

Data Model

Instructions:

You are the manager of a bioinformatics support service and need to build a database to manage data from your users' studies. Define a data model (entities, attributes and relationships) to hold data from a series of RNAseq (analysis).

Data should include:

- 1) Genes included in the study
 - 2) Reference, suppliers, for sequencing reagents and equipment used
 - 3) Sample and user details
 - 4) Results: genes, expression values, differential expression analysis
 - 5) References
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Entities:

1. Genes
2. Reference
3. Supplier
4. Sequencing Reagents
5. Equipment
6. Sample
7. User
8. Results
9. References

Attributes and Relationships:

1. Genes:

- Attributes:
 - o Gene_ID, Gene_Name, Gene_Description, Sequence
- Relationships:
 - o Many-to-Many with Results (genes involved in the analysis)

2. Reference:

- Attributes:
 - o Reference_ID, Title, Authors, Journal, Year
- Relationships:
 - o One-to-Many with Results (references used in the study)

3. Supplier:

- Attributes:

- Supplier_ID, Name, Contact_Info
- Relationships:
 - One-to-Many with Sequencing Reagents and Equipment

4. Sequencing Reagents:

- Attributes:
 - Reagent_ID, Name, Supplier_ID (foreign key)
- Relationships:
 - One-to-Many with Results

5. Equipment:

- Attributes:
 - Equipment_ID, Name, Model, Supplier_ID (foreign key)
- Relationships:
 - One-to-Many with Results

6. Sample:

- Attributes:
 - Sample_ID, Sample_Name, Sample_Type, User_ID (foreign key)
- Relationships:
 - One-to-Many with Results
 - Many-to-One with User

7. User:

- Attributes:
 - User_ID, Username, Email
- Relationships:
 - One-to-Many with Sample

8. Results:

- Attributes:
 - Result_ID, Gene_ID (foreign key), Sample_ID (foreign key), Expression_Values, Differential_Expression_Analysis
- Relationships:
 - Many-to-One with Genes
 - Many-to-One with Sample
 - Many-to-One with Reference

