```r
knitr::opts_chunk$set(echo = TRUE)
library(readr)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
library(tidyr)
library(ggplot2)
library(scales)
```

```
##
## Attaching package: 'scales'

## The following object is masked from 'package:readr':
##
##     col_factor
```

```r
library(tidytext)
library(textstem)
```

```
## Loading required package: koRpus.lang.en

## Loading required package: koRpus

## Loading required package: sylly

## For information on available language packages for 'koRpus', run
##
##   available.koRpus.lang()
##
## and see ?install.koRpus.lang()

##
## Attaching package: 'koRpus'

## The following object is masked from 'package:readr':
##
##     tokenize
```

```r
library(clinspacy)
```

```
## Welcome to clinspacy.

## By default, this package will install and use miniconda and create a "clinspacy" conda environment.

## If you want to override this behavior, use clinspacy_init(miniconda = FALSE) and specify an alternat
```

```r
library(topicmodels)
library('reshape2')
```

```
##
## Attaching package: 'reshape2'
```

```
## The following object is masked from 'package:tidyr':
##
##     smiths
```

```
library(stringr)
```

This practical is based on exploratory data analysis, named entity recognition, and topic modelling of unstructured medical note free-text data derived from electronic medical records (EMR). Real EMR data is very difficult to access without a specific need/request so this data set is derived from medical transcription data instead. I'll also caveat that the options of natural language processing (NLP) in R are far inferior to those available in Python.

First, install the packages in the setup block (`install.packages(c("readr", "dplyr", "tidyr", "ggplot2", "tidtext", "textstem", "clinspacy", "topicmodels", "reshape2"))`).

Note: To try and make it clearer which library certain functions are coming from clearer, I'll try to do explicit imports throughout this notebook.

Data Parsing

After that we can grab the dataset directly from the `clinspacy` library.

```
raw.data <- clinspacy::dataset_mtsamples()
dplyr::glimpse(raw.data)
```

```
## Rows: 4,999
## Columns: 6
## $ note_id           <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 1~
## $ description       <chr> "A 23-year-old white female presents with complaint ~
## $ medical_specialty <chr> "Allergy / Immunology", "Bariatrics", "Bariatrics", ~
## $ sample_name       <chr> "Allergic Rhinitis", "Laparoscopic Gastric Bypass Co~
## $ transcription     <chr> "SUBJECTIVE:,  This 23-year-old white female present~
## $ keywords          <chr> "allergy / immunology, allergic rhinitis, allergies,~
```

There is no explanation or data dictionary with this dataset, which is a surprisingly common and frustrating turn of events!

1 Using the output of dplyr's `glimpse` command (or rstudio's data viewer by clicking on `raw.data` in the Environment pane) provide a description of what you think each variable in this dataset contains.

note_id: The primary key of the data set.

description: A brief summary or description of the medical record.

medical_specialty: A categorical variable specifying the medical specialty associated with this record.

sample_name: The name or title of the medical record.

transcription: The full text of a medical record.

keywords: A list of keywords related to the record.

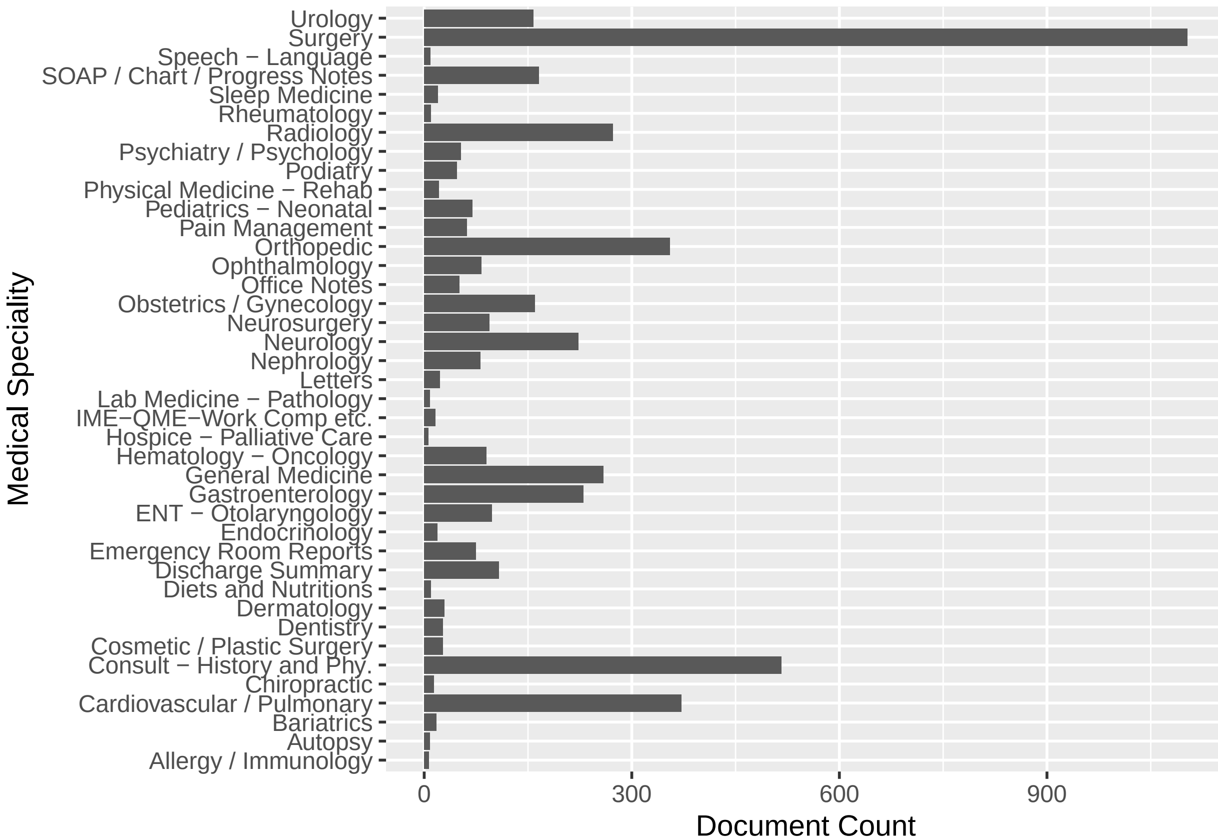
Let's see how many different medical specialties are featured in these notes:

```
raw.data %>% dplyr::select(medical_specialty) %>% dplyr::n_distinct()
```

```
## [1] 40
```

So, how many transcripts are there from each specialty:

```
ggplot2::ggplot(raw.data, ggplot2::aes(y=medical_specialty)) + ggplot2::geom_bar() + labs(x="Document C
```



Let's make our life easier and filter down to 3 specialties: a diagonstic/lab, a medical, and a surgical specialty

```
filtered.data <- raw.data %>% dplyr::filter(medical_specialty %in% c("Orthopedic", "Radiology", "Surgery
```

Text Processing

Let's now apply our standard pre-processing to the transcripts from these specialties.
We are going to use the `tidytext` package to tokenise the transcript free-text.
Let's remove stop words first. e.g., "the", "of", "to", and so forth. These are known as stop words and we can remove them relative easily using a list from `tidytext::stop_words` and `dplyr::anti_join()`

```
analysis.data <- filtered.data %>%
  unnest_tokens(word, transcription) %>%
  mutate(word = str_replace_all(word, "[^[:alnum:]]", "")) %>%
  filter(!str_detect(word, "[0-9]")) %>%
  anti_join(stop_words) %>%
  group_by(note_id) %>%
  summarise(transcription = paste(word, collapse = " ")) %>%
  left_join(select(filtered.data, -transcription), by = "note_id")
```

```
## Joining with `by = join_by(word)`
```

Now let's tokenize the `transcription` to words (unigram) By default this tokenises to words but other options include characters, n-grams, sentences, lines, paragraphs, or separation around a regular expression.

```
tokenized.data.unigram <- analysis.data %>% tidytext::unnest_tokens(word, transcription, to_lower=TRUE)
```

You can also do bi-grams

```
tokenized.data.bigram <- analysis.data %>% tidytext::unnest_tokens(bigram, transcription, token = "ngram
```

How many stop words are there in `tidytext::stop_words` from each lexicon?

```
tidytext::stop_words %>% dplyr::group_by(lexicon) %>% dplyr::distinct(word) %>% dplyr::summarise(n=dply
```

```
## # A tibble: 3 x 2
##   lexicon      n
##   <chr>    <int>
## 1 SMART      570
## 2 onix       398
## 3 snowball   174
```

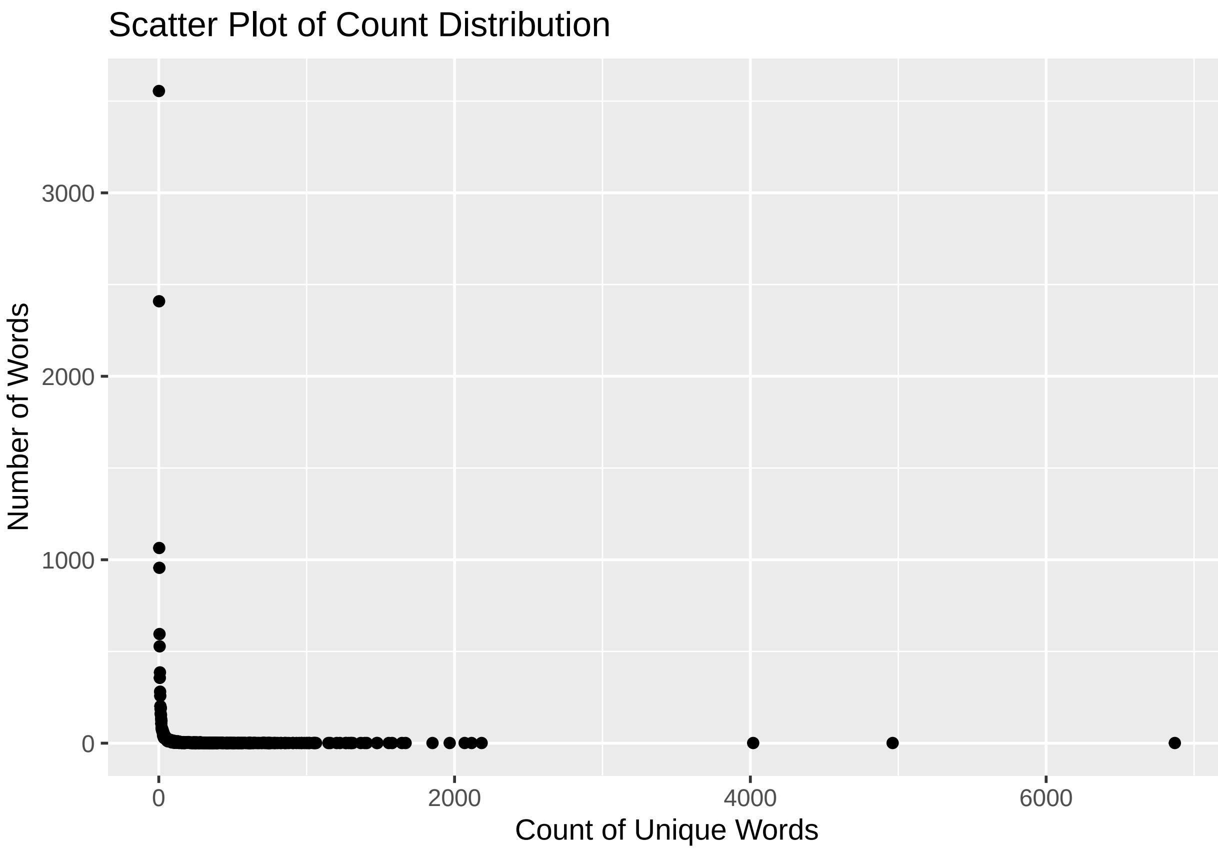
2 How many unique unigrams are there in the transcripts from each specialty:

```
unique_unigrams <- tokenized.data.unigram %>%
  group_by(medical_specialty) %>%
  summarise(unique_unigrams = n_distinct(word))

print(unique_unigrams)
```

```
## # A tibble: 3 x 2
##   medical_specialty unique_unigrams
##   <chr>                       <int>
## 1 Orthopedic                   7682
## 2 Radiology                    5935
## 3 Surgery                     11977
```

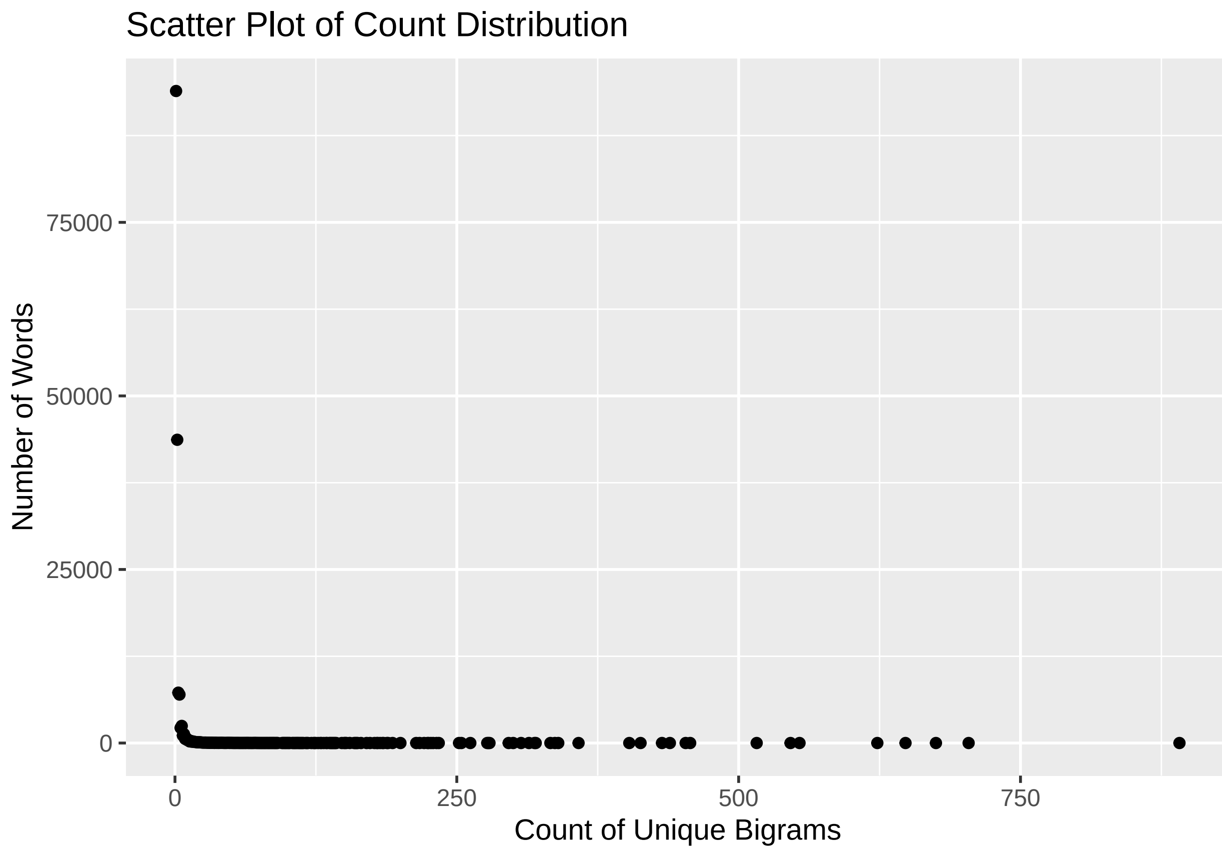
Let's plot some distribution of unigram tokens (words)

```
word_counts <- tokenized.data.unigram %>%
    group_by(word) %>%
    summarise(count = n()) %>%
    ungroup() %>%
    arrange(desc(count))

count_distribution <- word_counts %>%
  group_by(count) %>%
  summarise(num_words = n()) %>%
  ungroup()

 ggplot2::ggplot(count_distribution, aes(x = count, y = num_words)) +
  geom_point() +
  labs(title = "Scatter Plot of Count Distribution",
       x = "Count of Unique Words",
       y = "Number of Words")
```



Let's plot some distribution of bigram tokens (words)

```
word_counts <- tokenized.data.bigram %>%
    group_by(bigram) %>%
    summarise(count = n()) %>%
    ungroup() %>%
    arrange(desc(count))

count_distribution <- word_counts %>%
  group_by(count) %>%
  summarise(num_words = n()) %>%
  ungroup()

 ggplot2::ggplot(count_distribution, aes(x = count, y = num_words)) +
  geom_point() +
  labs(title = "Scatter Plot of Count Distribution",
       x = "Count of Unique Bigrams",
       y = "Number of Words")
```



3 How many unique bi-grams are there in each category without stop words and numbers?

```
unique_bigrams <- tokenized.data.bigram %>%
  group_by(medical_specialty) %>%
  summarise(unique_bigrams = n_distinct(bigram))

print(unique_bigrams)
```

```
## # A tibble: 3 x 2
##   medical_specialty unique_bigrams
##   <chr>                      <int>
## 1 Orthopedic                 55732
## 2 Radiology                  28297
## 3 Surgery                   130404
```

Sometimes we are interested in tokenising/segmenting things other than words like whole sentences or paragraphs.

4 How many unique sentences are there in each category? Hint: use `?tidytext::unnest_tokens` to see the documentation for this function.

```
tokenized.sentences <- analysis.data %>%
  unnest_tokens(sentence, transcription, token = "sentences")

unique_sentences <- tokenized.sentences %>%
  group_by(medical_specialty) %>%
  summarise(unique_sentences = n_distinct(sentence))

print(unique_sentences)
```

```
## # A tibble: 3 x 2
##   medical_specialty unique_sentences
##   <chr>                        <int>
## 1 Orthopedic                     354
## 2 Radiology                      273
## 3 Surgery                       1087
```

Now that we've tokenized to words and removed stop words, we can find the most commonly word used within each category:

```
tokenized.data.unigram %>%
  dplyr::group_by(medical_specialty) %>%
  dplyr::count(word, sort = TRUE) %>%
  dplyr::top_n(5)
```

```
## Selecting by n
```

```
## # A tibble: 15 x 3
## # Groups:   medical_specialty [3]
##    medical_specialty word           n
##    <chr>             <chr>      <int>
##  1 Surgery           patient     4855
##  2 Surgery           left        3263
##  3 Surgery           procedure   3243
##  4 Orthopedic        patient     1711
##  5 Surgery           anesthesia  1687
##  6 Surgery           incision    1641
##  7 Orthopedic        left         998
##  8 Orthopedic        pain         763
##  9 Radiology         left         701
## 10 Orthopedic        procedure    669
## 11 Radiology         normal       644
## 12 Orthopedic        lateral      472
## 13 Radiology         patient      304
## 14 Radiology         exam         302
## 15 Radiology         mild         242
```

We should lemmatize the tokenized words to prevent over counting of similar words before further analyses. Annoyingly, `tidytext` doesn't have a built-in lemmatizer.

5 Do you think a general purpose lemmatizer will work well for medical data? Why might it not?

I think general-purpose lemmatizers may not be suitable for medical data because they often cannot handle the specific terms, contexts, and polysemy in the medical domain.

Unfortunately, a specialised lemmatizer like in `clinspacy` is going to be very painful to install so we will just use a simple lemmatizer for now:

```
lemmatized.data <- tokenized.data.unigram %>% dplyr::mutate(lemma=textstem::lemmatize_words(word))
```

We can now calculate the frequency of lemmas within each specialty and note.

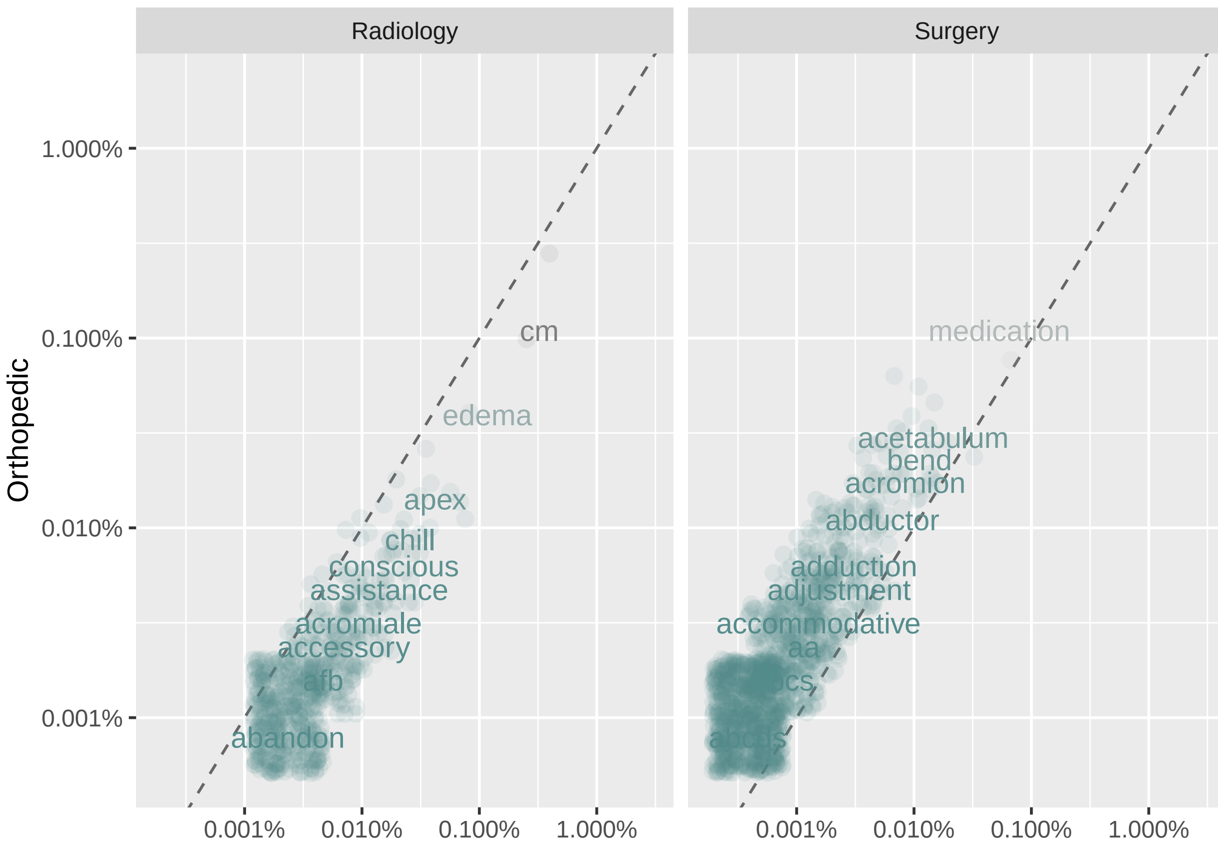
```
lemma.freq <- lemmatized.data %>%
  dplyr::count(medical_specialty, lemma) %>%
  dplyr::group_by(medical_specialty) %>%
  dplyr::mutate(proportion = n / sum(n)) %>%
  tidyr::pivot_wider(names_from = medical_specialty, values_from = proportion) %>%
  tidyr::pivot_longer(`Surgery`:`Radiology`,
               names_to = "medical_specialty", values_to = "proportion")
```

And plot the relative proportions

```r
ggplot2::ggplot(lemma.freq, ggplot2::aes(x=proportion,
                                          y=`Orthopedic`,
                                          color=abs(`Orthopedic` - proportion))) +
  ggplot2::geom_abline(color="gray40", lty=2) +
  ggplot2::geom_jitter(alpha=0.1, size=2.5, width=0.3, height=0.3) +
  ggplot2::geom_text(ggplot2::aes(label=lemma), check_overlap=TRUE, vjust=1.5) +
  ggplot2::scale_x_log10(labels=scales::percent_format()) +
  ggplot2::scale_y_log10(labels=scales::percent_format()) +
  ggplot2::scale_color_gradient(limits=c(0, 0.001), low="darkslategray4", high="gray75") +
  ggplot2::facet_wrap(~medical_specialty, ncol = 2) +
  ggplot2::theme(legend.position="none") +
  ggplot2:: labs(y="Orthopedic", x = NULL)
```

```
## Warning: Removed 36037 rows containing missing values or values outside the scale range
## (`geom_point()`).
```

```
## Warning: Removed 36037 rows containing missing values or values outside the scale range
## (`geom_text()`).
```



6

What does this plot tell you about the relative similarity of lemma frequencies between Surgery and Orthopedic and between radiology and Orthopedic? Based on what these specialties involve, is this what you would expect?

radiology and Orthopedic:

Most of the points are concentrated in the lower left corner, indicating that the frequency of many terms in these two specialties is very low, indicating that the terminology of orthopedics and radiology is very specialized. However, there are still some overlaps, such as series images and canal neural. These words do cover two different departments.

Surgery and Orthopedic:

Relatively speaking, the overlap is higher because the point is moving towards the upper right corner. There are also some high-frequency overlapping words, such as carpal ligament, etc. This is exactly what I expected.

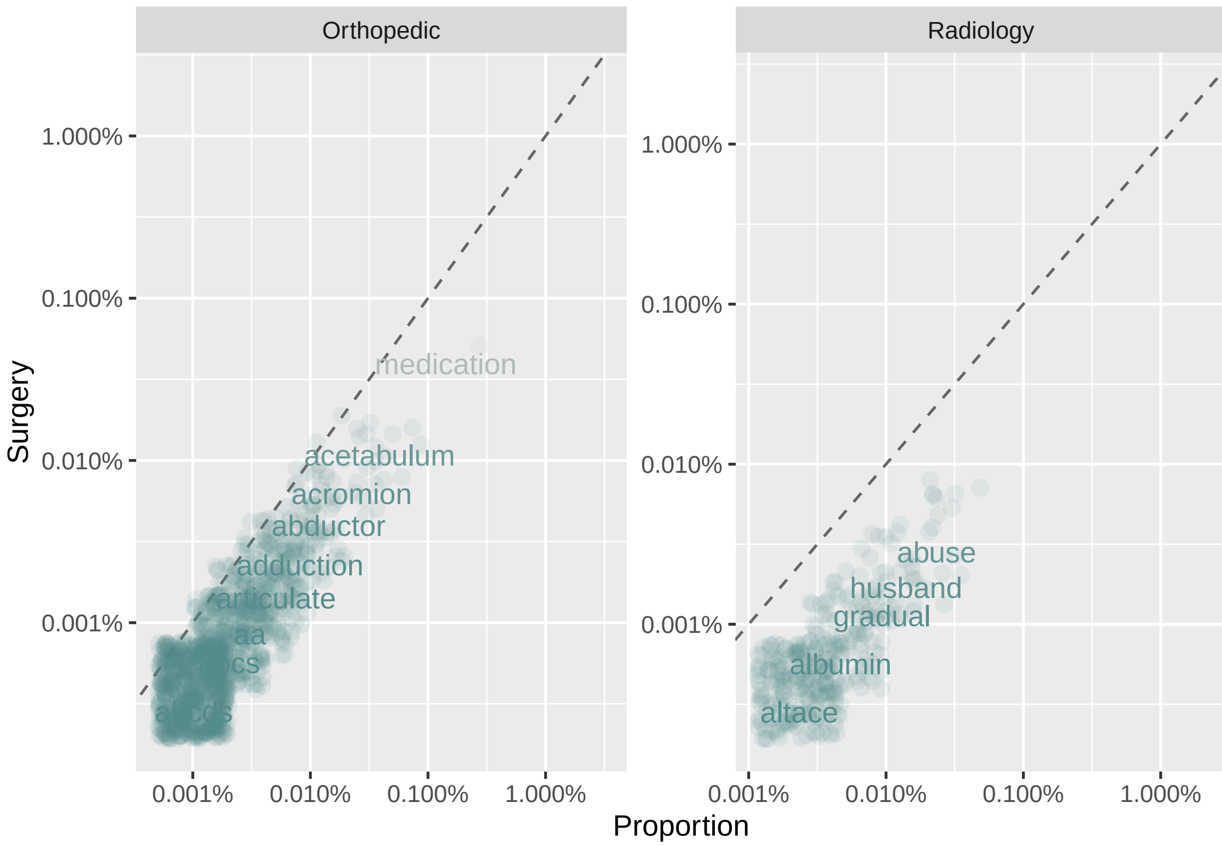
Most of the points are concentrated in the lower left corner, indicating that the frequency of many terms in these two specialties is very low, indicating that the terminology of orthopedics and radiology is very specialized. However, there are still some overlaps, such as series images and canal neural. These words do cover two different departments.

7 Modify the above plotting code to do a direct comparison of Surgery and Radiology (i.e., have Surgery or Radiology on the Y-axis and the other 2 specialties as the X facets)

```
lemma.freq <- lemmatized.data %>%
  dplyr::count(medical_specialty, lemma) %>%
  dplyr::group_by(medical_specialty) %>%
  dplyr::mutate(proportion = n / sum(n)) %>%
  tidyr::pivot_wider(names_from = medical_specialty, values_from = proportion) %>%
  tidyr::pivot_longer(`Orthopedic`:`Radiology`,
               names_to = "medical_specialty", values_to = "proportion")

ggplot2::ggplot(lemma.freq, ggplot2::aes(x = proportion, y = `Surgery`, color = abs(`Surgery` - proporti
  ggplot2::geom_abline(color = "gray40", lty = 2) +
  ggplot2::geom_jitter(alpha = 0.1, size = 2.5, width = 0.3, height = 0.3) +
  ggplot2::geom_text(ggplot2::aes(label = lemma), check_overlap = TRUE, vjust = 1.5) +
  ggplot2::scale_x_log10(labels = scales::percent_format()) +
  ggplot2::scale_y_log10(labels = scales::percent_format()) +
  ggplot2::scale_color_gradient(limits = c(0, 0.001), low = "darkslategray4", high = "gray75") +
  ggplot2::facet_wrap(~medical_specialty, scales = "free", ncol = 2) +
  ggplot2::theme(legend.position = "none") +
  ggplot2::labs(y = "Surgery", x = "Proportion")
```

```
## Warning: Removed 36279 rows containing missing values or values outside the scale range
## (`geom_point()`).
```

```
## Warning: Removed 36279 rows containing missing values or values outside the scale range
## (`geom_text()`).
```



TF-IDF Normalisation

Maybe looking at lemmas across all notes in a specialty is misleading, what if we look at lemma frequencies across a specialty.

```
lemma.counts <- lemmatized.data %>% dplyr::count(medical_specialty, lemma)
total.counts <- lemma.counts %>%
                      dplyr::group_by(medical_specialty) %>%
                      dplyr::summarise(total=sum(n))

all.counts <- dplyr::left_join(lemma.counts, total.counts)
```

```
## Joining with `by = join_by(medical_specialty)`
```

Now we can calculate the term frequency / invariant document frequency (tf-idf):

```
all.counts.tfidf <- tidytext::bind_tf_idf(all.counts, lemma, medical_specialty, n)
```

We can then look at the top 10 lemma by tf-idf within each specialty:

```
all.counts.tfidf %>% dplyr::group_by(medical_specialty) %>% dplyr::slice_max(order_by=tf_idf, n=10)
```

```
## # A tibble: 30 x 7
## # Groups:   medical_specialty [3]
##    medical_specialty lemma              n total      tf   idf   tf_idf
##    <chr>             <chr>          <int> <int>   <dbl> <dbl>    <dbl>
##  1 Orthopedic        drill            161 98129 0.00164 0.405 0.000665
##  2 Orthopedic        cement           114 98129 0.00116 0.405 0.000471
##  3 Orthopedic        interrupt        114 98129 0.00116 0.405 0.000471
##  4 Orthopedic        intraoperative   100 98129 0.00102 0.405 0.000413
```

```
##  5 Orthopedic        portal             97 98129 0.000988 0.405 0.000401
##  6 Orthopedic        phalanx            94 98129 0.000958 0.405 0.000388
##  7 Orthopedic        dissect            85 98129 0.000866 0.405 0.000351
##  8 Orthopedic        discectomy         81 98129 0.000825 0.405 0.000335
##  9 Orthopedic        retractor          75 98129 0.000764 0.405 0.000310
## 10 Orthopedic        musculoskeletal    27 98129 0.000275 1.10  0.000302
## # i 20 more rows
```

8 Are there any lemmas that stand out in these lists? Why or why not?

According to the tf-idf value, the top 10 lemmas of each major have high significance in their specific fields:

Orthopedic

drill,cement,intraoperative,phalanx,discectomy These lemmas are very common in orthopedic surgical records and are therefore prominent in this specialty.

Radiology

mci,spect,fetal,latency These terms are very common in radiology reports and reflect specific techniques and methods in the field.

Surgery

dissect, peritoneum, speculum, electrocautery, testis These terms are very common in surgical records and reflect the specific procedures and anatomy of the field.

We can look at transcriptions in full using these lemmas to check how they are used with `stringr::str_detect`

```
analysis.data %>% dplyr::select(medical_specialty, transcription) %>% dplyr::filter(stringr::str_detect
```

```
## # A tibble: 1 x 2
##   medical_specialty transcription
##   <chr>             <chr>
## 1 Surgery           preoperative diagnoses hallux rigidus left foot elevated me~
```

9 Extract an example of one of the other "top lemmas" by modifying the above code

```
analysis.data %>%
  dplyr::select(medical_specialty, transcription) %>%
  dplyr::filter(stringr::str_detect(transcription, 'dissect')) %>%
  dplyr::slice(1)
```

```
## # A tibble: 1 x 2
##   medical_specialty transcription
##   <chr>             <chr>
## 1 Surgery           title operation youngswick osteotomy internal screw fixatio~
```

Topic Modelling

In NLP, we often have collections of documents (in our case EMR transcriptions) that we'd like to divide into groups so that we can understand them separately. Topic modeling is a method for unsupervised classification of such documents, similar to clustering on numeric data.

Latent Dirichlet allocation (LDA) is a particularly popular method for fitting a topic model. It treats each document as a mixture of topics, and each topic as a mixture of words. This allows documents to "overlap" each other in terms of content, rather than being separated into discrete groups, in a way that mirrors typical use of natural language.

- Every document is a mixture of topics. We imagine that each document may contain words from several topics in particular proportions. For example, in a two-topic model we could say "Document 1 is 90% topic A and 10% topic B, while Document 2 is 30% topic A and 70% topic B."
- Every topic is a mixture of words. For example, we could imagine a two-topic model of American news, with one topic for "politics" and one for "entertainment." The most common words in the politics topic might be "President", "Congress", and "government", while the entertainment topic may be made up of words such as "movies", "television", and "actor". Importantly, words can be shared between topics; a word like "budget" might appear in both equally.

LDA is a mathematical method for estimating both of these at the same time: finding the mixture of words that is associated with each topic, while also determining the mixture of topics that describes each document. There are a number of existing implementations of this algorithm, and we'll explore one of them in depth.

First lets calculate a term frequency matrix for each transcription:

```
lemma.counts <- lemmatized.data %>% dplyr::count(note_id, lemma)
total.counts <- lemma.counts %>%
                      dplyr::group_by(note_id) %>%
                      dplyr::summarise(total=sum(n))

all.counts <- dplyr::left_join(lemma.counts, total.counts)
```

```
## Joining with `by = join_by(note_id)`
```

```
emr.dcm <- all.counts %>% tidytext::cast_dtm(note_id, lemma, n)
```

Then we can use LDA function to fit a 5 topic (`k=5`) LDA-model

```
emr.lda <- topicmodels::LDA(emr.dcm, k=5, control=list(seed=42))
emr.topics <- tidytext::tidy(emr.lda, matrix='beta')
```

Then we can extract the top terms per assigned topic:

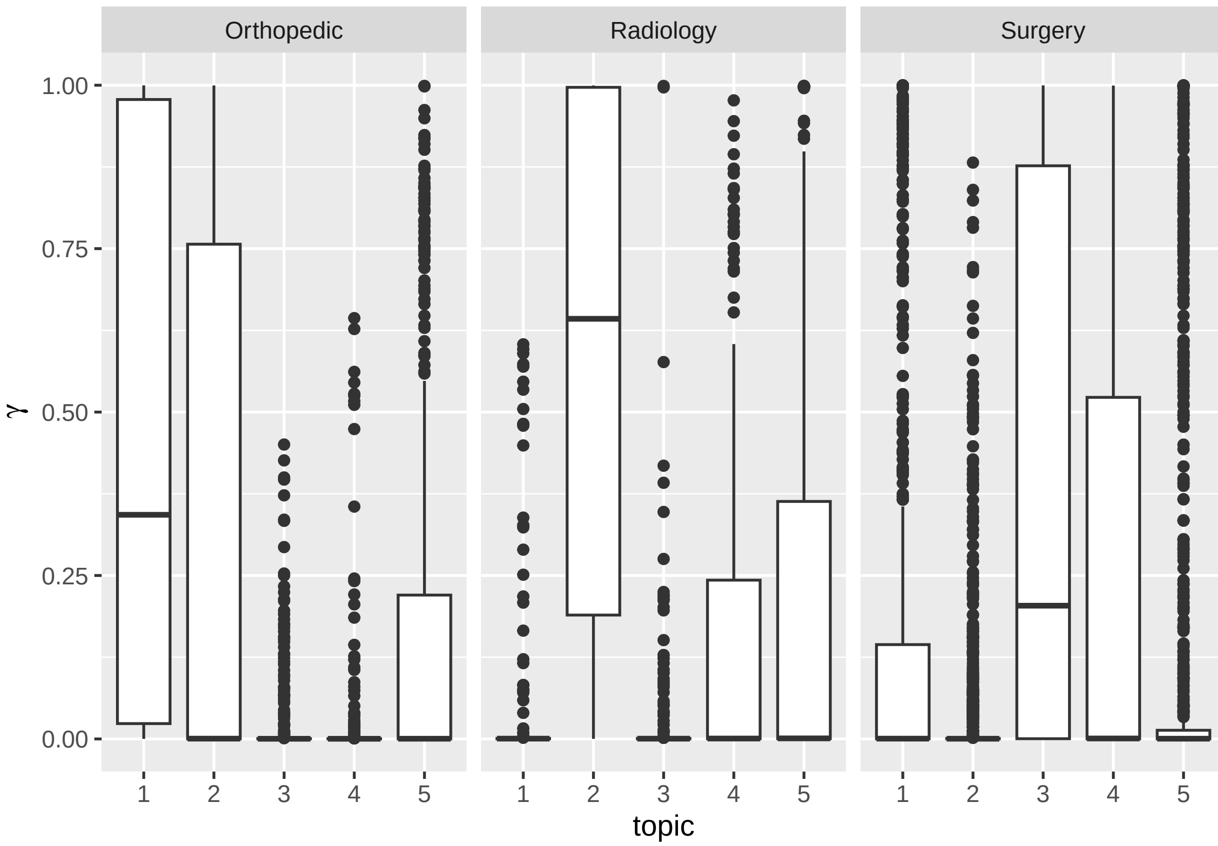
```
top.terms <- emr.topics %>% dplyr::group_by(topic) %>%
  dplyr::slice_max(beta, n=10) %>%
  dplyr::ungroup() %>%
  dplyr::arrange(topic, -beta)


top.terms %>%
  dplyr::mutate(term=tidytext::reorder_within(term, beta, topic)) %>%
  ggplot2::ggplot(ggplot2::aes(beta, term, fill=factor(topic))) +
    ggplot2::geom_col(show.legend=FALSE) +
    ggplot2::facet_wrap(~ topic, scales='free')  +
    ggplot2::theme(axis.text.x = element_text(angle = 45,vjust = 1,hjust = 1)) +
    tidytext::scale_y_reordered()
```

Now we can ask how well do these assigned topics match up to the medical specialties from which each of these transcripts was derived.

```
specialty_gamma <- tidytext::tidy(emr.lda, matrix='gamma')

# we need to join in the specialty from the note_id
note_id_specialty_mapping <- lemmatized.data %>%
  dplyr::mutate(document=as.character(note_id)) %>%
  dplyr::select(document, medical_specialty) %>%
  dplyr::distinct()

specialty_gamma <- dplyr::left_join(specialty_gamma, note_id_specialty_mapping)
```

```
## Joining with `by = join_by(document)`
```

```
specialty_gamma %>%
  dplyr::mutate(medical_specialty = reorder(medical_specialty, gamma * topic)) %>%
  ggplot2::ggplot(ggplot2::aes(factor(topic), gamma)) +
  ggplot2::geom_boxplot() +
  ggplot2::facet_wrap(~ medical_specialty) +
  ggplot2::labs(x = "topic", y = expression(gamma))
```



Interestingly, Surgery, Orthopedic, and Radiology assign mostly to a single topics. We'd possibly expect this from radiology due to referring to imaging for many different diagnoses/reasons. However, this may all just reflect we are using too few topics in our LDA to capture the range of possible assignments.

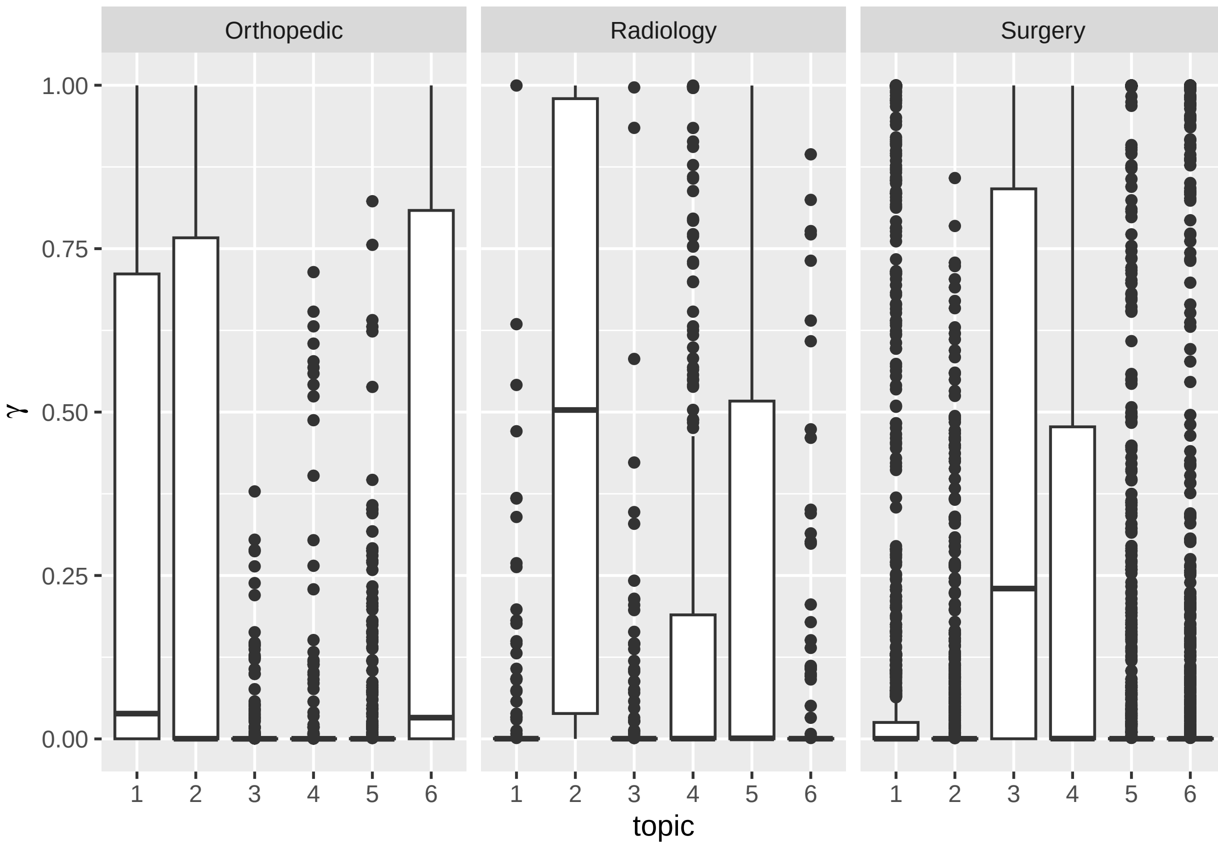
10 Repeat this with a 6 topic LDA, do the top terms from the 3 topic LDA still turn up? How do the specialties get split into sub-topics?

```
emr.lda6 <- topicmodels::LDA(emr.dcm, k=6, control=list(seed=42))
emr.topics6 <- tidytext::tidy(emr.lda6, matrix='beta')
top.terms6 <- emr.topics6 %>% dplyr::group_by(topic) %>%
    dplyr::slice_max(beta, n=10) %>%
    dplyr::ungroup() %>%
    dplyr::arrange(topic, -beta)

top.terms6 %>%
    dplyr::mutate(term=tidytext::reorder_within(term, beta, topic)) %>%
    ggplot2::ggplot(ggplot2::aes(beta, term, fill=factor(topic))) +
    ggplot2::geom_col(show.legend=FALSE) +
    ggplot2::facet_wrap(~ topic, scales='free') +
    ggplot2::theme(axis.text.x = element_text(angle = 45,vjust = 1,hjust = 1)) +
    tidytext::scale_y_reordered()
```


```
specialty_gamma6 <- tidytext::tidy(emr.lda6, matrix='gamma')

specialty_gamma6 <- dplyr::left_join(specialty_gamma6, note_id_specialty_mapping)
```

```
## Joining with `by = join_by(document)`
```

```
specialty_gamma6 %>%
    dplyr::mutate(medical_specialty = reorder(medical_specialty, gamma * topic)) %>%
    ggplot2::ggplot(ggplot2::aes(factor(topic), gamma)) +
    ggplot2::geom_boxplot() +
    ggplot2::facet_wrap(~ medical_specialty) +
    ggplot2::labs(x = "topic", y = expression(gamma))
```



###Comparison of main terms in the topic:

From the comparison of terms, many main terms will still appear again, but the model of six topics has made a more detailed segmentation of terms. For example, some terms in topic 1 and topic 3 in the model of three topics are respectively classified into topic 1 and topic 3 in the model of six topics. At the same time, the newly added topics 4, 5 and 6 in the model of six topics provide new classifications for the terms originally classified into topic 1 or topic 3, making the topic division more detailed.

###Subtopic segmentation:

The subtopic distribution of each profession is more detailed in the model of six topics. For example, Orthopedic is more distributed in topic 1 and topic 6, while Surgery is most distributed in topic 3. This shows that the model of six topics can better capture the subtle differences in each profession, thus providing more detailed information for analysis.

In general, the LDA model of six topics provides more detailed topic division and term classification than the model of three topics, making the subtopic analysis of different professions more detailed.

Credits

Examples draw heavily on material (and directly quotes/copies text) from Julia Slige's `tidytext` textbook.