1. Databases can be made either by manually curating the tools/studies or by using a text mining/computational assembly method like Szklarczyk outlines.
2. The main benefit of a public database is that anyone can access it and learn the information that they need. It is also convenient to have several similar articles/tools in the same location because it increases the ease by which a reader can search for specific resources.
3. Only using one database can lead to being exposed to a very limited portion of all the relevant literature that exists. Papers only make it into the database if either someone or an algorithm deems that it fits the criteria. However, both these methods may overlook some relevant papers. Public databases also do not include literature that is in journals with fees/paywalls so the reader may lose out on potentially relevant information due to only using public databases.
4. The only databases that I use currently are pubmed and PLOS. I am interested in finding databases that compile helpful tools for bioinformatics projects.