Module 1: Getting Started

Course Overview

- Every Wednesday: 3 hr lab
- Every Monday: 1 hr lecture
- Module 12 (July 21): Guest lecturer(s)
- Email: alice.chen@humber.ca
- Respond within 4-6 business hours

Course Overview

Assessment	Weight
In-Class Participation	10%
Group Discussion Assignments	15%
Lab Assignments	50%
Group Report – Clinical Case Study	25%
Total	**100%**

Class Participation

- Weekly class poll
- 1% per lecture * (9 out of 12 lectures)
- Lab 0 completion counts as 1%

Course Overview

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Group Discussion Assignments	15%
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Group Discussion Assignments

- Complete as a group after class
- 3 assignments x 5%
- Use the content to build knowledge towards completing the final group report

Course Overview

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Group Discussion Assignments	15%
Lab Assignments	50%
Group Report – Clinical Case Study	25%
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Lab Assignments

- 5 lab assignments x 10%
- Each assignment is split into two parts (Part A and B) and due on the Sunday 11:59 PM after Part B
- For each assignment,
  total mark of the assignment =
  total of Part A + total of Part B.

Course Overview

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Group Report - Clinical Case Study

- Run a Nextflow pipeline as a group and write a case study report.
- The lab on July 9 is reserved for group work and technical troubleshooting.

Missed and Late Evaluation Policy

- All students requesting an extension must follow the missed and late evaluation policy.
- **(Mandatory)** Complete this form for each missed assignment at least 24h before the assignment deadline.
- Evaluation of missed and late assignments is subjected to my approval.
- My email: alice.chen@humber.ca

Class Policy on AI Usage

- Humber College's AI Policy (link)
- Contends that un-cited and/or other unauthorized use of AI in assessments and assignments constitutes academic misconduct as defined in Humber's Academic Regulations.
- **Do not provide ChatGPT (or any other AI tool) human information that is not open access.**
- **Cite which tool you used and its contribution to your assignment.**
- **You are responsible for the accuracy of your answers.**

Class Policy on AI Usage

Lab Assignments

Code Example:

```
def foo():
    # some code here
    return answer

# Source: My code was generated by claude
```

Short Answer Example:

```
This figure shows that Gene A in fruit fly is upregulated in the treatment group.
Source: I made ChatGPT read the figure.
```

Class Policy on AI Usage

Group Assignments & Group Report

- Communicate with your group members how you used AI tools in your contributions
- Cite this information at the end of your group submission

```
AI Sources:
- Member A used ChatGPT to proofread the Introduction section
```

Learning Strategies

- Coding is a technical skill that requires continuous learning.
- Software manuals and documentations are your friends.
- Use your creativity to find answers ethically. Most knowledge is publicly available.

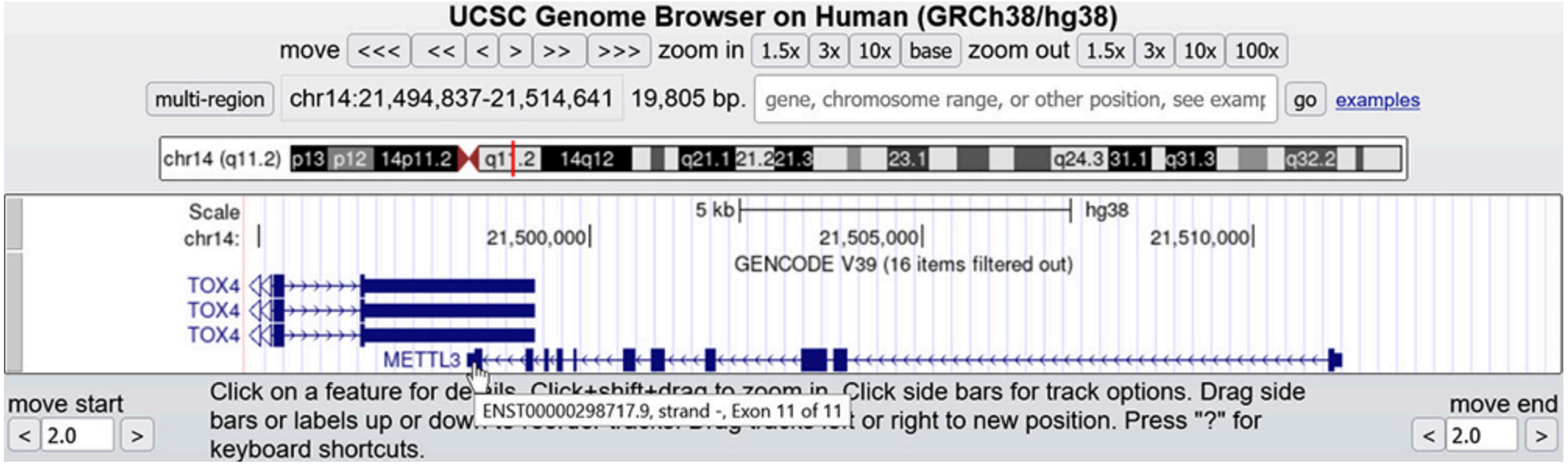
Applications of genomics in clinical medicine [1]

- ***Clinical diagnosis***: Used as diagnostics criteria for medical conditions.
- ***Disease gene identification***: Identify the role of specific genes in heritable diseases.
- ***Cancer genomics***: Used to understand how genomic variants in somatic cells are involved in the initiation and progression of cancer.
- ***Disease treatment***: Inform targeted gene therapies to treat patient monogenic disorders in personalized medicine.
- ***Prenatal diagnosis***: Risk assessment for genetic disorders in pregnancies.

Critical Path

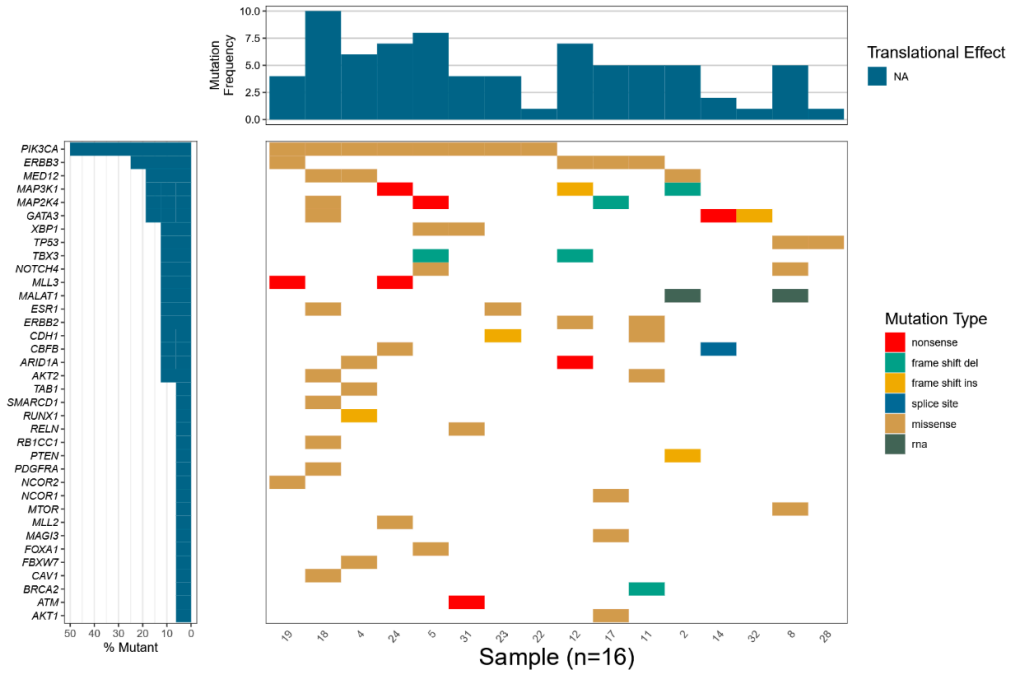
- The lecture materials provide information to support the lab components:
  - Understanding the genetic basis of heritable diseases using public resources
  - RNASeq using Nextflow
  - Gene expression profiling using Nextflow
  - Somatic variant analysis using Nextflow
  - Linkage analysis and clinical applications of GWAS
- Find more details in the Critical Path

Public Databases



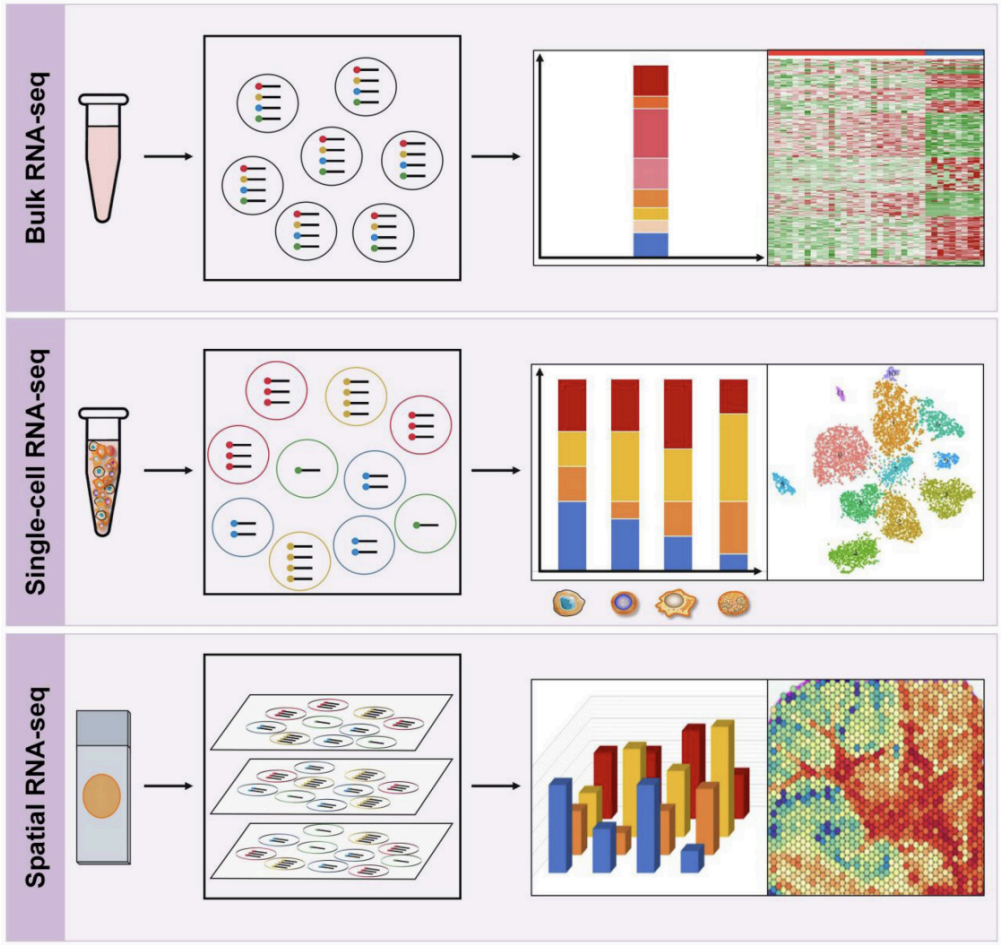
- Public databases that provide biological and medical information to prepare a clinical report.

GenVisR: “Genomic Visualizations in R”



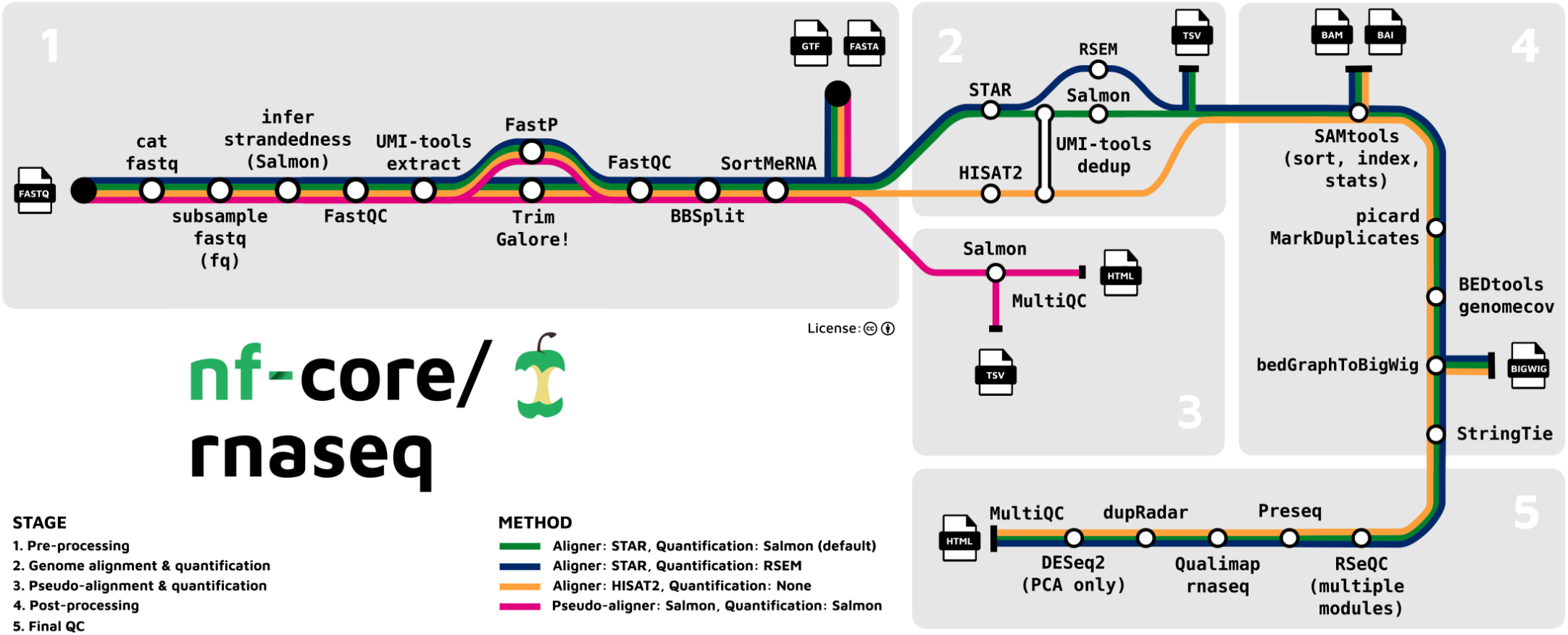
- An R package that creates highly customizable publication-quality graphics supporting multiple species and focused primarily on a cohort level (i.e., multiple samples/patients).

RNA Sequencing [2]

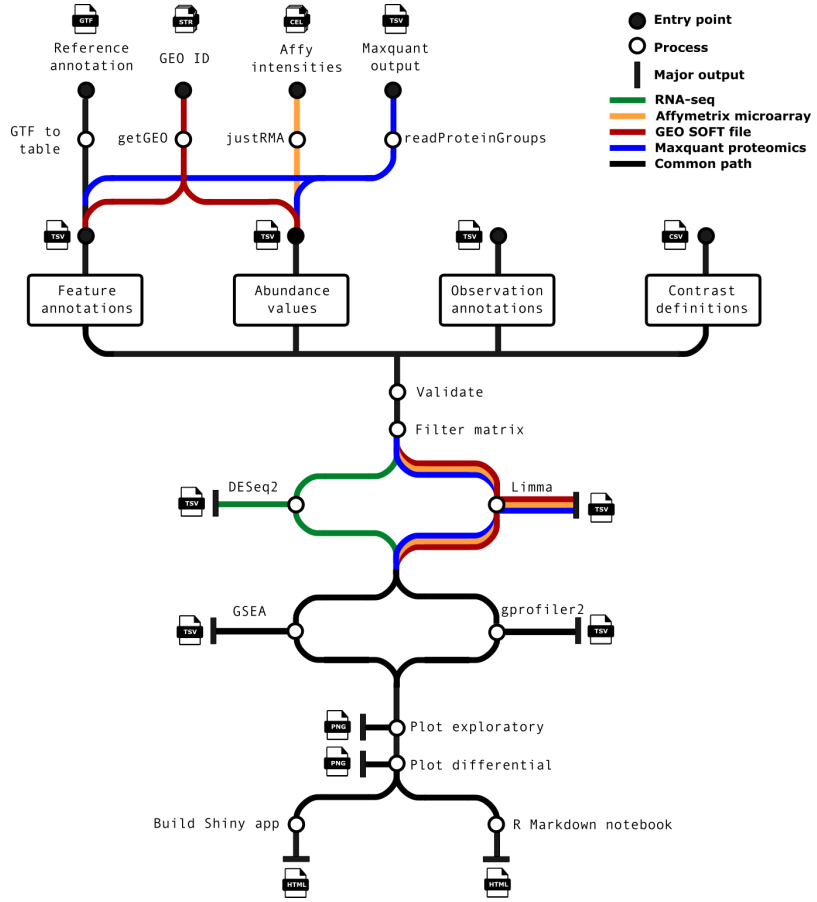


- **Bulk RNA-Seq** provides an average measure of gene expression across the entire population of cells.
- **scRNA-Seq** analyzes gene expression at the single-cell level, which helps to study cellular diversity and identify unique cell types
- **Spatial RNA-Seq** profiles gene expression with spatial resolution in a 3D context within tissue samples.

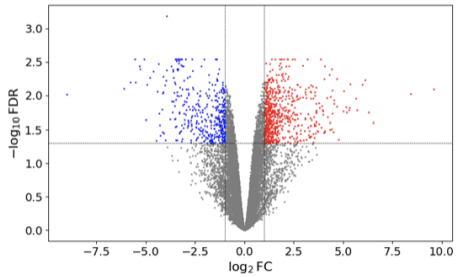
Bulk RNASeq using Nextflow [3]



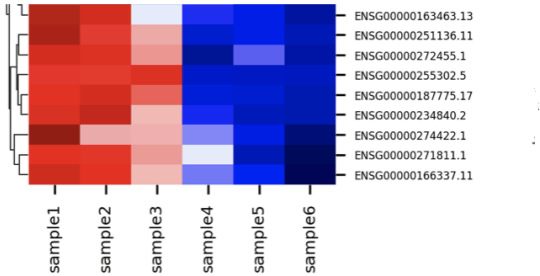
Differential Expression Analysis using Nextflow [3]



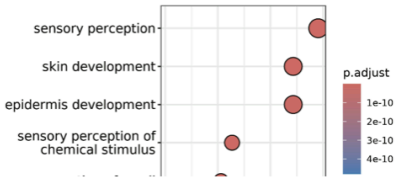
Volcano plot



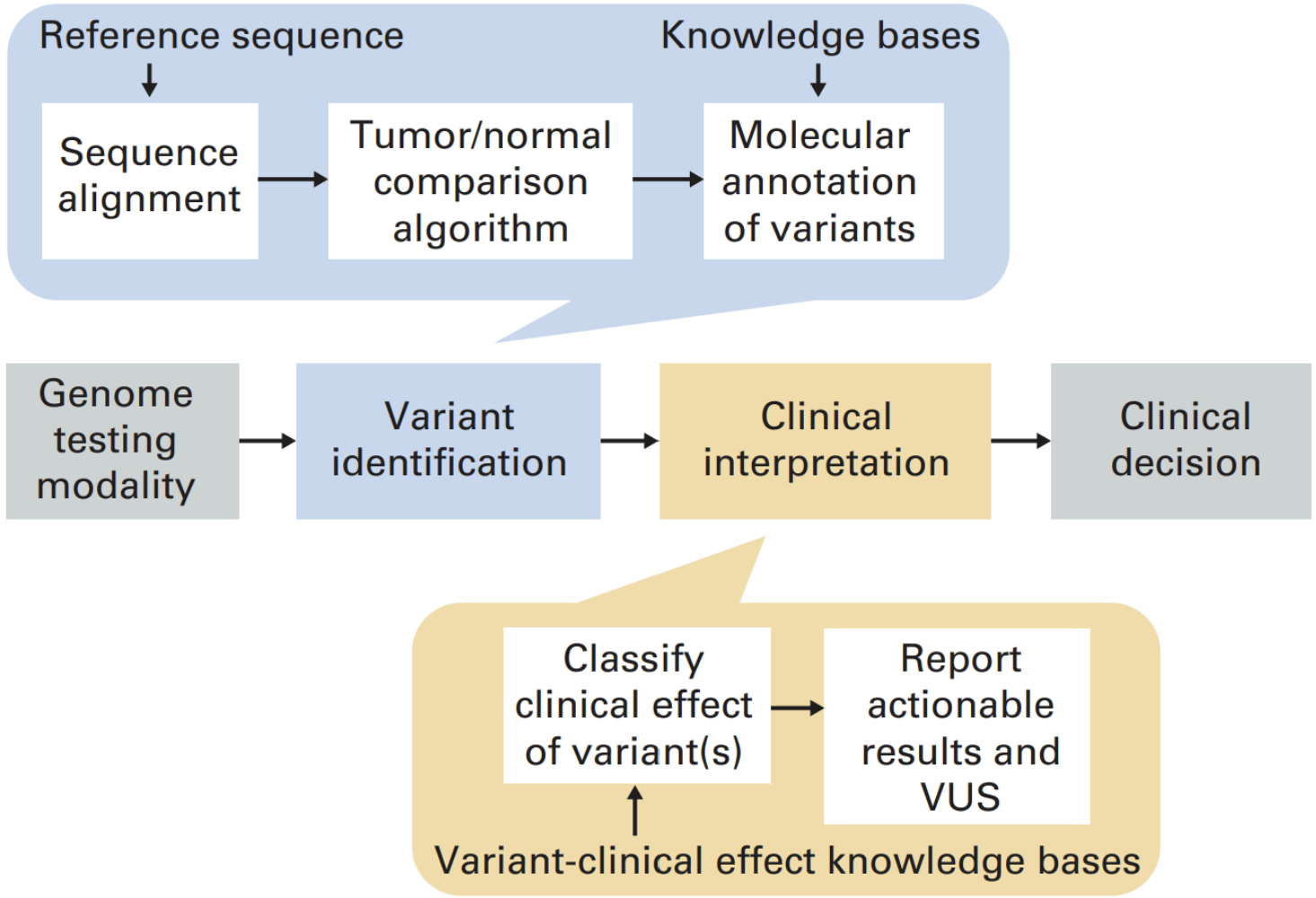
Heatmap



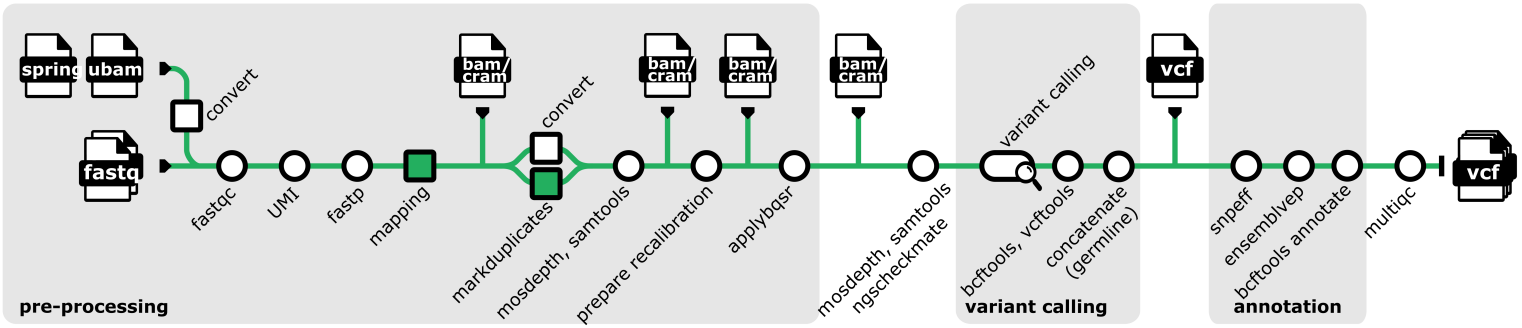
Gene Ontology/Pathway Analysis

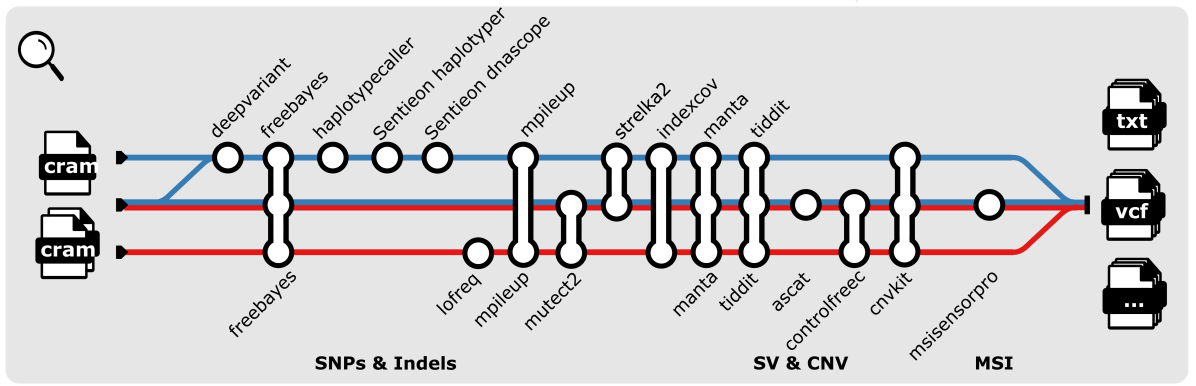


Clinical workflow for tumor genome analysis [4]



Somatic Variant Analysis using Nextflow [3]





Example analysis pathways

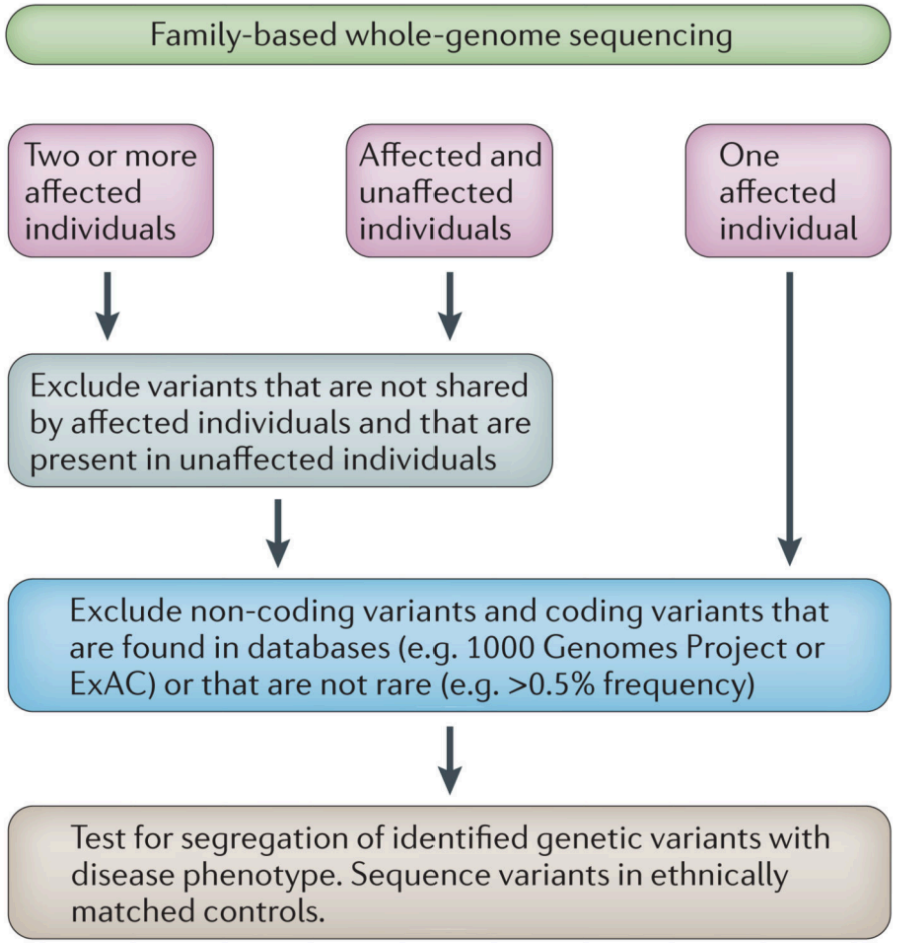
nf-core/sarek

Mandatory
Optional
Optionally Sentieon accelerated

Core workflow
Germline variant calling
Tumor only variant calling
Tumor-normal pair variant calling

Adapted from: Fellows Yates, James A., et al. PeerJ 9 (2021).

Linkage Analysis [5]



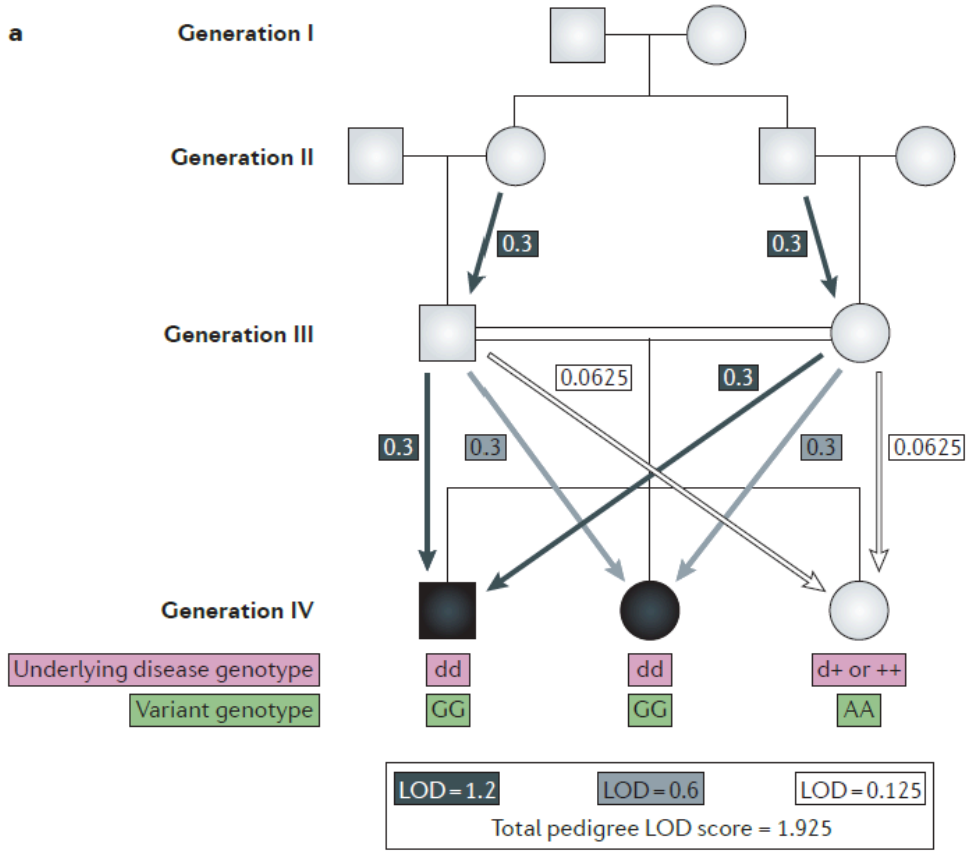
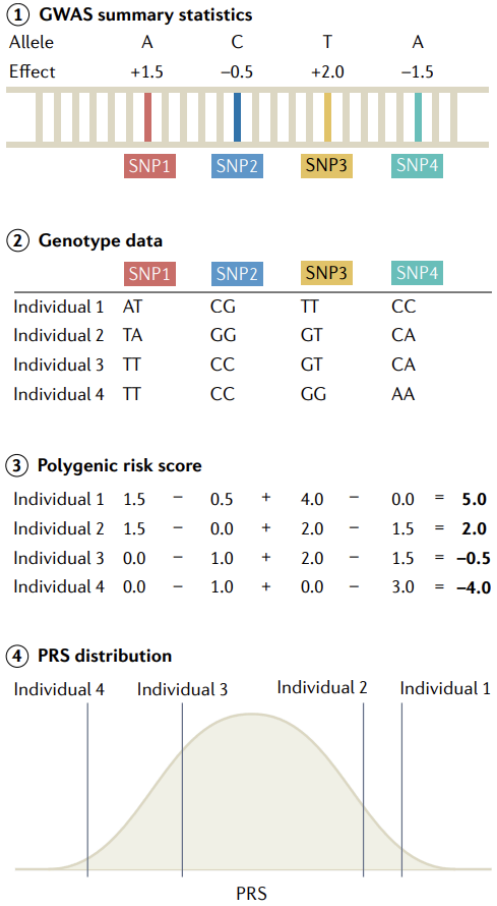


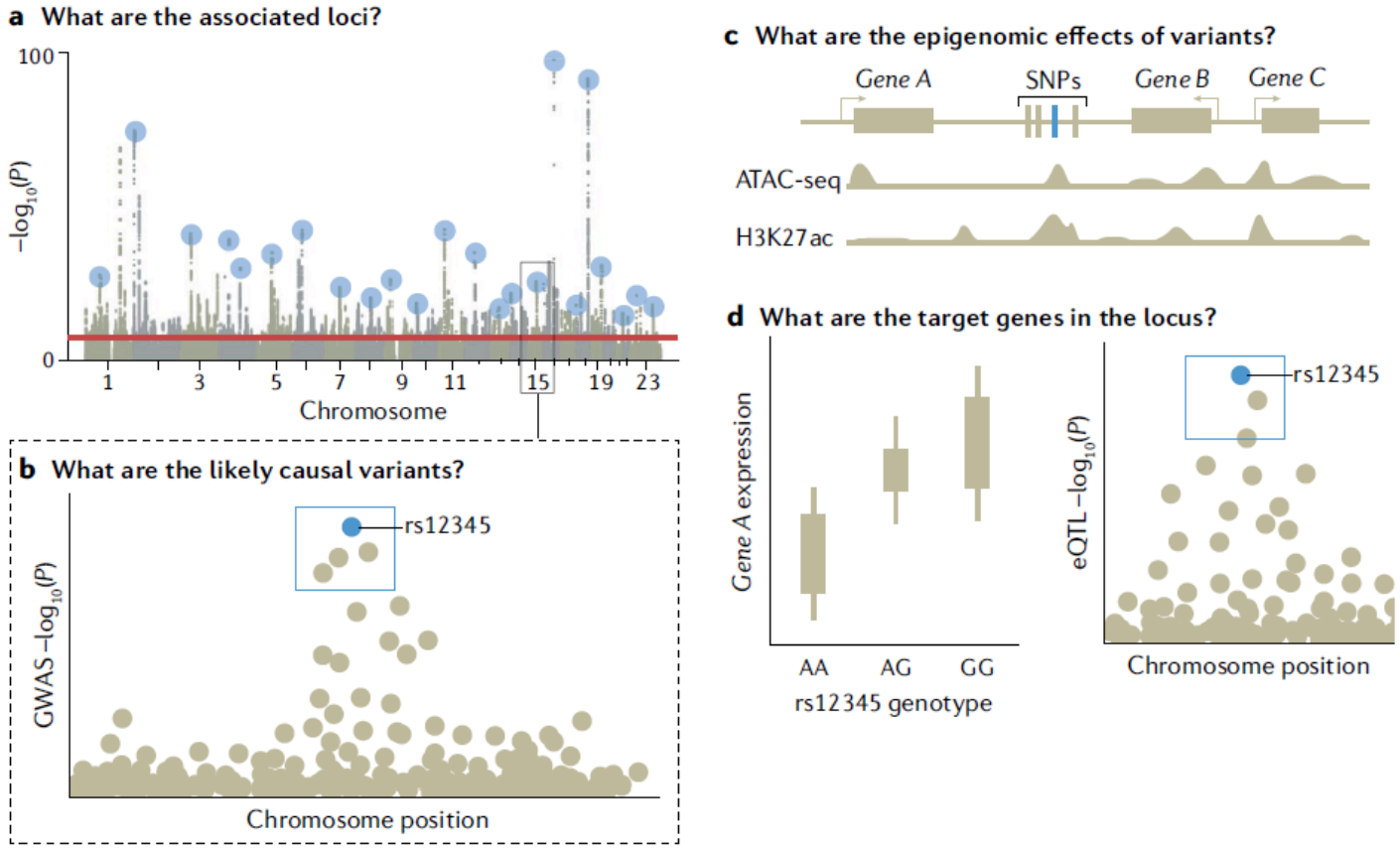
Figure 1. Workflow for the whole-genome sequencing filtering approach in human family data

Clinical Applications of GWAS [6]

(1) Polygenic Risk Score



(2) Functional Analysis



Class Survey (1%)

What do you want to learn from this course?

References:

1. Pyeritz, R.E. Medicine in a genetic and genomic context. In *Emery and Rimoin's Principles and Practice of Medical Genetics and Genomics* (7th edn) (eds. Pyeritz, R.E., Korf, B.R. & Grody, W.W.) 1–20 (Academic Press, 2019).
2. Yan, H., Ju, X., Huang, A. & Yuan, J. Advancements in technology for characterizing the tumor immune microenvironment. *Int. J. Biol. Sci.* **20**, 2151–2167 (2024).
3. Ewels, P. *et al.* The nf-core framework for community-curated bioinformatics pipelines. *Nat. Biotechnol.* **38**, 276–278 (2020).
4. Van Allen, E.M., Wagle, N. & Levy, M.A. Clinical analysis and interpretation of cancer genome data. *J. Clin. Oncol.* **31**, 1825–1833 (2013).
5. Ott, J., Wang, J. & Leal, S.M. Genetic linkage analysis in the age of whole-genome sequencing. *Nat. Rev. Genet.* **16**, 275–284 (2015).