RGGS Comparative Genomics 2 – Computational Methods (Session 11)

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ICG conference room

Session 11 outline

- **Final project description due**

- **Paper presentations**

- **Quiz 2 (oral recapitulation of previous topics), if time permits**

Final project description due

- A short description (~350 words) of your proposed research question for the final project is due today (November 14)

- The description should outline the research question and the methods you plan to use

- Provide the project title and description in a Word document

- We will review your document and provide feedback

Mid-term project presentations

- **Today, each student will deliver a 10-15-minute presentation on a cutting-edge genomics approach and lead a classroom discussion on the topic**

- **The objective is for students to gain insight into advanced methods that, while not directly applicable to their PhD work, are valuable for a comprehensive understanding of the field**

- **The presentation should provide an overview of the chosen approach, including its fundamental techniques, associated costs, and requirements. It should also address the types of research questions the approach can effectively tackle, as well as its current limitations in terms of application or accessibility**

- **For the discussion segment, the presenting student should prepare at least one question for the class to explore**

- **Additionally, each student is required to include an annotated bibliography of relevant publications**

Mid-term project presentations

- **Long read sequencing -> Amanda**

- **Direct sequencing of RNA -> Joseph**

- **Metagenomics -> Lina**

- **Spatial transcriptomics -> Violet**

- **NGS platforms -> Daniela**

- **Gene/genome editing -> Kate**

`Oral recapitulation quiz`

- **Getting data from public repositories**
  - Name two public repositories where you can download genomic or transcriptomic data.
- **Processing Illumina reads: QC, trimming, and filtering**
  - What is the purpose of trimming and filtering Illumina reads before further analysis?
- **Genome and transcriptome assembly from Illumina reads**
  - What is the difference between genome assembly and transcriptome assembly?
- **Assembly assessment**
  - Name a common metric used to assess the quality of an assembled genome.

- **Structural annotation of genomes and transcriptomes**
  - What does structural annotation involve in genome analysis?
- **Repeat identification and masking**
  - Why identify and mask repetitive elements in genome assemblies?
- **Homology-based functional annotation**
  - What is homology-based functional annotation, and why is it used?
- **The principles and practice of BLAST searches**
  - What is the main purpose of a BLAST search in genomics?
- **Domain-based functional annotation**
  - Why are protein domains important for functional annotation?
- **InterProScan and other protein databases**
  - What is InterProScan used for in genomics?
- **GO annotation**
  - What is its purpose of GO annotation?

Additional matters

- **Reschedule Session 13 — November 28**
  - Morning or afternoon:
    - Mon, Dec 3
    - Tue, Dec 4
    - Fri, Dec 6