

There are 9 regions from the wheat genome (triticum aestivum ) to annotate.

The annotation project is to be submitted by groups of 2 or 3:

think about the potential difficulties of annotating wheat before you start predicting genes (hexaploid genome, homeologous genes, 80% of transposable elements)

you must completely annotate the given sequence:

- genes: complete coordinates of intron-exon structure and UTR, , validation by the presence of transcribed sequences and/or homologous genes. [mRNA, RNAseq](#)
- proteins : potential protein functions, motifs and domaines analyze blast results, also go back to publications to analyze the biological functions (not just biochemical ones)
- transposable elements: [coordinates](#) and [family](#) of the transposable element. only these 2, not the complete seq

The report must be written in laboratory notebook format. It must be made in such a way that I can repeat the analysis you have carried out with all parameters for each tool write each step of the project, define the technical part of the tools (with all the parameters)  
define each tool u use for annotation, why this and not that  
can add some screenshots, make tables... no limitation

Send me a table with the names in each groups and the sequence to be annotated.

deadline : end of december, submission on ecampus

N. Boudet

[try to detect if it corresponds to A or B or D](#)