**Let us construct an ER model for the following Bioinformatics Application:**

* A Patient has a unique MSP number, a Patient name, a Date of Birth, a Tissue Type and an indicator denoting whether the tissue is cancerous or normal.
* A patient library associates a patient with multiple tags
* Each tag has a unique tag number and a unique nucleotide sequence.
* For each tag in the patient library, a count is given to record the number of times the tag occurs in the library. In general, the same tag can be associated with any number of patients.
* A tag may be mapped to a gene. Each gene has a unique gene name and a type.
* In general, multiple tags may be mapped to the same gene. However, two different genes cannot be mapped to the same tag.
* Finally, an article is identified by a unique article number and a journal name. An article may analyze multiple genes and a gene may be analyzed by multiple articles.