the breakthroughs in theoretical population genetics that they inspire.

Time Zone: Asia/Oceania

Symposium Title: Recombination rate variation: implications to genome and organismal evolution

Organizers: Nadia Singh, Judith Mank

Overview: Recombination is fundamental to multiple evolutionary processes, and the rate of recombination is a key variable in determining the adaptive potential of a genomic region. Recent advances have greatly expanded our understanding of the causes and consequences of recombination rate variation spanning multiple levels of biological complexity from within the genome, across individuals, and among related populations and species. In this symposium, we will bring together a diversity of approaches and study systems to the investigation of recombination rate variation and evolution, including work on high-density multigenerational pedigrees, models and methods of inferring linkage disequilibrium from genome data, and experimental manipulation. The symposium will highlight the important role of recombination in studies of evolution and adaptation, and synthesize recent work into a cohesive understanding of the approaches and key questions in the field.

Time Zone: Americas

Symposium Title: Genotype-by-environment interactions in the genomics era

Organizers: Luisa F Pallares, Amanda J Lea, Julien F Ayroles

Overview: The current quantitative genetics paradigm is driven by a prevailing view that additive genetic models, focused on the mean effects of alternative alleles, adequately explain variation for most phenotypes. However, both theoretical and empirical work suggests that the relationship between genotype and phenotype is often environmentally-dependent, and that such “genotype x environment (GxE)” interactions are often key contributors to complex trait variation. However, until recently, GxE interactions have been difficult to study in practice, due to a lack of cost-effective technology for mapping the genotype-phenotype relationship across many individuals and environments. The growing ability to perform large-scale genomic work thus promises to answer many outstanding questions about GxE interactions with relevance to evolution, ecology, and human health, namely: (i) how much of the genome appears “irrelevant” for phenotypic variation under one set of conditions, but plays a fundamental role in other environments?; (ii) how do GxE interactions evolve, and in turn what role do they play in the evolutionary processes when species are exposed to new environments?; and (iii) to what degree do GxE interactions explain variation in fitness-related traits in natural populations, including disease-related traits in humans? Addressing these questions is essential for revealing the context-dependency of allelic effects, a major knowledge gap in our understanding of the genetic basis of complex traits. We encourage researchers working on diverse study organisms and from diverse fields to join us in discussing recent advances in the field of GxE interactions, as well as the challenges for the years to come.

Time Zone: Americas

Symposium Title: Population genetics of identity-by-descent and runs of homozygosity: causes, consequences, and utility

Organizers: Jazlyn Mooney, Zachary Szpiech

Overview: Long stretches of identical-by-descent (IBD) haplotypes are regions that are inherited from a recent common ancestor, and runs of homozygosity (ROH) are a special case of IBD that manifest in individual genomes. Recent work has established a formal connection between IBD and ROH and has shown that there is value in analyzing and examining these genomic phenomena jointly. In humans, wild animals, and domesticated animals, the length and abundance of ROH and IBD has been informative about recent demographic history, gene flow, and selection, and has proven useful for characterizing the genetic architecture of complex traits. As access to genome-wide data grows substantially in non-model organisms, IBD-based methods are well-positioned to explore how evolutionary processes have shaped genetic variation in populations of conservation concern as well. This symposium brings together empirical and theoretical researchers with the goal of exploring the evolutionary consequences of IBD in populations and individual genomes.

Time Zone: Americas

Symposium Title: Efficient methods for dating evolutionary divergences

Organizers: Qiqing Tao, Beatriz Mello

Overview: Reliable divergence time estimates from different species, genes, and strains are crucial to decipher the micro- and macro-evolutionary temporal patterns. Ongoing advances in sequencing technologies have led to a fast expansion in the size of molecular datasets. This expansion necessitates the development of innovative and efficient methods to infer divergence times from genome-scale datasets that often scale to hundreds of species. However, the power and potential of these methods are not fully recognized. In this symposium, we will bring together the community to highlight studies of efficient dating methods, including the theoretical foundation of emerging computational efficient dating methods and tools, extensive evaluations of these methods using simulated and empirical datasets, and their new practical applications. Focus will be on the molecular dating analysis of phylogenomic data. This symposium will promote an open discussion on each method's strengths and weaknesses, providing practical guidelines for using these methods effectively.

Time Zone: Americas

Symposium Title: Phylomedicine of Tumor Evolution

Organizers: Sayaka Miura, Li Liu

Overview: Cancer is widely recognized as an evolutionary disease. Knowledge about evolutionary patterns and processes during cancer progression is fundamental in biological and clinical studies. Yet, the power of molecular phylogenetics in estimating clone phylogenies and dating, inferring mutational processes and selection detection, building metastatic migration histories, and translating phylogenetic discoveries to improve patient care remains to be fully harnessed. In this symposium, we will bring together the community to highlight integrated phylogenetic and tumor evolution studies, including new discoveries and emerging computational methods and techniques. Focus will be on (1) evolutionary analysis of tumor sequencing data, including data generated by bulk sequencing, single cell sequencing, RNA sequencing, and multi-modal sequencing technologies, and (2) clinical applications of evolutionary discoveries. This symposium will bridge the gap between cancer biology and molecular evolution and phylogenetics, which is timely because tumor sequencing is fast expanding with the genome-scale data from a large number of cells.

Time Zone: Americas

Symposium Title: Large-scale phylogeny using novel computational and statistical tools

Organizers: Yariv Aizenbud, Ariel Jaffe, Yuval Kluger

Overview: Advances in sequencing technologies led to the accumulation of large and diverse datasets amenable to phylogenetic analysis. The number of taxa, sequence length as well as the need to incorporate data from different sources pose enormous computational and statistical challenges. Such challenges appear in phylogenomic species tree estimation, gene tree estimation, studying the evolution of infectious diseases and lineage tracing. These problems motivate the development of scalable algorithms with strong performance guarantees as well as statistical tools for analyzing phylogenetic data obtained from diverse sources and environments.

The symposium is focused on the following topics:

1) Divide-and-conquer algorithms for recovery of large-scale trees:

One of the leading approaches to recover large trees is based on the idea of "divide-and-conquer", where a tree structure is inferred separately for multiple subsets of terminal nodes. The full tree is then derived by merging the small trees. We will present different divide-and-conquer algorithms and their application in a variety of problems, including lineage tracing in metastatic cancer, and incomplete lineage sorting.

2) Statistical tools for analyzing phylogenetic data from multiple sources:

The recent plethora of available phylogenetic datasets intensify the need for new approaches to quantify similarity between different trees. These include new metrics for tree comparisons and computing summary statistics of tree distributions. The importance of such statistics is showcased by studying the evolution of SARS–CoV-2.

Time Zone: Americas

Symposium Title: The effects of selection at linked sites and population history on levels and patterns of genomic variation

Organizers: Parul Johri, Jeffrey Jensen

Overview: It has become increasingly clear that the effects of selection on linked sites are pervasive genome-wide. As these hitchhiking effects - both constant background selection and episodic selective sweeps - shape patterns of variation at neutral sites, these deviations from neutral expectations can result in demographic mis-inference, as standard approaches assume complete neutrality. Relatedly, because natural populations often experience changes in population size, these demographic dynamics may similarly result in the mis-inference of selection parameters, as standard approaches assume constant size. In this symposium, we will highlight both recent theoretical and computational approaches that allow for the improved inference of selection by accounting for population history, the improved inference of demographic history by accounting for direct and linked selection effects, and recent efforts to jointly estimate these parameters. Empirical and experimental studies that contribute to a better understanding of the joint effects of demography and selection will also be most welcome.

Time Zone: Americas

Symposium Title: Open Symposia

Organizers: TBD

Overview: Open Symposia

Time Zone: All