

Reproducibility in Cancer Transcriptomics Research

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Bioinformatics Scientist

Community Lead



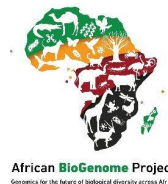
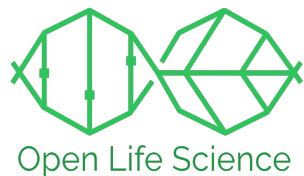
Member

Contributor

Co-Chair
Data Analysis Committee

Submission Moderator

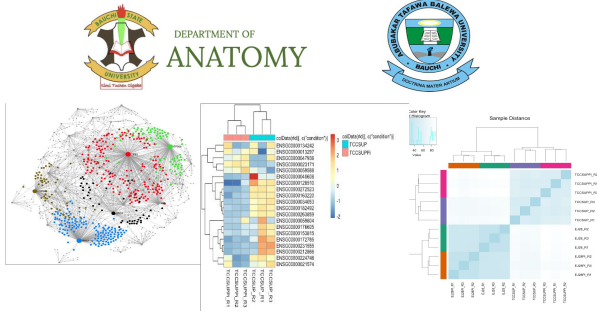
Project Lead



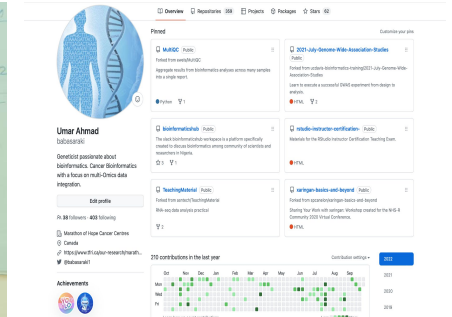
African BioGenome Project
Genetics for the future of biological diversity across Africa



Computational Cancer Research



Training & Mentoring



Bioinformatics & Data Science services



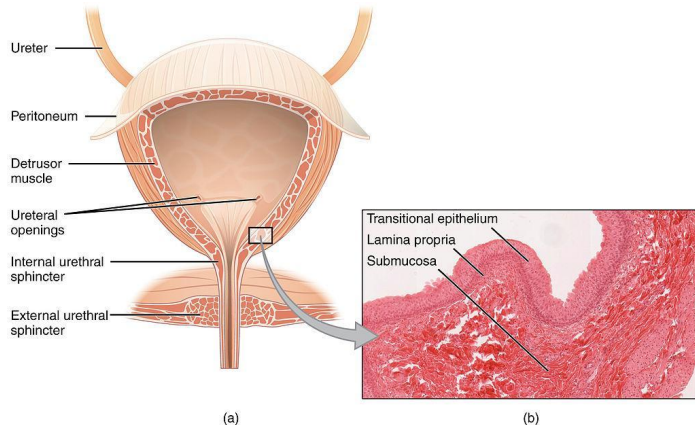


**Reproducibility
in cancer omics**

Background

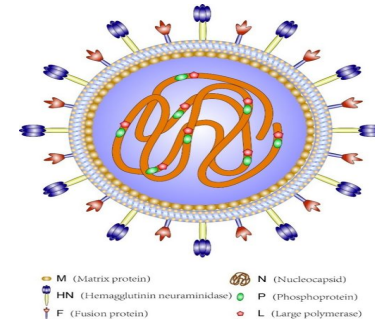
Urothelial carcinoma

- 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).



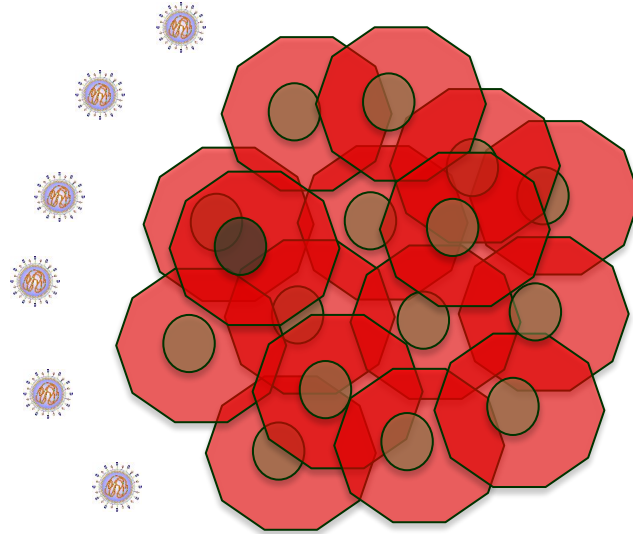
High rates of recurrence & Progression to muscle invasive disease

Newcastle disease virus (NDV)

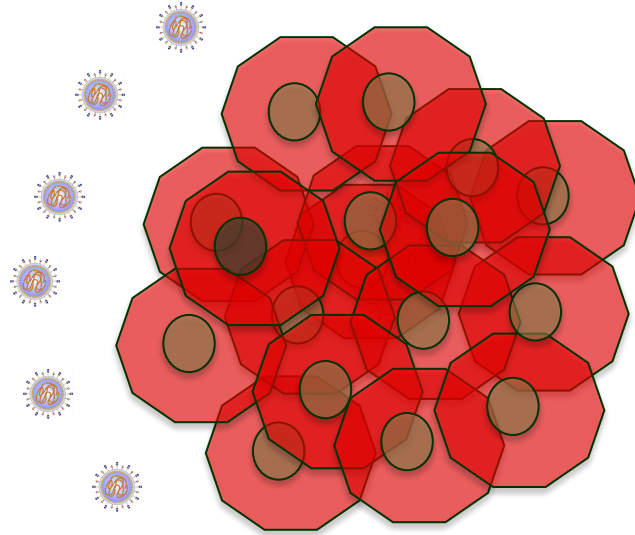


- **Persistency of infection** in subpopulation of cancer cells
- without causing cell death.

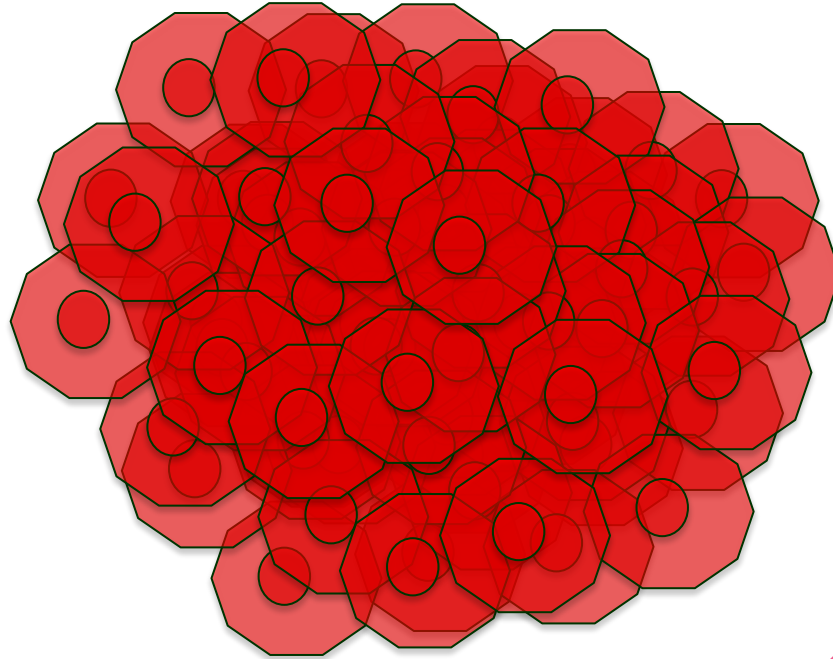
NDV mediated oncolysis



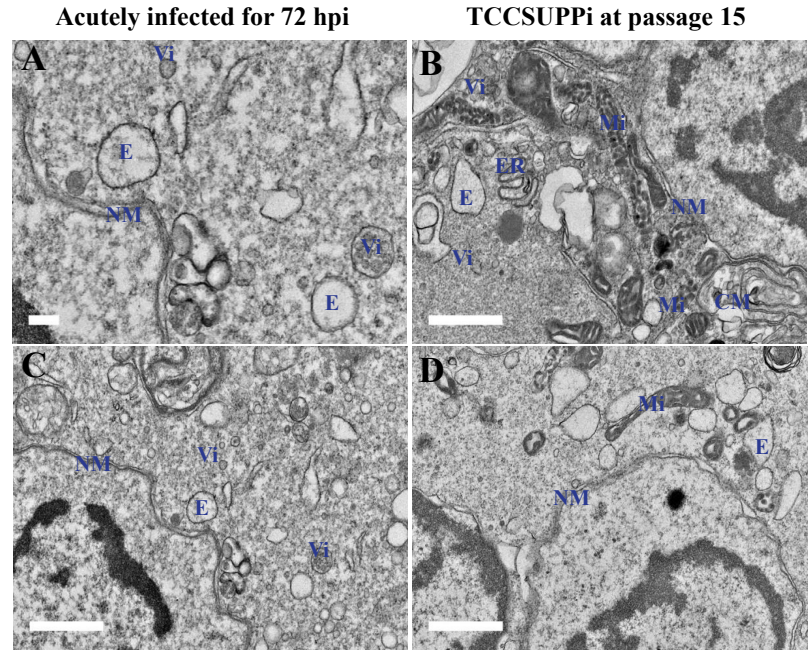
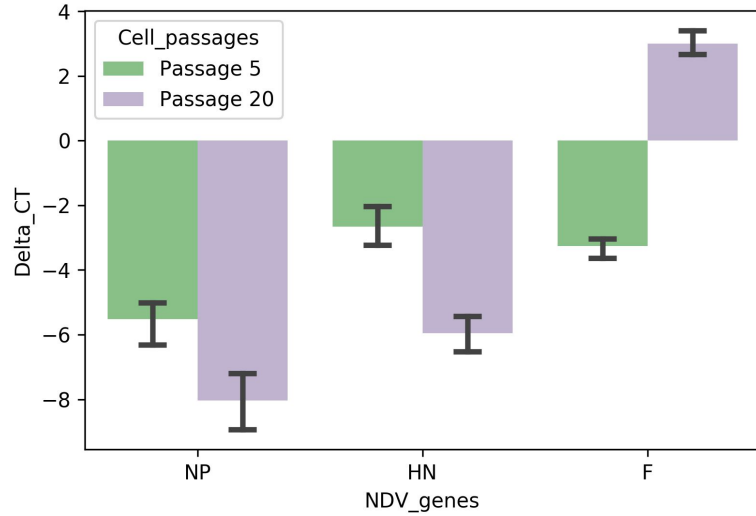
Persistent infection



Failure of therapy

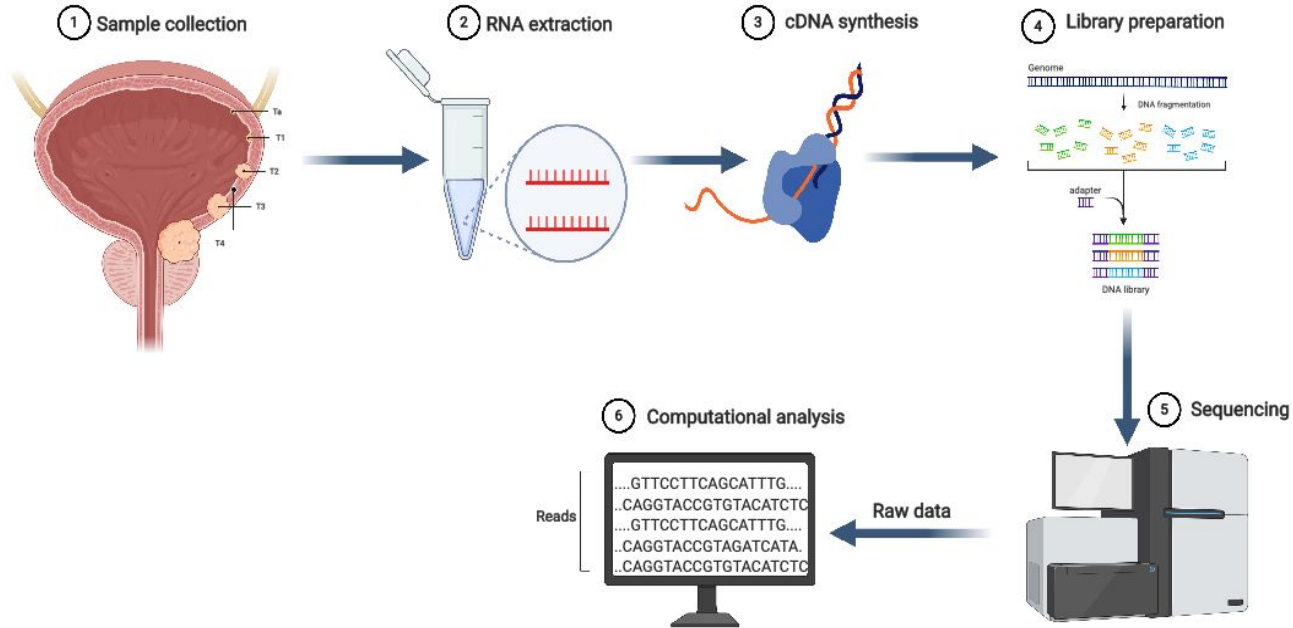


Expression of NDV genes in TCCSUPPi cells

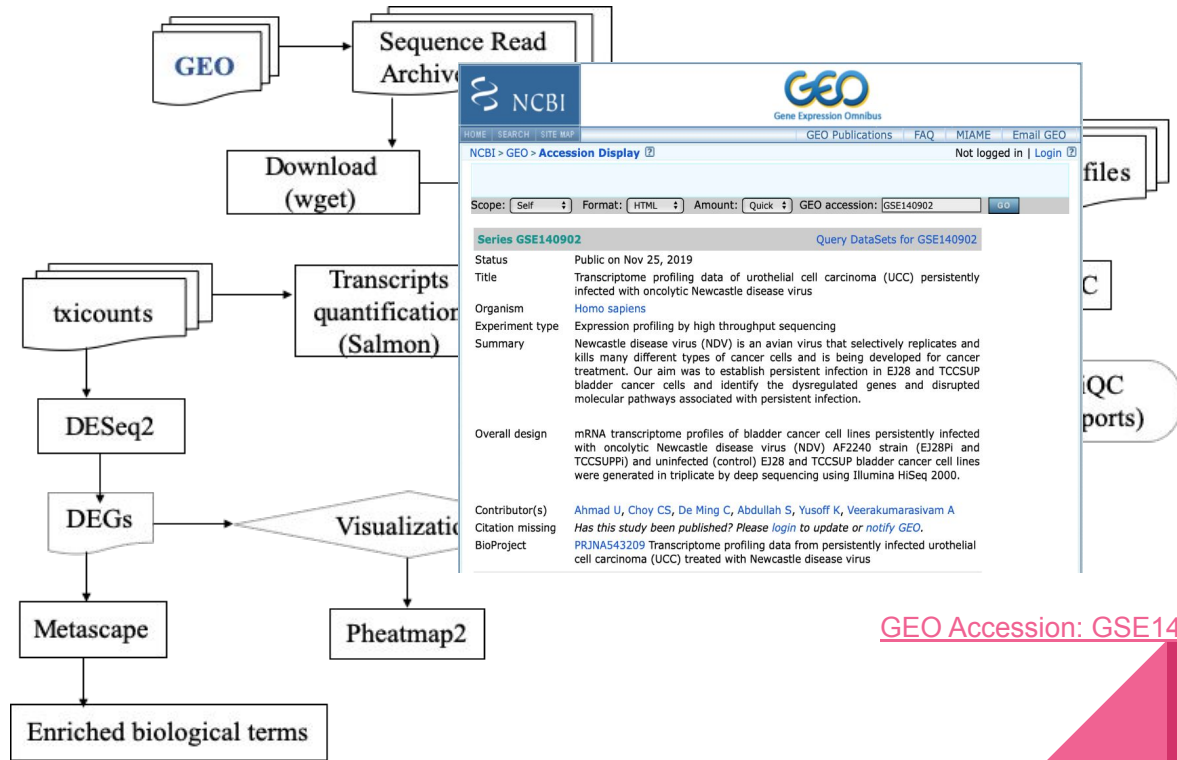


Transcriptomics workflow

RNA sequencing workflow



Uploading the raw datasets

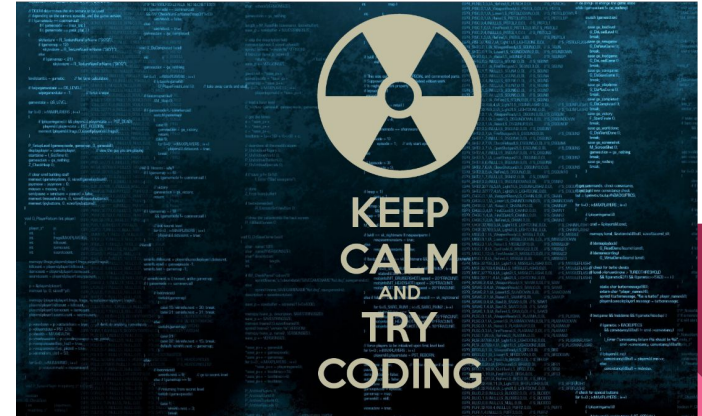


Bioinformatics – Analysis of transcriptomics data




AGTAATCAGCTACCTTTATCCCTAGCCCCCTGCGCCCCGCGCCCTTGGCA
GSTATGGTGAGGTCTGCTCTGGGTCCCTCGCCACCATGTACGTGAGC
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CGGGGCGCTGCCGAGCCAACGCGGTAGCCACGGCCTCAATGGT
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GCGCTGCGCCTCCGATTGCTGCAGACGCTCAACCCCGGCCCTCCA
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GAAGCCAAGGTATGCGGTGCTGGGGCGCGCCCCTGGTCCC
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ACCTCGTTGGCAACCTCGGGACCCCTTCGGAAGCTCCCGGTAGTGT
AGCAGAATCGCGTCCTTTAGTTGGCTGCCACCAGCATTCTTACACC
SGGTGATTGGATTCCCTTGCCGAGCCTACTCAACTAGCTACCCACTCT

```
umarahmad@umarahmad-VirtualBox:~$ ls
Desktop  Downloads  Pictures  Share      Videos
Documents Music      Public   Templates
umarahmad@umarahmad-VirtualBox:~$ cd Share/
umarahmad@umarahmad-VirtualBox:~/Share$ ls
BAB40370.1      Lockdown-Learning.Rproj  Q9BYF1.txt  testfile
BAB40370.1.fasta  'newfile '                temp        Umar.txt
BAB40370.1.txt   Q9BYF1.fasta              test        week1
umarahmad@umarahmad-VirtualBox:~/Share$
```



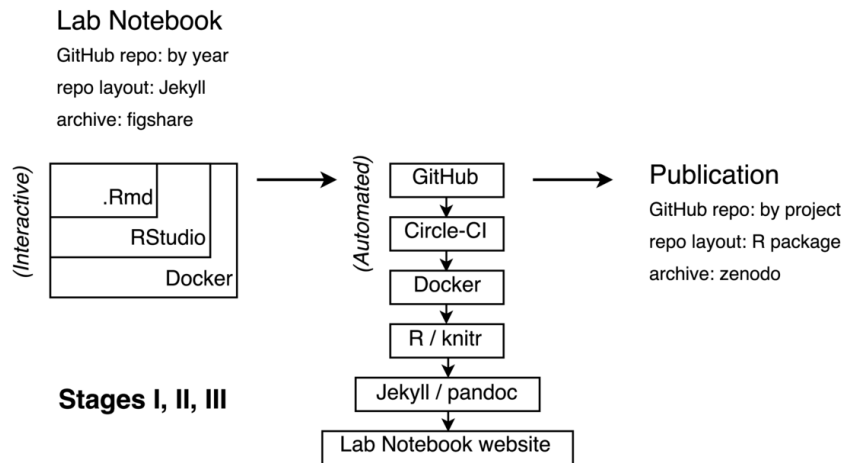
Challenges in reproducibility in omics experiments ?

- 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



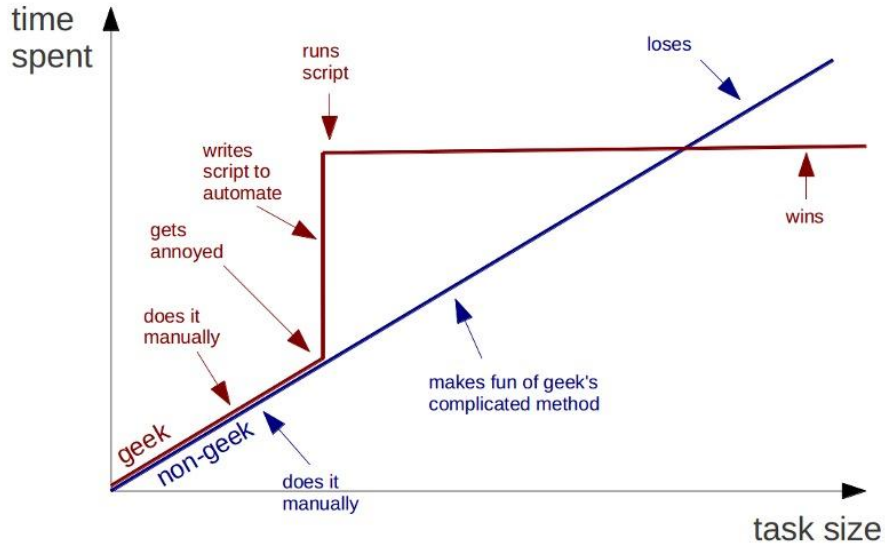
- Git version control and Github/GitLab/Gitbucket repo
- Jupyter notebook/Rmarkdown - documentation
- Containers (docker, singularity, biocontainers <https://biocontainers.pro/>)



Kitzes *et al.*, 2021

Automate to make your research more reproducible

Geeks and repetitive tasks



- 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.

nextflow

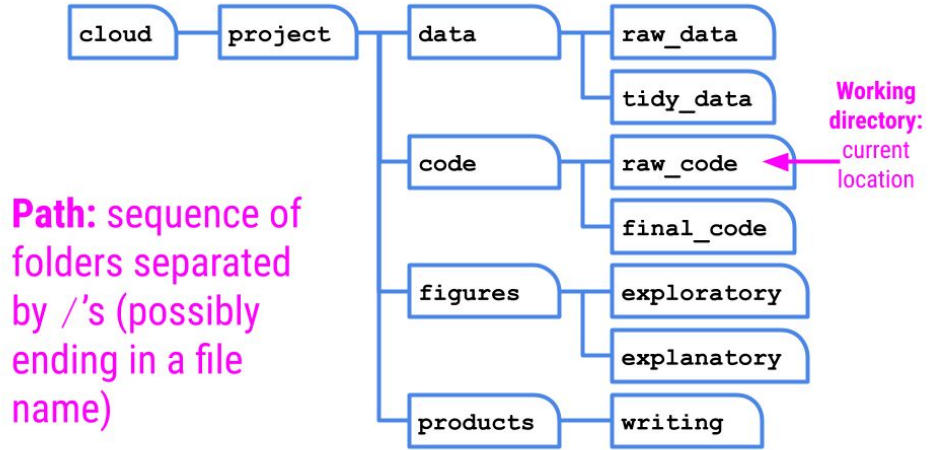


docker



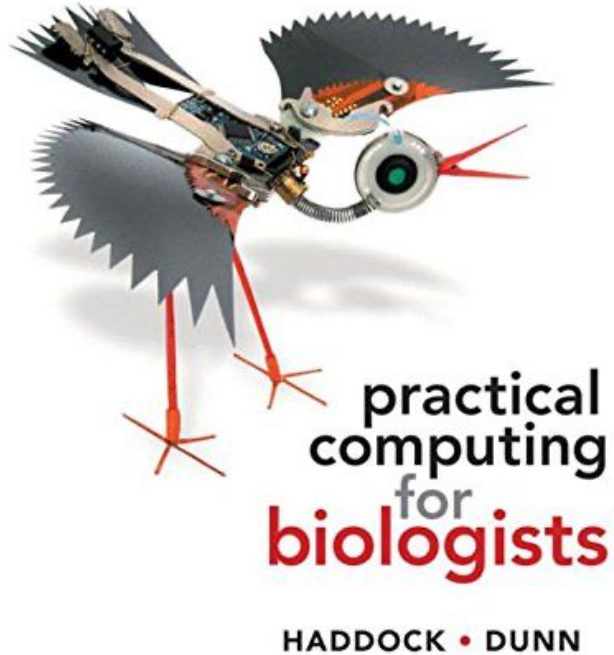
Important skills for reproducibility

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

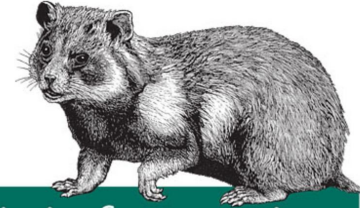


Peng *et al.*, 2021

Learn by doing

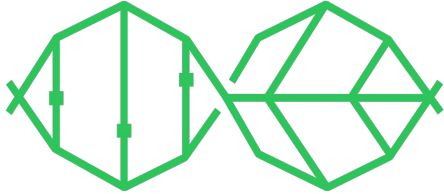


O'REILLY



Vince Buffalo

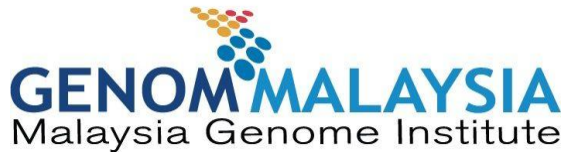
Acknowledgement



Open Life Science



KEMENTERIAN SAINS,
TEKNOLOGI DAN INOVASI
MINISTRY OF SCIENCE, TECHNOLOGY AND INNOVATION



Need help in your NGS analyses & Training services ?

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Have questions?

