Choose a team partner, immediately, and send me and the T.A. email (ASAP).

1. Choose a team partner, immediately, and send me and the T.A. email (ASAP).
2. Compile the logical Rose model to a DDL and insert that into MySQL
      Once you create the .ddl you should modify it by
      i. Remove the non-null constraint for an attribute that is not required, such as computedFunction.
      ii. Extend the storage type for long data. For example, use TEXT type for protein sequence.
   b. Insert the .ddl into MySQL, you can use the instructions from Homework 5.
3. Turn in the results of the execution of two queries, either in text or screenshot form:
   a. The query
      SELECT name
      FROM t_protein, t_proteinsource
      WHERE dbName = 'Genbank' AND
      organism = 'EColi' AND
      t_protein.t_proteinsource_id = t_proteinsource.t_proteinsource_id
   b. A query of your invention

4. The following questions refer to the UML diagram that comprises the published solution to homework 4: [http://www.cs.utexas.edu/~parnell/courses/2008/fall/hw4_soln.pdf](http://www.cs.utexas.edu/~parnell/courses/2008/fall/hw4_soln.pdf)

Recall, Rational Rose compiles inheritance as follows:
A) Per the model above, and in the style of the textbook, [invent] and draw out the table contents comprising at least,
- one person who is not an employee or a student,
- two employees
- two students

B) The following questions refer to the UML diagram that comprises the published solution to homework 4 [http://www.cs.utexas.edu/~parnell/courses/2008/fall/hw4_soln.pdf].
- Consider the DbxRef class and the classes whose contents have provenance by virtue of association with the DbxRef class. It would seem natural to simply have those classes inherit from the DbxRef class. Explain if this is a good or bad idea, and if it is feasible or infeasible.

5. Below is the UML diagram for the Biosequence package in the MAGE-OM. The following questions apply to this diagram answer the question.

**Diagram: BioSequence / Overview**

A) Note this model differs from our usual sequence model as the sequences being referred to are more commonly probe sequences in the wells of the chips rather than full length gene or protein sequences typical of Genbank.
i) SequencePosition has a multiplicity of 1 to 1, quite different than our usual model. Why do you suppose that is? (Hint: see next two questions).

ii) For a given sequence feature how many times may it appear in a sequence?

iii) Observe the association Subregions. What do you suppose this represents?