

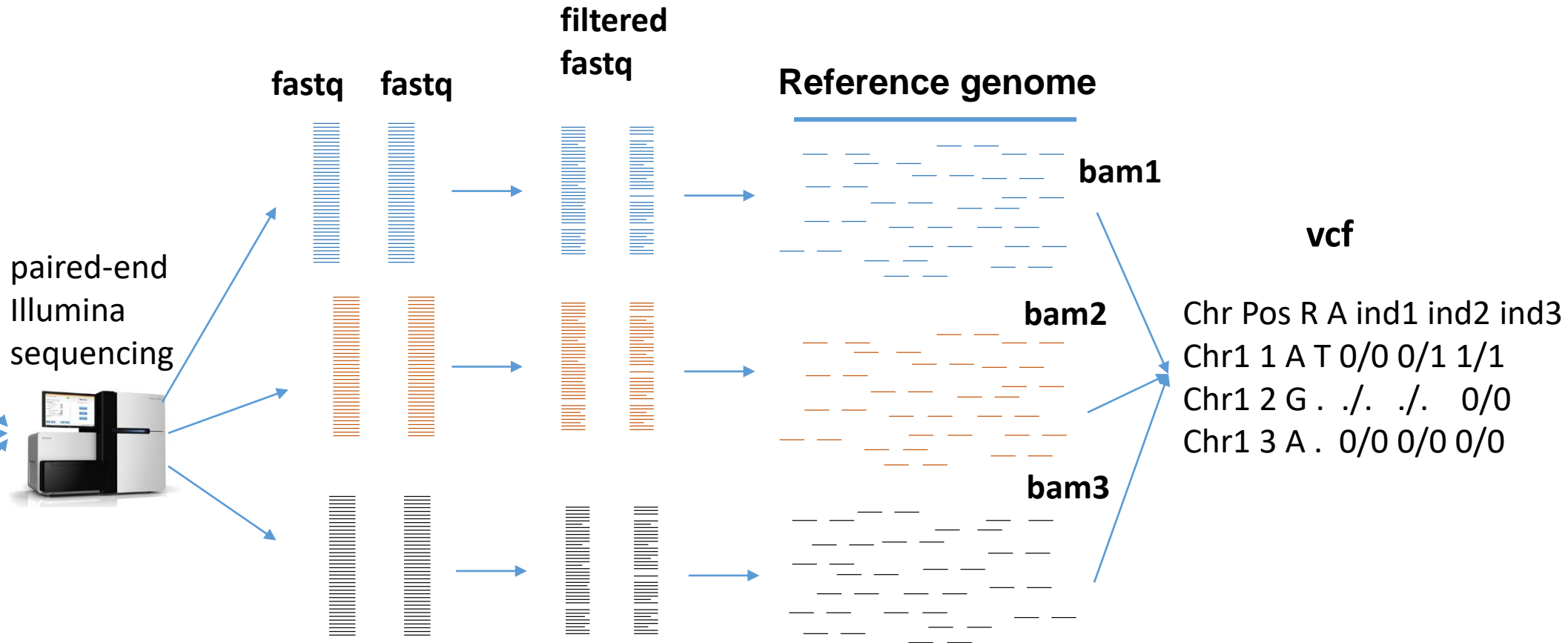
Course summary and further learning opportunities

from butterflies to a vcf file

fastp:
filtering &
trimming reads

bwa-mem2:
alignment to
a reference
genome

bcftools:
genotype and
variant calling

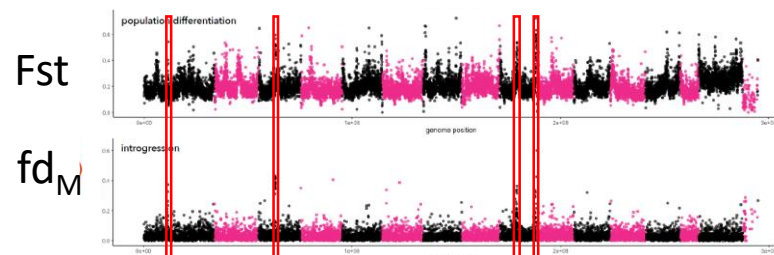
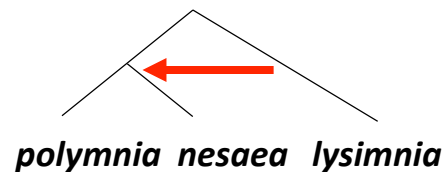
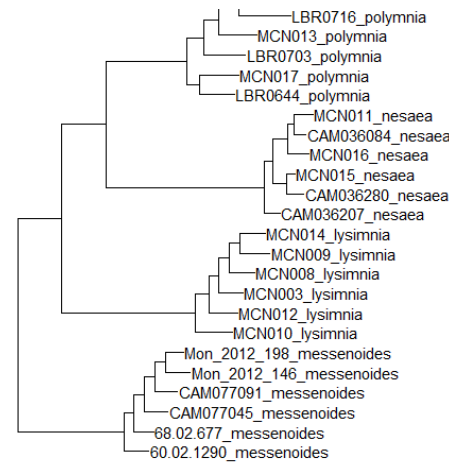
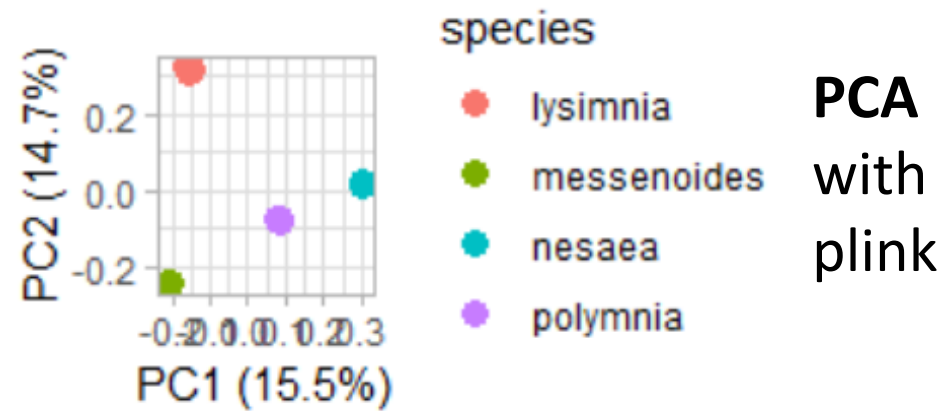


Using the vcf file for biodiversity genomics

vcftools:
Filtering sites and genotypes

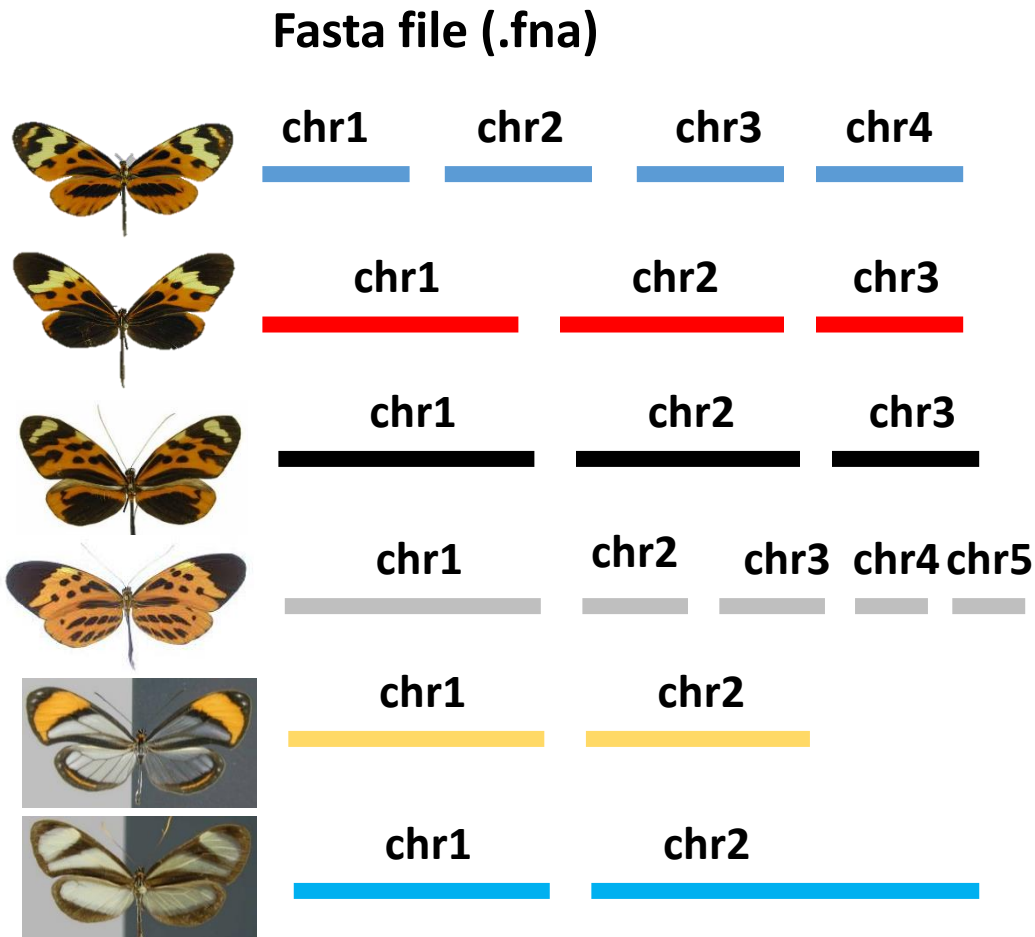
Filtered vcf

Chr Pos R A ind1 ind2 ind3
Chr1 1 A T 0/0 0/1 1/1
Chr1 3 A . 0/0 0/0 ./.

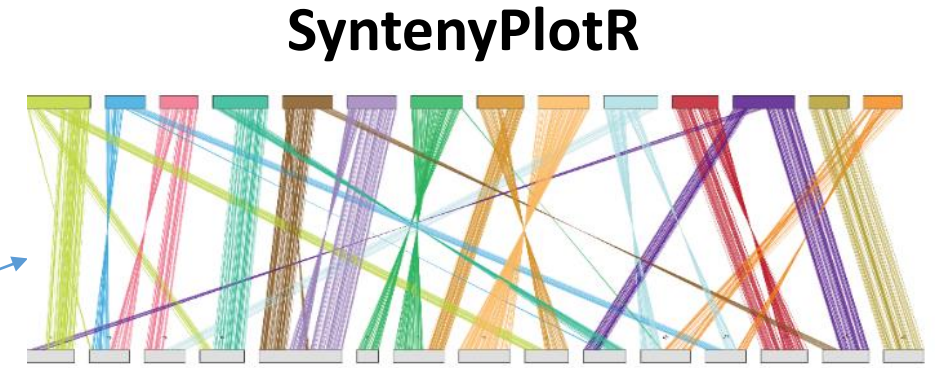


Comparative genomics

Download genomes from
<https://www.ncbi.nlm.nih.gov/>



Minimap2:
 whole-genome
 alignment

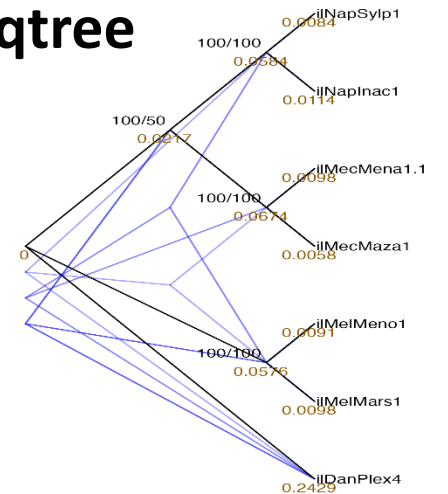


Orthofinder + Mafft

Fasta alignment file
 per BUSCO gene

gene1	gene2	gene3
>ind1	>ind1	>ind1
ATCTG	CTGAA	CCCTA
>ind2	>ind2	>ind2
ATCTC	CTGGA	CCGTA
>ind3	>ind3	>ind3
ACCTC	CTAGA	CGGTA

**Gene trees with
 iqtree**



Learning more:

<https://www.biodiversitygenomicsconference.org/bga24>

mail

Calendar

Calendar

WhatsApp

Quip

Netflix

Republik

TolQC

Notion

Twitter

Zoom

Fred

STS

Benchling

Faculty ToL WIP

Okta

AWS instance

NZZ

BG24

Programme

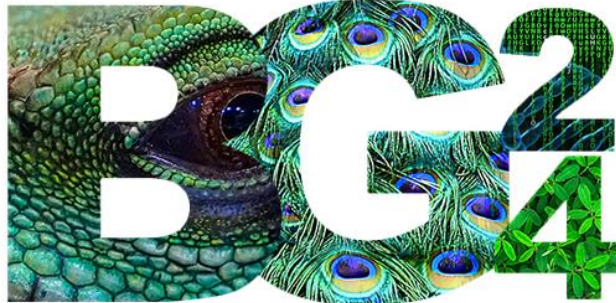
Registration and Abstracts

General Information

Sponsorships

BGA24

Legal Information



BioDiversity Genomics Conference 2024

28th October - 1st November 2024
open | online | global

Biodiversity Genomics 2024 (BG24) is back for a fifth year. It will again be open, online and global.

BG24 is free to attend, thanks to the generosity of sponsors and core support from the Wellcome Sanger Institute Tree of Life Programme. Please engage with us using #BG24 on social media.

Join thousands of researchers worldwide to hear all the latest findings and ideas as we strive to complete the goals of the [Earth Biogenome Project](#) (EBP):
"sequencing life for the future of life."

Day	Date	Timezone
Day 2	29th October	Daytime in the Americas.
Day 3	30th October	Daytime in Africa and Europe
Day 4	31st October	Daytime in Australasia and Asia

<https://thebgacademy.org/>



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Homepage for BGA24!

Workflow Tracks for 2024

> glossary

About us

Bioinfo Basics

Welcome to The BioDiversity Genomics Academy Homepage!

Jun 10, 2024, 2 min read



Join us between October 1st - 26th

 Info

https://speciationgenomics.github.io



Speciation & Population Genomics: a how-to-guide

Home

LEARNING UNIX

- Getting used to Unix
- Going further with Unix
- awk tutorial

HANDLING NGS DATA

- Understanding NGS data
- Filtering reads
- Mapping to a reference genome
- Variant calling
- Filtering and handling VCFs
- Checking for PCR duplication problems, contamination, etc.

LEARNING R

- Introduction to R
- Data manipulation and visualisation in R

Welcome to the [Physalia](#) December 2021 course run by Mark Ravinet & Joana Meier.

Follow the links on the lefthand side to take part in the course modules.

The [presentations](#) we gave during the course and the [scripts](#) and [datasets](#) can be downloaded from our [Speciation genomics github page](#). You can either clone the repositories (see [here](#) how to do that) or just download them as a zip file. Individual text files can be downloaded by clicking on `raw`. The scripts directory contains a number of scripts we used throughout the course (`bash` and `R`), plus several others that might be of use.

The course GitHub

https://github.com/rapidspeciation/biodiversity_genomics_course

Publications we recommend:

Reviews on biodiversity genomics:

- How genomics can help biodiversity conservation [Theissinger et al. 2023](#)
- Genomics and the origin of species [Seehausen et al. 2015](#)

Publications related to the examples in the course:

- Genomics of Neotropical biodiversity indicators: two butterfly radiations with rampant chromosomal rearrangements and hybridisation [van der Heijden et al. 2024](#)
- Genomic evidence reveals three *M. outcome* fusions in Heliconius butterflies [Briede](#)

If you do not have access to a cluster

- Making an **Amazon server** as we did for the course:

<https://us-west-2.console.aws.amazon.com/ec2>

- **Cloud development environment:**
Launch and enter Virtual Machines

<https://gitpod.io>

50 free hours per calendar month

Used for teaching BGA23:

<https://gitpod.io/#https://github.com/bgacademy23/test>