Lab 2 Ally Seamone

```
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 in this dataset contains.

NoteID: an integer value used to number/describe each medical record in the data set

Description: an explanation of why individuals are visiting the hospital/ (character)

Medical Specialty: specialized department of the hospital the patient will go to based on their medical condition (character)

Sample Name: medical name of the condition the patient is experiencing (character)

Transcription: written description of the entire medical record/doctors information taken down when with patient (character)

Keywords: medical terms that could be important identifiers of the medical condition (character)

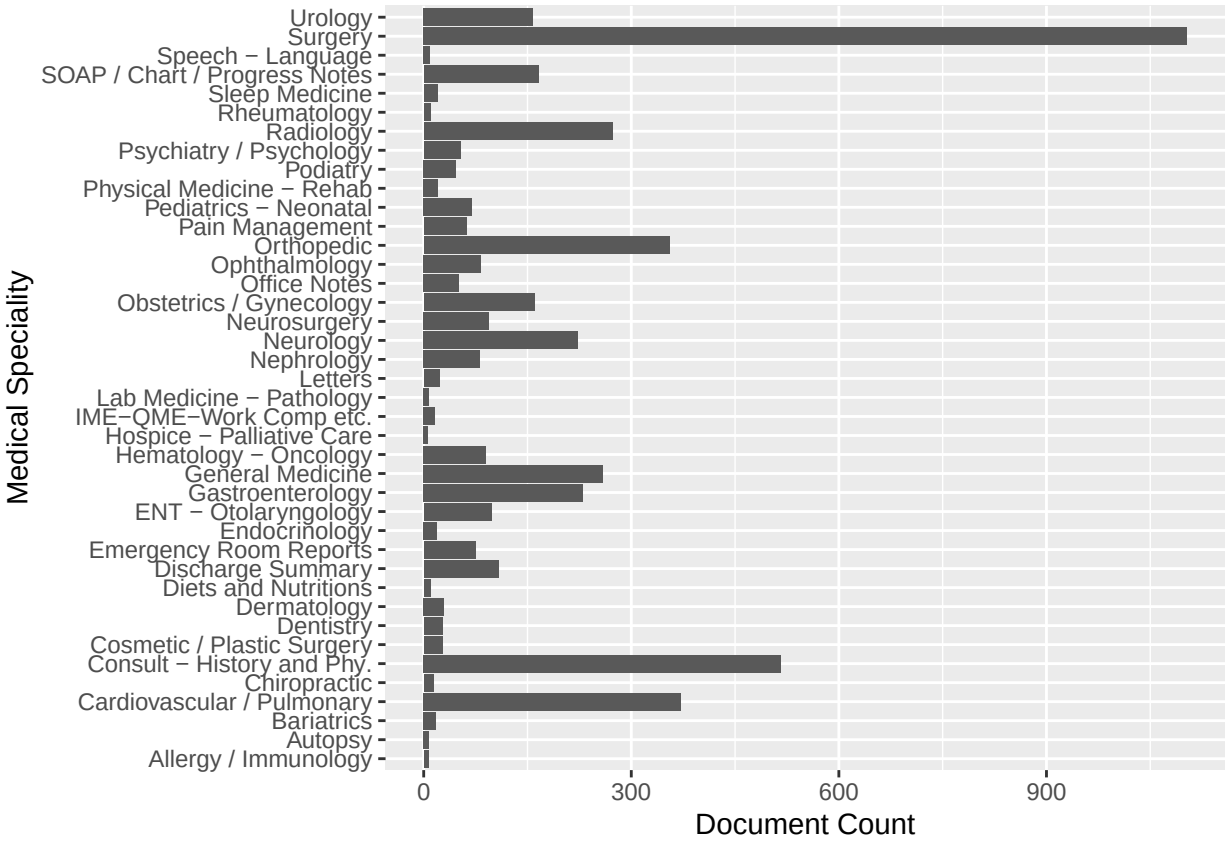
Let's see how many different medical specialties are featured in these notes:

```
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 Co
```



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
```

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

Orthopedic has 7682 unique tokens, radiology has 5935, and surgery has 11977.

```
tokenized.data.unigram %>% dplyr::group_by(medical_specialty) %>% dplyr::distinct(word) %>% dplyr::summa
```

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

For bigram

```
tokenized.data %>% dplyr::group_by(medical_specialty) %>% dplyr::distinct(ngram) %>% dplyr::summarise(n=
```

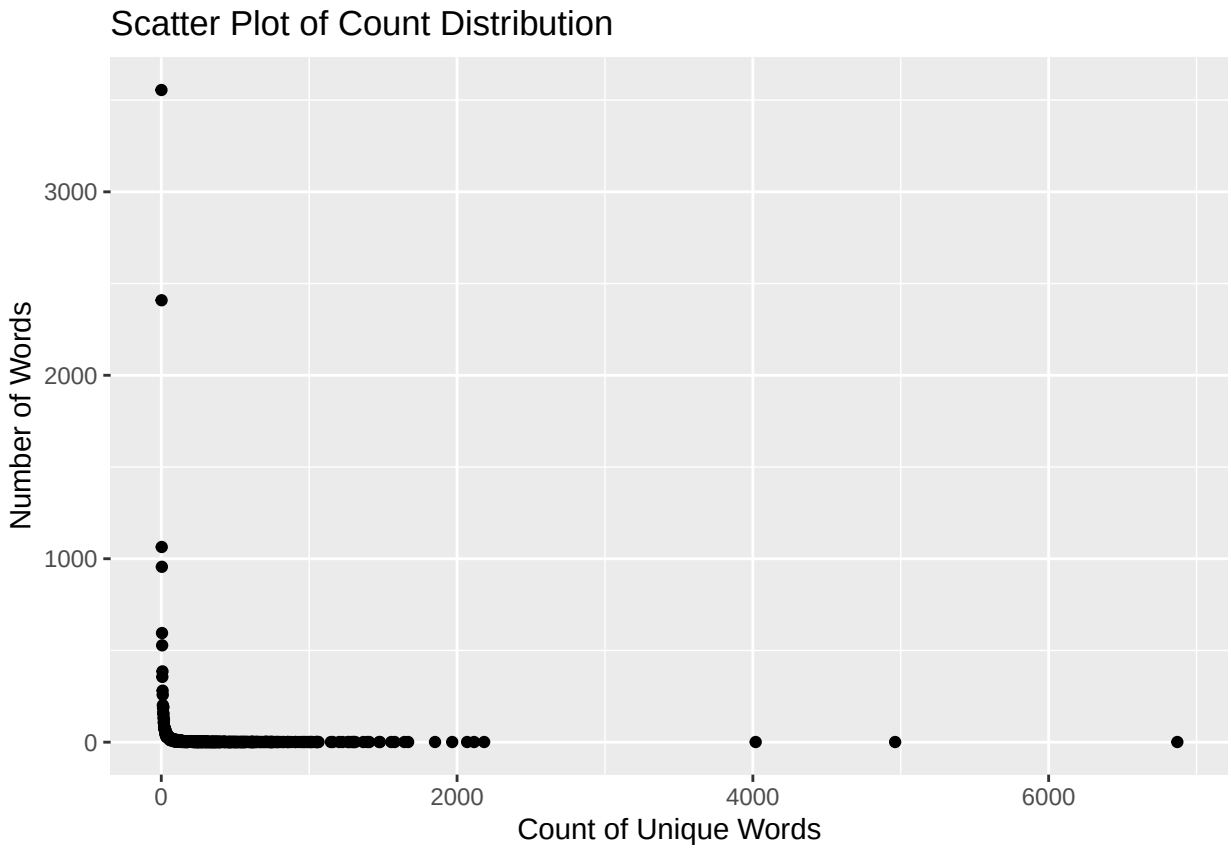
```
## # A tibble: 3 x 2
##   medical_specialty      n
##   <chr>              <int>
## 1 Orthopedic         55732
## 2 Radiology          28297
## 3 Surgery           130404
```

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")
```

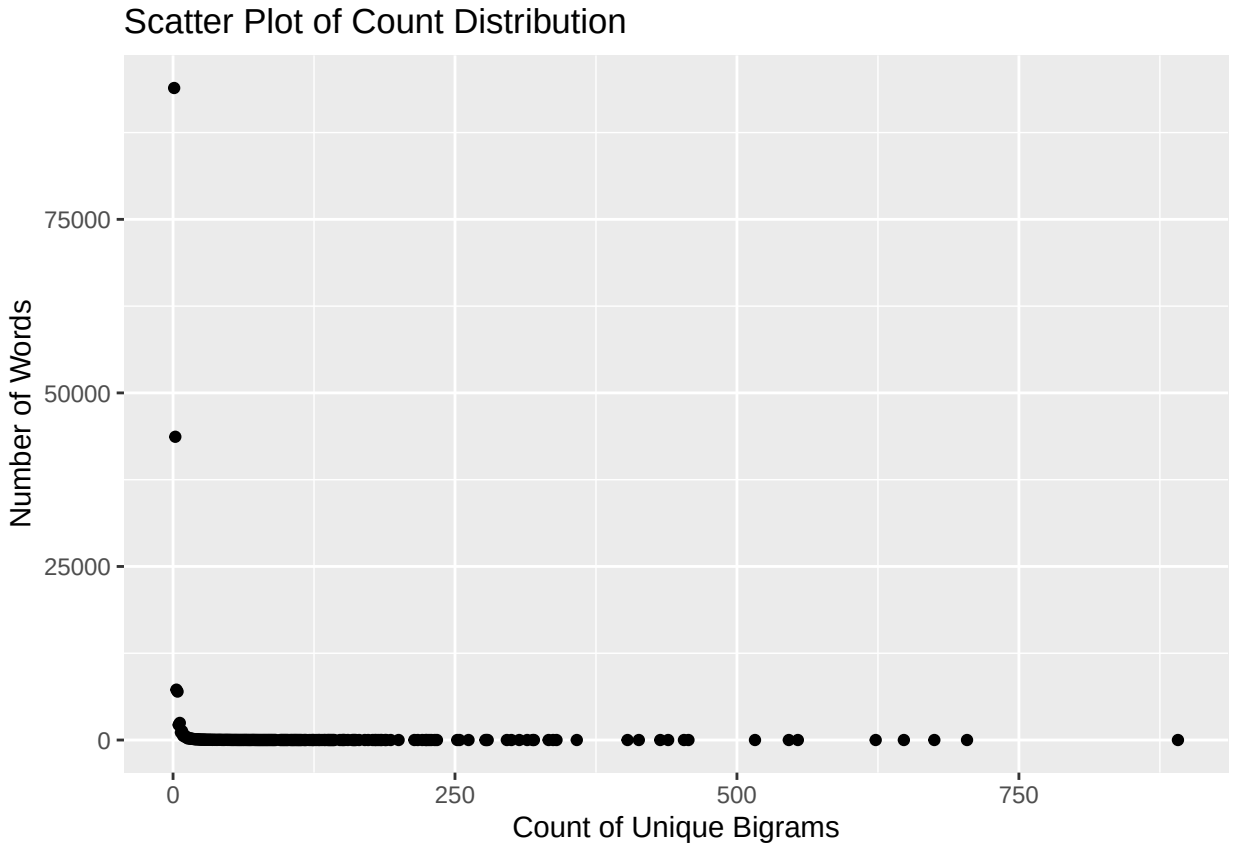


Let's plot some distribution of bigram tokens (words)

```
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 words are there in each category without stop words and numbers? **DO IT FOR BIGRAMS**

Orthopedic has 55732, radiology has 28297, and surgery has 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.

For orthopedic there are 354, radiology has 273, and surgery has 1087 unique sentences.

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

```
tokenized.data.sentence %>% dplyr::group_by(medical_specialty) %>% dplyr::distinct(sentences) %>% dplyr
```

```
## # A tibble: 3 x 2
##   medical_specialty     n
##   <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 %>%
  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 not?

I do not think a general purpose lemmatizer would work well for medical data. I think that terms in medicine are very specific to certain things, and similar words can mean different things. When using a lemmatizer to group words in medical records could be difficult because very small prefixes or suffixes can mean entirely different things or indicate that a different specialty should be used to manage the condition.

For example, hypertension and hypotension mean different things and have a very small wording/spelling differences.

Also depending on certain aspects of where an illness occurs can indicate which specialty is needed to treat it. For example, if a blood clot is in a patients brain then it would be a neurology treatment, or if it was in someones heart that it would need a cardiology treatment. The same word could also mean different things/procedures depending on the specialty. Therefore many specific small differences can indicate differences in medical data, which could impact lemmatization. Depending on the doctor could indicate different uses/orders of words or short hand versions of words could be difficult. Doctors could use different terms to mean the same thing as well.

Therefore, a specailized medical lemmatizer would be the best option here as medical words are very specific.

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) %>%
```

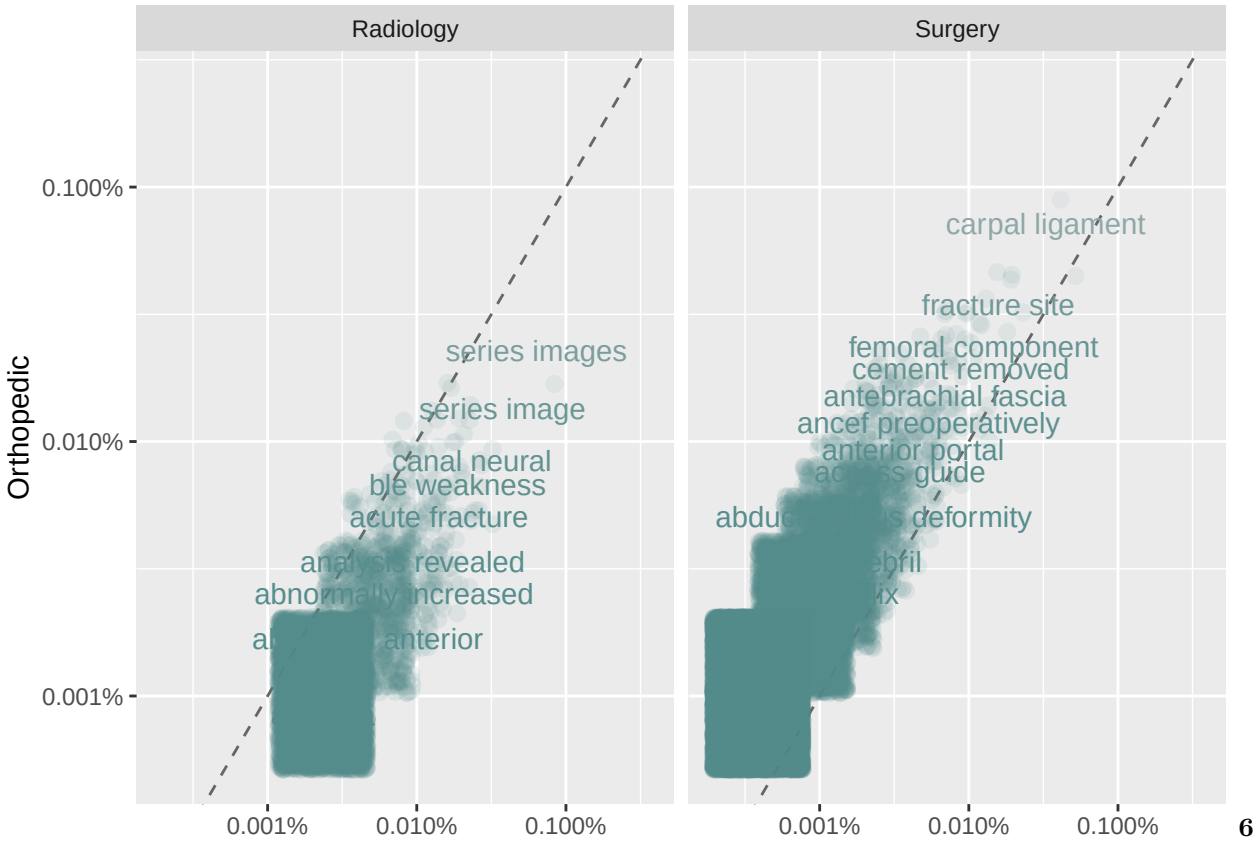
```
  tidyr::pivot_longer(`Surgery`:`Radiology`,
                      names_to = "medical_specialty", values_to = "proportion")
```

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 (`geom_point()`).
```

```
## Warning: Removed 314404 rows containing missing values (`geom_text()`).
```



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 plot tells us that the lemma frequencies of orthopedics and surgery are more related than orthopedics and radiology. Since most of the data points are above the predicted/trend line for surgery and orthopedics then this means they share more terms compared to radiology and orthopedics. Since most points are below the predicted/trend line for radiology then there are less shared words between radiology and orthopedics.

This does make sense since orthopedic medicine is a type of surgery and radiology is not a type of surgery.

Since radiology and surgery are both part of the x axis then we cannot directly compare them, this would just be a comparison of each of them in relation to orthopedic, as explained above.

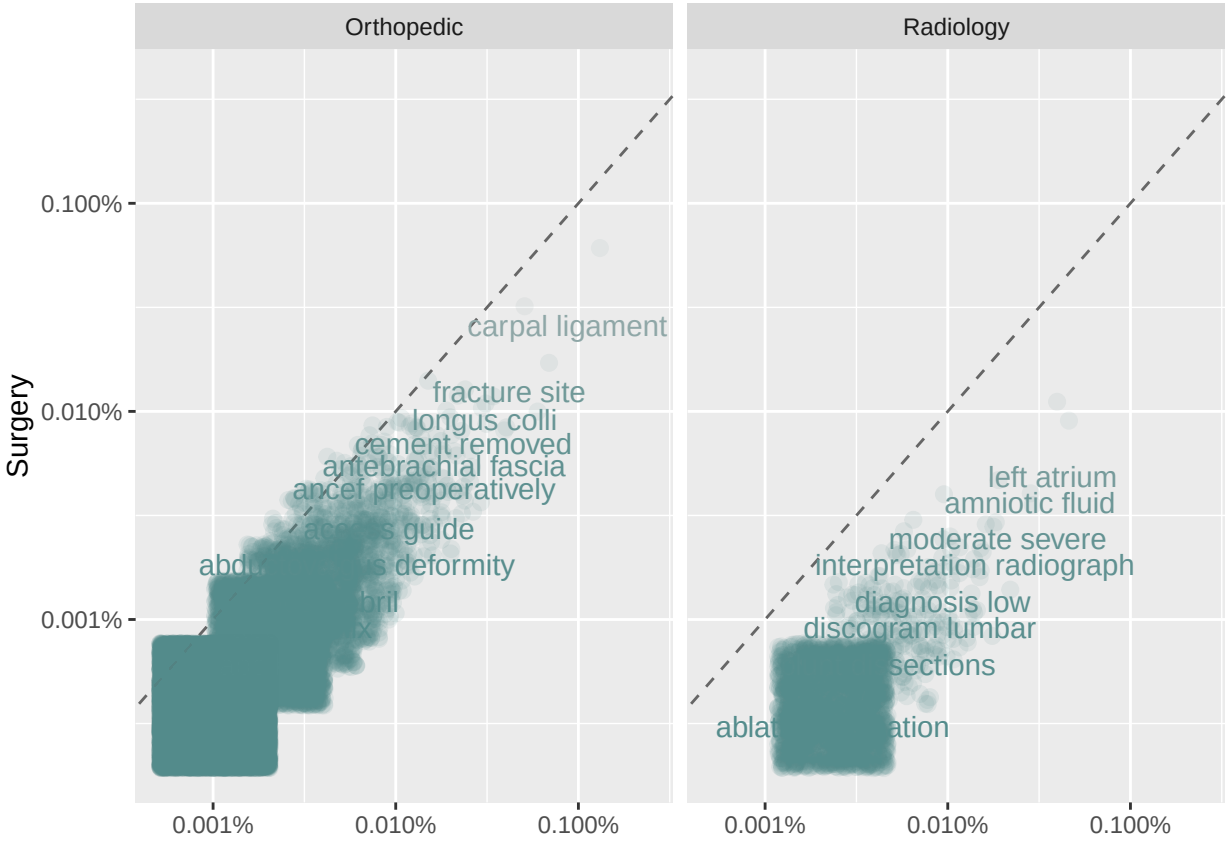
7 Modify the above plotting code to do a direct comparison of Surgery and Radiology (i.e., have Surgery or Radiology on the Y-axis and the other 2 specialties as the X facets)

```
lemma.freq.2 <- 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.2, 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 (`geom_point()`).
```

```
## Warning: Removed 317820 rows containing missing values (`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?

There are a few lemmas that stand out in these lists. "range motion" in orthopedic, has the highest tf value of 0.00142, and "left ventricular" in radiology, has the second highest tf value of 0.00117.

"Steri strips" also stands out as it is on the list twice, in surgery and orthopedics.

Another two terms that stand out are "anesthesia endotracheal" and "endotracheal anethesia", which are both in surgery. This is a reason why a general purpose lemmatizer may not be the best for medical termonology, as different doctors could use terms in different orders but means the same thing.

We can look at transcriptions using these unusual 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 thrombosed left forearm loop fistula~
```

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

```
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 fractured retained lumbar subarachno~
```

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)
```

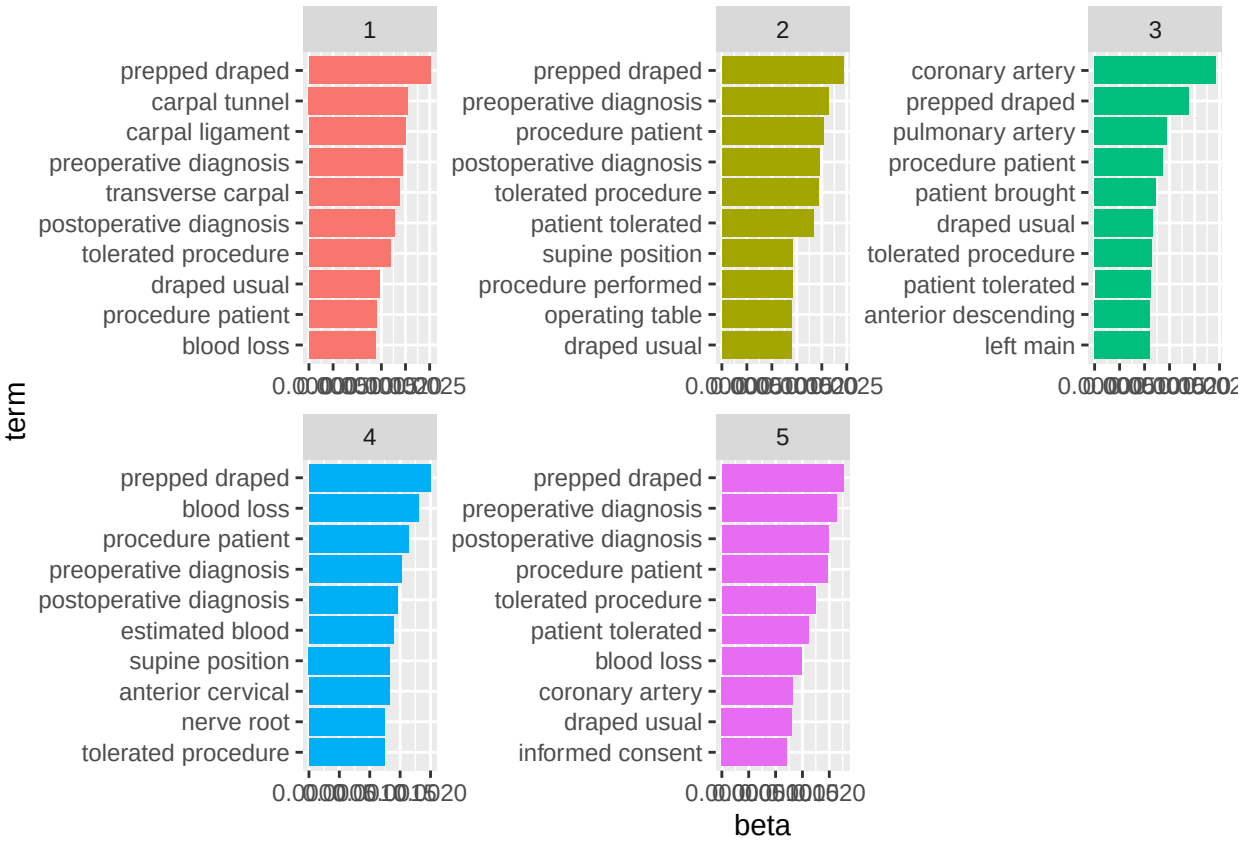
Then we can use LDA function to fit a 5 topic (k=5) LDA-model

```
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')  +
    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.

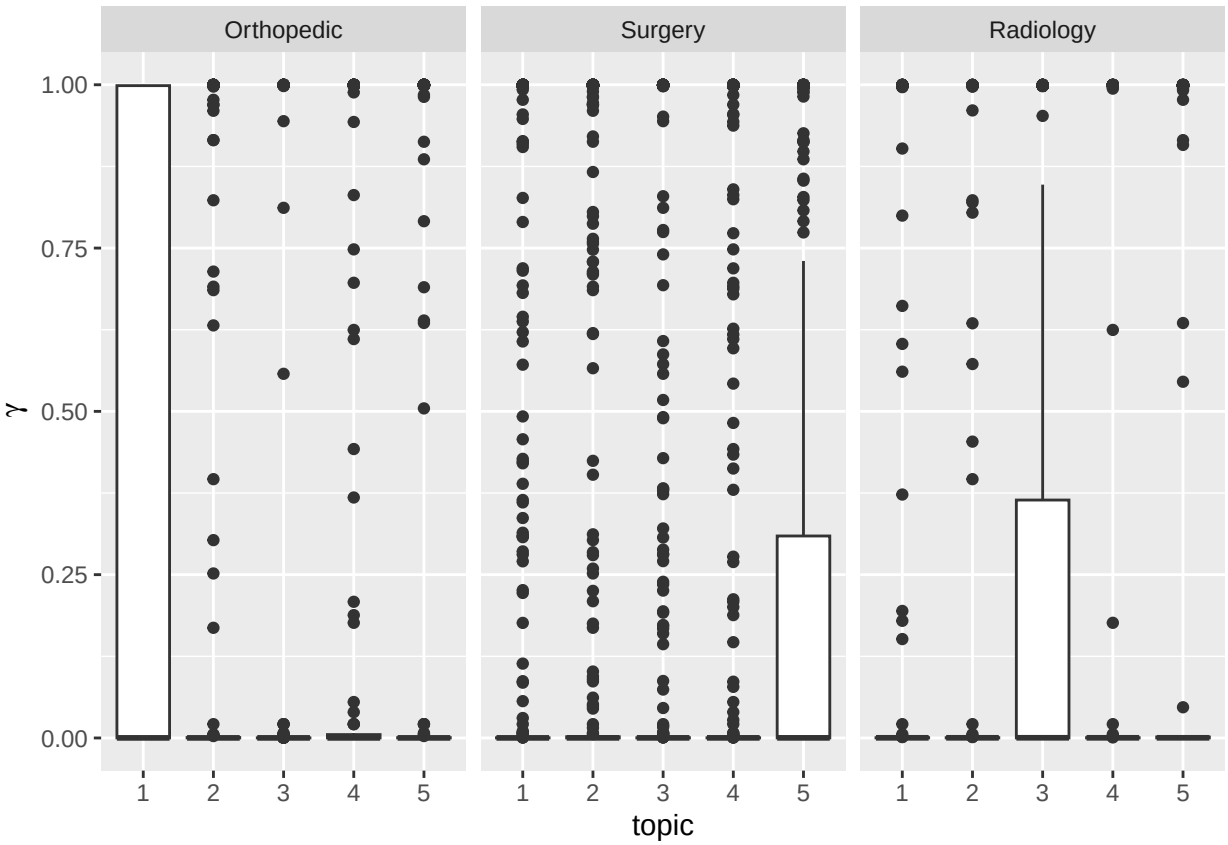
```
specialty_gamma <- tidytext::tidy(emr.lda, matrix='gamma')

# 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 assigns mostly to a single topic but radiology and Orthopedic are both more diverse in transcriptions. 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?

From the six topic LDA, most of the top terms from the five topic LDA still do turn up. Some of the top terms do not show up here and the terms are in different orders or included in a differet sub-topic.

The specialties get split into sub-topics by the content of the words. Each of the six documents/sub-topics are a mixture of words that are similar in terms of content or meaning. The content of the words are grouped together by the higher proportions of the words that are most related.

The LDA finds words that are most related with each specialty and at the same time determining the combination of topics that most closely describes each document.

```
lemma.counts.2 <- lemmatized.data %>% dplyr::count(note_id, lemma)
total.counts.2 <- lemma.counts.2 %>%
                    dplyr::group_by(note_id) %>%
                    dplyr::summarise(total=sum(n))

all.counts.2 <- dplyr::left_join(lemma.counts.2, total.counts.2)
```

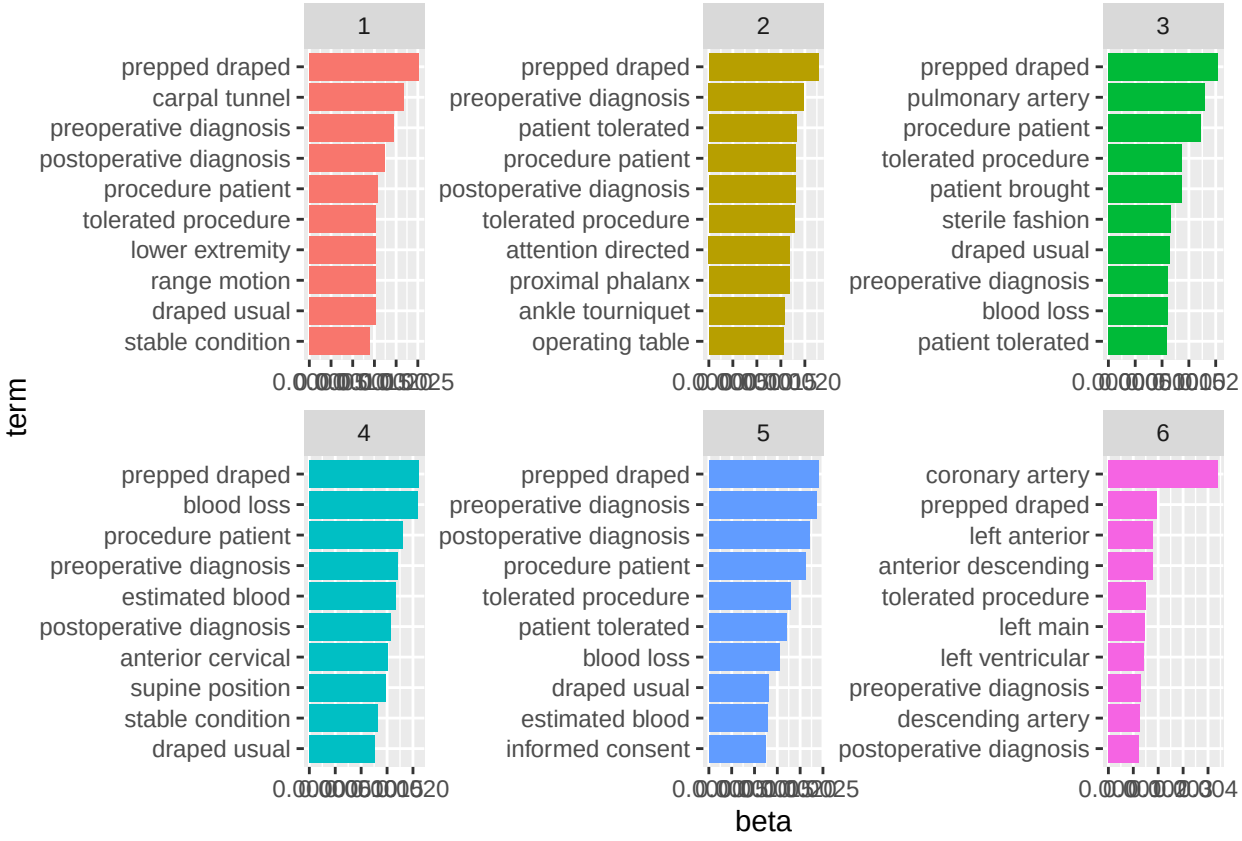
```
## Joining with `by = join_by(note_id)`
```

```
emr.dcm.2 <- all.counts %>% tidytext::cast_dtm(note_id, lemma, n)
```

```
emr.lda.2 <- topicmodels::LDA(emr.dcm.2, k=6, control=list(seed=42))
emr.topics.2 <- tidytext::tidy(emr.lda.2, matrix='beta')
```

```
top.terms.2 <- emr.topics.2 %>% dplyr::group_by(topic) %>%
  dplyr::slice_max(beta, n=10) %>%
  dplyr::ungroup() %>%
  dplyr::arrange(topic, -beta)


top.terms.2 %>%
  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')  +
    tidytext::scale_y_reordered()
```



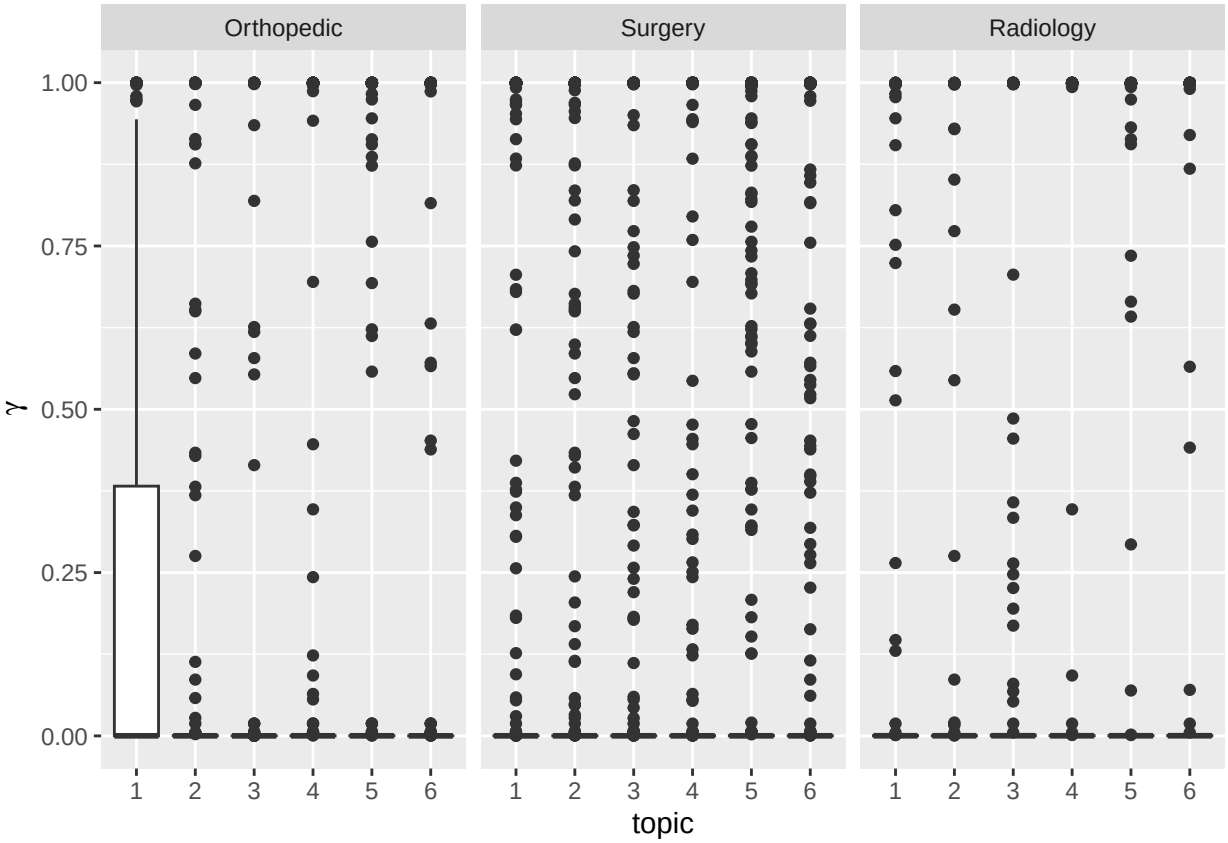

```
specialty_gamma.2 <- tidytext::tidy(emr.lda.2, matrix='gamma')

# we need to join in the specialty from the note_id
note_id_specialty_mapping.2 <- lemmatized.data %>%
  dplyr::mutate(document=as.character(note_id)) %>%
  dplyr::select(document, medical_specialty) %>%
  dplyr::distinct()

specialty_gamma.2 <- dplyr::left_join(specialty_gamma.2, note_id_specialty_mapping.2)
```

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

```
specialty_gamma.2 %>%
  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))
```



Credits

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