EINES INFORMÀTIQUES PER A LA BIOINFORMÀTICA. PAC2
Amelia Martínez Sequera.

1. Descripción del catálogo de genes.

Primero descargamos la tabla refGene.sql y los archivos de los 4 genomas del navegador genómico de UCSC:

Entramos en mysql y cargamos la tabla en el database "genomas". Comprobamos:

Cargamos el genoma humano en la tabla refGene:

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```
mysql> LOAD DATA LOCAL INFILE 'hg38.txt'INTO TABLE refGene;
Query OK, 172767 rows affected, 10 warnings (1.94 sec)
Records: 172767  Deleted: 0  Skipped: 0  Warnings: 10

mysql> SELECT DISTINCT chrom FROM refGene WHERE chrom NOT LIKE '%\_%';
+-------+
| chrom |
+-------+
| chr1  |
| chr10 |
| chr11 |
| chr12 |
| chr13 |
| chr14 |
| chr15 |
| chr16 |
| chr17 |
| chr18 |
| chr19 |
| chr2  |
| chr20 |
| chr21 |
| chr22 |
| chr3  |
| chr4  |
| chr5  |
```

Para la levadura:

```
student@ubuntuM0151: ~
File  Edit  View  Search  Terminal  Help
mysql> LOAD DATA LOCAL INFILE 'cer3.txt'INTO TABLE refGene;
Query OK, 6126 rows affected, 10 warnings (0.06 sec)
Records: 6126  Deleted: 0  Skipped: 0  Warnings: 10

mysql> SELECT name2, name, chrom, txStart, txEnd FROM refGene ORDER BY name2 LIMIT 10;
+-------+----------------+---------+---------+--------+
| name2 | name           | chrom   | txStart | txEnd  |
+-------+----------------+---------+---------+--------+
| AAC1  | NM_001182554.1 | chrXIII |  387314 | 388244 |
| AAC3  | NM_001178433.3 | chrII   |  415982 | 416906 |
| AAD10 | NM_001181813.1 | chrX    |  727404 | 728271 |
| AAD14 | NM_001183169.1 | chrXIV  |   16117 |  17248 |
| AAD15 | NM_001183418.1 | chrXV   |    1646 |   2078 |
| AAD3  | NM_001178814.1 | chrIII  |  313889 | 314981 |
| AAD4  | NM_001180303.1 | chrIV   |   17576 |  18566 |
| AAH1  | NM_001182979.1 | chrXIV  |  359595 | 360639 |
| AAP1  | NM_001179177.1 | chrVIII |  198739 | 201310 |
| AAR2  | NM_001178314.1 | chrII   |   86721 |  87789 |
+-------+----------------+---------+---------+--------+
10 rows in set (0.00 sec)

mysql> SELECT DISTINCT chrom FROM refGene WHERE chrom NOT LIKE '%\_%';
+--------+
| chrom  |
+--------+
```

Para el caballo:

```
mysql> TRUNCATE TABLE refGene;
Query OK, 0 rows affected (0.00 sec)

mysql> LOAD DATA LOCAL INFILE 'cab3.txt'INTO TABLE refGene;
Query OK, 76581 rows affected, 10 warnings (0.88 sec)
Records: 76581  Deleted: 0  Skipped: 0  Warnings: 10

mysql> SELECT name2, name, chrom, txStart, txEnd FROM refGene ORDER BY name2 LIMIT 10;
+--------+----------------+-------+----------+----------+
| name2  | name           | chrom | txStart  | txEnd    |
+--------+----------------+-------+----------+----------+
| A1BG   | XM_023651550.1 | chr10 | 28405572 | 28409265 |
| A1CF   | XM_014733382.2 | chr1  | 41813428 | 41889961 |
| A2ML1  | XM_023643099.1 | chr6  | 36959093 | 37019643 |
| A2ML1  | XM_014740589.2 | chr6  | 36982882 | 37019643 |
| A2ML1  | XM_014740588.2 | chr6  | 36982882 | 37019643 |
| A3F2   | XM_023631192.1 | chr28 | 37093256 | 37097738 |
| A3GALT2| XM_023634015.1 | chr2  | 23764126 | 23778484 |
| A4GALT | XM_023631773.1 | chr28 | 40288953 | 40315193 |
| A4GNT  | XM_023619735.1 | chr16 | 74432232 | 74442579 |
| A4GNT  | NM_001163877.1 | chr16 | 74434598 | 74441156 |
+--------+----------------+-------+----------+----------+
10 rows in set (0.00 sec)
```

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1. Número de cromosomas distintos.

% SELECT DISTINCT chrom FROM refGene WHERE chrom NOT LIKE ´%\ _%´;

Hay que restarle 1 de "chrom".

Para el caballo: 33

Para el pollo: 34

2. Número de genes distintos.

% SELECT COUNT(DISTINCT name2) FROM refGene;

Para la levadura:

Caballo:

```
mysql> SELECT COUNT(DISTINCT name2) FROM refGene;
+----------------------+
| COUNT(DISTINCT name2) |
+----------------------+
|                29517 |
+----------------------+
1 row in set (0.02 sec)
```

3. Número de transcritos distintos.

% SELECT COUNT(DISTINCT name) FROM refGene;

Levadura:

```
mysql> SELECT COUNT(DISTINCT name) FROM refGene;
+---------------------+
| COUNT(DISTINCT name) |
+---------------------+
|                6126 |
+---------------------+
1 row in set (0.00 sec)
```

Caballo:

```
mysql> SELECT COUNT(DISTINCT name) FROM refGene;
+---------------------+
| COUNT(DISTINCT name) |
+---------------------+
|               76581 |
+---------------------+
1 row in set (0.03 sec)
```

4. Número de transcritos codificantes distintos. Para la levadura:

% SELECT COUNT(DISTINCT name) FROM refGene where name LIKE ´%NM%´;

```
mysql> SELECT COUNT(DISTINCT name) FROM refGene where name LIKE '%NM%';
+---------------------+
| COUNT(DISTINCT name) |
+---------------------+
|                5983 |
+---------------------+
1 row in set (0.01 sec)
```

Caballo:

```
mysql> SELECT COUNT(DISTINCT name) FROM refGene where name LIKE '%NM%';
+---------------------+
| COUNT(DISTINCT name) |
+---------------------+
|                1114 |
+---------------------+
1 row in set (0.02 sec)
```

5. Número de transcritos no codificantes distintos. Para el caballo:

% SELECT COUNT(DISTINCT name) FROM refGene where name LIKE ´%NR%´;

```
mysql> SELECT COUNT(DISTINCT name) FROM refGene where name LIKE '%NR%';
+---------------------+
| COUNT(DISTINCT name) |
+---------------------+
|                 689 |
+---------------------+
1 row in set (0.03 sec)
```

```
mysql> SELECT COUNT(DISTINCT name) FROM refGene where name LIKE '%NR%';
+----------------------+
| COUNT(DISTINCT name) |
+----------------------+
|                18297 |
+----------------------+
1 row in set (0.06 sec)
```

6. Número de transcritos por cada gen (en promedio)

% SELECT name2, count(name) AS totales FROM refGene GROUP BY name2 LIMIT 10;

Para el caballo:

Primero creamos "totales":

```
mysql> SELECT name2, COUNT(name) AS totales FROM refGene GROUP BY name2 LIMIT 10
;
+---------+---------+
| name2   | totales |
+---------+---------+
| A1BG    |       1 |
| A1CF    |       1 |
| A2ML1   |       3 |
| A3F2    |       1 |
| A3GALT2 |       1 |
| A4GALT  |       1 |
| A4GNT   |       2 |
| AAAS    |       3 |
| AACS    |       2 |
| AADACL2 |       1 |
+---------+---------+
```

Y calculamos la media:

% SELECT AVG(tmp.totales) from (SELECT name2, COUNT(name) AS totales FROM refGene GROUP BY name2) tmp;

```
 File  Edit  View  Search  Terminal  Help
mysql> SELECT AVG(tmp.totales) from (SELECT name2, COUNT(name) AS totales FROM r
efGene GROUP BY name2) tmp;
+------------------+
| AVG(tmp.totales) |
+------------------+
|           2.5945 |
+------------------+
1 row in set (0.12 sec)
```

Para el pollo:

```
mysql> SELECT name2, COUNT(name) AS totales FROM refGene GROUP BY name2 LIMIT 10
;
+---------+---------+
| name2   | totales |
+---------+---------+
| 2KTGRL  |       9 |
| 44G24.1 |       1 |
| A1CF    |       3 |
| A2M     |       2 |
| A2ML1   |       1 |
| A2ML2   |       6 |
| A2ML3   |       1 |
| A2ML4   |       1 |
| A4GALT  |       2 |
| A4GNT   |       1 |
+---------+---------+
10 rows in set (0.01 sec)
```

```
efGene GROUP BY name2) tmp;
+------------------+
| AVG(tmp.totales) |
+------------------+
|           2.6203 |
+------------------+
1 row in set (0.09 sec)
```

Humano:

5

```
mysql> SELECT name2, COUNT(name) AS totales FROM refGene GROUP BY name2 LIMIT 10
;
+----------+---------+
| name2    | totales |
+----------+---------+
| A1BG     |       1 |
| A1BG-AS1 |       1 |
| A1CF     |      12 |
| A2M      |       5 |
| A2M-AS1  |       3 |
| A2ML1    |       9 |
| A2MP1    |       1 |
| A3GALT2  |       1 |
| A4GALT   |      11 |
| A4GNT    |       3 |
+----------+---------+
10 rows in set (0.00 sec)
```

```
mysql> SELECT AVG(tmp.totales) from (SELECT name2, COUNT(name) AS totales FROM r
efGene GROUP BY name2) tmp;
+------------------+
| AVG(tmp.totales) |
+------------------+
|           4.4814 |
+------------------+
1 row in set (0.20 sec)
```

7. Número de exones por transcrito (en promedio)

% SELECT AVG(exonCount) FROM refGene;

Para la levdura:

```
mysql> SELECT AVG(exonCount) FROM refGene;
+----------------+
| AVG(exonCount) |
+----------------+
|         1.0583 |
+----------------+
1 row in set (0.00 sec)
```

Para el caballo:

```
mysql> SELECT AVG(exonCount) FROM refGene;
+----------------+
| AVG(exonCount) |
+----------------+
|        12.2290 |
+----------------+
1 row in set (0.02 sec)
```

Para el pollo:

```
mysql> SELECT AVG(exonCount) FROM refGene;
+----------------+
| AVG(exonCount) |
+----------------+
|        12.8119 |
+----------------+
1 row in set (0.02 sec)
```

8. Número de nucleótidos por transcrito (en promedio)

% SELECT AVG(txEnd – txStart +1) FROM refGene;

Para la levadura:

```
mysql> SELECT AVG(txEnd-txStart+1) FROM refGene;
+---------------------+
| AVG(txEnd-txStart+1) |
+---------------------+
|           1467.6996 |
+---------------------+
1 row in set (0.00 sec)
```

Para el caballo:

```
mysql> SELECT AVG(txEnd-txStart+1) FROM refGene;
+---------------------+
| AVG(txEnd-txStart+1) |
+---------------------+
|          66577.4442 |
+---------------------+
1 row in set (0.03 sec)
```

Para el pollo:

```
mysql> SELECT AVG(txEnd-txStart+1) FROM refGene;
+---------------------+
| AVG(txEnd-txStart+1) |
+---------------------+
|          47617.6525 |
+---------------------+
1 row in set (0.02 sec)

mysql> TRUNCATE TABLE refGene;
Query OK, 0 rows affected (0.00 sec)
```

Genoma	1	2	3	4	5	6	7	8
H. sapiens (hg38)	24	38552	163989	60847	18297	4.48	11.6	76709.7
E. caballus (EcuCab3.0)	33	29517	76581	1114	689	2.6	12.23	66576.4
G. gallus (GRCg6a)	34	23727	62161	6401	776	2.62	12.8	47616.7
S. cerevisiae (sacCer3)	17	6126	6126	5983	123	1	1.06	1466.7

2.Datos de expresión.

Visualizamos los datos de " **GTEx_Analysis_v8_Annotations_SubjectPhenotypesDS.txt",** que se han descargado con el nombre de Phenotypes.txt. Se elimina la primera línea con grep -v SUBJID, y lo llamamos Pheno.txt.

```
File  Edit  View  Search  Terminal  Help
student@ubuntuM0151:~$ head Phenotypes.txt
SUBJID   SEX    AGE      DTHHRDY
GTEX-1117F    2      60-69    4
GTEX-111CU    1      50-59    0
GTEX-111FC    1      60-69    1
GTEX-111VG    1      60-69    3
GTEX-111YS    1      60-69    0
GTEX-11220    2      60-69    0
GTEX-1128S    2      60-69    2
GTEX-113IC    1      60-69
GTEX-113JC    2      50-59    2
student@ubuntuM0151:~$ grep -v SUBJID Phenotypes.txt > Pheno.txt
student@ubuntuM0151:~$ head Pheno.txt
GTEX-1117F    2      60-69    4
GTEX-111CU    1      50-59    0
GTEX-111FC    1      60-69    1
GTEX-111VG    1      60-69    3
GTEX-111YS    1      60-69    0
GTEX-11220    2      60-69    0
GTEX-1128S    2      60-69    2
GTEX-113IC    1      60-69
GTEX-113JC    2      50-59    2
GTEX-117XS    1      60-69    2
student@ubuntuM0151:~$
```

Del archivo de las muestras, " **GTEx_Analysis_v8_Annotations_SampleAttributesDS.txt** ", seleccionamos las columnas necesarias.

Hay dos columnas separadas por un tabulador. Llamamos al nuevo archivo Sample.txt.

Creamos un database "gtex" y creamos la tabla "pheno", en la que cargaremos los datos de Pheno.txt. Como ha valores ausentes, para evitar que aparezca como un 0 escribimos:

% LOAD DATA LOCAL INFILE ´Pheno.txt´ INTO TABLE pheno(subid, sex, age, @vdthhrdy) SET dthhrdy = NULLIF(@vdthhrdy, ´ ´);

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Comprobamos:

1. Rango de edad más frecuente del que se tienen muestras.

Contamos y ordenamos la columna age de forma descendiente.

% SELECT age, COUNT(age) FROM pheno GROUP BY age ORDER BY COUNT(age) DESC;

La franja de 60-69 es la que tiene más muestras.

2. Tipo de muerte más frecuente por género.

El tipo de muerte es la columna dthhrdy. Se utiliza sex=1 o 2 para distinguir entre los dos géneros:

% SELECT dthhrdy , COUNT(dthhrdy) FROM pheno WHERE sex=´1´GROUP BY dthhrdy ORDER BY COUNT(dthhrdy) DESC;

En ambos géneros la causa más frecuente es la ´0´, Ventilator Case.

3. ¿Cuántos tipos de regiones del cerebro (brain) podemos encontrar?

Los tipos de regiones se encuentran en la columna regions, y contienen la palabra ´Brain´.

Creamos la tabla ´sample´ y cargamos ´Sample.txt´, teniendo en cuenta que hay datos ausentes:

% SELECT DISTINCT(regions) FROM sample WHERE regions LIKE ´%Brain%´ORDER BY regions;

Existen 13 tipos.

4. Paciente que más muestras tiene:

Primero se crea una nueva columna ´subid´ en la tabla sample:

% ALTER TABLE sample ADD subid VARCHAR(20) NOT NULL;

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Esta columna nos permite relacionar sample con pheno.

% ALTER TABLE sample ADD FOREIGN KEY (subid) REFERENCES pheno(subid);

Se rellenan los datos teniendo en cuenta que hay valores ausentes:

```
mysql> UPDATE sample
    -> SET subid= IF(sampleid IS NULL, 0, substring_index(sampleid, '-',2));
Query OK, 22951 rows affected (0.41 sec)
Rows matched: 22951  Changed: 22951  Warnings: 0
```

Comprobamos:

```
File  Edit  View  Search  Terminal  Help
------+------------+
10 rows in set (0.01 sec)

mysql> mysql> SELECT * FROM sample LIMIT 10;
+-----------------------------+---------------------------+------------+---------------+-------------+------------+
| sampleid                    | regions                   | splitreads | tipomuestra   | mappeunique | subid      |
+-----------------------------+---------------------------+------------+---------------+-------------+------------+
| GTEX-1117F-0003-SM-58Q7G    | Whole Blood               |       NULL | Blood         |        NULL | GTEX-1117F |
| GTEX-1117F-0003-SM-5DWSB    | Whole Blood               |       NULL | Blood         |        NULL | GTEX-1117F |
| GTEX-1117F-0003-SM-6WBT7    | Whole Blood               |       NULL | Blood         |        NULL | GTEX-1117F |
| GTEX-1117F-0011-R10a-SM-AHZ7F | Brain - Frontal Cortex (BA9) |    NULL | Brain         |        NULL | GTEX-1117F |
| GTEX-1117F-0011-R10b-SM-CYKQ8 | Brain - Frontal Cortex (BA9) |    NULL | Brain         |        NULL | GTEX-1117F |
| GTEX-1117F-0226-SM-5GZZ7    | Adipose - Subcutaneous    |   11999300 | Adipose Tissue |    66833200 | GTEX-1117F |
| GTEX-1117F-0426-SM-5EGHI    | Muscle - Skeletal         |   11550200 | Muscle        |    59963600 | GTEX-1117F |
| GTEX-1117F-0526-SM-5EGHJ    | Artery - Tibial           |   11000300 | Blood Vessel  |    59839400 | GTEX-1117F |
| GTEX-1117F-0626-SM-5N9CS    | Artery - Coronary         |   11617900 | Blood Vessel  |    69859200 | GTEX-1117F |
| GTEX-1117F-0726-SM-5GIEN    | Heart - Atrial Appendage  |    9266070 | Heart         |    62885700 | GTEX-1117F |
+-----------------------------+---------------------------+------------+---------------+-------------+------------+
10 rows in set (0.01 sec)
```

Pacientes con más muestras:

% SELECT subid, COUNT(subid) FROM sample GROUP BY subid ORDER BY COUNT(subid) DESC LIMIT 10;

```
> s
mysql> SELECT subid, COUNT(subid) FROM sample GROUP BY subid ORDER BY count(subid) DESC LIMIT 10;
----------+--------------+
| subid     | COUNT(subid) |
----------+--------------+
| K-562     |          217 |
| GTEX-NPJ8 |           72 |
| GTEX-RU72 |           59 |
| GTEX-Q2AG |           58 |
| GTEX-N7MS |           56 |
| GTEX-YEC3 |           51 |
| GTEX-N7MT |           50 |
| GTEX-RNOR |           50 |
| GTEX-OHPN |           49 |
| GTEX-T5JC |           49 |
----------+--------------+
10 rows in set (0.02 sec)
```

El K-562 es el que tiene más: 217.

5. Cuáles son las 7 muestras con más Split Reads.

% SELECT subid, sampleid, splitreads FROM sample ORDER BY splitreads DESC LIMIT 7;

```
mysql> SELECT subid, sampleid, splitreads FROM sample ORDER BY splitreads DESC LIMIT 10;
+------------+---------------------------+------------+
| subid      | sampleid                  | splitreads |
+------------+---------------------------+------------+
| GTEX-14BMU | GTEX-14BMU-1526-SM-5TDE6  |   99228600 |
| GTEX-14JFF | GTEX-14JFF-0526-SM-62LFL  |   81794300 |
| GTEX-QMRM  | GTEX-QMRM-0426-SM-4R1K2   |   80654100 |
| GTEX-1JMQI | GTEX-1JMQI-2026-SM-CMKGP  |   68568100 |
| GTEX-1JJE9 | GTEX-1JJE9-0006-SM-CGQEB  |   64031800 |
| GTEX-13G51 | GTEX-13G51-0011-R8b-SM-5LZZ4 | 60748600 |
| GTEX-18D9B | GTEX-18D9B-0008-SM-EAZBT  |   57394000 |
| GTEX-1IDJU | GTEX-1IDJU-0326-SM-CGQEE  |   57307700 |
| GTEX-UJMC  | GTEX-UJMC-1026-SM-4IHKN   |   56677200 |
| GTEX-1LKK1 | GTEX-1LKK1-0005-SM-CXZIT  |   56454200 |
+------------+---------------------------+------------+
10 rows in set (0.01 sec)
```

6. Mediante el comando "join" responder a, ¿cuántas mujeres han muerto de manera violenta y tienen muestras de sangre? ¿y cuál es la media de " mapped unique" de esta selección?

Subid es el elemento común entre pheno y sample: pheno.subid=sample.subid para hacer el JOIN.

Las otras variables a tener en cuenta son: sex=2 (mujer), dthhrdy=1(muerte violenta), tipomuestra que contenga "Blood".

% SELECT DISTINCT(pheno.subid), pheno.sex, pheno.dthhrdy, sample.subid, sample.tipomuestra FROM pheno JOIN sample on pheno.subid=sample.subid WHERE sex=2 AND dthhrdy=1 AND tpomuestra LIKE '%Blood%' AND tipomuestra NOT LIKE '%Vessel%';

```
mysql> SELECT DISTINCT(pheno.subid), pheno.sex, pheno.dthhrdy, sample.subid, sample.tipomuestra FROM ph
eno JOIN sample ON pheno.subid=sample.subid WHERE sex=2 AND dthhrdy=1 AND tipomuestra LIKE '%Blood%'AND
 tipomuestra NOT LIKE '%Vessel%';
+------------+------+---------+------------+-------------+
| subid      | sex  | dthhrdy | subid      | tipomuestra |
+------------+------+---------+------------+-------------+
| GTEX-12ZZX |    2 |       1 | GTEX-12ZZX | Blood       |
| GTEX-15ER7 |    2 |       1 | GTEX-15ER7 | Blood       |
| GTEX-1F7RK |    2 |       1 | GTEX-1F7RK | Blood       |
| GTEX-1GZHY |    2 |       1 | GTEX-1GZHY | Blood       |
| GTEX-1PBJI |    2 |       1 | GTEX-1PBJI | Blood       |
| GTEX-1POEN |    2 |       1 | GTEX-1POEN | Blood       |
| GTEX-RNOR  |    2 |       1 | GTEX-RNOR  | Blood       |
| GTEX-T2IS  |    2 |       1 | GTEX-T2IS  | Blood       |
| GTEX-WRHU  |    2 |       1 | GTEX-WRHU  | Blood       |
| GTEX-YFC4  |    2 |       1 | GTEX-YFC4  | Blood       |
| GTEX-ZVZQ  |    2 |       1 | GTEX-ZVZQ  | Blood       |
+------------+------+---------+------------+-------------+
11 rows in set (0.01 sec)
```

11 mujeres.

Y hacemos la media de mapped unique:

% SELECT AVG(mappeunique) FROM pheno JOIN sample ON pheno.subid=sample.subid WHERE sex = 2 AND dthhrdy = 1 AND tipomuestra LIKE '%Blood%' AND tipomuestra NOT LIKE '%Vessel%';

```
mysql> SELECT AVG(mappeunique) FROM pheno JOIN sample ON pheno.subid=sample.subid WHERE sex=2 AND dthhr
dy=1 AND tipomuestra LIKE '%Blood%'AND tipomuestra NOT LIKE '%Vessel%';
+------------------+
| AVG(mappeunique) |
+------------------+
|    92580733.3333 |
+------------------+
1 row in set (0.02 sec)
```

3. Servicio web de consulta de genes.

En el database "genoma" se crean 4 tablas, una para cada una de las especies.
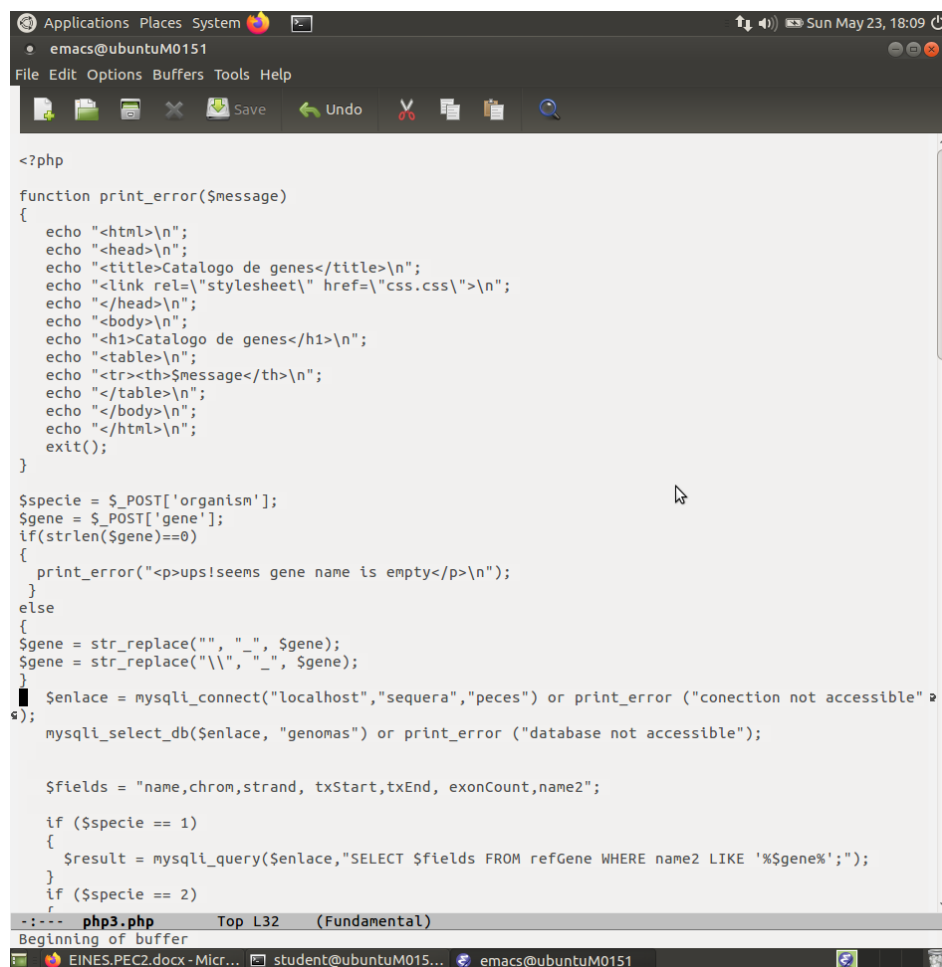
Código HTML: (html2.html)

PHP: (php3.php)

Primero establecemos la función print_error. Luego las 2 variables a introducir (form method=post), una tipo <select> y la otra tipo <input type=text>.

Con $enlace nos conectamos a mysql. Luego seleccionamos database con mysqli_select_db.

Antes de hacer la query, establecemos las columnas a consultar con $fields, y establecemos un condicional en función de la especie seleccionada. Se muestra el resultado mediante mysqli_affected_rows en una tabla html, además de un link para UCSC, también en función de la especie seleccionada.

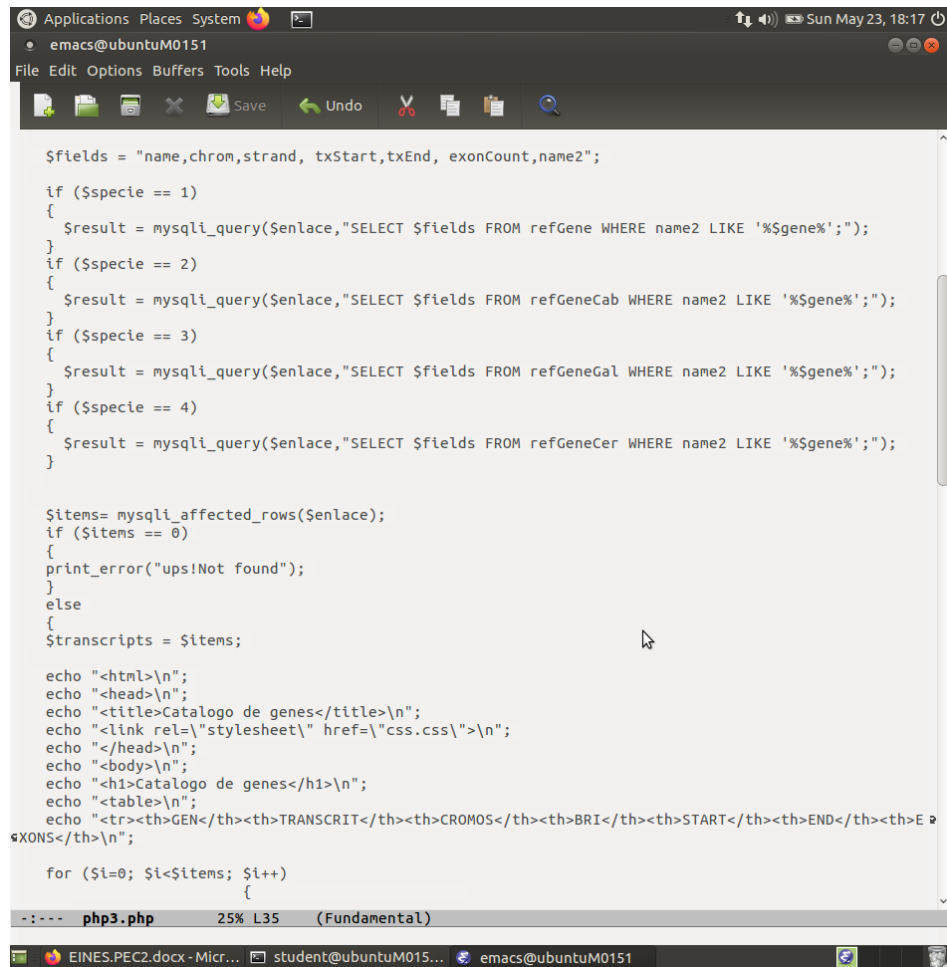Se incluyen, además, mensajes de error para campos en blanco o genes que no existen.

```php
$fields = "name,chrom,strand, txStart,txEnd, exonCount,name2";

if ($specie == 1)
{
  $result = mysqli_query($enlace,"SELECT $fields FROM refGene WHERE name2 LIKE '%$gene%';");
}
if ($specie == 2)
{
  $result = mysqli_query($enlace,"SELECT $fields FROM refGeneCab WHERE name2 LIKE '%$gene%';");
}
if ($specie == 3)
{
  $result = mysqli_query($enlace,"SELECT $fields FROM refGeneGal WHERE name2 LIKE '%$gene%';");
}
if ($specie == 4)
{
  $result = mysqli_query($enlace,"SELECT $fields FROM refGeneCer WHERE name2 LIKE '%$gene%';");
}


$items= mysqli_affected_rows($enlace);
if ($items == 0)
{
print_error("ups!Not found");
}
else
{
$transcripts = $items;

echo "<html>\n";
echo "<head>\n";
echo "<title>Catalogo de genes</title>\n";
echo "<link rel=\"stylesheet\" href=\"css.css\">\n";
echo "</head>\n";
echo "<body>\n";
echo "<h1>Catalogo de genes</h1>\n";
echo "<table>\n";
echo "<tr><th>GEN</th><th>TRANSCRIT</th><th>CROMOS</th><th>BRI</th><th>START</th><th>END</th><th>E
XONS</th>\n";

for ($i=0; $i<$items; $i++)
        {
```

-:--- **php3.php**   25% L35   (Fundamental)

```php
echo "<html>\n";
echo "<head>\n";
echo "<title>Catalogo de genes</title>\n";
echo "<link rel=\"stylesheet\" href=\"css.css\">\n";
echo "</head>\n";
echo "<body>\n";
echo "<h1>Catalogo de genes</h1>\n";
echo "<table>\n";
echo "<tr><th>GEN</th><th>TRANSCRIT</th><th>CROMOS</th><th>BRI</th><th>START</th><th>END</th><th>E
XONS</th>\n";

for ($i=0; $i<$items; $i++)
                {

$row= mysqli_fetch_array($result);

    $name2 = $row["name2"];
    $name = $row["name"];
    $chrom = $row["chrom"];
    $strand = $row["strand"];
    $txStart = $row["txStart"];
    $txEnd = $row["txEnd"];
    $exonCount = $row["exonCount"];


    echo "<tr><td>$name2</td><td>$name</td><td>$chrom</td><td>$strand</td>";
    echo "<td>$txStart</td><td>$txEnd</td><td>$exonCount</td>\n";
                }



            echo "</table><br><br>\n";
            }

            echo "<h1>Link UCSC</h1>\n";
            if ($specie==1)
            {
            echo "<a href='https://genome-euro.ucsc.edu/cgi-bin/hgTracks?hgsid=265595631
&_4T4EMyZSagWEj8HfDVNfDbJhKaP1&org=Human&db=hg38&position=$name2&pix=1234'>Clik $name2</a>";
            }
            if ($specie==2)
            {
            echo "<a href='https://genome-euro.ucsc.edu/cgi-bin/hgTracks?hgsid=265595631
&_4T4EMyZSagWEj8HfDVNfDbJhKaP1&org=Mouse&db=mm10&position=$name2&pix=1234'>Clik $name2</a>";
```
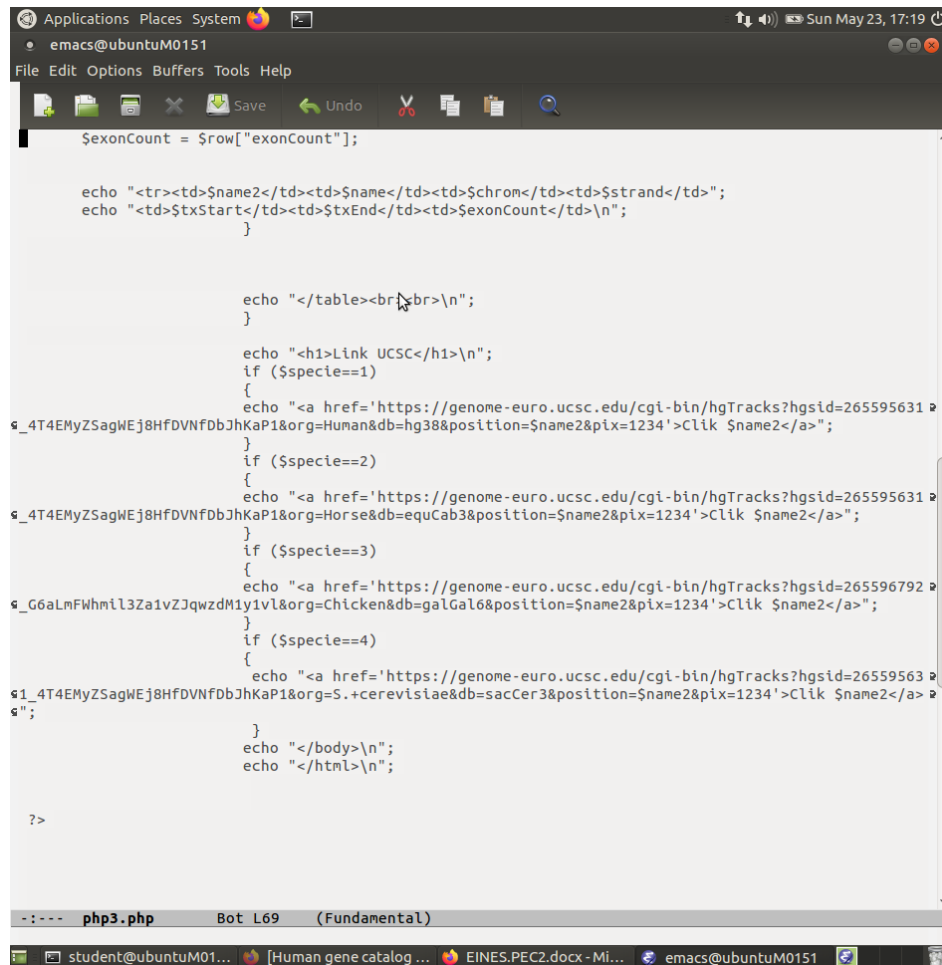
EINES INFORMÀTIQUES PER A LA BIOINFORMÀTICA. PAC2
Amelia Martínez Sequera.

CSS: (css.css)

```css
body
{
    background-color:#DDDDDD;
    padding-top: 20px;
    padding-bottom: 20px;
    padding-left: 50px;
    padding-right: 50px;
}

h1
{
    background: white;
    width: 100%;
```

```css
  border: 0px solid black;

  border-radius: 25px;

  color: darkblue;

  height: 35px;

  font-family: verdana, sans-serif;

  font-size: 18pt;

  font-weight: bold;

  text-align: center;

}


p
{

  font-family: verdana, sans-serif;

}



table
{

  border: 5px solid #FFA500;

  border-radius: 25px;

  padding: 20;

  width: 100%;

  font-family: verdana, sans-serif;

}


td
{

  padding: 30;

  font-weight: bold;

  font-size: 12pt;

  border: 1px solid #D0D0D0;

  border-radius: 25px;

}
```

```css
th
{
    padding: 10;
    font-weight: bold;
    font-size: 18pt;
    text-align: left;
    text-transform: uppercase;
}

a:link, a:visited
{
    color: blue;
    text-decoration: none;
    font-weight: bold;
}

a:hover
{
    color: white;
    background: darkblue;
}

input
{
    width:300px;
}
```