

stemmatology: An R Stemmatology Package

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Abstract

Stemmatology is the name of the field dedicated to studying text genealogies and establishing genealogical tree-like graphs known as *stemma codicum*.

This package includes various functions for stemmatological analysis. It particularly implements functions following the Poole-Camps-Cafiero method, as well as functions to import data.

Keywords: stemmatology, philology, network, graphs.

1. Input

Most of the functions take, as input a *numeric matrix*, with witnesses in columns, variant locations in rows, and readings coded by a number, e.g.

	A	B	C	D	E	H	I	J	K	O
1	0	1	1	1	NA	1	1	NA	1	1
2	1	1	1	1	NA	1	1	NA	1	1
3	1	1	1	1	NA	1	1	NA	1	1
4	1	1	1	2	NA	1	1	NA	1	1
5	1	1	1	2	NA	1	1	NA	1	1
6	1	1	1	1	NA	1	1	NA	1	1

where A, B, \dots, O are the various witnesses in columns, $1 \dots 6$ the various variant locations, in rows, and the different readings are coded either 0 (omission), $1, 2, \dots, n$. NA is used for the lack of information (physical lacuna, absence of observation, variant location not applicable to a given witness, etc.).

Alternatively, if `alternateReadings = TRUE`, the input can be a *character matrix*, with witnesses in columns, variant locations in rows, and, in each cell, one or several readings, coded by numbers and separated by a comma (e.g. '1,2,3', if the witness has three different readings), e.g.

	A	D	F	T	P
1	"1"	"2"	"2"	"2"	"1,2"
2	"1"	"2"	"1,2"	"2"	"1"
3	"1"	"1"	"1"	"1"	"2"
4	"1,3"	"1,2"	"1"	"2"	"3"

Notice how a witness can bear several readings (e.g., P at VL 1).

1.1. Create or import data

Data can be created inside R or imported. They can be imported by reading a csv file, for instance (e.g. with `read.csv`). They can also be imported from a TEI encoded apparatus in parallel-segmentation, either by using an XSL stylesheet, or the built-in function `import.TEIApparatus`.

The function `import.TEIApparatus` allows to import a TEI P5 encoded apparatus into a stemmatological matrix usable with other functions. It has some parameters to refine the import (variant types, ...), and can read either from disk or from an URL.

2. PCC Method

Functions are made available for the PCC method (See Camps and Cafiero 2014 or PCC for more details). The most important are

`PCC.global.shell` for the PCC functions;

`PCC.Exploratory` global function for exploratory methods of the PCC family;

`PCC.Stemma` Building the Stemma Codicum.

3. Other functions

The package contains also various other functions, particularly aimed at detecting contamination. It contains for instance the function `PCC.contam`.

The package aims at making available various other stemmatological methods, including further functions for contamination detection, or for theoretical stemmatology.

References

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Poole, Eric, 'The Computer in Determining Stemmatic Relationships'. *Computers and the Humanities*, 8-4 (1974), p. 207-16.

Bugs and Issues

Please report issues with this package to <https://github.com/Jean-Baptiste-Camps/stemmatology>.

Example of use

```
> # Interactive mode
> # Load data
> data(fournival)
> # or alternatively, import it
> fournival = import.TEIApparatus(file = "myFournival.xml",
+   appTypes = c("substantive"))
> # Analyse it with the PCC functions
> PCC(fournival)
> # Complete step-by-step non interactive use
> data("fournival")
> # look for conflicts
> myConflicts = PCC.conflicts(fournival)
> # remove conflicting VL
> myConflicts = PCC.overconflicting(myConflicts, ask = FALSE, threshold = 0.06)
> myNewData = PCC.elimination(myConflicts)
> # look for competing genealogies
> myConflicts = PCC.conflicts(myNewData)
> myNewData = PCC.equipollent(myConflicts, ask = FALSE, scope = "W", wits = "D")
> # build a stemma
> PCC.Stemma(myNewData$databases[[3]], ask = FALSE)
```

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