



For the majority of the task I'll perform on my project, I won't need a spreadsheet, but here is the structure of the database I designed to host key information I will be needing for my project. This database is composed of 3 tables. The species Info table includes individual info on the taxonomy and ploidy level of each species. The species source info table contains source information of each sample, which were pulled from another database using voucher_ID. The phasing statistics table provides the statistics for each sample, for e.g. No_of_loci (how many loci had a DNA sequence for this sample). Primary keys are in italics and foreign keys are in bold. The goFlagID is a unique number assigned to each species/sample and it is the foreign key that connects all the tables