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# Bioinformatics up to Date

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## Inside…..





## About us

The Bioinformatics Infrastructure Facility (BIF) at Biotechnology division, CSIR NEIST, Jorhat runs under the Biotechnology Information System Network (BTISnet) programme of DBT, Ministry of Science & Technology, and Government of India. The Centre was established on 2nd February, 2008 to promote innovation in Biological research and education through Bioinformatics accomplishment. The main goal is to facilitate and expose students and researchers from different academic institutions of North East India in Bioinformatics. The center conduct training and workshops for enlightening the use of bioinformatics applications in biological research and development. The Centre has access to global information through 24 hour high speed internet facility, and also e-journal facilities with DeLCON, Science Direct etc. To date the Centre has profoundly extended support in R & D work with a great intensity to different biological discipline including medicinal chemistry, computer aided drug design, genomics and proteomic data analysis etc.

## Cas9-deaminase barcoding system: A genome editing strategy for lineage tracing

Understanding cell lineage and function illuminates the underlying mechanisms of human physiology and pathology. Human genome consists vast number of repetitive elements. By amplifying and characterizing human L1 retrotransposons as target regions for cell barcoding system, Byungjin Hwang, *et al.,* developed a genome editing strategy utilizing a cytidine deaminase fused with nickase Cas9 (nCas9) to specifically target endogenous interspersed repeat regions in mammalian cells. Using targeted mutagenesis with single guide RNA (sgRNA), mutation was induced leveraging C-to-T substitution events, and subsequent read out by a single primer pair. The resulting mutation patterns is used as a genetic barcode. By analysing interspersed mutation signatures, they showed the accurate reconstruction of cell lineage using both bulk cell and single-cell data.

*Source: Byungjin Hwang, et al. J Nature Communications, 2019*

## LEMON: A framework for rapid mining of structural information from the PDB

The protein data bank (PDB) is an essential online database resource providing 3D structures of proteins and nucleic acids. PDB currently holds over 140,000 biomolecular structures and continues to release new structures on a weekly basis. It is one of the essential databases for structural bioinformatics to develop software that mine, use, categorize, and analyze such data. Computational biology methods utilize 3D experimentally determined structures and structural features of proteins and nucleic acids from the PDB. For rapid query of 3D descriptors of the entire PDB and to generate desired structural features, Jonathan Fine, et al. proposed a new approach named Lemon framework, a C++11 library with Python bindings. Lemon provides a consistent workflow methodology for selecting biomolecular interactions based on user criterion and computing desired 3D structural features. Lemon uses MacroMolecule Transmission Format (MMTF) to reduce the computational cost of reading text-based formats. This framework can analyse and characterize the entire PDB in less than ten minutes on modern, multithreaded hardware.

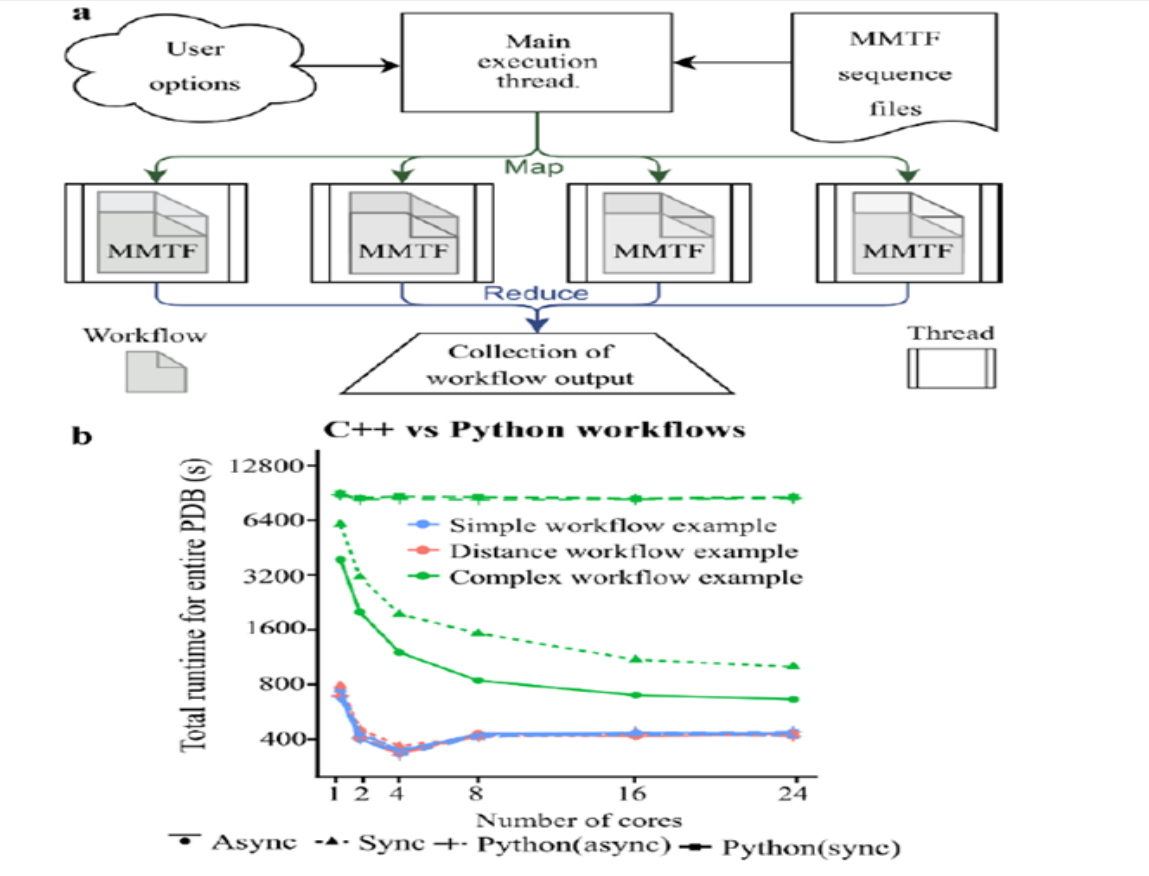


Figure: Overall Workflow of Lemon

*Source: Jonathan Fine, et al. J Oxford Bioinformatics, 2019,* https://github.com/chopralab/lemon.

## *Bioinformatics Animation*

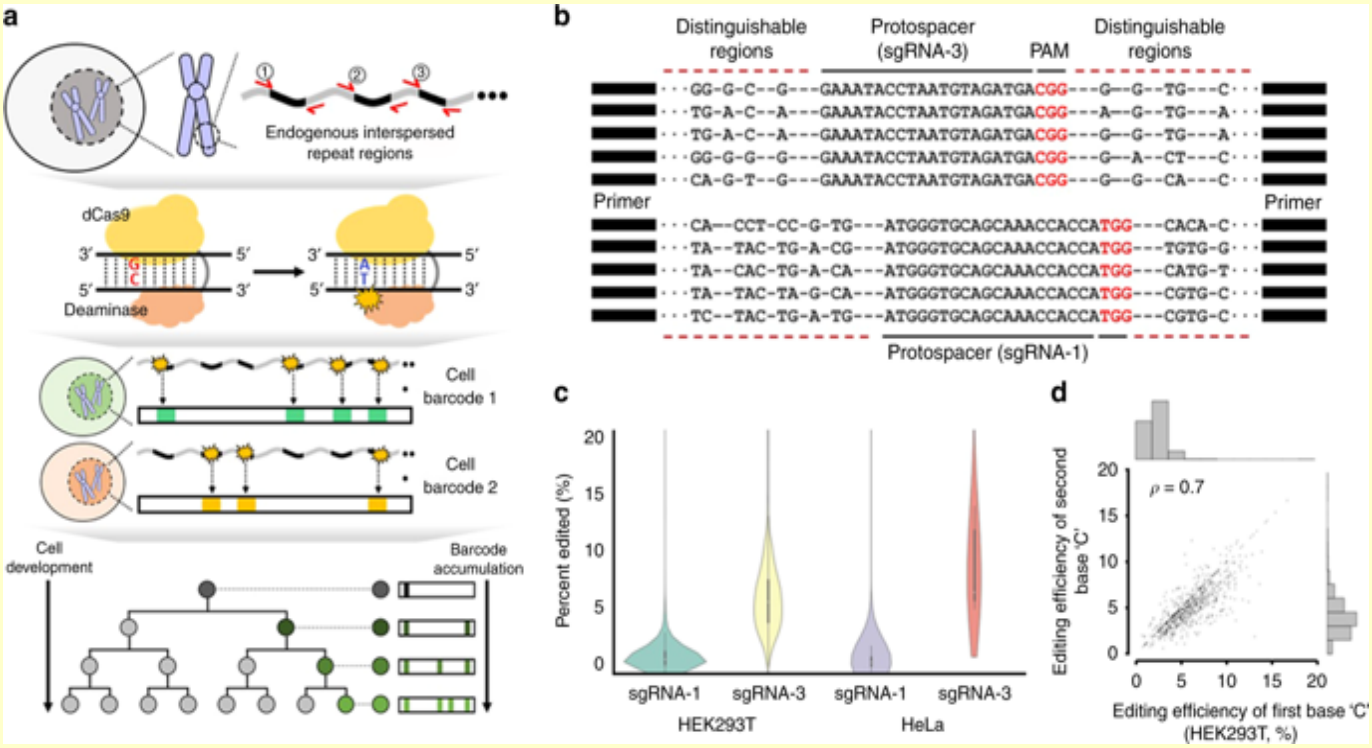


**Fig: Workflow of Cas9 Deaminase barcoding system for lineage tracing**

*Source*: *Byungjin Hwang, et al. J Nature Communications, 2019*

## Upcoming Events



http://www.iaria.org/conferences2019/BIOTECHNO19.html
https://www.explara.com/e/nextgenerationsequencing-genome-editing-crispr-training-dubai

# Measles Virus Proteins

*Six proteins in measles to infect cells*

Measles is a highly contagious disease caused by the rubeola virus. Despite the availability of safe and effective vaccine, globally the disease remains as a major cause of death among young children. It is transmitted through the droplets from nose, mouth and throat. Disease symptoms usually appear 10-12 days after the infection which includes high fever, runny nose, uncomfortable rash on the face and upper neck spreading downwards. The disease has not been eradicated fully.

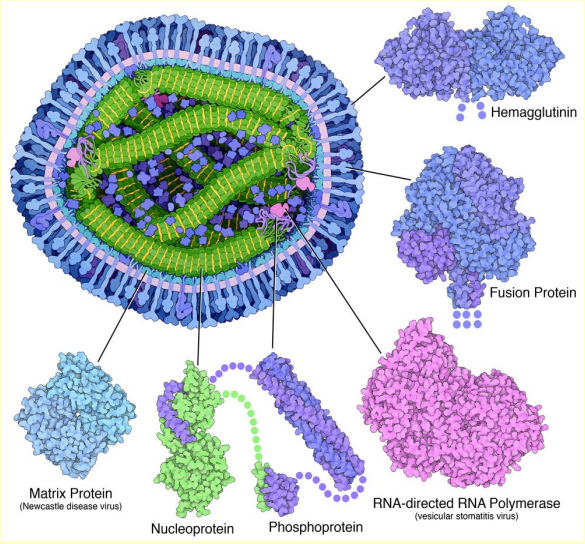


Figure: Measles virus cross section showing the structures of six viral proteins.

## *Measles Proteins*

Measles virus genome is composed of RNA which encodes six proteins. Three proteins ( RNA-directed RNA polymerase, phosphoprotein and nucleoprotein) are responsible for genome replication and maintenance. The flexible tails of phosphoprotein tether the polymerase to the nucleoprotein to undergo the replication and transcription of the genome.

## *Surface Proteins*

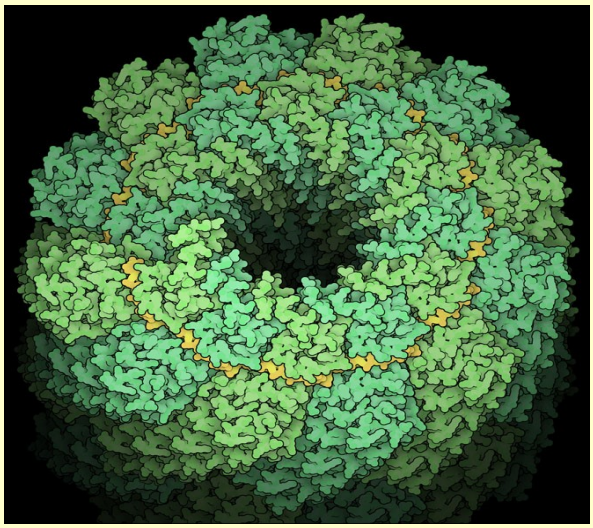

Figure: Nucleoprotein (green) and RNA (yellow) Measles virus

The virus is enclosed by a lipid membrane consisting of hemagglutinin protein and fusion protein. Hemagglutinin protein (PDB entry 2zb5) finds new cells and attaches to the receptor proteins on the surface of cell membrane while the fusion protein (PDB entry 5yxw) binds the viral membrane to the cells and fuses to the cell membrane, transferring the viral RNA. Weakened form of the virus is utilized for the production of widely used vaccines that stimulate the immune system to produce antibodies against the surface proteins.

## *The Matrix and Nucleocapsid*

The matrix assists the budding of new viruses from the infected cells and also ensures that the viral RNA is included. The matrix associates with the membrane and the nucleocapsid to produce the new viruses. The measles nucleocapsid forms a large helical complex with RNA and chaperone the process of replication and transcription. It is the binding site of polymerase/phosphoprotein complex.

Source: http://pdb101.rcsb.org/motm/230

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