Read metadata and barcode maps in CSV / TSV & TXT format

Read and collate FASTQ and FASTA sequence data efficiently.

Call variants using inbuilt variant caller or minimap2

Open Source!

Write your own plugin modules in Python

Graphical User Interface, little programming experience required!

CountESS

a user-friendly platform for analysing MAVE data

Nick Moore[1] and Alan F Rubin[1,2]

[1]: The Walter and Eliza Institute of Medical Research, Parkville, VIC, Australia
[2]: The University of Melbourne, Parkville, VIC, Australia

Save configurations as a simple, revision-control friendly .INI file

Built on top of **DuckDB** and Python, and Apache Arrow, and Biobear.

install with

`pip install countess`

on Linux / Windows / MacOS

Design a pipeline in the GUI, run from the command line on an HPC cluster

Built-in support for SGE, VAMP-seq, LABEL-seq and custom assays and methodologies

https://countess-project.github.io/