

Purpose of the Project

- Two tracks in Diagnostic Genetics and Genomics (DGG) master's program at SHP: Molecular Genetics and Genomics (MGG) and Cytogenetics and Cytogenomics (CGG)
- Overarching goal of DGG-MGG: to train technologists/scientists with expertise in high capacity data generation (wet lab) and bioinformatic/computational analyses (dry lab)
- To serve one of the institution's core values, <u>Discovery</u>, we strive to introduce cutting-edge technologies to maintain our program at the forefront of graduate education.
- The current project aims to incorporate the innovative Nanopore sequencing technology ^[1] into our curriculum.

Rationale for Integration into Curriculum

- The existing MGG core curriculum deploys first-generation sequencing (Sanger method) and next-generation sequencing (NGS, Illumina platform) for the first-year students' training.
- Third-generation sequencing (TGS) offers high speed and long sequence reads and is increasingly being used in genomic studies ^[2] as well as pathogen surveillance ^[3].
- Benefits of including the emerging TGS technology in the core curriculum: (a) expand our sequencing platforms; (b) supplement and help fill the gaps in genome assemblies made from short reads generated by NGS
- MinION (launched in 2015), along with the associated MinIT (2018), is a portable TGS device from Oxford Nanopore Technologies (ONT) that is readily meeting our teaching need.

Educational Goal and Performance Objectives

- Goal: Students in the MGG teaching lab will demonstrate an understanding of the principle of Nanopore sequencing to be applied in hands-on practice by generating and analyzing bacterial whole genome sequencing (WGS) data and presenting results.
- **Objectives**:
- 1. Explain the concept of Nanopore sequencing and elaborate how it works (intellectual skill)
- 2. Prepare libraries for WGS using MinION and perform sequencing (psychomotor skill)
- 3. Analyze sequencing data using bioinfomatic tools (intellectual & psychomotor)
- 4. Summarize data from both wet and dry labs and present results in groups (cognitive & social)

Background of Nanopore Sequencing

- Concept and mechanism
- Video https://nanoporetech.com/applications/dna-nanopore-sequencing

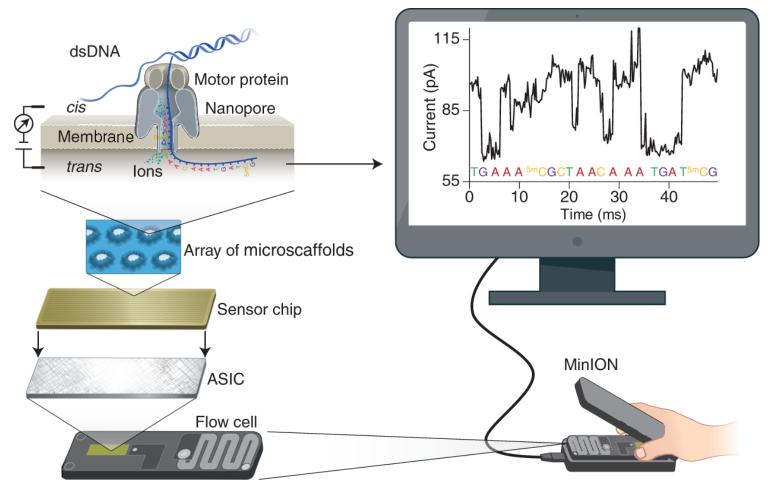
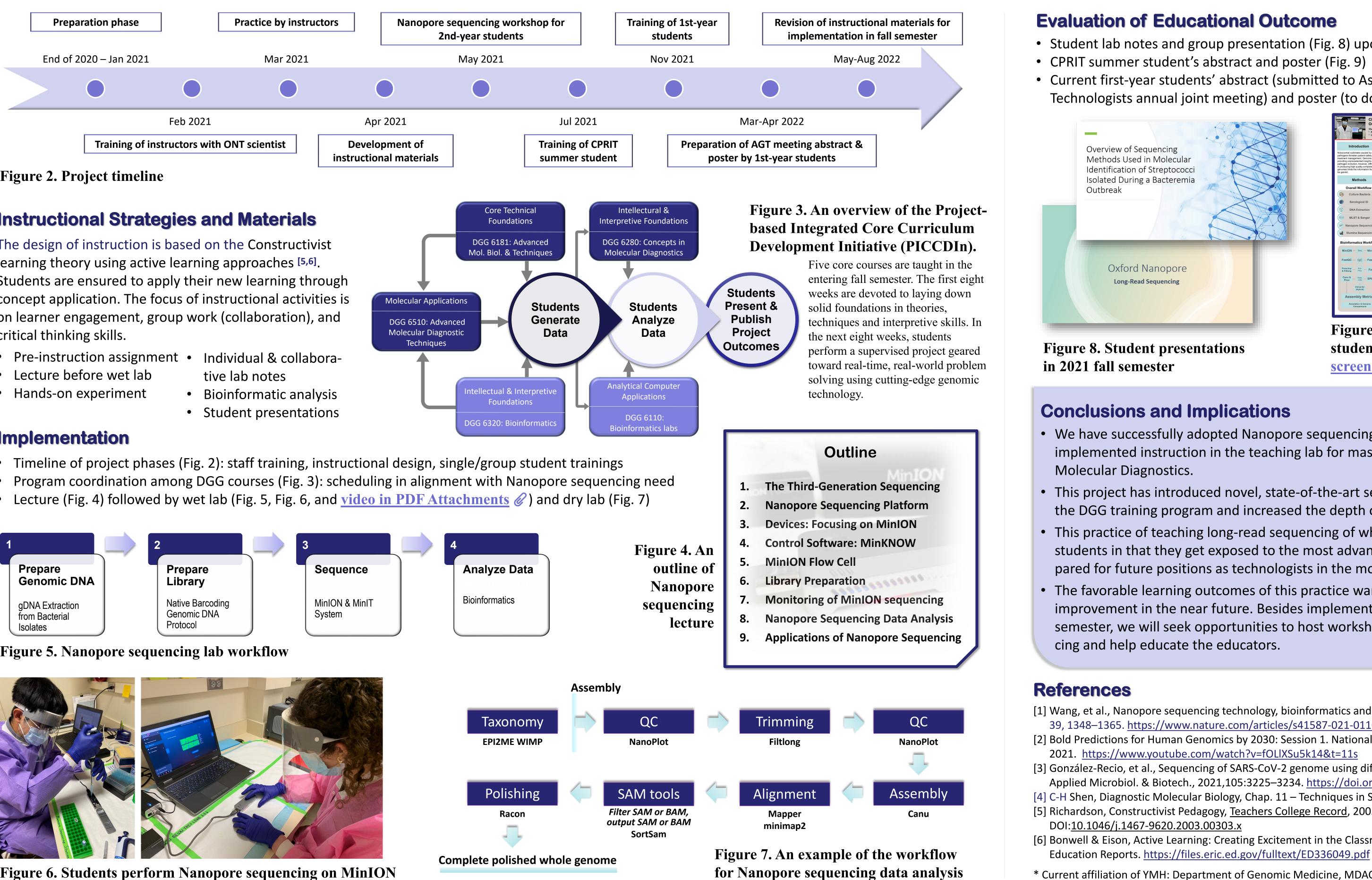


Figure 1. **Principle of** Nanopore sequencing (only MinION device shown) ^[1]

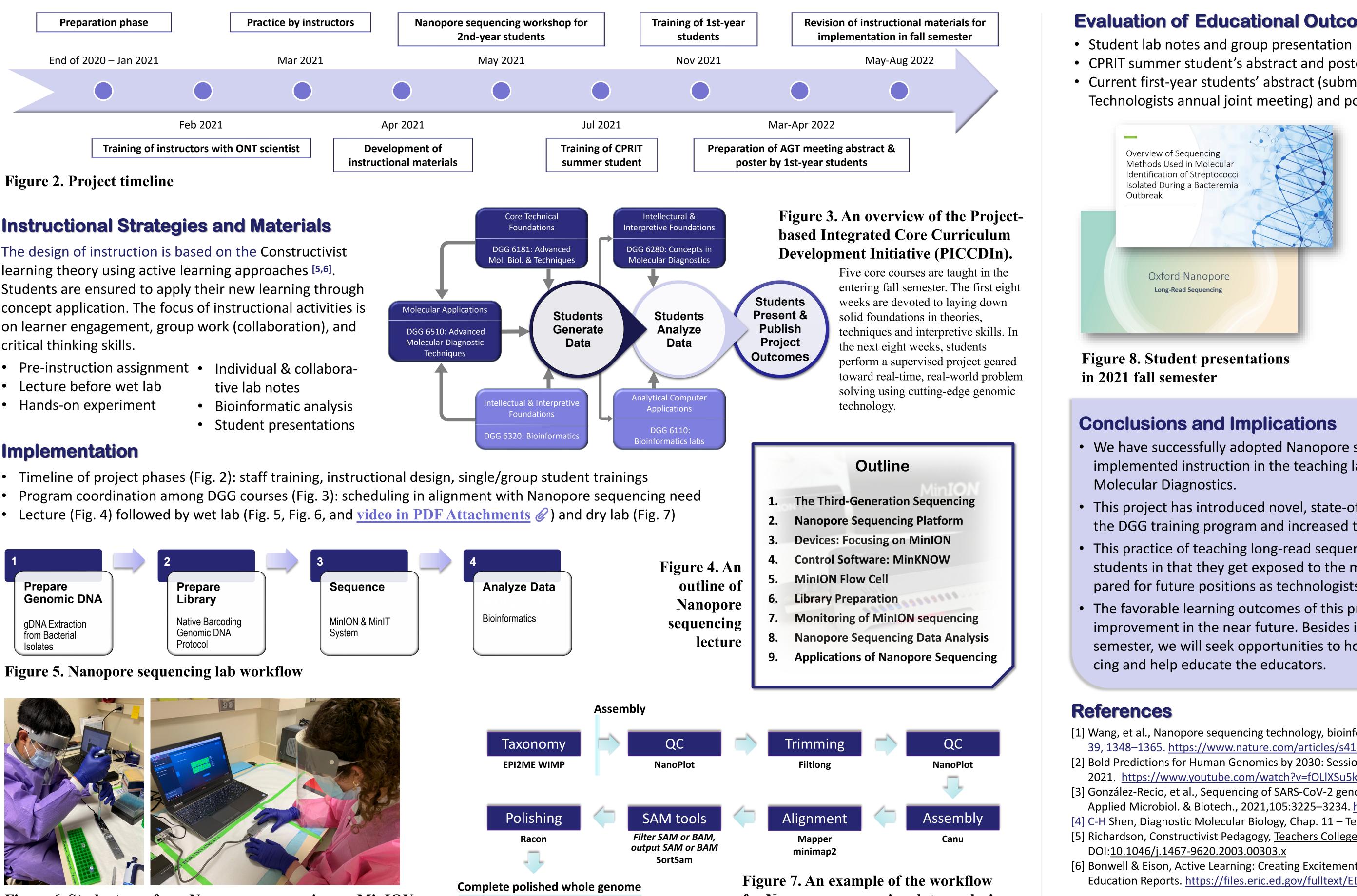
- Advantages over Illumina-based NGS platform ^[4]
- a. Long read (> 5k bp), high speed (1 bp/ns), and real-time base calling
- b. Fluorescent tag-free detection of bases
- Less sensitive to temperature throughout sequencing; reliable outcome
- d. Shortened hands-on time

Integration of Long-Read Whole Genome Sequencing in Graduate **Curriculum of Diagnostic Genetics and Genomics**

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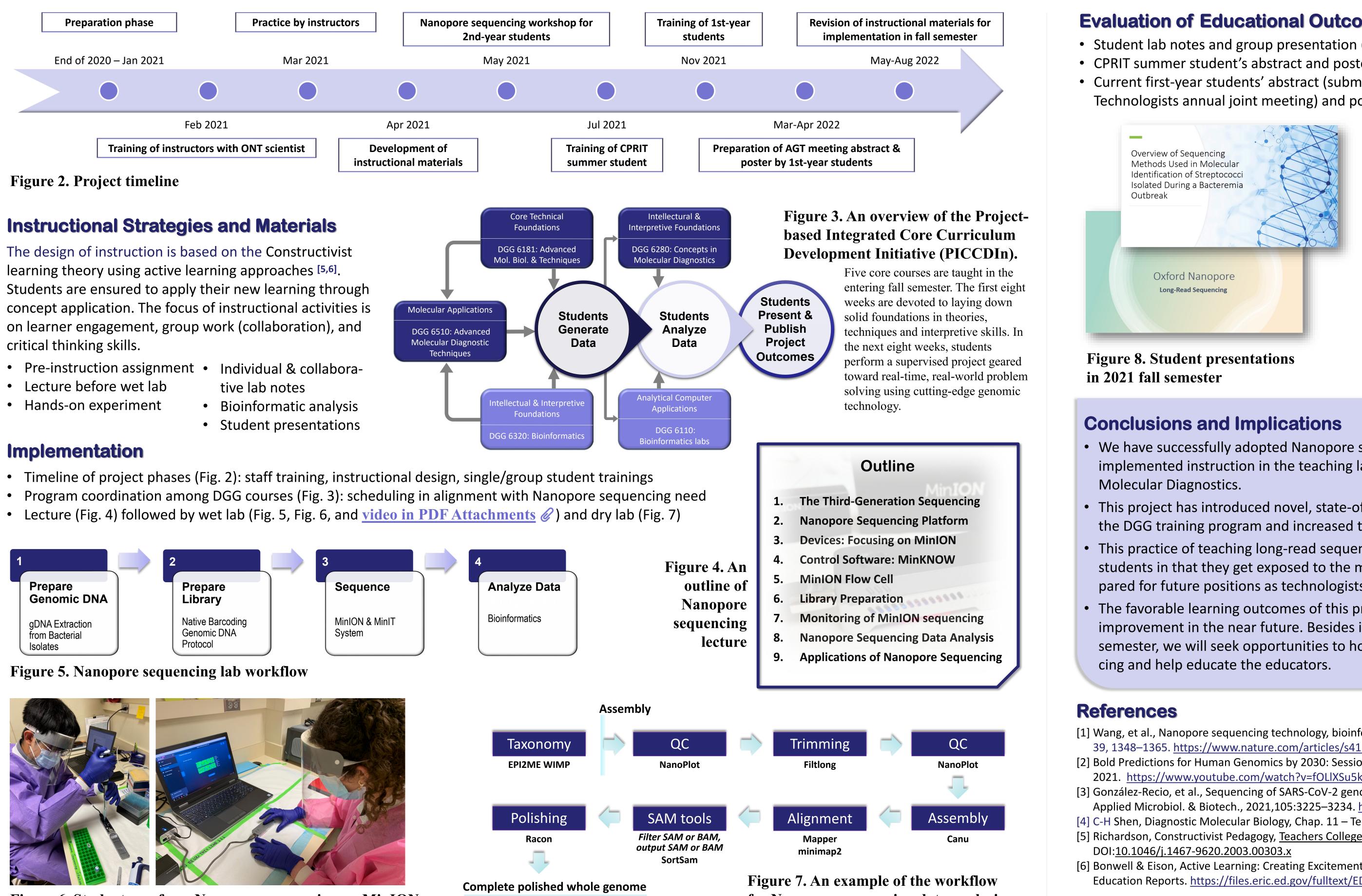
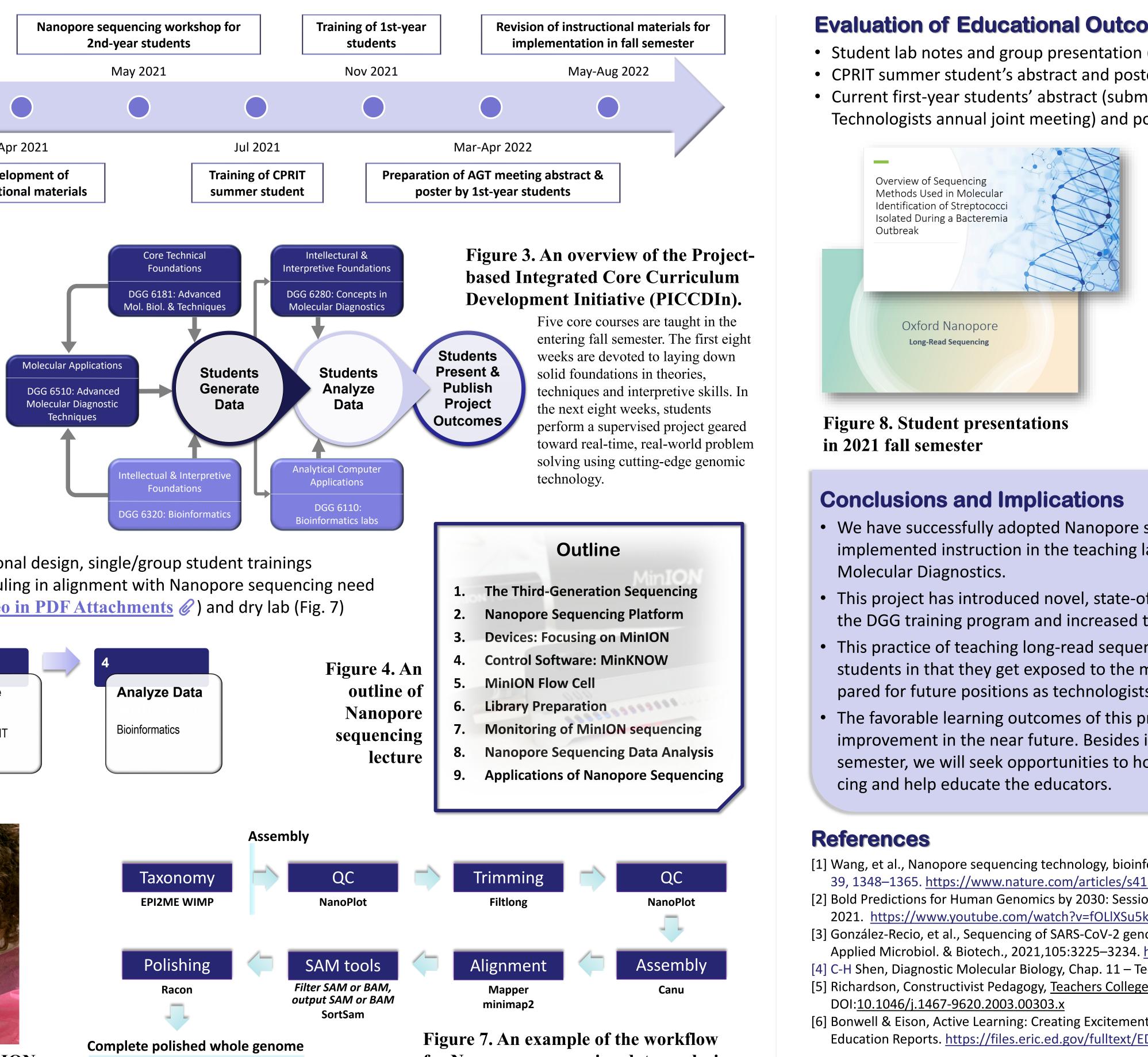
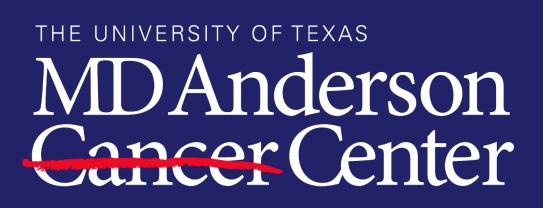


Figure 6. Students perform Nanopore sequencing on MinION



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Making Cancer History[®]

• Student lab notes and group presentation (Fig. 8) upon completion of instruction

• Current first-year students' abstract (submitted to Association of Genetic Technologists annual joint meeting) and poster (to do in April-May 2022)

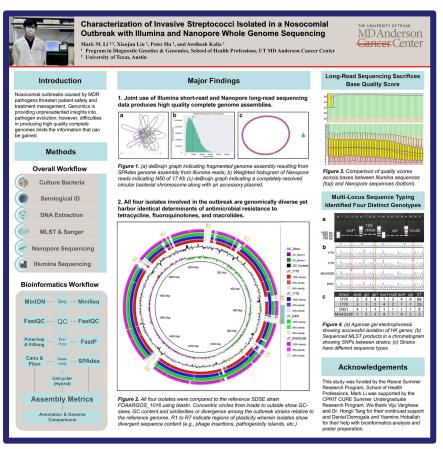


Figure 9. 2021 CPRIT summer student's poster, also seen in a screencast in PDF Attachments @

We have successfully adopted Nanopore sequencing technology (MinION) and implemented instruction in the teaching lab for master's students specialized in

This project has introduced novel, state-of-the-art sequencing technology into the DGG training program and increased the depth of the teaching curriculum.

This practice of teaching long-read sequencing of whole genomes benefit DGG students in that they get exposed to the most advanced technology and prepared for future positions as technologists in the molecular diagnostics field.

The favorable learning outcomes of this practice warrant replication and improvement in the near future. Besides implementation in the upcoming fall semester, we will seek opportunities to host workshops on Nanopore sequen-

[1] Wang, et al., Nanopore sequencing technology, bioinformatics and applications. Nature Biotech., 2021, 39, 1348–1365. https://www.nature.com/articles/s41587-021-01108-x.pdf

[2] Bold Predictions for Human Genomics by 2030: Session 1. National Human Genome Research Institute,

[3] González-Recio, et al., Sequencing of SARS-CoV-2 genome using different nanopore chemistries. Applied Microbiol. & Biotech., 2021,105:3225–3234. <u>https://doi.org/10.1007/s00253-021-11250-w</u> [4] C-H Shen, Diagnostic Molecular Biology, Chap. 11 – Techniques in Sequencing, 2019: 277-302, Elsevier. [5] Richardson, Constructivist Pedagogy, <u>Teachers College Record</u>, 2003, 105(9):1623-1640.

[6] Bonwell & Eison, Active Learning: Creating Excitement in the Classroom. 1991 ASHE-ERIC Higher