Assessing Keyness using Permutation Tests

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Abstract

We propose a resampling-based approach for assessing keyness in corpus linguistics based on suggestions by Gries (2006, 2022). Traditional approaches based on hypothesis tests (e.g. Likelihood Ratio) model the copora as independent identically distributed samples of tokens. This model does not account for the often observed uneven distribution of occurences of a word across a corpus. When occurences of a word are concentrated in few documents, large values of LLR and similar scores are in fact much more likely than accounted for by the token-by-token sampling model, leading to false positives. We replace the token-by-token sampling model by a model where corpora are samples of documents rather than tokens, which is much closer to the way corpora are actually assembled. We then use a permutation approach to approximate the distribution of a given keyness score under the null hypothesis of equal frequencies and obtain p-values for assessing significance. We do not need any assumption on how the tokens are organized within or across documents, and the approach works with basically *any* keyness score. Hence, appart from obtaining more accurate p-values for scores like LLR, we can also assess significance for e.g. the logratio which has been proposed as a measure of effect size. An efficient implementation of the proposed approach is provided in the `R` package `keyperm` available from github.

1 Introduction

In this paper, we consider the *keyness problem*, namely, assessing whether some words appear significantly more often in one corpus A than in another corpus B. Most existing approaches are based on *statistical hypothesis tests*, i.e. differences in frequencies of a word between two corpora A and B are judged to be significant if they are so large that they would be very unlikely under a *random sampling model*. Examples of these approaches are the well-known *Log-Likelihood-Ratio-Test*, χ^2*-tests* and *Fisher's Exact Test*. Other measures like the so-called *Log-Ratio* are also sometimes used, but these do not directly take into account random variation in the sampling process and hence tend to give very high scores to differences in very rare words which might well be due to chance.

Approaches based on statistical hypothesis tests are necessarily tied to some assumption of randomness. All methods currently used – as far as they are based on hypothesis testing – are justified under the assumption that the corpora A and B are samples of larger populations, say Pop_A and Pop_B. These are typically not larger corpora of actually existing texts from which a random selection was taken but some form of abstract infinite populations like "all texts that could have been produced by some author", "all texts that could have been published in a given newspaper in a given year", "the discourse on…", "actual use of language in certain media" etc. This is not a special feature of linguistics but very common in other applications of statistics, as we typically view a sample of e.g. patients with a certain type of disease not as a subset of all people who currently have the desease but also representative of patients that will develop the illness in the future, some of whom might not even be born yet. Hence, assuming the corpus is a random sample from some larger (abstract) population is not a problem per se.

The problem is rather the specific random sampling mechanism that is assumed. Here, we follow an argument also put forward in Gries (2006, 2022); see also Evert (2006) for a discussion of randomness and different sampling models. While assuming the corpora to be random samples of *texts* from larger populations of

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(potentially fictitious) texts seems reasonable in many cases, the assumption actually underlying the hypothesis tests as currently used is that the corpora are samples of *tokens*, i.e. the corpora are modeled as constructed by *independently* drawing single tokens, one by one, from the two populations. The reason is of course that the distributions of the relevant test statistics are known at least approximately under this assumption (χ_1^2 for LLR- and χ^2-tests, hypergeometric for Fisher's).

Apart from the fact that the smallest unit added to a corpus at a time is always a whole text (perhaps a very short one like in sentence corpora) this is unrealistic in at least two ways:

- Within a text, grammatical constraints limit which words can follow other words. The assumption of independence hence allows for ungrammatical as well as nonsensical texts.
- Words are generally not evenly distributed in corpora, i.e. they may appear several times in some texts and not at all in others.

While the first issue has also been used to criticize the use of hypothesis testing in this context (Killgariff 2005), the second issue seems to be more severe. The phenomenon itself is well known, and measures have been developed to measure uneven distribution (see eg. Gries (2008)). In addition, other procedures like topic modelling that are routinely performed on the same corpora start from the assumption that the distribution is uneven. Yet, the implications for keyness analyses are routinely ignored.

It might not be obvious why sampling in units larger than single tokens is a problem for keyness analyses at all. Word frequencies are measured by counting occurences across the corpus and dividing by the total number of tokens. This is also directly reflected in all currently used measures of keyness. While the measures are rightly interpreted with respect to tokens, as also pointed out by Gries (2006, 2022), the sampling distributions of the measures are much wider when taking into account that we sample *texts*, not single *tokens* at a time. We show some empirical examples later, but the idea can be seen as follows: Think of some word whose occurences are very unevenly spread, i.e. when we add a new text to the corpus, the occurence will be either much less or much more than "on average", i.e. the relative frequency in the new text will greatly deviate from the relative frequency across the whole population in either direction. On the other hand, if instead we independently added a corresponding number of tokens independently drawn, each of which has a probability of being equal to the word under consideration equal to the relative frequency in the population, the relative frequency of occurences will be much closer to the overall average. Hence, the ratio of occurences to total size in tokens changes much more when sampling larger units than it does when sampling single tokens. However, the latter model is used for judging how extreme a given score is, while more extreme values are actually much more likely just by chance under the much more realistic model of sampling text-by-text.

The increased variability due to not sampling independently token-by-token cannot be amended by just setting stricter thresholds, as the exact impact is generally unknown beforehand, may vary from corpus to corpus and, more severely, between words within the same corpus, depending on how unevenly distributed they are. Hence, two words might have the same LLR score, but due to differences in dispersion one might well be much more extreme than what would be expected by chance while the other may not.

In the following, we propose an approach based on *permutation tests*, that allows us to simulate (to arbitrary precision) the distribution of any conventionally used keyness score as well as new ones under the null hypothesis of equal frequencies in the two populations (technically speaking, we are actually testing a somewhat stonger hypothesis). This means we are not tied to measures for which the distribution is "known" (under a assumptions known to be blatantly wrong), but we can use a measure that is also more interpretable. The downside is that we cannot rely on standard critical values for judging significance, as the distributions will be different for each word in each corpus – meaning we have to be willing to utilize more computational resources. Permutation tests (see also Gries 2006) are computationally very similar to the *bootstrap* approach advocated in Gries (2022), but are conceptually different and are based on different assumptions.

The rest of the paper is organized as follows: In Section 2, we review some of the theory behind hypothesis testing for keyness analysis and explain the differences between the widely used sampling-token-by-token model and our sampling-text-by-text model in more detail. In Section 3, we point out some of the undesired effects of using current approaches by means of a numerical example. In Section 4, we give some further remarks on practical implementation.

The procedure introduced in this article is available in an R-package `keyperm` that can be installed from github[1]. Submission to CRAN is planned. In keyness analysis, we need high precision in the p-values in order to compare them, hence we need many simulation runs. To make this approach efficient, the core resampling part of the procedure has been implemented in `C++` using the `Rcpp` interface (Eddelbuettel et al. 2023).

2 Significance testing for keyword analysis

We consider the following problem: We have two Corpora A and B which are regarded as *samples* from larger populations Pop_A and Pop_B of (potential) texts. *Keywords* are words which appear more fruequently in Pop_A than Pop_B (sometimes we also want those that are more frequent in Pop_B). Often, B will be a *reference corpus*.

The general approach is a three-step procedure:

1. Calculate a *keyness score* for each word that appears at least once in one of A or B (usually directly equivalent to a *p-value*)
2. Filter the word list by setting a threshold on the scores (preferably taking into account multiple testing issues) and perhaps additional criteria
3. Order the words that pass the filter

Steps 2 and 3 are often mixed, i.e. the score is used for ordering the list and words are excluded based on a cut-off for the same score. This is not really appropriate as criteria like LLR measure *significance*, i.e. strength of evidence against the null hypothesis of equal frequencies in Pop_A and Pop_B. As such, they do not directly measure the *strength of the effect* and are therefore useful for filtering but not for ranking. Effect size measures like the *log-ratio* on the other hand do not take into account random variation and tend to be extreme for very small numbers occurences, making them unsuitable for filtering but useful for ranking. Hence, it generally makes sense to *filter by significance* and *order by effect size* (supported by `CQPweb` and recent versions of `AntConc`).

We will almost exclusively focus on step 1 in this article, as the currently used tests are not even valid for testing for a difference in frequencies for a single word. Hence, it is most important to get the tests (and associated p-values) right before considering problems of combining the results (which involve issues of multiple testing).

2.1 Tests of significance in contingency tables

For a potential keyword, consider the following contingency table:

	freq. of *word*	freq. of all other words	total
Corpus A	a	c	$n_A = a + c$
Corpus B	b	d	$n_B = b + d$
Total	$n_{word} = a + b$	$n_{\neg word} = c + d$	$n = n_A + n_B$

Log-Likelihood-Ratio (LLR) measures deviation of the table from what would be expected if the relative frequencies of *word* in Pop_A and Pop_B are the same.

$$LLR = -2\left(a\log\left(\frac{a}{E_a}\right) + b\log\left(\frac{b}{E_b}\right) + c\log\left(\frac{c}{E_c}\right) + d\log\left(\frac{d}{E_d}\right)\right),$$

where $E_a = \frac{a}{a+b} \cdot \frac{a}{a+c}$ and similiar for E_b, E_c, E_d.

Formally, LLR is a *test statistic* for testing

[1]The current development version can be installed by `remotes::install_github("thmild/keyperm")`

H_0: $\pi_A = \pi_B$ vs. H_1: $\pi_A \neq \pi_B$

where π_A and π_B are the "true" frequencies, i.e. the frequencies in Pop_A and Pop_B. π_A hence is the probability that a single token drawn from Pop_A is equal to the word under consideration and $(1 - \pi_A)$ is the probability that it is some other word. If H_0 is true, i.e. the probabilities (or population frequencies) are the same, the distribution of LLR is (approximately) known *under the assumption of independence*, i.e. under the model where corpus A is obtained by randomly drawing tokens from Pop_A, one by one, independent of each other, and similarly for corpus B. LLR then approximately follows a χ^2-distribution with 1 degree of freedom (χ^2_1). Since this distribution is known, it is easy to judge whether the LLR-value calculated for a given word is within the range of what one would expect by random variation or whether it is much larger. Usually, cut-offs are chosen from quantiles of this distribution, for example $\chi^2_{1,0.95} = 3.8414588$, i.e. if $\pi_A = \pi_B$, the LLR-score will only be larger than 3.84 with probability 5% and in this case one would declare the observed difference significant at the 5% level. This means than whenever $\pi_A = \pi_B$ a significant difference is only declared 5% of the time.

Equivalently, the p-value can be calculated as the probability for a LLR-value as large or larger than the value that was actually observed given that H_0 is true, i.e. $\pi_A = \pi_B$. The result is declared significant at level α if the p-value is smaller than or equal to α. A common value for α is 0.05, although α should be much smaller when more than one word is considered (as is the case in keyness analysis) and adjustments are available in most software packages.

Even under the token-by-token sampling assumption, the χ^2_1-distribution of LLR under the null is only approximate. The χ^2-test for contingency tables uses a test statistic with a different formula which however often results in similar values and also approximately follows a χ^2_1-distribution under the null. It has been argued that the LLR-statistic is more appropriate for keyness analysis than the χ^2-test because the approximation is more accurate in the case of skewness (Dunning 1993). In any case the model assumes that the corpora are drawn independently token-by-token, which in unrealistic, making the argument somewhat irrelevant.

While the (approximate) χ^2_1-distribution can be derived analytically, the true distribution can be approximated to arbitrary precision using a *permutation approach*, and this approach is easily adapted for the more realistic assumption that tokens are not drawn one-by-one but arrive in larger batches (one text at a time).

First we note that under the model where the tokens are drawn independently one-by-one from Pop_A and Pop_B, the row totals n_A and n_B (corpus sizes) and the column totals n_{word} and $n_{\neg word}$ (total frequencies of the word under consideration and all other words combined) do not contain *any* information on whether $\pi_A = \pi_B$ as long as none of a, b, c, d is known. Hence, we can regard these as *fixed*, although under the model the total number of occurrences of a word across both corpora would be subject to random fluctuations.

The distribution of LLR under H_0, i.e. assuming $\pi_A = \pi_B$ could now be obtained by performing (or simulating) the following experiment:

1. For every token in corpus A or B fill out a little sheet of paper. Put an "X" on the paper whenever the token is the word under consideration and leave the paper unmarked for any other word. This results in n slips of paper, n_{word} of these correspond to occurences of the word and $n_{\neg word} = n - n_{word}$ to occurences of other words.
2. Put the n sheets into a big box and shuffle well.
3. Randomly draw n_A sheets from the box and note how many of these are marked. Put this number in the a-field of the contingency table.
4. Fill out the other fields of the table – these can be obtained from a and the row and column totals.
5. Calculate the LLR score and record the value.
6. Repeat steps 2–5 a large number of times.

The resulting empirical distribution is an approximation of the theoretical distribution of LLR under H_0. Alternatively, the distribution can also be obtained numerically as given the row and column totals, LLR is a function of a and under this model, a follows a hypergeometrical distribution. The simulation approach, however, can easily be adapted to the more realistic sampling model described below.

Generally, sampling tokens one-by-one from two different population is a poor model of how corpora are actually created. Usually, whole documents are added to the corpus, i.e. tokens arrive in larger sets. Also, many words are distributed quite unevenly across the corpus and they often occur in a few documents with a much higher frequency and not all in others. Hence, adding a single document to a corpus leads to much greater changes in a test statistic like LLR compared to independently drawing the same number of tokens according to the independence model described above.

We therefore propose the treat the corpora as samples of *documents*, not as samples of *tokens* and assume random sampling of documents, independently of each other. This is arguably more realistic than the sampling-by-token model, although of course it may also be an oversimplification in some situations. While the sampling units are now documents, we still want to make statements about frequencies of words in the populations (e.g. in occurences per million), not about frequencies per document.

We still want to test the hypothesis

$$H_0 : \pi_A = \pi_B \quad \text{vs.} \quad H_1 : \pi_A \neq \pi_B$$

where π_A and π_B again are the frequencies of a given word in Pop_A and Pop_B, but we actually test the somewhat stronger hypothesis

$$H_0 : (n_A, N_A - n_A) \stackrel{d}{=} (n_B, N_B - N_b),$$

i.e. the pair of random variables (number of occurrences of *word* in Text, number of other *tokens* in text) has the same distribution among both Pop_A and Pop_B. Apart from the frequencies being the same this implies that the number of tokens per text is not systematically different. See chapter 3 of Good (2005) for a more technical discussion on assumptions for permutation tests.

Hence, for what follows, we assume that:

- Documents in both A and B are *homogenous*, i.e. not a mixture of different types
- Documents in A and B are *comparable* in size and type, e.g. texts in A are not systematically longer than those in B.
- We have frequency information *by document* for both corpora (e.g. as a term-document-matrix)

We do *not* need to assume that

- All the texts have the same length
- A and B consist of the same number of texts
- The order of tokens *in* a text is in any way random

Examples where we would use the method include:

- A and B are corpora of texts from the same newspaper but cover different years
- A and B are corpora of records of parliamentary debates from the same country but cover different years
- A and B are corpora of two quality newspapers from the same year.
- A and B are corpora of contemporary poetry written by men and women, respectively

Examples where it should probably not be used include:

- A and B are corpora of a tabloid and quality newspaper from the same year (debatable).
- A is a corpus of poems and B a corpus of short stories from the same author.
- A consists of written texts and B of transcriptions of spoken language.
- A and B both consist of crawled web forums, tweets and newspaper articles from the same sources but different years.

Most of these cases could be treated with similar methods using more sophisticated resampling schemes. These are part of ongoing research and here, we will only focus on the simple case of two homogenuous corpora which are similar in all other respects except for word frequencies.

The difference in the sampling scheme is now that we assume we sample document-by-document, not token-by-token, i.e. a whole set of tokens arrives at a time and the number of occurrences of the word under consideration is allowed to be much larger or much smaller compared to what would be expected from randomly drawing token-by-token. After sampling the two corpora document-by-document, we can create the same 2 x 2 - table as above by counting occurences and totals, and we can calculate the same score (for example LLR) as in the token-by-token case; the result will be the same.

The difference is the *distribution* of the score, as the larger fluctuation results in a wider distribution. This means that under this model, scores that are regarded *extreme* in the token-by-token-sampling-model may well occur quite frequently randomly, even if the population frequencies do not differ. It is not obvious how the distribution of the score under the document-by-document-sampling could be treated analytically, but it is possible to use a simulation approach similar to the one described above for token-by-token sampling.

If $\pi_A = \pi_B$, i.e. there is no systematic difference in frequencies in the populations, and under the assumption that the document length do not differ systematically, a document with a given total number of tokens and a given number of occurences of the word under consideration could equally well come from Pop_A or Pop_B. Hence, the actually observed table or the score calculated from it should not be very different from what would have been obtained when the labels of the documents had been randomly assigned. We can then approximate the distribution of LLR (or other statistics) by not *shuffling and randomly drawing tokens*, but by *shuffling and randomly drawing documents*. In contrast to the token-by-token model the number of tokens in the randomly generated corpora is not fixed, but the number of documents in the corpora is.

This results in the following experiment, which can easily be simulated on a computer:

1. For every *document* in corpus A or B fill out a little sheet of paper. Put the number of occurences of the word under consideration and the total number of tokens in the document on the paper. This results in $N = N_A + N_B$ slips of paper, where N_A and N_B are the numbers of documents in A and B.
2. Put the N sheets into a big box and shuffle well.
3. Randomly draw N_A sheets from the box and add up the occurrences of the word under consideration as field a and the total number of tokens n_A in the table.
4. Fill out the other fields of the table.
5. Calculate the LLR score and record the value.
6. Repeat steps 2–5 a large number of times.

We now use the empirical distribution of the LLR scores obtained in this way as an approximation of the (unknown) theoretical distribution of the scores. The extremeness of a given score value is now judged against this distribution, which is typically considerably wider than the χ_1^2 distribution or the simulated distribution obtained under the token-by-token model. This is especially pronounced if the occurrences are concentrated in a small number of documents.

3 Numerical Expriment: Dail corpus

A numerical example shows that the actually much wider null distribution is a considerable problem. We use a recently released corpus of transcripts of parliamentary debates in Ireland (Herzog and Mikhaylov 2017). We assign the 919 transcripts from 2001 − 2010 to Corpus A and the 925 transcipts from 1991 − 2000 to corpus B. Since different parliamentary sessions treat different topics, the different dispersion of words between texts should be especially pronounced in this example: many words should appear very frequently in some transcripts and not at all in others.

We run the standard approach of calculating LLR scores for every word. All in all, there are 193170 different words in both corpora combined. About 40% of these are significantly more frequent in A or B ($p < 0.05$), 29% have $p < 0.01$, according to the standard LLR approach (token-by-token) using a comparison with quantiles of the χ_1^2 distribution.
We now *shuffle the labels*: Of all 1844 texts, we randomly label 919 as A and the remaining 925 as B. Now there are no *systematic* differences in word usage in A and B, and words can only appear more frequently in one of the corpora by chance (so there are no true keywords here!).

We re-run the Log-Likelihood-Ratio test on these new randomized data. We repeat this 100 times. This results in the following procedure:

1. Calculate the test statistic (LLR) for every potential keyword
2. Shuffle the labels: Randomly assign the texts to A or B so that the same number is assigned to each corpus as in the original labelling
3. Calculate the test statistic (LLR) for every potential keyword based on the shuffled labels and record it
4. Repeat steps 2-3 a large number of times
5. For each potential keyword, obtain a p-value by comparing with the χ_1^2 distribution.

We do expect a few *false positives*: On average 5% of the words should have a p-value smaller than or equal to 0.05, 1% should have a p-value smaller than or equal to 0.01 etc. But, as Figure 1 shows, the numbers of false positives are actually much larger when naively comparing the values of LLR to a χ_1^2-distribution (red) vs. comparing to the simulated null distribution based on text-by-text-sampling (blue) as well as a permutation test based on the log-ratio (see also section 4). We see that for most random relabellings, the naive approach yields many more false positives than expected, while for the permutation approaches, most random relabellings do not produce a high number of false positives.

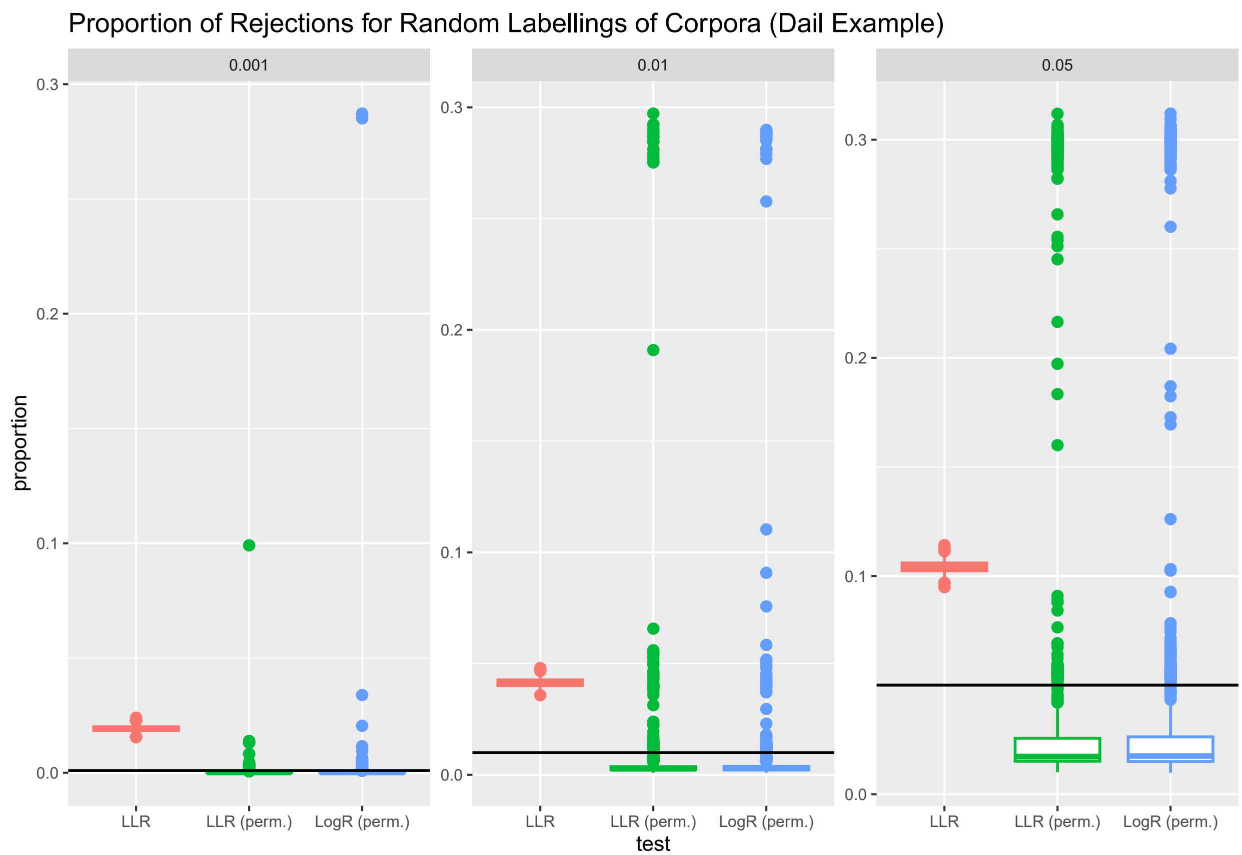


Figure 1: Simulation results: Boxplots of the proportion of significant words at different significance levels from randomly reassignment of the texts to corpora A and B (dots) when the usual LLR-approach is used (red) vs. our permutation-based approach using LLR (blue) or the log-ratio (green, see sec. 4).

We now look at the simulated null distribution for one word, "simon". As a proper noun, we can expect this word to be quite unevenly distributed, because a person named "Simon" could be mentioned frequently in the same document and not at all in others. Figure 2 shows the histogram of the simulated null distribution compared to the usually used χ_1^2 distribution. We see that the simulated distribution is wider, meaning that it frequently produces values that would be considered extreme relative to the χ_1^2 distribution.

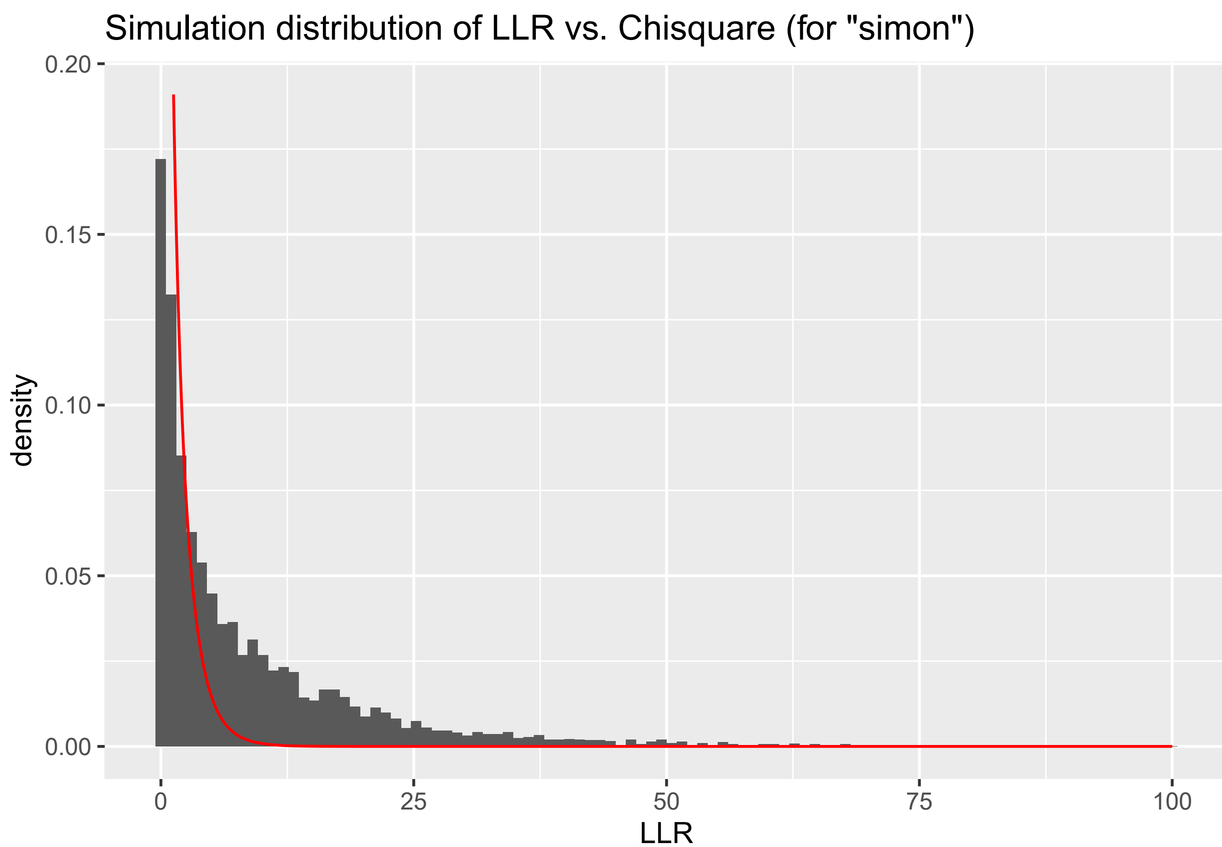
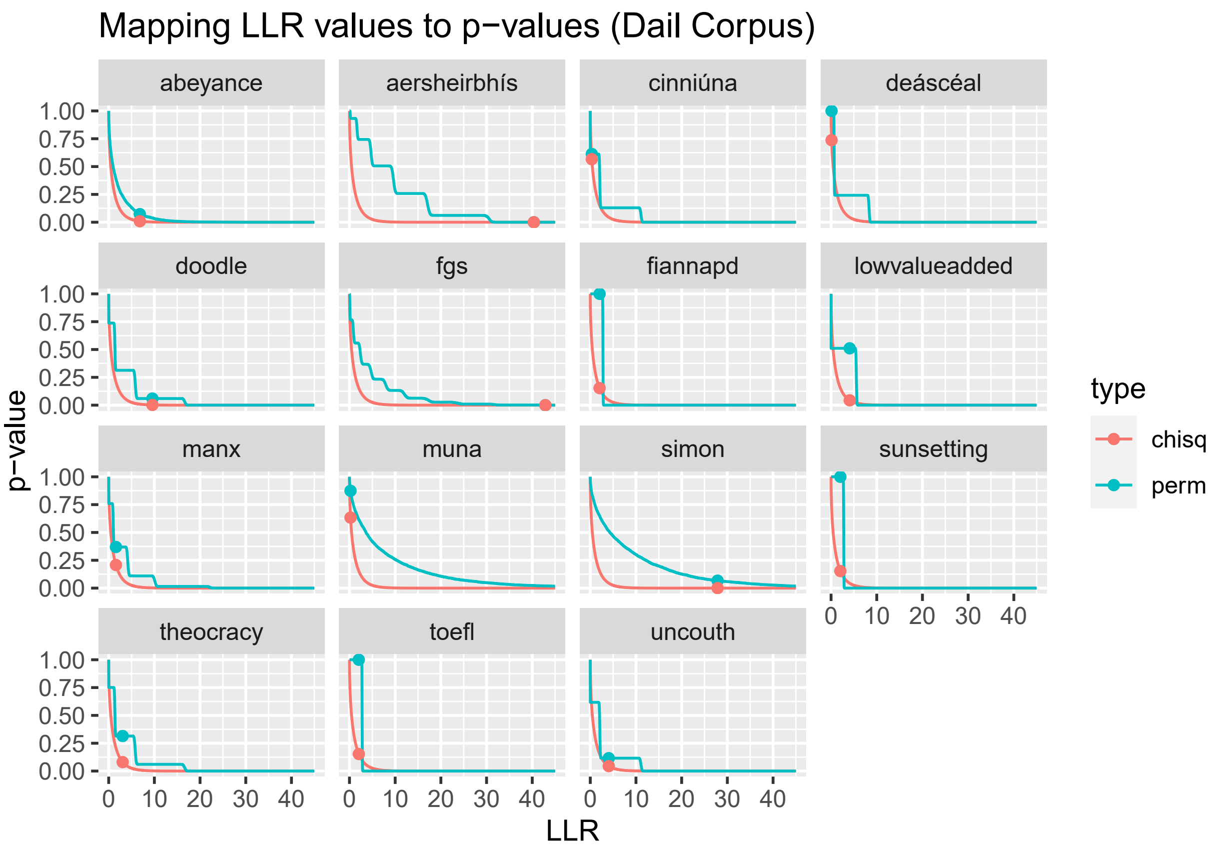


Figure 2: Simulated null distribution (histogram) vs. χ_1^2 distribution (red)

Generally, the distribution of a test statistic under H_0 can be very different even if two words occur with the same frequencies in A and B. Very often, the distributions put more mass on larger values than the χ^2_1. Especially when occurrences of a word are concentrated in only a few texts (lumping), large values of LLR have a much higher probability than they would according to the χ^2_1 distribution. With our approach, the *same* LLR value can lead to *very different* p-values for different words, and this is desired!

Figure 3 shows p-values versus value of the LLR statistic for a random selection of words from the corpora. The red curves are based on the commonly used χ^2_1 distribution and are the same for all words, while the blue ones ares based on the permutation approach. The dots mark the realized value, and we see that p-values based on the permutation approach are usually larger, sometimes much larger, than those based on the χ^2_1-distribution, meaning that under the more realistic text-by-text sampling model, the χ^2_1-distribution (based on the token-by-token sampling model) produces too many significant results.



Our approach is computationally costly. The test produces valid p-values if the observed test statistic on the original data set is included in the permutation distribution, but the test is a bit conservative in this case and the minimum possible p-value is $1/(n_{simulations} + 1)$. This means that if a multiple testing correction is used, we are especially interested in very small p-values and we need a huge number of simulations to obtain a reasonable accuracy. This is considered in more detail in the next section.

4 Implementation and extensions

4.1 Choice of Test Statistic

The approach based on permutation tests allows us to approximate the null distribution of *any* test statistic related to keyness. This includes the commonly used LLR and $Chisquare$ statistics. However, these are basically only used because their distribution under the null hypothesis are approximately known – under the inappropriate token-by-token-sampling model. Otherwise, they have a number of drawbacks:

- LLR and $Chisquare$ are not very well interpretable, they are essentially measuring the deviation from a null model. In addition, this null model is itself also based on the inappropriate token-by-token-sampling assumption, making the interpretation of the measure questionable under more realistic assumptions.
- LLR and $Chisquare$ do not give an indication of the effect size, although $Chisquare$-based effect sizes are available in the literature.
- LLR and $Chisquare$ are directionless in the sense that they do not discriminate between $\pi_A > \pi_B$ and $\pi_A < \pi_B$. If only departures in one direction are to be detected, one has to resort to ad-hoc filtering based on observed frequencies.
- LLR and $Chisquare$ are based on 2x2 contingency tables and are symmetric with respect to occurrences and non-occurrences. In classical keyness analysis counting non-occurences is straightforward. If one is for example interested in constructs consiting of several words, the definition of non-occurences becomes difficult.

Since we need to simulate the distribution anyway, there is no reason for using these test statistics. We can as well use a test statistic that is more interpretable. An obvious candidate is the *logratio* statistic:

$$Logratio = \log_2 \frac{\frac{a}{n_A}}{\frac{b}{n_B}}$$

This statistic is well-established for keyness-analysis. It has a few advantages over $LLR/Chisquare$:

- It directly measures the effect size, and hence is very interpretable. An increase by one unit means that the ratio of the relative frequencies doubles.
- The logratio gives the direction of the effect, positive values mean that the word is more frequent in A, negative values mean it is more frequent in B
- The logratio is based on the number of occurrences and the sizes of the corpora as measured by the number of tokens, hence it does not require the calculation of non-occurrences.

So far, the logratio has only been used as an effect size, as the sampling distribution is not known, so it is commonly not used to assess statistical significance, and indeed values can be large for very rare words as it is easy to have a large increase in relative frequencies by chance in this case. This is either taken care of by ad-hoc-filtering by a minimum number of occurrences or by using some other significance-based statistic like LLR for filtering. `CQPweb` also offers the option to use an approximate confidence interval for the Logratio for filtering. However, the calculation is also based on the token-by-token sampling model.

For our approach, we can readily approximate the null distribution also for the logratio statistic. It is important to note that the distribution will also be different for each pair of corpora and for each word under consideration, depending on the absolute number of occurrences and the evenness of the distribution (dispersion). Two words may well have the same logratio value, but the resulting p-values could be very different, making one significant while the other is not.

We can then filter by significance using the p-values obtained using the random permutations, and order the words surviving the filtering step by the size of the logratio.

One problem with the logratio statistic is that it can take (positive or negative) infinite values if one of the relative frequencies in the numerator or the denominator is zero. Note that not both can be zero if there is at least one occurrence of the word. This is unconvenient, as zero occurences in Corpus B lead to a value of $+\infty$, regardless of whether the word appears in A exactly one time or several thousand times. Even if the observed Logratio is finite, infinite values can also easily occur when calculating the null distribution, as occasionally the random permutation may assign all documents containing the word to one of the corpora.

For this reason, it may be helpful to slightly modify the definition using and add a typically small number $k > 0$:

$$Logratio = \log_2 \frac{\frac{a+k}{n_A+k}}{\frac{b+k}{n_B+k}}$$

This amounts to adding k occurences of the word to both corpora and also increasing the total number of tokens in both by k; $k = 0$ corresponds to the original definition. The simplest choice is $k = 1$, but k need not be an integer. This makes the logratio take a finite value also when either a or b is zero. In the case where $b = 0$, the logratio will increase with a, which intuitively makes sense - a high keyness score should be assigned to a word that occurs very often in A but not at all in B, while one occurrence in A and none in B is not an indicator of keyness. The trick of adding a small amount to avoid zeros is often called a *Laplace-correction* and well known in statistics. The *simple math* statistic introduced in Kilgariff (2009) is – apart from not taking logarithms – based on a similar idea, although it is only suggested for use as a descriptive measure.

4.2 Implementation

Whether *LLR*, *Chisquare*, Logratio or any other statistics is used, the basic steps to obtain a p-value are the following:

1. Calculate the test statistic for every potential keyword
2. Shuffle the labels: Randomly assign the texts to A or B so that the same number is assigned to each corpus as in the original labeling
3. Calculate the test statistic for every potential keyword based on the shuffled labels and record it
4. Repeat steps 2-3 a large number of times
5. For each potential keyword, obtain a *p-value* by calculating the fraction of values of the test statistic that are as extreme or more extreme than the one obtained for the original labeling.

The implementation is conceptually most straightforward if the frequencies are given as a term-document matrix T, with counts for term i in document j stored in T_{ij}, although this is not the most efficient data structure in terms of speed and memory usage. If the columns are originally arranged such that columns $1, \ldots, N_A$ correspond to the documents in A and columns $N_A + 1, \ldots, N_A + N_B$ correspond to those in B, the shuffling of documents corresponds to randomly permuting the columns and assigning the first N_A columns to corpus A and the others to B before re-calculating the statistic.

Note that we shuffle the documents (or columns of the term-document matrix) once before re-calculating the statistics for *all* terms under consideration. In this way, also dependencies between occurrences of different words are kept intact during resampling. While this is not needed for the calculation of p-values, it is computationally more efficient, and it may be of interest for other analyses. In addition, some corrections for multiple testing require knowledge of correlations between different p-values.

For the calculation of p-values we follow Chihara and Hesterberg (2019, ch. 3.3): valid (slightly conservative) p-values are calculated easily in the following way. For a one-sided test (right side), we count the number of random permuations that resulted in a value of the test statistic that was greater or equal to the observed value of the original, unpermuted data:

$$\text{p-value}_{right} = \frac{\text{no. greater} + \text{no. equal} + 1}{\text{no. of permutations} + 1}$$

and similar for the left-sided test:

$$\text{p-value}_{left} = \frac{\text{no. less} + \text{no. equal} + 1}{\text{no. of permutations} + 1}$$

Adding 1 in both the numerator and denominator amounts to including the observed value. This results in a slightly conservative p-value, but guarantees that the test is valid for any number of random permutations. It also means that never a p-value of zero is returned but the minimum possible p-value is $1/(\text{no. permutations} + 1)$.

The two-sided p-value is calculated by

$$\text{p-value}_{twosided} = 2 \cdot \min\{\text{p-value}_{left}, \text{p-value}_{right}\}$$

(values larger than 1 are set to 1).

The approximation of the p-values by randomly drawing permutations is more accurate if the number of iterations is larger. The construction as given above (add 1 in numerator and denominator), however, ensures that we err on the conservative side. If the null hypothesis is true, the probability of obtaining a p-value smaller that α is never greater than α, although it may be considerably smaller than α if the number of random permutations is small. Hence, the test is valid for any number of permutations, but the power may be low if the number of permutations is small.

Since keyness analysis typically involves testing a large number of words, some kind of multiple testing correction should be employed. For this, p-values are compared to a much smaller threshold than the conventionally used $\alpha = 0.05$ for single tests. This means that we need very high accuracy especially for the very small p-values, an in addition, the minimum p-value than can possibly be obtained with a given number of random draws is $1/(\text{no. permutations} + 1)$ for one-sided tests and $2/(\text{no. permutations} + 1)$ in the two-sided case. So the number of permutations should be chosen as large as feasible (in the millions), but must in any case be large enough that it is possible to obtain p-values smaller than the significance threshold.

This makes the method somewhat computationally costly, and an efficient implementation is needed. The `keyperm` package for `R` uses code partly written in `C++` that utilizes an efficient data structure. This is made possible by use of the `Rcpp` package (Eddebuettel et al. 2023, Eddelbuettel 2012). In addition, the calculations can be trivially parallelized and results of several runs on different cores can be easily combined. It should also be noted that only the small p-values are needed with high accuracy; p-values far away from any reasonable significance threshold need to be known only very approximately. This suggests performing an initial run of only a few thousand random permutations to decide on the words for which more accurate p-values are needed. Only for these more extensive runs are needed. The package also includes some helper functions and example code to enable this.

4.3 R Example

We now give a simple example of use of the `keyperm` package using small Reuters corpora. We first load the package, as well as the `tm` package (Fleinerer and Hornik 2023) which includes the example corpora. These are loaded as well:

```r
library(keyperm)
library(tm)

# load subcorpora "acq" and "crude" from Reuters

data(acq)
data(crude)
```

We then calculate a term-document matrix for both corpora separately and combine them into one `tdm` object. Currently, `tdm` objects using the `tm` package are the only supported input format for the `keyperm` package. We then also create a logical vector that indicates which columns of the term-document matrix belong to which corpus.

```r
# convert to term-document-matrices and combine into single tdm

acq_tdm <- TermDocumentMatrix(acq, control = list(removePunctuation = TRUE))
crude_tdm <- TermDocumentMatrix(crude, control = list(removePunctuation = TRUE))
tdm <- c(acq_tdm, crude_tdm)

# generate a logical that indicates whether document comes from "acq" or "crude"

ndoc_A <- dim(acq_tdm)[2]
ndoc_B <- dim(crude_tdm)[2]
corpus <- rep(c(TRUE, FALSE), c(ndoc_A, ndoc_B))
```

Now we convert the `tdm` object to what we call an indexed frequency list, containing the same information but in an optimized data structure especially suitable for fast computations.

```r
# generate an indexed frequency list, the data structure used by keyperm

reuters_ifl <- create_ifl(tdm, corpus = corpus)
```

We now calculate the LLR values along with p-values from the conventionally used χ^2_1-distribution, which – as we argued above – is wrong because it is based on a token-by-token sampling model.

```r
# calculate Log-Likelihood-Ratio scores for all terms and calculate
# p-values according to the (wrong) token-by-token sampling model

llr <- keyness_scores(reuters_ifl, type = "llr", laplace = 0)
head(round(pchisq(llr, df = 1, lower.tail = FALSE), digits = 4), n = 10)
```

```
##        125        150     200000      50000    acquire additional       also
##     0.1072     0.3886     0.9483     0.3523     0.0003     0.1884     0.2315
##        and        any        are
##     0.1437     0.4504     0.3589
```

Now we obtain permutation-based p-values using the `keyperm()` function, which are usually, but not always, larger. We pass the indexed frequency list, and the original LLR values and indicate that we want 10000 permutation values of the LLR statistic:

```r
# generate permutation distribution and p-values based on document-by-document sampling model

keyp <- keyperm(reuters_ifl, llr, type = "llr",
                laplace = 0, output = "counts", nperm = 10000)
head(p_value(keyp, alternative = "greater"), n = 10)
```

```
##        125        150     200000      50000    acquire additional       also
## 0.05139486 0.69863014 0.95930407 0.34696530 0.00489951 0.34696530 0.38326167
##        and        any        are
## 0.17118288 0.52484752 0.40865913
```

We can also get p-values not using the LLR but the log-ratio. To avoid dividing by zero, we use a laplace correction adding 1 both in the numerator as well as the denominator. We do a first run with 1000 permutations:

```r
# generate observed log-ratio values and (one-sided) p-values based
# on the permutation distribution (document-by-document sampling model)
# laplace-correction used (adding one occurence to both corpora)

logratio <- keyness_scores(reuters_ifl, type = "logratio", laplace = 1)
keyp2 <- keyperm(reuters_ifl, logratio, type = "logratio",
                laplace = 1, output = "counts", nperm = 1000)
head(p_value(keyp2, alternative = "greater"), n = 10)
```

```
##         125         150      200000       50000     acquire  additional
## 0.023976024 0.676323676 0.557442557 0.064935065 0.003996004 0.064935065
##        also         and         any         are
## 0.209790210 0.096903097 0.256743257 0.781218781
```

We now filter the small p-values, and run 9000 further simulations for the corresponding words, as we need higher accuracy in the small p-values. Note that 10000 simulations are usually not enough for real practical applications.

```r
pvals <- p_value(keyp2, alternative = "greater")
table(pvals > 0.1)
```

```
##
## FALSE  TRUE
##  1330  1042
```

```r
small_p <- which(pvals < 0.1)

# subset the original logratio values and create a new, smaller, indexed frequency list:

logratio_subset <- logratio[small_p]
reuters_ifl_subset <- create_ifl(tdm, subset_terms = small_p, corpus = corpus)

keyp2_subset <- keyperm(reuters_ifl_subset, logratio_subset, type = "logratio",
                 laplace = 1, output = "counts", nperm = 9000)
```

We can use the `combine_results()` function to combine the results from both simulation runs. Note that this works despite the fact that in the second simulation only a subset of words was used. The function is also useful for parallelization where different simulation runs may run on different cores or computers.

```r
# combine counts from both runs using the combiner

keyp2_combined <- combine_results(keyp2, keyp2_subset)

# smaller p-values are based on 1000, the larger ones on 10000 random permutations
# note that 10000 is still far too small for real applications

head(p_value(keyp2_combined, alternative = "greater"), n = 10)
```

```
##        125        150     200000      50000    acquire additional       also
## 0.01679832 0.67632368 0.55744256 0.05479452 0.00259974 0.05479452 0.20979021
##        and        any        are
## 0.09549045 0.25674326 0.78121878
```

5 Discussion and Outlook

We presented a permutation test approach to keyness analysis, based on a *text-by-text* sampling model, in contrast to the conventionally used methods, which are implicitly based on a *token-by-token* sampling model. Unevenness of distrbiution of words makes the more realtistic *text-by-text* sampling distribution of a test statistic typically wider than the conventionally used reference distributions, meaning that seemingly extreme values of test statistics are actually much more common than predicted by e.g. the χ_1^2 distribution.

The idea can easily be extendended, and indeed proposals based on similar ideas have been put forward by Gries (2006, 2022). For example, if the two different corpora are from different years and both contain tweets and newspaper articles (a case we excluded in our discussion above), we could shuffle lables between tweets and articles separately, not mixing the two, hence keeping the number of tweets and articles constant in each resampling step. Also possible would be the use of test statistics which compare more than two corpora at once.

Computationally similar to permutation tests but conceptually different are bootstrap methods, which could be implemented similarly (see Gries 2022). These may be used to construct confidence intervals of a measure instead of performing a test, and they could also be used for one-sample problems, as sometimes it may be appropriate to treat a reference corpus as fixed and only the corpus compared with it as a random sample.

Currently, only the basic version of the permutation test is implemented in our `R` package `keyperm`, but the extensions sketched here are part of ongoing investigations and some of these may be added at a later date. Also, the package is currently available on github but submission to CRAN is planned in the near future.

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