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RAGE
Rabies Accessible
Genomic Epidemiology

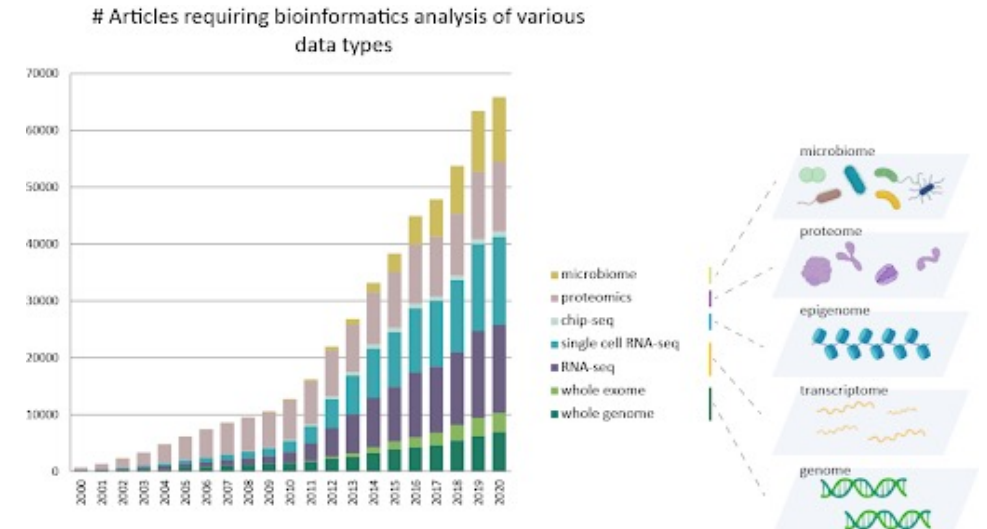
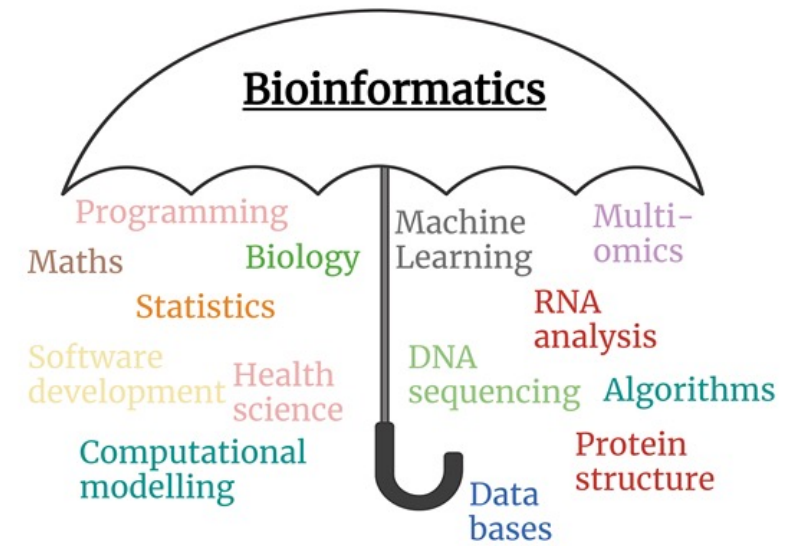
Bioinformatics in action: Current Techniques and Tools Used in Our Lab

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Introduction

- Coined in 1970 by Paulien Hogeweg and Ben Hesper
- Utilization of computational tools and analytical methods for capturing and interpreting biological data
- Biological data (genomics, transcriptomics, proteomics and metabolomics)
- Plays a crucial role in modern biology and medicine, facilitating the understanding of complex biological processes

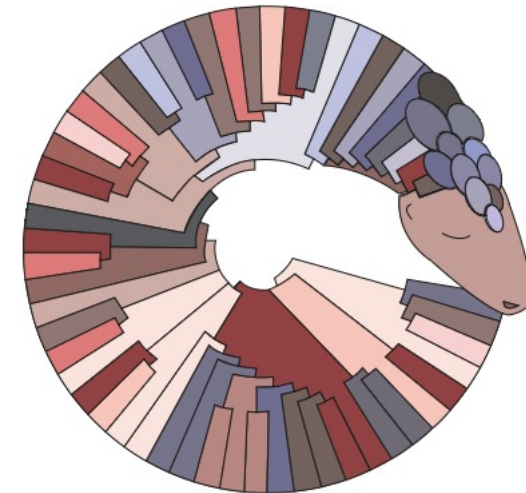
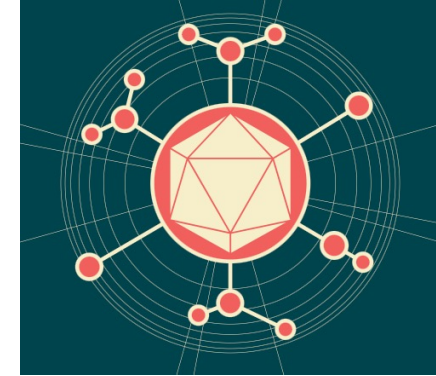


Bioinformatics role during the pandemic

- Rapid Genome Sequencing and Analysis
- Tracking Virus Evolution and Spread
- Vaccine Development
- Therapeutic Targets
- Understanding Host Response
- Public Health and Epidemiological Studies

Bioinformatics tools gained popularity during the pandemic

- Pangolin (Phylogenetic Assignment of Named Global Outbreak Lineages)
- ARTIC network
- Nextstrain
- GISAID (Global Initiative on Sharing Avian Influenza Data)
- Bioconductor and COVID-19 Data Portal

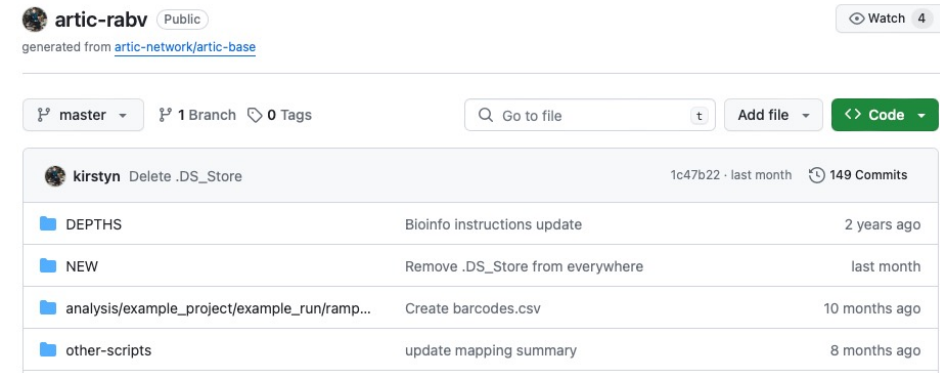


Computation facility at UofG

- Alpha2
 - RAM: 4TB
 - Processing cores: ~250
 - GPU's: 4 x 32 GB
- HPC cluster
 - RAM: 300GB
 - Processor: ~100
 - GPU's: 2 x 32 GB
- MARS
 - RAM: 2TB
 - Processing cores: ~200
 - GPU's: ~120 GB

Current bioinformatics practice

- Shell/Python/R
- Pipelines (Snakemake)
- Web-based resources



RABV-GLUE Home Sequence Data Analysis Offline version About

RABV-GLUE

A Sequence Data Resource for Rabies Virus

Rabies virus (RABV) is a neglected zoonotic disease that causes around 59,000 human deaths each year, with a near 100% mortality rate after the onset of symptoms. The virus is a member of the Lyssavirus genus, within the Rhabdoviridae family, which is characterised by a single stranded, negative-sense RNA genome.

Infection with RABV can occur in all species of mammal, but up to 99% of human rabies cases arise from bites from infected domestic dogs. Vaccinating dogs to interrupt transmission is therefore paramount, and a major focus of the 'Zero by 30' global strategy to eliminate human deaths from dog-mediated rabies by 2030.

RABV-GLUE is a data-centric bioinformatics resource which organises RABV genome sequence data along evolutionary lines. RABV-GLUE aims to leverage new and existing RABV sequences in order to improve our understanding of the epidemiology and pathology of RABV.

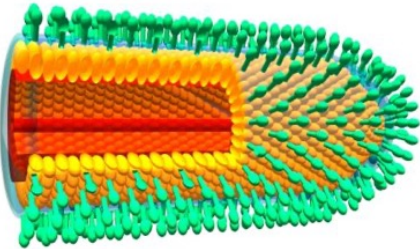
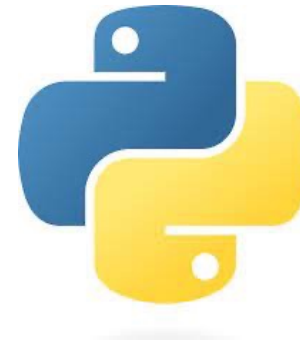


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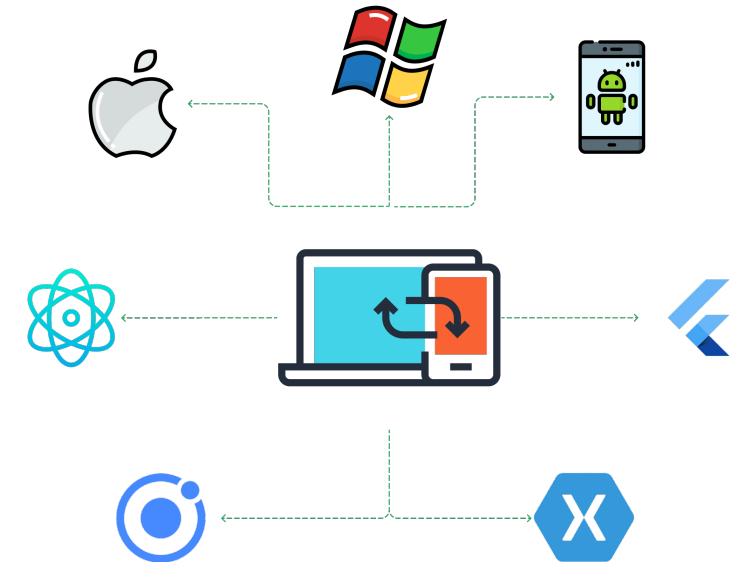
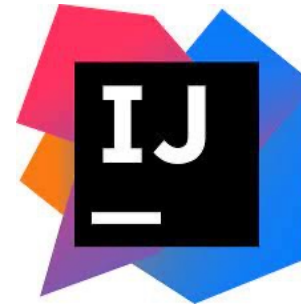


Current challenges at our lab

- Tools and the complexities (execution, parameters)
- Internet issues at field work (remote location)
- Intermediate/advanced bioinformatics skills
- Hardware facilities to run massive informatics

Future implementation

- AWS implementation
- Pipeline developments
- GUI's to develop and support cross platform





Thank you

Reference to images

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