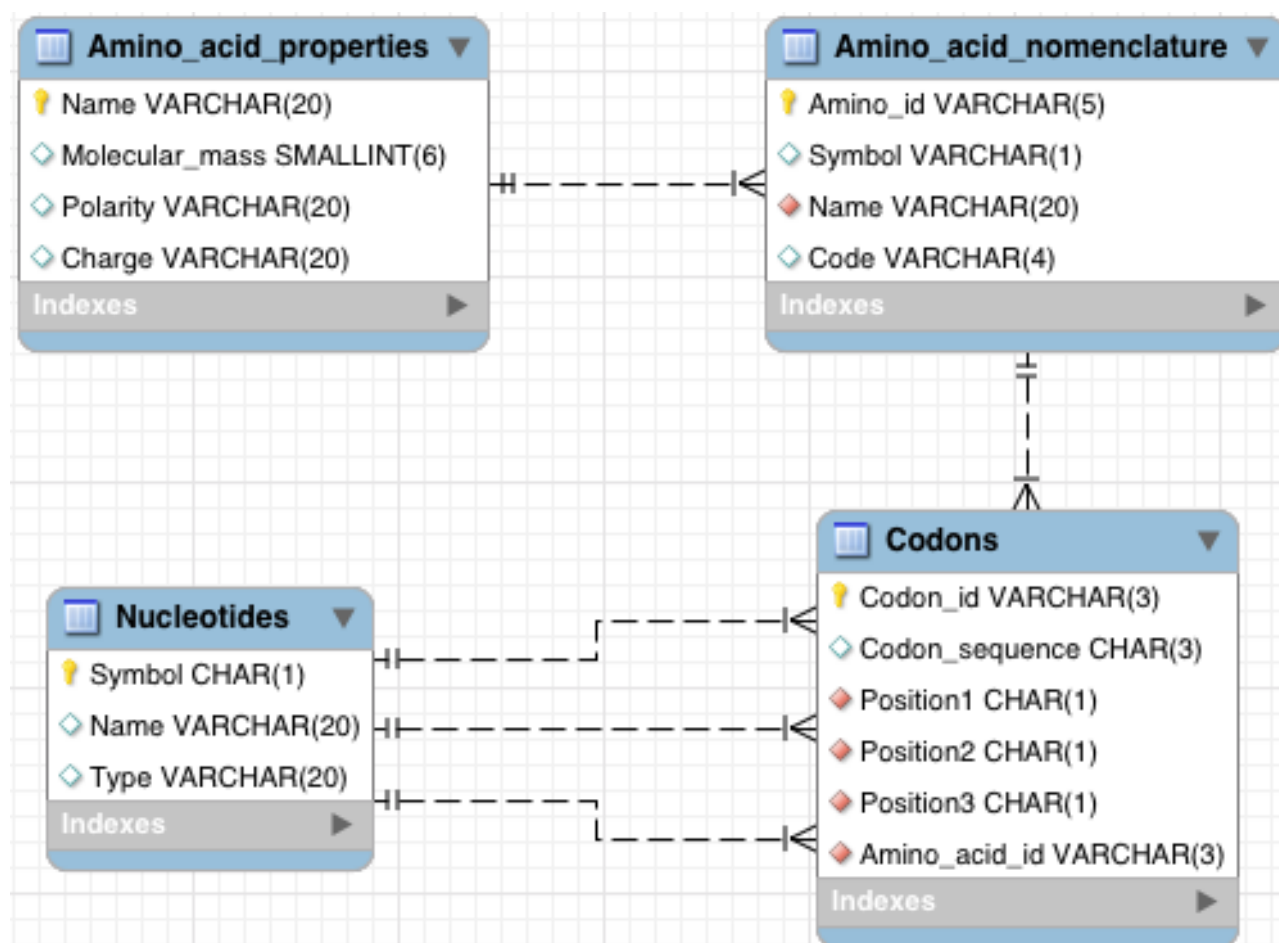


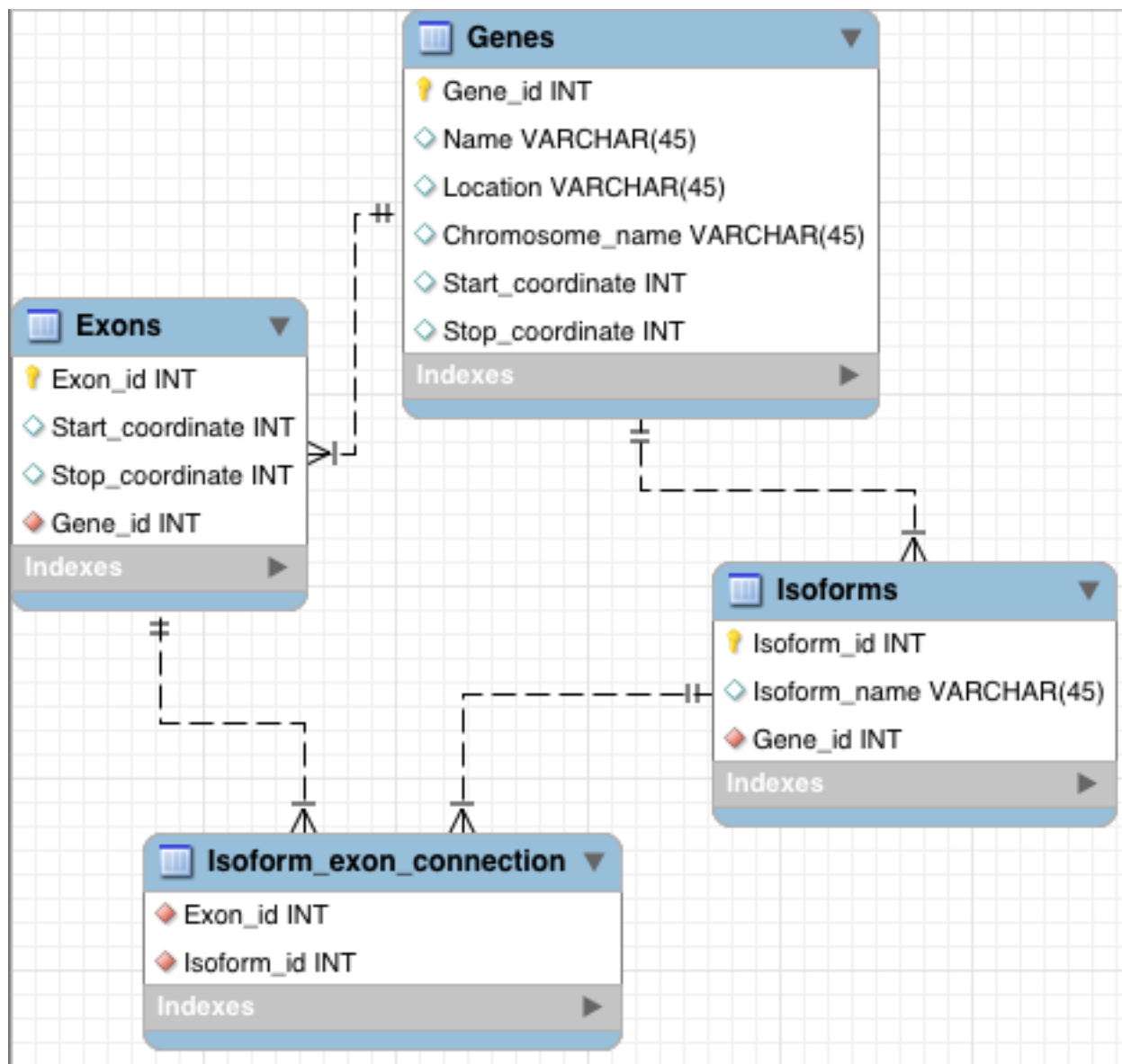
1)



2.i)

Genes, Exons, Isoforms

2.ii)



2.iii)

Genes(#Gene_id, Name, Location, Chromosome_name, Start_coordinate, Stop_coordinate)

Exons(#Exon_id, Start_coordinate, Stop_coordinate, Gene_id*)

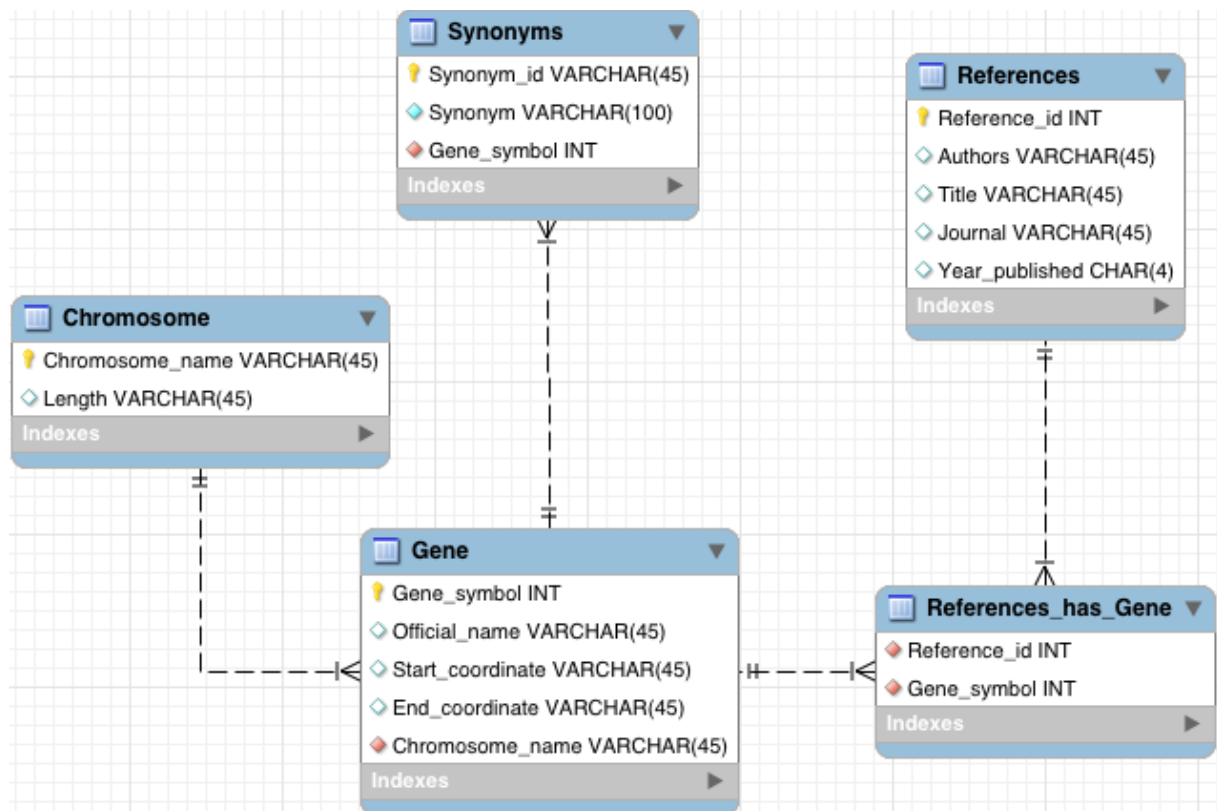
Isoforms(#Isoform_id, Isoform_name, Gene_id*)

Isoform_exon_connection(Exon_id*, Isoform_id*)

3.i)

Chromosome, Gene, Synonyms, References

3.ii)



3.iii)

Gene(#Gene_symbol, Official_name, Start_coordinate, End_coordinate, #Chromosome_name, Chromosome_length)

Synonyms(#Synonym_id, Synonym, Gene_symbol*)

References(#Reference_id, Authors, Title, Journal, Year_published)

References_has_Gene(Reference_id*, Gene_symbol*)

3.iv)

Chromosome(#Chromosome_name, Length)

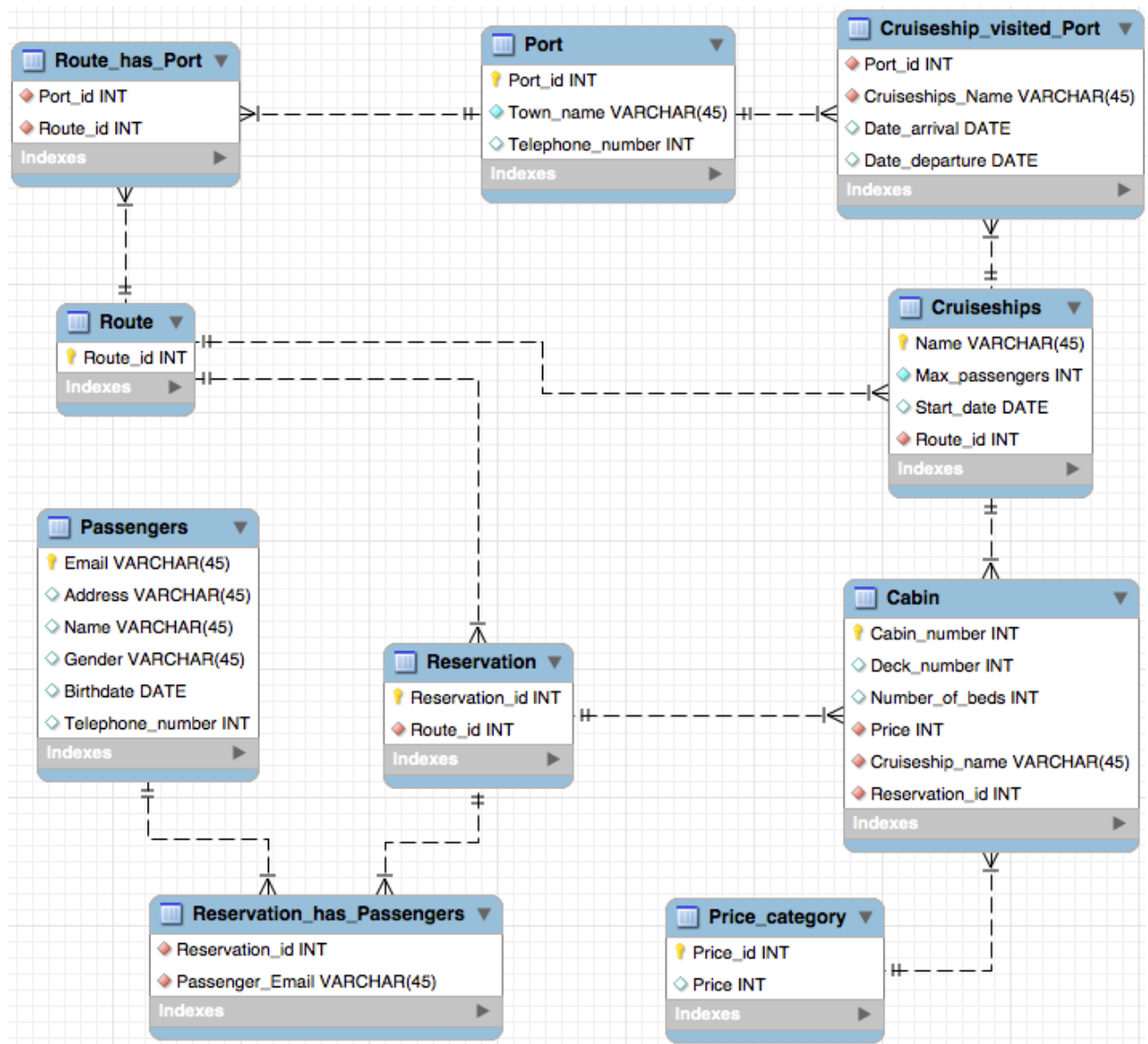
Gene(#Gene_symbol, Official_name, Start_coordinate, End_coordinate, Chromosome_name*)

Synonyms(#Synonym_id, Synonym, Gene_symbol*)

References(#Reference_id, Authors, Title, Journal, Year_published)

References_has_Gene(Reference_id*, Gene_symbol*)

4)



5i)

This solution is problematic because it is a breach of the second normal form; Registration_year, Model and Maximum_weight are all dependent on the Registration_number.

5ii)

Registration_number -> Registration_year

Registration_number -> Model

Model -> Maximum_weight

5iii)

Registration_number

5iv)

Container_type (#Type_id, Type_name, Max_weight, Cubic_quantity, Nightly_rate)

Container (#Container_number, Type_id*)

Customer (#Telephone_number, Address)

Assignment (#Assignment_number, Telephone_number*, Container_number*, Start_date, End_date)

Truck (Registration_number*, Assignment_number*)

Truck_registration(#Registration_number, Registration_year, Model_name*)

Model(#Model_name, Maximum_weight)