An educational guide for nanopore sequencing in the classroom

Assignment 1 : Abstract And Introduction Summary

- Abstract :

1-The last decade has witnessed a remarkable increase in our ability to measure genetic information. Advancements of sequencing technologies are challenging the existing methods of data storage and analysis.

2-Future generations of biologists must be more computationally aware and capable. This means they should be trained to give them the computational skills to keep pace with technological developments.

- Introduction :

1-what defines a biologist? In short, a biologist is a person who studies life and living organisms.

2-Biology covers diverse topics such as molecular biology, structural biology, ecology, evolution, genetics, microbiology, immunology, and biotechnology. Importantly, most (if not all) of these topics have undergone incredible progress due to rapid discoveries and technological advances [1,2]. As such, a modern biologist has the inevitable tasks of adapting to rapid change and mastering new knowledge and technology.

3-One of the most important revolutions in the field of biology was caused by the development of next-generation sequencing (NGS) technologies. Using massively parallel processing of samples, NGS dramatically reduces sequencing time and costs, enabling the sequencing of entire genomes.

4-Currently, genome sequencing and analysis have become a crucial component in biology, as evidenced by recent scientific breakthroughs [3,4] and by the exponential increase of reported genomes on GenBank (e.g., from 30,000 sequenced prokaryotic genomes in 2014 [5] to 183,000 in 2018.

5-not only do biologists need to adapt and learn how to use these emerging technologies, they also need to learn how to mine the ever-growing mountain of genomic information they generate, which requires bioinformatics skills. Now, the question is how do we train this generation of biologists so that they have the required computational skills?

-Related works:

Twenty-four groups of 4 students (96 total) prepared their own DNA libraries of various single-isolate bacterial, bacteriophage, and metagenomic samples in the classroom. Number of groups and their size were determined to allow for sufficient supervision within the available lab space. If possible, smaller groups are preferable to increase the hands-on time of each student

We would like to emphasize the benefits of having multiple groups working on different related samples (e.g., each barcode represents a similar but different microbial isolate). This allows groups to initiate discussions about differences in their own findings.

1-Karas M, Hillenkamp F. Laser desorption ionization of proteins with molecular masses exceeding 10000 daltons. Anal Chem. 1988; 60: 2299–301.
https://doi.org/10.1021/ac00171a028 PMID:3239801

2-Norton ME. Noninvasive prenatal testing to analyze the fetal genome. Proc Natl Acad Sci U S A. 2016;
113: 14173–14175. https://doi.org/10.1073/pnas.1617112113
PMID: 27911833

3- Kim D, Song L, Breitwieser FP, Salzberg SL. Centrifuge: rapid and sensitive classification of metagenomic sequences. Genome Res. 2016; 26: 1721–1729.
https://doi.org/10.1101/gr.210641.116 PMID: 27852649

Name : Omnya Abd El Fattah Ali

3rd year Bioinformatics Department