

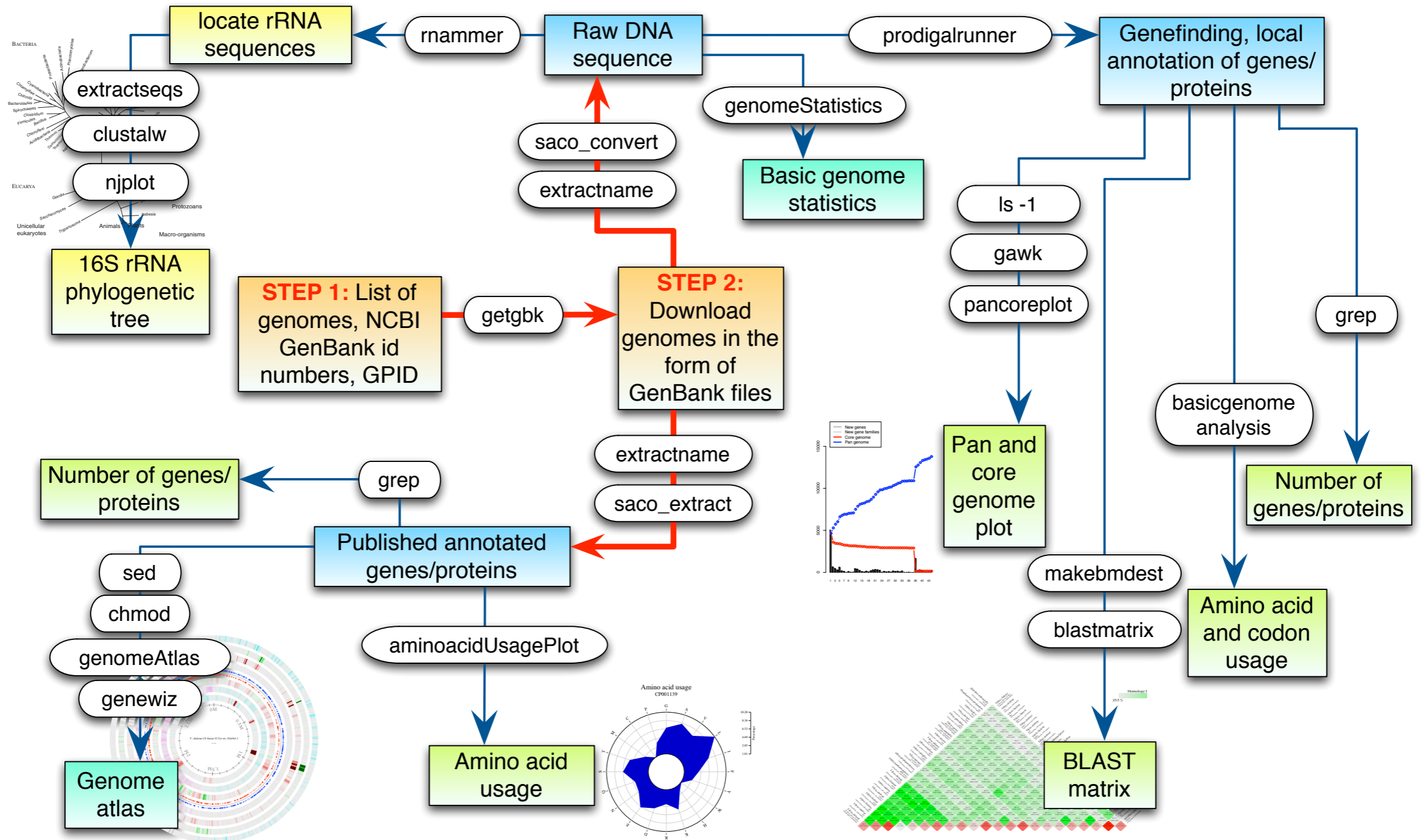
Comparative Microbial Genomics

Exercises for course 27104 -

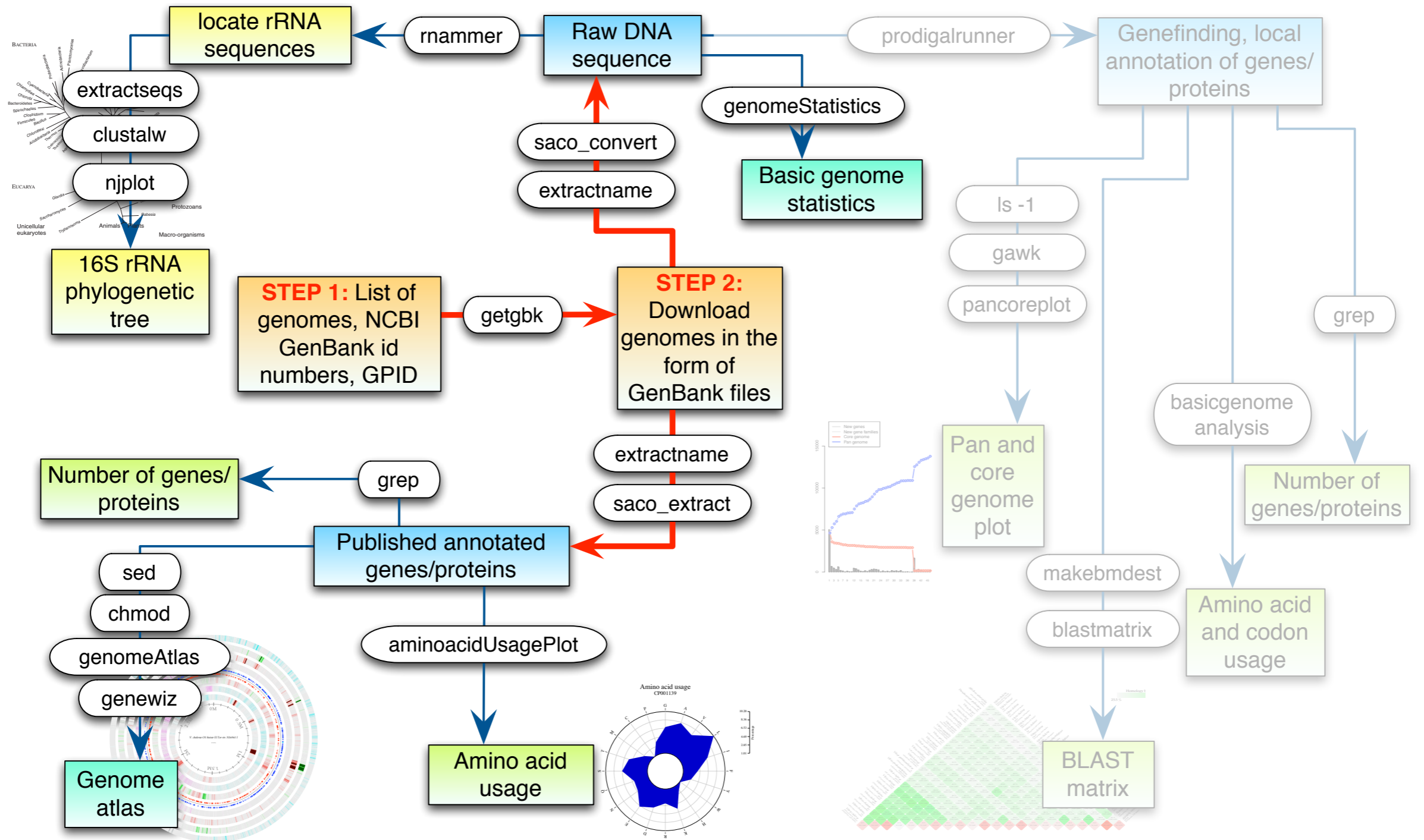
- Wednesday 21 Sep.:
 - Genefinding using prodigalRunner
 - Number of genes/proteins
 - Amino acid and codon usage
- Thursday 22 Sep.:
 - BLAST matrix

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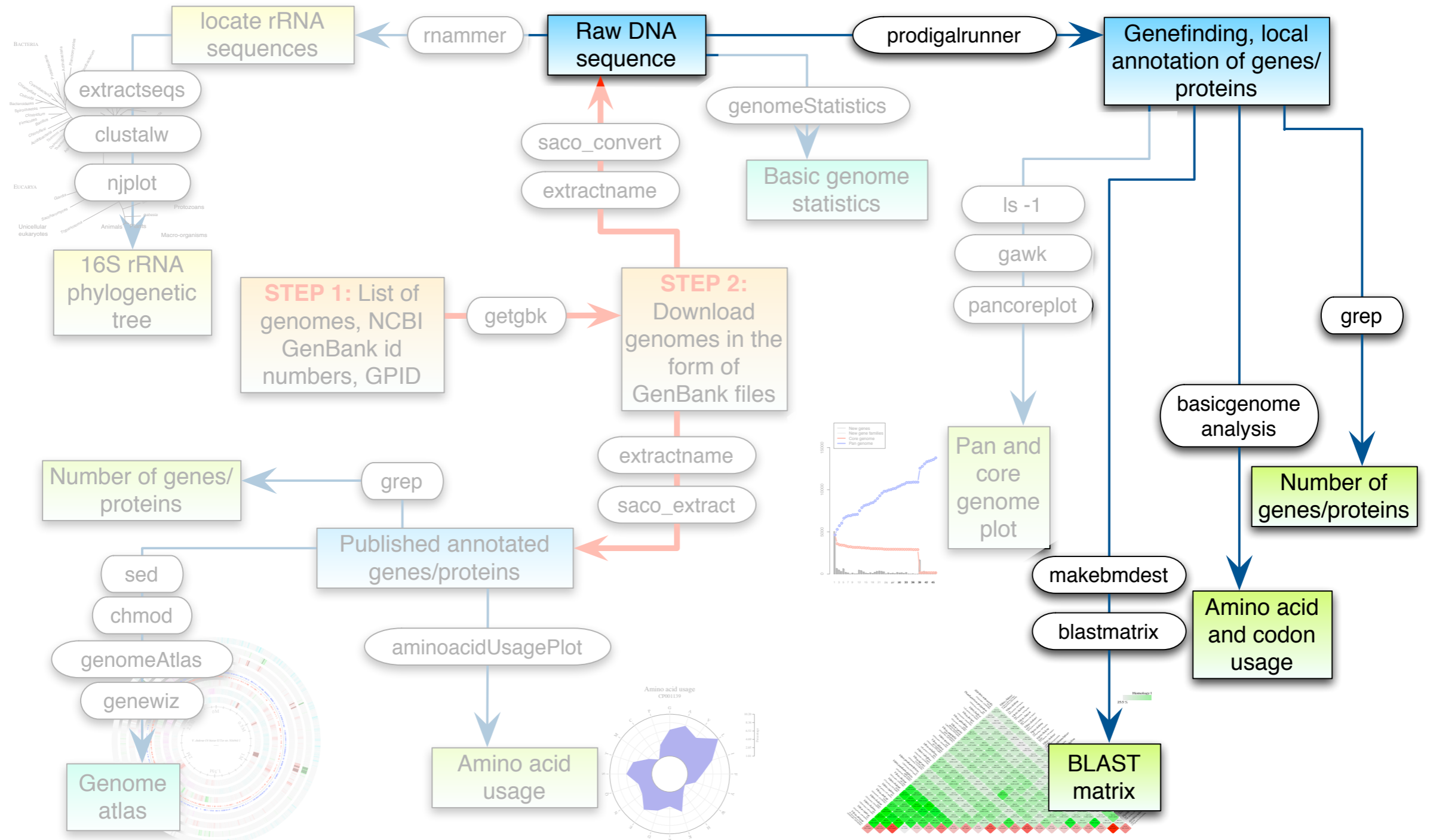
Work flow:



Progress so far:



Wednesday/Thursday work flow:



Wednesday tasks:

- Run genefinding on whole genome DNA sequences
 - ▶ `prodigalrunner <name>.fna`
- Count number of published genes/proteins
 - ▶ `grep ">" <name>_prodigal.orf.fsa`
- Compare protein count with published annotation counts, differences?
- Construct graphical basic statistics for selected genomes
 - ▶ `basicgenomeanalysis <name>_prodigal /usr/bin/gnuplot`

Thursday tasks:

- Construct a BLAST matrix comparing protein profiles of genomes
 - Create directory to hold the BLAST matrix input/output files
 - ▶ `mkdir TestMatrix`
 - Copy selected files into the working directory:
 - ▶ `cp <genome1>_prodigal.orf.fsa TestMatrix/`
 - Construct a configuration file for the BLAST matrix program:
 - ▶ `makebmdes . > bmdes.xml`
 - Run BLAST matrix program
 - ▶ `blastmatrix bmdes.xml > blastmatrix.ps`

Output of the week:

- Files containing genes and proteins from local genefinding.
- Table of local gene/protein counts compared to published counts
- One-page basic statistics for selected genomes
- BLAST matrix for selected test-set and complete matrix