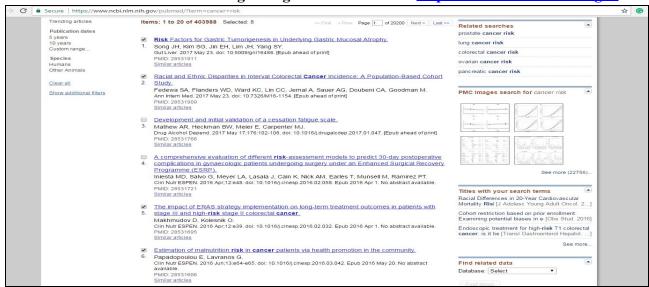
A tutorial outline on PubMed.MineR package

First I downloaded several data regarding Cancer risk from https://www.ncbi.nlm.nih.gov.



Then I opened the Rstudio and installed the pubmed.mineR package. After installation, I loaded the pubmed.mineR library.

```
# loading pubmed.mineR package
library(pubmed.mineR)
```

And the output:

```
> library(pubmed.mineR)
> |
```

At first, I need to read the abstracts in R:

```
# To read abstracts
readabs("cancer_text.txt")
```

```
| Section | Sect
```

To read the abstracts in a variable:

```
# To read the abstracts in a variable
cancerabs <- readabs("cancer_text.txt")
diabetesabs <- readabs("diabetes_text.txt")</pre>
```

The output:

```
> cancerabs <- readabs("cancer_text.txt")
> diabetesabs <- readabs("diabetes_text.txt")
> |
```

There were many abstracts on the downloaded file. I needed some abstracts for a specific year. For this:

```
# To retrive the abstracts for a year with the specific terms
currentabs_fn("2017", "cancer", cancerabs)
```

```
> currentabs_fn("2017", "cancer", cancerabs)
[1] "5 abstracts cancer"
An object of class "Abstracts"
Slot "Journal":
[1] "2. Ann Intern Med. 2017 May 23. doi: 10.7326/M16-1154. [Epub ahead of print]"
[2] "5. Int J Qual Health Care. 2017 May 20. doi: 10.1093/cid/cix475. [Epub ahead of print]"
[3] "6. Clin Infect Dis. 2017 May 20. doi: 10.1093/carcin/bgx046. [Epub ahead of print]"
[4] "7. Carcinogenesis. 2017 May 20. doi: 10.1093/carcin/bgx046. [Epub ahead of print]"
[5] "8. J Clin oncol. 2017 May 22:ICO2016716902. doi: 10.1200/JCO.2016.71.6902. [Epub"
Slot "Abstract":
[1] "Racial and Ethnic Disparities in Interval Colorectal Cancer Incidence: A Population-Based Cohort Study. Fedewa SA(1), Flanders Wp(1), Ward Kc(1), Lin Cc(1), Jemal A(1), Sauer AG(1), Doubeni Ca(1), Goodman M(1). Author information: (1)From Surveillance and Health Services Research, American Cancer Society, and Emory University, Atlanta, Georgia, and Perelman School of Medicine, University of Pennsylvania, Philadelphia, Pennsylvania. Background: Interval Colorectal cancer (CRC) a Ccounts for 3% to 8% of all cases of CRC in the United States. Data on interval CRC by race/ethnicity and whether this potential variation is accounted for by differences in the quality of colonoscopy, as measured by physicians' polyp detection rate (PDR). Design: Population-based cohort study. Setting: Medicare program. Participants: Patients aged 66 to 75 years who received colonoscopy betw... <truckets.</td>

[2] "of print] A diabetes pay-for-performance program and the competing causes of death among cancer survivors with type 2 diabetes in Taiwan. Hsieh HM(1,)(2,)(3), Chiu HC(4,)(5), Lin YT(6), Shin SJ(7,)(8). Author information: (1)Department of Public Health, Kaohsiung Medical University Hospital, 100 Shih-Chuan 1st Road, Kaohsiung 80708, Taiwan. (5)Department of Health. Roadshiung Medical University Hospital, 100 Shih-Chuan 1st Road, Kaohsiung 80708, Taiwan. (6)Department of Health (1)Division of Family Medicine, Kaohsiung Medical University Hospit
```

I need the word which mentioned most of the time in the abstracts. So, I used the word atomizations code:

```
# To automize the words word_atomizations(cancerabs)
```

The output:

	1	
> word_atomizations(cancerabs)		
	words	Freq
195	cancer	31
641	were	21
532	risk	19
638	was	16
41	1	14
233	crc	14
465	patients	12
582	survivors	11
14	(hr	10
477	persons	10
58	2	
145	age	9 9 9 9 9 8 8
372	interval	9
422	mortality	9
651	years	9
159	among	8
248	diabetes	8
342	hpv	8
402	math	8
402	matri	0

Then I felt that it will be better to find abstracts with gene:

```
# To automize with gene
gene_atomization(cancerabs)
```

```
gene_atomization(cancerabs)
     Gene_symbol
                    Genes
                                                                          Freq
                 "ES cell expressed Ras"
     "ERAS"
                                                                           "1"
[1,]
                                                                          "1"
    "HR"
                 "hair growth associated"
[2,]
[3,] "IRF5"
                 "interferon regulatory factor 5"
                                                                          "1"
[4,] "KRAS"
                 "v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
                                                                          "1"
[5,] "TP53"
                                                                          "1"
                 "tumor protein p53"
>
```

To know more about the downloaded abstracts, I used some codes to find out frequency of any specific term mentioned in the abstracts:

```
# To findout a given term in each abstract
tc = c("risk", "survivor", "patients")
tdm_for_lsa(cancerabs, tc)
```

The output:

```
> tdm_for_lsa(cancerabs, tc)
         [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]
risk
                 4
                       1
                            1
                                 3
                                       1
                                            1
                                                10
survivor
            0
                 0
                       0
                            0
                                  9
                                       0
                                            0
                                                 3
patients
            2
                       1
                            1
                                       0
                                            5
                                                  0
```

I already got the list of genes which mentioned in the abstracts. Now, I thought that I should know about those lines which contained these genes. Then, I used codes like this:

```
# Getting sentences for a genes (ERAS)
get_gene_sentences("ERAS", cancerabs, "ERAS_sentence.txt")
```

The output :

As above, I also got some sentences with a specific term like cancer, risk, patient, and survivor:

```
# Getting sentences for a query term (cancer)
contextSearch(cancerabs, "cancer")
```

The output:

```
Untitled1* × tex cancer.tex ×
                                                                                                                                                                                                                                                                                     -
 No TeX installation detected. Please install TeX before compiling.
      1 \documentclass[11pt]{article}
                title { cancer search}
             \begin{document}
             \maketitle
             %\section{}
            %\subsection{}
             Results of context search
      8 \newline [ 1 ] Racial and Ethnic Disparities in Interval Colorectal Cancer Incidence: A Population
              -Based Cohort Study. Fedewa SA(1), Flanders WD(1), Ward KC(1), Lin CC(1), Jemal A(1), Sauer AG(1), Doubeni CA(1), Goodman M(1). Author information: (1)From Surveillance and Health Services Research,
              American Cancer Society, and Emory University, Atlanta, Georgia, and Perelman School of Medicine,
              University of Pennsylvania, Philadelphia, Pennsylvania. Background: Interval colorectal cancer } (CRC) accounts for 3% to 8% of all cases of CRC in the United States.

| (CRC) accounts for 3% to 8% of all cases of CRC in the United States.
| (CRC) accounts for 3% to 8% of all cases of CRC in the United States.
             // (RCC) In accounts for interval
// (Newline [ 2 ] Compared with white persons, black persons had significantly higher risk for interval
// (CRC (HR, 1.31 [95% CI, 1.13 to 1.51]); the disparity was more pronounced for \textbf { cancer } of
// the rectum (HR, 1.70 [CI, 1.25 to 2.31]) and distal colon (HR, 1.45 [CI, 1.00 to 2.11]) than for cancer
// of the proximal colon (HR, 1.17 [CI, 0.96 to 1.42]).
                                                     ]
                                                               Conclusion: Among elderly Medicare enrollees, the risk for interval CRC was higher in in white persons; the difference was more pronounced for \textbf { cancer } of
              black persons than in white persons; the difference was more pronounced for
              the distal colon and rectum and for physicians with higher PDRs.
             \newline [ 4 ] Apr 1. The impact of ERAS strategy implementation on long-term treatment outcomes in patients with stage III and high-risk stage II colorectal \textbf { cancer } . Makhmudov D(1), Kolesnik O(1). Author information: (1)Abdominal Cavity and Retroperitoneal Tumors, National Cancer Institute of Ukraine, Kiev, Ukraine. DOI: 10.1016/j.clnesp.2016.02.032 \newline [ 5 ] 2016 May 20. Estimation of malnutrition risk in \textbf { cancer } patients via health promotion in the community. Papadopoulou E(1), Lavranos G(1). Author information: (1)European University, Nicosia, Cyprus. DOI: 10.1016/j.clnesp.2016.03.042 \newline [ 6 ] of print] A diabetes pay-for-performance program and the competing causes of death among \textbf { cancer } survivors with type 2 diabetes in Taiwan. Hsieh HM(1,)(2,)(3), Chiu HC(4,)(5), Lin YT(6), Shin SJ(7,)(8). Author information: (1)Department of Public Health, Kaohsiung Medical University, 100 Shih-Chuan 1st Road, Kaohsiung 80708, Taiwan. (2)Department of Medical Research, Kaohsiung Medical University Hospital, 100 Shih-Chuan 1st Road, Kaohsiung 80708, Taiwan. (3)Department of Community Medicine, Kaohsiung Medical University Hospital, 100 Shih-Chuan 1st Road, Kaohsiung 80708, Taiwan. (4)Research Education and Epidemiology Center, Changhua Christian Hospital, 135 Nan-Hsiao St.,
                                           4 ] Apr 1. The impact of ERAS strategy implementation on long-term treatment outcomes in
             Taiwan. (4)Research Education and Epidemiology Center, Changhua Christian Hospital, 135 Nan-Hsiao St., Changhua City 50006, Taiwan. (5)Department of Healthcare Administration and Medical Informatics,
                                                                                                                                                                                                                                                                                    TeX $
```

The downloaded file contained many abstracts of several years. To know about their year of publication:

```
# Searching abstracts yearwise
Yearwise(cancerabs, c("2016", "2017"))
```

The output:

```
> Yearwise(cancerabs, c("2016", "2017"))
[1] "3 abstracts 2016" "3 abstracts 2017"
```

I also found the number of abstracts for a specific gene:

```
# Searching abstracts genewise
Genewise(cancerabs, "ERAS")
```

```
> Genewise(cancerabs, "ERAS")
[1] "1 abstracts ERAS"
```

Some of the abstracts were short and some were very long. So, it was time consuming and hard to learn about their information such as diseases, chemical, genes etc. To get a descriptive result on it, I used the PMID number (publication number) with the code named publication:

```
# Getting information of PMID about Gene, Chemical, Mutation, Species and Diseases pubtator_function(28531909)
```

The output:

```
> pubtator_function(28531909)
$Genes
NULL
$Diseases
[1] "Colorectal Cancer"
[3] "CRC"
[5] "cancer"
                                                "colorectal cancer"
                                                 "cancer of the rectum"
                                                "cancer of the distal colon and rectum"
[7] "Cancer"
$Mutations
NULL
$Chemicals
NULL
$Species
[1] "patients"
                     "Participants" "Patients"
                                                      "person"
                                                                       "persons"
$PMID
[1] 28531909
```

After all of these, a question came to my mind that if I get some abstracts later, then I need to add them with previous one. Then I will be able to analyze them together. For this:

```
# Combining several abstracts in a variable
combo = combineabs(diabetesabs, cancerabs)
```

The output:

```
> combo = combineabs(diabetesabs, cancerabs)
[1] "9 combined abstracts for above terms"
> |
```

When I need to remove some abstracts with a specific term:

```
# Removing abstracts for a specific term
removeabs(cancerabs, "cancer", TRUE)
```

```
> removeabs(cancerabs, "cancer", TRUE)
[1] "7 abstracts removed abstracts for term cancer"
An object of class "Abstracts"
Slot "Journal":
[1] "1. Gut Liver. 2017 May 23. doi: 10.5009/gnl16488. [Epub ahead of print]"

Slot "Abstract":
[1] "Risk Factors for Gastric Tumorigenesis in Underlying Gastric Mucosal Atrophy. Song JH(1), Kim SG(2), Jin EH(1), Lim JH(1), Yang SY(1). Author information: (1)Department of Internal Medicine, Healthcare Research Inst itute, Seoul National University Hospital Healthcare System Gangnam Center, Seoul, Korea. (2)Department of Internal Medicine and Liver Research Institute, Seoul National University College of Medicine, Seoul, Korea. Backgro und/Aims: Atrophic gastritis is considered a premalignant lesion. We aimed to evaluate the risk factors for gast ric tumorigenesis in underlying mucosal atrophy. Methods: A total of 10,185 subjects who underwent upper gastrointestinal endoscopy between 2003 and 2004 were enrolled in this retrospective cohort study. Follow-up endoscopy was performed between 2005 and 2014. Atrophic gastritis and intestinal metaplasia were assessed by endoscopy using the Kimura-Takemoto classification. Helicobacter pylori infection was evaluated based on serum immuno... <tru ncated>
Slot "PMID":
[1] 28531911
```

There are many codes to analyze the abstracts with the pubmed.mineR package. But, they are mostly similar to each other like the code of *sentence_token* and *context_search* provides similar result. So, I only showed the use of anyone from them.