Package ‘textir’

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Title Inverse Regression for Text Analysis

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Suggests MASS


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Ideology in Political Speeches

Description

Phrase counts and ideology scores by speaker for members of the 109th US congress.

Details

This data originally appear in Gentzkow and Shapiro (GS; 2010) and considers text of the 2005 Congressional Record, containing all speeches in that year for members of the United States House and Senate. In particular, GS record the number times each of 529 legislators used terms in a list of 1000 phrases (i.e., each document is a year of transcripts for a single speaker). Associated sentiments are repshare – the two-party vote-share from each speaker’s constituency (congressional district for representatives; state for senators) obtained by George W. Bush in the 2004 presidential election – and the speaker’s first and second common-score values (from http://voteview.com). Full parsing and sentiment details are in Taddy (2013; Section 2.1).

Value

- congress109Counts
  A dgCMatrix of phrase counts indexed by speaker-rows and phrase-columns.

- congress109Ideology
  A data.frame containing the associated repshare and common scores $\{cs1, cs2\}$, as well as speaker characteristics: party (‘R’epublican, ‘D’emocrat, or ‘I’ndependent), state, and chamber (‘H’ouse or ‘S’enate).

Author(s)

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References


See Also

srproj, pls, dmr, we8there
**Examples**

```r
data(congress109)

## Bivariate sentiment factors (roll-call vote common scores)
covars <- data.frame(gop=congress109Ideology$party=="R",
cscore=congress109Ideology$cs1)
covars$cscore <- covars$cscore -
tapply(covars$cscore,covars$gop,mean)[covars$gop+1]
rownames(covars) <- rownames(congress109Ideology)

## cl=NULL implies a serial run.
## To use a parallel library fork cluster,
## uncomment the relevant lines below.
## Forking is unix only; use PSock for windows
cl <- NULL
# cl <- makeCluster(detectCores(), type="FORK")
## small nlambda for a fast example
fitcs <- dmr(cl, covars, congress109Counts, gamma=1, nlambda=10)
## stopCluster(cl)

## plot the fit
par(mfrow=c(1,2))
for(j in c("estate.tax","death.tax")){
  plot(fitcs[[j]], col=c("red","green"))
mtext(j,line=2)
}
legend("topright",bty="n",fill=c("red","green"),legend=names(covars))

## plot the IR sufficient reduction space
Z <- srproj(fitcs, congress109Counts)
par(mfrow=c(1,1))
plot(Z, pch=21, bg=c(4,3,2)[congress109Ideology$party], main="SR projections")
## two pols
Z[c(68,388),]
```

---

**corr**

2nd moments of sparse matrices

**Description**

Correlation and deviation in sparse matrices.

**Usage**

```r
corr(x, y)
sdev(x)
```
Arguments

x       A dgCMatrix or matrix of counts.
y       A matrix with nrow(y)=nrow(x).

Value

corr returns the ncol(x) by ncol(y) matrix of correlation between x and y, and sdev returns the column standard deviations.

Author(s)

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See Also

pls, congress109

Examples

# some congress examples
data(congress109)
r <- corr(congress109Counts, congress109Ideology$repshare)
## 20 terms for Democrats
sort(r[,1])[1:20]
## 20 terms for Republicans
sort(r[,1], decreasing=TRUE)[1:20]
## 20 high variance terms
colnames(congress109Counts)[
order(-sdev(congress109Counts))[1:20]]
## S3 method for class 'pls'
print(x, ...)

## S3 method for class 'pls'
plot(x, K=NULL, xlab="response", ylab=NULL, ...)

### Arguments

- **x**: The covariate matrix, in either dgCMatrix or matrix format. For plot and print: a pls output object.
- **y**: The response vector.
- **K**: The number of desired PLS directions. In plotting, this can be a vector of directions to draw, otherwise directions 1:fit$K are plotted.
- **scale**: An indicator for whether to scale x; usually a good idea. If scale=TRUE, model is fit with x scaled to have variance-one columns.
- **verb**: Whether or not to print a small progress script.
- **object**: For predict and summary: a pls output object.
- **newdata**: For predict, an ncol(x)-column matrix of new observations. Can be either a simple matrix or a simple_triplet_matrix.
- **type**: For predict, a choice between output types: predictions scaled to the original response for "response", fitted partial least squares directions for "reduction".
- **xlab**: For plot, the x-axis label.
- **ylab**: For plot, the y-axis label. If null, will be set to ‘pls(k) fitted values’ for each k.
- **...**: Additional arguments.

### Details

**pls** fits the Partial Least Squares algorithm described in Taddy (2012; Appendix A.1). In particular, we obtain loadings loadings[k] as the correlation between X and factors factors[k], where factors[1] is initialized at scale(as.numeric(y)) and subsequent factors are orthogonal to to the k'th pls direction, an ortho-normal transformation of x*loadings_shift.

**predict.pls** returns predictions from the object$fw$mod forward regression \( \alpha + \beta * z \) for projections \( z = x*loadings_shift \) derived from new covariates, or if type="reduction" it just returns these projections. **summary.pls** prints dimension details and a quick summary of the corresponding forward regression. **plot.pls** draws response versus fitted values for least-squares fit onto the K pls directions.

### Value

Output from **pls** is a list with the following entries

- **y**: The response vector.
- **x**: The unchanged covariate matrix.
- **directions**: The pls directions: x*%loadings_shift.
loadings  The pls loadings.
shift     Shift applied after projection to center the PLS directions.
fitted    $K$ columns of fitted $y$ values for each number of directions.
fwdmod    The $\text{lm}$ object from forward regression $\text{lm}(\text{as.numeric}(y)\sim\text{directions})$.

$\text{predict.pls}$ outputs either a vector of predicted response or an $\text{nrow(newcounts)} \times \text{ncol(object}$\$loadings$ matrix of pls directions for each new observation. Summary and plot produce return nothing.

Author(s)
Matt Taddy <taddy@chicagobooth.edu>

References


See Also
normalize, sdev, corr, congress109

Examples

data(congress109)
x <- t(t(congress109Counts)/rowSums(congress109Counts))
summary(fit <- pls(x, congress109Ideology$repshare, K=3))
plot(fit, pch=21, bg=c(4,3,2)[congress109Ideology$party])
predict(fit, newdata=x[c(68,388),])

srproj       *Multinomial Inverse Regression (MNIR)*

Description
Estimation of MNIR sufficient reduction projections. Note that $\text{mnlm}$ is just a call to $\text{dmr}$ from the $\text{distrom}$ package.

Usage

srproj(obj, counts, dir=1:K, ...)  
mnlm(cl, covars, counts, mu=NULL, bins=NULL, verb=0, ...)
Arguments

cl  A parallel library socket cluster. See the same argument in help(dmr) for details.
covars A dense matrix or sparse Matrix of covariates. This should not include the intercept. See the same argument in help(dmr) for details.
counts A dense matrix or sparse matrix of response counts (e.g., token counts in text mining). See the same argument in help(dmr) for details. For srproj, this must have the same number of columns as the response dimensions (vocabulary size) in obj.
mu Pre-specified fixed effects for each observation in the Poisson regression linear equation. See the same argument in help(dmr) for details.
bins Number of bins into which we will attempt to collapse each column of covars. bins=NULL does no collapsing. See the same argument in help(dmr) for details.
verb Whether to print some info. See the same argument in help(dmr) for details.
obj Either a dmr object, as returned from mnlm, or the dmrcoef object obtained by calling coef on the output of mnlm or dmr. The latter will be faster, since coef.dmr is called inside srproj otherwise.
dir The attribute (covar) dimensions onto which you want to project. The default is all dimensions: 1:K, where K is the number of columns in the covars argument to mnlm.
...

Additional arguments to gamlr from dmr (or mnlm), and to coef.dmr from srproj. See help(gamlr) and help(dmr) for details.

Details

These functions provide the first two steps of multinomial inverse regression (see MNIR paper).
mnlm fits multinomial logistic regression parameters under gamma lasso penalization on a factorized Poisson likelihood. The mnlm function, which remains in this package for backwards compatibility only, is just call to the dmr function of the distrom library (see DMR paper). For simplicity, we recommend using dmr instead of mnlm. For model selection, coefficients, prediction, and plotting see the relevant functions in help(dmr).
srproj calculates the MNIR Sufficient Reduction projection from text counts on to the attribute dimensions of interest (covars in mnlm or dmr). In particular, for counts C, with row sums m, and mnlm/dmr coefficients \( \phi_j \) corresponding to attribute \( j \), \( z_j = C' \phi_j / m \) is the SR projection in the direction of \( j \). The MNIR paper explains how \( V = [v_1...v_K] \), your original covariates/attributes, are independent of text counts \( C \) given SR projections \( Z = [z_1...z_K] \).

The final step of MNIR is ‘forward regression’ for any element of \( V \) onto \( Z \) and the remaining elements of \( V \). We do not provide a function for this because you are free to use whatever you want; see the MNIR and DMR papers for linear, logistic, and random forest forward regression examples.

Note that if you were previously using textir not for inverse regression, but rather just as fast code for multinomial logistic regression, you probably want to work directly with the gamlr (binary response) or dmr (multinomial response) packages.
srproj returns a matrix with columns corresponding to directions dir, plus an additional column m holding the row totals of counts. mnlm returns a dmr s3 object. See help(dmr) for details.

Author(s)

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References

Taddy (2013, JASA), Multinomial Inverse Regression for Text Analysis (MNIR).

Taddy (2015, AoAS), Distributed Multinomial Regression (DMR).

Taddy (2016, JCGS), The Gamma Lasso (GL).

See Also

congress109, we8there, dmr

Examples

```r
### Ripley's Cushing Data; see help(Cushings) ###
library(MASS)
data(Cushings)
Cushings[,1:2] <- log(Cushings[,1:2])
train <- Cushings[Cushings$Type!="u",]
newdata <- as.matrix(Cushings[Cushings$Type == "u", 1:2])

# fit, coefficients, predict, and plot

# you could replace 'mnlm' with 'dmr' here.
fit <- mnlm(NULL,
covars=train[,1:2],
counts=factor(train$Type))

# dmr applies corrected AICc selection by default
round(coef(fit),1)
round(predict(fit, newdata, type="response"),1)
par(mfrow=c(1,3))
for(j in c("a","b","c")){
    plot(fit[[j]]); mtext(j,line=2) }

# see we8there and congress109 for MNIR and srproj examples
```
tfidf

**Description**

term frequency, inverse document frequency

**Usage**

```r
tfidf(x, normalize=TRUE)
```

**Arguments**

- `x` A dgCMatrix or matrix of counts.
- `normalize` Whether to normalize term frequency by document totals.

**Value**

A matrix of the same type as `x`, with values replaced by the tf-idf

\[ f_{ij} \cdot \log\left[ \frac{n}{(d_j + 1)} \right], \]

where \( f_{ij} \) is \( x_{ij}/m_i \) or \( x_{ij} \), depending on `normalize`, and \( d_j \) is the number of documents containing token \( j \).

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**See Also**

`pls`, `we8there`

**Examples**

```r
data(we8there)
## 20 high-variance tf-idf terms
colnames(we8thereCounts)[
  order(-sdv(tfidf(we8thereCounts)))[1:20]]
```
On-Line Restaurant Reviews

Description

Counts for 2804 bigrams in 6175 restaurant reviews from the site www.we8there.com.

Details

The short user-submitted reviews are accompanied by a five-star rating on four specific aspects of restaurant quality - food, service, value, and atmosphere - as well as the overall experience. The reviews originally appear in Maua and Cozman (2009), and the parsing details behind these specific counts are in Taddy (MNIR; 2013).

Value

we8thereCounts A dgCMatrix of phrase counts indexed by review-rows and bigram-columns.
we8thereRatings
A matrix containing the associated review ratings.

Author(s)

Matt Taddy, <mataddy@gmail.com>

References

Taddy (2013, JASA), Multinomial Inverse Regression for Text Analysis.
Taddy (2013, AoAS), Distributed Multinomial Regression.

See Also
dmr, srproj

Examples

## some multinomial inverse regression
## we'll regress counts onto 5-star overall rating
data(we8there)

## cl=NULL implies a serial run.
## To use a parallel library fork cluster,
## uncomment the relevant lines below.
## Forking is unix only; use PSOCK for windows
c1 <- NULL
# c1 <- makeCluster(detectCores(), type="FORK")
## small nlambda for a fast example
```r
fits <- dmr(cl, we8thereRatings[, 'Overall', drop=FALSE],
we8thereCounts, bins=5, gamma=1, nlambda=10)
# stopCluster(cl)

## plot fits for a few individual terms
terms <- c("first date","chicken wing",
"ate here","good food",
"food fabul","terribl servic")
par(mfrow=c(3,2))
for(j in terms)
{ plot(fits[[j]]); mtext(j,font=2,line=2) }

## extract coefficients
B <- coef(fits)
mean(B[2,]==0) # sparsity in loadings
## some big loadings in IR
B[2,order(B[2,])[1:10]]
B[2,order(-B[2,])[1:10]]

## do MNLR projection onto factors
z <- srproj(B,we8thereCounts)

## fit a fwd model to the factors
summary(fwd <- lm(we8thereRatings$Overall ~ z))

## truncate the fwd predictions to our known range
fwd$fitted[fwd$fitted<1] <- 1
fwd$fitted[fwd$fitted>5] <- 5
## plot the fitted rating by true rating
par(mfrow=c(1,1))
plot(fwd$fitted ~ factor(we8thereRatings$Overall),
varwidth=TRUE, col="lightslategrey")
```
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