



Notes:

1. This model that covers most genomic projects. Processes of sequencing and assembly can be subdivided into more specific parts, with their own inputs and outputs. Likewise, some of them can be omitted from a project (either because they didn't occur or because there is no information about them).
2. Rather than specifying subclasses for sequencing and assembly, we will use "type" metadata to specify the specific type of sequencing or assembly process (e.g., sanger sequencing, RNAseq, metagenomic sequencing). CVs for these will be supplied. Likewise, we will have a type vocabulary for analysis.
3. isPartOf and hasPart relations are transitive..