

Team 1 Functional Annotation Homework

- Please submit homework as a zip file (Lastname_Firstname_HW3.zip) to team1.annotation2018@gmail.com. Sending email to the same email address if you have questions about homework, we will try to respond within 24 hrs
 - Please remember to modify your .bashrc file and use source to update it before you start, this homework is not hard, but still, don't wait until the last minutes
 - Deadline: April 5th midnight
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Question 1: (20 points)

What is Prokka? Choose one genome from server to run Prokka. Write down your command and take a screenshot of your result.

Running Prokka:

```
./prokka --outdir /wherever/you/want --kingdom TheKingdomOfKlebsiella --rfam(this is just a flag telling prokka to search for ncRNAs with Infernal+Rfam) --gram(pos or neg depending on what Klebsiella is. If you are unsure please feel free to google it.)  
/your/input/should/be/something/like/this/team1_GenePrediction/Prodigal_output_all/assemblies/SRR#####.skesa.fa
```

Question 2: (20 points)

Read <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4539851/> and <https://www.ncbi.nlm.nih.gov/books/NBK174280/>

Identify the challenges and advantages of doing genome annotation on bacteria; Explain what makes BEACON meaningful.

Question 3: (20 points)

Compare and contrast SignalP & LipoP. What do they do? Why do we need them for functional annotation? What input file and parameters would you use to run them? (No need to actually run them)

Question 4: (20 points)

Choose one genome to run DeepARG. How long does it take and how many output files do you get? Take a screenshot for the first ten lines of output files.

(http://bench.cs.vt.edu/deeparg_analyze/)

Question 5: (20 points)

What is function of CRISPR? Briefly introduce its development.