**Annotated bibliography:**

1. da Fonseca, R. R., Albrechtsen, A., Themudo, G. E., Ramos-Madrigal, J., Sibbesen, J. A., Maretty, L., Zepeda-Mendoza, M.L., Campos, P.F., Heller, R., Pereira, R. J. (2016). Next-generation biology: sequencing and data analysis approaches for non-model organisms*. Marine genomics*, 30, 3-13.

Fonseca et al . 2016 present a detailed review about the next generation sequencing technologies available for biological studies along with the bioinformatic tools at that time available for analyzing NGS data. Within their review the authors explain the different NGS outputs such as: 1) Restriction-site associated (RADseq) 2) Target sequencing (e.g. UCEs), 3) Transcriptomic sequencing (RNA-seq), and 4) whole genome sequencing. They specifically explain the advantages and disadvantages of each sequencing techniques and explain if they are useful to answer questions at a deep (phylogenetic) or recent (population genetics) evolutionary scale. They also have a section and comparative table showing the different NGS platforms including information about the detection method, library types, maximum read length and error rate related to these tools.

1. Taishan Hu, Nilesh Chitnis, Dimitri Monos, Anh Dinh. (2021) Next-generation sequencing technologies: An overview. Human Immunology, 82(11), 801-811.

This article is a very complete review paper that explain how the next generation and third generation sequencing platforms work. It is particularly useful because the authors review the most important steps and consideration that researchers should include while doing library preparation of their samples and how this step may differ depending on the target output ( e.g. whole exonic regions, whole genomes, target sequences, RNA-seq). The authors also explain the chemistry behind the sequencing plataforms of: 1) Illumina, 2) Ion Torrent, 3) PacBio, and 4) NanoPore.

1. Lam, H. Y., Clark, M. J., Chen, R., Chen, R., Natsoulis, G., O'huallachain, M., ... & Snyder, M. (2012). Performance comparison of whole-genome sequencing platforms. Nature biotechnology, 30(1), 78-82.

This article compares the accuracy and completeness of genome sequencing between two platforms: Illumina and Complete Genomics. Their results show that both platforms have similar outcomes with around 88% of the SNVs obtained from variant calling being the same. This article seems important since it considers how different sequencing platforms may generate slightly different results in the sequences obtained, thus making emphasis on the importance to consider machine errors when interpretating genomic data.

1. Stoler, N., & Nekrutenko, A. (2021). Sequencing error profiles of Illumina sequencing instruments. NAR genomics and bioinformatics, 3(1), lqab019

This study evaluates the error rates of Illumina platforms using 1943 online databases, finding that the more expensive and recent platforms of Novaseq and HiSeq exhibiting less error rates. The authors find that the HiSeq X Ten is easily the most consistent platform compared to other illumina platforms. In addition to the type of platforms used, the authors mentioned that error rate can also strongly be influenced by the individual handling of experiments.

1. Quail, M. A., Smith, M., Coupland, P., Otto, T. D., Harris, S. R., Connor, T. R., ... & Gu, Y. (2012). A tale of three next generation sequencing platforms: comparison of Ion Torrent, Pacific Biosciences and Illumina MiSeq sequencers. BMC genomics, 13, 1-13.

This article compares the performance of three widely used next-generation sequencing (NGS) technologies: Ion Torrent, Pacific Biosciences and Illumina MiSeq. It explains the benefits and disadvantages of each sequencing platform giving useful information about how these three platforms are different in their: workflow, genome coverage and GC bias, error rate and performance in downstream analysis such as SNP calling.