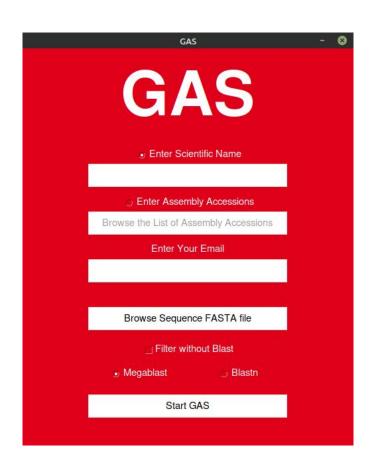
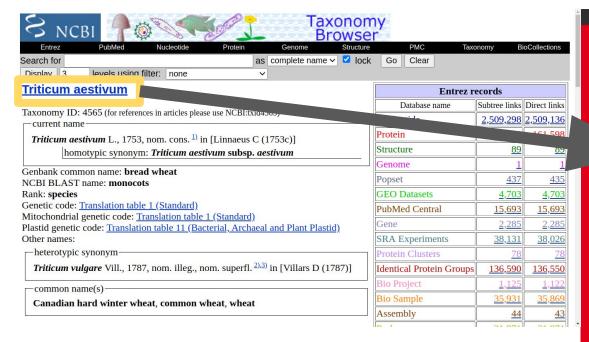
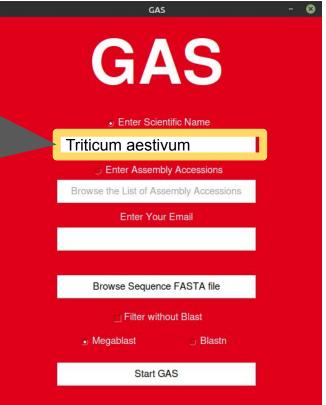
GAS User Guide

Ahmed Karam

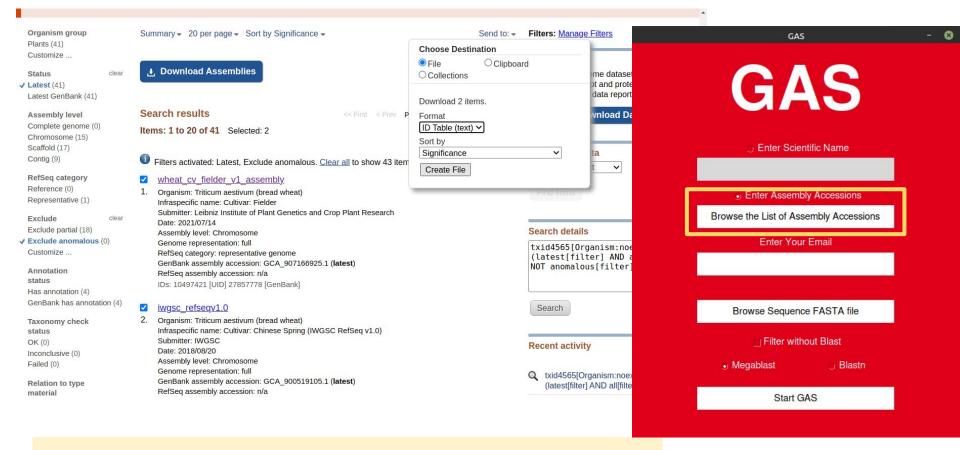
ahmedkaram.edu@gmail.com



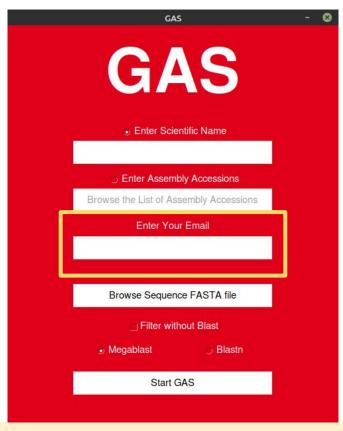




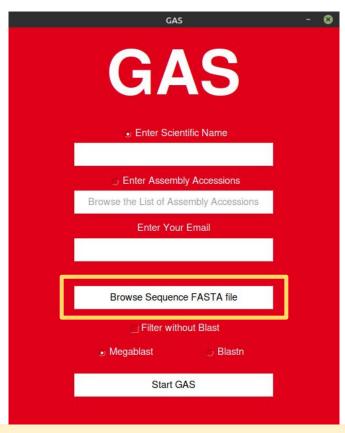
Copy correct scientific name and paste (or write it correctly)



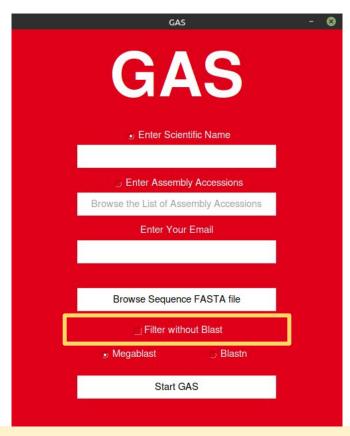
Search by scientific name in the assembly database, choose the assembly, download the ID table, and browse the table through GAS.



Enter your email and this is what NCBI requires to contact you if anything happens.



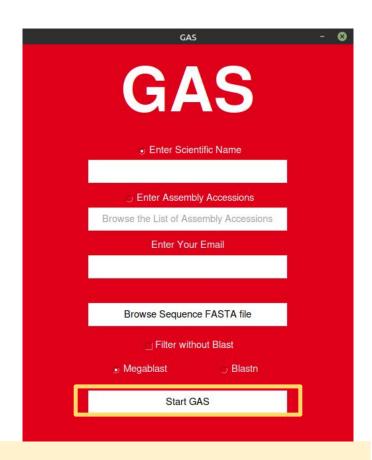
Enter a FASTA file that contains only one sequence and is less than 1000 bases.

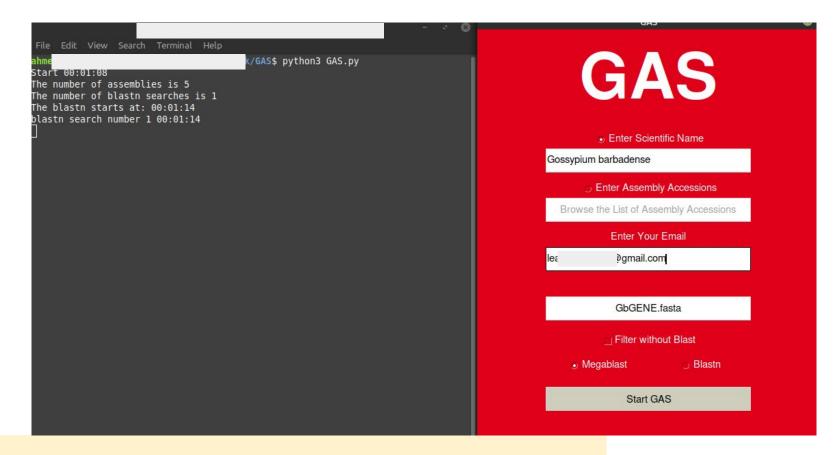


It filters all files that are similar to the name of the entered fasta file that are in the same folder without blastn action.



Choose megablast or blastn





Follow the steps of the GAS through the CMD or the terminal