Laying a string NOT filling a vessel:
Genome papers as an active teaching and learning tool

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Introduction

- "**Laying a string**" and "**Filling a vessel**" , as described by Noam Chomsky, are two models of education that are strikingly different in approach and outcome.

- "**Laying a string**" model is an active teaching and learning method where students are provided with a string that can guide them through their learning journey. The active experience is likely to enhance students information retention abilities.

- "**Filling a vessel**" model is comparably a passive method and students are likely to serve as vessels that get filled with information that is returned during exams and never retained.

- **Genomics** is a relatively new field of biology that relies on understanding the entire genetic content that is referred to as "**genome**".

- Genomics is an interdisciplinary field that lies in the intersection of biology, genetics, bioinformatics, computer science, and engineering.

- Genomics is responsible for understanding of the basics of living organisms and is applied in medicine, agriculture, food production, and industry.
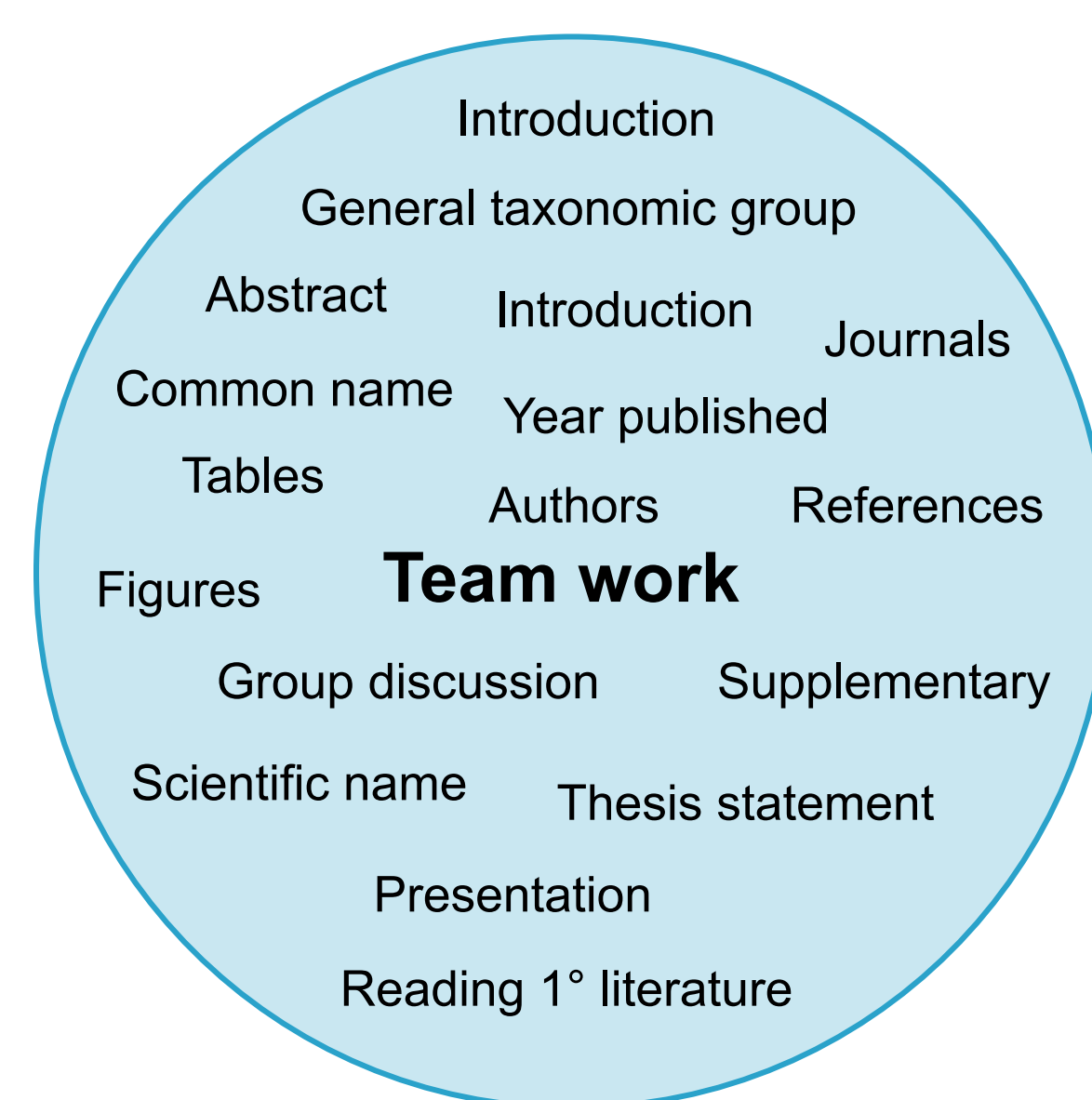
Objectives

- **Applying "Laying a string" model in the teaching of genomics course (485).**

- **Using published peer-reviewed genome papers as a "string" to guide students in discovering:**

    1) Academic concepts - "Academic string".

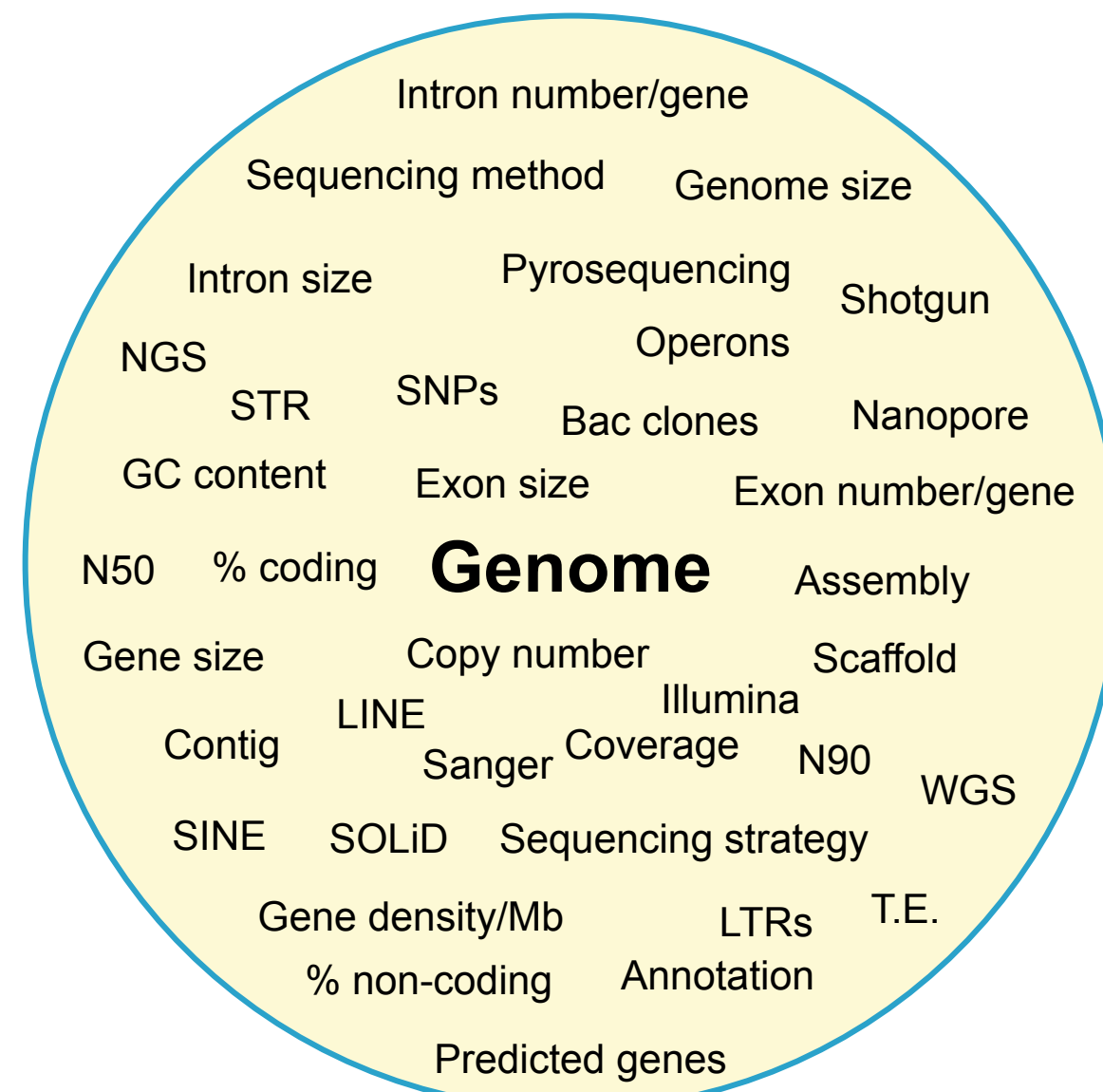   **2) Genome and genomics concepts – "Genomics string".**

Strategies

- The "string" laid out for students was as follows:

1. Select three organisms that are taxonomically related.
2. Conduct a literature search and find the genome papers of the three organisms.
3. One paper can be old (before 2010) and two must be published after 2010.
4. Download and/or print the three papers and related supplementary material.
5. Understand the structure and content of scientific papers using the "Academic string" (see below) and its concepts.
6. Independently, search for concepts as an assignment.
7. Discuss and share the learned academic concepts with peers in groups.
8. Review peers' findings by exchanging papers in class.
9. Change group formation every class.
10. Apply the same strategy to the "genomics string" (see below).

Academic String

Genomics String

"Academic string" outcome

- Students experienced searching for peer-reviewed articles and learned the difference between open access journal and subscription based ones.

- 28 genome papers were selected 9 of which were of model organisms and 19 of non-model (6 prokaryotes and 22 eukaryotes).

- Students identified paper elements (title, abstract, introduction etc.) and were able to locate the expected information in each element. For example, the title should contain the common name and/or scientific name of the organism and the word genome.

- Students Gained the ability to correctly extract information from their selected papers and verify the extracted information from their peers' papers.

- While focusing on their papers, students were given the chance to review all other paper during the group discussion session and the paper exchange activity.

- Students learned the basics of presenting their selected papers using a comparative genomics approach and focusing on specific hypotheses.

"Genomics string" outcome

- Using the genome paper as a string, students first explored the various genome sequencing strategies (Bac clone sequencing and whole genome shotgun (WGS sequencing).

- DNA sequencing methods (Sanger, illumina, Pyro etc.) were covered as students idntified the methods in their papers.

- Genome assembly process and the measure of assembly quality (contig N50 or scaffold N50) were illustrated as students found variation in these measure across the genome papers.

- The reported genes in each genome paper guided introducing structural annotation of sequenced genome while distinguishing it from the laborious functional annotation.

- The coding portion of genomes (genes) and its different components was covered as students identified them in their papers and supplementary material accompanying the papers.

- The variation in non-coding component of eukaryotic genomes was used as a guide to introduce tandom and interspersed repeats.

- Intra-species sequence variation represented by (single nucleotide polymorphisms – SNPs) found in each genome paper facilitated teaching and learning about the usability of variation to deduce evolutionary history and mapping of traits.

Stretching the "Genomics string"

- The student extracted data from their genome papers was used collectively to answer questions raised as genomic concepts were covered. Below are examples of questions and their answers.

- **How often are the different sequencing strategies implemented in the past two decades?**

The WGS is the predominant sequencing strategy in recent years and a reduced implementation of sequencing back clones due to its labor intensive and time consuming nature (**Fig. 1a**).

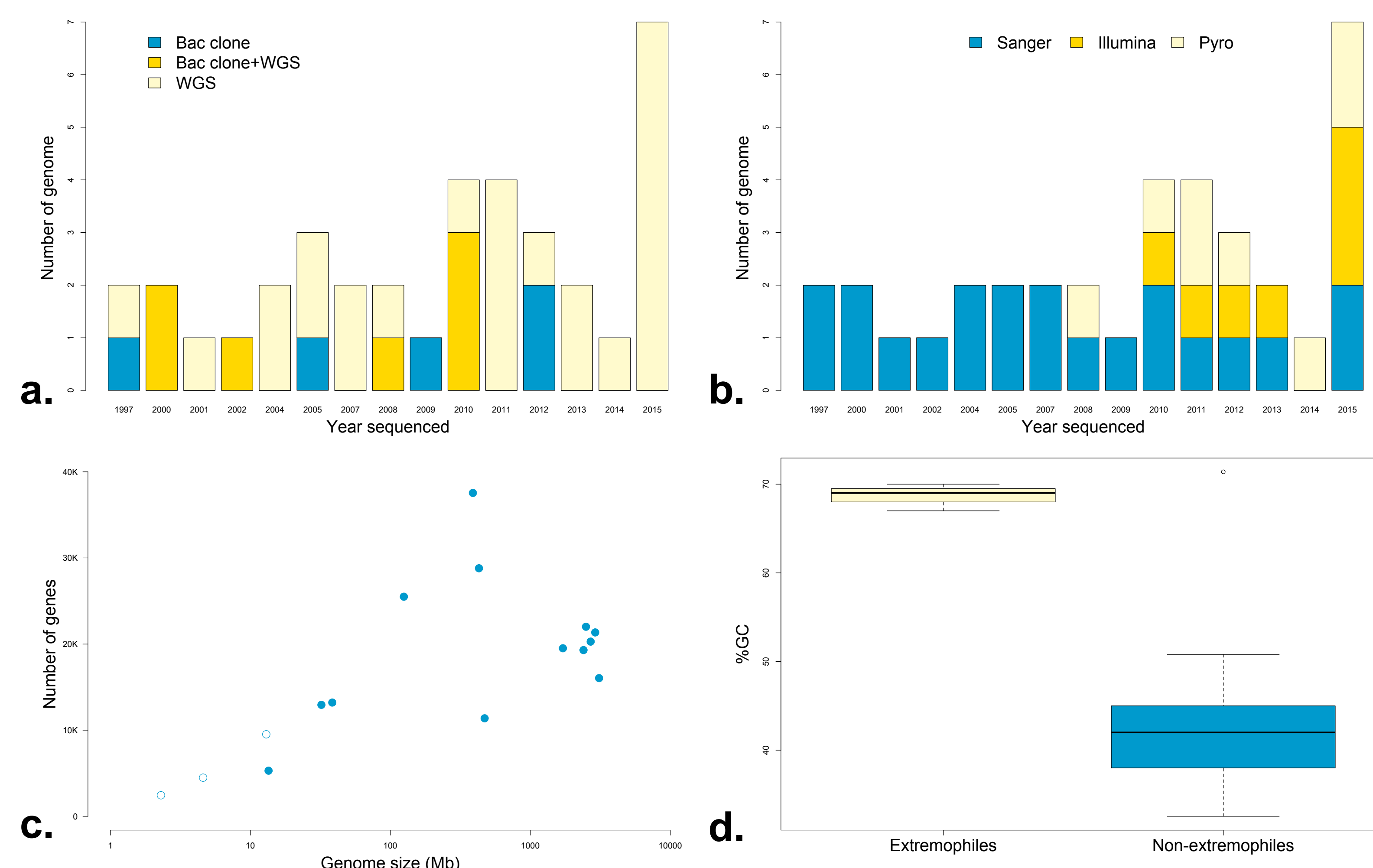- **What is the evolution of sequencing methods in the past two decades?**

Sanger remains a powerful sequencing method due to the length of the reads generated. The sequencing methods referred to as "Next Generation Sequencing -NGS" are relatively recent methods that focuses on the high throughput of short reads (**Fig. 1b**).

- **What is the relationship between genome size and number of genes?**

While prokaryotic genomes may show a linear relationship between genome size and gene number, the size of eukaryotic genomes (including ours!) is not, which is a result of the inflation in the non-coding (repetitive) genomic content (**Fig. 1c**).

- **Is there a difference in nucleotide composition of extremophiles vs. non-extremophiles?**

The genomes of extremophiles exhibits higher percentage of GC content than their non-extremophile counterparts to insure the survival and stability of the genetic material (**Fig. 1d**).

Fig.1. Comparative genomic analysis of students' extracted data. a-b) Graphs showing the genome sequencing strategy and method, respectively, over 18 years period. **c)** Relationship between genome size and number of genes across range of organisms. Empty circles represent prokaryotic genomes and filled circles represent eukaryotic genomes. **d)** Comparison between the GC content of extremophile genome versus non-extremophile genome.

Conclusion

The active teaching and learning method of "laying a string" has, as students testified, proven to be a fun and versatile way to learn about the science of genomes, engage in discussions, and independently answer significant biological questions.