Notes:
1. This is the most fundamental model for a genomics project. The simplest project would have no processes beyond sequencing, and thus only have specimen, sequencing, and sequence file as parts of the project. More complex projects will have additional processes, with their inputs and outputs, but all the entities will usually be a subclass of one of the entities shown here.
2. Even though specimen collection is an important process, metadata for the collection process is usually associated with the specimen itself (as in BioSamples). We adopt that practices here for our proof of concept, but fully support the notion that a separate entity should be created for that process.
3. isPartOf relations are transitive.
4. Results can have entities other than data files as parts, such as conclusions, figures, publications.