

#### A SERIES OF WORKSHOPS FROM The FLS bioinformatics society

#### INTRODUCTION TO SQL MARK REARDON

Database programming for biologists

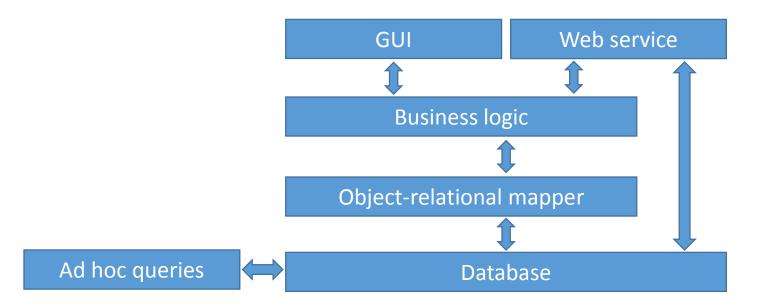
**4-5<sup>™</sup>, FRIDAY 13-11-15** STOPFORD 1.065-1.066 uombio.info ♥ f UoMBioinfoSoc

#### Introduction

- Databases help us model the relationships between datasets
- Spreadsheets are not databases (please don't call them that!)
- There are many database engines
  - (MySQL, SQL Server, Oracle, Postgres, etc.)
- I'm good at SQL Server so we're using that
  - SQL Server Express is free and really quite powerful
- <u>www.microsoft.com/en-us/server-cloud/products/sql-server-editions/sql-server-express.aspx</u>
  - Just click 'Next' a few times and you'll probably be alright

#### Where do databases fit in?

- They can be standalone and used for ad hoc queries (this lecture)
- They can be a layer in a more complex application:

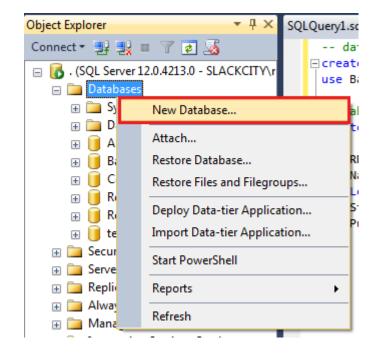


#### Creating a database

#### SQL

use Basics;

#### **Management Studio**



#### Creating a table to hold rows of data

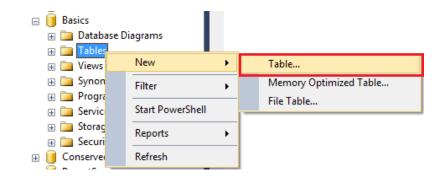
SQL

);

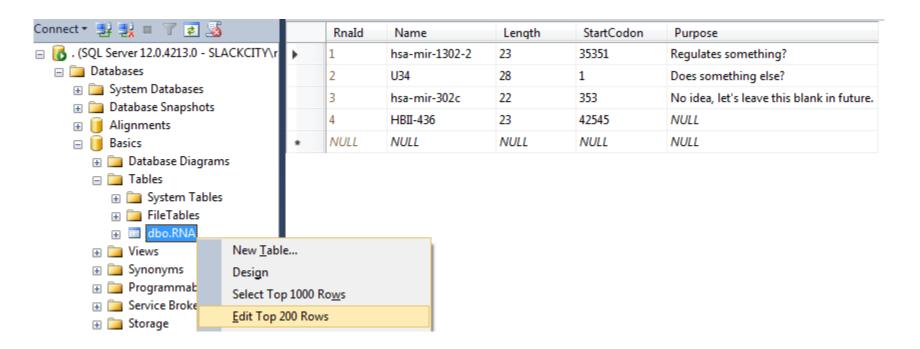
```
-- create a table create table RNA
```

```
RnaId int identity(1,1) primary key,
Name varchar(50) not null,
Length int not null,
StartCodon int not null,
Purpose varchar(255) null
```

#### **Management Studio**



	Column Name	Data Type	Allow Nulls
8	RnaId	int	
	Name	varchar(50)	
	Length	int	
	StartCodon	int	
	Purpose	varchar(255)	$\checkmark$



- Create, Retrieve, Update and Delete
- This covers pretty much everything you do to data

Creating and retrieving data

```
-- create data
   insert RNA (Name, Length, StartCodon, Purpose)
     values ('hsa-mir-1302-2', 23, 35351, 'Regulates something?'),
             ('U34', 28, 1, 'Does something else?'),
             ('hsa-mir-302c', 22, 353, 'No idea, let''s leave this blank in future.'),
             ('HBII-436', 23, 42545, null);
     -- retrieve data
     select * from RNA where Name like 'hsa%';
100 % - 4
 Results
              Messages
     Rnald
            Name
                         Length
                                 StartCodon
                                           Purpose
            hsa-mir-1302-2
                                 35351
                                            Regulates something?
                         23
                                 353
 2
      3
            hsa-mir-302c
                          22
                                            No idea, let's leave this blank in future.
```

• Tip: select a part of the script and hit F5 to run that bit alone

• Updating data

```
-- update data
    update RNA set Purpose = null where Name = 'U34';
     select * from RNA where Name = 'U34';
100 % 🚽 🖪
🔠 Results
          Messages
                 Length StartCodon
     Rnald
           Name
                                   Purpose
    2
            U34
                  28
                         1
                                   NULL
 1
```

• Deleting data

```
-- delete data
delete from RNA where Name = 'U34';
select * from RNA;
```

100 % 👻 🖪

		🔢 Results 📑 Messages							
Rna		Length	StartCodon	Purpose					
1 1	hsa-mir-1302-2	23	35351	Regulates something?					
2 3	hsa-mir-302c	22	353	No idea, let's leave this blank in future.					
3 4	HBII-436	23	42545	NULL					

## Slicing and dicing

• Three statements and three result sets:

slicing and dicing data select distinct Length from RNA; select Length, count(*) as [Count] from RNA group by Length; select * from RNA order by StartCodon;							
100 %	6 👻 🗧						
	Results	Messages					
	Length						
1	22						
2	23						
	Length	Count					
1	22	1					
2	23	2					
	Rnald	Name	Length	StartCodon	Purpose		
1	3	hsa-mir-302c	22	353	No idea, let's leave this blank in future.		
2	1	hsa-mir-1302-2	23	35351	Regulates something?		
3	4	HBII-436	23	42545	NULL		

## Primary keys

• Each record should have a way of uniquely identifying it

```
-- create a table
create table RNA
(
    RnaId int identity(1,1) primary key,
    Name varchar(50) not null,
    Length int not null,
    StartCodon int not null,
    Purpose varchar(255) null
);
```

 Records in other tables can be unambiguously linked to a record in this table (we'll see how in a moment)

#### Natural or arbitrary keys?

- You *could* use the RNA name as the key instead...
  - What if you want to change the name but it's been used elsewhere?
  - You'd have to find and change everywhere else the name has been used
  - You'd have to do this update everywhere simultaneously...
- Don't do it! Use auto-incrementing integers. Always.
  - Predictable Id mechanism
  - Field data can be edited without breaking links
  - The 'payload' fields can anyway be set to be unique if required
  - This argument was settled a long time ago

# Foreign keys

- A foreign key field is used to relate one table's data to another's
- Referential integrity: the database engine will enforce these links
  - This is one of the main advantages of relational databases
- But first, we need another table:

```
-- another table
create table Chromosomes
(
    ChromosomeId int identity(1,1) primary key,
    Name varchar(50)
);
```

#### Digression: Importing data

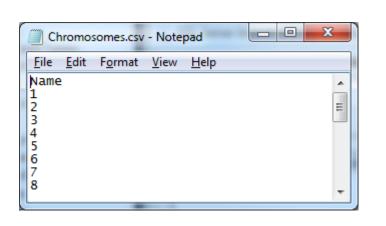
- Right-click on the database, choose Tasks, Import Data
- The source and destination matter most, just click 'Next' for the rest

	port and Export Wizard							
	Choose a Data Source Select the source from which to copy data.							
<u>D</u> ata source:	📑 Flat Fi	le Source	•					
U General	Select a file and specify t	the file properties and the file format.						
Columns	File name:	ching\Database basics\Chromosomes.csv	Bro <u>w</u> se					
Preview	Locale:	English (United Kingdom)	□ <u>U</u> nicode					
	<u>C</u> ode page:	1252 (ANSI - Latin I)	•					
	For <u>m</u> at:	Delimited	•					
	Text <u>q</u> ualifier:	<none></none>						
	Header row delimiter:	{CR}{LF}	•					
	Header rows to <u>s</u> kip:	0	÷					
	Column n <u>a</u> mes in t	he first data row						
A Columns are	e not defined for this connection	on manager.						
<u>H</u> elp		< <u>Back</u> <u>N</u> ext > <u>Finish</u> >>	Cancel					

	Specify where to copy data to				0
Authentication    Authentication    Use <u>Mindows</u> Authentication   Use SQL Server Authentication  User name:  Password:  Database:  Basics  Refree	Destination:	🗐 sqi	Server Native Client 11.0		
	erver name:				
User name: Password: Dajabase: Basics		on			
Password:	C Use SQL Server Authentic	ation			
Database: Basics <u>R</u> efree	<u>U</u> ser name:				
· · · · · · · · · · · · · · · · · · ·	<u>P</u> assword:				
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					N <u>e</u> w
Help < Back Next > Finish >>  C	Help		< Back Next >	Finis	1>>I Canc

### Digression: Still importing data

- SQL Server has spotted that we have a table with the right name
- It also maps to the right field because we named everything sensibly



	ect Source Tables and View Choose one or more tables and views				1
					V
_	es and views:				
- Januari	Source:		Destination: .		
	C:\Users\mark\iCloudDrive\MSc\	Teachi	[dbo].[Chromosomes	]	
			Edit Mappings	Previ	iew
			East mappinga		·····

#### Digression: Imported data

- The CSV has imported to the correct field as well
- SQL Server assigned Id values to each record

### Foreign keys continued

• We need a link field in RNA to match the Id field in Chromosomes:

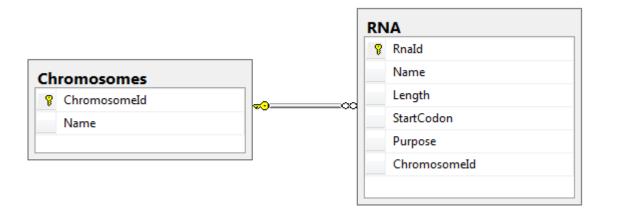
-- add a link field
alter table RNA add ChromosomeId int not null default(1);

• We relate the two tables with a 'foreign key constraint':

```
-- create the foreign key
alter table RNA add constraint FK_RNA_Chromosomes
   foreign key (ChromosomeId)
    references Chromosomes (ChromosomeId)
   on delete cascade;
```

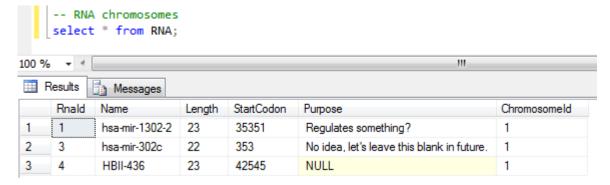
#### Digression: database diagrams

- Right-click on Database Diagrams and New Database Diagram
- Select both tables and click Add and then Close



# Foreign keys

- Why did we just do all this?
  - The RNAs are now all associated with a chromosome
  - RNAs have to have a chromosome (thanks to referential integrity)
  - Chromosomes can have associated RNAs (but they don't have to)
    - This is a one-to-many relationship



#### Joins

- Join relate data from different tables together
- Takes into account the relationships between the tables

#### • There are various types:

- Inner joins results have values in both tables
- Left outer joins results have values in at least the left hand table
- Cross joins, full outer joins, etc. you'll hardly ever need these

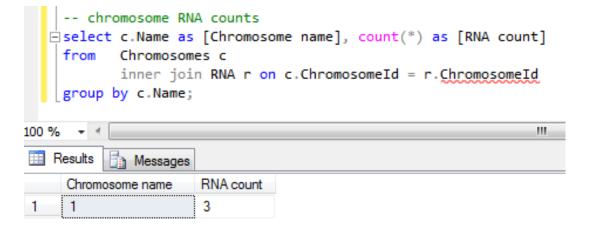
#### Inner joins

3 1

- Combines records from two tables using a common field
- Only common values that are in both tables participate

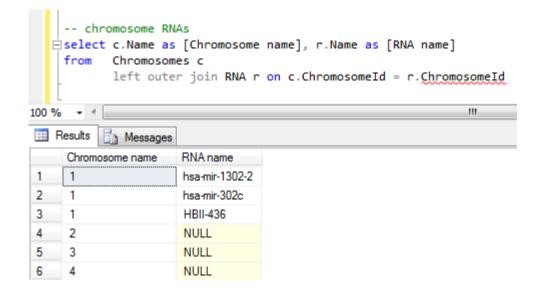
	from Chromosome	[Chromosome es c	name], r.Name as [RNA name] .ChromosomeId = r.ChromosomeId					
100	100 %							
	Results Messages							
	Chromosome name	RNA name						
1	1	hsa-mir-1302-2						
2	1	hsa-mir-302c						

HBII-436



## Left outer joins

- Combines records from two tables using a common field (like inner)
- Common values that are in left table are always present
- Missing values in right table are null



#### Putting it all together

Add some more RNA

-- add some more RNAs
insert RNA (Name, Length, StartCodon, Purpose, ChromosomeId)
values ('U10', 23, 565, null, 2),
 ('U11', 23, 565, null, 2),
 ('U12', 23, 565, null, 2),
 ('Xist', 22, 4453, 'Inactivates one X chromosome in females', 23),
 ('T', 23, 7987, null, 24);
select \* from RNA;

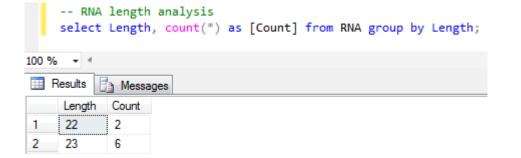
100 % 👻 🖪

	📰 Results 🎒 Messages							
	Rnald	Name	Length	StartCodon	Purpose	Chromosomeld		
1	1	hsa-mir-1302-2	23	35351	Regulates something?	1		
2	3	hsa-mir-302c	22	353	No idea, let's leave this blank in future.	1		
3	4	HBII-436	23	42545	NULL	1		
4	5	U10	23	565	NULL	2		
5	6	U11	23	565	NULL	2		
6	7	U12	23	565	NULL	2		
7	8	Xist	22	4453	Inactivates one X chromosome in females	23		
8	9	Т	23	7987	NULL	24		

#### Putting it all together

Chromosome RNA counting and length analysis

	chromosome RNA counts select c.Name as [Chromosome name], count(*) as [RNA count] from Chromosomes c inner join RNA r on c.ChromosomeId = r.ChromosomeId group by c.Name;						
100	% 🔹						
	Results 🔒 Messages						
	Chromosome name	RNA count					
1	1	3					
2	2	3					
3	X	1					
4	Y	1					



#### Putting it all together

• RNA chromosome names

	from Chrom	osome names e as [RNA name], c.Name as [Chromosome name] osomes c join RNA r on c.ChromosomeId = r.ChromosomeId
.00	% - <	
	Results 📑 Mess	ages
	RNA name	Chromosome name
1	hsa-mir-1302-2	1
2	hsa-mir-302c	1
3	HBII-436	1
3 4 5	U10	2
5	U11	2
6	U12	2
7	Xist	X
8	Т	Y

#### Summary

- Create databases and tables
- CRUD
- Import data
- Create relationships between data
- Exploit those relationships to answer questions about the data
- Referential integrity prevents the data from becoming malformed

## Next steps (next lecture?)

#### Indexes

- Primary keys are clustered indexes by default
- Foreign key fields should have indexes so joins are fast
- Fields that are part of queries should also have indexes

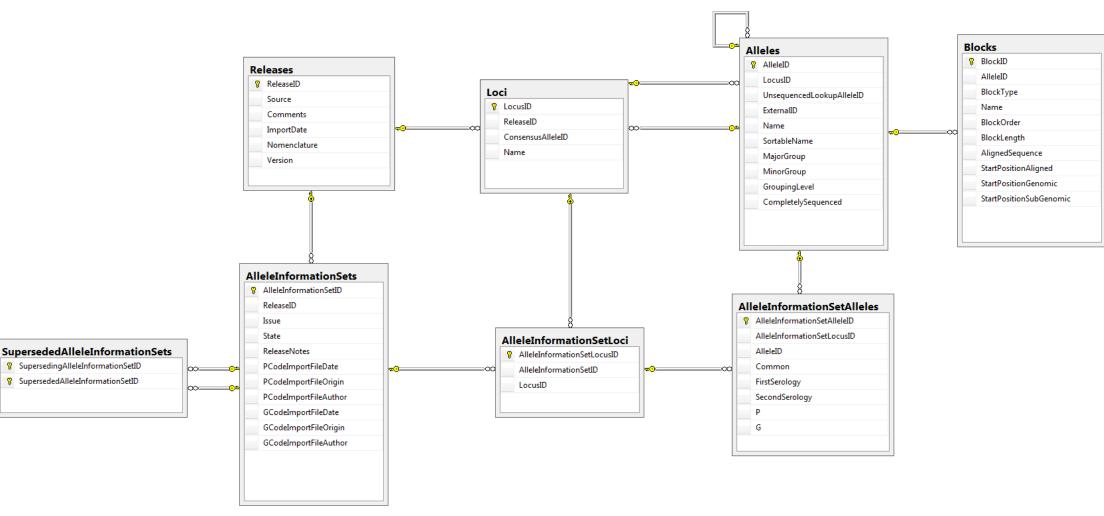
#### Stored procedures and functions

- Motivation
- Examples

#### Transactions

- Motivation
- Examples

#### Real world example 1



#### Real world example 2

