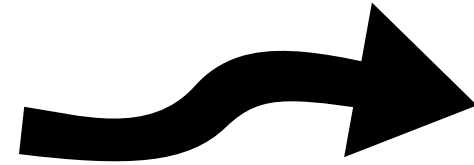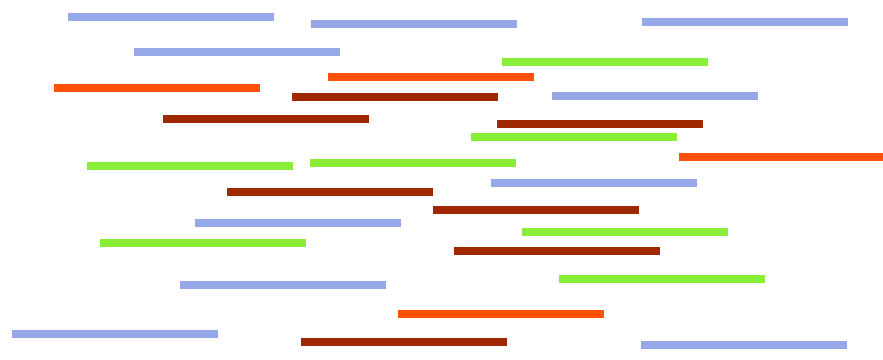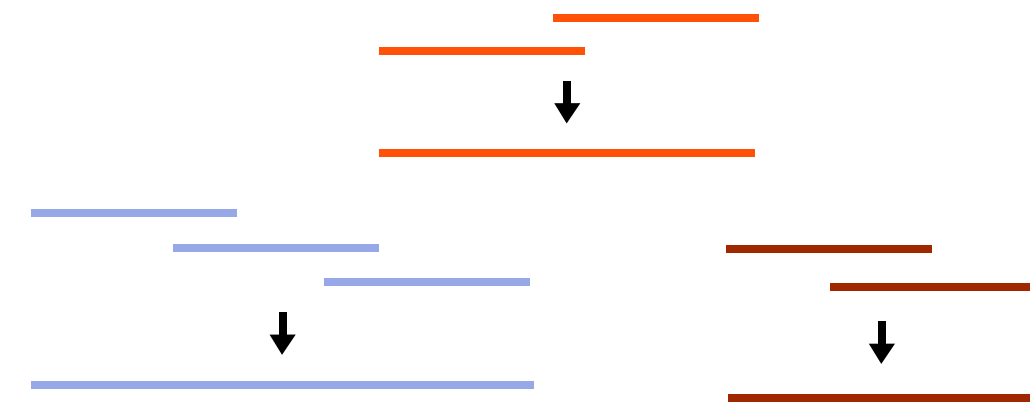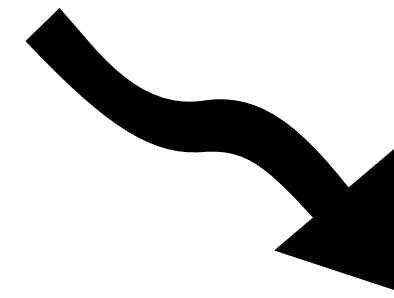Alignment of metagenome reads
to reference NOG sequences

DIAMOND
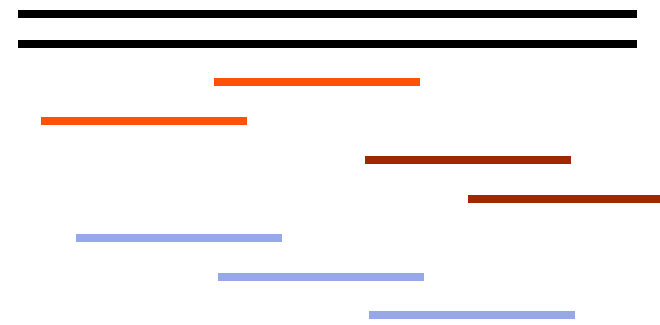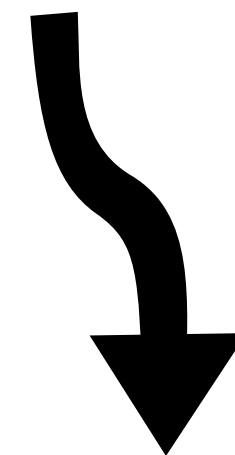
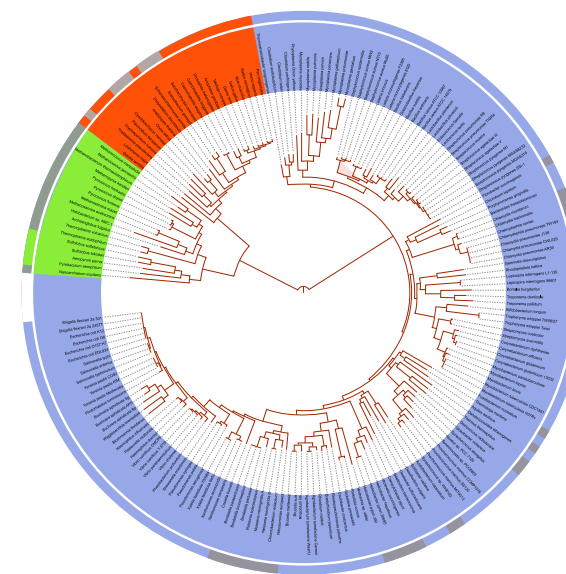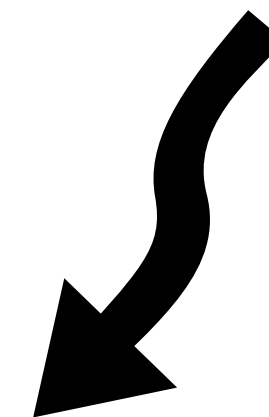Gene-centric assembly of
reads per NOG

MEGAN6

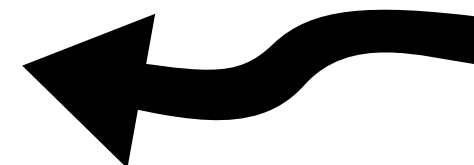Multiple sequence
alignment

MAFFT

PhyloMagnet

Phylogenetic
tree reconstruction

FastTree or *IQ-TREE*

Discard samples
Whole-metagenome assembly
and extraction of MAGs

"Magnetizing" trees to
detect lineages of interest

ETE3