Package ‘corlink’

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Title Record Linkage, Incorporating Imputation for Missing Agreement Patterns, and Modeling Correlation Patterns Between Fields

Version 1.0.0

Description A matrix of agreement patterns and counts for record pairs is the input for the procedure. An EM algorithm is used to impute plausible values for missing record pairs. A second EM algorithm, incorporating possible correlations between per-field agreement, is used to estimate posterior probabilities that each pair is a true match - i.e. constitutes the same individual.

Depends R (>= 3.2.4)

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corlink functions

linkd

`linkd` *Function to impute missing agreement patterns and then to link data*

Description

Function to impute missing agreement patterns and then to link data

Usage

```
linkd(d, initial_m = NULL, initial_u = NULL, p_init = 0.5,
  fixed_col = NULL, alg = "m")
```

Arguments

`d`	Matrix of agreement patterns with final column counting the number of times that pattern was observed. See Details
`initial_m`	starting probabilities for per-field agreement in record pairs, both records being generated from the same individual. Defaults to NULL
`initial_u`	starting probabilities for per-field agreement in record pairs, with the two records being generated from differing individuals Defaults to NULL
`p_init`	starting probability that both records for a randomly selected record pair is associated with the same individual
`fixed_col`	vector indicating columns that are not to be updated in initial EM algorithm. Useful if good prior estimates of the mis-match probabilities. See details
`alg`	character; see Details

Details

`d` is a numeric matrix with N rows corresponding to N record pairs, and L+1 columns the first L of which show the field agreement patterns observed over the record pairs, and the last column the total number of times that pattern was observed in the database. The code 0 is used for a field that differs for two record, 1 for a field that agrees, and 2 for a missing field. `fixed_col` indicates the components of the `u` vector (per field probabilities of agreement for 2 records from differing individuals) that are not to be updated when applying the EM algorithm to estimate components of the Feligi Sunter model. `alg` has four possible values. The default `'m'` fits a log-linear model for the agreement counts only within the record pairs that corresponds to the same individual, `'b'` fits differing log-linear models for the 2 clusters, `'i'` corresponds to the original Feligi Sunter algorithm, with probabilities estimated via the EM algorithm, `'a'` fits all the previously listed models

Value

A list, the first component is a matrix - the posterior probabilities of being a true match is the last column, the second component are the fitted models used to generate the predicted probabilities

Examples

```
# Simulate data
m_probs <- rep(0.8,6)
u_probs <- rep(0.2,6)
means_match <- -1*qnorm(1-m_probs)
means_mismatch <- -1*qnorm(1-u_probs)
missingprobs <- rep(.2,6)
thedata <- do_sim(cor_match=0.2,cor_mismatch=0,nsample=10^4,pi_match=.5,
m_probs=rep(0.8,5),u_probs=rep(0.2,5),missingprobs=rep(0.4,5))
colnames(thedata) <- c(paste("V",1:5,sep="_"),"count")
output <- linkd(thedata)
output$fitted_probs
```

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