

DNA Sequencing Technologies

Gepoliano Chaves, Ph. D.

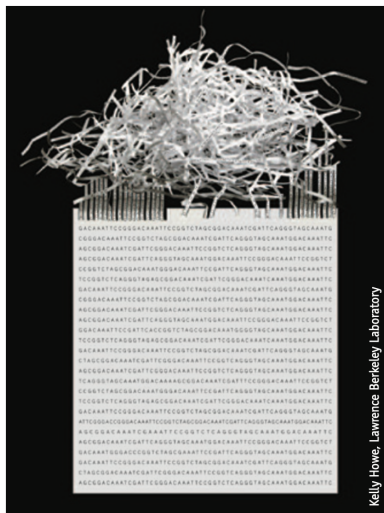
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Overview

After completing today's session, students should:

- ▶ Think about the problem of genome assembly
- ▶ Know how DNA is extracted, sequencing libraries are prepared and analysed

Genome Assembly



Kelly Howe, Lawrence Berkeley Laboratory

Figure 1: Genome assemblies need a lot of sequencing data and complex informatics algorithms to put the sequence back together. Figure from Baker (2012).

The DNA sequencing Machine: Flow Cell

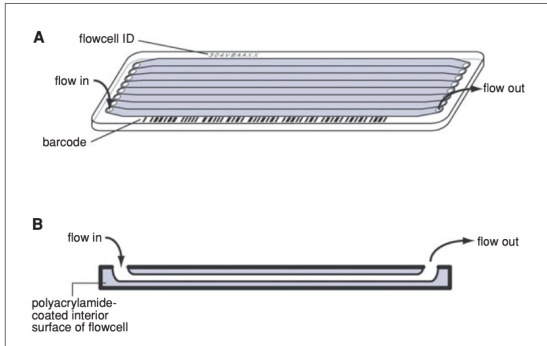


Figure 2: Flow-cell. Figure from Quail (2009).

The DNA sequencing Machine: Cluster amplification

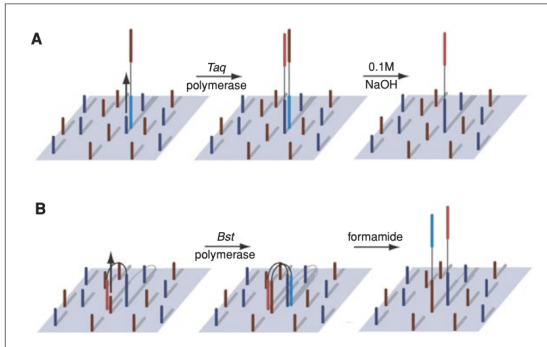


Figure 3: Cluster amplification. Figure from Quail (2009).

Gene Prediction and Annotation

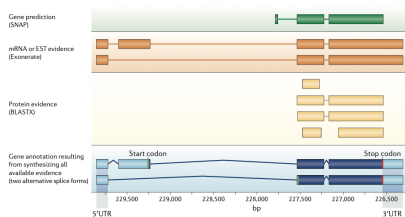


Figure 5: Gene prediction and annotation. Figure from Yandell and Ence (2012)

References

- Baker, Monya. 2012. *De Novo Genome Assembly: What Every Biologist Should Know*.
- Quail, Michael. 2009. *Improved Protocols for the Illumina Genome Analyzer Sequencing System*.
<https://pubmed.ncbi.nlm.nih.gov/19582764/>.
- Yandell, Mark, and Daniel Ence. 2012. *A Beginner's Guide to Eukaryotic Genome Annotation*.