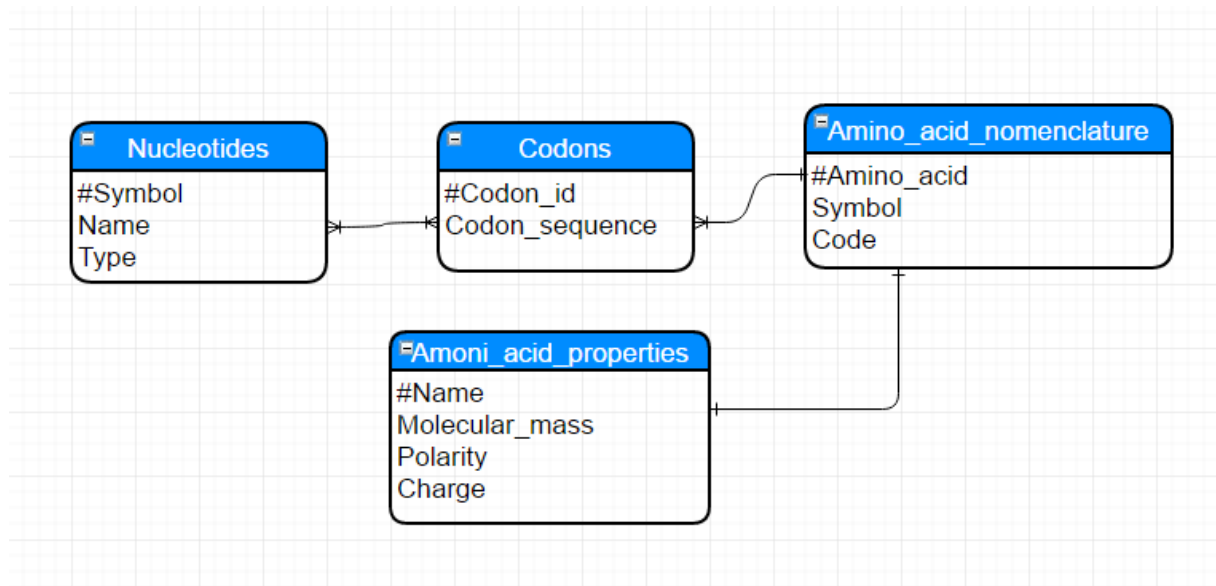


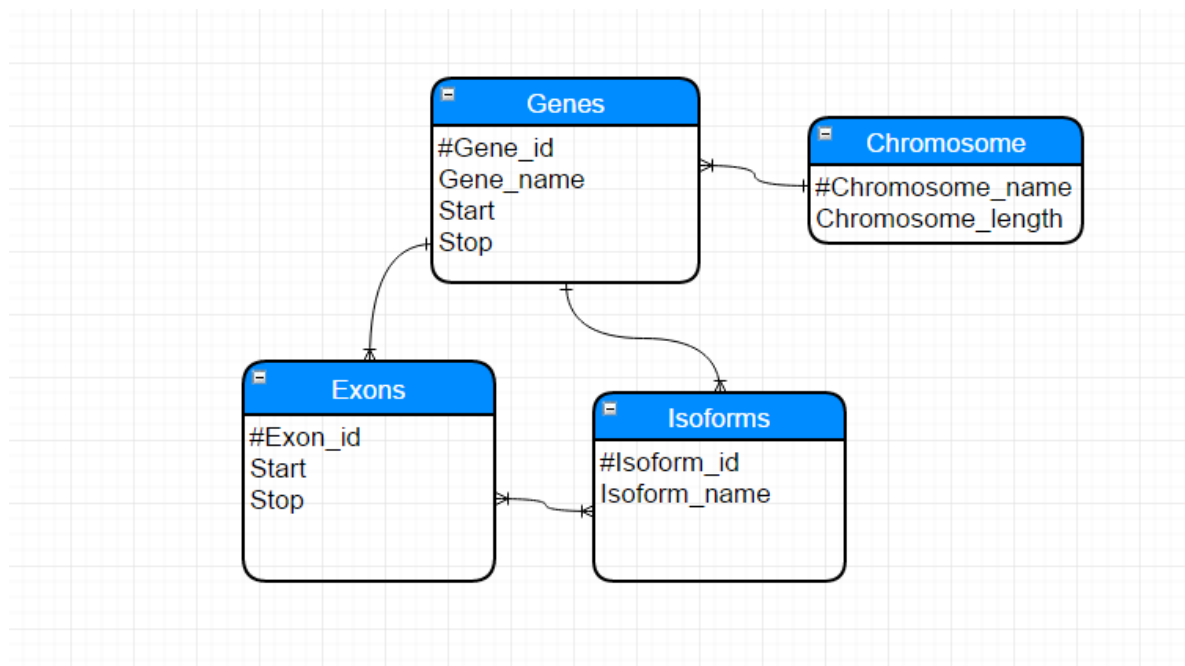
1.



2. I

Genes, Chromosome, Exons, Isoforms.

2 II.



2. III

Genes(#Gene_id, Gene_name, Chromosome_name*, Exon_id*, Isoform_id*, Start, Stop)

Chromosome(#Chromosome_name, Chromosome_length)

Exons(#Exon_id, Gene_id*, Start, Stop)

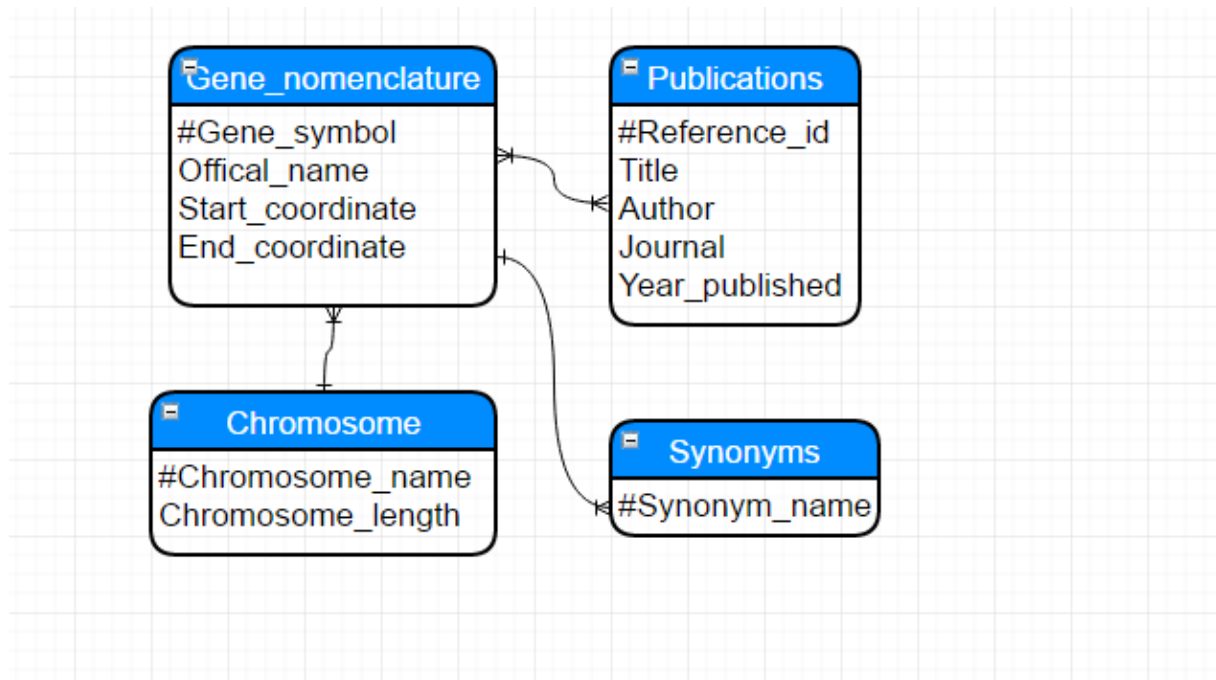
Exons_isoforms(#Exon_id*, #Isoform_id*)

Isoforms(#Isoform_id, Isoform_name, Gene_id*)

3.I

Gene_nomenclature, Publications, Chromosome, Synonyms

3. II



3.III

Gene_nomenclature(#Gene_symbol, #Synonym_name, #Reference_id, Official_name, Chromosome_name, Chromosome_lenght, Start_coordinate, End_coordinate, Authors, Title, Journal, Year_published)

3 IV.

Gene_nomenclature(#Gene_symbol, Official_name, Chromosome_name*, Reference_id*, Start_coordinate, End_coordinate)

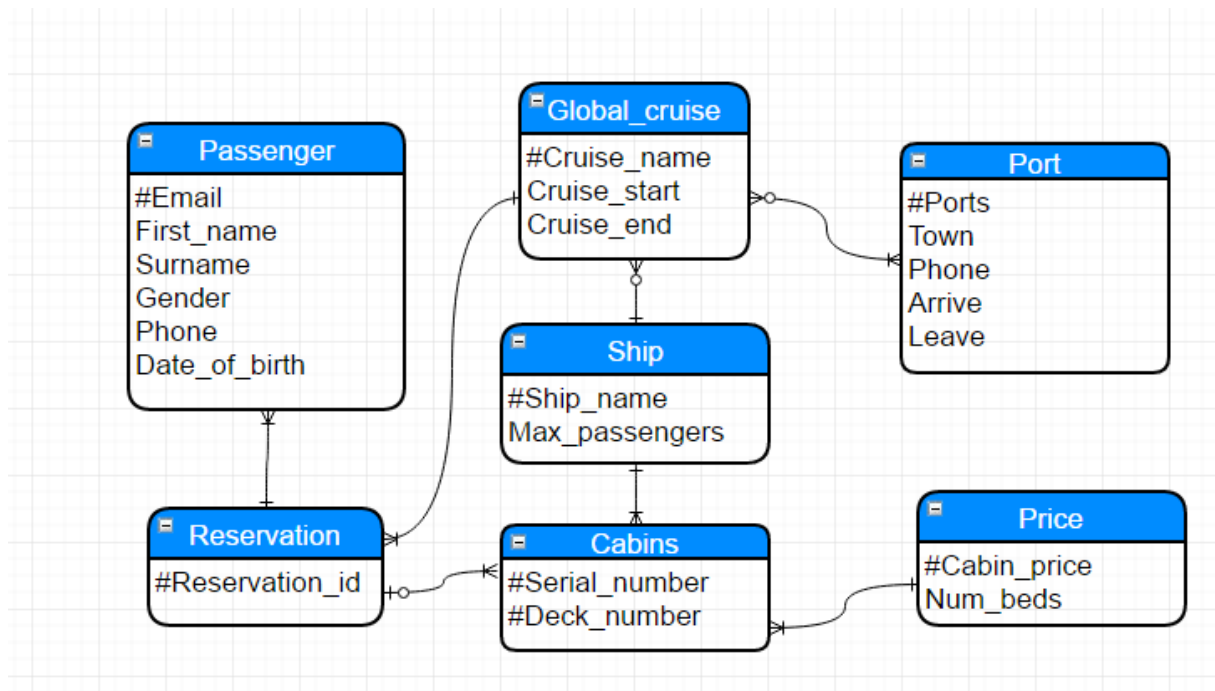
Gene_publications(#Reference_id*, #Gene_symbol*)

Publications(#Reference_id, Author, Title, Journal, Year_published)

Chromosome(#Chromosome_name, Chromosome_length)

Synonyms(#Synonym_name, Gene_symbol*)

4.



5. I

Problematic to not have a primary key. One can't identify a specific row without a primary key and a table without a primary key may create duplicates of the same truck (Registration_number).

5. II

Registration_number -> (Registration_year, Model)

Model -> Maximum_weight

5. III

(Registration_number, Model) is a possible candidate key, because then the table would be functionally dependent -> Truck(#Registration_number, #Model, Registration_year, Maximum_weight, Assignment_number*).

5. IV

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)

Assignment_truck(#Assignment_number*, #Registration_number*)

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

Model(#Model, Maximum_weight)