reading from mySQL

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install.packages("RMySQL", repos = "http://cran.us.r-project.org")

##   
## The downloaded binary packages are in  
## /var/folders/qv/s711tc7s1q37hcfz2ngtmwdr0000gp/T//RtmpmafC9e/downloaded\_packages

install.packages("DBI", repos = "http://cran.us.r-project.org")

##   
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library(DBI)  
library(RMySQL)

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

## [1] TRUE

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

## [1] 12551

allTables[1:5]

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

dbListFields(hg19, "affyU133Plus2")

## [1] "bin" "matches" "misMatches" "repMatches" "nCount"   
## [6] "qNumInsert" "qBaseInsert" "tNumInsert" "tBaseInsert" "strand"   
## [11] "qName" "qSize" "qStart" "qEnd" "tName"   
## [16] "tSize" "tStart" "tEnd" "blockCount" "blockSizes"   
## [21] "qStarts" "tStarts"

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

## count(\*)  
## 1 58463

affyData <- dbReadTable(hg19, "affyU133Plus2")

## Warning in .local(conn, statement, ...): Unsigned INTEGER in col 0 imported as  
## numeric

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## numeric

head(affyData)

## bin matches misMatches repMatches nCount qNumInsert qBaseInsert tNumInsert  
## 1 585 530 4 0 23 3 41 3  
## 2 585 3355 17 0 109 9 67 9  
## 3 585 4156 14 0 83 16 18 2  
## 4 585 4667 9 0 68 21 42 3  
## 5 585 5180 14 0 167 10 38 1  
## 6 585 468 5 0 14 0 0 0  
## tBaseInsert strand qName qSize qStart qEnd tName tSize tStart  
## 1 898 - 225995\_x\_at 637 5 603 chr1 249250621 14361  
## 2 11621 - 225035\_x\_at 3635 0 3548 chr1 249250621 14381  
## 3 93 - 226340\_x\_at 4318 3 4274 chr1 249250621 14399  
## 4 5743 - 1557034\_s\_at 4834 48 4834 chr1 249250621 14406  
## 5 29 - 231811\_at 5399 0 5399 chr1 249250621 19688  
## 6 0 - 236841\_at 487 0 487 chr1 249250621 27542  
## tEnd blockCount  
## 1 15816 5  
## 2 29483 17  
## 3 18745 18  
## 4 24893 23  
## 5 25078 11  
## 6 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,  
## 3 690,10,32,33,376,4,5,15,5,11,7,41,277,859,141,51,443,1253,  
## 4 99,352,286,24,49,14,6,5,8,149,14,44,98,12,10,355,837,59,8,1500,133,624,58,  
## 5 131,26,1300,6,4,11,4,7,358,3359,155,  
## 6 487,  
## qStarts  
## 1 34,132,278,541,611,  
## 2 87,165,540,647,818,1123,1484,1682,2343,2545,2546,2808,3058,3133,3206,3317,3472,  
## 3 44,735,746,779,813,1190,1195,1201,1217,1223,1235,1243,1285,1564,2423,2565,2617,3062,  
## 4 0,99,452,739,764,814,829,836,842,851,1001,1016,1061,1160,1173,1184,1540,2381,2441,2450,3951,4103,4728,  
## 5 0,132,159,1460,1467,1472,1484,1489,1497,1856,5244,  
## 6 0,  
## tStarts  
## 1 14361,14454,14599,14968,15795,  
## 2 14381,14454,14969,15075,15240,15543,15903,16104,16853,17054,17232,17492,17914,17988,18267,24736,29320,  
## 3 14399,15089,15099,15131,15164,15540,15544,15549,15564,15569,15580,15587,15628,15906,16857,16998,17049,17492,  
## 4 14406,20227,20579,20865,20889,20938,20952,20958,20963,20971,21120,21134,21178,21276,21288,21298,21653,22492,22551,22559,24059,24211,24835,  
## 5 19688,19819,19845,21145,21151,21155,21166,21170,21177,21535,24923,  
## 6 27542,

query <- dbSendQuery(hg19, "select \* from affyU133Plus2 where misMatches between 1 and 3")

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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 once done with data subtract  
dbDisconnect(hg19)

## [1] TRUE

#RMySQL vignette: http://cran.r-project.org/web/packages/RMySQL/RMySQL.pdf  
#List of commands: http://www.pantz.org/software/mysql/mysqlcommands.html  
#blog post with summary of some other commands: http://www.r-bloggers.com/mysql-and-r/