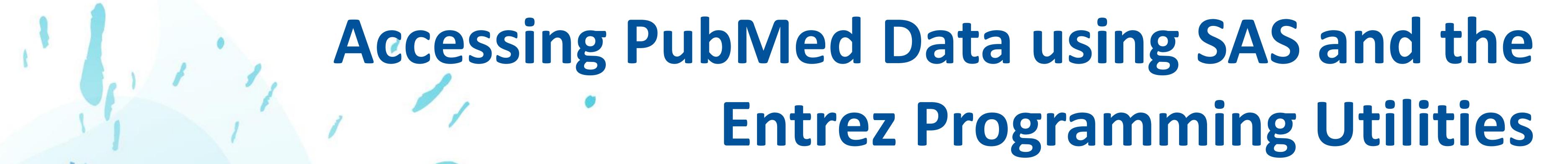
# SAS® GLOBAL FORUM 2016

IMAGINE. CREATE. INNOVATE.



South Australian Health and Medical Research Institute,
Australia.

Click to start

MENU (click on heading)

Introduction

Methods - 1

Methods - 2

Results & Conclusion



Introduction Methods - 1 Methods - 2 Results & Conclusion

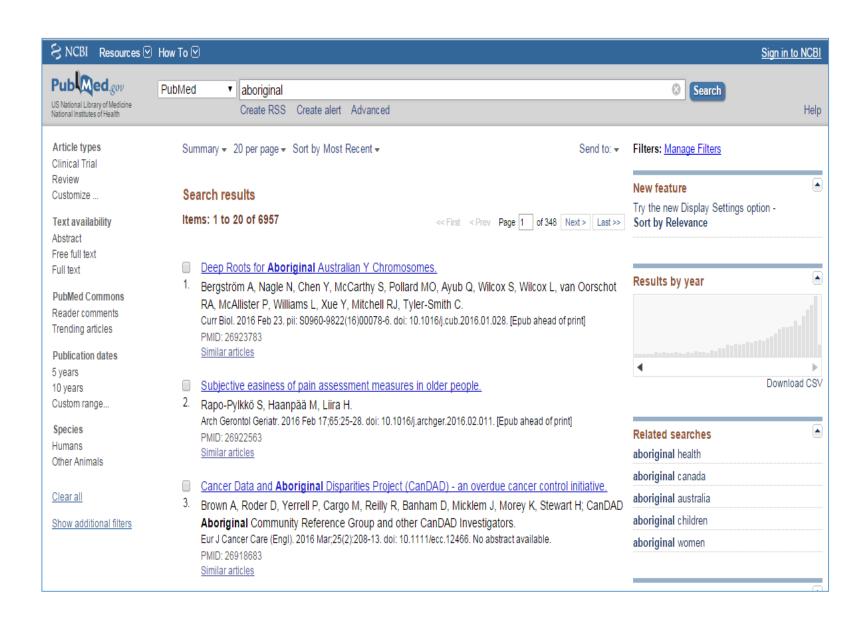
Craig Hansen, PhD South Australian Health and Medical Research Institute



#### What is PubMed?

PubMed (http://www.ncbi.nlm.nih.gov/pubmed) is a free search engine within MEDLINE and has become one of the standard databases to search for scientific abstracts.

MEDLINE is a suite of indexed databases developed and maintained by the National Center for Biotechnology Information (NCBI) at the United States National Library of Medicine (NLM).



Deep Roots for Aboriginal Australian Y Chromosomes. Bergström A<sup>1</sup>, Nagle N<sup>2</sup>, Chen Y<sup>1</sup>, McCarthy S<sup>1</sup>, Pollard MO<sup>3</sup>, Ayub Q<sup>1</sup>, Wilcox S<sup>4</sup>, Wilcox L<sup>2</sup>, van Oorschot RA<sup>5</sup>, McAllister P<sup>6</sup>, Williams L<sup>7</sup>, Xue Y<sup>1</sup>, Mitchell Author information Australia was one of the earliest regions outside Africa to be colonized by fully modern humans, with archaeological evidence for human presence by 47,000 years ago (47 kya) widely accepted [1, 2]. However, the extent of subsequent human entry before the European colonial age is less clear. The dingo reached Australia about 4 kya, indirectly implying human contact, which some have linked to changes in language and stone tool technology to suggest substantial cultural changes at the same time [3]. Genetic data of two kinds have been proposed to support gene flow from the Indian subcontinent to Australia at this time, as well: first, signs of South Asian admixture in Aboriginal Australian genomes have been reported on the basis of genome-wide SNP data [4]; and second, a Y chromosome lineage designated haplogroup C\*, present in both India and Australia, was estimated to have a most recent common ancestor around 5 kya and to have entered Australia from India [5]. Here, we sequence 13 Aboriginal Australian Y chromosomes to re-investigate their divergence times from Y chromosomes in other continents, including a comparison of Aboriginal Australian and South Asian haplogroup C chromosomes. We find divergence times dating back to ∼50 kya, thus excluding the Y chromosome as providing evidence for recent gene flow from India into Australia. Copyright © 2016 The Authors. Published by Elsevier Ltd.. All rights reserved.

Figure 1. Pubmed search results

Figure 2. Journal article abstract

**PROBLEM TO SOLVE:** I want to create a database of all the journal articles based on a search term. I don't want to do this manually!

**SOLUTION TO PROBLEM:** Entrez Programming Utilities allows you to extract all this information into data formats (then convert to SAS datasets)

#### Entrez Programming Utilities (APIs)

Entrez is the information retrieval system that gives you direct access to the 40 databases with over 1.3 billion records within the NCBI.

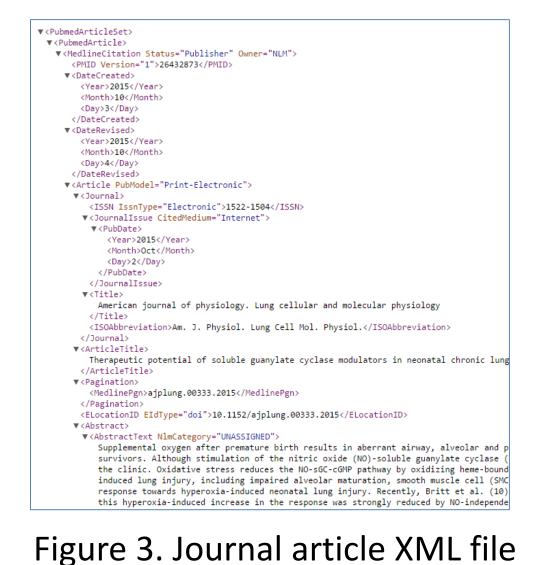
You can access these records by using the eight e-utilities (einfo, esearch, summary, efetch, elink, einfo, epost and egquery) - the NCBI application programming interfaces (APIs).

Base URL: <a href="http://eutils.ncbi.nlm.nih.gov/entrez/eutils/">http://eutils.ncbi.nlm.nih.gov/entrez/eutils/</a>

elnfo: Provides information about each database http://eutils.ncbi.nlm.nih.gov/entrez/eutils/einfo.fcgi?db=pubmed

**eSearch:** Provides a list of the UIDs (e.g. IDs for records in a particular database) for a search term http://eutils.ncbi.nlm.nih.gov/entrez/eutils/esearch.fcgi?db=pubmed&term=asthma

**eFetch:** Provides formatted output for a list of UIDs (for PUBMED it will be PMIDs). This example we will fetch the information for the first PMID listed in the XML that was generated. http://eutils.ncbi.nlm.nih.gov/entrez/eutils/efetch.fcgi?db=pubmed&id=26432873&retmode=xml



Mapper

Use the API to search journal articles

- **Extract the XML files using SAS PROC HTTP**
- Map the XML file to dataset using SAS XML

Introduction
Methods - 1
Methods - 2

Results & Conclusion

Craig Hansen, PhD

South Australian Health and Medical Research Institute



### 1. Run eSearch to get max # of records

```
/** SET UP MACRO VARIABLES **/
* - XML file to save;
%LET FILE = C:\SAS\Global Forum 2016\eSearchHistory.xml;
* - Search term URL;
%LET URL = http://eutils.ncbi.nlm.nih.gov/entrez/eutils/esearch.fcgi?
db=pubmed%nrstr(&term)=aboriginal[TIAB]%nrstr(&RETMAX)=1;
/** RUN eSearch TO GET THE MAXIMUM NUMBER OF RECORDS TO RETURN **/
* - Proc HTTP;
FILENAME test1 "&FILE." encoding="UTF-8";
PROC HTTP
        OUT=test1
                                      Need to create an XML map in
        URL="&URL."
                                         SAS XML mapper first
        METHOD="get";
RUN;
* - Map the XML file;
FILENAME Maxsrch 'C:\SAS\Global Forum 2016\eSearchMax.xml';
FILENAME MyMap 'C:\SAS\Global Forum 2016\PubmedIDs.map';
         Maxsrch xmlv2 xmlmap=MyMap ACCESS=READONLY;
LIBNAME
        * - Put the count variable into a macro variable;
PROC SQL NOPRINT;
SELECT DISTINCT
        PUT (Count, BEST12.), QueryTranslation
        INTO :MYCOUNT TRIMMED, :QUERY TRIMMED
FROM MaxSrch.eSearchResult;
                              Get the max# records from the eSearchResults table
QUIT;
                              and create macro variables for the next step
```

### 2. Run eSearch - "usehistory=y" parameter

```
* - Run eSearch with the "&usehistory=y" paremeter,
        this will save all the PMIDs in the ENTREZ database for later use;
%LET FILE = C:\SAS\Global Forum 2016\eSearchHistory.xml;
%LET URL = http://eutils.ncbi.nlm.nih.gov/entrez/eutils/esearch.fcgi?
db=pubmed%nrstr(&term)=aboriginal[TIAB]%nrstr(&retmax)=&MYCOUNT.%nrstr(&usehistory)=y;
FILENAME test1 "&FILE." encoding="UTF-8";
PROC HTTP
        OUT=test1
        URL="&URL."
       METHOD="get";
RUN;
* - Map the XML file;
                        'C:\SAS\Global Forum 2016\eSearchHistory.xml';
FILENAME eSearch
FILENAME
                        'C:\SAS\Global Forum 2016\eSearchHistory.map';
         MyMap
                        xmlv2 xmlmap=MyMap ACCESS=READONLY;
LIBNAME
         eSearch
* - Get the "&query key" and "&WebEnv" paremeters;
PROC SQL NOPRINT;
SELECT PUT (querykey, BEST12.), WebEnv INTO :QK TRIMMED, :WEBENVKEY TRIMMED
FROM eSearch.eSearchResult;
                             Get the "querykey" and "WebEvn" and create macro variables
QUIT;
                             to use in the next step
```

<sup>\*\*</sup> The step above is optional – however it is best to use this when you have a large output of articles \*\*

<sup>\*\*</sup> Using the "usehistory=y" saves the results (e.g. PMIDs) in the Entrez server ready for extraction by running a query with the QueryKey and WebEnv values given in the eSearchResults table \*\*

Introduction Methods - 1

Methods - 2

Results & Conclusion

Craig Hansen, PhD

South Australian Health and Medical Research Institute



#### 3. Run eFetch to get the final results

```
* - Run eFetch with the Query Key and WebEnv paremeters;
%LET FILE = C:\SAS\Global Forum 2016\eSearchHistoryResults.xml;
%LET URL = http://eutils.ncbi.nlm.nih.gov/entrez/eutils/efetch.fcgi?
db=pubmed%nrstr(&query key)=&QK.%nrstr(&WebEnv)=&WEBENVKEY.%nrstr(&usehist
ory) = y%nrstr(&retmode) = xml;
FILENAME test1 "&FILE." encoding="UTF-8";
PROC HTTP
       OUT=test1
        URL="&URL."
       METHOD="get";
RUN;
          eFetch 'C:\SAS\Global Forum 2016\eSearchHistoryResults.xml';
                       'C:\SAS\Global Forum 2016\eFetch.map';
FILENAME
          MyMap
                       xmlv2 xmlmap=MyMap ACCESS=READONLY;
LIBNAME
          eFetch
```

#### 4. Create final tables from XML

```
PROC SQL;

CREATE TABLE eFetch_AUTHORS AS
SELECT DISTINCT

A.PMID,
B.Author_ORDINAL,
B.AuthorList_ORDINAL,
B.LastName,
B.ForeName,
B.ForeName,
B.Initials

FROM eFetch.PMID AS A, eFetch.Author AS B
WHERE A.MedlineCitation_ORDINAL=B.AuthorList_ORDINAL
ORDER BY PMID, AuthorList_ORDINAL;
QUIT;
```

#### 4. (continued) Create final tables from XML

```
* - Articles;
                                                             Create 'Articles' dataset
PROC SQL;
CREATE TABLE eFetch ARTICLE AS
SELECT DISTINCT
        A.MedlineCitation Status,
        A.MedlineCitation Owner,
        B.PMID,
        C.YEAR AS CREATED YEAR,
        C.MONTH AS CREATED MONTH,
        C.DAY AS CREATED DAY,
.....More code here
FROM
                eFetch.MedlineCitation AS A
                eFetch.PMID AS B ON A.PubmedArticle ORDINAL=B.MedlineCitation ORDINAL
LEFT JOIN
.....More code here
                eFetch.PubmedData AS M ON
LEFT JOIN
B.MedlineCitation ORDINAL=M.PubmedData ORDINAL
....etc
QUIT;
                                                            Create 'Abstract' dataset
Abstract;
.....Use similar SQL to create ABSTRACT table
                                                          Create 'Affiliations' dataset

    Author Affiliations;

.....Use similar SQL to create AUTHOR AFFILIATIONS table
```

Introduction
Methods - 1
Methods - 2
Results & Conclusion

Craig Hansen, PhD
South Australian Health and Medical Research Institute



#### **RESULTS: SAS Datasets**

The main SAS datasets generated from the XML file and SQL joins are:

- ARTICLE
- AUTHOR
- AUTHOR AFFILIATION
- ABSTRACT

Relational database design with lots of information

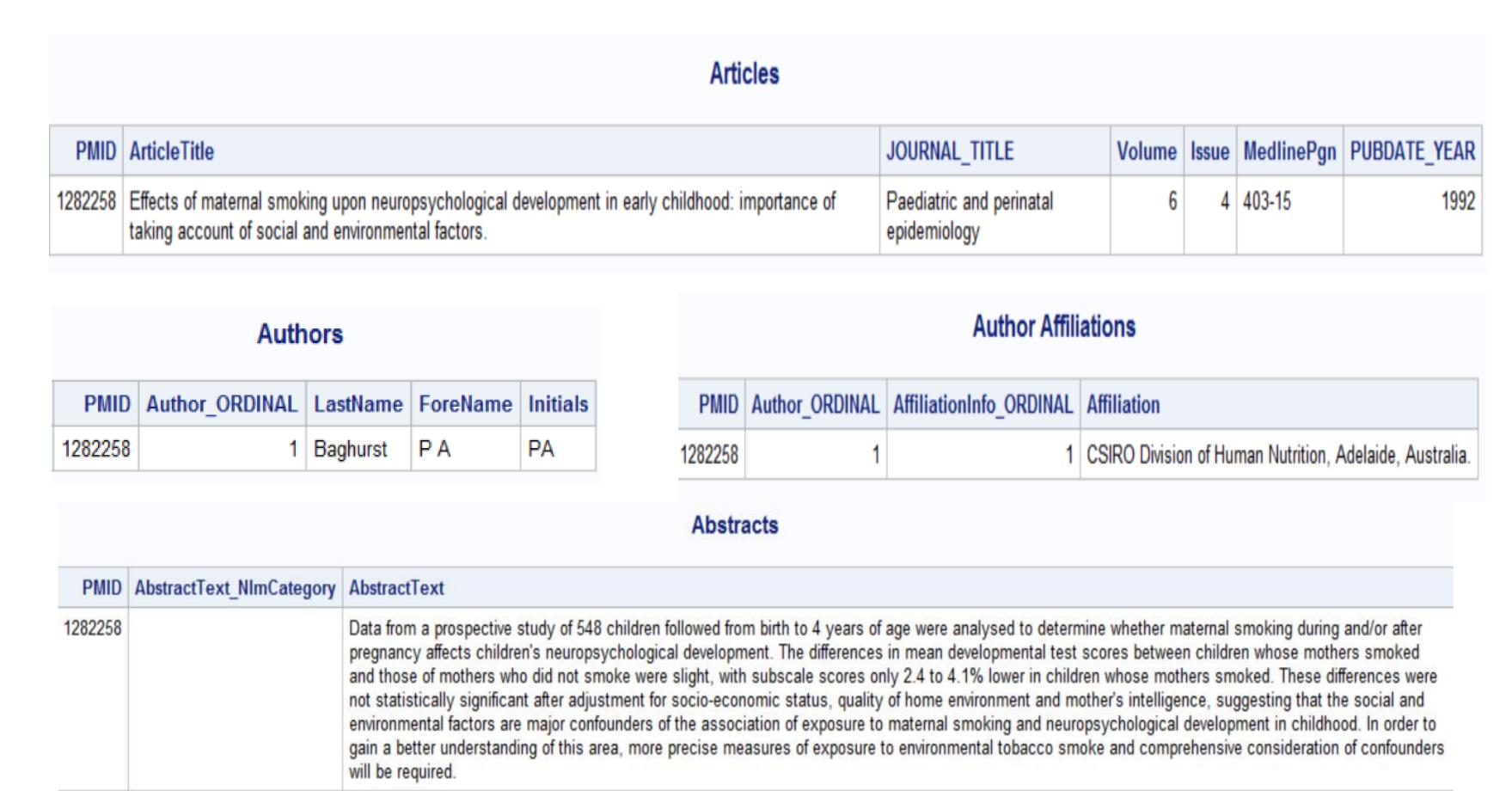


Figure 4. Example SAS datasets generated – these can be linked via the PMID field

#### CONCLUSION

#### **PROS**

- Using the APIs with PROC HTTP is a very efficient method to get data from PubMed
- Create PubMed datasets automatically based on different searches
- Extract large amounts of data in one go (e.g. no looping required for limits)
- Can create macros to perform multiple searches and append results

#### **CONS**

- Documentation on the Entrez Programming Utilities could be improved with more information on different parameters used in the URL
- There are many tables generated by the XML mapper and it takes a while to workout the linkages
- No bibiolmetric data in PubMed (e.g. times a journal article is cited, and by who etc)
- Truncation of data fields without knowing the length

#### REFERENCES AND READING

Introduction to E-Utilities. <a href="http://www.ncbi.nlm.nih.gov/books/NBK25501/">http://www.ncbi.nlm.nih.gov/books/NBK25501/</a>
E-Utilities Introduction (YouTube). <a href="https://www.youtube.com/watch?v=BCG-M5k-gvE">https://www.youtube.com/watch?v=BCG-M5k-gvE</a>
SAS PROC HTTP Documentation.

http://support.sas.com/documentation/cdl/en/proc/61895/HTML/default/viewer.htm#a003286672.htm

McNeill, B. (2013). The Ins and Outs of Web-Based Data with SAS., SAS Institute Inc., Cary, NC

https://support.sas.com/resources/papers/proceedings13/024-2013.pdf

Litton, I & Ottesen, R. (2013). %GrabTweet: A SAS® Macro to Read JSON Formatted Tweets.

http://www.lexjansen.com/wuss/2013/103 Paper.pdf

Martell, C. (2008). SAS® XML Mapper to the Rescue.

http://www2.sas.com/proceedings/forum2008/099-2008.pdf

MENU (click on heading)
Introduction
Methods - 1
Methods - 2
Results & Conclusion



# SAS® GLOBAL FORUM 2016

IMAGINE. CREATE. INNOVATE.

#### THANK YOU FOR YOUR INTEREST

Craig Hansen, PhD
South Australian Health and Medical Research Institute
Craig.Hansen@sahmri.com

LAS VEGAS | APRIL 18-21 #SASGF