

# Assignment 3

- Predict the operons (defined as longest contiguous multi-gene transcriptional units) using the PTT files (attached) for the following genomes. (Tip: adjacent co-directional genes with intervening distance less than 50bp can be considered to be in the same operon)
  - 1) *Escherichia coli* K12
  - 2) *Bacillus Subtilis*
  - 3) *Halobacterium*
  - 4) *Synechocystis*
- Now predict the operons in a Crop microbiome from Hoatzin (IMG id 2088090036 obtained from <http://img.jgi.doe.gov/cgi-bin/m/main.cgi>) using the attached gff file (which is equivalent to ptt file although not identical). The first column comprises of the contig with the fourth and fifth columns comprising the gene start and stops.