```
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
```

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

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

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

```
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
```

```
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 alternati
```

```
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.

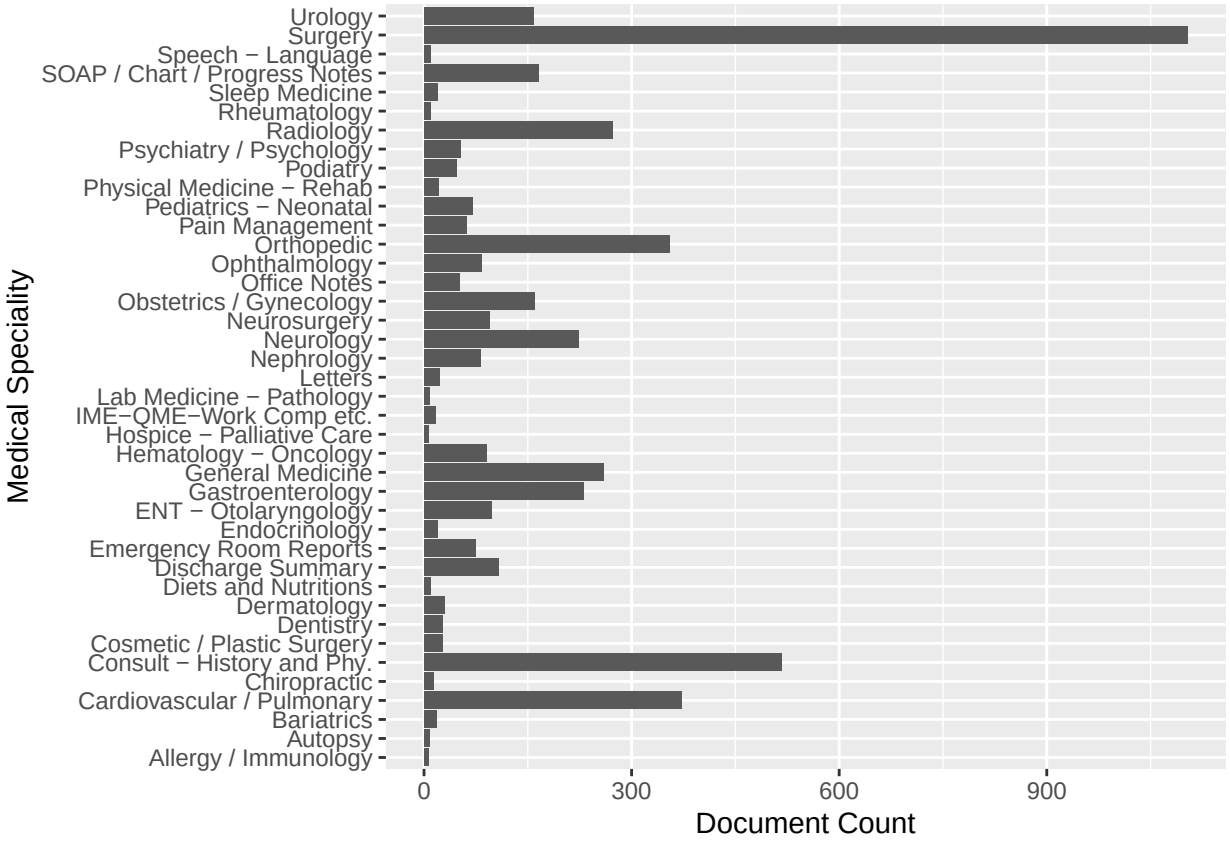
Let's see how many different medical specialties are featured in these notes:

```
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 <- analysis.data %>% tidytext::unnest_tokens(ngram, transcription, token = "ngrams", n=2
```

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=dplyr
```

```
## # 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:

```
#Insert code here.
unigram_counts <- tokenized.data.unigram %>% group_by(medical_specialty, word) %>% summarise(count = n()
  arrange(medical_specialty, desc(count))

# Count the unique unigrams based on specialty
unique_unigram_counts <- unigram_counts %>% group_by(medical_specialty) %>% summarise(unique_unigrams =

# View the unique unigrams
unique_unigram_counts
```

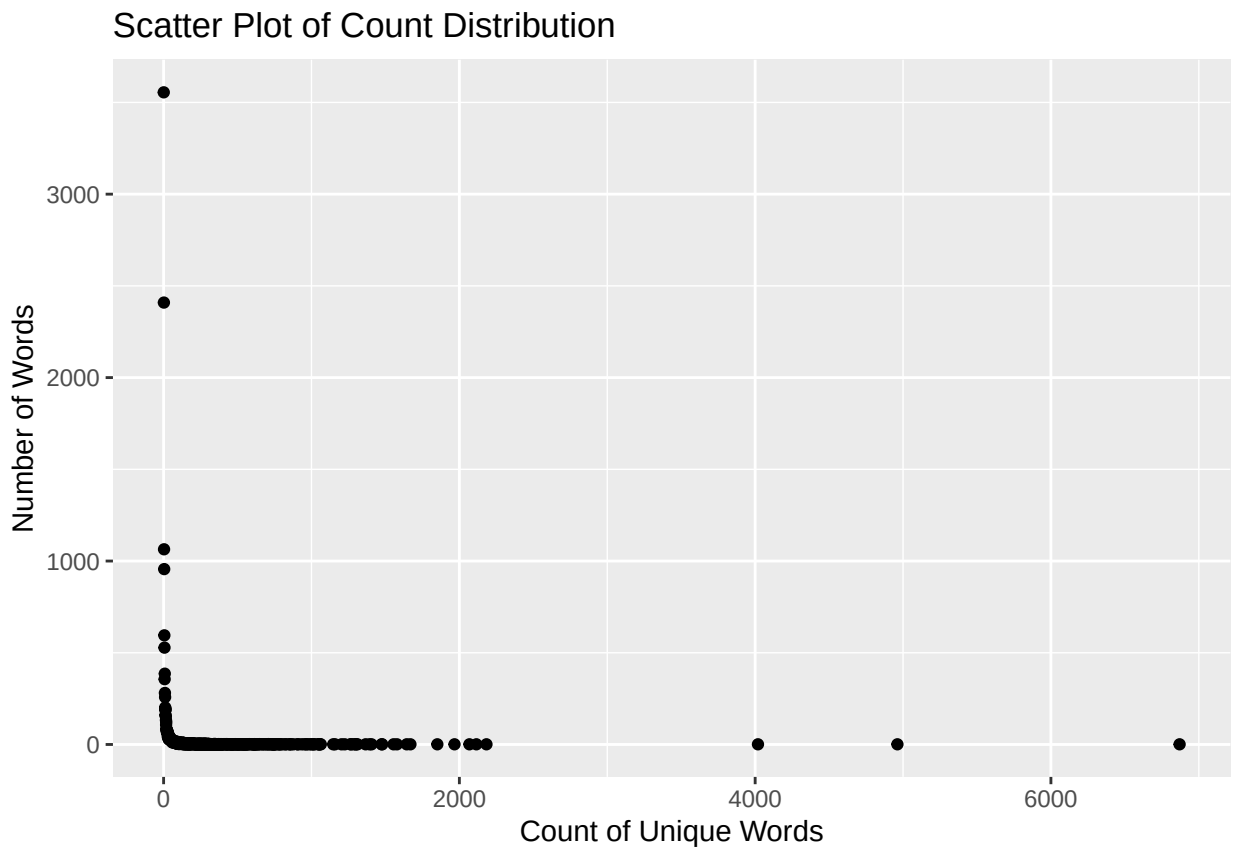
```
## # A tibble: 3 x 2
##   medical_specialty unique_unigrams
##   <chr>                       <int>
## 1 Orthopedic                   7682
## 2 Radiology                    5935
## 3 Surgery                     11977
```

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")
```

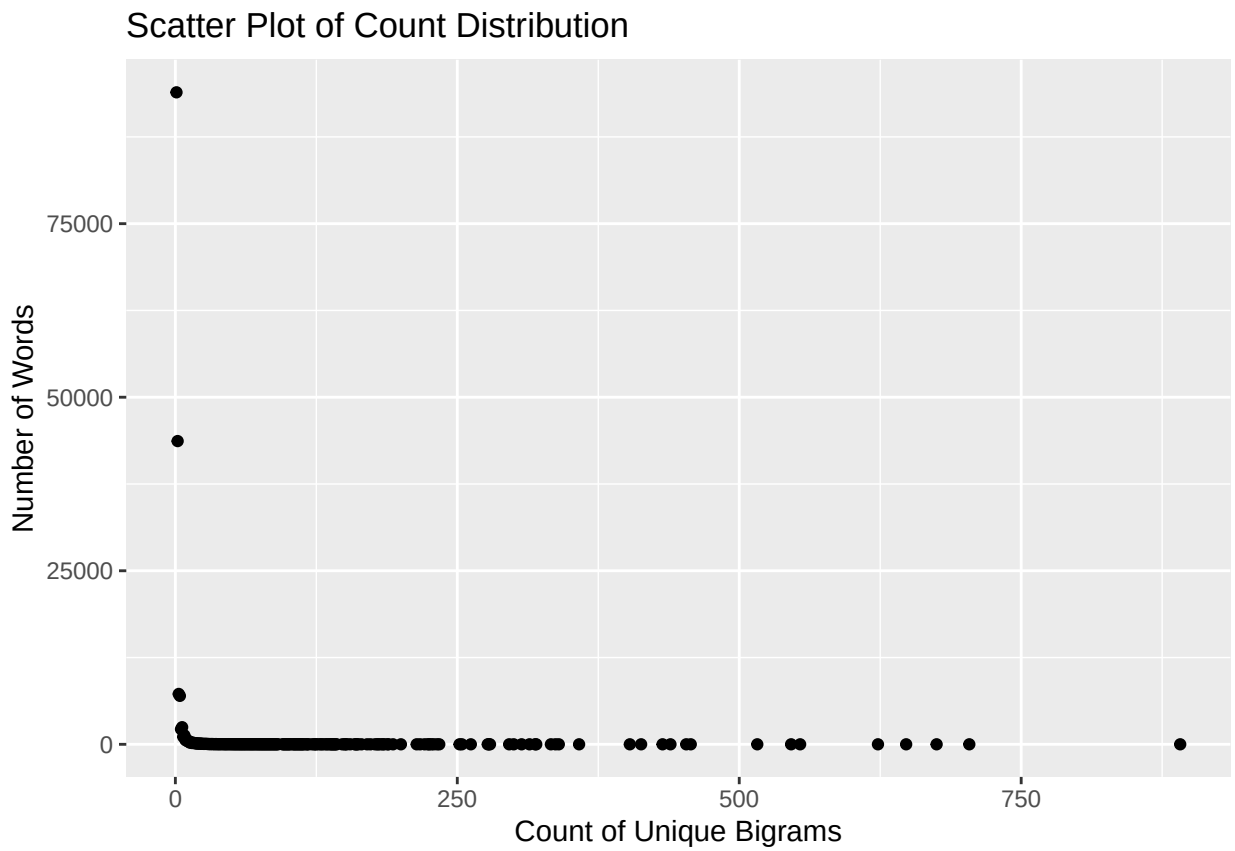


Let's plot some distribution of bigram tokens (words)

```
word_counts <- tokenized.data %>%
    group_by(ngram) %>%
    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?

```
# tokenized.data already have bigrams
# Let's divide the bigrams into single words
bigrams_seperated <- tokenized.data %>% separate(ngram, into=c("word1","word2"), sep = " ")

# Remove all non-alpha numeric characters, numbers and stop words (analysis.data is already filtered fo
bigrams_cleaned <- bigrams_seperated %>%
  mutate(word1 = str_replace_all(word1, "[^[:alnum:]]",""),
         word2 = str_replace_all(word2, "[^[:alnum:]]", "")) %>%
  filter(!str_detect(word1, "[0-9]"), !str_detect(word2, "[0-9]")) %>%
  anti_join(stop_words, by = c("word1" = "word")) %>%
  anti_join(stop_words, by = c("word2" = "word"))

# Then reunite them to bigrams
bigrams_cleaned <- bigrams_cleaned %>% unite(ngram, word1, word2, sep = " ")

# Then count the unique bigrams for each specialty
unique_bigrams_counts = bigrams_cleaned %>% group_by(medical_specialty, ngram) %>% summarise(count = n()
  arrange(medical_specialty, desc(count))

# Count the number of unique bigrams for each specialty
unique_bigrams_summary <- unique_bigrams_counts %>% group_by(medical_specialty) %>% summarise(unique_big

unique_bigrams_summary
```

```
## # A tibble: 3 x 2
```

```
##   medical_specialty unique_bigrams
##   <chr>                      <int>
## 1 Orthopedic                 55732
## 2 Radiology                  28296
## 3 Surgery                   130403
```

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.

```
# Let's take the filtered data and tokenize the transcription to sentences
sentences.data <- filtered.data %>% unnest_tokens(sentence, transcription, token = "sentences", to_lowe
  mutate(sentence = str_replace_all(sentence, "[^[:alnum:][:space:]]","")) %>%
  filter(!str_detect(sentence,"[0-9]")) %>%
  anti_join(stop_words, by = c("sentence" = "word"))

# Ensure the medical specialty column is present with the help of note_id
# sentences.data <- sentences.data %>% left_join(select(filtered.data, note_id, medical_specialty), by =

# Count the unique sentences for each specialty
unique_sentences_count <- sentences.data %>% group_by(medical_specialty, sentence) %>% summarise(count =

# Count the number of unique sentences for each specialty
unique_sentences_summary <- unique_sentences_count %>% group_by(medical_specialty) %>% summarise(uniqe_s

unique_sentences_summary
```

```
## # A tibble: 3 x 2
##   medical_specialty uniqe_sentences
##   <chr>                       <int>
## 1 Orthopedic                   7376
## 2 Radiology                    2515
## 3 Surgery                     19890
```

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

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

```
## Selecting by n
```

```
## # A tibble: 16 x 3
## # Groups:   medical_specialty [3]
##    medical_specialty ngram                       n
##    <chr>             <chr>                   <int>
##  1 Surgery           prepped draped            696
##  2 Surgery           preoperative diagnosis    555
##  3 Surgery           procedure patient         551
##  4 Surgery           postoperative diagnosis   518
##  5 Surgery           tolerated procedure       515
##  6 Orthopedic        prepped draped            183
##  7 Orthopedic        preoperative diagnosis    141
##  8 Orthopedic        lower extremity           139
```

```
##  9 Orthopedic        range motion              139
## 10 Orthopedic        postoperative diagnosis   124
## 11 Radiology         carotid artery             59
## 12 Radiology         heart rate                 52
## 13 Radiology         reason exam                51
## 14 Radiology         left ventricular           50
## 15 Radiology         coronary artery            43
## 16 Radiology         exam unremarkable          43
```

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?

A general purpose lemmatizer might not work well for medical data because of various reasons. Medical records contain specialized terminology/vocabulary including some complex abbreviations or compound terms. General purpose lemmatizer is trained on common languages, so it may not recognise or wrongly lemmatize the specific medical terminology. Some of the words in medical data like 'aspirin', 'Ibuprofen' should not be lemmatized but general purpose lemmatizer might lemmatize these words too which can lead to improper results. Sometimes it might not breakdown the complex terminology where there's scope to lemmatize but the lemmatizer might fail. Acronyms are frequently used in medical terminology, which might not be recognised by these general-purpose lemmatizer. Considering all these challenges, we should avoid using such general purpose lemmatizer for medical data.

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 %>% dplyr::mutate(lemma=textstem::lemmatize_words(ngram))
```

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

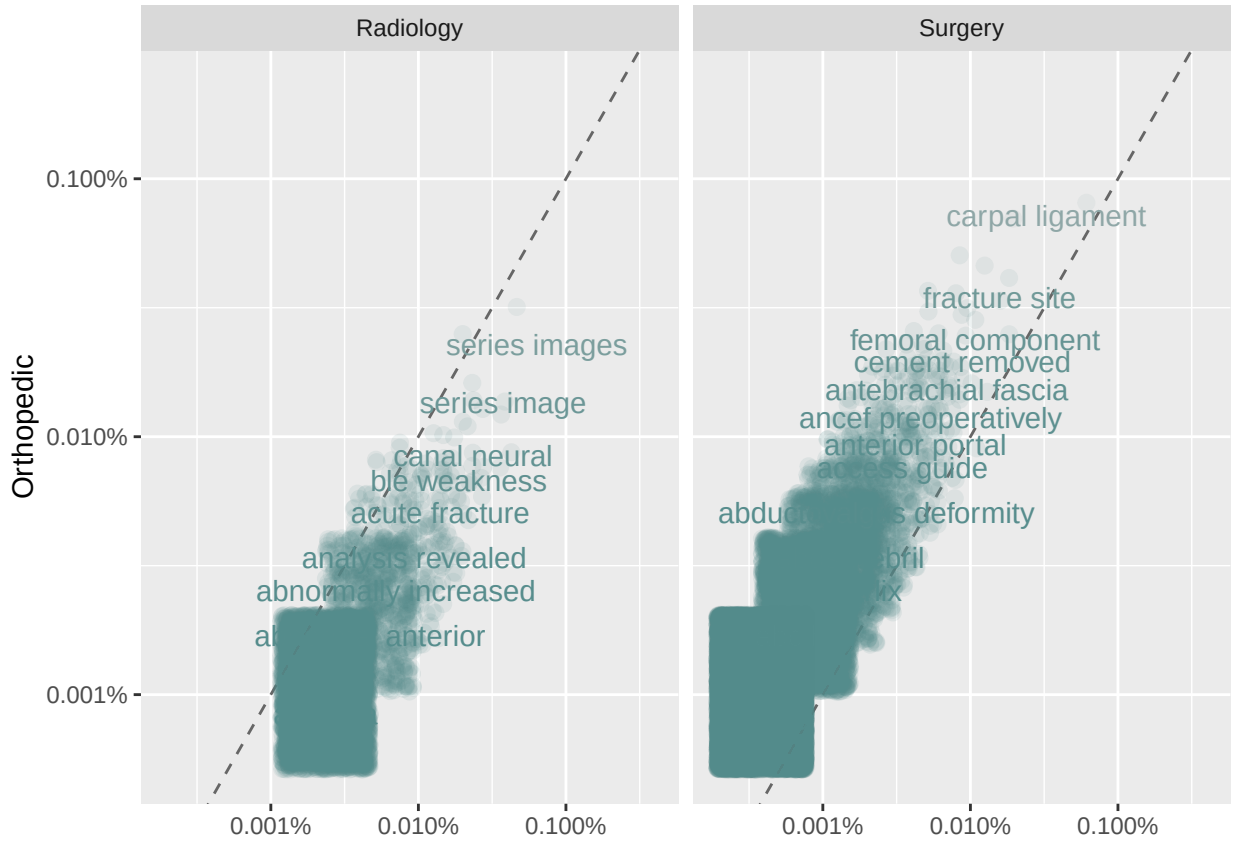
```
lemma.freq <- lemmatized.data %>%
  dplyr::count(medical_specialty, lemma) %>%
  dplyr::group_by(medical_specialty) %>%
  dplyr::mutate(proportion = n / sum(n)) %>%
  tidyr::pivot_wider(names_from = medical_specialty, values_from = proportion) %>%
  tidyr::pivot_longer(`Surgery`:`Radiology`,
   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

And plot the relative proportions

```
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 314404 rows containing missing values or values outside the scale range
## (`geom_point()`).
```

```
## Warning: Removed 314404 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 Surgery? Based on what these specialties involve, is this what you would expect?

The graphs show the lemma frequencies between different medical specialities. The first graph which shows the lemma frequency between orthopedic and radiology indicates that they are relatively different because the points are little farther from the diagonal line. Some of the lemmas are series images, acute fracture which align well with radiology since these phrases are common for this medical speciality. While there is some overlap (Orthopedic procedures often rely on radiological imaging for diagnosis), Radiology includes a broader range of imaging modalities and diagnostic techniques across different parts of the body, leading to different terminologies. This broader range in Radiology causes the lemma frequencies to diverge more from those in Orthopedic.

Other graph shows the lemma frequency between orthopedic and surgey medical specialities. This graph indicates that lemma frequencies are more similar since the points align with diagonal line. Lemmas like "fracture site" and "acute fracture" appear frequently which makes sense because these terms are part of surgerical procedures and similar terminology. Both specialties deal extensively with the musculoskeletal system, surgical procedures, and related terms. It makes sense that their vocabulary would overlap significantly, as both fields often involve treatments for similar conditions (e.g., fractures, ligament injuries).

The plot aligns with expectations based on what these specialties involve. The closer similarity between Orthopedic and Surgery reflects their shared focus on surgical interventions and musculoskeletal conditions, while the greater divergence between Orthopedic and Radiology reflects Radiology's broader diagnostic focu

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)

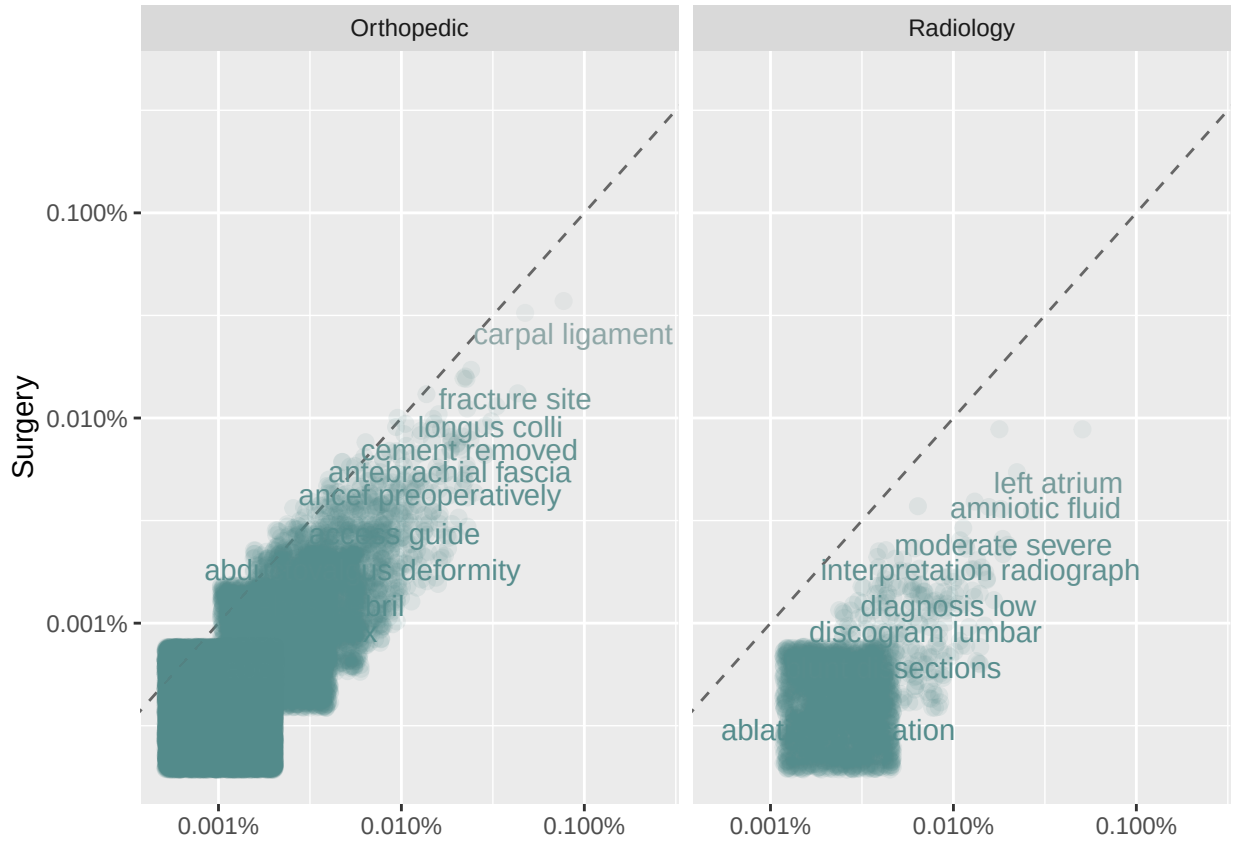
```
lemma.freq_1 <- lemmatized.data %>%
  dplyr::count(medical_specialty, lemma) %>%
```

```
  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_1, ggplot2::aes(x=proportion,
                                           y=`Surgery`,
                                           color=abs(`Surgery` - 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="Surgery", x = NULL)
```

```
## Warning: Removed 317819 rows containing missing values or values outside the scale range
## (`geom_point()`).
```

```
## Warning: Removed 317820 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        range motion           139 97774 0.00142  0.405 0.000576
##  2 Orthopedic        carpal ligament         85 97774 0.000869 0.405 0.000352
##  3 Orthopedic        transverse carpal       81 97774 0.000828 0.405 0.000336
##  4 Orthopedic        extremity prepped       79 97774 0.000808 0.405 0.000328
##  5 Orthopedic        proximal phalanx        75 97774 0.000767 0.405 0.000311
##  6 Orthopedic        department anesthesia   63 97774 0.000644 0.405 0.000261
##  7 Orthopedic        dissection carried      63 97774 0.000644 0.405 0.000261
##  8 Orthopedic        steri strips            59 97774 0.000603 0.405 0.000245
##  9 Orthopedic        closed vicryl           58 97774 0.000593 0.405 0.000241
## 10 Orthopedic        dressing applied        58 97774 0.000593 0.405 0.000241
## # i 20 more rows
```

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

Looking at the tables, we can understand from the simple analysis that there are few lemmas which have high tf-idf scores.

For Orthopedic medical speciality lemmas like range motion, carpal ligament, extremity prepped and proximal phalanx have high tf-idf values. Range motion is commonly used in orthopedic evaluations and treatments related to the mobility of joints. Carpal ligament is relevant to conditions like carpal tunnel syndrome, which is frequently addressed in orthopedic practice. Extremity prepped is often used in surgical preparation and procedures involving limbs. Proximal phalanx is a specific anatomical term frequently used in orthopedic discussions about finger and toe bones.

For Surgery speciality lemmas like anterior chamber, lithotomy position, external oblique and closed vicryl have high tf-idf values. Anterior chamber refers to a part of the eye often involved in surgical procedures like cataract surgery, lithotomy position is a common surgical position used in various types of surgeries, particularly in gynecological and urological procedures. External oblique is a muscle that may be involved in surgical procedures or assessments of the abdominal area and closed vicryl is a specific type of suture material used frequently in surgeries.

For Radiology speciality lemmas like myocardial perfusion, calcific plaque, needle emg and left ventricular have high tf-idf values. Myocaridal infusion is a specific imaging study often conducted in radiology to assess the blood flow to the heart muscle, calcific plaque is commonly identified in imaging studies related

to cardiovascular health. Needle emg refers to a diagnostic procedure involving needle electrodes to assess muscle and nerve function and left ventricular pertains to the left ventricle of the heart, frequently examined in radiological imaging for cardiac assessments.

The lemmas that stand out in these lists are aligned with the primary focus and activities of each medical specialty. They are specific to the common procedures, anatomical terms, and diagnostic studies related to Orthopedic, Radiology, and Surgery, respectively. Overall, these standout lemmas highlight the specialized vocabulary inherent to each medical field, underscoring the importance of using domain-specific lemmatization and text analysis techniques in medical data processing.

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

```
# Extract the top 10 lemmas by tf-idf for each medical specialty
top_lemmas <- all.counts.tfidf %>%
  dplyr::group_by(medical_specialty) %>%
  dplyr::slice_max(order_by = tf_idf, n = 10)

# Extract an example lemma for a specific medical specialty
Orthopedic_lemma <- top_lemmas %>%
  filter(medical_specialty == "Orthopedic") %>%
  slice(1)

# View the result
Orthopedic_lemma
```

```
## # A tibble: 1 x 7
## # Groups:   medical_specialty [1]
##   medical_specialty lemma            n total      tf   idf   tf_idf
##   <chr>             <chr>        <int> <int>   <dbl> <dbl>    <dbl>
## 1 Orthopedic        range motion   139 97774 0.00142 0.405 0.000576
```

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)
```

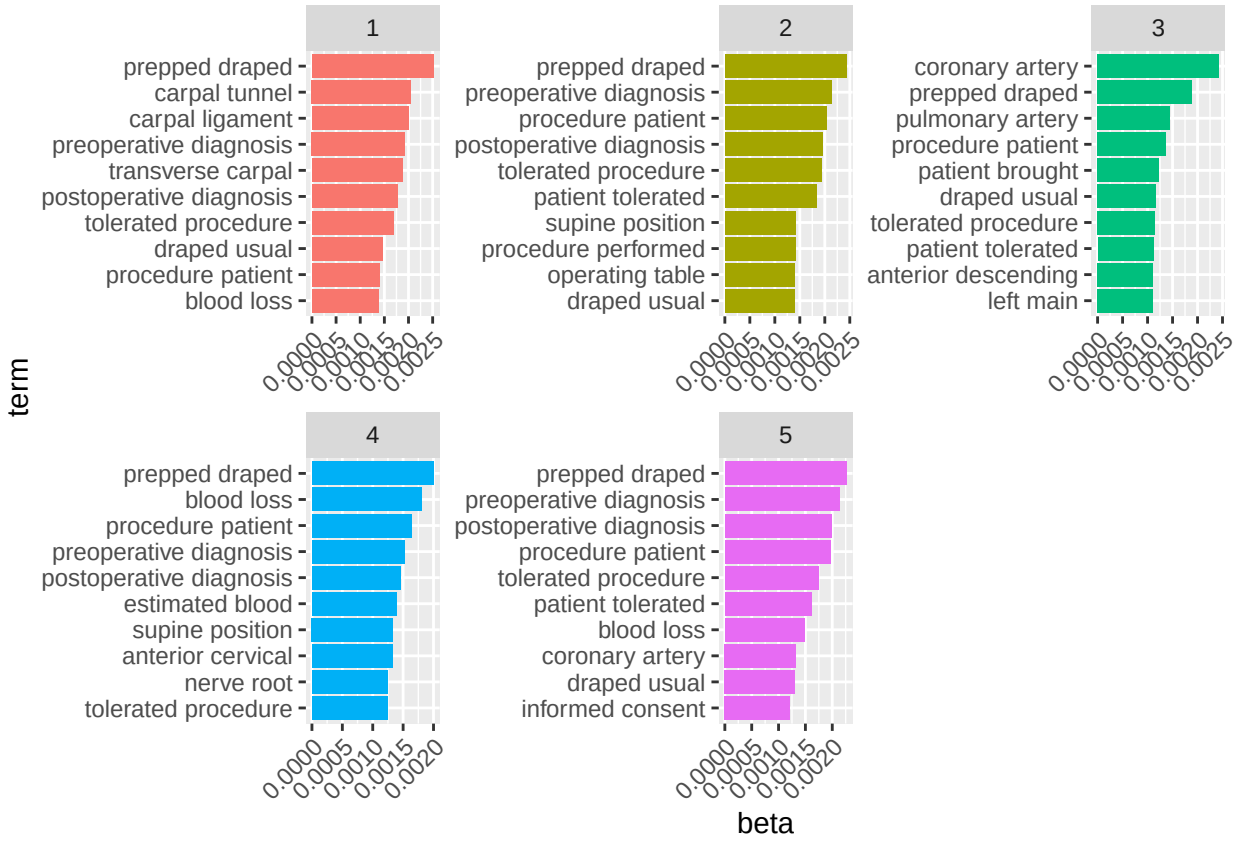
Then we can use LDA function to fit a 5 topic (k=5) LDA-model

```
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.

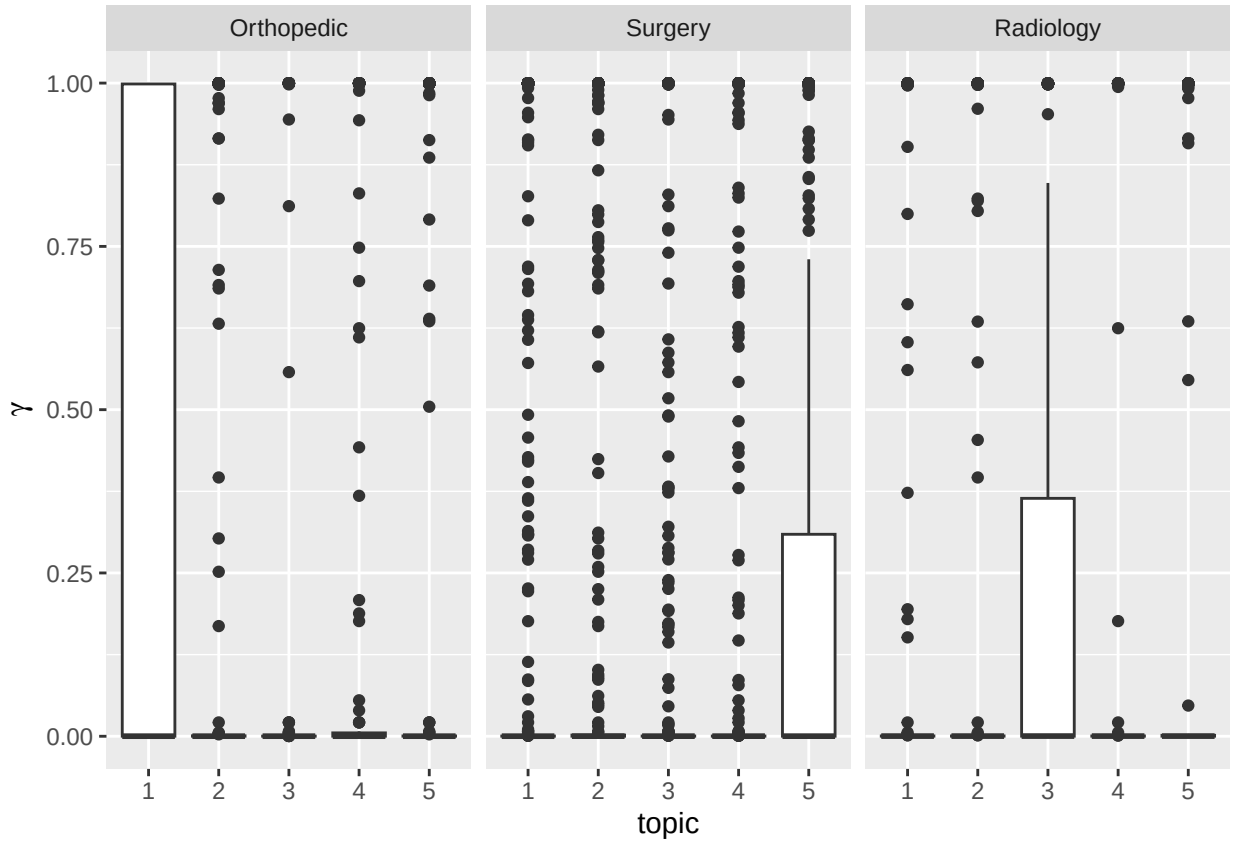
```
specialty_gamma <- tidytext::tidy(emr.lda, matrix='gamma')

# 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))
```



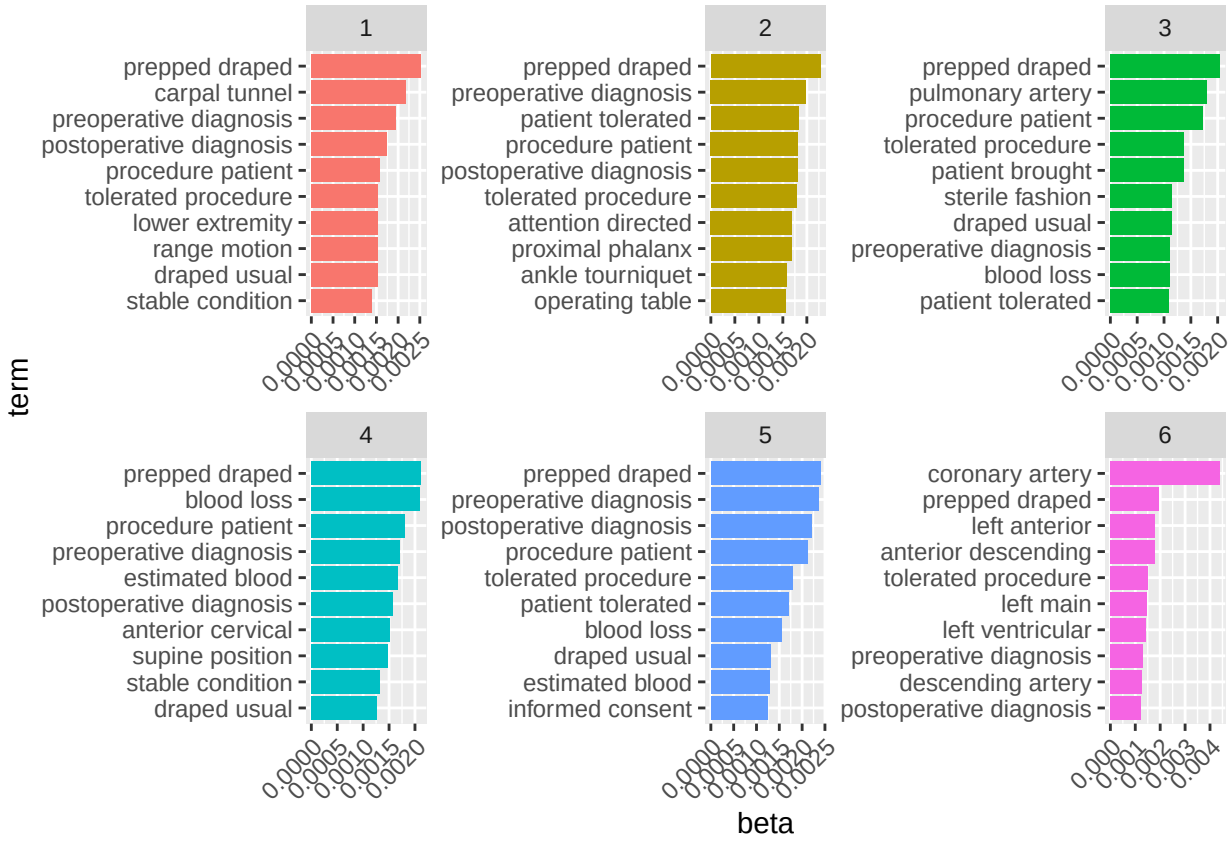
Interestingly, Surgery, Orthopedic, and Radiology assign mostly to a single topics. We'd possibly expect this from radiology due to referring to imaging for many different diagnoses/reasons. However, this may all just reflect we are using too few topics in our LDA to capture the range of possible assignments.

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?

```
k <- 6
emr_1.lda <- topicmodels::LDA(emr.dcm, k = k, control = list(seed = 42))
emr_1.topics <- tidytext::tidy(emr_1.lda, matrix = "beta")

top_1.terms <- emr_1.topics %>%
  dplyr::group_by(topic) %>%
  dplyr::slice_max(beta, n = 10) %>%
  dplyr::ungroup() %>%
  dplyr::arrange(topic, -beta)

top_1.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()
```

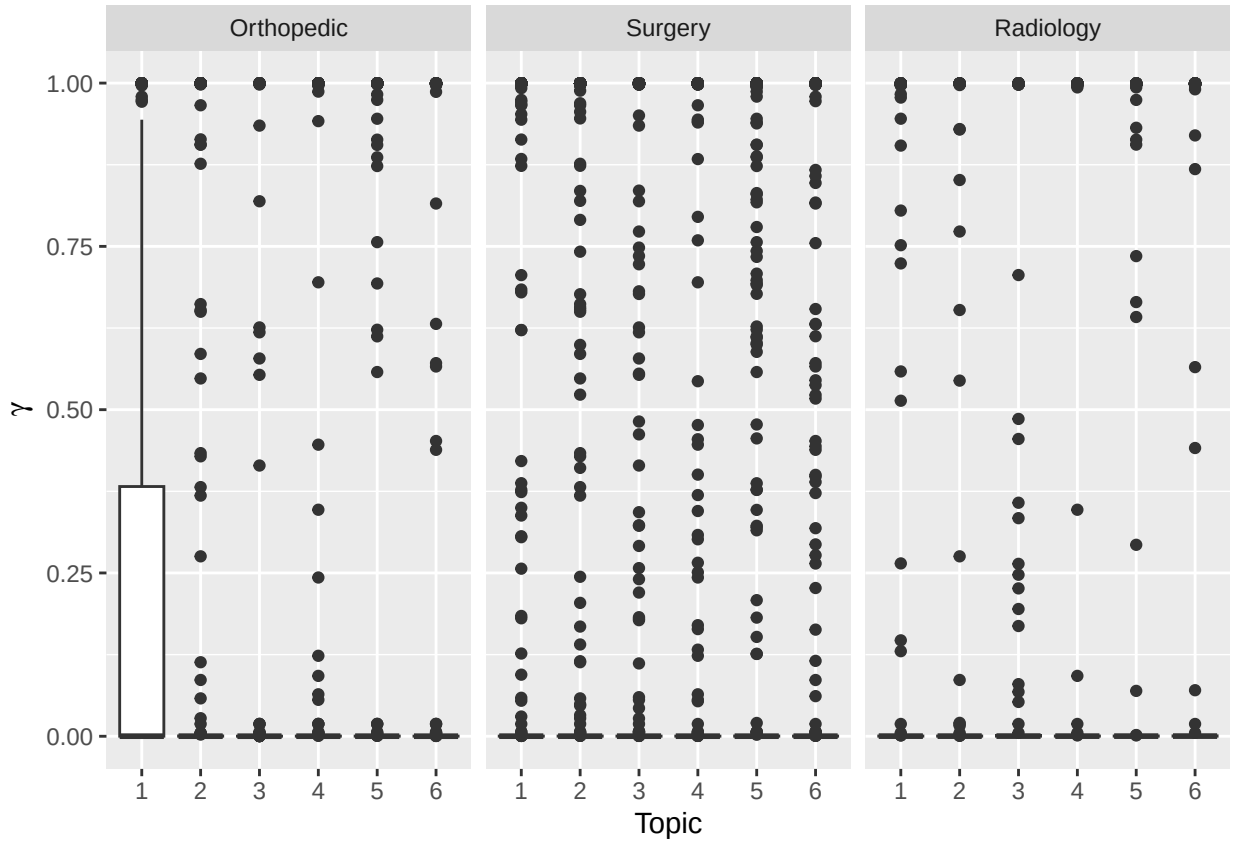



```
specialty_gamma_1 <- tidytext::tidy(emr_1.lda, matrix = 'gamma')

# Join the medical_specialty from the note_id
note_id_specialty_mapping_1 <- lemmatized.data %>%
  dplyr::mutate(document = as.character(note_id)) %>%
  dplyr::select(document, medical_specialty) %>%
  dplyr::distinct()

specialty_gamma_1 <- dplyr::left_join(specialty_gamma_1, note_id_specialty_mapping_1, by = "document")

specialty_gamma_1 %>%
  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))
```



Let's analyze the 6 topic LDA model, top terms for each topic are as follows:

Topic 1: Includes terms like "prepped draped," "carpal tunnel," "preoperative diagnosis," etc. This topic appears similar to one of the topics from the 5-topic model, indicating procedural terms and preparatory steps commonly used in surgeries.

Topic 2: Includes terms like "prepped draped," "preoperative diagnosis," "patient tolerated," etc. This topic also seems to emphasize preoperative and procedural aspects.

Topic 3: Includes terms like "coronary artery," "prepped draped," "pulmonary artery," etc. This topic is specific to cardiovascular procedures, which was also present in the 5-topic model.

Topic 4: Similar to Topic 1, with terms like "prepped draped," "blood loss," "procedure patient," etc., indicating overlap with surgical preparatory and procedural terms.

Topic 5: Terms like "prepped draped," "preoperative diagnosis," "procedure patient," similar to previous topics, indicating the focus on procedural aspects.

Topic 6: Focuses on cardiovascular procedures with terms like "coronary artery," "prepped draped," "left anterior," etc., similar to Topic 3.

Distribution of specialities into topics:

Orthopedic: The plot indicates that Orthopedic topics are primarily assigned to Topic 1 and Topic 4. This reflects procedural and preoperative terminologies common in Orthopedic procedures.

Surgery: Surgery topics are more evenly distributed across Topics 1, 2, 4, and 5. This suggests that surgical procedures involve a wide range of terminologies, covering different aspects of the surgical process.

Radiology: Radiology topics are mostly assigned to Topics 3 and 6. This makes sense as these topics include terms related to cardiovascular imaging and diagnostic procedures, which are common in Radiology.

- Many top terms from the 5-topic model reappear in the 6-topic model, indicating consistency in identifying key terms related to each specialty. Terms like "prepped draped," "coronary artery," and "preoperative diagnosis" are common across both models.
- The additional topic in the 6-topic model provides a more granular view of the specialties. For instance, Surgery is split into more sub-topics, reflecting the diverse nature of surgical procedures.

By comparing the results of both models, we can conclude that while increasing the number of topics provides a more granular view, the core terminologies remain consistent, validating the effectiveness of the topic modeling approach.

Credits

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