



Reading mySQL

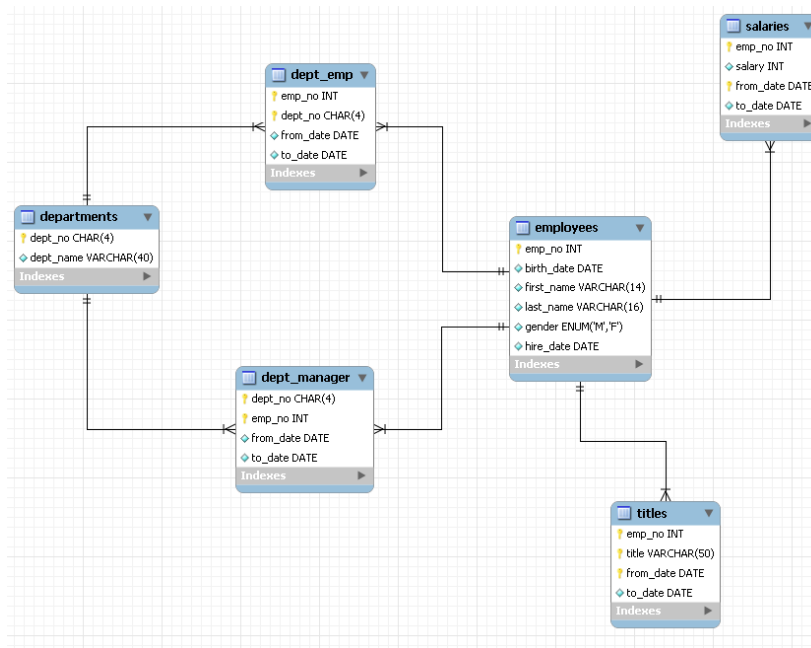
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MySQL

- Free and widely used open source database software
- Widely used in internet based applications
- Data are structured in
 - Databases
 - Tables within databases
 - Fields within tables
- Each row is called a record

<http://en.wikipedia.org/wiki/MySQL> <http://www.mysql.com/>

Example structure



<http://dev.mysql.com/doc/employee/en/sakila-structure.html>

Step 1 - Install MySQL

The screenshot shows a web browser window with the URL `dev.mysql.com/doc/refman/5.7/en/installing.html`. The page is titled "Chapter 2. Installing and Upgrading MySQL". On the left, there is a "Documentation Library" sidebar with a "Table of Contents" section listing manuals for MySQL 5.7, 5.6, 5.5, 5.1, 5.0, and 3.23/4.0/4.1. Below this is a "Search manual:" field with a "Go" button. The main content area has a "Table of Contents" section with links to sections 2.1 through 2.13. The text of the chapter begins with "This chapter describes how to obtain and install MySQL. A summary of the procedure follows and later sections provide the details. If you plan to upgrade an existing version of MySQL to a newer version rather than install MySQL for the first time, see [Section 2.11.1, "Upgrading MySQL"](#), for information about upgrade procedures and about issues that you should consider before upgrading." It then states "If you are interested in migrating to MySQL from another database system, you may wish to read [Section B.8, "MySQL 5.7 FAQ: Migration"](#), which contains answers to some common questions concerning migration issues." Finally, it says "Installation of MySQL generally follows the steps outlined here:" followed by a list of steps that is partially obscured by a horizontal line.

MySQL :: MySQL 5.7 Reference Manual

dev.mysql.com/doc/refman/5.7/en/installing.html

Documentation Library

Table of Contents

- MySQL 5.7 Manual
- MySQL 5.6 Manual
- MySQL 5.5 Manual
- MySQL 5.1 Manual
- MySQL 5.0 Manual
- MySQL 3.23/4.0/4.1 Manual

Search manual:

Chapter 2. Installing and Upgrading MySQL

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- [2.7. Installing MySQL on HP-UX](#) [v-]
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- [2.9. Installing MySQL from Source](#) [v-]
- [2.10. Postinstallation Setup and Testing](#) [v-]
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This chapter describes how to obtain and install MySQL. A summary of the procedure follows and later sections provide the details. If you plan to upgrade an existing version of MySQL to a newer version rather than install MySQL for the first time, see [Section 2.11.1, "Upgrading MySQL"](#), for information about upgrade procedures and about issues that you should consider before upgrading.

If you are interested in migrating to MySQL from another database system, you may wish to read [Section B.8, "MySQL 5.7 FAQ: Migration"](#), which contains answers to some common questions concerning migration issues.

Installation of MySQL generally follows the steps outlined here:

- 1. Obtain the MySQL source code or binaries.
- 2. Install the MySQL binaries.
- 3. Configure the MySQL server.
- 4. Start the MySQL server.
- 5. Create the MySQL database.
- 6. Create the MySQL user.
- 7. Create the MySQL database.
- 8. Create the MySQL user.
- 9. Create the MySQL database.
- 10. Create the MySQL user.

« 1.9.5 Supporters of MySQL

2.1 General Installation Guidance »

Section Navigation [Toggle]

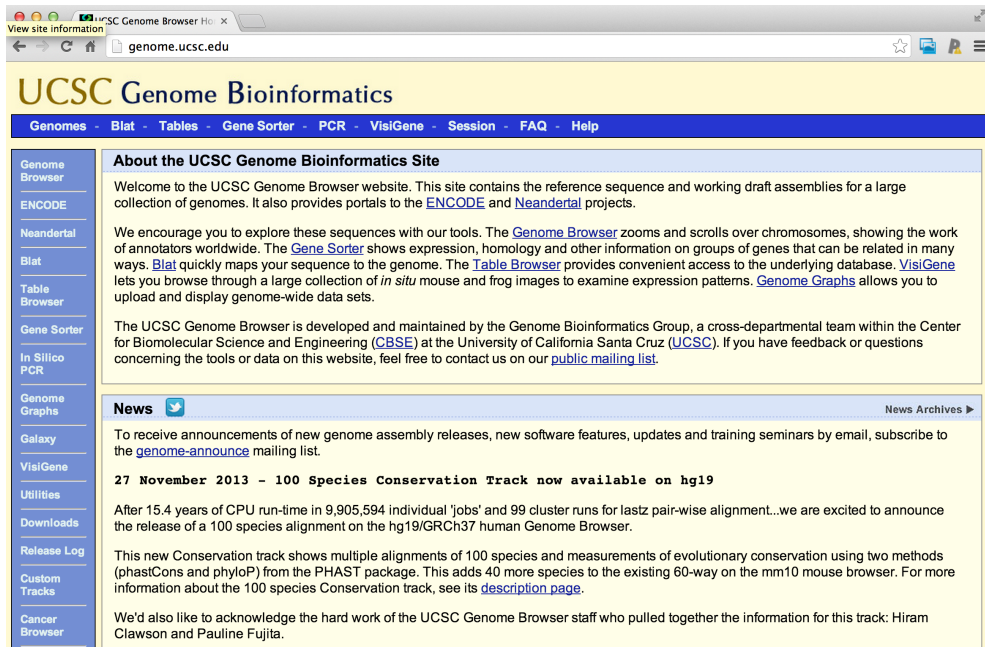
- Preface and Legal Notices
- 1 General Information
- 2 Installing and Upgrading MySQL
 - 2.1 General Installation Guidance
 - 2.2 Installing MySQL on Unix/Linux Using Generic Binaries
 - 2.3 Installing MySQL on Microsoft Windows
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- 6 Security
- 7 Backup and Recovery
- 8 Optimization
- 9 Language Structure
- 10 Globalization

<http://dev.mysql.com/doc/refman/5.7/en/installing.html>

Step 2 - Install RMySQL

- On a Mac: `install.packages("RMySQL")`
- On Windows:
 - Official instructions - <http://biostat.mc.vanderbilt.edu/wiki/Main/RMySQL> (may be useful for Mac/UNIX users as well)
 - Potentially useful guide - <http://www.ahschulz.de/2013/07/23/installing-rmysql-under-windows/>

Example - UCSC database



The screenshot shows the UCSC Genome Browser website in a web browser. The address bar displays 'genome.ucsc.edu'. The page has a yellow header with the 'UCSC Genome Bioinformatics' logo. Below the header is a blue navigation bar with links: Genomes, Blat, Tables, Gene Sorter, PCR, VisiGene, Session, FAQ, and Help. A left sidebar contains a list of tools: Genome Browser, ENCODE, Neandertal, Blat, Table Browser, Gene Sorter, In Silico PCR, Genome Graphs, Galaxy, VisiGene, Utilities, Downloads, Release Log, Custom Tracks, and Cancer Browser. The main content area is titled 'About the UCSC Genome Bioinformatics Site' and contains a welcome message, a description of the site's resources, and a section for news. The news section includes a tweet icon and a link to 'News Archives'. The latest news item is dated '27 November 2013' and discusses the release of a 100 species conservation track.

UCSC Genome Bioinformatics


Genomes - Blat - Tables - Gene Sorter - PCR - VisiGene - Session - FAQ - Help

About the UCSC Genome Bioinformatics Site

Welcome to the UCSC Genome Browser website. This site contains the reference sequence and working draft assemblies for a large collection of genomes. It also provides portals to the [ENCODE](#) and [Neandertal](#) projects.

We encourage you to explore these sequences with our tools. The [Genome Browser](#) zooms and scrolls over chromosomes, showing the work of annotators worldwide. The [Gene Sorter](#) shows expression, homology and other information on groups of genes that can be related in many ways. [Blat](#) quickly maps your sequence to the genome. The [Table Browser](#) provides convenient access to the underlying database. [VisiGene](#) lets you browse through a large collection of *in situ* mouse and frog images to examine expression patterns. [Genome Graphs](#) allows you to upload and display genome-wide data sets.

The UCSC Genome Browser is developed and maintained by the Genome Bioinformatics Group, a cross-departmental team within the Center for Biomolecular Science and Engineering ([CBSE](#)) at the University of California Santa Cruz ([UCSC](#)). If you have feedback or questions concerning the tools or data on this website, feel free to contact us on our [public mailing list](#).

News  [News Archives](#)

To receive announcements of new genome assembly releases, new software features, updates and training seminars by email, subscribe to the [genome-announce](#) mailing list.

27 November 2013 - 100 Species Conservation Track now available on hg19

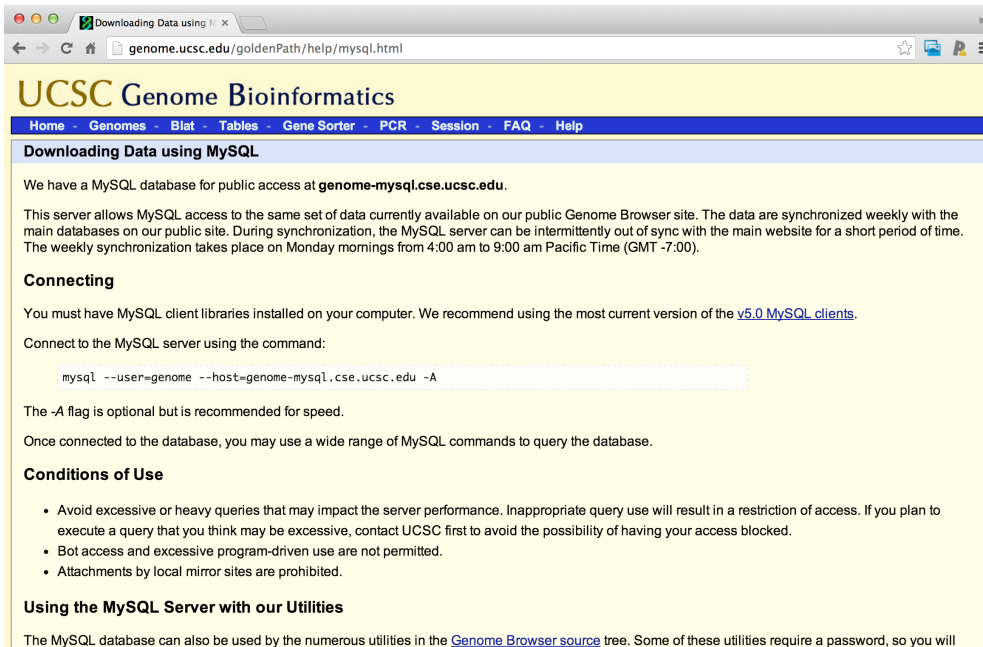
After 15.4 years of CPU run-time in 9,905,594 individual 'jobs' and 99 cluster runs for lastz pair-wise alignment...we are excited to announce the release of a 100 species alignment on the hg19/GRCh37 human Genome Browser.

This new Conservation track shows multiple alignments of 100 species and measurements of evolutionary conservation using two methods (phastCons and phyloP) from the PHAST package. This adds 40 more species to the existing 60-way on the mm10 mouse browser. For more information about the 100 species Conservation track, see its [description page](#).

We'd also like to acknowledge the hard work of the UCSC Genome Browser staff who pulled together the information for this track: Hiram Clawson and Pauline Fujita.

<http://genome.ucsc.edu/>

UCSC MySQL



The screenshot shows a web browser window with the address bar displaying `genome.ucsc.edu/goldenPath/help/mysql.html`. The page title is "UCSC Genome Bioinformatics". Below the title is a navigation bar with links: Home, Genomes, Blat, Tables, Gene Sorter, PCR, Session, FAQ, and Help. The main heading is "Downloading Data using MySQL". The text explains that a MySQL database is available for public access at `genome-mysql.cse.ucsc.edu`. It states that the server allows MySQL access to the same set of data currently available on the public Genome Browser site, with data synchronized weekly. The weekly synchronization takes place on Monday mornings from 4:00 am to 9:00 am Pacific Time (GMT -7:00). The section "Connecting" advises that users must have MySQL client libraries installed and recommends using the most current version of the [v5.0 MySQL clients](#). It instructs users to connect to the MySQL server using the command: `mysql --user=genome --host=genome-mysql.cse.ucsc.edu -A`. It notes that the `-A` flag is optional but recommended for speed. The section "Conditions of Use" lists three bullet points: avoid excessive or heavy queries that may impact server performance; if a query is thought to be excessive, contact UCSC first; and bot access and excessive program-driven use are not permitted. Attachments by local mirror sites are also prohibited. The section "Using the MySQL Server with our Utilities" states that the MySQL database can also be used by numerous utilities in the [Genome Browser source](#) tree, and that some of these utilities require a password.

UCSC Genome Bioinformatics

Home - Genomes - Blat - Tables - Gene Sorter - PCR - Session - FAQ - Help

Downloading Data using MySQL

We have a MySQL database for public access at [genome-mysql.cse.ucsc.edu](#).

This server allows MySQL access to the same set of data currently available on our public Genome Browser site. The data are synchronized weekly with the main databases on our public site. During synchronization, the MySQL server can be intermittently out of sync with the main website for a short period of time. The weekly synchronization takes place on Monday mornings from 4:00 am to 9:00 am Pacific Time (GMT -7:00).

Connecting

You must have MySQL client libraries installed on your computer. We recommend using the most current version of the [v5.0 MySQL clients](#).

Connect to the MySQL server using the command:

```
mysql --user=genome --host=genome-mysql.cse.ucsc.edu -A
```

The `-A` flag is optional but is recommended for speed.

Once connected to the database, you may use a wide range of MySQL commands to query the database.

Conditions of Use

- Avoid excessive or heavy queries that may impact the server performance. Inappropriate query use will result in a restriction of access. If you plan to execute a query that you think may be excessive, contact UCSC first to avoid the possibility of having your access blocked.
- Bot access and excessive program-driven use are not permitted.
- Attachments by local mirror sites are prohibited.

Using the MySQL Server with our Utilities

The MySQL database can also be used by the numerous utilities in the [Genome Browser source](#) tree. Some of these utilities require a password, so you will

<http://genome.ucsc.edu/goldenPath/help/mysql.html>

Connecting and listing databases

```
ucscDb <- dbConnect(MySQL(),user="genome",  
                    host="genome-mysql.cse.ucsc.edu")  
result <- dbGetQuery(ucscDb,"show databases;"); dbDisconnect(ucscDb);
```

```
[1] TRUE
```

```
result
```

| | Database |
|---|--------------------|
| 1 | information_schema |
| 2 | ailMel1 |
| 3 | allMis1 |
| 4 | anoCar1 |
| 5 | anoCar2 |
| 6 | anoGam1 |
| 7 | apiMel1 |
| 8 | apiMel2 |

Connecting to hg19 and listing tables

```
hg19 <- dbConnect(MySQL(),user="genome", db="hg19",  
                  host="genome-mysql.cse.ucsc.edu")  
allTables <- dbListTables(hg19)  
length(allTables)
```

```
[1] 10949
```

```
allTables[1:5]
```

```
[1] "HInv"          "HInvGeneMrna" "acembly"       "acemblyClass" "acemblyPep"
```

Get dimensions of a specific table

```
dbListFields(hg19, "affyU133Plus2")
```

```
[1] "bin"          "matches"      "misMatches"   "repMatches"   "nCount"       "qNumInsert"
[7] "qBaseInsert"  "tNumInsert"   "tBaseInsert"  "strand"       "qName"        "qSize"
[13] "qStart"       "qEnd"         "tName"        "tSize"        "tStart"       "tEnd"
[19] "blockCount"   "blockSizes"   "qStarts"      "tStarts"
```

```
dbGetQuery(hg19, "select count(*) from affyU133Plus2")
```

```
count(*)
1      58463
```

Read from the table

```
affyData <- dbReadTable(hg19, "affyU133Plus2")
head(affyData)
```

| | bin | matches | misMatches | repMatches | nCount | qNumInsert | qBaseInsert | tNumInsert | tBaseInsert | strand |
|---|-----|---------|------------|------------|--------|------------|-------------|------------|-------------|--------|
| 1 | 585 | 530 | 4 | 0 | 23 | 3 | 41 | 3 | 898 | - |
| 2 | 585 | 3355 | 17 | 0 | 109 | 9 | 67 | 9 | 11621 | - |
| 3 | 585 | 4156 | 14 | 0 | 83 | 16 | 18 | 2 | 93 | - |
| 4 | 585 | 4667 | 9 | 0 | 68 | 21 | 42 | 3 | 5743 | - |
| 5 | 585 | 5180 | 14 | 0 | 167 | 10 | 38 | 1 | 29 | - |
| 6 | 585 | 468 | 5 | 0 | 14 | 0 | 0 | 0 | 0 | - |

| | qName | qSize | qStart | qEnd | tName | tSize | tStart | tEnd | blockCount |
|---|--------------|-------|--------|------|-------|-----------|--------|-------|------------|
| 1 | 225995_x_at | 637 | 5 | 603 | chr1 | 249250621 | 14361 | 15816 | 5 |
| 2 | 225035_x_at | 3635 | 0 | 3548 | chr1 | 249250621 | 14381 | 29483 | 17 |
| 3 | 226340_x_at | 4318 | 3 | 4274 | chr1 | 249250621 | 14399 | 18745 | 18 |
| 4 | 1557034_s_at | 4834 | 48 | 4834 | chr1 | 249250621 | 14406 | 24893 | 23 |
| 5 | 231811_at | 5399 | 0 | 5399 | chr1 | 249250621 | 19688 | 25078 | 11 |
| 6 | 236841_at | 487 | 0 | 487 | chr1 | 249250621 | 27542 | 28029 | 1 |

| | blockSizes |
|---|---|
| 1 | 93,144,229,70,21, |
| 2 | 73,375,71,165,303,360,198,661,201,1,260,250,74,73,98,155,163, |

Select a specific subset

```
query <- dbSendQuery(hg19, "select * from affyU133Plus2 where misMatches between 1 and 3")  
affyMis <- fetch(query); quantile(affyMis$misMatches)
```

```
0%  25%  50%  75% 100%  
1    1    2    2    3
```

```
affyMisSmall <- fetch(query,n=10); dbClearResult(query);
```

```
[1] TRUE
```

```
dim(affyMisSmall)
```

```
[1] 10 22
```

Don't forget to close the connection!

```
dbDisconnect(hg19)
```

```
[1] TRUE
```

Further resources

- RMySQL vignette <http://cran.r-project.org/web/packages/RMySQL/RMySQL.pdf>
- List of commands <http://www.pantz.org/software/mysql/mysqlcommands.html>
 - **Do not, do not, delete, add or join things from ensembl. Only select.**
 - In general be careful with mysql commands
- A nice blog post summarizing some other commands <http://www.r-bloggers.com/mysql-and-r/>