## Getting Data from the Web with R Part 8: Getting Data via Web APIs

Gaston Sanchez

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#### Readme

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#### Lectures Menu

#### Slide Decks

- 1. Introduction
- 2. Reading files from the Web
- 3. Basics of XML and HTML
- 4. Parsing XML / HTML content
- 5. Handling JSON data
- 6. HTTP basics and the RCurl package
- 7. Getting data via Web Forms
- 8. Getting data via Web APIs

## Web APIs

#### Goal

#### Data via Web APIs

The goal of the present slides is to give you an overview of **how data can be accessed via APIs** with  ${\sf R}$ 

### Synopsis

#### In a nutshell

We'll cover the following topics:

- ► API basics
- ► API consederations
- Case Study PubMed

#### Some References

- XML and Web Technlogies for Data Sciences with R by Deb Nolan and Duncan Temple Lang
- RESTful Web Services
   by Leonard Richardson and Sam Ruby
- ► The ROAuth Package

  http://cran.r-project.org/web/packages/ROAuth/index.html
- ► CRAN Task View: Web Technologies and Services
  http://cran.r-project.org/web/views/WebTechnologies.html

## **API** Basics

#### API

"In computer programming, an application programming interface (API) specifies how some software components should interact with each other."

"When used in the context of web development, an API is typically defined as a set of Hypertext Transfer Protocol (HTTP) request messages, along with a definition of the structure of response messages"

http://en.wikipedia.org/wiki/Application\_programming\_interface

#### About APIs

#### What's an API?

API stands for **Application Programming Interface**. Broadly speaking, API refers to a set of programming instructions that allow different software to interact with another.

#### Web API?

A Web API uses HTTP requests to access information from Web-based software application.

#### About APIs

#### What's an API?

By definition, an API is an interface, that is, something that **defines** the way in which two software communicate.

#### How Web APIs communicate?

With Web APIs, the communication between applications is handled through a collection of standards and protocols (eg  $\mathsf{HTTP}$ )

#### **Importance**

#### Why should we care?

A lot of companies allow users to freely access data from their websites by means of APIs. So it is important to have some exposure on how to work and get data with APIs.

#### Everybody who's anybody has an API

Web APIs are becoming increasingly popular for any company, almost mandatory if they want to stay "connected" with the rest of the world, and have a presence with their users/customers. A good starting point for finding more websites with APIs is **Programmable Web**:

http://www.programmableweb.com

#### Web API Examples: Google APIs

#### ← → C a https://developers.google.com

#### Master our APIs and Technologies



Increase traffic and engagement to your content by using Google+ plugins and APIs



Use Google APIs in your Android apps.



Build and run your websites and apps on Google's infrastructure.

Chrome

Create high performance web apps using the latest technologies the open web has to offer.

Games

Build high powered and interactive web and mobile games using cutting-edge technologies.



#### Google Maps

The easy way to build interactive data visualizations on a map and location-based apps.



#### Google Apps

Extend the Google Apps experience for your users.



#### Google TV

Build apps for the big screen.



#### Google Wallet

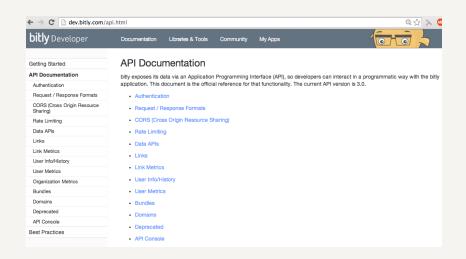
Increase conversions, process payments, and engage customers with offers and loyalty programs.



#### YouTube

Integrate YouTube's video content and functionality into your website, app, or device.

#### Web API Examples: Bitly





#### Using the API

Request a Key Data Sets

#### **Download Data**

To download full data sets. visit our FTP Server

#### Developer Forum

Need help? Join our Developer Forum - to submit questions, share your apps, and provide feedback.

#### The Census Bureau API

To improve access to data and encourage innovation, the Census Bureau has begun to provide API access to some data sets. We invite developers to use these APIs, join our Developer Forum, and provide feedback to help us move forward with continued API development.

Please read the Terms of Service for using the API

#### Now available: The Economic Indicators Time Series Database - see details

The Economic Indicator Database is now available via the API. This database includes statistics, primarily at the national level, for measuring key sectors of the U.S. economy.

#### Discovery Tool (in Beta)

http://api.census.gov/data.ison

The machine-readable dataset discovery service is now available in beta release. The http://api.census.gov/data.ison URI produces a JSON document describing all available datasets. The content of this JSON document is based largely on the Open Project Data Common Core Metadata Schema, and extended to include metadata specific to Census Bureau datasets. The http://api.census.gov/data.xml URI may he used to access the same information as XMI.

In addition to the above URIs dataset discovery is available for the entire vintage/dataset hierarchy as well. For example, the http://api.census.gov/data/2010.ison and http://api.census.gov/data/2010.xml URIs may be used to discover all datasets within the 2010 vintage.

## Web API Considerations

#### We're just here for the data

We're interested in Web APIs because they allow us to download content and data. And as with any other tool, there's the good, the bad, and the ugly about Web APIs.

#### The Good

- ▶ Obviously, we get access to data
- ▶ No need to buy or pay for data
- We can get access in a programmatically way
- ► There are some R packages for working with specific Web APIs http://cran.r-project.org/web/views/WebTechnologies.html
- Under ideal circumnstances, data is in nice formats and decent structure

#### The Bad

- You first have to learn how to use a given Web API
- ► Learning about an API and reading the documentation may take you some time
- ► The documentation may be very limited, outdated, and poorly explained
- ▶ Sometimes the data is not what you were expecting

#### The Ugly

- APIs change and evolve, so if you're planning to use one over a long period of time, you have to check it constantly
- ▶ You may need to register, get credentials, use authentication
- Usually there are rate and quota limits on how much data you can download and how frequently
- ► Some APIs can be very complex to use (not user friendly)

#### Working with Web APis

#### Checklist for working with Web APIs

- ► Read the API's documentation (check the examples!)
- ▶ Read terms of service (what you're allowed or not to do)
- Typically you may need an API key
- ▶ You may need to register and open a developer account
- ▶ You may need to authenticate (just another step in the pipeline)
- ▶ See what kind of data you have access to
- ▶ See what kind of formats are available

#### Working with Web APIs

#### Working with Web APIs and R

This is our main concern: figure out how to interact with Web APIs and do things in  $\ensuremath{\mathsf{R}}$ 

- Understand how the API works (eg REST, SOAP)
- Understand what kind of requests you need to use (GET, POST, etc)
- ► Experiment first with simple examples
- Usually you begin with some kind of query or search
- Check what R packages you must load (eg XML, RCurl, SSOAP, ROAuth, httpRequest, RJSONIO)
- Write functions and scripts (programmatically)

# Case Study E-utilities with PubMed

### Case Study Outline

#### Outline

We'll work with a **small but real life example**, which means you might get lost with all the descriptive information.

Hopefully this brief outline will help you to navigate through this case study:

- ► NCBI Website (central site containing everything else)
- ▶ Database PubMed (this is where we want to get data from)
- ► Web API **E-Utilities** (this is the API we'll be playing with)
- ► ESearch and ESummary (in particular, we'll use these 2 functions)

### National Center for Biotechnology Information



#### About NCBI

#### **NCBI**

The National Center for Biotechnology Information (NCBI) provides access to biomedical information

http://www.ncbi.nlm.nih.gov

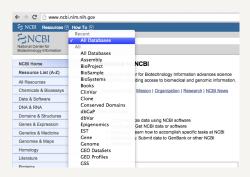
#### Mind you

- ► The NCBI website is kind of ugly and confusing. (I told you this is a real life example!)
- ► Looking at the website, it's not evident what you are supposed to do first or where to begin with.
- ► For our example, the important parts of the website are the **Databases** and the **Tools**.

#### About NCBI

#### **NCBI** Databases

The real juice of the NCBI website is the data in it. There are **38 databases** covering a variety of biomedical data. Among them, there is the database *PubMed*.



#### API: F-Utilities

#### E-Utilities

The NCBI makes accessible the information in their databases with its API Entrez Programming Utilities also known as E-Utilities

http://www.ncbi.nlm.nih.gov/books/NBK25501/

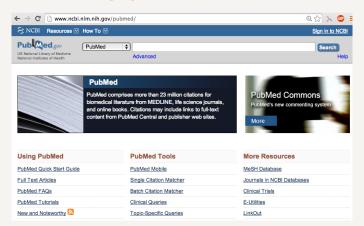


#### About PubMed

#### PubMed Database

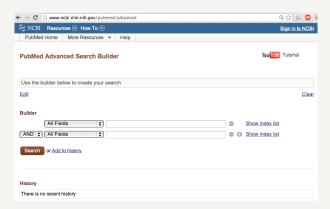
PubMed comprises more than 23 million citations for biomedical literature from MEDLINE, life science journals, and online books.

http://www.ncbi.nlm.nih.gov/pubmed/



#### Searching PubMed

Although we can use the Advanced Search forms to query PubMed (http://www.ncbi.nlm.nih.gov/pubmed/advanced), we'll see how to use the E-utilities API to get some data.



#### Mission

#### Ultimate Goal

Your mission is to download the PubMed IDs for articles published in 2012, and containing the term "human genome" in their titles

Good Luck!

# Basics of E-utilities (NCBI Web API)

#### E-Utilities

#### E-Utilities provides 8 different applications or utilities:

Application	Description
EInfo	database statistics
ESearch	text searches
EPost	Unique Identification (UID) uploads
ESummary	document summary downloads
EFetch	data record downloads
ELink	Entrez links
EGQuery	global query
ESpell	spelling suggestions
ECitMatch	batch citation searching in PubMed

We'll focus on *ESearch* and *ESummary* 

#### E-Utilities Documentation

#### Documentation

Like many other Web APIs, there's an extensive documentation about E-Utilities ... and it's not beginner friendly.

But this is a good example of the things you will find when working with APIs. Usually you will struggle reading and understanding the provided documentation.

#### **E-Utilities Applications**

#### How does E-utilities work?

In essence, we use E-utilities by specifying URL's and send requests

- 1. All E-utilities calls share the same URL: http://eutils.ncbi.nlm.nih.gov/entrez/eutils/
- 2. Each E-utility has its own structure and parameters:
  - esearch.fcgi?db=<database>&term=<query>
  - esummary.fcgi?db=<database>&id=<uid\_list>
- 3. All E-utilities are appended to the base url:

http://eutils.ncbi.nlm.nih.gov/entrez/eutils/esearch.fcgi?db=<database>&term=<query>

# ESearch and ESummary

## ESearch & ESummary 2-step process

The way you'll work with ESearch and ESummary is using a two-step procedure:

- 1. you **search for a particular query** in order to get a list of UIDs (unique identification). This is done with **ESearch**
- 2. you use the list of UIDs to get a summary of the resources you are looking for. This is done with **ESummary**

### **ESearch**

#### About ESearch

ESearch allows us to specify a search query on a given database.

An ESearch call has the following structue:

```
esearch.fcgi?db=<database>&term=<query>
```

#### **Parameters**

- <database> represents the name of the database
- <query> represents the terms forming the query

# Defining an ESearch Call

## Example

We want to searh *PubMed* and get a list of UIDs for those articles containing the term *human genome* in the title, and that were published in *2012*.

#### **Parameters**

database: pubmed

query: human+genome[title]+AND+2012[pdat]

#### ESearch Call

esearch.fcgi?db=pubmed&term=human+genome[title]+AND+2012[pdat]

### ESearch with R

```
# load XMI.
library(XML)
# E-utilities base url
base_url = "http://eutils.ncbi.nlm.nih.gov/entrez/eutils/"
# define database variable: PubMed
db = "pubmed"
# define query variable
query = "human+genome[title]+AND+2012[pdat]"
# assemble ESearch call
esearch = sprintf("esearch.fcgi?db=%s&term=%s", db, query)
# create URL to make search request
search_url = paste(base_url, esearch, sep = '')
# ESearch request to get the list of UIDs
# (the list will be contained in an XML document)
search doc = xmlParse(search url)
```

# ESearch XML file output

```
<?xml version="1.0" ?>
<!DOCTYPE eSearchResult PUBLIC ...>
<eSearchResult>
  <Count>103</Count>
  <RetMax>20</RetMax>
  <RetStart>0</RetStart>
  <QueryKey>1</QueryKey>
  <WebEnv>NCID 1 282865897 130.14.18.34 9001 1399488846 694838780/WebEnv>
  <TdList>
    <Id>23959643</Id>
    <Id>23730202</Id>
  </IdList>
</eSearchResult>
```

There's a Count of 103 articles. Each article has its corresponding Id. By default (RetMax) just 20 Ids are retrieved

### ESearch with R

In order to get the 103 articles, we need to change the default maximum number of retrieved results:

```
# let's add the retmax parameter
retmax = 200

# redefine assemble ESearch
new_esearch = sprintf("esearch.fcgi?db=%s&term=%s&retmax=%s", db, query, retmax)

# update URL to make request
new_search_url = paste(base_url, new_esearch, sep = '')

# ESearch request to get the list of UIDs
# (the list will be contained in an XML document)
new_search_doc = xmlParse(new_search_url)
```

#### ESearch with R

We need to get the list of <Id>'s that are in the XML node <IdList>. One way to get those values is by using xpathSApply()

```
# get UIDs in a vector
ids = xpathSApply(new search doc, path = "//IdList/Id", fun = 'xmlValue')
# we should have 103 TDs
length(ids)
## [1] 103
# take a peek
head(ids)
## [1] "23959643" "23730202" "23520917" "23281708" "23281599" "23266811"
tail(ids)
## [1] "22057813" "22057783" "22050290" "22031941" "21945885" "21559844"
```

# **ESummary**

### About ESummary

ESummary allows us to get *document summaries* for a list of input UIDs. An ESummary call has the following structure:

```
esummary.fcgi?db=<database>&id=<uid_list>
```

#### **Parameters**

- <database> represents the name of the database
- <uid\_list> represents the list of UIDs

# **ESummary**

## Example

With ESearch we retrieve the list of UIDs for the articles we're looking for. Now we need to pass the list to ESummary

#### **Parameters**

database: pubmed

uid\_list: 23959643,23730202,23520917,...

## ESummary Call

esummary.fcgi?db=pubmed&id=23959643,23730202,23520917,...

# ESummary with R

### Now we need to use ESummary to get summaries of each article:

```
# concatenate all IDs, separated by commas
# (we'll pass this list to ESummary)
id_list = paste(ids, collapse = ',')

# assemble ESummary call
esummary = sprintf("esummary.fcgi?db=%s&id=%s", db, id_list)

# create URL to make request
sum_url = paste(base_url, esummary, sep = '')

# ESummary request to get document summaries
# (the summaries will be contained in an XML document)
summary_doc = xmlParse(sum_url)
```

## ESummary output

### You should get something like this from ESummary:

```
## <?xml version="1.0" encoding="UTF-8"?>
## <!DOCTYPE eSummaryResult PUBLIC "-//NLM//DTD esummary v1 20060131//EN" "http://eutils.ncbi.nlm.nih.gov/
## <eSummaryResult>
## <DocSum>
## <Td>23959643</Td>
## <Item Name="PubDate" Type="Date">2012 Dec</Item>
## <Item Name="EPubDate" Type="Date"></Item>
## <Item Name="Source" Type="String">Hum Biol</Item>
## <Item Name="AuthorList" Type="List">
## <Item Name="Author" Type="String">Casto AM</Item>
## <Item Name="Author" Type="String">Henn BM</Item>
## <Item Name="Author" Type="String">Kidd JM</Item>
## <Item Name="Author" Type="String">Bustamante CD</Item>
## <Item Name="Author" Type="String">Feldman MW</Item>
## </Ttem>
## <Item Name="LastAuthor" Type="String">Feldman MW</Item>
   <Item Name="Title" Type="String">A tale of two haplotypes: the EDA2R/AR Intergenic region is the most
## <Item Name="Volume" Type="String">84</Item>
   <Item Name="Issue" Type="String">6</Item>
## <Item Name="Pages" Type="String">641-94</Item>
## <Item Name="LangList" Type="List">
## <Item Name="Lang" Type="String">English</Item>
## </Ttem>
## <Item Name="NlmUniqueID" Type="String">0116717</Item>
## <Item Name="ISSN" Type="String">0018-7143</Item>
```

### Journal Names

The summary document of each <Id> article is composed of several <Item>'s such as "PubDate", "AuthorList", "Title", "Lang", and "FullJournalName", among others.

The **journal name** of each article is in an element: <Item Name="FullJournalName" Type="String">

For instance, the first article of the list (<Id>23959643</Id>) was published in *Human Biology*:

<Item Name="FullJournalName" Type="String">Human
biology</Item>

## ESummary with R

If we want to get the journal names in which each article was published, we can use xpathSApply() like so:

```
# journal names
journals = xpathSApply(summary doc, "//Item[@Name='FullJournalName']", xmlValue)
# first 5 journals
head(journals, n = 5)
## [1] "Human biology"
## [2] "Current genomics"
## [3] "Revista de derecho y genoma humano = Law and the human genome review / Catedra de Derecho y Genoma
## [4] "BMC genomics"
## [5] "BMC genomics"
# last 5 journals
tail(journals, n = 5)
## [1] "Human genetics"
                                    "Tissue antigens"
## [3] "Journal of virology"
                                    "Human molecular genetics"
## [5] "Journal of medical systems"
```