



# Understanding Life: Using Largescale Biodiversity Reference Genomes

27–29 October 2025

Wellcome Genome Campus, UK and Virtual

## Workshops at a Glance

Monday 27 October 2025

Workshop session 1: 15:15 – 17:15 GMT

1. AI and annotation	
<b>Workshop Leads</b>	<i>Francoise Thibaud-Nissen, National Center for Biotechnology Information (NCBI), USA</i> <i>Katharina Hoff, University of Greifswald, Germany</i>
<b>What it's about</b>	Gene annotation is a gateway to unlocking the functional meaning of genomes. This workshop explores the fast-evolving world of annotation tools — from traditional pipelines to cutting-edge AI and deep learning methods. You will learn about benchmarking strategies, explore how machine learning is reshaping standards, and gain insights into the strengths and limitations of current approaches.
<b>Why attend</b>	If you work with eukaryotic genomes, this session will give you the confidence to apply next-generation annotation methods, integrate AI into your workflows, and move from raw data to biological discovery more effectively.

2. Sequencing the holobiont - how to disentangle species	
<b>Workshop Lead</b>	<i>Ellen Cameron, Earlham Institute, UK</i>
<b>What it's about</b>	In sequencing, what may look like “contamination” can be a source of discovery. Holobionts — hosts and their associated microorganisms — reveal rich biological context when analysed together. This workshop will explore bioinformatic tools and strategies for recovering and characterizing microbial genomes from holobiont data.
<b>Why attend</b>	If you want to move beyond single-species genomics, this session will show you how to turn complex data into insights about host–microbe interactions.

<b>3. Curation of assemblies</b>	
<b>Workshop Lead</b>	<i>Jo Wood, Wellcome Sanger Institute, UK</i>
<b>What it's about</b>	High-quality genome assemblies often require more than raw data and automatic pipelines — they depend on rigorous curation. This workshop focuses on tools and workflows to improve assembly quality, correct errors, and ensure reliability for downstream analyses. You will gain a practical understanding of both manual and automated approaches.
<b>Why attend</b>	If you generate or use genome assemblies, this session will give you strategies to boost genome quality and potentially uncover new insights into your assemblies.

<b>4. Advances in Genomic Technologies</b>	
<b>Workshop Lead</b>	<i>Ana Conesa, CSIC Valencia, Spain</i>
<b>What it's about</b>	Large-scale biogenome projects depend on efficient, high-quality data acquisition. This workshop explores the latest methods and technologies designed to improve and streamline these processes, from sequencing innovations to new standards and analytical tools. Participants will gain insights into the techniques driving progress in genome assembly, annotation, and large-scale analysis.
<b>Why attend</b>	This session is ideal for professionals developing pipelines, standards, and methodologies for genomic data, as well as early-stage researchers eager to adopt innovative technologies to advance their work.

<b>5. Project Psyche Showcase</b>	
<b>Workshop Leads</b>	<i>Joana Meier, Wellcome Sanger Institute, UK</i> <i>Charlotte Wright, Wellcome Sanger Institute, UK</i>
<b>What it's about</b>	Project Psyche is a pan-European initiative to sequence reference genomes for all 11,000 species of butterflies and moths in Europe. With over 1,000 genomes already sequenced, the project is opening new horizons for Lepidoptera research. This workshop introduces Project Psyche, its visualization platform LepBase, and features talks from leading analysis groups.
<b>Why attend</b>	If you're an early-career researcher or interested in large-scale genome analysis, this session is your chance to learn, connect, and get involved in one of the most ambitious biodiversity genomics projects in Europe.

**Tuesday 28 October 2025**

**Workshop session 2: 15:45 – 17:45 GMT**

<b>6. Bat1K showcase</b>	
<b>Workshop Leads</b>	<i>Michael Hiller, LOEWE Centre for Translational Biodiversity Genomics, Germany</i> <i>Emma Teeling, University College Dublin, Ireland</i> <i>Sonja Vernes, University of St Andrews, UK</i>
<b>What it's about</b>	The Bat1K project brings together over 530 members from 67 countries with one bold mission: to generate reference-quality genome assemblies for all living bat species. With more than 300 genomes underway and 100+ already released, Bat1K provides an unparalleled resource for studying evolution, ecology, immunity, longevity, and biodiversity. This workshop will showcase cutting-edge research powered by Bat1K's genomes.
<b>Why attend</b>	Whether your interest lies in evolution, sensory biology, conservation, or emerging diseases, this session highlights how bat genomics is advancing science and addressing global challenges.

<b>7. Aquatic symbiosis genomics</b>	
<b>Workshop Lead</b>	<i>Jose V. Lopez, Nova Southeastern University, USA</i>
<b>What it's about</b>	Symbiotic and interspecies interactions shape ecosystems, yet their genomic foundations are only beginning to be understood. This workshop will explore how genomics can illuminate the mechanisms, dynamics, and maintenance of aquatic symbioses, providing a deeper perspective on host–symbiont partnerships.
<b>Why attend</b>	While the focus is on aquatic systems, researchers from all fields are welcome. This session is ideal for anyone interested in using genomic tools to better understand interspecies interactions and their ecological significance.

<b>8. Let's be FAIR: using pipelines in genomics research</b>	
<b>Workshop Lead</b>	<i>Chris Wyatt, University College London, UK</i>
<b>What it's about</b>	FAIR means Findable, Accessible, Interoperable, and Reusable — the gold standard for scientific data. This workshop introduces best practices in bioinformatics pipeline development, showing how the omics community builds, shares, and reuses workflows. Participants will learn practical strategies to run pipelines, streamline analyses, and increase the impact of their data.
<b>Why attend</b>	From beginners looking for inspiration to seasoned bioinformaticians, this session provides tools and insights to make your research more robust, shareable, and collaborative.

<b>9. Population genomics and conservation</b>	
<b>Workshop Leads</b>	<i>Ilik Saccheri, University of Liverpool, UK</i> <i>Niklas Wahlberg, Lund University, Sweden</i>
<b>What it's about</b>	Population genomics offers crucial insights into species conservation — but it comes with challenges. This workshop will spark discussion on best practices, opportunities using new reference genomes, and limitations in applying genomics to conservation biology. Topics include genetic diversity and evolutionary potential, adaptation to environmental change, inbreeding depression, reintroduction genetics, museomics, and prioritization informed by phylogeny.
<b>Why attend</b>	If you're using or planning to use reference genomes in conservation and population genetics, this is an open forum to align methods, share experiences, and push the field forward.