**SQL**

CREATE TABLE lipids(lipidID INT, common\_name VARCHAR(255), systematic\_name VARCHAR(255), formula VARCHAR(255), mass INT, publicID VARCHAR(255), structure\_image VARCHAR(255), categories\_categoryID INT );

CREATE TABLE organisms(organismID INT, organism\_name VARCHAR(255));

CREATE TABLE categories(categoryID INT, category\_name VARCHAR(255));

CREATE TABLE lipid\_references(referenceID INT, reference\_name VARCHAR(255), reference \_description VARCHAR(255), reference\_link VARCHAR(255), lipids\_lipidID INT);

CREATE TABLE cross\_references(cross\_referenceID INT, cross\_reference\_ link VARCHAR(255), lipids\_lipidID INT, sources\_sourceID INT);

CREATE TABLE sources(sourceID INT, source\_name VARCHAR(255));

CREATE TABLE spectroscopy\_images(imageID INT, image VARCHAR(255), image\_description VARCHAR(255), lipids\_lipidID INT);

CREATE TABLE modifications\_lipids(lipids\_1ID INT, lipids\_2ID INT, modification\_typeID INT);

CREATE TABLE modifications(modification\_typeID INT, modification\_type\_name VARCHAR(255));

CREATE TABLE found\_in(lipidID INT, organismID INT);

INSERT INTO Lipids (common\_name, systemaics\_name, formula, publicID, mass, structure\_image, categoryID) VALUES ( X,Y ,Z ,M ,N ,L ,O ,P);

INSERT INTO categories (categoryID , category\_name) VALUES (X ,Y );

INSERT INTO organisms( organismID, organism\_name) VALUES ( X, Y);

INSERT INTO lipid\_references (referenceID, reference\_name, reference \_description ,reference\_link, lipids\_lipidID) VALUES (X ,Y ,Z ,M ,N );

INSERT INTO cross\_references (cross\_referenceID, cross\_reference\_link, lipids\_lipidID, sources\_sourceID) VALUES (X ,Y , Z,M );

INSERT INTO sources (sourceID, source\_name) VALUES (X ,Y );

INSERT INTO spectroscopy\_images(imageID, image, image\_description, lipids\_lipidID) VALUES (Z ,X ,Y ,M);

INSERT INTO modifications\_lipids(lipids\_1ID, lipids\_2ID, modification\_typeID) VALUES (X ,Y ,Z );

INSERT INTO modifications(modification\_typeID, modification\_type\_name ) VALUES (X ,Y );

INSERT INTO found\_in(lipidID, organismID) VALUES (X ,Y );

SELECT \* FROM Lipids WHERE mass =< A AND mass => B;

SELECT \* FROM Lipids WHERE Systematic\_name = X OR Common\_name = X;

SELECT \* FROM Lipids WHERE Formula = X;

SELECT \* FROM Lipids WHERE publicID = X;

SELECT \* FROM Lipids WHERE Organism = X;

SELECT \* FROM Lipids WHERE Category ID = X;

SELECT publicID FROM Lipids WHERE mass IN (A,B,C);

SELECT publicID FROM lipids WHERE mass NOT IN (D,E,F);

SELECT publicID,common\_name,mass FROM lipids WHERE categoryID IN (A,B,C,D);

SELECT publicID,common\_name FROM lipids L organisms O WHERE O.organismID IN (A,B,C);

DELETE FROM sources WHERE cross\_reference\_link = X;

DELETE FROM lipids WHERE mass =< A AND mass => B;

**RELATIONAL ALGEBRA:** π σ

SELECT \* FROM Lipids WHERE mass =< A AND mass => B;

σ mass =< a and mass =>b Lipids ;

SELECT \* FROM Lipids WHERE Systematic\_name = X OR Common\_name = X;

σ systematic\_name = x v common\_name = x Lipids;

SELECT \* FROM Lipids WHERE Formula = X;

σ formula = x Lipids;

SELECT \* FROM Lipids WHERE publicID = X;

σ publicid = x Lipids;

SELECT \* FROM Lipids WHERE Organism = X;

σ organism = x Lipids;

SELECT \* FROM Lipids WHERE Category ID = X;

σ category id = x Lipids;

SELECT publicID FROM Lipids WHERE mass IN (A,B,C);

π publicID ( σ mass = ‘A’ v mass = ‘B’ v mass = ‘C’ Lipids)

SELECT publicID FROM lipids WHERE mass NOT IN (D,E,F);

π publicID ( )

SELECT publicID,common\_name,mass FROM lipids WHERE categoryID IN (A,B,C,D);

π publicID,common\_name,mass ( σ categoryID = ‘A’ v categoryID = ‘B’ v categoryID = ‘C’ v categoryID = ‘D’ Lipids)

SELECT publicID,common\_name FROM lipids L organisms O WHERE O.organismID IN (A,B,C);

π publicID,common\_name (σ organismID = ‘A’ v organismID = ‘B’ v organismID = ‘C’ Lipids ⋈ Organisms )

**Normalization**

lipids

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| lipidID | common\_name | systematic\_name | formula | mass | publicID | structure\_image | categories\_categoryID |

organisms

|  |  |
| --- | --- |
| organismID | organism\_name |

categories

|  |  |
| --- | --- |
| categoryID | category\_name |

lipid\_references

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| referenceID | reference\_name | reference \_description | reference\_link | lipids\_lipidID |

cross\_references

|  |  |  |  |
| --- | --- | --- | --- |
| cross\_referenceID | cross\_reference\_ link | lipids\_lipidID | sources\_sourceID |

sources

|  |  |
| --- | --- |
| sourceID | source\_name |

spectroscopy\_images

|  |  |  |  |
| --- | --- | --- | --- |
| imageID | image | image\_description | lipids\_lipidID |

modifications\_lipids

|  |  |  |
| --- | --- | --- |
| lipids\_1ID | lipids\_2ID | modification\_typeID |

modifications

|  |  |
| --- | --- |
| modification\_typeID | modification\_type\_name |

found\_in

|  |  |
| --- | --- |
| lipidID | organismID |

The first normal form (1NF) states that all values in any given table are atomic.

The second normal form (2NF) states that every non-key attribute is fully functionally dependent on the primary key.

The third normal form (3NF) states that all columns must depend on the primary key only, and not on any other non-key attribute.

The Boyce-Codd normal form (BCNF) states that all redundancy due to functional dependencies has been removed.

As indicated by the arrows, all our tables comply with the mentioned normal forms, and are in BCNF.