Downloading files

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Get/set your working directory

- A basic component of working with data is knowing your working directory
- The two main commands are `getwd()` and `setwd()`.
- Be aware of relative versus absolute paths
  - **Relative** - `setwd("./data")`, `setwd("../")`
  - **Absolute** - `setwd("/Users/jtleek/data/")`
- Important difference in Windows `setwd("C:\\Users\\Andrew\\Downloads")`

Checking for and creating directories

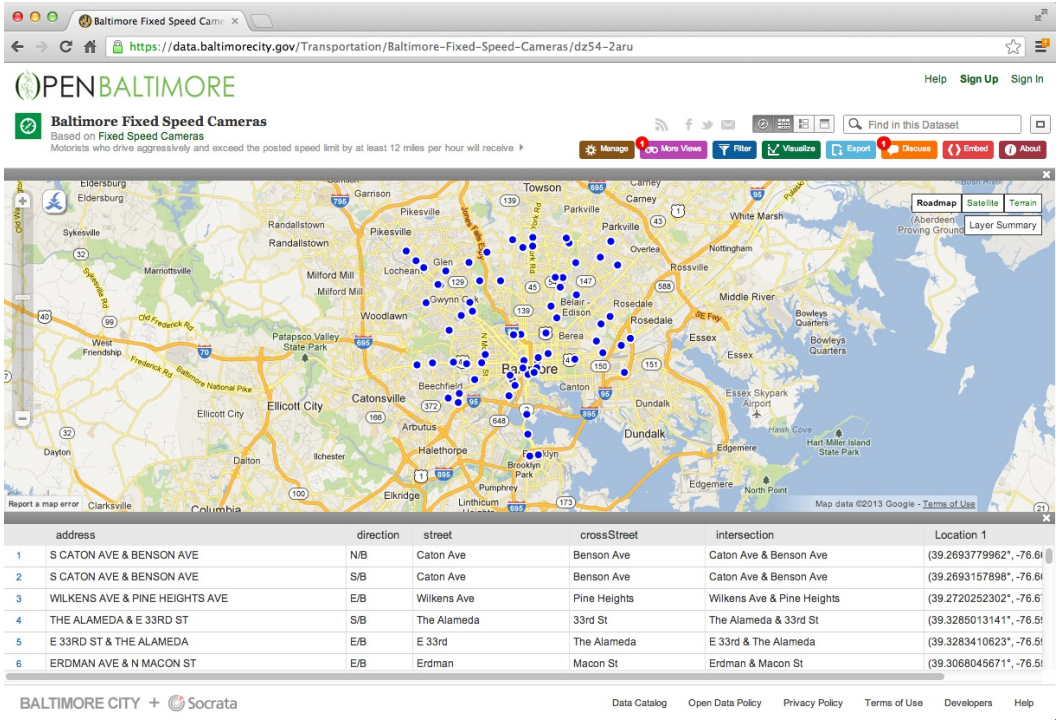
- `file.exists("directoryName")` will check to see if the directory exists
- `dir.create("directoryName")` will create a directory if it doesn't exist
- Here is an example checking for a "data" directory and creating it if it doesn't exist

```
if (!file.exists("data")) {
    dir.create("data")
}
```

Getting data from the internet - download.file()

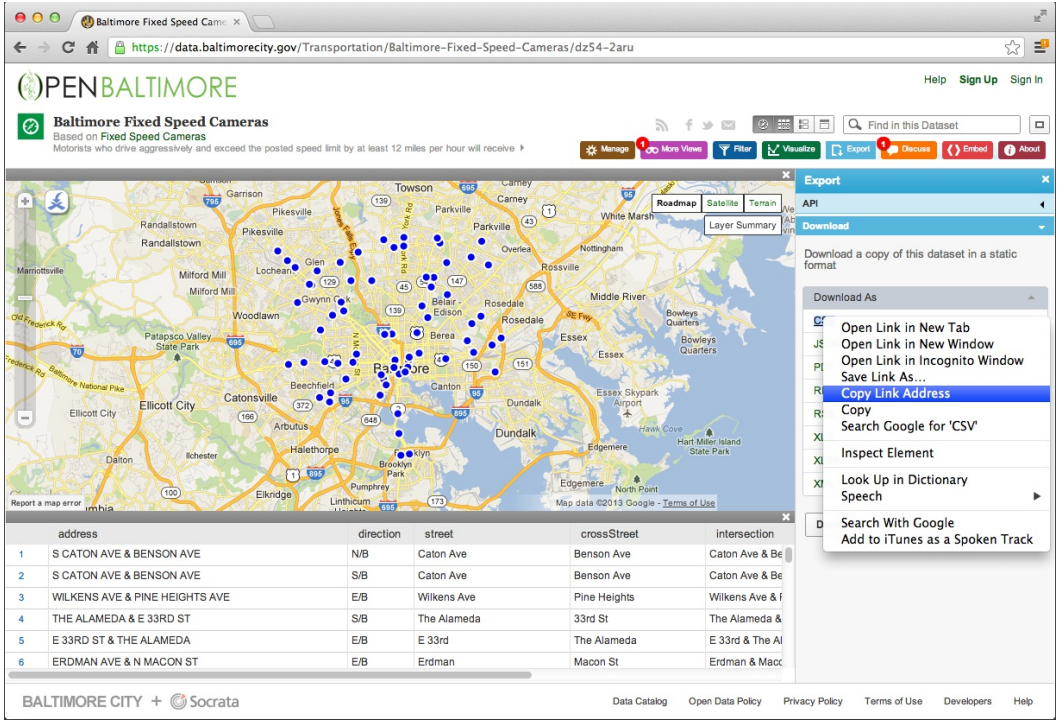
- Downloads a file from the internet
- Even if you could do this by hand, helps with reproducibility
- Important parameters are *url*, *destfile*, *method*
- Useful for downloading tab-delimited, csv, and other files

Example - Baltimore camera data



https://data.baltimorecity.gov/Transportation/Baltimore-Fixed-Speed-Cameras/dz54-2aru

Example - Baltimore camera data



https://data.baltimorecity.gov/Transportation/Baltimore-Fixed-Speed-Cameras/dz54-2aru

Download a file from the web

```
fileUrl <- "https://data.baltimorecity.gov/api/views/dz54-2aru/rows.csv?accessType=DOWNLOAD"
download.file(fileUrl, destfile = "./data/cameras.csv", method = "curl")
list.files("./data")
```

```
## [1] "cameras.csv"
```

```
dateDownloaded <- date()
dateDownloaded
```

```
## [1] "Sun Jan 12 21:37:44 2014"
```

Some notes about download.file()

- If the url starts with *http* you can use download.file()
- If the url starts with *https* on Windows you may be ok
- If the url starts with *https* on Mac you may need to set *method="curl"*
- If the file is big, this might take a while
- Be sure to record when you downloaded.

Reading local flat files

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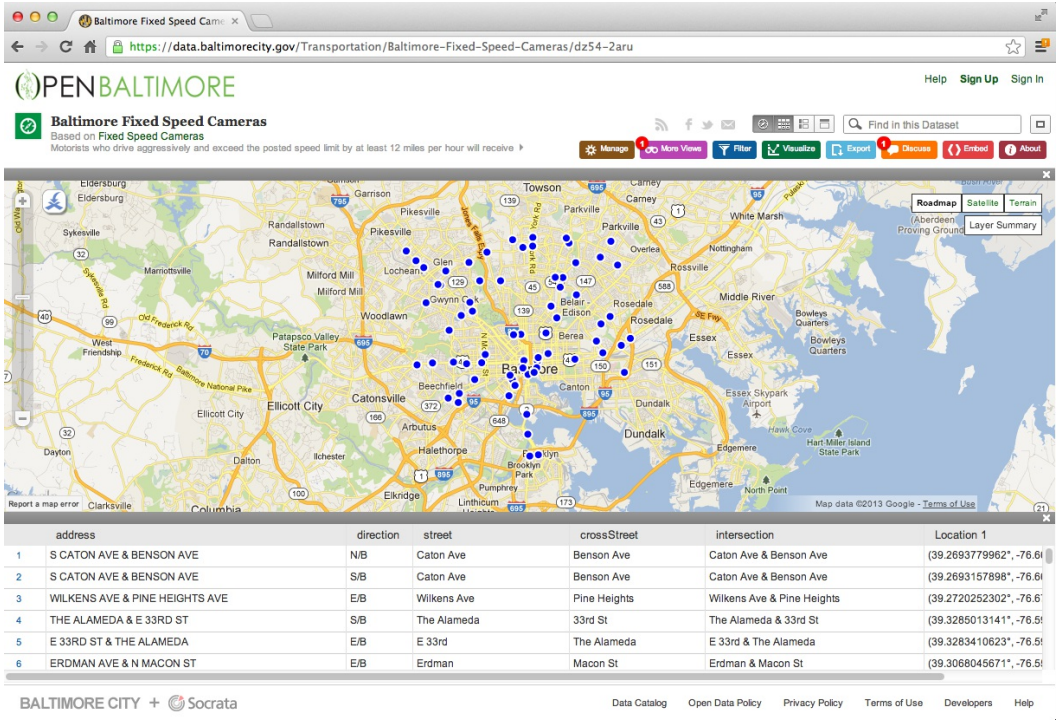
Example - Baltimore camera data



https://data.baltimorecity.gov/Transportation/Baltimore-Fixed-Speed-Cameras/dz54-2aru

Download the file to load

```
if (!file.exists("data")) {
    dir.create("data")
}
fileUrl <- "https://data.baltimorecity.gov/api/views/dz54-2aru/rows.csv?accessType=DOWNLOAD"
download.file(fileUrl, destfile = "cameras.csv", method = "curl")
dateDownloaded <- date()
```

Loading flat files - read.table()

- This is the main function for reading data into R
- Flexible and robust but requires more parameters
- Reads the data into RAM - big data can cause problems
- Important parameters *file*, *header*, *sep*, *row.names*, *nrows*
- Related: *read.csv()*, *read.csv2()*

Baltimore example

```
cameraData <- read.table("./data/cameras.csv")
```

```
## Error: line 1 did not have 13 elements
```

```
head(cameraData)
```

```
## Error: object 'cameraData' not found
```

Example: Baltimore camera data

```
cameraData <- read.table("./data/cameras.csv", sep = ",", header = TRUE)
head(cameraData)
```

```
##                         address direction      street  crossStreet
## 1       S CATON AVE & BENSON AVE       N/B   Caton Ave   Benson Ave
## 2       S CATON AVE & BENSON AVE       S/B   Caton Ave   Benson Ave
## 3 WILKENS AVE & PINE HEIGHTS AVE       E/B Wilkens Ave Pine Heights
## 4        THE ALAMEDA & E 33RD ST       S/B The Alameda      33rd St
## 5        E 33RD ST & THE ALAMEDA       E/B      E 33rd  The Alameda
## 6        ERDMAN AVE & N MACON ST       E/B      Erdman     Macon St
##                intersection                      Location.1
## 1     Caton Ave & Benson Ave (39.2693779962, -76.6688185297)
## 2     Caton Ave & Benson Ave (39.2693157898, -76.6689698176)
## 3 Wilkens Ave & Pine Heights  (39.2720252302, -76.676960806)
## 4     The Alameda  & 33rd St (39.3285013141, -76.5953545714)
## 5      E 33rd  & The Alameda (39.3283410623, -76.5953594625)
## 6         Erdman  & Macon St (39.3068045671, -76.5593167803)
```

Example: Baltimore camera data

read.csv sets *sep=","* and *header=TRUE*

```
cameraData <- read.csv("./data/cameras.csv")
head(cameraData)
```

```
##                         address direction      street  crossStreet
## 1       S CATON AVE & BENSON AVE       N/B   Caton Ave   Benson Ave
## 2       S CATON AVE & BENSON AVE       S/B   Caton Ave   Benson Ave
## 3 WILKENS AVE & PINE HEIGHTS AVE       E/B Wilkens Ave Pine Heights
## 4        THE ALAMEDA & E 33RD ST       S/B The Alameda      33rd St
## 5        E 33RD ST & THE ALAMEDA       E/B      E 33rd  The Alameda
## 6        ERDMAN AVE & N MACON ST       E/B      Erdman     Macon St
##                intersection                       Location.1
## 1     Caton Ave & Benson Ave (39.2693779962, -76.6688185297)
## 2     Caton Ave & Benson Ave (39.2693157898, -76.6689698176)
## 3 Wilkens Ave & Pine Heights  (39.2720252302, -76.676960806)
## 4     The Alameda  & 33rd St (39.3285013141, -76.5953545714)
## 5      E 33rd  & The Alameda (39.3283410623, -76.5953594625)
## 6         Erdman  & Macon St (39.3068045671, -76.5593167803)
```

Some more important parameters

- *quote* - you can tell R whether there are any quoted values quote="" means no quotes.
- *na.strings* - set the character that represents a missing value.
- *nrows* - how many rows to read of the file (e.g. nrows=10 reads 10 lines).
- *skip* - number of lines to skip before starting to read

In my experience, the biggest trouble with reading flat files are quotation marks ` or " placed in data values, setting quote="" often resolves these.

Reading Excel files

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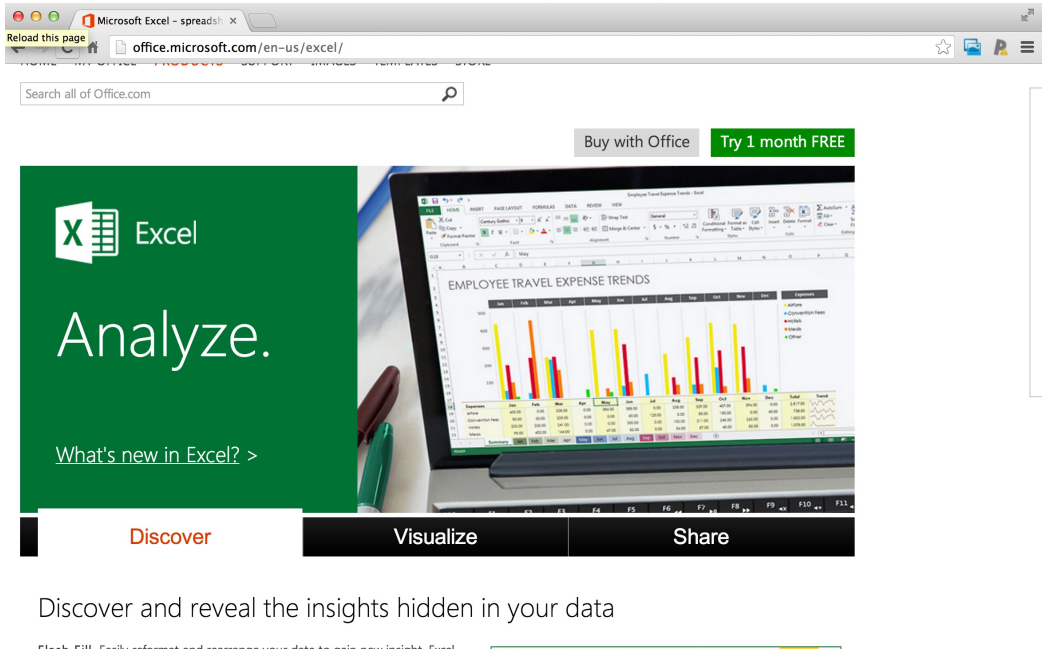
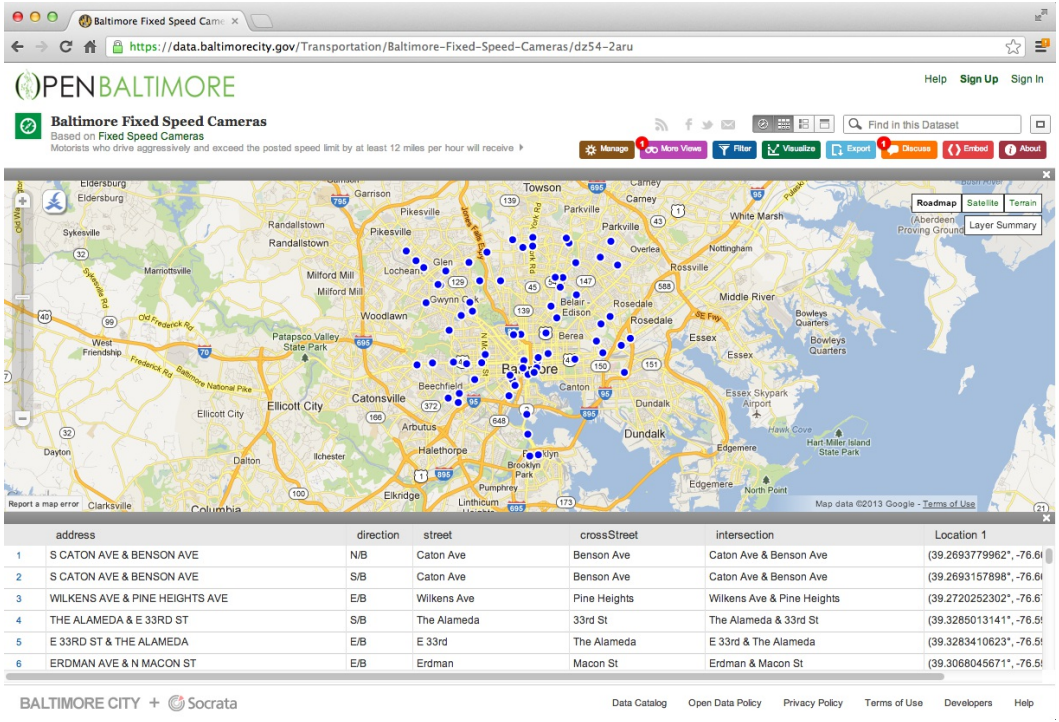
Excel files

Still probably the most widely used format for sharing data



http://office.microsoft.com/en-us/excel/

Example - Baltimore camera data



https://data.baltimorecity.gov/Transportation/Baltimore-Fixed-Speed-Cameras/dz54-2aru

Download the file to load

```
if(!file.exists("data")){dir.create("data")}
fileUrl <- "https://data.baltimorecity.gov/api/views/dz54-2aru/rows.xlsx?accessType=DOWNLOAD"
download.file(fileUrl,destfile="./data/cameras.xlsx",method="curl")
dateDownloaded <- date()
```

read.xlsx(), read.xlsx2() {xlsx package}

```
library(xlsx)
cameraData <- read.xlsx("./data/cameras.xlsx",sheetIndex=1,header=TRUE)
head(cameraData)
```

```
                        address direction      street  crossStreet                intersection
1       S CATON AVE & BENSON AVE       N/B   Caton Ave   Benson Ave     Caton Ave & Benson Ave
2       S CATON AVE & BENSON AVE       S/B   Caton Ave   Benson Ave     Caton Ave & Benson Ave
3 WILKENS AVE & PINE HEIGHTS AVE       E/B Wilkens Ave Pine Heights Wilkens Ave & Pine Heights
4        THE ALAMEDA & E 33RD ST       S/B The Alameda       33rd St     The Alameda  & 33rd St
5        E 33RD ST & THE ALAMEDA       E/B      E 33rd  The Alameda      E 33rd  & The Alameda
6
1 (39.2693779962, -76.6688185297)
2 (39.2693157898, -76.6689698176)
3  (39.2720252302, -76.676960806)
4 (39.3285013141, -76.5953545714)
5 (39.3283410623, -76.5953594625)
6 (39.3068045671, -76.5593167803)
```

Reading specific rows and columns

```
colIndex <- 2:3
rowIndex <- 1:4
cameraDataSubset <- read.xlsx("./data/cameras.xlsx",sheetIndex=1,
                              colIndex=colIndex,rowIndex=rowIndex)
cameraDataSubset
```

```
  direction      street
1       N/B   Caton Ave
2       S/B   Caton Ave
3       E/B Wilkens Ave
```

Further notes

- The *write.xlsx* function will write out an Excel file with similar arguments.
- *read.xlsx2* is much faster than *read.xlsx* but for reading subsets of rows may be slightly unstable.
- The XLConnect package has more options for writing and manipulating Excel files
- The XLConnect vignette is a good place to start for that package
- In general it is advised to store your data in either a database or in comma separated files (.csv) or tab separated files (.tab/.txt) as they are easier to distribute.

Reading JSON

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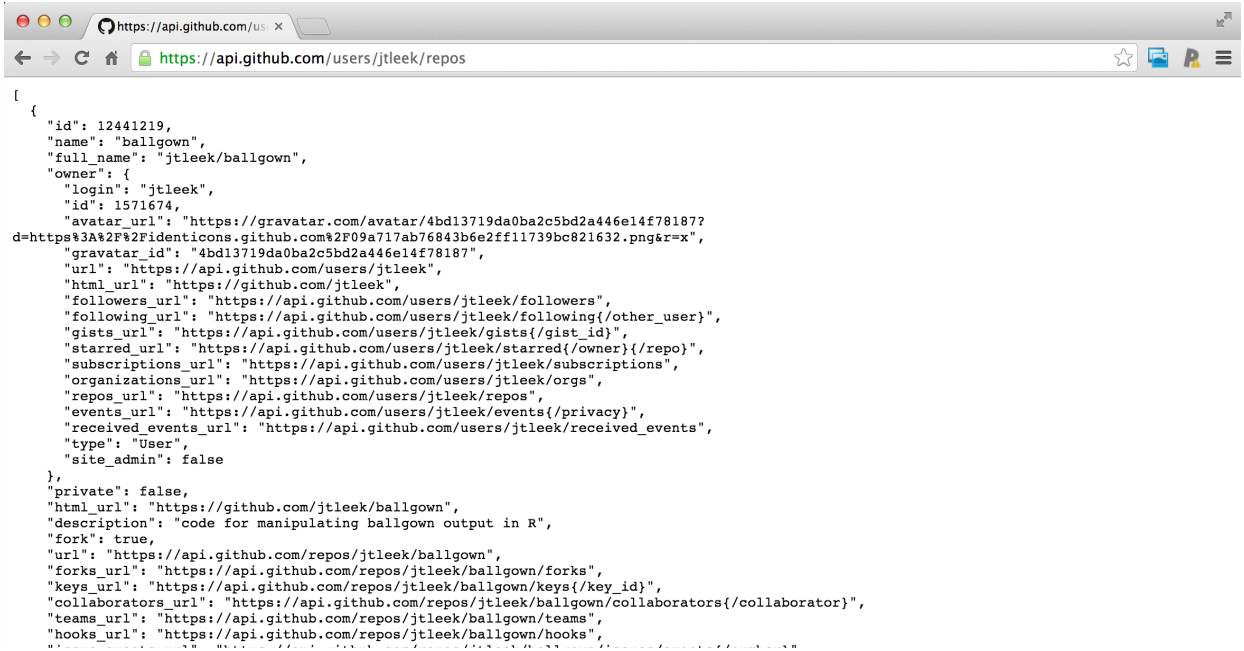
JSON

- Javascript Object Notation
- Lightweight data storage
- Common format for data from application programming interfaces (APIs)
- Similar structure to XML but different syntax/format
- Data stored as
  - Numbers (double)
  - Strings (double quoted)
  - Boolean (*true* or *false*)
  - Array (ordered, comma separated enclosed in square brackets *[]*)
  - Object (unorderd, comma separated collection of key:value pairs in curley brackets *{}*)

http://en.wikipedia.org/wiki/JSON

Example JSON file




```
[
  {
    "id": 12441219,
    "name": "ballgown",
    "full_name": "jtleek/ballgown",
    "owner": {
      "login": "jtleek",
      "id": 1571674,
      "avatar_url": "https://gravatar.com/avatar/4bd13719da0ba2c5bd2a446e14f781877
d=https%3A%2F%2Fidenticons.github.com%2F09a717ab76843b6e2ff11739bc821632.png&r=x",
      "gravatar_id": "4bd13719da0ba2c5bd2a446e14f78187",
      "url": "https://api.github.com/users/jtleek",
      "html_url": "https://github.com/jtleek",
      "followers_url": "https://api.github.com/users/jtleek/followers",
      "following_url": "https://api.github.com/users/jtleek/following{/other_user}",
      "gists_url": "https://api.github.com/users/jtleek/gists{/gist_id}",
      "starred_url": "https://api.github.com/users/jtleek/starred{/owner}{/repo}",
      "subscriptions_url": "https://api.github.com/users/jtleek/subscriptions",
      "organizations_url": "https://api.github.com/users/jtleek/orgs",
      "repos_url": "https://api.github.com/users/jtleek/repos",
      "events_url": "https://api.github.com/users/jtleek/events{/privacy}",
      "received_events_url": "https://api.github.com/users/jtleek/received_events",
      "type": "User",
      "site_admin": false
    },
    "private": false,
    "html_url": "https://github.com/jtleek/ballgown",
    "description": "code for manipulating ballgown output in R",
    "fork": true,
    "url": "https://api.github.com/repos/jtleek/ballgown",
    "forks_url": "https://api.github.com/repos/jtleek/ballgown/forks",
    "keys_url": "https://api.github.com/repos/jtleek/ballgown/keys{/key_id}",
    "collaborators_url": "https://api.github.com/repos/jtleek/ballgown/collaborators{/collaborator}",
    "teams_url": "https://api.github.com/repos/jtleek/ballgown/teams",
    "hooks_url": "https://api.github.com/repos/jtleek/ballgown/hooks",
```

Reading data from JSON {jsonlite package}

```
library(jsonlite)
jsonData <- fromJSON("https://api.github.com/users/jtleek/repos")
names(jsonData)
```

```
 [1] "id"               "name"             "full_name"        "owner"
 [5] "private"          "html_url"         "description"      "fork"
 [9] "url"              "forks_url"        "keys_url"         "collaborators_url"
[13] "teams_url"        "hooks_url"        "issue_events_url" "events_url"
[17] "assignees_url"    "branches_url"     "tags_url"         "blobs_url"
[21] "git_tags_url"     "git_refs_url"     "trees_url"        "statuses_url"
[25] "languages_url"    "stargazers_url"   "contributors_url" "subscribers_url"
[29] "subscription_url" "commits_url"      "git_commits_url"  "comments_url"
[33] "issue_comment_url" "contents_url"    "compare_url"      "merges_url"
[37] "archive_url"      "downloads_url"    "issues_url"       "pulls_url"
[41] "milestones_url"   "notifications_url" "labels_url"     "releases_url"
[45] "created_at"       "updated_at"       "pushed_at"        "git_url"
[49] "ssh_url"          "clone_url"        "svn_url"          "homepage"
[53] "size"             "stargazers_count" "watchers_count"   "language"
```

Nested objects in JSON

```
names(jsonData$owner)
```

```
 [1] "login"             "id"                "avatar_url"          "gravatar_id"
 [5] "url"               "html_url"          "followers_url"       "following_url"
 [9] "gists_url"         "starred_url"       "subscriptions_url"   "organizations_url"
[13] "repos_url"         "events_url"        "received_events_url" "type"
[17] "site_admin"
```

```
jsonData$owner$login
```

```
 [1] "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek"
[11] "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek"
[21] "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek" "jtleek"
```

Writing data frames to JSON

```
myjson <- toJSON(iris, pretty=TRUE)
cat(myjson)
```

```
[
    {
        "Sepal.Length" : 5.1,
        "Sepal.Width" : 3.5,
        "Petal.Length" : 1.4,
        "Petal.Width" : 0.2,
        "Species" : "setosa"
    },
    {
        "Sepal.Length" : 4.9,
        "Sepal.Width" : 3,
        "Petal.Length" : 1.4,
        "Petal.Width" : 0.2,
        "Species" : "setosa"
    },
    {
        "Sepal.Length" : 4.7,
```

Convert back to JSON

```
iris2 <- fromJSON(myjson)
head(iris2)
```

```
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          5.1         3.5          1.4         0.2  setosa
2          4.9         3.0          1.4         0.2  setosa
3          4.7         3.2          1.3         0.2  setosa
4          4.6         3.1          1.5         0.2  setosa
5          5.0         3.6          1.4         0.2  setosa
6          5.4         3.9          1.7         0.4  setosa
```

http://www.r-bloggers.com/new-package-jsonlite-a-smarter-json-encoderdecoder/

Further resources

- http://www.json.org/
- A good tutorial on jsonlite - http://www.r-bloggers.com/new-package-jsonlite-a-smarter-json-encoderdecoder/
- jsonlite vignette

Reading XML

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XML

- Extensible markup language
- Frequently used to store structured data
- Particularly widely used in internet applications
- Extracting XML is the basis for most web scraping
- Components
    - Markup - labels that give the text structure
    - Content - the actual text of the document

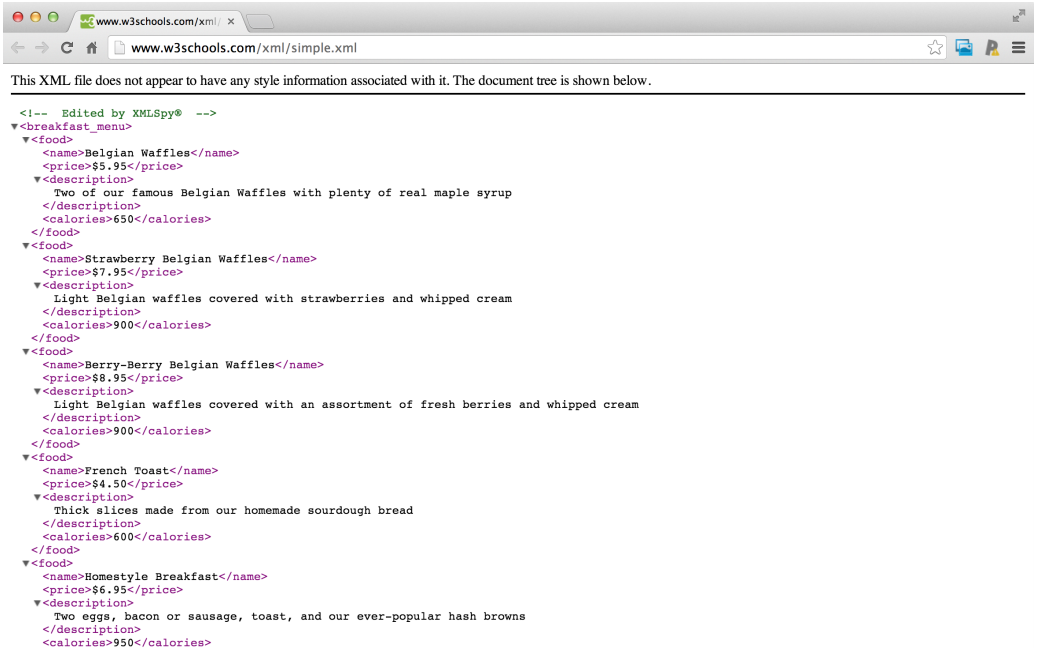
http://en.wikipedia.org/wiki/XML

Tags, elements and attributes

- Tags correspond to general labels
  - Start tags `<section>`
  - End tags `</section>`
  - Empty tags `<line-break />`
- Elements are specific examples of tags
  - `<Greeting> Hello, world </Greeting>`
- Attributes are components of the label
  - `<img src="jeff.jpg" alt="instructor"/>`
  - `<step number="3"> Connect A to B. </step>`

http://en.wikipedia.org/wiki/XML

Example XML file



http://www.w3schools.com/xml/simple.xml

Read the file into R

```
library(XML)
fileUrl <- "http://www.w3schools.com/xml/simple.xml"
doc <- xmlTreeParse(fileUrl,useInternal=TRUE)
rootNode <- xmlRoot(doc)
xmlName(rootNode)
```

```
[1] "breakfast_menu"
```

```
names(rootNode)
```

```
  food   food   food   food   food
"food" "food" "food" "food" "food"
```

Directly access parts of the XML document

```
rootNode[[1]]
```

```
<food>
  <name>Belgian Waffles</name>
  <price>$5.95</price>
  <description>Two of our famous Belgian Waffles with plenty of real maple syrup</description>
  <calories>650</calories>
</food>
```

```
rootNode[[1]][[1]]
```

```
<name>Belgian Waffles</name>
```

Programatically extract parts of the file

```
xmlSApply(rootNode,xmlValue)
```

```
                                "Belgian Waffles$5.95Two of our famous Belgian Waffles with plenty of rea

                          "Strawberry Belgian Waffles$7.95Light Belgian waffles covered with strawberries and

"Berry-Berry Belgian Waffles$8.95Light Belgian waffles covered with an assortment of fresh berries and

                                                    "French Toast$4.50Thick slices made from our homemade so

                          "Homestyle Breakfast$6.95Two eggs, bacon or sausage, toast, and our ever-popula
```

Programatically extract parts of the file

```
xmlSApply(rootNode,xmlValue)
```

```
                                "Belgian Waffles$5.95Two of our famous Belgian Waffles with plenty of rea

                          "Strawberry Belgian Waffles$7.95Light Belgian waffles covered with strawberries and

"Berry-Berry Belgian Waffles$8.95Light Belgian waffles covered with an assortment of fresh berries and

                                                        "French Toast$4.50Thick slices made from our homemade so

                           "Homestyle Breakfast$6.95Two eggs, bacon or sausage, toast, and our ever-popula
```

XPath

- */node* Top level node
- *//node* Node at any level
- *node[@attr-name]* Node with an attribute name
- *node[@attr-name='bob']* Node with attribute name attr-name='bob'

Information from: http://www.stat.berkeley.edu/~statcur/Workshop2/Presentations/XML.pdf

Get the items on the menu and prices

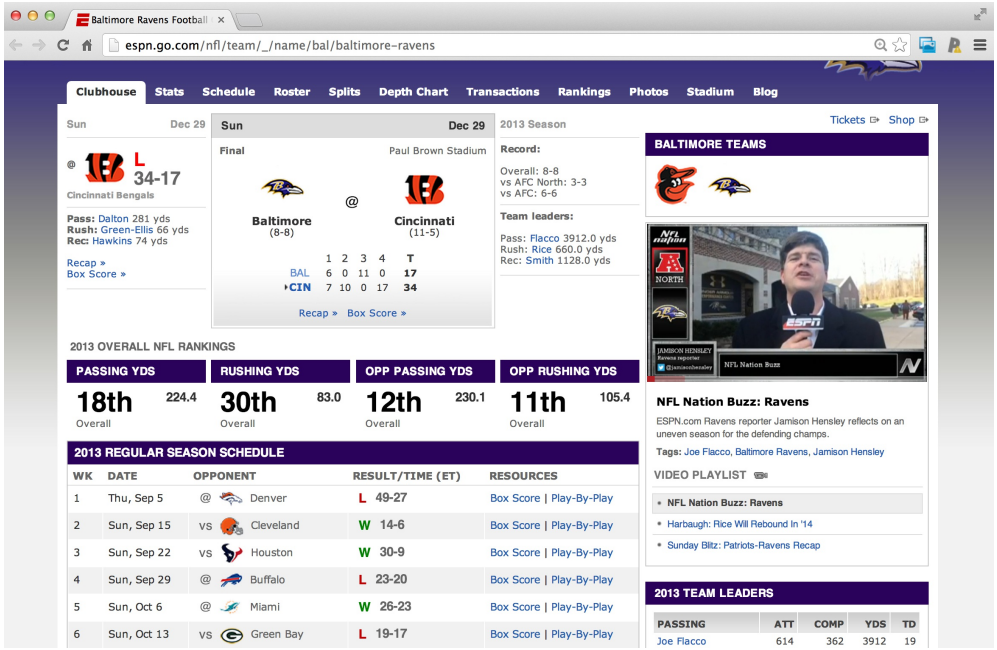
```
xpathSApply(rootNode,"//name",xmlValue)
```

```
[1] "Belgian Waffles"             "Strawberry Belgian Waffles"  "Berry-Berry Belgian Waffles"
[4] "French Toast"                "Homestyle Breakfast"
```

```
xpathSApply(rootNode,"//price",xmlValue)
```

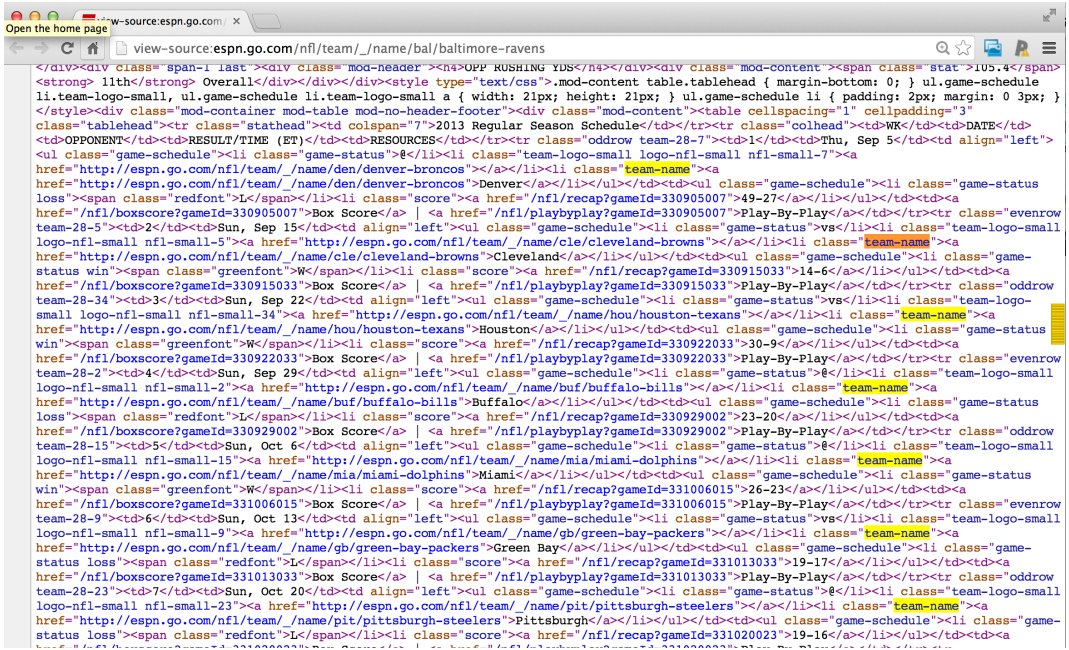
```
[1] "$5.95" "$7.95" "$8.95" "$4.50" "$6.95"
```

Another example



http://espn.go.com/nfl/team/_/name/bal/baltimore-ravens

Viewing the source



http://espn.go.com/nfl/team/_/name/bal/baltimore-ravens

Extract content by attributes

```
fileUrl <- "http://espn.go.com/nfl/team/_/name/bal/baltimore-ravens"
doc <- htmlTreeParse(fileUrl,useInternal=TRUE)
scores <- xpathSApply(doc,"//li[@class='score']",xmlValue)
teams <- xpathSApply(doc,"//li[@class='team-name']",xmlValue)
scores
```

```
 [1] "49-27"    "14-6"     "30-9"     "23-20"    "26-23"    "19-17"    "19-16"    "24-18"
 [9] "20-17 OT" "23-20 OT" "19-3"     "22-20"    "29-26"    "18-16"    "41-7"     "34-17"
```

```
teams
```

```
 [1] "Denver"       "Cleveland"    "Houston"      "Buffalo"      "Miami"        "Green Bay"
 [7] "Pittsburgh"   "Cleveland"    "Cincinnati"   "Chicago"      "New York"     "Pittsburgh"
[13] "Minnesota"    "Detroit"      "New England"  "Cincinnati"
```

Notes and further resources

- Official XML tutorials short, long
- An outstanding guide to the XML package

Using data.table

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data.table

- Inherets from data.frame
    - All functions that accept data.frame work on data.table
- Written in C so it is much faster
- Much, much faster at subsetting, group, and updating

Create data tables just like data frames

```
library(data.table)
DF = data.frame(x=rnorm(9),y=rep(c("a","b","c"),each=3),z=rnorm(9))
head(DF,3)
```

```
       x y        z
1 0.4159 a -0.05855
2 0.8433 a  0.13732
3 1.0585 a  2.16448
```

```
DT = data.table(x=rnorm(9),y=rep(c("a","b","c"),each=3),z=rnorm(9))
head(DT,3)
```

```
          x y      z
1: -0.27721 a 0.2530
2:  1.00158 a 1.5093
3: -0.03382 a 0.4844
```

See all the data tables in memory

```
tables()
```

```
     NAME NROW MB COLS  KEY
[1,] DT      9 1  x,y,z
Total: 1MB
```

Subsetting rows

```
DT[2,]
```

```
      x y     z
1: 1.002 a 1.509
```

```
DT[DT$y=="a",]
```

```
         x y      z
1: -0.27721 a 0.2530
2:  1.00158 a 1.5093
3: -0.03382 a 0.4844
```

Subsetting rows

```
DT[c(2,3)]
```

```
         x y      z
1:  1.00158 a 1.5093
2: -0.03382 a 0.4844
```

Subsetting columns!?

```
DT[,c(2,3)]
```

```
[1] 2 3
```

Column subsetting in data.table

- The subsetting function is modified for data.table
- The argument you pass after the comma is called an "expression"
- In R an expression is a collection of statements enclosed in curley brackets

```
{
  x = 1
  y = 2
}
k = {print(10); 5}
```

```
[1] 10
```

```
print(k)
```

```
[1] 5
```

Calculating values for variables with expressions

```
DT[,list(mean(x),sum(z))]
```

```
        V1     V2
1: 0.05637 0.5815
```

```
DT[,table(y)]
```

```
y
a b c
3 3 3
```

Adding new columns

```
DT[,w:=z^2]
```

```
          x y        z        w
1: -0.27721 a  0.25300 0.064009
2:  1.00158 a  1.50933 2.278091
3: -0.03382 a  0.48437 0.234619
4: -0.70493 b -1.22755 1.506885
5: -1.36402 b -0.64624 0.417631
6: -0.26224 b -0.51427 0.264475
7: -0.10929 c  1.21445 1.474901
8:  1.40234 c  0.07493 0.005614
9:  0.85494 c -0.56652 0.320948
```

Adding new columns

```
DT2 <- DT
DT[, y:= 2]
```

```
          x y        z        w
1: -0.27721 2  0.25300 0.064009
2:  1.00158 2  1.50933 2.278091
3: -0.03382 2  0.48437 0.234619
4: -0.70493 2 -1.22755 1.506885
5: -1.36402 2 -0.64624 0.417631
6: -0.26224 2 -0.51427 0.264475
7: -0.10929 2  1.21445 1.474901
8:  1.40234 2  0.07493 0.005614
9:  0.85494 2 -0.56652 0.320948
```

Careful

```
head(DT,n=3)
```

```
          x y      z       w
1: -0.27721 2 0.2530 0.06401
2:  1.00158 2 1.5093 2.27809
3: -0.03382 2 0.4844 0.23462
```

```
head(DT2,n=3)
```

```
          x y      z       w
1: -0.27721 2 0.2530 0.06401
2:  1.00158 2 1.5093 2.27809
3: -0.03382 2 0.4844 0.23462
```

Multiple operations

```
DT[,m:= {tmp <- (x+z); log2(tmp+5)}]
```

```
          x y        z        w     m
1: -0.27721 2  0.25300 0.064009 2.315
2:  1.00158 2  1.50933 2.278091 2.909
3: -0.03382 2  0.48437 0.234619 2.446
4: -0.70493 2 -1.22755 1.506885 1.617
5: -1.36402 2 -0.64624 0.417631 1.580
6: -0.26224 2 -0.51427 0.264475 2.078
7: -0.10929 2  1.21445 1.474901 2.610
8:  1.40234 2  0.07493 0.005614 2.695
9:  0.85494 2 -0.56652 0.320948 2.403
```

plyr like operations

```
DT[,a:=x>0]
```

```
          x y        z        w     m     a
1: -0.27721 2  0.25300 0.064009 2.315 FALSE
2:  1.00158 2  1.50933 2.278091 2.909  TRUE
3: -0.03382 2  0.48437 0.234619 2.446 FALSE
4: -0.70493 2 -1.22755 1.506885 1.617 FALSE
5: -1.36402 2 -0.64624 0.417631 1.580 FALSE
6: -0.26224 2 -0.51427 0.264475 2.078 FALSE
7: -0.10929 2  1.21445 1.474901 2.610 FALSE
8:  1.40234 2  0.07493 0.005614 2.695  TRUE
9:  0.85494 2 -0.56652 0.320948 2.403  TRUE
```

plyr like operations

```
DT[,b:= mean(x+w),by=a]
```

```
          x y        z        w     m     a      b
1: -0.27721 2  0.25300 0.064009 2.315 FALSE 0.2018
2:  1.00158 2  1.50933 2.278091 2.909  TRUE 1.9545
3: -0.03382 2  0.48437 0.234619 2.446 FALSE 0.2018
4: -0.70493 2 -1.22755 1.506885 1.617 FALSE 0.2018
5: -1.36402 2 -0.64624 0.417631 1.580 FALSE 0.2018
6: -0.26224 2 -0.51427 0.264475 2.078 FALSE 0.2018
7: -0.10929 2  1.21445 1.474901 2.610 FALSE 0.2018
8:  1.40234 2  0.07493 0.005614 2.695  TRUE 1.9545
9:  0.85494 2 -0.56652 0.320948 2.403  TRUE 1.9545
```

Special variables

`.N` An integer, length 1, containing the numbe r

```
set.seed(123);
DT <- data.table(x=sample(letters[1:3], 1E5, TRUE))
DT[, .N, by=x]
```

```
   x     N
1: a 33387
2: c 33201
3: b 33412
```

Keys

```
DT <- data.table(x=rep(c("a","b","c"),each=100), y=rnorm(300))
setkey(DT, x)
DT['a']
```

```
    x        y
  1: a  0.25959
  2: a  0.91751
  3: a -0.72232
  4: a -0.80828
  5: a -0.14135
  6: a  2.25701
  7: a -2.37955
  8: a -0.45425
  9: a -0.06007
 10: a  0.86090
 11: a -1.78466
 12: a -0.13074
 13: a -0.36984
 14: a -0.18066
 15: a -1.04973
```

Joins

```
DT1 <- data.table(x=c('a', 'a', 'b', 'dt1'), y=1:4)
DT2 <- data.table(x=c('a', 'b', 'dt2'), z=5:7)
setkey(DT1, x); setkey(DT2, x)
merge(DT1, DT2)
```

```
   x y z
1: a 1 5
2: a 2 5
3: b 3 6
```

Fast reading

```
big_df <- data.frame(x=rnorm(1E6), y=rnorm(1E6))
file <- tempfile()
write.table(big_df, file=file, row.names=FALSE, col.names=TRUE, sep="\t", quote=FALSE)
system.time(fread(file))
```

```
   user  system elapsed
  0.312   0.015   0.326
```

```
system.time(read.table(file, header=TRUE, sep="\t"))
```

```
   user  system elapsed
  5.702   0.048   5.755
```

Summary and further reading

- The latest development version contains new functions like `melt` and `dcast` for data.tables
  - https://r-forge.r-project.org/scm/viewvc.php/pkg/NEWS?view=markup&root=datatable
- Here is a list of differences between data.table and data.frame
  - http://stackoverflow.com/questions/13618488/what-you-can-do-with-data-frame-that-you-cant-in-data-table
- Notes based on Raphael Gottardo's notes https://github.com/raphg/Biostat-578/blob/master/Advanced_data_manipulation.Rpres, who got them from Kevin Ushey.

Reading mySQL

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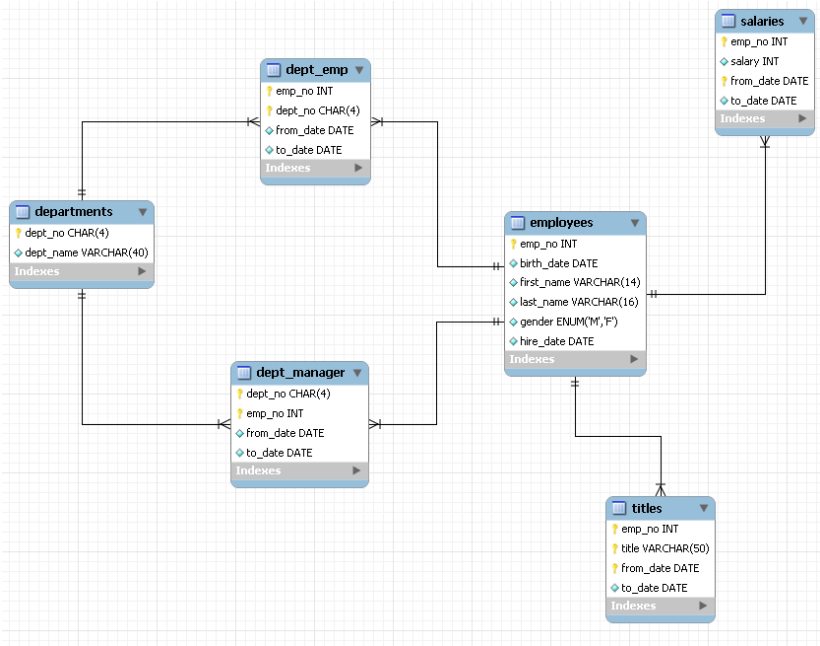
mySQL

- 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

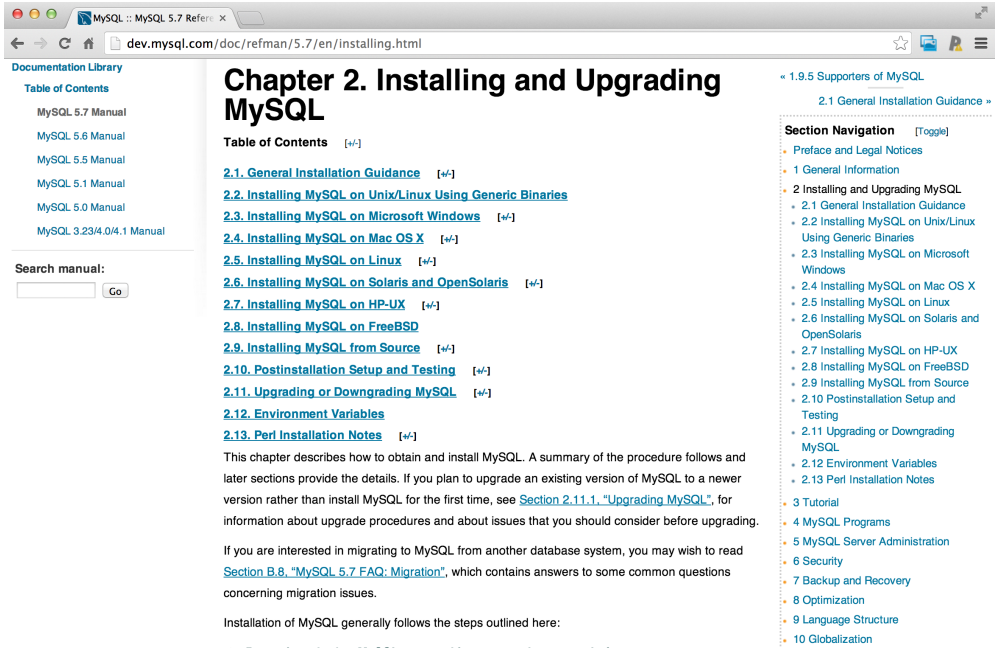
http://en.wikipedia.org/wiki/MySQL http://www.mysql.com/

Example structure



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

Step 1 - Install MySQL

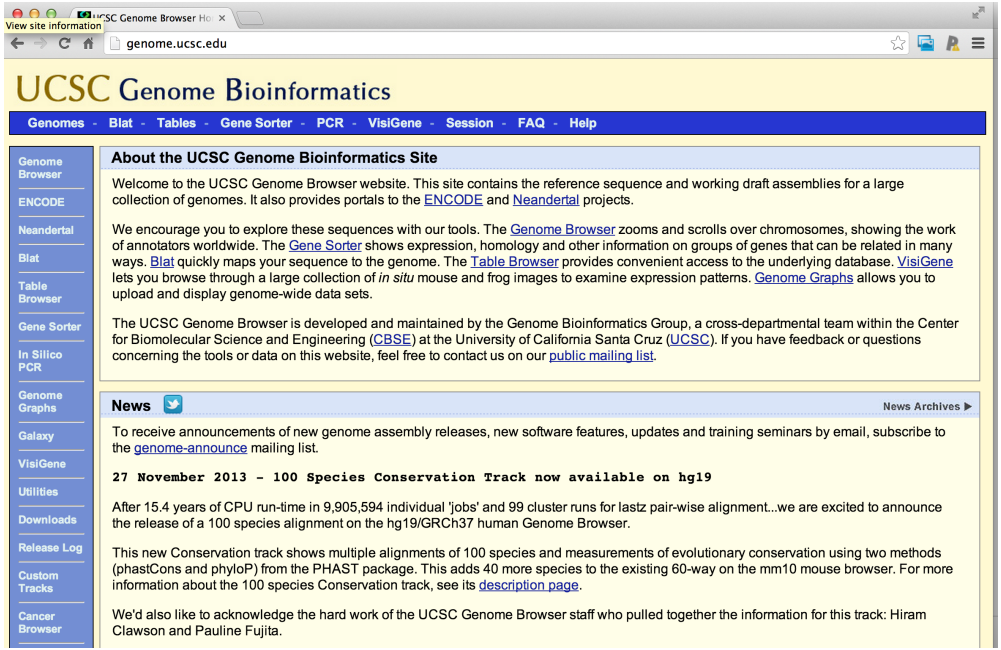


http://dev.mysql.com/doc/refman/5.7/en/installing.html

Step 2 - Install RMySQL

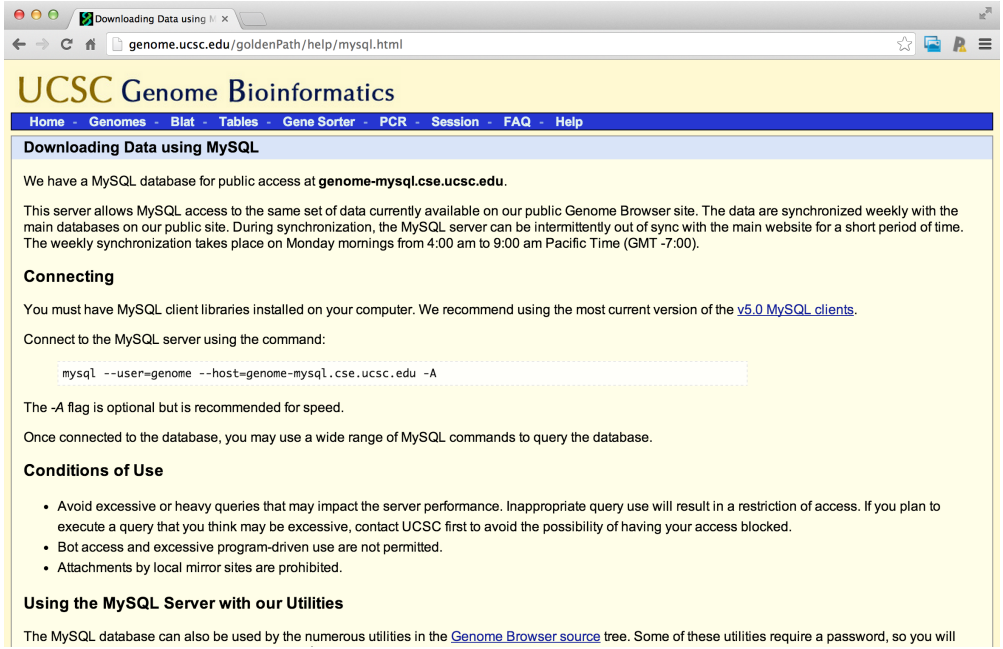
- On a Mac: `install.packages("RMySQL")`
- On Windows:
  - Official instructions - http://biostat.mc.vanderbilt.edu/wiki/Main/RMySQL (may be useful for Mac/UNIX users as well)
  - Potentially useful guide - http://www.ahschulz.de/2013/07/23/installing-rmysql-under-windows/

Example - UCSC database



http://genome.ucsc.edu/

UCSC MySQL



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/

Reading HDF5

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HDF5

- Used for storing large data sets
- Supports storing a range of data types
- Heirarchical data format
- *groups* containing zero or more data sets and metadata
  - Have a *group header* with group name and list of attributes
  - Have a *group symbol table* with a list of objects in group
- *datasets* multidmensional array of data elements with metadata
  - Have a *header* with name, datatype, dataspace, and storage layout
  - Have a *data array* with the data

http://www.hdfgroup.org/

R HDF5 package

```
source("http://bioconductor.org/biocLite.R")
biocLite("rhdf5")
```

```
library(rhdf5)
created = h5createFile("example.h5")
created
```

```
[1] TRUE
```

- This will install packages from Bioconductor http://bioconductor.org/, primarily used for genomics but also has good "big data" packages
- Can be used to interface with hdf5 data sets.
- This lecture is modeled very closely on the rhdf5 tutorial that can be found here http://www.bioconductor.org/packages/release/bioc/vignettes/rhdf5/inst/doc/rhdf5.pdf

Create groups

```
created = h5createGroup("example.h5","foo")
created = h5createGroup("example.h5","baa")
created = h5createGroup("example.h5","foo/foobaa")
h5ls("example.h5")
```

```
  group    name      otype dclass dim
0     /     baa H5I_GROUP
1     /     foo H5I_GROUP
2  /foo foobaa H5I_GROUP
```

Write to groups

```
A = matrix(1:10,nr=5,nc=2)
h5write(A, "example.h5","foo/A")
B = array(seq(0.1,2.0,by=0.1),dim=c(5,2,2))
attr(B, "scale") <- "liter"
h5write(B, "example.h5","foo/foobaa/B")
h5ls("example.h5")
```

```
        group   name       otype  dclass       dim
0           /    baa   H5I_GROUP                  
1           /    foo   H5I_GROUP                  
2        /foo      A H5I_DATASET INTEGER     5 x 2
3        /foo foobaa   H5I_GROUP                  
4 /foo/foobaa      B H5I_DATASET   FLOAT 5 x 2 x 2
```

Write a data set

```
df = data.frame(1L:5L,seq(0,1,length.out=5),
  c("ab","cde","fghi","a","s"), stringsAsFactors=FALSE)
h5write(df, "example.h5","df")
h5ls("example.h5")
```

```
        group   name       otype   dclass       dim
0           /    baa   H5I_GROUP                  
1           /     df H5I_DATASET COMPOUND         5
2           /    foo   H5I_GROUP                  
3        /foo      A H5I_DATASET  INTEGER     5 x 2
4        /foo foobaa   H5I_GROUP                  
5 /foo/foobaa      B H5I_DATASET    FLOAT 5 x 2 x 2
```

Reading data

```
readA = h5read("example.h5","foo/A")
readB = h5read("example.h5","foo/foobaa/B")
readdf= h5read("example.h5","df")
readA
```

```
     [,1] [,2]
[1,]    1    6
[2,]    2    7
[3,]    3    8
[4,]    4    9
[5,]    5   10
```

Writing and reading chunks

```
h5write(c(12,13,14),"example.h5","foo/A",index=list(1:3,1))
h5read("example.h5","foo/A")
```

```
     [,1] [,2]
[1,]   12    6
[2,]   13    7
[3,]   14    8
[4,]    4    9
[5,]    5   10
```

Notes and further resources

- hdf5 can be used to optimize reading/writing from disc in R
- The rhdf5 tutorial:
  - http://www.bioconductor.org/packages/release/bioc/vignettes/rhdf5/inst/doc/rhdf5.pdf
- The HDF group has informaton on HDF5 in general http://www.hdfgroup.org/HDF5/

Reading data from the web

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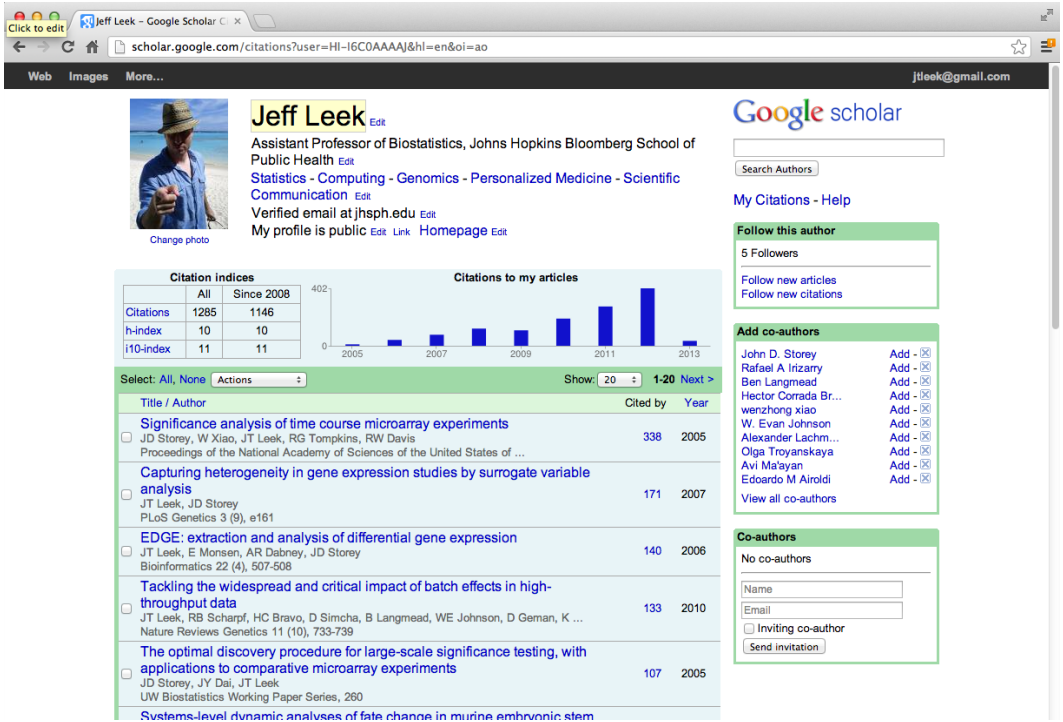
Webscraping

Webscraping: Programatically extracting data from the HTML code of websites.

- It can be a great way to get data How Netflix reverse engineered Hollywood
- Many websites have information you may want to programaticaly read
- In some cases this is against the terms of service for the website
- Attempting to read too many pages too quickly can get your IP address blocked

http://en.wikipedia.org/wiki/Web_scraping

Example: Google scholar



http://scholar.google.com/citations?user=HI-I6C0AAAAJ&hl=en

Getting data off webpages - readLines()

```
con = url("http://scholar.google.com/citations?user=HI-I6C0AAAAJ&hl=en")
htmlCode = readLines(con)
close(con)
htmlCode
```

```
[1] "<!DOCTYPE html><html><head><title>Jeff Leek - Google Scholar Citations</title><meta name=\"robots\
```

Parsing with XML

```
library(XML)
url <- "http://scholar.google.com/citations?user=HI-I6C0AAAAJ&hl=en"
html <- htmlTreeParse(url, useInternalNodes=T)

xpathSApply(html, "//title", xmlValue)
```

```
[1] "Jeff Leek - Google Scholar Citations"
```

```
xpathSApply(html, "//td[@id='col-citedby']", xmlValue)
```

```
 [1] "Cited by" "397"      "259"      "237"      "172"      "138"      "125"      "122"
 [9] "109"      "101"      "34"       "26"       "26"       "24"       "19"       "13"
[17] "12"       "10"       "10"       "7"        "6"
```

GET from the httr package

```
library(httr); html2 = GET(url)
content2 = content(html2,as="text")
parsedHtml = htmlParse(content2,asText=TRUE)
xpathSApply(parsedHtml, "//title", xmlValue)
```

```
[1] "Jeff Leek - Google Scholar Citations"
```

Accessing websites with passwords

```
pg1 = GET("http://httpbin.org/basic-auth/user/passwd")
pg1
```

```
Response [http://httpbin.org/basic-auth/user/passwd]
  Status: 401
  Content-type:
```

http://cran.r-project.org/web/packages/httr/httr.pdf

Accessing websites with passwords

```
pg2 = GET("http://httpbin.org/basic-auth/user/passwd",
    authenticate("user","passwd"))
pg2
```

```
Response [http://httpbin.org/basic-auth/user/passwd]
  Status: 200
  Content-type: application/json
{
  "authenticated": true,
  "user": "user"
}
```

```
names(pg2)
```

```
[1] "url"         "handle"      "status_code" "headers"     "cookies"     "content"
[7] "times"       "config"
```

Using handles

```
google = handle("http://google.com")
pg1 = GET(handle=google,path="/")
pg2 = GET(handle=google,path="search")
```

http://cran.r-project.org/web/packages/httr/httr.pdf

Notes and further resources

- R Bloggers has a number of examples of web scraping http://www.r-bloggers.com/?s=Web+Scraping
- The httr help file has useful examples http://cran.r-project.org/web/packages/httr/httr.pdf
- See later lectures on APIs

Reading data from APIs

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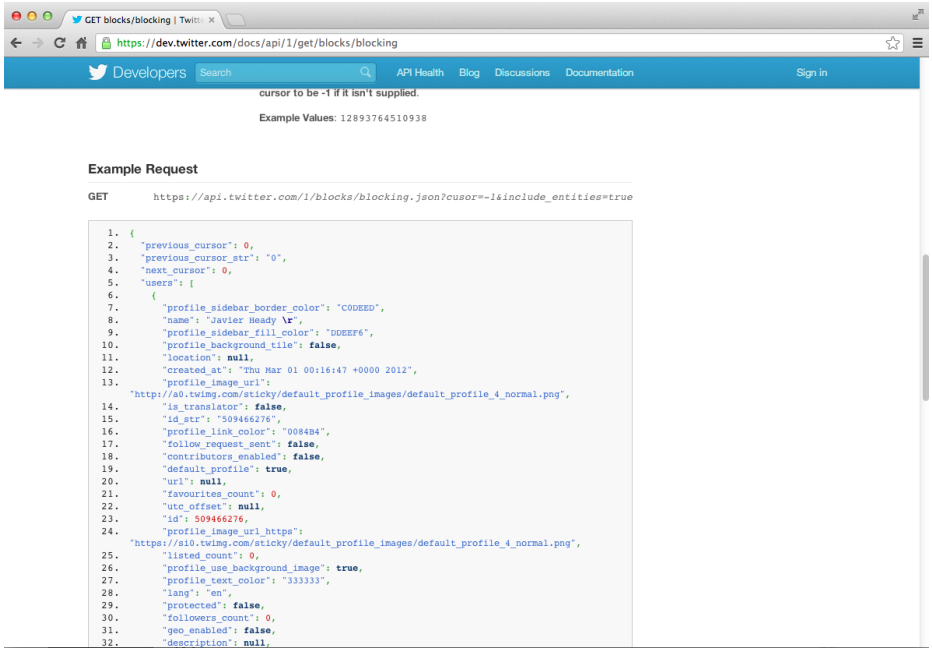
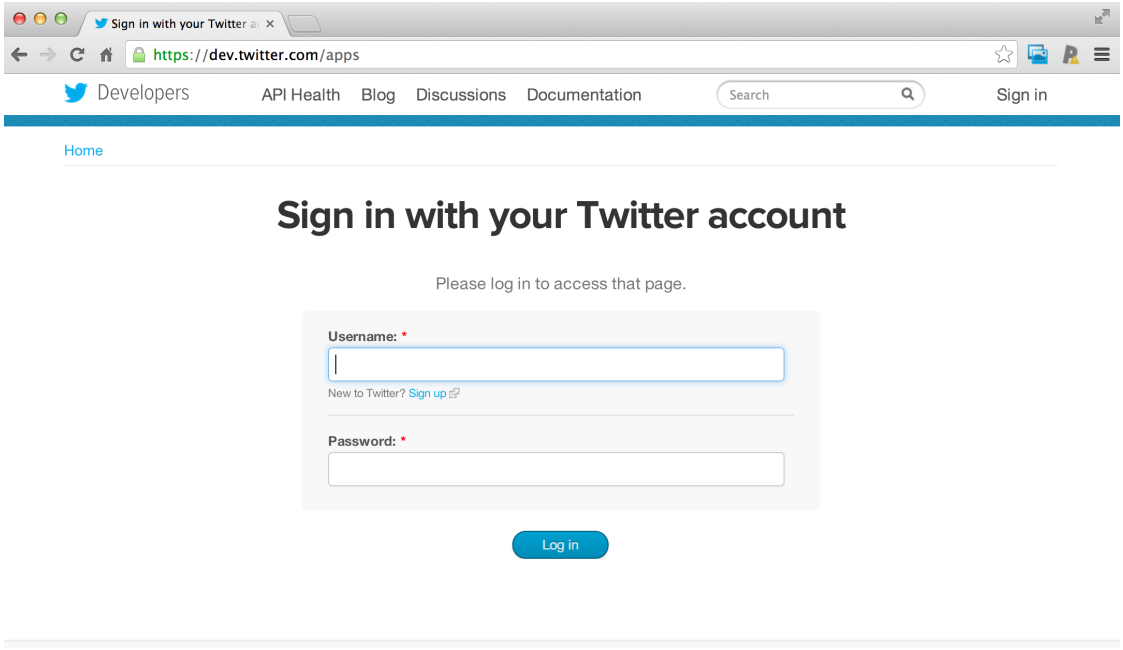
Application programming interfaces



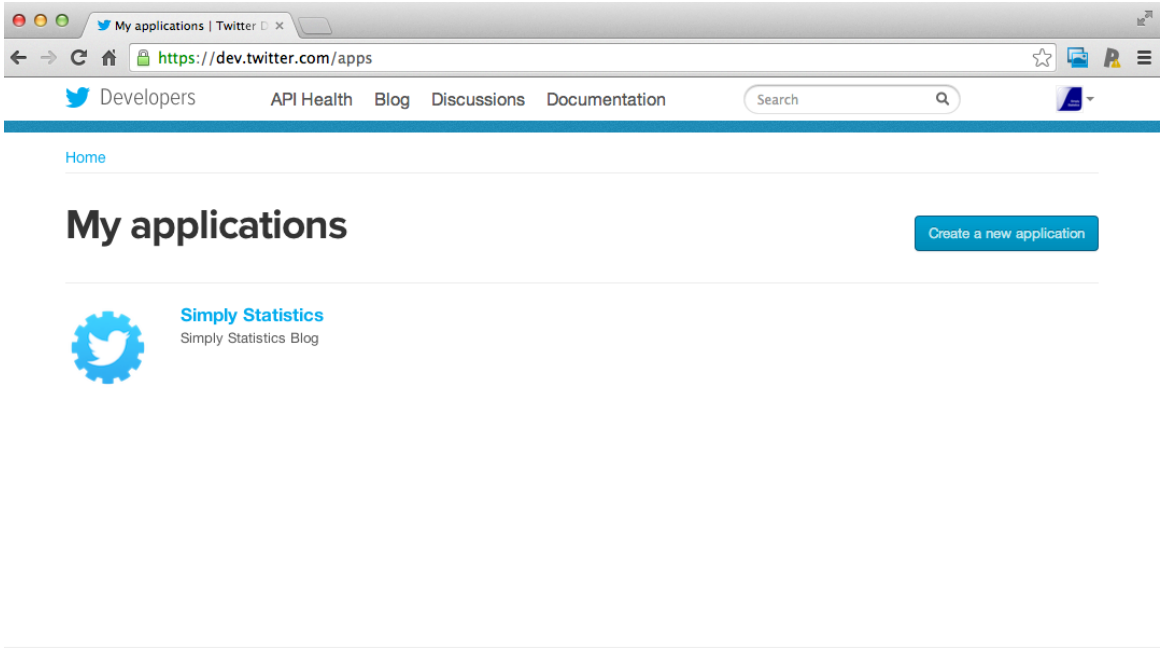
https://dev.twitter.com/docs/api/1/get/blocks/blocking

Creating an application

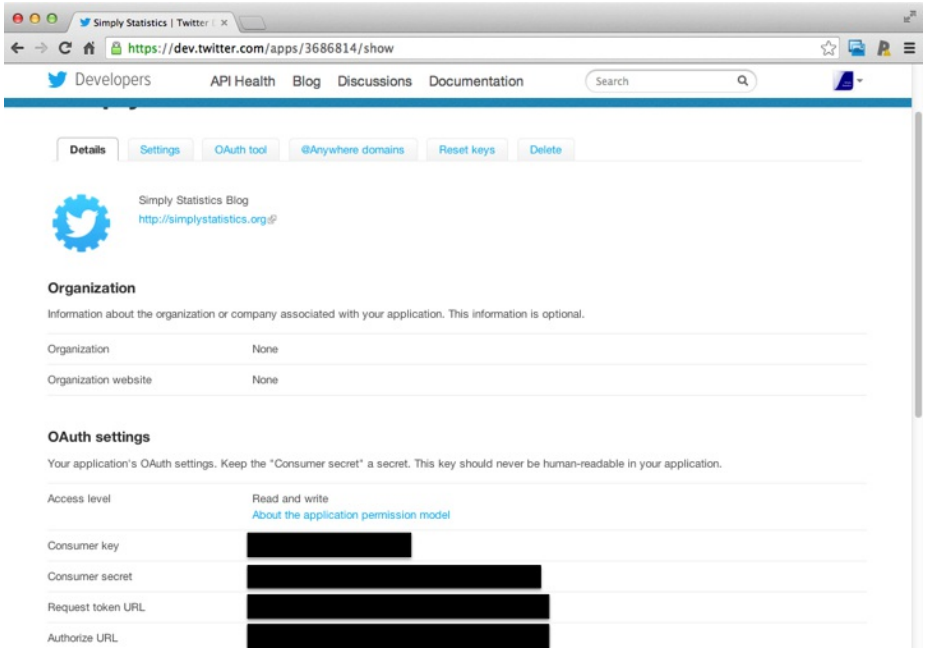


https://dev.twitter.com/apps)

Creating an application



Creating an application



Accessing Twitter from R

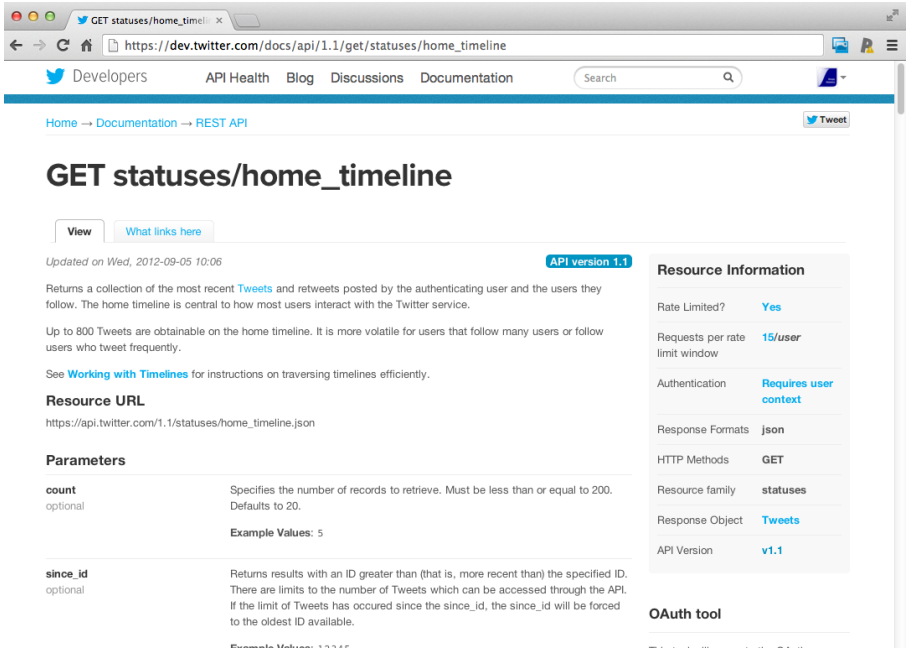
```
myapp = oauth_app("twitter",
                  key="yourConsumerKeyHere",secret="yourConsumerSecretHere")
sig = sign_oauth1.0(myapp,
                    token = "yourTokenHere",
                     token_secret = "yourTokenSecretHere")
homeTL = GET("https://api.twitter.com/1.1/statuses/home_timeline.json", sig)
```

Converting the json object

```
json1 = content(homeTL)
json2 = jsonlite::fromJSON(toJSON(json1))
json2[1,1:4]
```

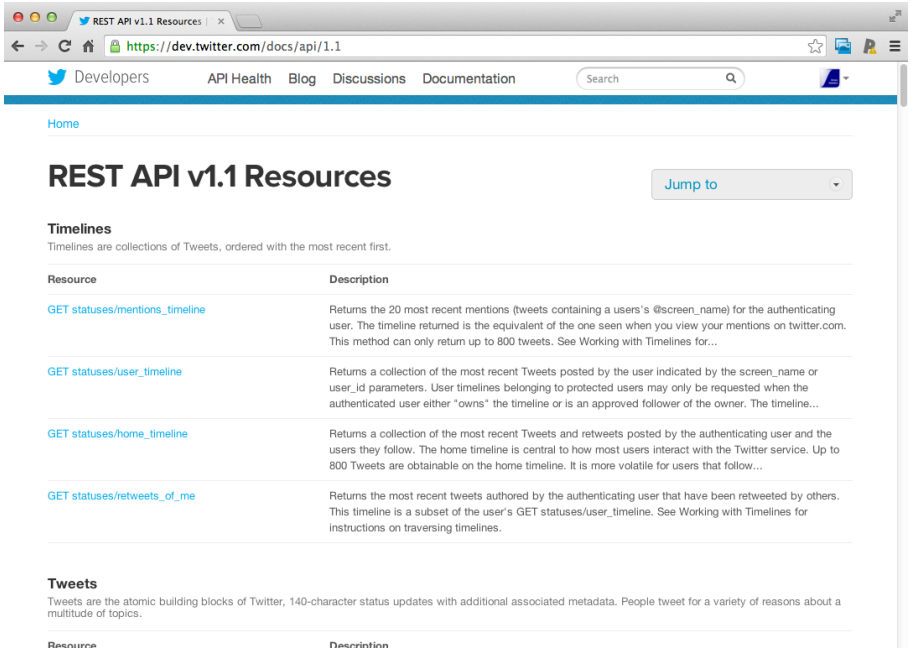
```
                    created_at           id             id_str
1 Mon Jan 13 05:18:04 +0000 2014 4.225984e+17 422598398940684288

1 Now that P. Norvig's regex golf IPython notebook hit Slashdot, let's see if our traffic spike tops th
```

How did I know what url to use?



https://dev.twitter.com/docs/api/1.1/get/search/tweets

In general look at the documentation



https://dev.twitter.com/docs/api/1.1/overview

In general look at the documentation

- httr allows `GET`, `POST`, `PUT`, `DELETE` requests if you are authorized
- You can authenticate with a user name or a password
- Most modern APIs use something like oauth
- httr works well with Facebook, Google, Twitter, Githb, etc.

Reading from other sources

Jeffrey Leek
Johns Hopkins Bloomberg School of Public Health

There is a package for that

- Roger has a nice video on how there are R packages for most things that you will want to access.
- Here I'm going to briefly review a few useful packages
- In general the best way to find out if the R package exists is to Google "data storage mechanism R package"
    - For example: "MySQL R package"

Interacting more directly with files

- file - open a connection to a text file
- url - open a connection to a url
- gzfile - open a connection to a .gz file
- bzfile - open a connection to a .bz2 file
- *?connections* for more information
- Remember to close connections

foreign package

- Loads data from Minitab, S, SAS, SPSS, Stata,Systat
- Basic functions *read.foo*
  - read.arff (Weka)
  - read.dta (Stata)
  - read.mtp (Minitab)
  - read.octave (Octave)
  - read.spss (SPSS)
  - read.xport (SAS)
- See the help page for more details http://cran.r-project.org/web/packages/foreign/foreign.pdf

Examples of other database packages

- RPostresSQL provides a DBI-compliant database connection from R. Tutorial-https://code.google.com/p/rpostgresql/, help file-http://cran.r-project.org/web/packages/RPostgreSQL/RPostgreSQL.pdf
- RODBC provides interfaces to multiple databases including PostgreQL, MySQL, Microsoft Access and SQLite. Tutorial - http://cran.r-project.org/web/packages/RODBC/vignettes/RODBC.pdf, help file - http://cran.r-project.org/web/packages/RODBC/RODBC.pdf
- RMongo http://cran.r-project.org/web/packages/RMongo/RMongo.pdf (example of Rmongo http://www.r-bloggers.com/r-and-mongodb/) and rmongodb provide interfaces to MongoDb.

Reading images

- jpeg - http://cran.r-project.org/web/packages/jpeg/index.html
- readbitmap - http://cran.r-project.org/web/packages/readbitmap/index.html
- png - http://cran.r-project.org/web/packages/png/index.html
- EBImage (Bioconductor) - http://www.bioconductor.org/packages/2.13/bioc/html/EBImage.html

Reading GIS data

- rdgal - http://cran.r-project.org/web/packages/rgdal/index.html
- rgeos - http://cran.r-project.org/web/packages/rgeos/index.html
- raster - http://cran.r-project.org/web/packages/raster/index.html

Reading music data

- tuneR - http://cran.r-project.org/web/packages/tuneR/
- seewave - http://rug.mnhn.fr/seewave/