TopicAnalysis

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Topic analysis

The goal in this task is to create an algorithm that classifies abstracts into a topic. Indeed, your goal is to group abstracts based on their semantic similarity. Given that this is an unsupervised learning task we can set the number of topics at convenience but not the type of topics.

Solution description

This is a NLP topic modelling task. For this case, most of the libraries are written in R and even if I have some personal bias towards Python. I prefer to work with R in this case. The process is summarized in the following

1. Data extraction

2. Data frame creation

3. Natural language processing functions

4. Topic analysis

5. Conclusion

Data Extraction

As standard procedure, the first thing to do is to import the libraries

```
library(xml2)
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse
1.3.1 --
```

```
## v ggplot2 3.3.5     v purrr   0.3.4
## v tibble  3.1.3     v dplyr   1.0.7
## v tidyr   1.1.3     v stringr 1.4.0
## v readr   2.0.0     v forcats 0.5.1
```

```
## -- Conflicts ------------------------------------------
tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(tidyverse) # general utility & workflow functions
library(tidytext) # tidy implimentation of NLP methods
library(topicmodels) # for LDA topic modelling
library(tm) # general text mining functions, making document term matrixes
```

```
## Loading required package: NLP
```

```
##
## Attaching package: 'NLP'
```

```
## The following object is masked from 'package:ggplot2':
##
##     annotate
```

```
library(SnowballC) # for stemming
library(tm)
library(tmap)
```

The first thing done was to get an abstract from a file

```
## [1] "This is the abstract"
```

```
## [1] "Head and heart development are closely intertwined during embryonic
development in vertebrates. They share molecular regulatory mechanism as well
as some progenitor cell populations. Both head and heart, are made from a
multitude of cells, which include mesodermal cells that form musculature and
neural crest cells which form connective tissue. Mesodermal and neural crest
cells are also important for the development of cartilages and bones in head
and neck and for proper septation of the heart. The identity of cells that
constitute these tissues is specified very early during embryogenesis via a
specific set of genes (specifiers), then follow their trajectory to become
muscle, connective tissue, etc.<br/>One early specifier, gastrulation-brain-
homeobox 2 (Gbx2), is essential for the migration (movement) and survival of
neural crest cells. Neural crest cells and mesodermal cells interact during
their migration to form head and heart structures. While mesodermal cells are
not directly effected by change in Gbx2 expression, neural crest cells are
effected and will alter the communication with mesodermal cells, leading to
changes in mesoderm derived structures (e.g., muscles). This project aims to
understand how Gbx2 guides neural crest development, and how changes in Gbx2
expression influences head (muscle, cartilage, bone, cranial nerve) and heart
development. <br/>Traditionally the fields of comparative, developmental and
evolutionary biology have been unsuccessful in recruiting students and
scientists of diverse backrounds. This project will promote collaborations
between researchers from non-traditional backgrounds in these areas of
biology and historically black universities, Howard University and University
of the District of Columbia.  This award is funded by the NSF Excellence in
Research Program.<br/><br/><br/>Technical paragraph<br/>Cranial neural crest
cells (CNCCs) are involved in the development of cranial ganglia, cranial
nerves, cranium, connective tissue of head muscles, heart septation,
pharyngeal arch artery development, etc. The gastrulation-brain-homeobox
(Gbx) transcription factor family member, Gbx2, regulates diverse
```

```
developmental processes, including anteroposterior patterning within the
anterior hindbrain and migration and survival of CNCCs. Since CNCCs are
involved in many different developmental processes during head and heart
development, this project aims to analyze target genes under direct control
of Gbx2, that regulate migration and survival of CNCCs in homozygous Gbx2neo
embryos. Furthermore, this project will include analyses of the impact of
changes of Gbx2 expression on the morphogenesis of the neural system, and
craniofacial and cardiovascular structures. The latter part is of
significance as neural crest cells influence the development and
differentiation of surrounding tissues and vice versa. During head and haert
development the interaction of CNCCs and mesoderm is of particular interest
for this project because the mesodermal progenitor cells for most of the head
and heart musculature derives from a common progenitor field, called the
cardiopharyngeal field. In case Gbx2 is somehow involved in the gene
regulatory network underlying the differentiation of that mesodermal
progenitor field, directly via altering the transcription of genes or
indirectly via altering the neural crest - mesodermal interaction during
development, this project will lead to insights into mechanisms regulating
head and heart development as well as cranial ganglia and nerve
development.<br/><br/>This award reflects NSF's statutory mission and has
been deemed worthy of support through evaluation using the Foundation's
intellectual merit and broader impacts review criteria."
```

Now that we know that we can get an abstract we proceed to the dataframe creation

Data frame creation

Let's ge all the xml files from the folder and put it into a variable

```
filenames <- Sys.glob("D:/Globant/Task1/data/*.xml")
```

The next thing to do is to load everything into a dataframe. This dataframe will have the address of the file and teh abstract. Since there are some files that have no abstract, they will have a value that will help to remove them later. This code chunk takes a while to run

The next process is to clean the dataset from the elements that have no abstract. Since the files and the abstract have the same text if there's no abstract, we can remove in a simple way with the following code

Now that the DataFrame is cleared, we need to pre process the data. We have to remove stopwords, and apply different natural language processing algorithms to get the important words that will allow us to extract the topics. In this case, I added a couple of stop words from the original code, since this is an abstract compilation, it makes sense to remove the word research, project and students.

Compared to the cleared data frame, this one looks not readable for the human but for the machine is clear and it allows to get the topic

Natural language processing functions

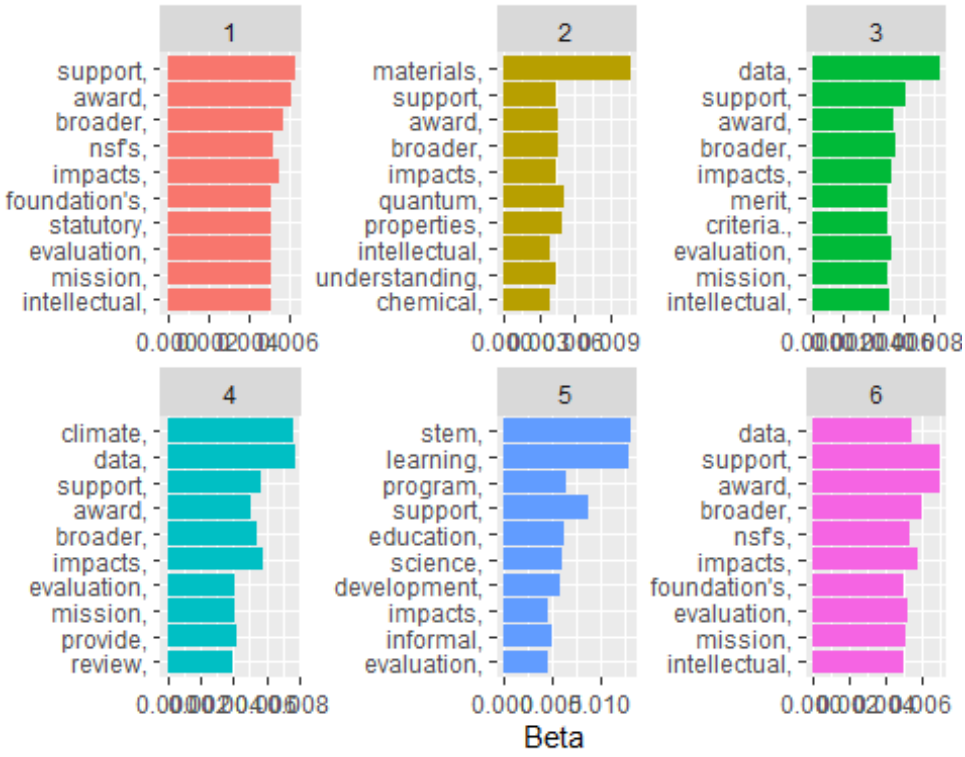
In this function the corpus is created and with the Latent Dirichlet Allocation (LDA), the topics can be modelled.

```
top_terms_by_topic_LDA <- function(input_text, # should be a columm from a
dataframe
                                   plot = T, # return a plot? TRUE by defult
                                   number_of_topics = 4) # number of topics
(4 by default)
{
    # create a corpus (type of object expected by tm) and document term
matrix
    Corpus <- Corpus(VectorSource(input_text)) # make a corpus object
    DTM <- DocumentTermMatrix(Corpus) # get the count of words/document

    # remove any empty rows in our document term matrix (if there are any
    # we'll get an error when we try to run our LDA)
    unique_indexes <- unique(DTM$i) # get the index of each unique value
    DTM <- DTM[unique_indexes,] # get a subset of only those indexes

    # preform LDA & get the words/topic in a tidy text format
    lda <- LDA(DTM, k = number_of_topics, control = list(seed = 1234))
    topics <- tidy(lda, matrix = "beta")

    # get the top ten terms for each topic
    top_terms <- topics  %>% # take the topics data frame and..
      group_by(topic) %>% # treat each topic as a different group
      top_n(10, beta) %>% # get the top 10 most informative words
      ungroup() %>% # ungroup
      arrange(topic, -beta) # arrange words in descending informativeness

    # if the user asks for a plot (TRUE by default)
    if(plot == T){
        # plot the top ten terms for each topic in order
        top_terms %>% # take the top terms
          mutate(term = reorder(term, beta)) %>% # sort terms by beta value
          ggplot(aes(term, beta, fill = factor(topic))) + # plot beta by
theme
          geom_col(show.legend = FALSE) + # as a bar plot
          facet_wrap(~ topic, scales = "free") + # which each topic in a
seperate plot
          labs(x = NULL, y = "Beta") + # no x label, change y label
          coord_flip() # turn bars sideways
    }else{
        # if the user does not request a plot
        # return a list of sorted terms instead
        return(top_terms)
    }
}
```

Topic analysis

Now that we have the algorithm ready, let's model some topics. We're going to start with 6 topics

```
top_terms_by_topic_LDA(cleaned_documents$terms, number_of_topics = 6)
```



In this case we can see that the main topic is related to an award from the Naturla Science Foundation. Another important topic is related to the understanding of quantum, probably computing. The third topic is in the evaluation. The fift topic is interesting because it is related to the climate change. While the 6th topic is the education

Conclusion

NLP provides very useful tools to understand a big group of datasets and have an idea of it. Manually reading the over 2000 abstracts is a tedious tasks while NLP in less time can give an insight

Aknowledgments

Special thanks for Rachael Tatman for her NLP code that was the reference
https://www.kaggle.com/rtatman/nlp-in-r-topic-modelling/data?select=deceptive-opinion.csv