

VAGUE, Prokka & Neson

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The tools

- VAGUE

- Velvet assembler GUI

- Prokka

- Microbial genome annotator

- Neson

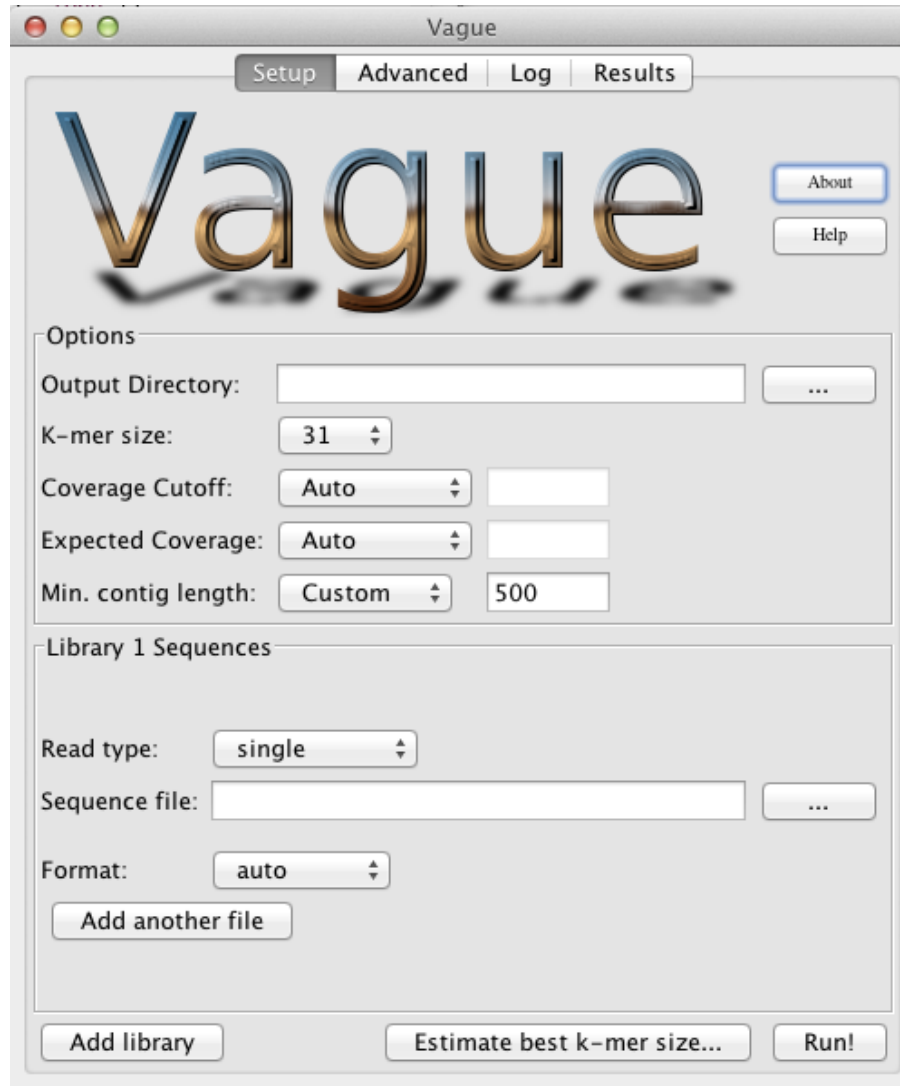
- Microbial NGS toolkit / pipeline

VAGUE

What is VAGUE?

- Velvet
Assembler
Graphical
User
Environment
- Essentially a GUI for Velvet
- Velvet is a command-line genome assembler popular with microbians (us).

VAGUE screenshot



VAGUE features

- Supports

- separate paired reads (left and right files)
- gz and bz2 compression

- No parameters to choose

- Even can find a good k-value for you

- Examine results in the GUI

Prokka

Prokka

- “Prokaryotic Annotation”
- Turn lifeless FASTA files into richly annotated GBK/GFF files you can view in Artemis, IGV, etc
- Find all gene, CDS, tRNA, rRNA features and label them usefully (and correctly)

Why?

•Previously

- Ad hoc set of scripts for initial annotation
- Load into Wasabi and curate
- Iterative battle with NCBI & Sequin to submit

•Now

- Prokka produces GFF3, GBK, SQN
- Over 99% features pass NCBI scrutiny

Nesoni

Nesoni

- A pipeline system
 - Python based, using 'futures'
- You write tools as modules
 - Get a command line version for free
 - Modules are composable
- Pre-written tools for microbial NGS tasks

Features

- Read alignment to reference
 - SNP/indel calling amongst 100s of samples
 - Core/accessory genome
- Read cleaning
 - Trimming, quality, adaptors, lengths
- RNA-Seq
 - Uses edgeR/Limma to do gene expression
- Plus lots more!

Install them next week!

Get the source

<http://bioinformatics.net.au/>



That's all Folks!