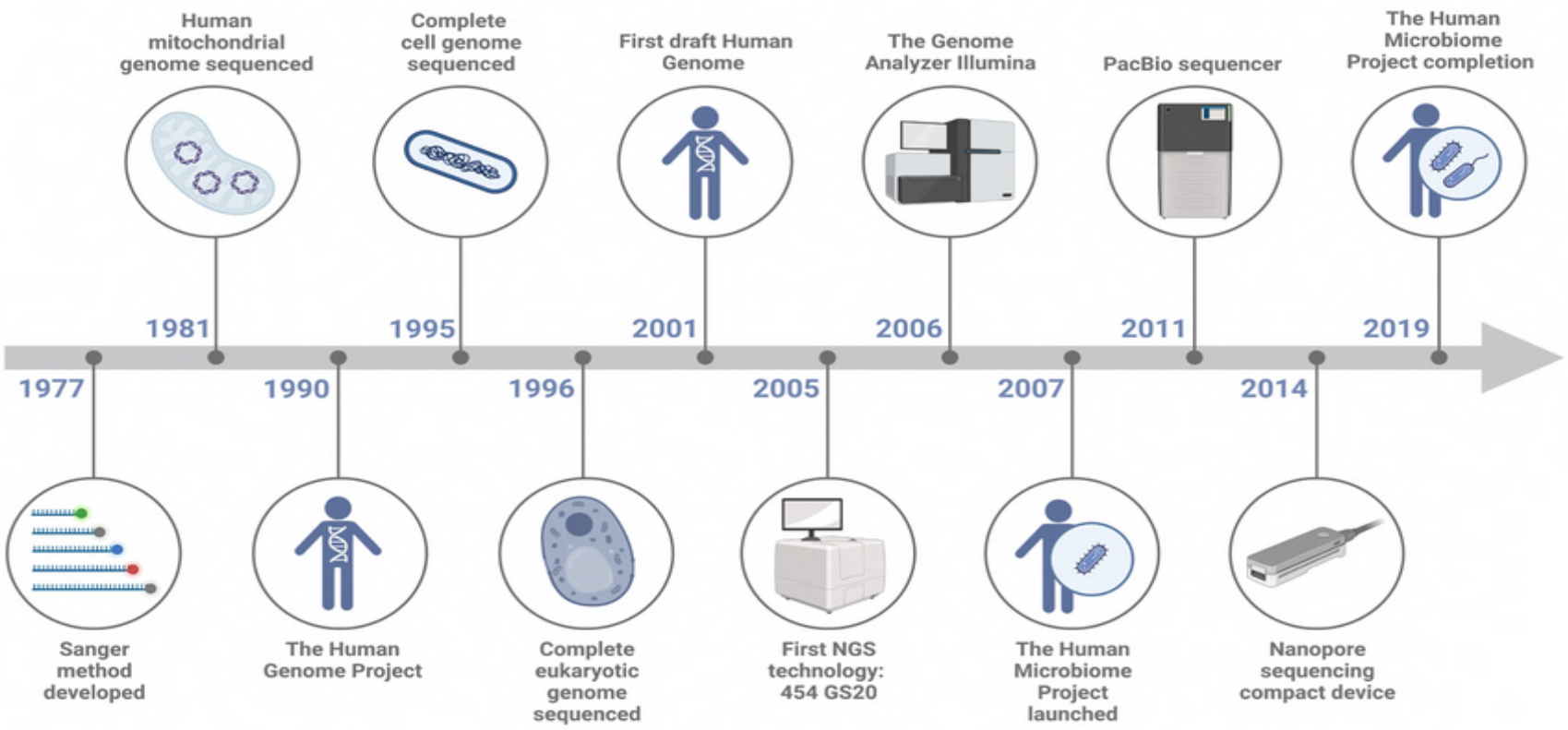
Genome Sequencing

Dr. Varun CN
SSO, Neurovirology
NIMHANS

What are we discussing about ?

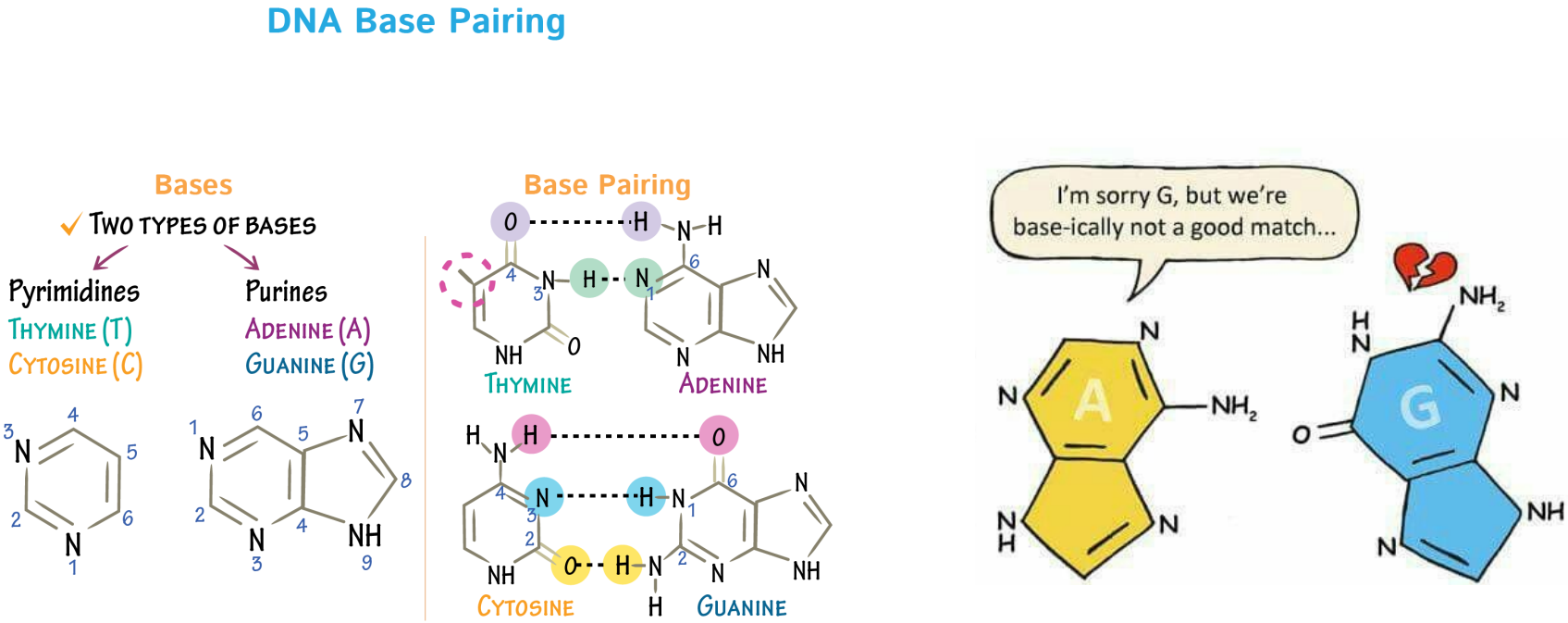
- Genome Sequencing with examples
  - First Generation
  - Second Generation
  - Third Generation
- Our Experience in sequencing Rabies Virus

Genome sequencing (Landmark events)



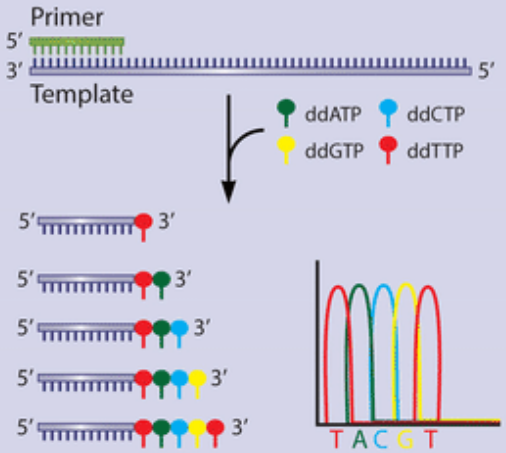
McEwen, Juan & Gomez, Oscar. (2023)

The core concept



Sequencing Technologies

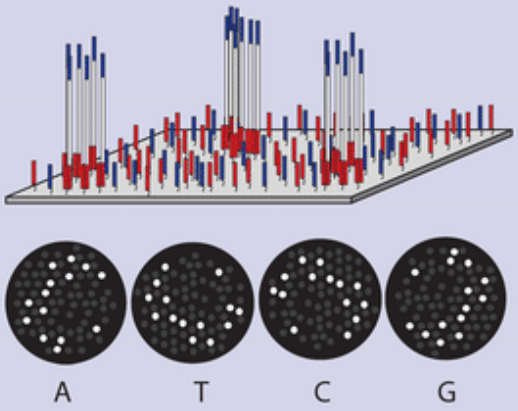
First Generation
Shotgun Sequencing



- Sequencing by synthesis
- High accuracy
- Long read lengths
- Relatively small amount of data generated

e.g., ABI capillary sequencer (ABI)

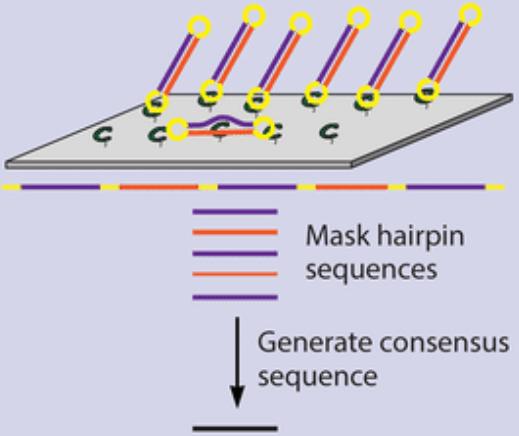
Second Generation
Massively Parallel Sequencing



- Sequencing by synthesis
- Amplified templates are generated during sequencing, reducing the requirements for starting material
- High accuracy
- Short read lengths

e.g., MiSeq (Illumina), Ion Torrent (Thermo Fisher Scientific)

Third Generation
Single-molecule Sequencing

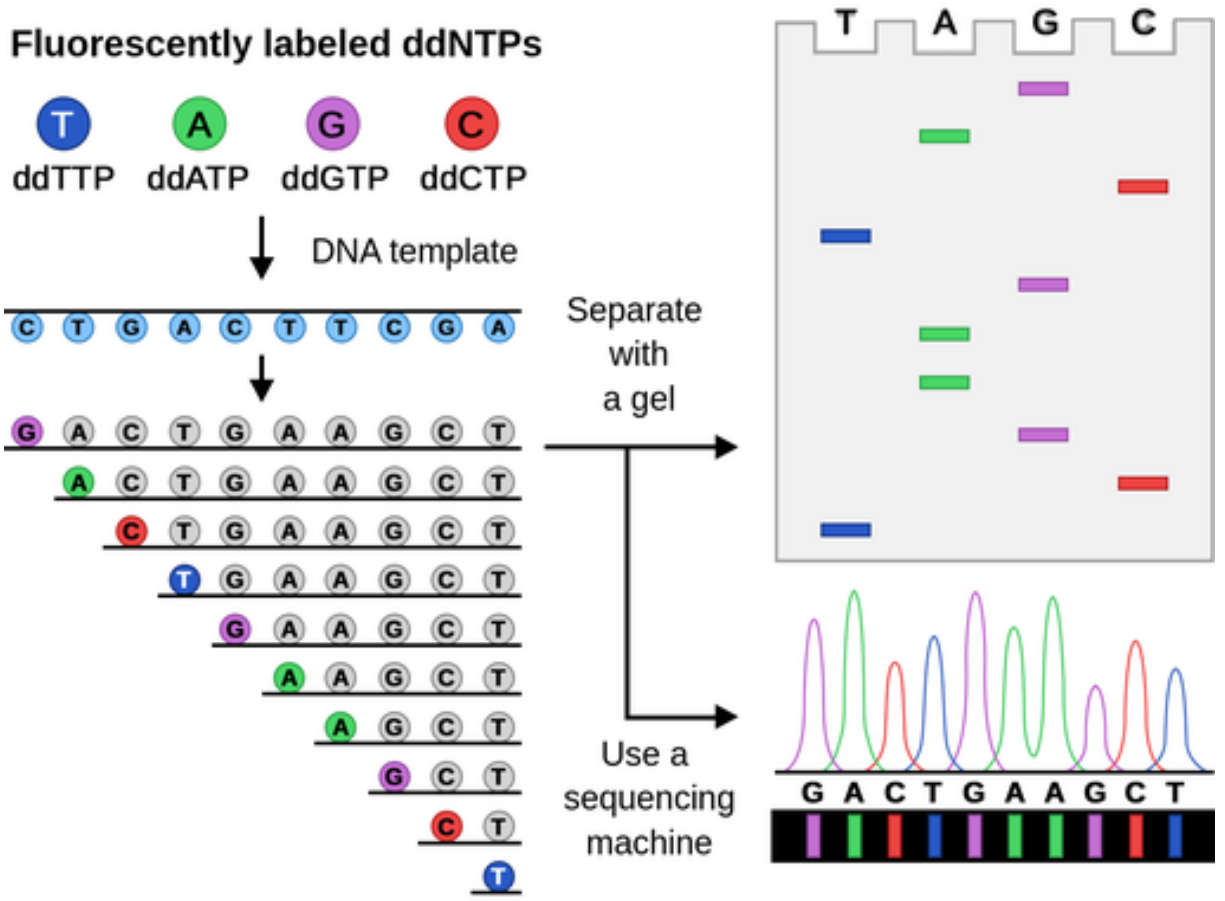


- Single-molecule templates
- Low accuracy
- Long read lengths

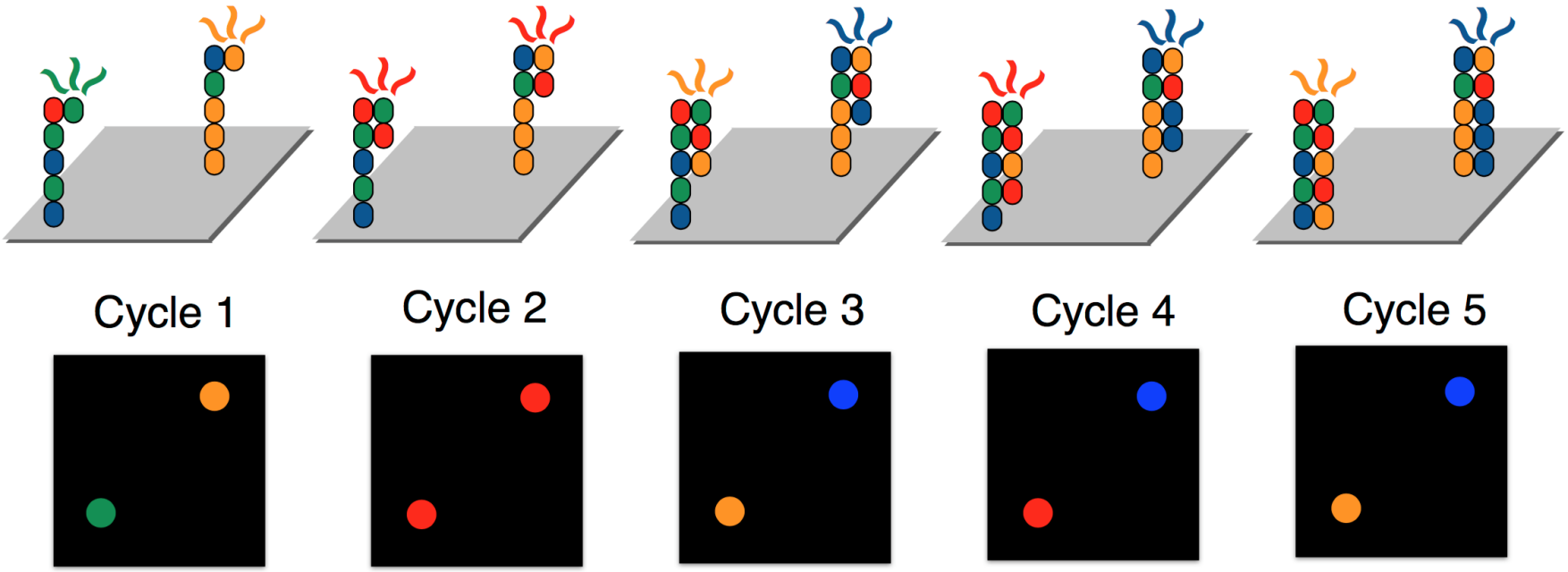
e.g., Single-Molecule Real-Time (SMRT) — Sequencing (Pacific Biosciences), MinION (Oxford Nanopore Technologies)

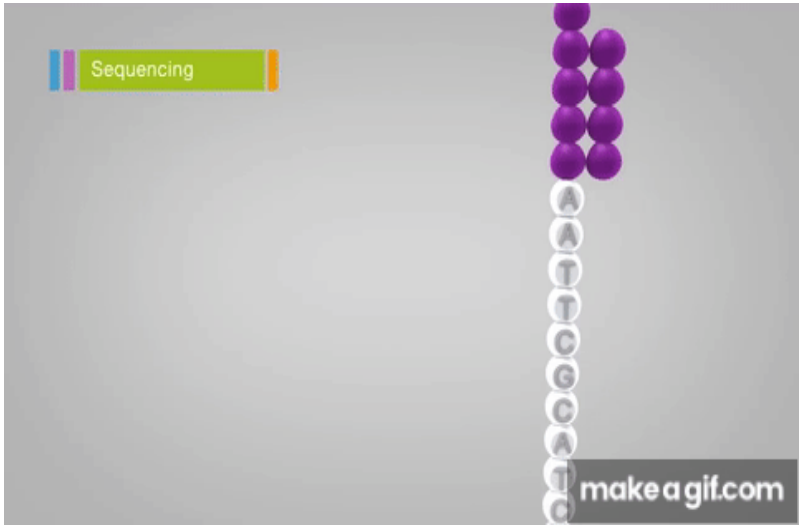
Ronholm J, Nasheri N, Petronella N, Pagotto F. 2016. Clin Microbiol Rev 29:837–857

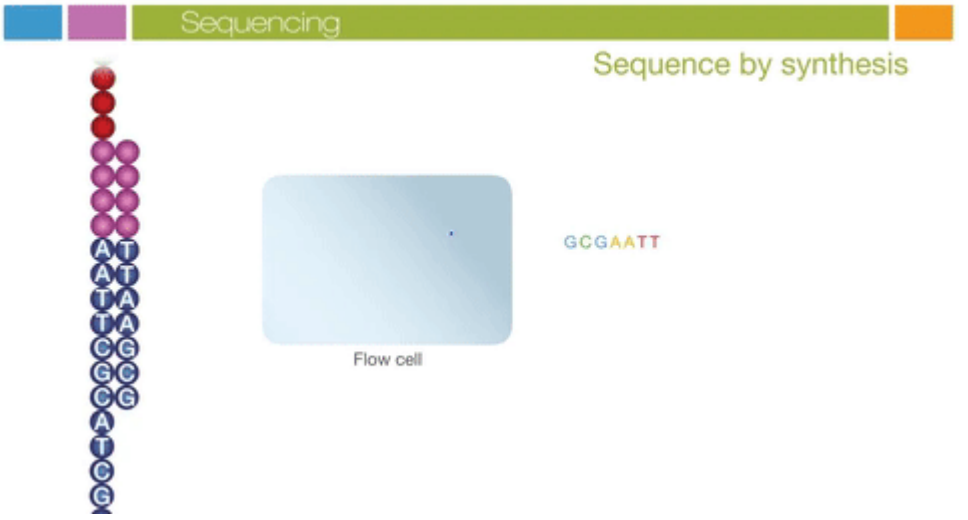
First Generation

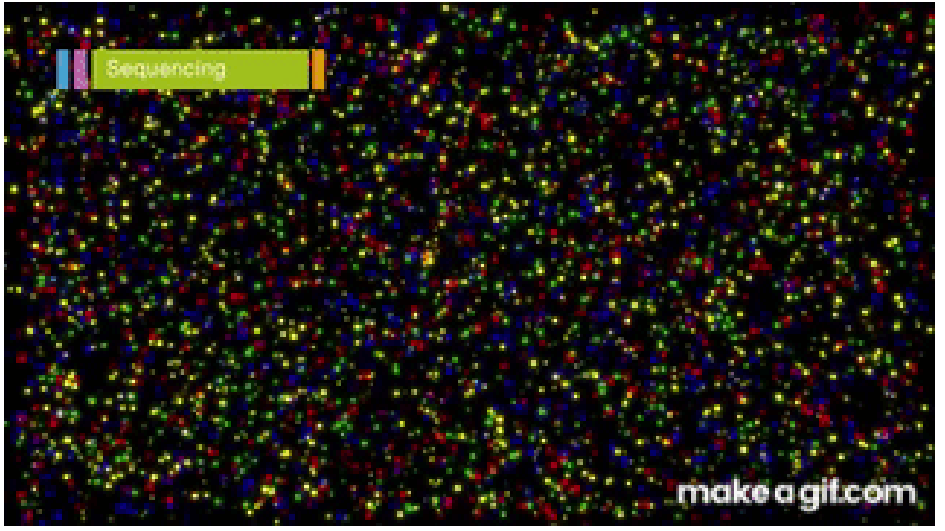


Second Generation

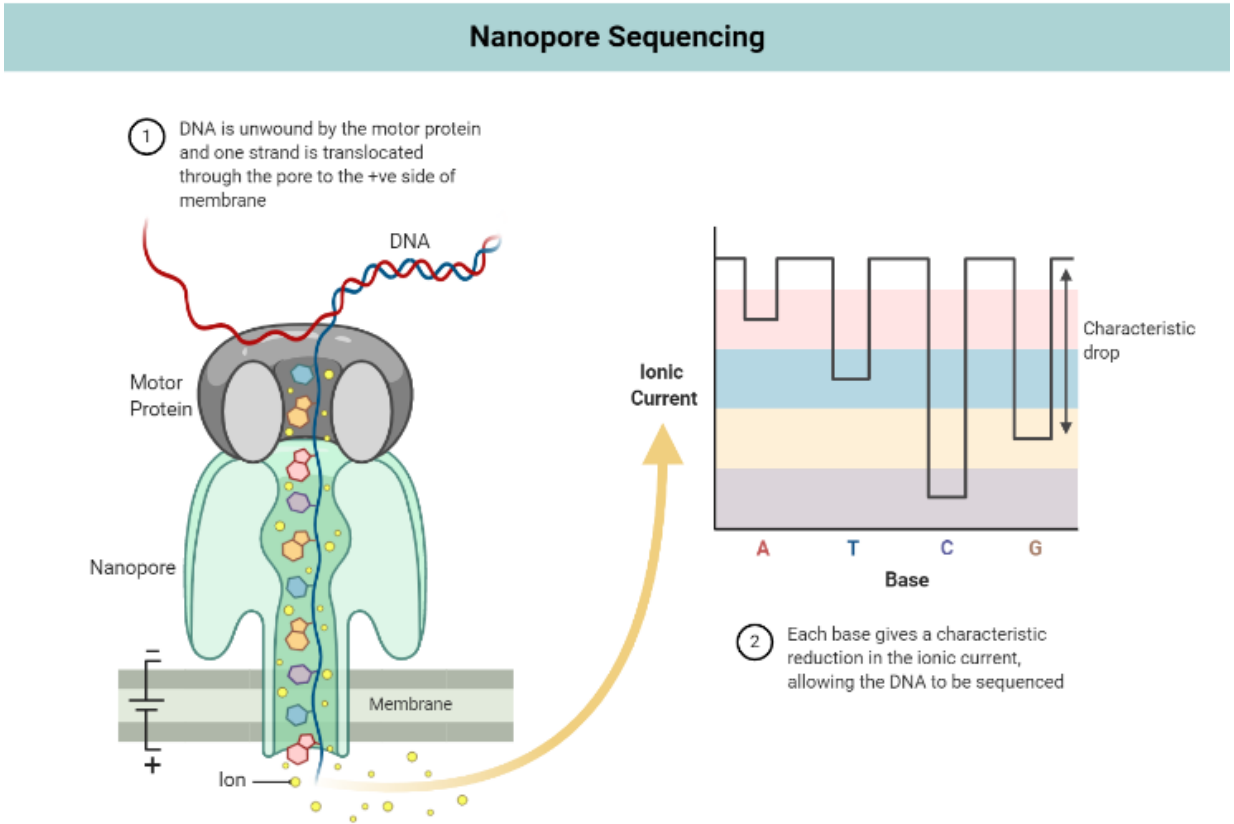


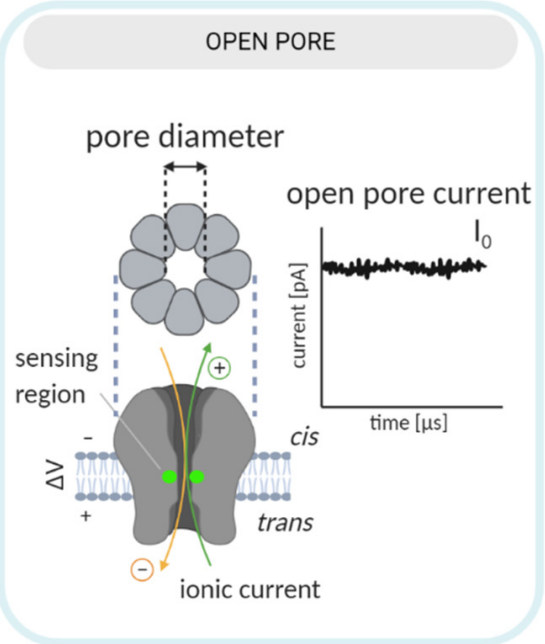

Sequencing
make a gif.com

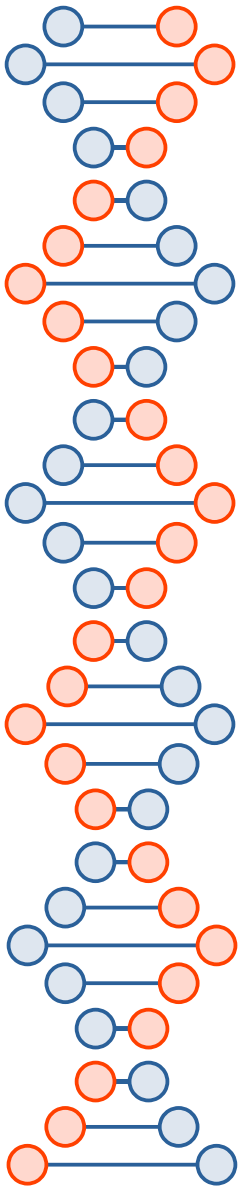

Sequencing
Sequence by synthesis
Flow cell
GCGAATT

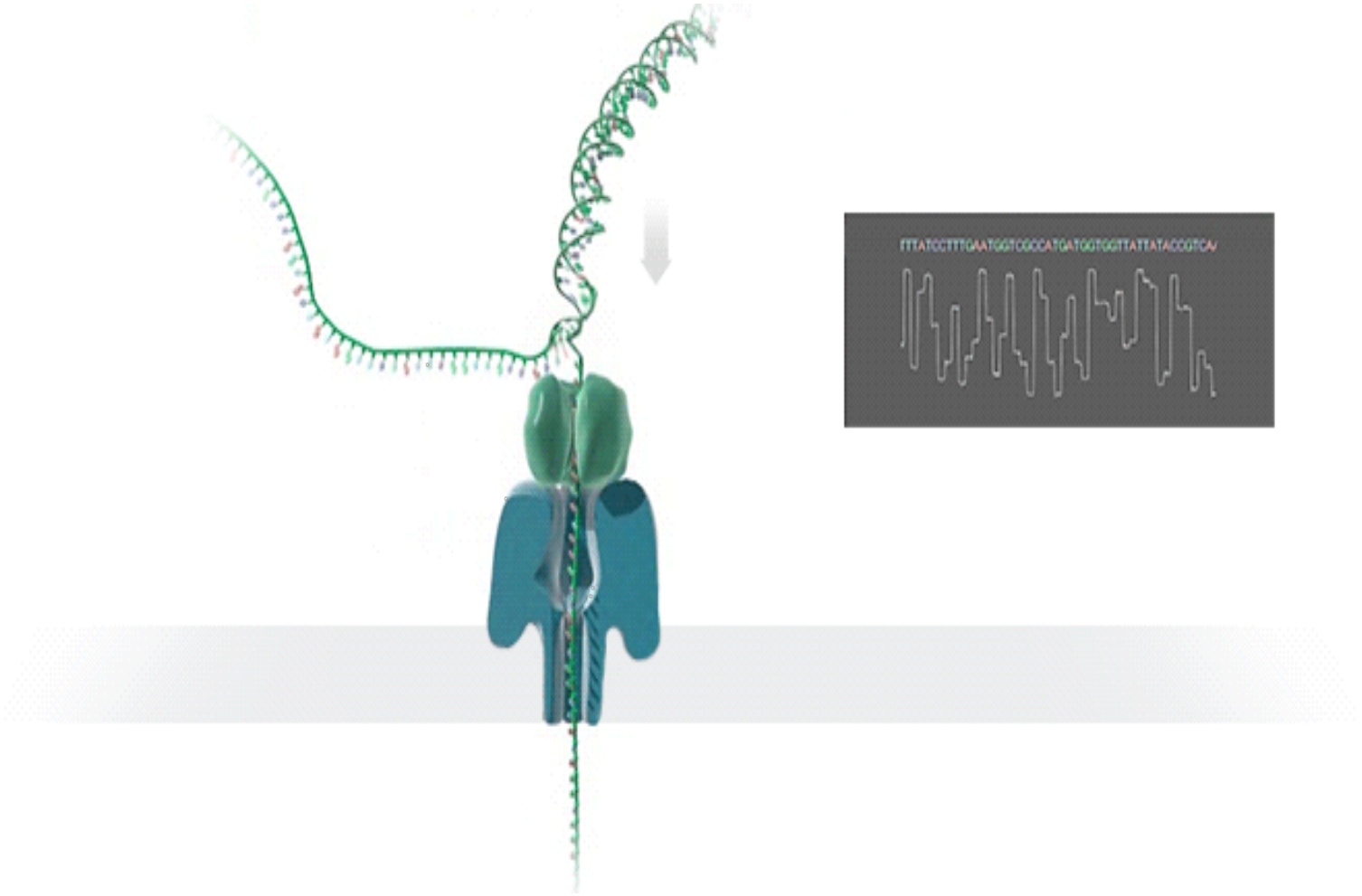

Sequencing
make a gif.com

Third Generation









Rabies Virus Genome Sequencing
Our Experience, thus far

Jan 28, 2024

Rabies Virus Sequencing using Illumina- MiSeq

DOI
dx.doi.org/10.17504/protocols.io.ewov1qbrogr2/v1

Chakrakodi N Varun[1], Dhanya K[1], Ashwini M Ananda[1], Reeta Mani[1]
[1]Department of Neurovirology, NIMHANS

Chakrakodi N Varun
Department of Neurovirology, NIMHANS

OPEN ACCESS

DOI: dx.doi.org/10.17504/protocols.io.ewov1qbrogr2/v1

Jan 11, 2023

MinION Sequencing protocol for Rabies virus of Arctic lineage

Forked from MinION Sequencing protocol for Rabies virus of Indian subcontinental lineage

DOI
dx.doi.org/10.17504/protocols.io.3byl4jzb8lo5/v1

pramadaprasad[1], Harsha P.K.[1], Chitra Pattabiraman[1]
[1]National Institute of Mental Health and Neuro Sciences

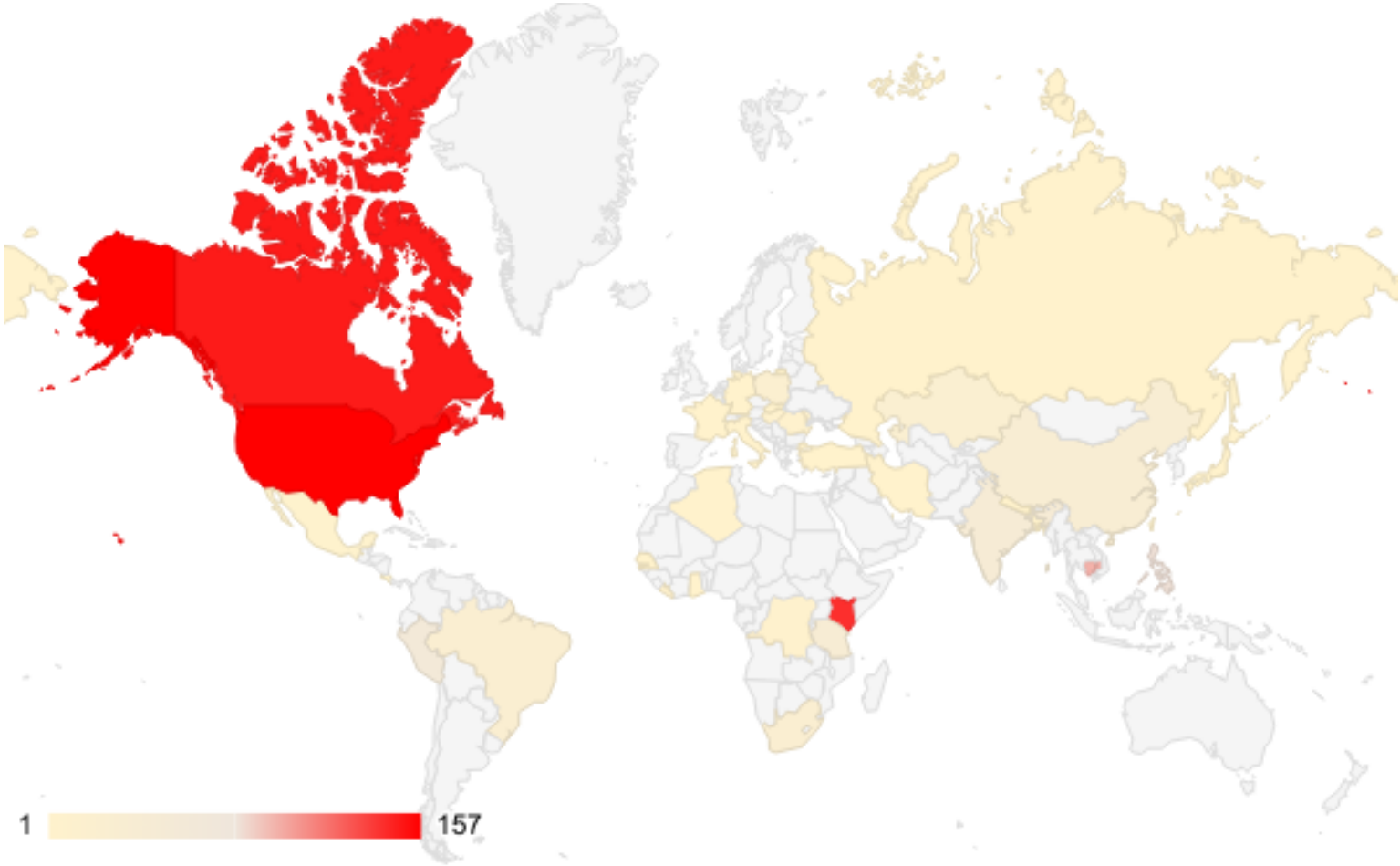
NIMHANS

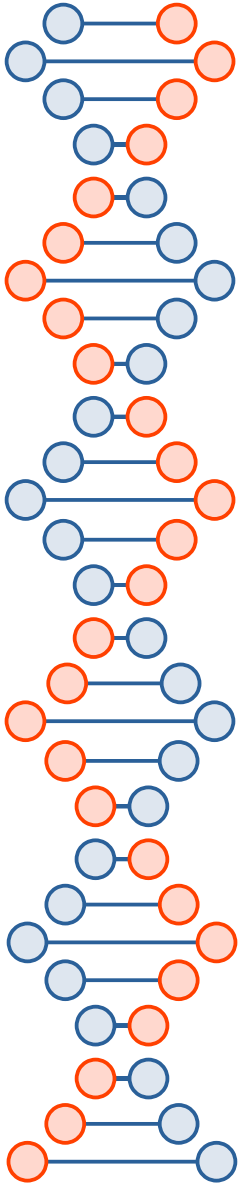
pramadaprasad

OPEN ACCESS

DOI: dx.doi.org/10.17504/protocols.io.3byl4jzb8lo5/v1

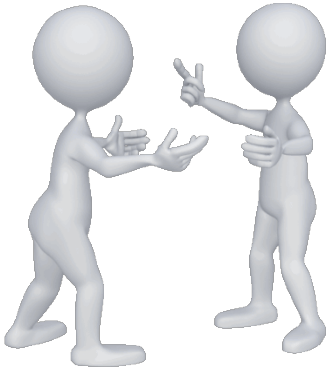
RABV Sequence Availability





Whole genome sequencing: Why

- **Epidemiological Studies**
  - Circulating Genotypes
  - Cross Contamination Event Predictions
- **Mutation**
  - Importance for successful vaccine designs
- **Phylodynamics**



cha6203@nimhans.ac.in