Reproducibility in Cancer Transcriptomics Research

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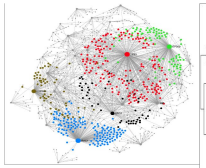
African BioGenome Project
Genomics for the future of biological diversity across Africa

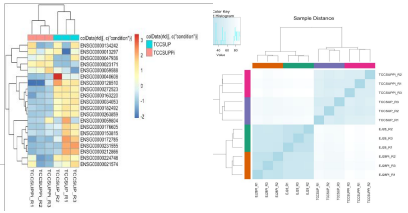
Submission Moderator

AfricArXiv

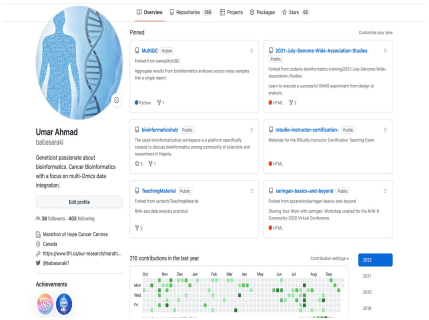
Computational Cancer Research

DEPARTMENT OF ANATOMY





Training & Mentoring



Nigeria

HB

Bioinformatics & Data Science services

python™

BIOSEQ

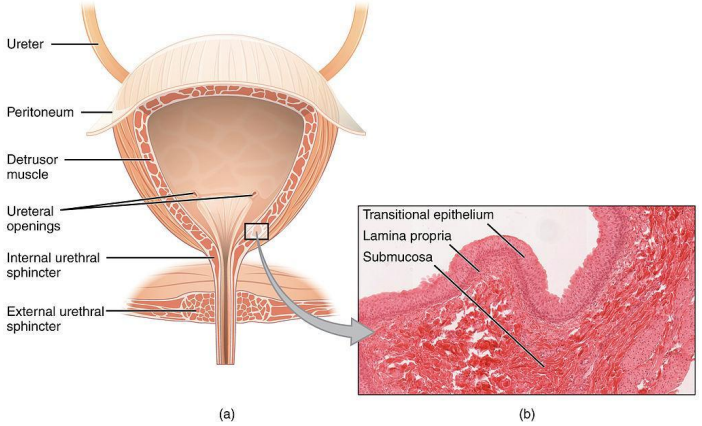
software carpentry

Reproducibility in cancer omics

Background

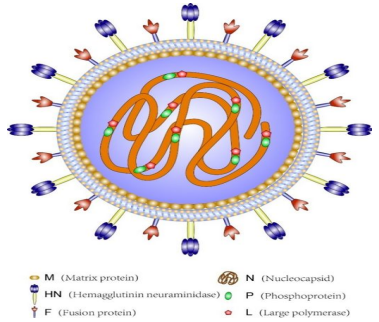
Urothelial carcinoma

- Bladder cancer ~ malignant disease that develops from cells of bladder.
- Most common type is TCC or UCC that account for 90% of cases (Dmitriy *et al*., 2016).



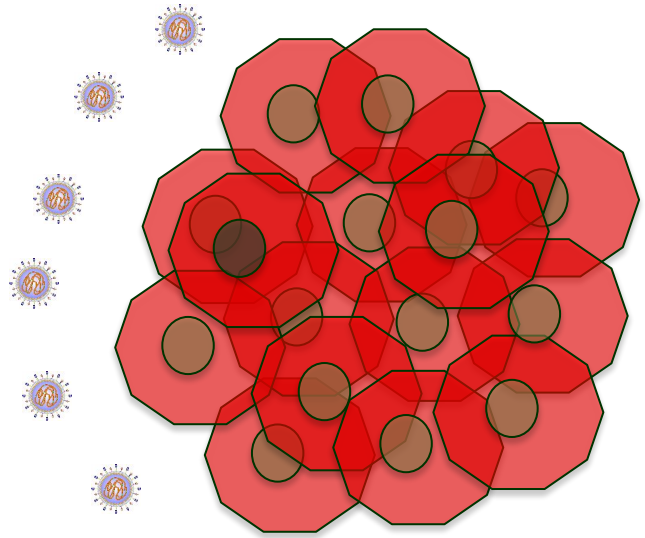
High rates of recurrence & Progression to muscle invasive disease

Newcastle disease virus (NDV)

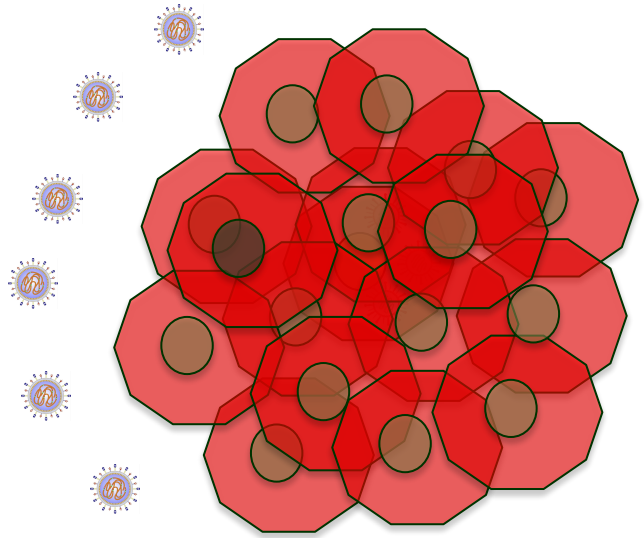


- **Persistency of infection** in subpopulation of cancer cells
  - without causing cell death.

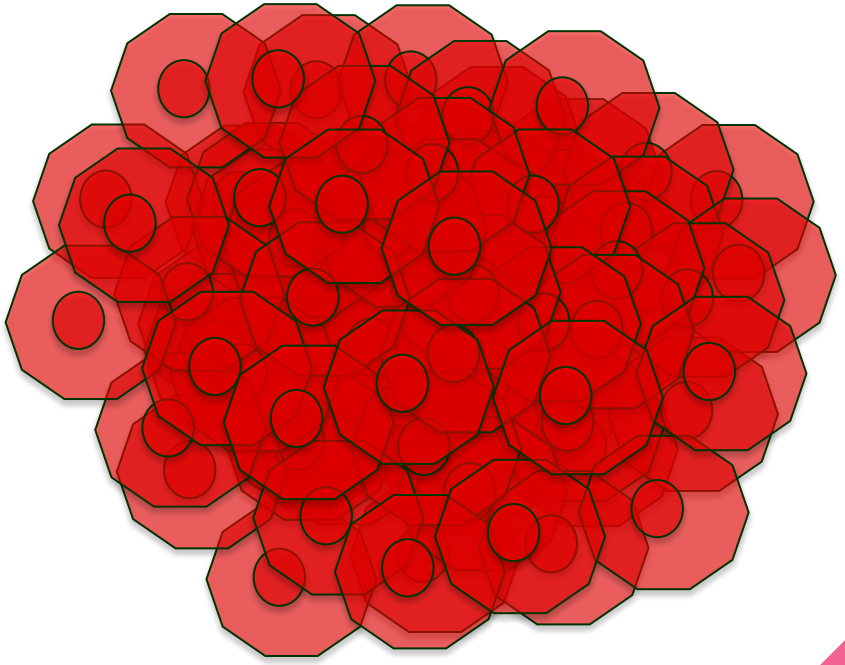
NDV mediated oncolysis



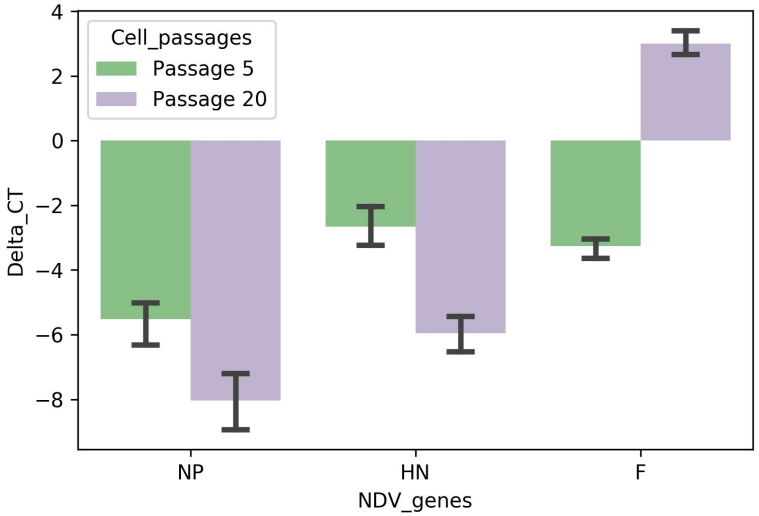
Persistent infection

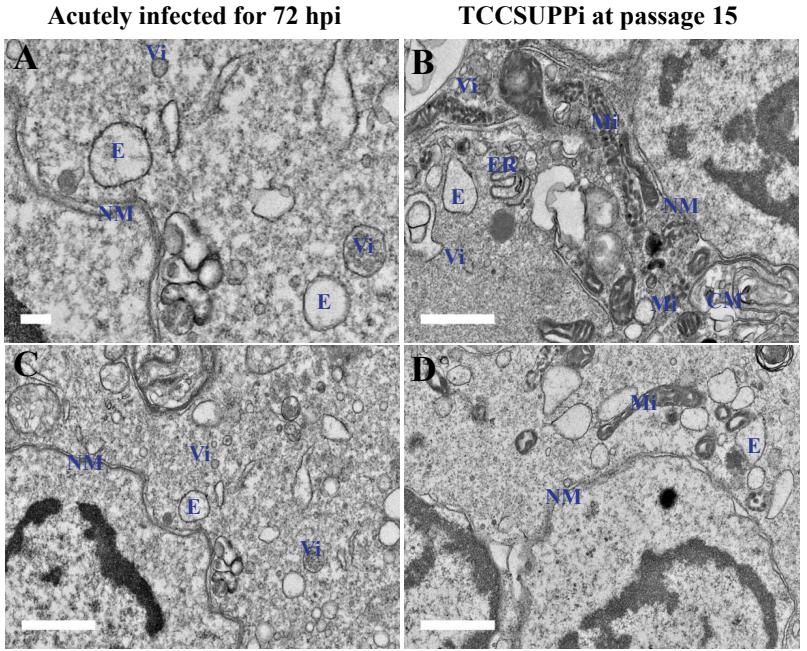


Failure of therapy

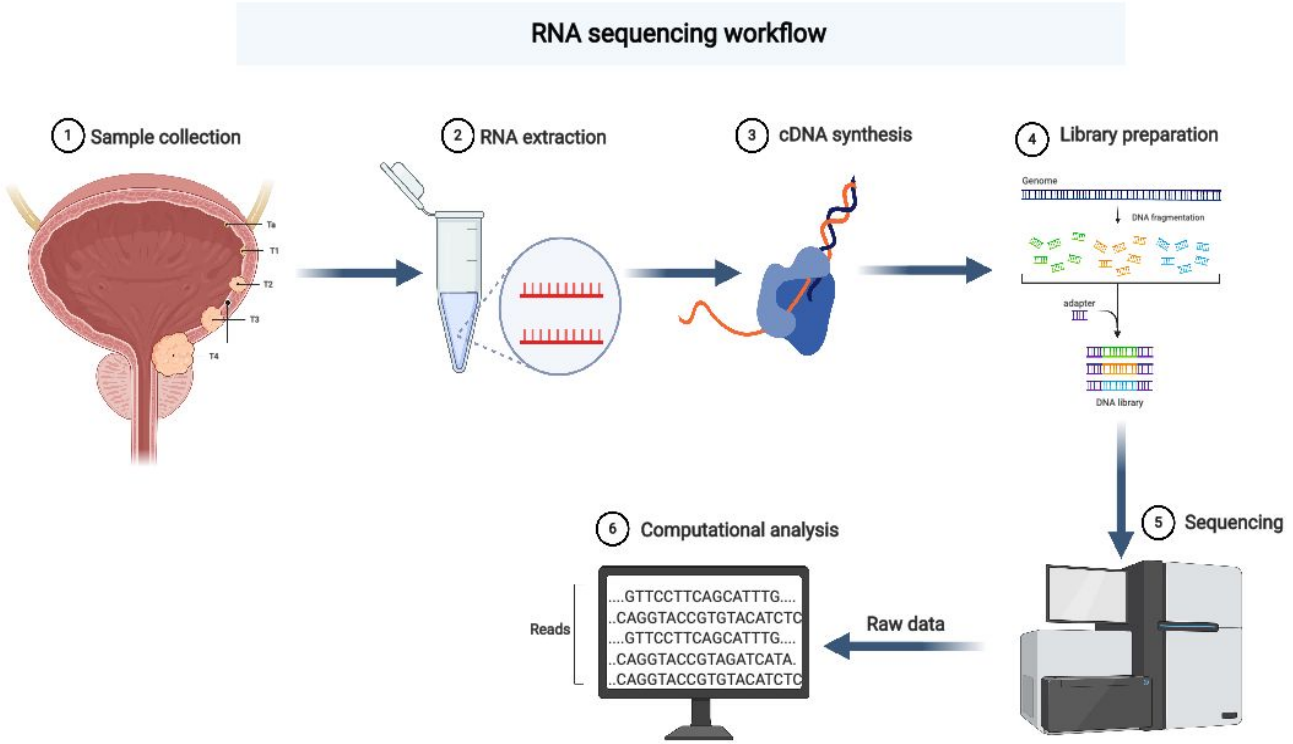


Expression of NDV genes in TCCSUPPi cells



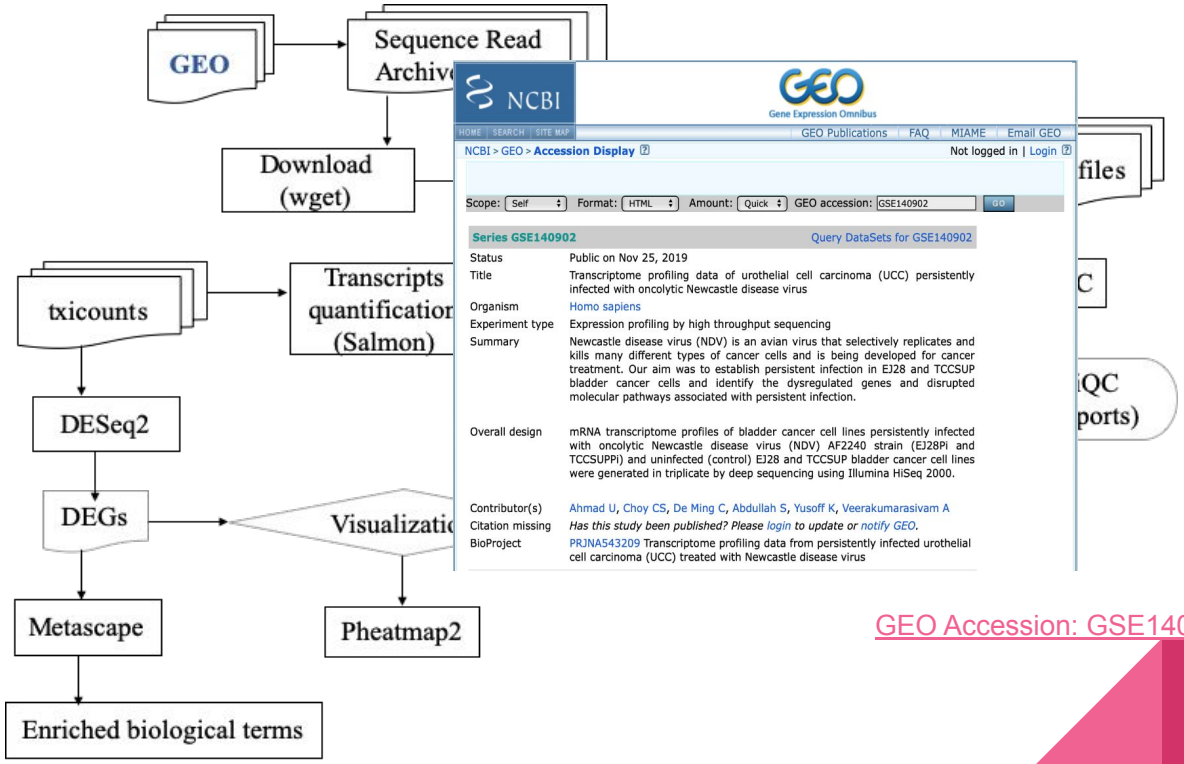


Transcriptomics workflow



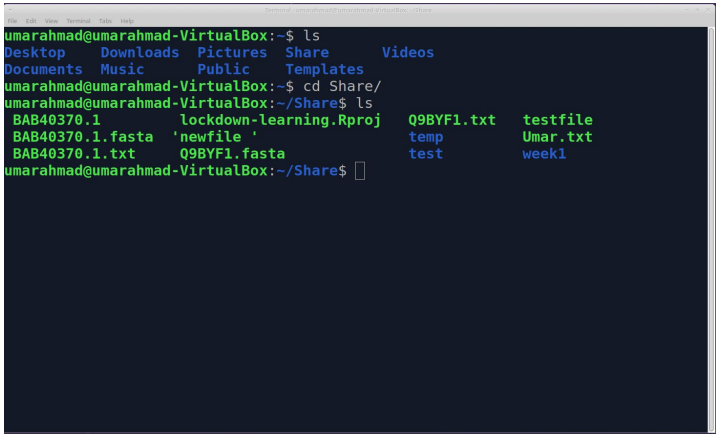
Ahmad *et al*., 2020

Uploading the raw datasets



GEO Accession: GSE140902

Bioinformatics – Analysis of transcriptomics data

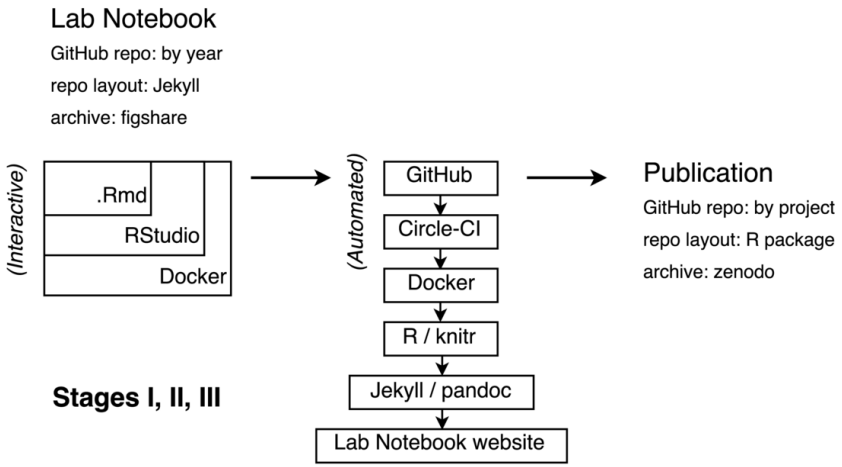


Challenges in reproducibility in omics experiments ?

- Non availability of raw data generated
- Authors mentioning scripts and code are available upon request
- Rewarding novel findings and undervalues negative results
- Lack of clear methodological description
- Difference in version of tools/packages
- Difference in operating system (e.g. Linux vs Windows)

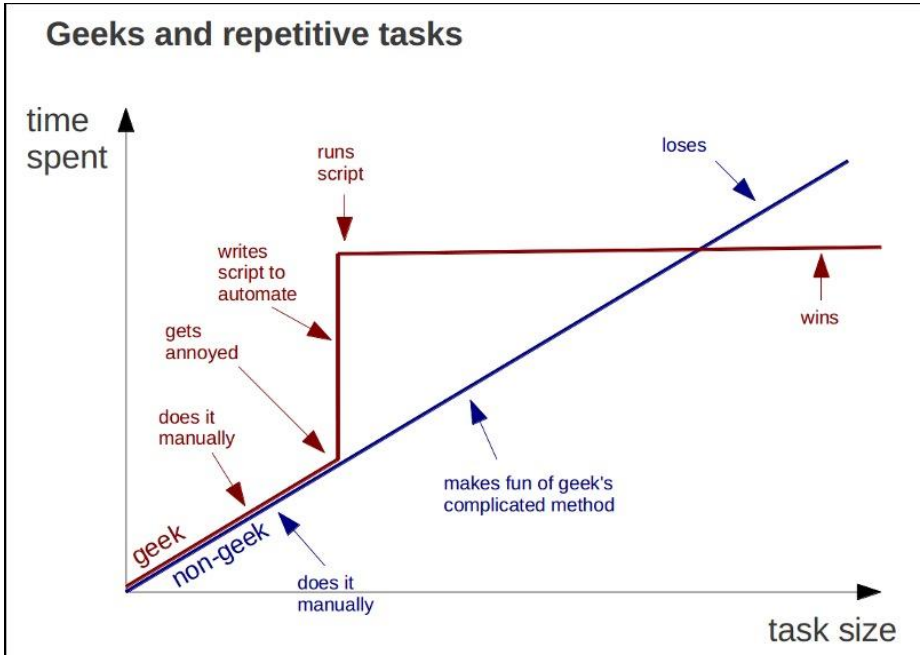
To ensure reproducibility

- Git version control and Github/GitLab/Gitbucket repo
- Jupyter notebook/Rmarkdown - documentation
- Containers (docker, singularity, biocontainers https://biocontainers.pro/)



Kitzes *et al.*, 2021

Automate to make your research more reproducible



- Best documentation is automation
- Write scripts for everything
- Markdown (https://www.mkdocs.org/)

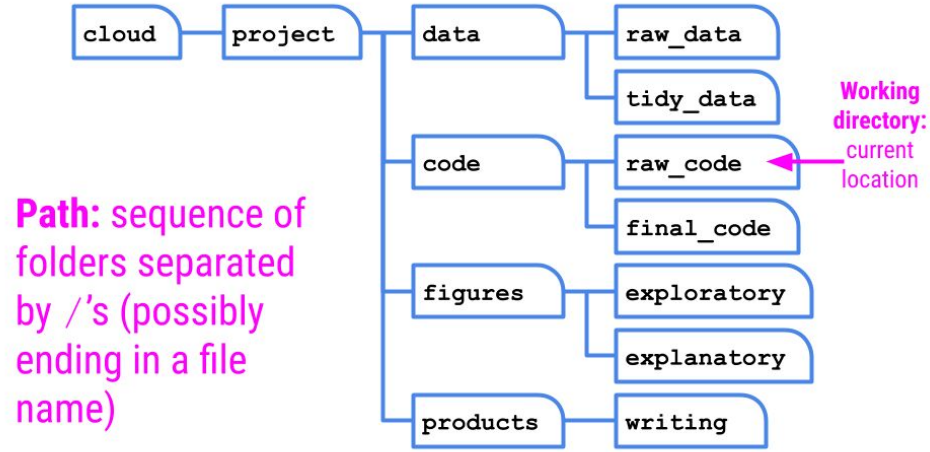
Tips for automation

- If your task is repetitive, develop a shell script e.g. rna-seq-analysis.sh.

- Workflow management such as: Snakemake, WDL, Nextflow etc.

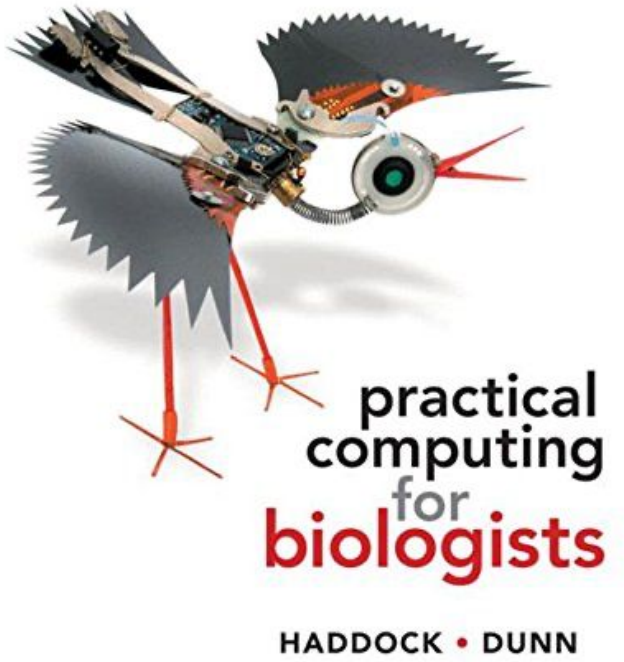
Important skills for reproducibility

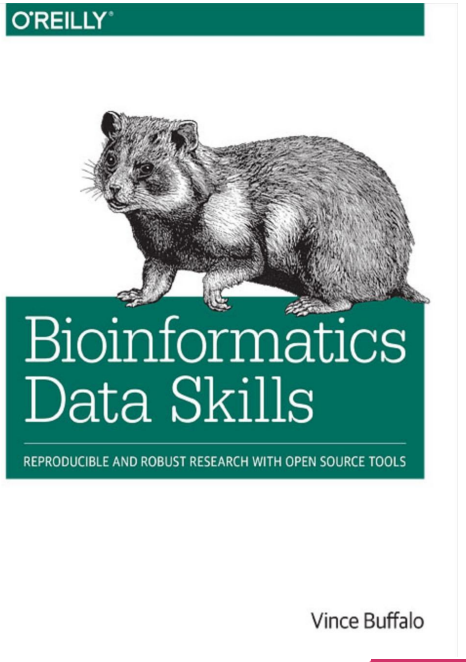
- Naming files
- Project organisation
- Data organisation/ backup plans



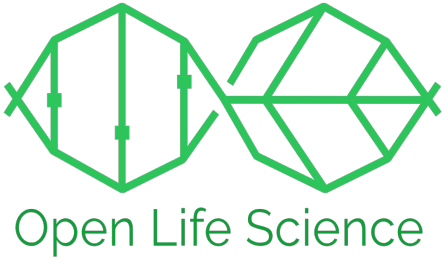
Peng *et al.*, 2021

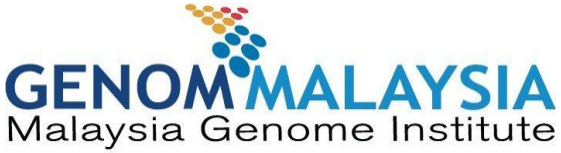
Learn by doing





Acknowledgement





Need help in your NGS analyses & Training services ?

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Have questions?