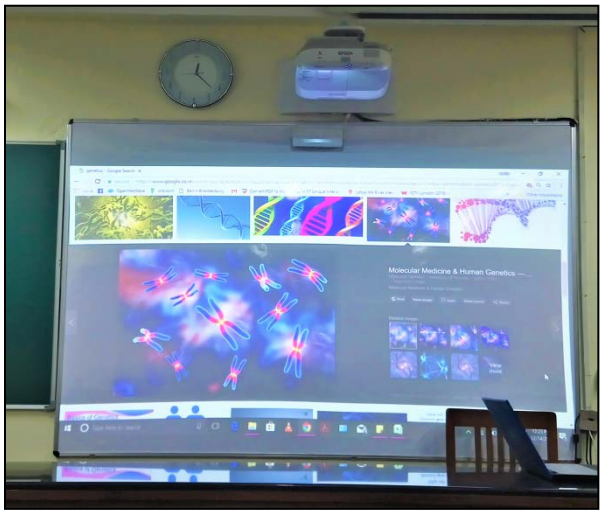
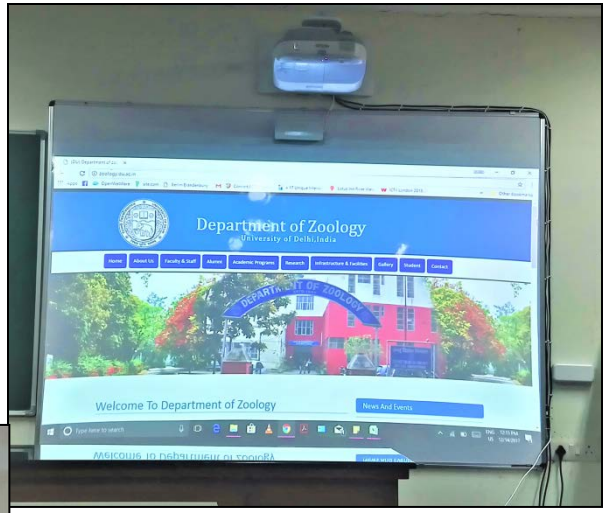
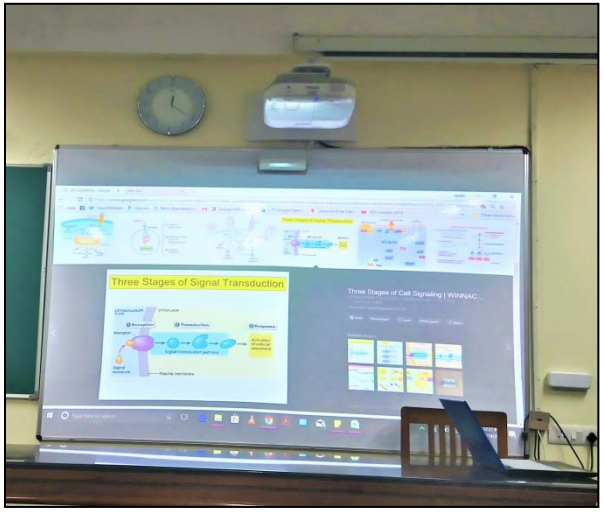
Smart Boards in Classrooms Department of Zoology

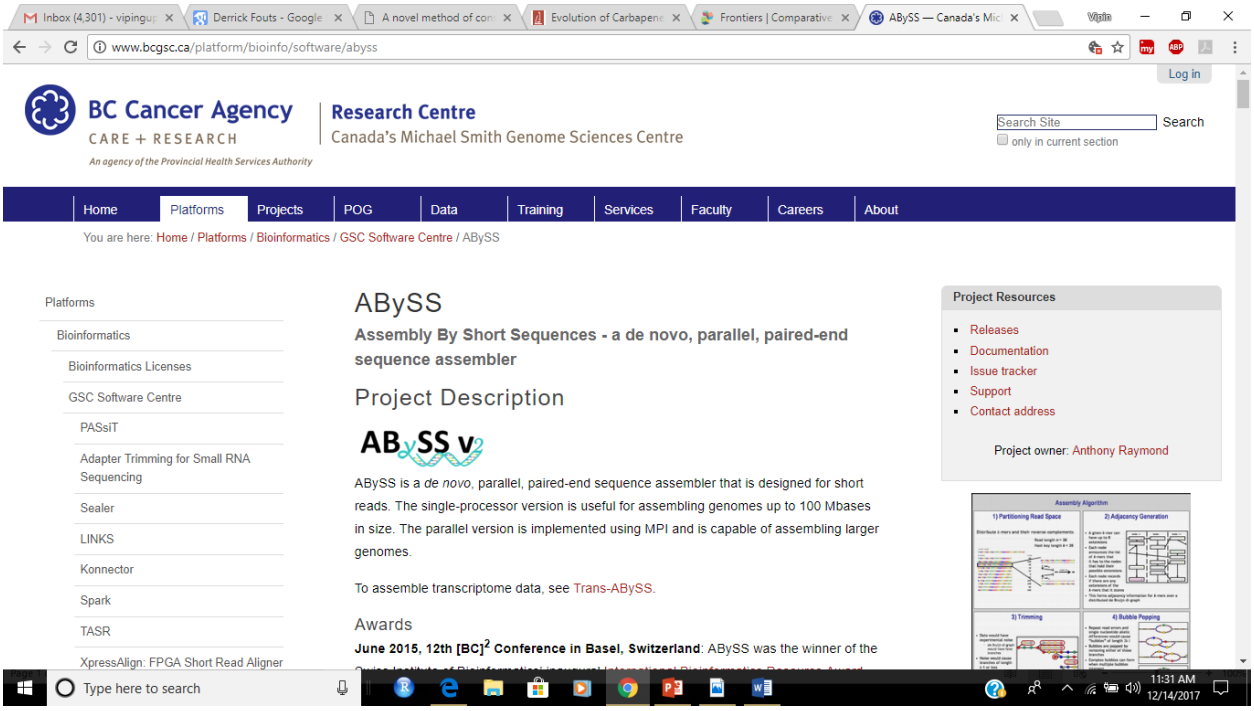




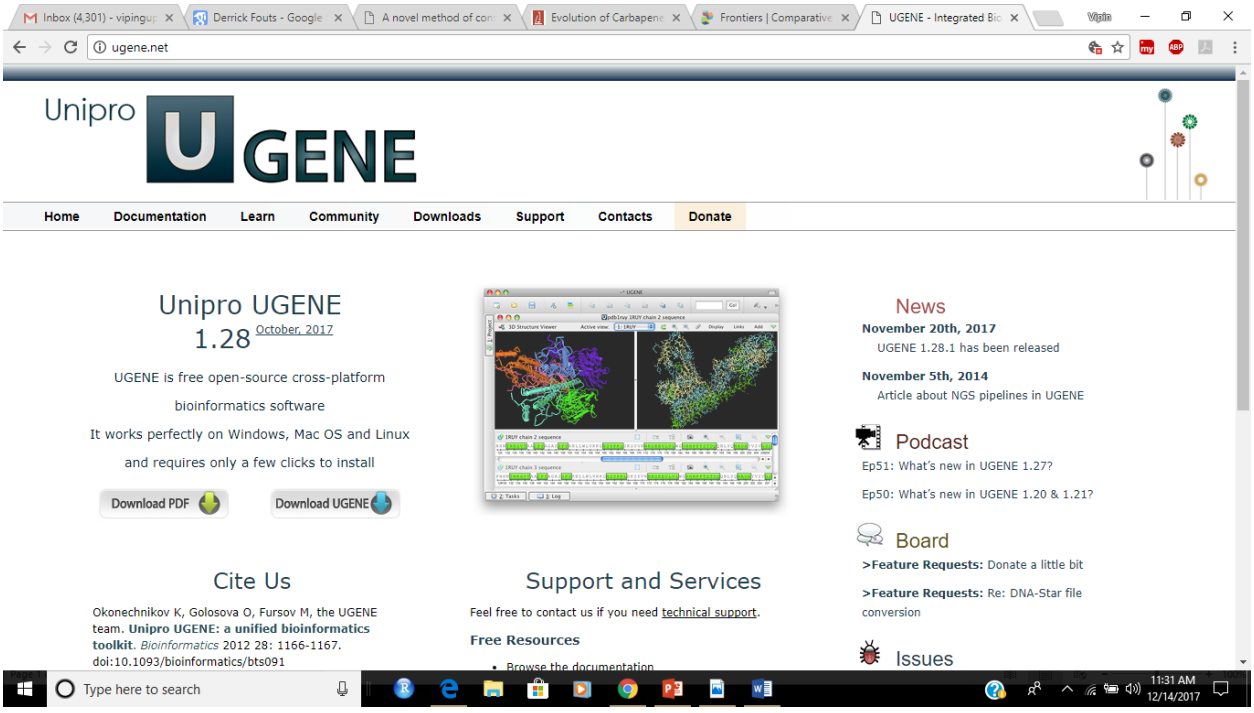



STRENGTH
hp

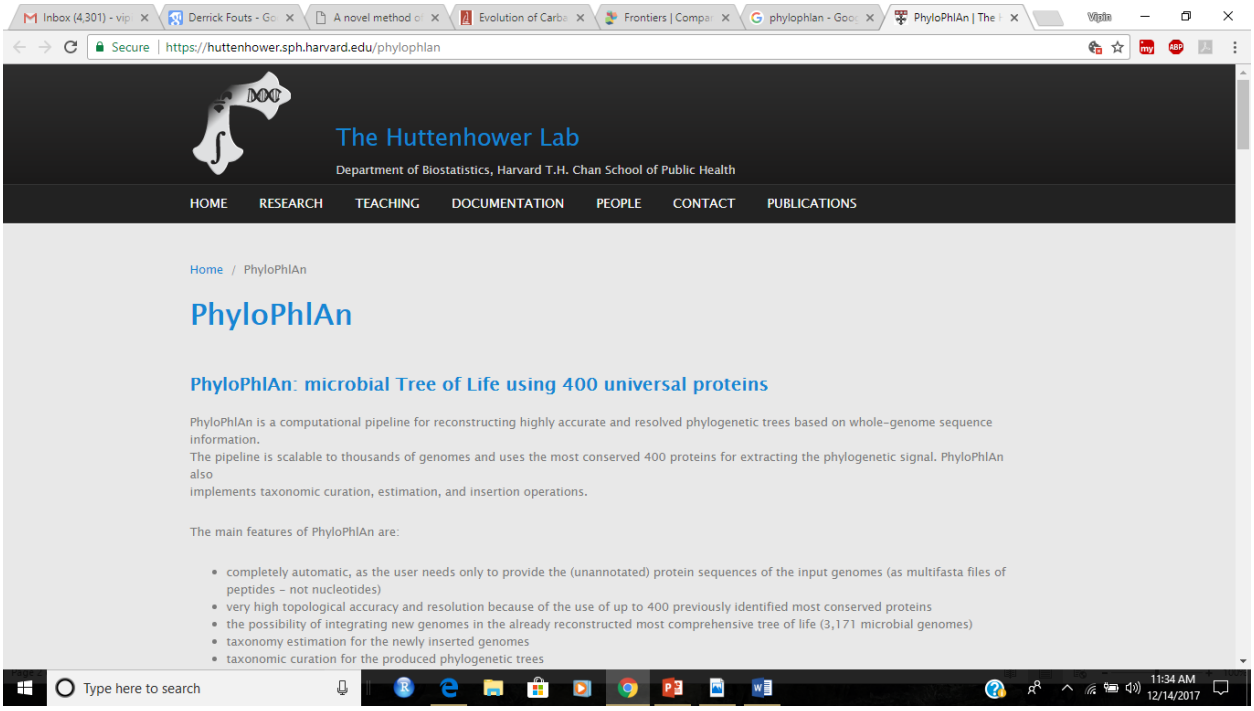
ABySS: A parallel assembler for short read sequence data



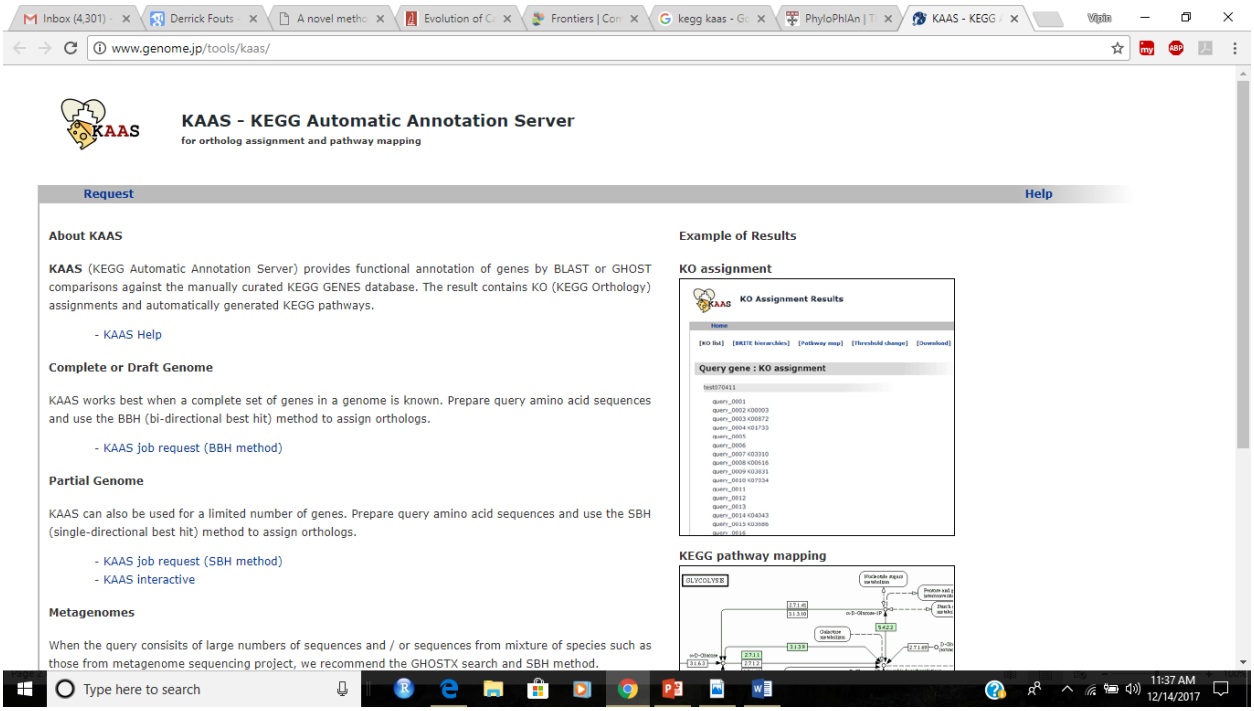
UGENE is a free bioinformatics software for multiple sequence alignment, genome sequencing data analysis, amino acid sequence visualization.



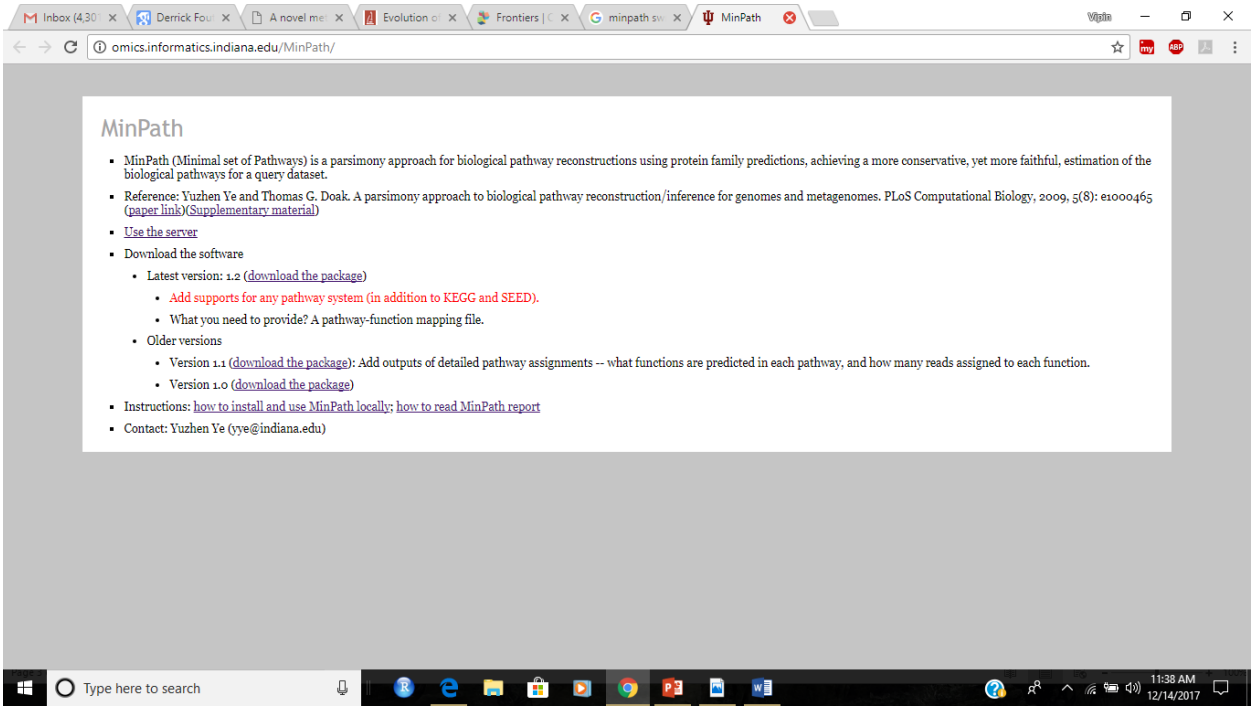
PhyloPhlAn is a computational pipeline for reconstructing highly accurate and resolved phylogenetic trees based on whole-genome sequence information.



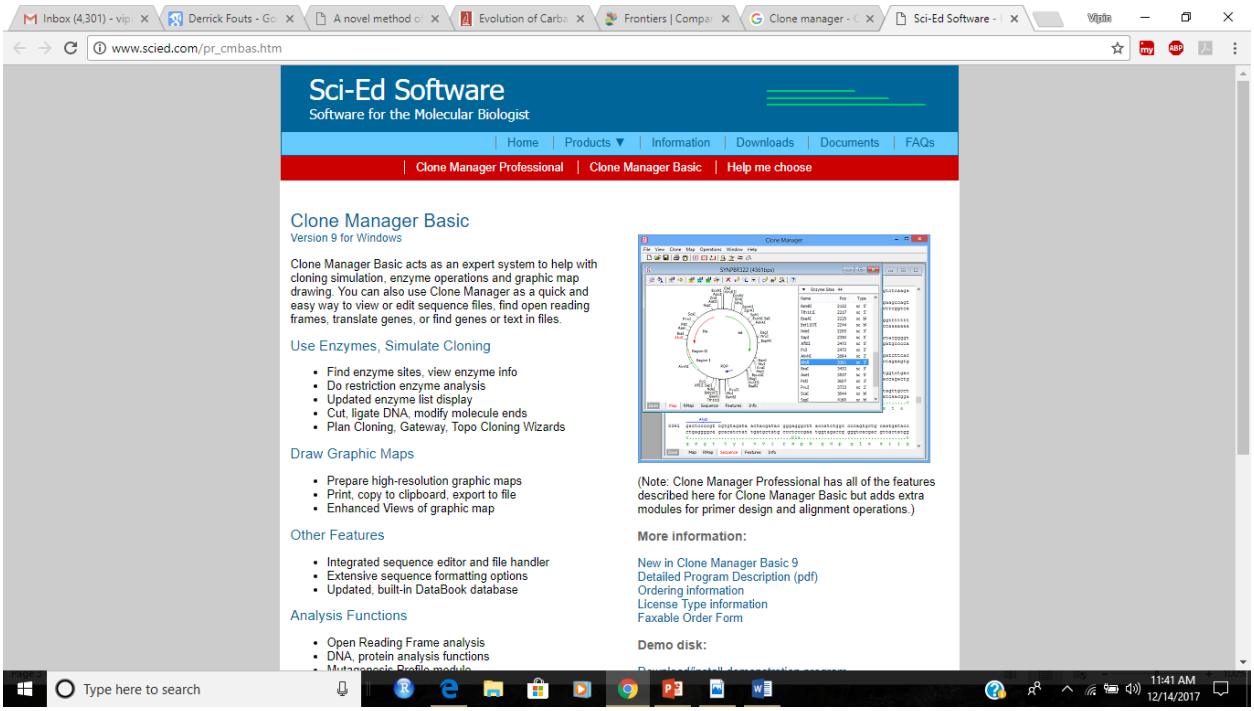
KAAS. **KAAS** (**KEGG** Automatic Annotation Server) provides functional annotation of genes by BLAST or GHOST comparisons against the manually curated **KEGG** GENES database.



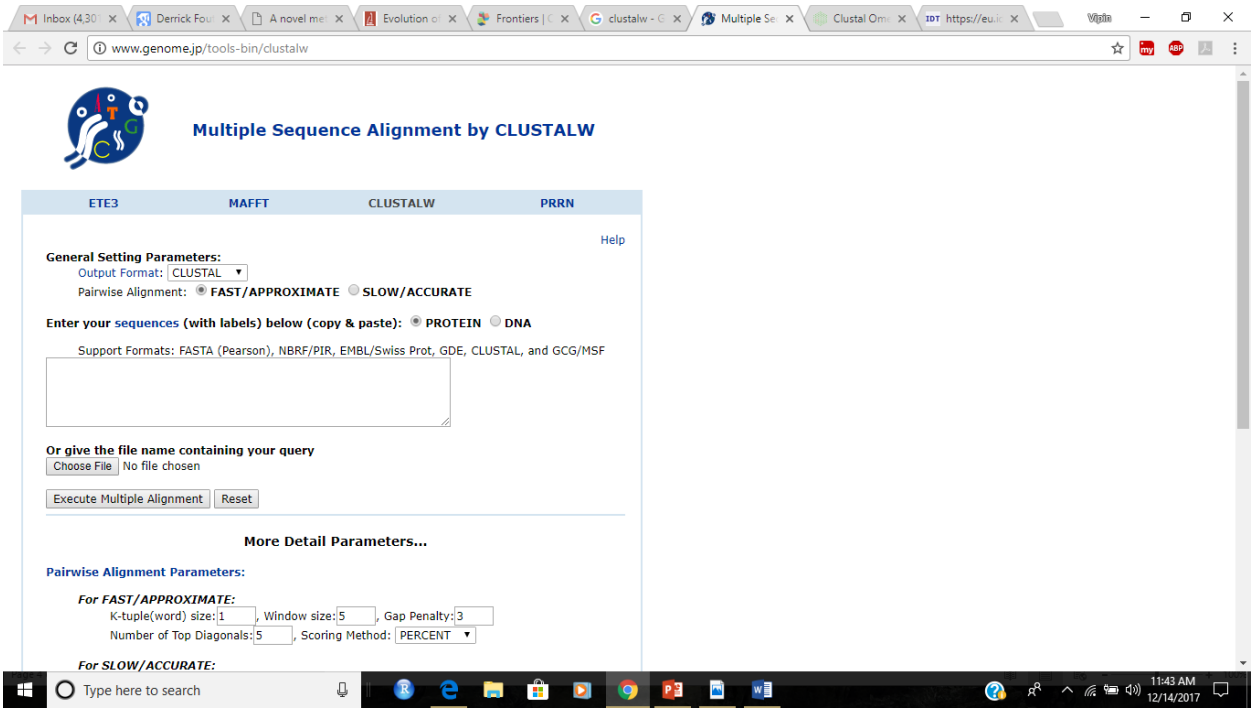
MinPath (Minimal set of Pathways) is a parsimony approach for biological pathway reconstructions using protein family



Clone manager



Multiple Sequence Alignment by CLUSTALW



Primer-BLAST: Finding primers specific to your PCR template