## Practice of variant calling. Comparing two genomes of *Synechocystis* for SNPs.

*Synechocystis* sp. PCC 6803 is a cyanobacterium able to perform oxygenic photosynthesis. We are interested in to explore two weird phenotypes we got in the pass with two mutant in the *gene_x. Both mutant have the same mutation, but we suspect that during the mutant generation parallel mutation were selected. Could you help us?.*

Perform a variant calling analysis in the two mutant strains: BC3 and CM, and compare the SNPs you obtain in both strains with the WT strain of *Synechocystis*. Note: don't analyze the INDELs, only SNPs for that use *samtools mpileup with -I option.*

Files available at Zenodo Practica_1_vcf for this practice:

- BC3_Synechocystis.fastq
- CM_Synechocystis.fastq
- Wt_Synechocystis.fastq
- Pcc6803.genome.fasta (reference genome)
- Syn6803TSS.gff (annotated genome in GFF format)

Do you think the coverage obtains in these fastQ was enough to perform this analysis?. Try to annotate the SNPs that you found using the Syn6803TSS.gff. For that you could use ChIPseeker (R Bioconductor package), or pipelines using python, and other many options (google) explore it and try it!!. How many SNP do you find?