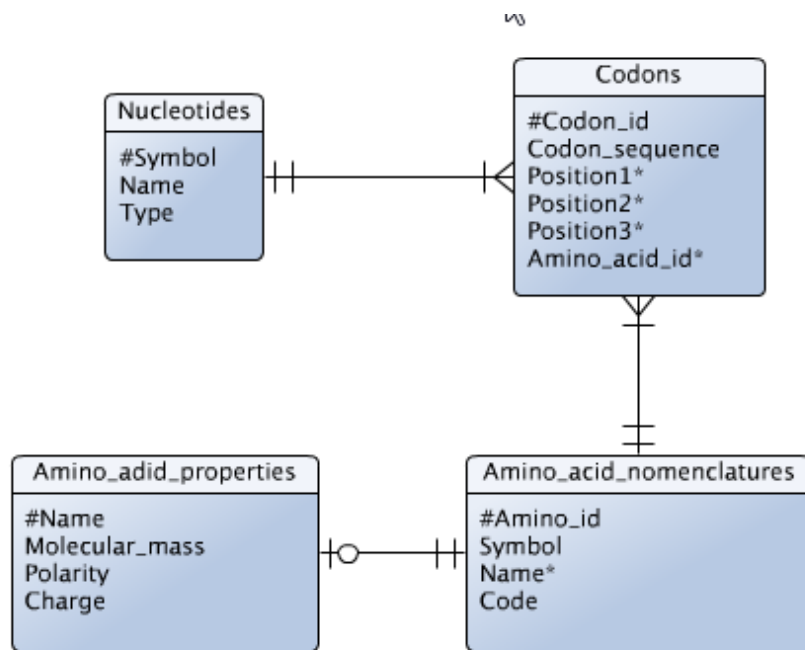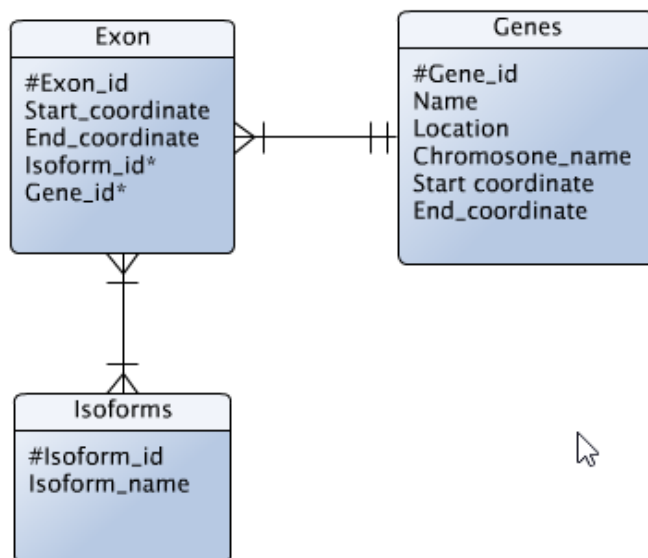1)

2 i) Exon, Genes, Isoforms

ii)

iii)

Exon(#Exon_id,Start_coordinate,End_coordinate,Isoform_id*)

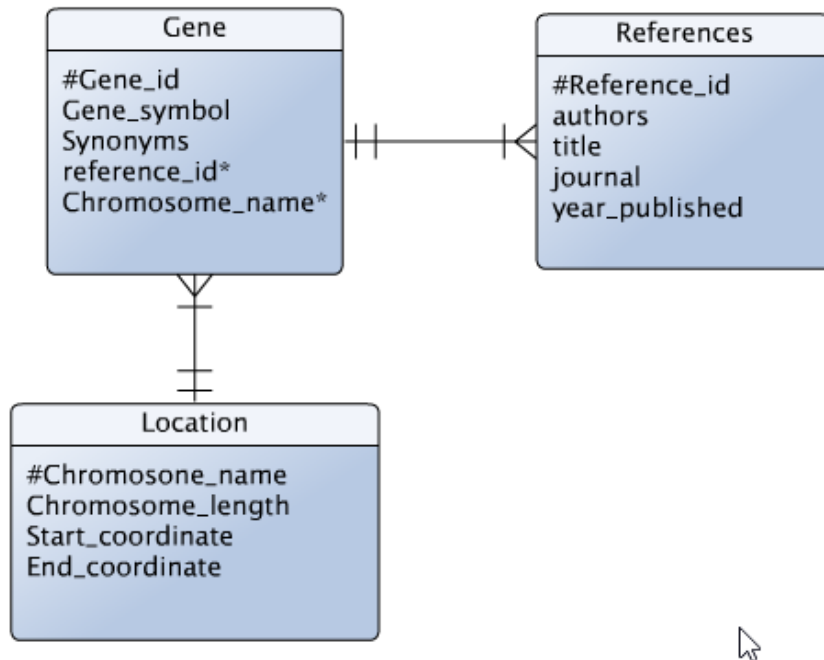Genes(#Gene_id,Name,Location,Chromosome_name*,exon_id*)

Chromosome(#Chromosome_name,start coordinate,end_coordinate)

Isoforms(#Isoform_id,Isoform_name)

3 i)

Entities: Gene, Location, references

ii)

iii)

Gene(#Gene_id*, Official name, Reference_id*,chromosome_name*)

Location(#Chromosome_name,Chromosome_length, Start_coordinate, End_coordinate)

References(#Reference_id*,title,journal,year_published)

Synonyms(#Gene_id, Gene_symbols)

Authors(#Reference_id, Author_name)

iv)

Gene(#Gene_id*, Official name, Reference_id*,chromosome_name*)
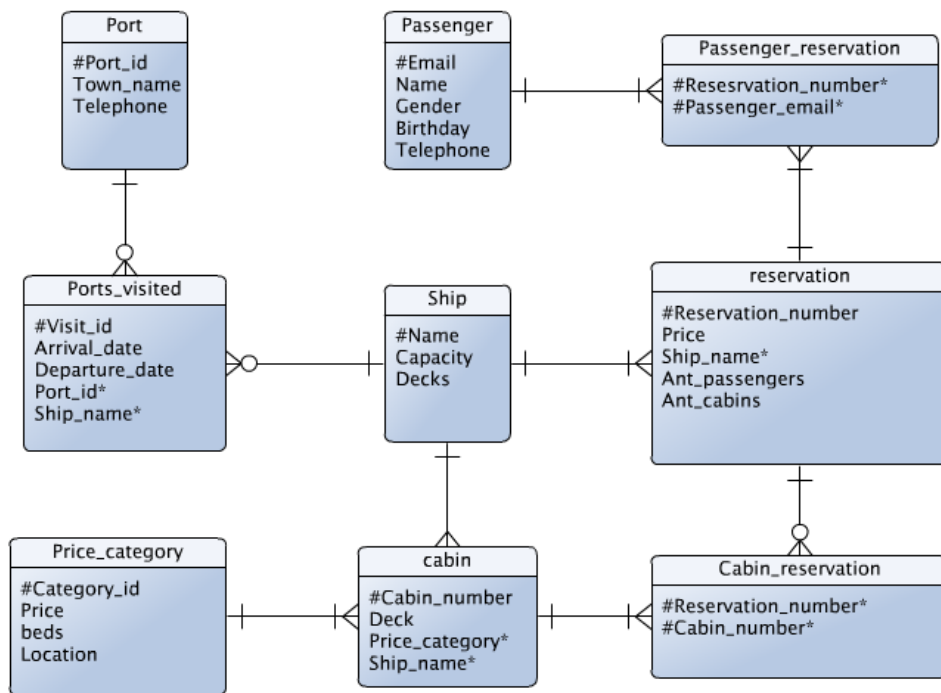
Location(#Chromosome_name, Start_coordinate, End_coordinate)

References(#Reference_id*,title,journal,year_published)

Synonyms(#Gene_id, Gene_symbols)

Authors(#Reference_id, Author_name)

Chromosome(#Chromosome_name,Chromosome_length)

4)

5

 i) You get a many to many relationship when a truck gets new assignments

ii) Registration_number→Registration_year

   Model→Maximum_weight

iii) Registration_number

iv)

Container_type(#Type_name, Max_weight ,Cubic_quantity ,Nightly rate)

Container (#Container_number, Type_name*)

Assignment(#Assignment_number, Customer_id*, Start_date, End_date)

Truck(#registration_number, Registration_year,Assignment_number*, Model*)

Truck_model(#model, Maximum_weight)