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Heat Map with Hierarchical Clustering: Multivariate Visualization Method for Corpus-based Language Studies

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Abstract

An advantage of corpus-based language studies is that global descriptions of linguistic texts can be obtained by examining a broad range of linguistic features. However, multivariate statistical techniques are required to analyze the multiple linguistic features found in a number of texts. This study compared the strengths and weaknesses of several multivariate statistical techniques, thereby demonstrating the effectiveness of using heat map with hierarchical clustering as a powerful method for visualizing multivariate data. Explanations are also provided for how these techniques can be used in the R programming language as well as indicating how the results obtained can be interpreted.*

Key words: multivariate visualization, corpus analysis, heat map, hierarchical clustering, R

1. Introduction

An advantage of corpus-based language studies is that global descriptions of linguistic texts can be obtained by examining a broad range of linguistic features. However, multivariate statistical techniques are required to analyze the multiple linguistic features found in a number of texts. These techniques can identify the complex interrelationships among linguistic features and texts, as well as the associated patterns between linguistic features and texts. The appropriateness of these techniques for analyzing language has been confirmed in the past few decades. For example, Burrows (1987) employed principal components analysis to analyze the idiolects of the major characters in Jane Austen's novels. Biber (1988) applied factor analysis to describe the linguistic characteristics of speech and writing. Nakamura and Sinclair (1995) used Hayashi's Quantification Method Type III, a method that is mathematically identical to correspondence analysis, to compare the frequencies of the collocates of the word *woman* in four components of the Bank of English, a representative subset of the COBUILD Corpus. Moreover, Hoover (2003) used cluster analysis to distinguish texts written by different authors using commonly occurring words in these texts. In the present study, I compared the strengths and weaknesses of several multivariate statistical techniques, thereby demonstrating the effectiveness of using heat map with hierarchical clustering as a powerful method for visualizing multivariate data. I also explain how these techniques are used with R (Ihaka and Gentleman 1996) and how the results can be interpreted.

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2. Multivariate visualization methods

Visualization is useful for identifying meaningful patterns in multivariate data comprising a large number of samples (e.g., texts and corpora) and variables (e.g., letters, words, and grammatical features). It also provides an intuitive understanding of the significant associations among samples and variables.

2.1 Correspondence analysis

One of the most common ways of visualizing multivariate data is using a scatter plot. Scatter plots can be utilized to visualize the results of factor analysis, principal components analysis, correspondence analysis, and multidimensional scaling (Baayen 2008). In particular, correspondence analysis is most popular in the fields of stylometry and corpus linguistics (e.g., Linmans 1998, Nakamura 1993, Tabata 2002, Wilson 2005). Correspondence analysis is an exploratory technique for mathematically summarizing the relationships between samples and variables, which graphically represents them in a two- or three-dimensional scatter plot (Glynn 2014).

Several packages are available for conducting correspondence analysis in R (e.g., `ade4`, `amap`, `anacor`, `ca`, `FactoMineR`, `homals`, `pamctdp`, and `vegan`). In this study, I selected the `ca` package (Nenadic and Greenacre 2007) because the author dataset containing the counts for the 26 letters of the alphabet in 12 different text samples is included as a sample dataset in this package. The letter counts do not include proper nouns.

Table 1: Part of the author dataset in the `ca` package

	<i>a</i>	<i>b</i>	<i>c</i>	<i>d</i>	...	<i>z</i>
three daughters (buck)	550	116	147	374	...	3
drifters (michener)	515	109	172	311	...	5
lost world (clark)	590	112	181	265	...	10
east wind (buck)	557	129	128	343	...	4
farewell to arms (hemingway)	589	72	129	339	...	2
sound and fury 7 (faulkner)	541	109	136	228	...	1
sound and fury 6 (faulkner)	517	96	127	356	...	5
profiles of future (clark)	592	151	251	238	...	20
islands (hemingway)	576	120	136	404	...	5
pendorric 3 (holt)	557	97	145	354	...	4
asia (michener)	554	108	206	243	...	6
pendorric 2 (holt)	541	93	149	390	...	2

The R script used to perform correspondence analysis for this dataset is as follows.

```
> # Installing the package
> install.packages("ca", dependencies = TRUE)
> # Loading the package
> library(ca)
> # Performing correspondence analysis
> ca.res <- ca(author)
> plot(ca.res)
```

Figure 1 shows the scatter plot obtained by running the correspondence analysis. The coordinates in the figure reflect the interrelationships between 12 text samples, the relative proximity between the 26 letters of the alphabet, and the association patterns between text samples and letters.

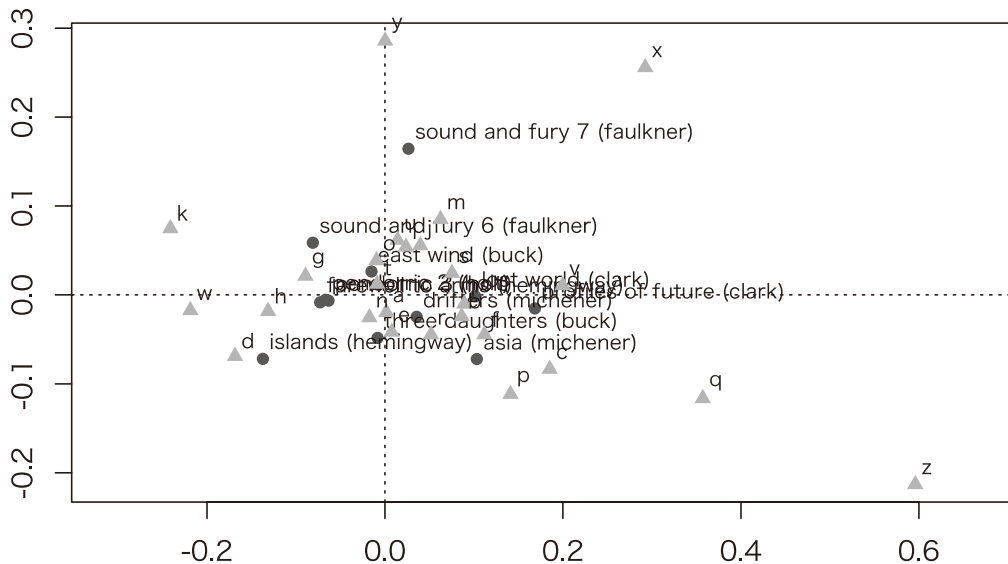


Figure 1: Correspondence analysis (samples and variables)

Figure 1 graphically illustrates both the samples and variables in two-dimensional space. Therefore, it is difficult to verify the relationships between them in cases where many samples and variables are plotted in the scatter plot. An alternative option is to display only the samples or variables in the plot to facilitate their readability.

```
> # Plotting only text samples
> plot(ca.res, what = c("all", "none"))
```

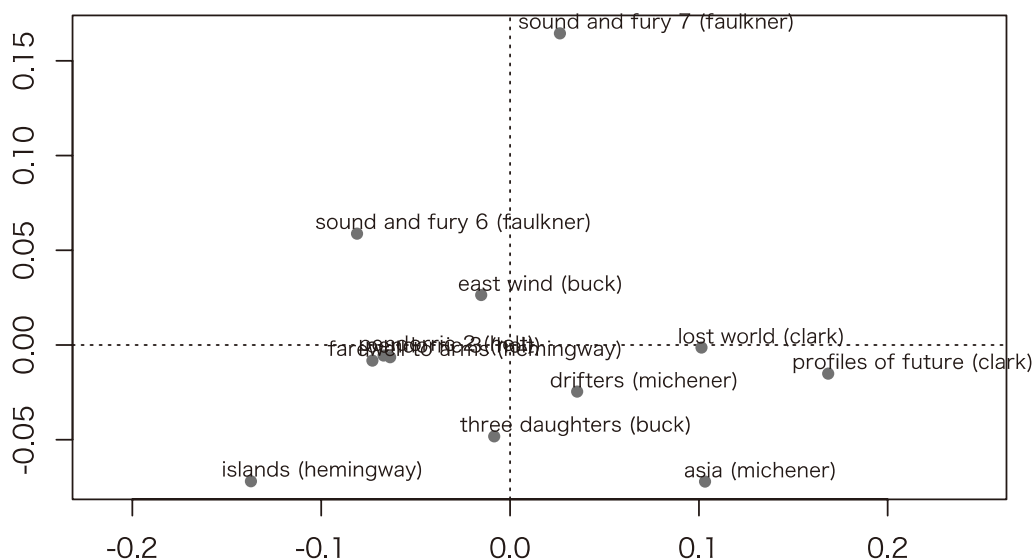


Figure 2: Correspondence analysis (samples)

Figure 2 shows the similarities among 12 text samples written by six novelists. Each pair of samples by the same author has been plotted relatively close to each other. For example, both *Lost World* (Clark) and *Profiles of Future* (Clark) are distributed on the right-hand side of the figure, while *Asia* (Michener) and *Drifters* (Michener) are positioned at the bottom of the plot. These pairs have similar frequency patterns for the 26 letters of the alphabet.

Scatter plots are helpful for grouping the samples and/or variables in a dataset. However, they are sometimes interpreted in an arbitrary manner, i.e., in “an informal way, grouping ‘by eye’ the points lying one near the other on the plot,” and thus “a more formal method” would be useful to better understand these plots (Alberti 2013: 40).

2.2 Cluster analysis

Cluster analysis is a method for organizing information regarding the similarity of items (i.e., samples or variables) so groups (or “clusters”) can be formed (Divjak and Fieller 2014). This method provides tree-like categorizations, where small groups of highly similar items are included within much larger groups of less similar items (Oakes 1998). This technique has been utilized in a wide variety of language studies including authorship attribution (Hoover 2003), lexical semantics (Gries 2012), and phonetic variation (Wieling, Shackleton Jr., and Nerbonne 2013).

Cluster analysis can be conducted with the `dist` and `hclust` functions. The `dist` function calculates a distance matrix and the `hclust` function then performs hierarchical clustering based on the distance matrix. The Euclidean distance measure and complete linkage method (Divjak and Fieller 2014) are selected for these functions, respectively, according to the default settings.

```

> # Calculating relative frequencies
> author.r <- author / apply(author, 1, sum)
> # Calculating a distance matrix
> d1 <- dist(author.r)
> # Performing hierarchical clustering
> hcl <- hclust(d1)
> # Creating a dendrogram
> plot(hcl, hang = -1, main = NA)

```

Figure 3 shows a dendrogram representing the results of cluster analysis, where each pair of text samples by the same author is highly similar in terms of the frequencies of the 26 letters. These results also suggest that there is a gap in the frequency patterns between three novelists on the left-hand side (i.e., Holt, Buck, and Hemingway) and three on the right (i.e., Faulkner, Michener, and Clark).

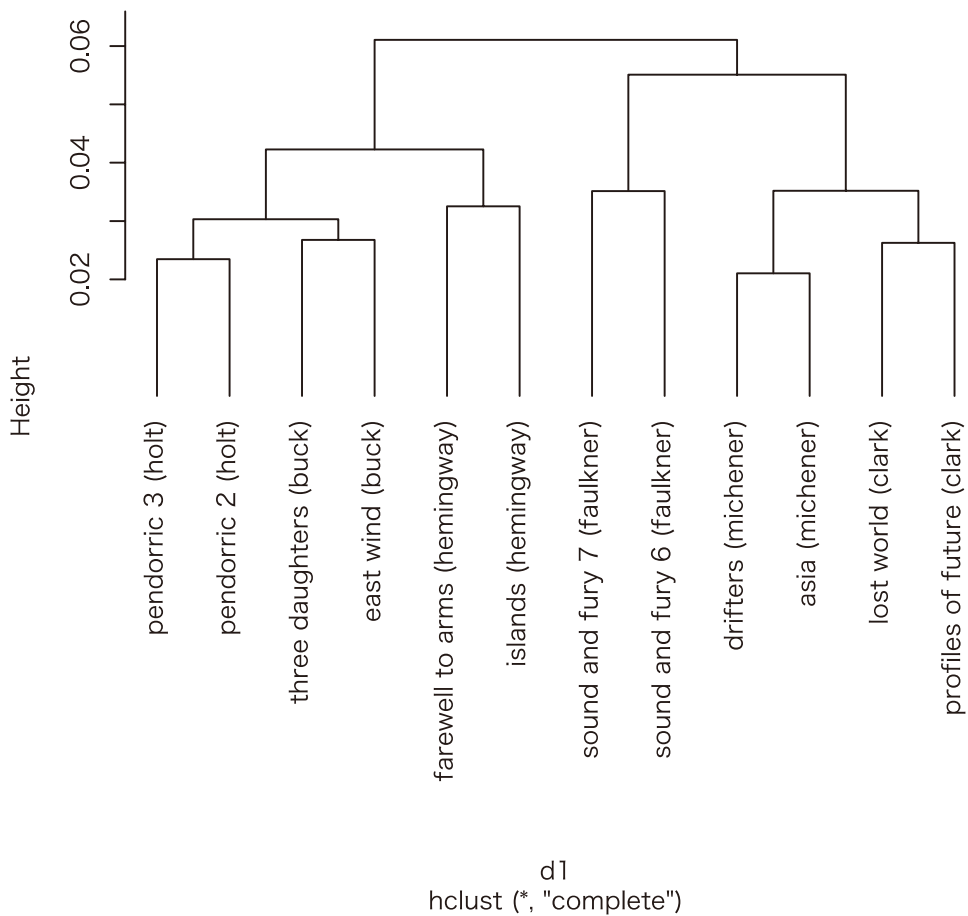


Figure 3: Cluster analysis (samples)

The 26 letters can be grouped by transposing the frequency table used for cluster analysis.

```
> d2 <- dist(t(author.r))
> hc2 <- hclust(d2)
> plot(hc2, hang = -1, main = NA)
```



Figure 4: Cluster analysis (variables)

More sophisticated clustering methods are available using R packages such as `amap`, `ape`, `cluster`, `FactoMineR`, `fpc`, `mclust`, `pvclust`, and `tclust`. Various types of distance measures are also available in the `proxy` package. Different distance measures or clustering methods can yield different clustering results, so it is necessary to carefully compare several combinations. The robustness of the clustering results obtained can be assessed by examining the widths of the silhouettes using the `silhouette` function in the `cluster` package and by computing the p -value for each cluster in a dendrogram after multiscale bootstrap resampling using the `pvclust` function in the `pvclust` package (Divjak and Fieller 2014). Moreover, multiple trees created with different measures and methods can be statistically integrated into a single consensus tree using the `consensus` function in the `ape` package (Baayen 2008).

The graphical representations of cluster analyses are easier to interpret than those obtained by correspondence analysis in terms of the grouping of items (Glynn 2014). However, cluster analysis does not provide information about the associations between samples and variables because the samples and variables cannot be visualized simultaneously in a single dendrogram.

2.3 Heat map

A heat map is a method for visualizing multivariate data where the individual values contained in

a frequency matrix are represented as colors. Heat maps are used widely in the natural sciences, especially in the biological sciences (Wilkinson and Friendly 2009), and they can be applied to language studies such as diachronic corpus analysis (Kehoe and Gee 2009) and stylometric analysis (Saccenti and Tenori 2012).

A very simple heat map can be made using the `image` function, but more sophisticated heat maps can be produced with the `ggplot2` and `reshape2` packages.

```
> # Installing the packages
> install.packages(c("ggplot2", "reshape2"))
> # Loading the packages
> library(ggplot2)
> library(reshape2)
> # Creating a heat map
> author.m <- melt(author.r)
> ggplot(author.m, aes(Var2, Var1)) + geom_tile(aes(fill =
value), colour = "white") + scale_fill_gradient(low = "white",
high = "black")
```

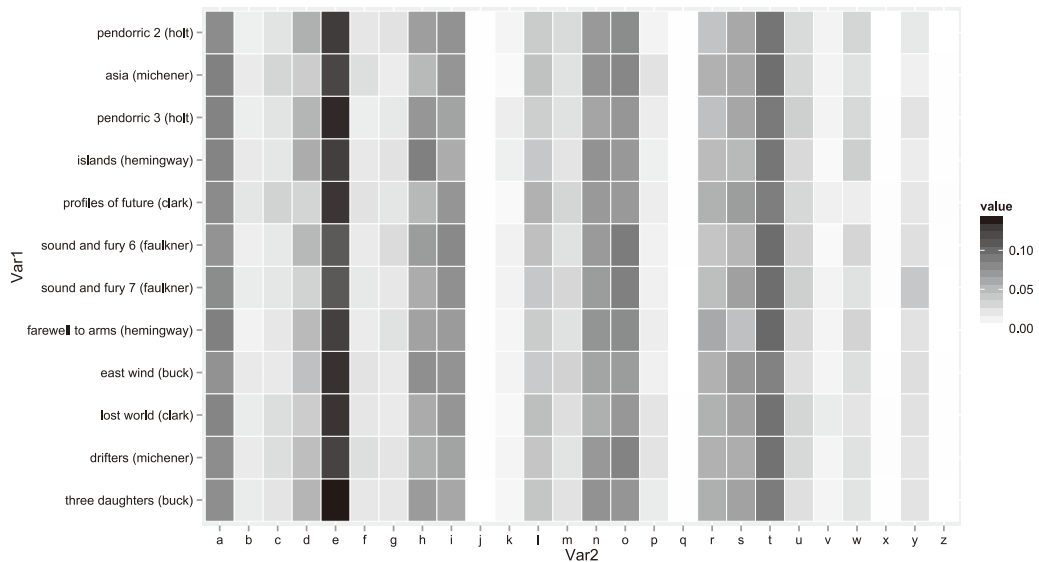


Figure 5: Heat map

Figure 5 shows a heat map generated based on the frequencies of the 26 letters occurring in 12 text samples. This diagram compares the samples where more frequent letters are represented by darker cells and less frequent letters are denoted by lighter cells. The frequency distributions of the 26 letters are quite similar in all of the samples, and *a*, *e*, *h*, *i*, *n*, *o*, *r*, *s*, and *t* are more common than other letters. However, *y* is more frequent in Faulkner's "sound and fury 7" than the other samples, and *c* is more common in the four samples written by Clark and Michener.

The visual representation of the heat map is based directly on the original frequency table. Therefore, it is highly intelligible, especially in cases where the tables contain small numbers of samples and variables. However, heat maps are not necessarily effective at interpreting larger frequency tables because, unlike correspondence analysis and cluster analysis, any information included in them is not statistically summarized.

3. Heat maps with hierarchical clustering

Each of the multivariate visualization methods compared in the previous sections has various advantages and disadvantages. However, a combination of multiple methods can perform better than any single method in terms of the visualization and interpretation of a frequency table. The best combination is cluster analysis with a heat map, which is known as heat map with hierarchical clustering. This method can be used to display the results obtained from clustering samples and variables, while simultaneously generating a heat map from the permuted frequency table in two-dimensional space. Using heat map with hierarchical clustering, Chaussabel (2004) examined the relationships among 239 categories and 517 keywords in biomedical research articles. Kobayashi (2014) also investigated the frequency patterns of 42 types of lexical and grammatical errors in seven different stages in English-language acquisition using the same visualization method.

Heat maps with hierarchical clustering can be created with the `heatmap` function.

```
> # Creating a heat map with hierarchical clustering
> heatmap(as.matrix(author.r), scale = "none", col =
colorRampPalette(c("white", "black"))(256), margin = c(4,0))
```

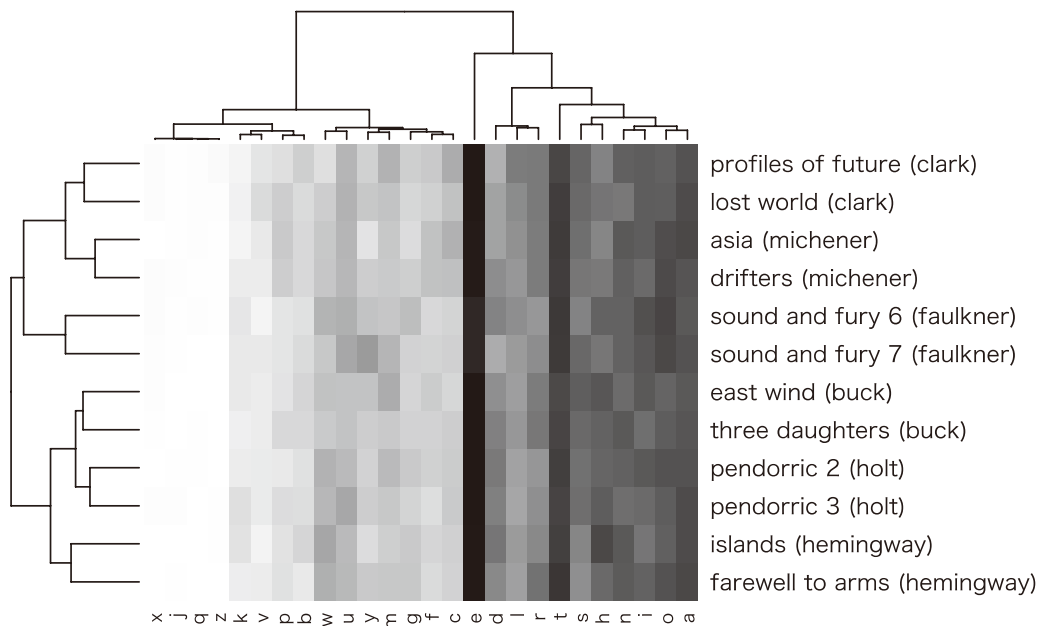


Figure 6: Heat map with hierarchical clustering

The two dendrograms in Figure 6 show exactly the same clustering results as those in Figures 3 and 4, but they are different in appearance due to the different algorithms used to visualize the tree. The rows and columns in the heat map are permuted according to the clustering results obtained for the samples and variables. By combining these three diagrams, this visualization method overcomes the disadvantages of correspondence analysis, cluster analysis, and heat maps discussed in the previous sections. The figure shows the interactions between samples and variables by combining the two dendrograms, thereby providing a more intelligible graphical representation compared with correspondence analysis in terms of the groupings of samples and variables. Furthermore, the arbitrary interpretation and misreading of results can be avoided by referring to the heat map, which represents the frequency distributions and co-occurrence patterns of each sample and variable included in the original frequency table.

Heat maps with hierarchical clustering can also be generated with the `d3heatmap`, `dendextend`, `fheatmap`, `gapmap`, `GMD`, `gplots`, `heatmap.plus`, `heatmap3`, `Heatplus`, `made4`, `NMF`, and `pheatmap` packages. The relative frequencies can be placed within each cell using the `heatmap.2` function in the `gplots` package.

```
> # Installing the package
> install.packages("gplots")
> # Loading the package
> library(gplots)
> # Creating a heat map with hierarchical clustering and relative frequencies
> heatmap.2(as.matrix(author.r), col = colorRampPalette(c(
  "#ffffff", "#7f878f"))(256), cellnote = round(author.r, 2),
  notecol = "black", notecex = 0.5, density.info = "none",
  trace = "none", margin = c(2, 12), cexRow = 0.7, cexCol =
  0.7, key = FALSE)
```

The implementation of the script given above is shown in Figure 7. The clustering results can be interpreted better by examining the relative frequencies and cell colors in the heat map. Furthermore, a close investigation of specific frequency patterns can be implemented in combination with statistical hypothesis testing and effect sizes (Gries 2014). For instance, the significance of inter-cluster differences can be determined by conducting analysis of variance (ANOVA) using the `aov` and `anova` functions, or by implementing the Kruskal-Wallis rank sum test using the `kruskal.test` function. Quantitative research approaches are more reliable than qualitative approaches in terms of replicability, provided that an identical conclusion can be obtained using different analytical methods.

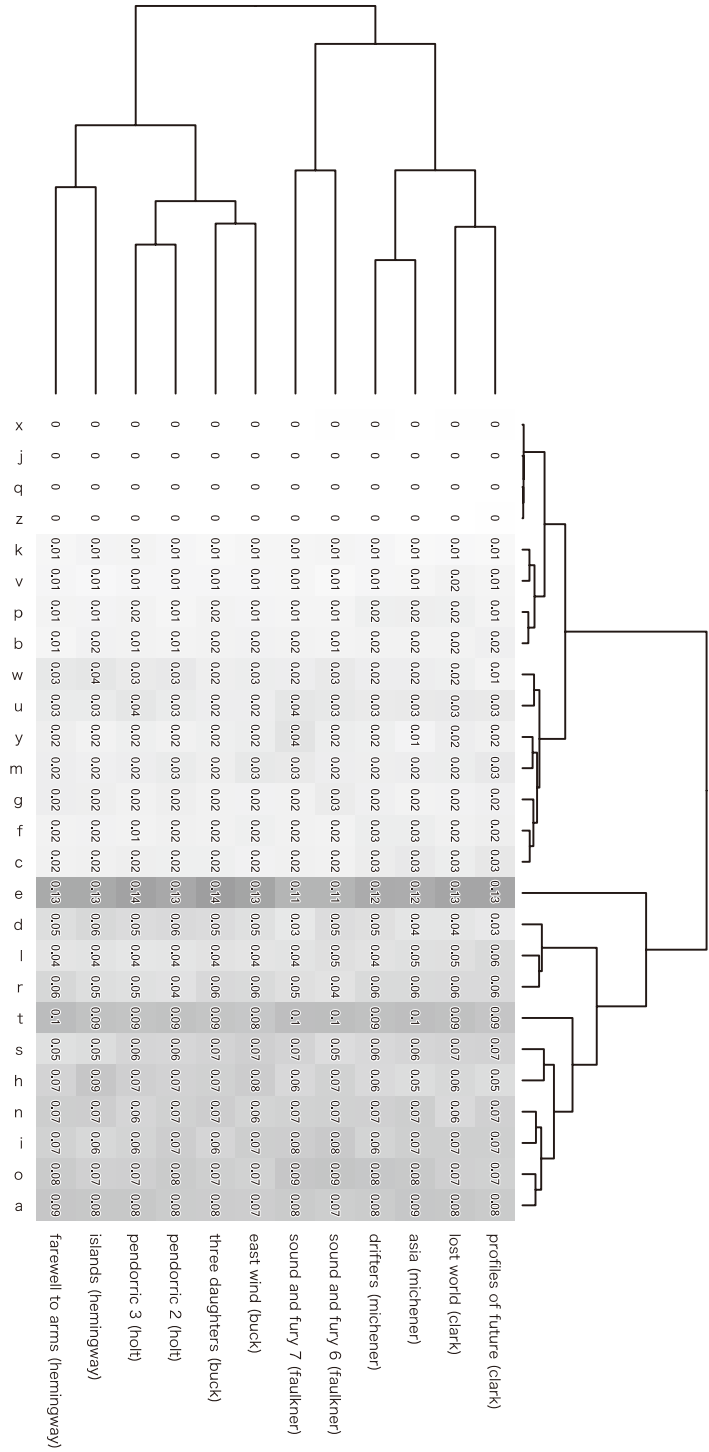


Figure 7: Heat map with hierarchical clustering and relative frequencies

4. Conclusion

Heat map with hierarchical clustering is a powerful method for visualizing multivariate data, such as large frequency tables for linguistic analysis, where the graphical representation obtained provides a statistical summary of complex frequency patterns, as well as the original frequency information contained in the data. Therefore, the underlying meaningful patterns between samples and variables can be detected easily in multiple dendrograms. Moreover, the interpretation of these patterns can be validated by referring to the heat map. This multivariate statistical method will become increasingly important as the size of corpora increases and as corpus-based language studies cover a broader range of linguistic features.

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ヒートマップと階層型クラスタリング ——コーパスに基づく言語研究のための多変量視覚化手法——

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要旨

コーパスに基づく言語研究の利点は、広範な言語項目を分析対象とすることで、言語データを包括的に記述できることである。しかしながら、複数のデータにおける多数の言語項目を効率的に分析するためには、多変量解析などの統計手法に関する知識が求められる。本稿では、言語研究で活用することができる複数の多変量解析の長所と短所を比較検討し、ヒートマップと階層型クラスター分析を組み合わせる用いることの有効性を論じる。それに加えて、R言語を用いた解析方法と、その解析結果を解釈する方法を提示する。

キーワード：多変量データの視覚化、コーパス分析、ヒートマップ、階層型クラスタリング、R言語