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Type Package

Title Hierarchical Bayesian Analysis of Recognition Memory

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Depends R (>= 1.8.0), methods

Description Contains functions for fitting hierarchical versions of
EVSD, UVSD, DPSD, DPSD with d’ restricted to be positive, and
our gamma signal detection model to recognition memory
confidence-ratings data.

License LGPL (>= 2.0)

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Description

Contains functions for fitting hierarchical versions of EVSD, UVSD, DPSD, and our gamma signal detection model to recognition memory confidence-ratings data.

Details

Package: hbmem
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Author(s)

Michael S. Pratte <prattems@gmail.com>

References

Morey, Pratte, and Rouder (2008); Pratte, Rouder, and Morey (2009); Pratte and Rouder (2012).
See Also

'uvsdSample' to fit hierarchical UVSD model, 'uvsdSim' to simulate data from the hierarchical UVSD model, 'dpsdSample' to fit the hierarchical DPSD model, 'dpsdSim' to simulate data from the hierarchical DPSD model, 'dpsdPosSim' and 'dpsdPosSample' for the DPSD model with positive sensitivity, and datasets from our publications.

Examples

# In this example data are simulated from EVSD
# They are then fit by both UVSD and DPSD

library(hbmem)
sim=uvsdSim(s2aS2=0,s2bS2=0) # Simulate data from hierarchical EVSD
dat=as.data.frame(cbind(sim@subj,sim@item,sim@Scond,sim@cond,sim@lag,sim@resp))
colnames(dat)=c("sub","item","Scond","cond","lag","resp")

M=10 # Set way low for speed
keep=2:M
# For real analysis we run 105000 iterations
# with the first 5000 serving as burnin, and
# only keep every 10th iteration for analysis,
# i.e., thinning the chains to mitigate autocorrelation.
evsd=uvsdSample(dat,M=M,keep=keep,equalVar=TRUE) # Fit EVSD
uvsd=uvsdSample(dat,M=M,keep=keep,freeSig2=TRUE) # Fit UVSD w/ Sigma2
dpsd=dpsdSample(dat,M=M,keep=keep) # Fit DPSD

# Look at available information
slotNames(uvsd)
slotNames(dpsd)

# Compare DIC; smaller is better
evsd@DIC
uvsd@DIC
dpsd@DIC

# Effective parameters. Because there are no
# real effects on studied-item variance, the
# hierarchical models are drastically shrinking these
# effect parameters to zero, so that they do not
# count as full parameters.
evsd@pd
uvsd@pd
dpsd@pd

# PLOTS FROM UVSD FIT
par(mfrow=c(3,2),pch=19,pty='s')
# Make sure chains look OK
matplot(uvsd@blockN[,uvsd@muN],t='l',xlab="Iteration",ylab="Mu-N")
abline(h=sim@muN,col="blue")
matplot(uvsd@blockS[,uvsd@muS],t='l',xlab="Iteration",ylab="Mu-S")
abline(h=sim@muS,col="blue")
# Estimates of Alpha as function of true values
plot(uvsd@estN[uvsd@alphaN]~sim@alphaN,xlab="True Alpha-N",ylab="Est. Alpha-N"); abline(0,1,col="blue")
plot(uvsd@estS[uvsd@alphaS]~sim@alphaS,xlab="True Alpha-S",ylab="Est. Alpha-S"); abline(0,1,col="blue")

# Estimates of Beta as function of true values
plot(uvsd@estN[uvsd@betaN]~sim@betaN,xlab="True Beta-N",ylab="Est. Beta-N"); abline(0,1,col="blue")
plot(uvsd@estS[uvsd@betaS]~sim@betaS,xlab="True Beta-S",ylab="Est. Beta-S"); abline(0,1,col="blue")

### Look at Sigma2 and Recollection from UVSD and DPSD###
par(mfrow=c(2,3), pch=19, pty='s')
plot(sqrt(exp(uvsd@blockS2[,uvsd@salphaS])), t='l',ylab="Sigma", main="Grand Mean")
abline(h=1,col="blue")
hist(uvsd@blockS2[,uvsd@s2alphaS], main="Participant Effect")
hist(uvsd@blockS2[,uvsd@s2betaS], main="Item Effect")
plot(pnorm(dpsd@blockR[,dpsd@muS]), t='l',ylab="P(Recollection)", main="Grand Mean")
abline(h=0,col="blue")
hist(dpsd@blockR[,dpsd@s2alphaS], main="Participant Effect")
hist(dpsd@blockR[,dpsd@s2betaS], main="Item Effect")

# See what DPSD does with EVSD effects
par(mfrow=c(2,3))
plot(dpsd@estN[dpsd@alphaN]~sim@alphaN,xlab="DPSD Alpha-N",ylab="DPSD Alpha-N"); abline(0,1,col="blue")
plot(dpsd@estS[dpsd@alphaS]~sim@alphaS,xlab="DPSD Alpha-S",ylab="DPSD Alpha-S"); abline(0,1,col="blue")
plot(dpsd@estR[dpsd@alphaS]~sim@alphaS,xlab="DPSD Alpha-R",ylab="DPSD Alpha-R"); abline(0,1,col="blue")

plot(dpsd@estN[dpsd@betaN]~sim@betaN,xlab="DPSD Beta-N",ylab="DPSD Beta-N"); abline(0,1,col="blue")
plot(dpsd@estS[dpsd@betaS]~sim@betaS,xlab="DPSD Beta-S",ylab="DPSD Beta-S"); abline(0,1,col="blue")
plot(dpsd@estR[dpsd@betaS]~sim@betaS,xlab="DPSD Beta-R",ylab="DPSD Beta-R"); abline(0,1,col="blue")

dpsd-class

Class "dpsd"~~~

Description

Holds all information returned from posterior simulations of dual-process models
**Slots**

- `muN`: Object of class "numeric"
- `alphaN`: Object of class "numeric"
- `betaN`: Object of class "numeric"
- `s2alphaN`: Object of class "numeric"
- `s2betaN`: Object of class "numeric"
- `thetaN`: Object of class "numeric"
- `muS`: Object of class "numeric"
- `alphaS`: Object of class "numeric"
- `betaS`: Object of class "numeric"
- `s2alphaS`: Object of class "numeric"
- `s2betaS`: Object of class "numeric"
- `thetaS`: Object of class "numeric"
- `estN`: Object of class "numeric"
- `estS`: Object of class "numeric"
- `estR`: Object of class "numeric"
- `estCrit`: Object of class "matrix"
- `blockN`: Object of class "matrix"
- `blockS`: Object of class "matrix"
- `blockR`: Object of class "matrix"
- `s.crit`: Object of class "array"
- `pD`: Object of class "numeric"
- `DIC`: Object of class "numeric"
- `M`: Object of class "numeric"
- `keep`: Object of class "numeric"
- `b0`: Object of class "matrix"
- `b0Crit`: Object of class "numeric"

**Description**

Returns the probability of making confidence ratings given parameters of DPSD.

**Usage**

dpsdProbs(r,d,crit)
Arguments

- `r` Probability of recollection.
- `d` Mean of the signal-detection distribution. In the common parameterization of the model, this would be zero for new-item trials, and d’ for studied-item trials. In the PRM09 parameterization, these are dn and ds for new and studied-item trials, respectively.
- `crit` Criteria (not including -Inf or Inf).

Details

For new-item trials, simply set r=0.

Value

The function returns the probability of making each response for the parameters given.

Author(s)

Michael S. Pratte

References

See Pratte, Rouder, & Morey (2009)

See Also

hbmem

Examples

```r
# Low r
dpsdProbs(.2,1,c(-1,-.5,0,.5,1)) # studied
dpsdProbs(0,-.1,c(-1,-.5,0,.5,1)) # new

# High r
dpsdProbs(.6,1,c(-1,-.5,0,.5,1)) # studied
dpsdProbs(0,-.1,c(-1,-.5,0,.5,1)) # new
```

dpsdRNSample

Fit DPSD model with R restricted to be function of N

Description

This is a dual process model in which the person and item effects on probability of recollection are linear functions of those effects for the new-item distribution.
dpsdRNSim

Usage

dpsdRNSample(dat, M = 5000, keep = (M/10):M, getDIC = TRUE, jump = 0.001)

Arguments

dat Data frame that must include variables Scond,cond,sub,item,lag.resp. Scond indexes studied/new, whereas cond indexes conditions nested within the studied or new conditions. Indexes for Scond,cond, sub, item, and respone must start at zero and have no gaps (i.e., no skipped subject numbers). Lags must be zero-centered.

M Number of MCMC iterations.

keep Which MCMC iterations should be included in estimates and returned. Use keep to both get ride of burn-in, and thin chains if necessary.

getDIC Logical. Should the function compute DIC value? This takes a while if M is large.

jump The criteria and decorrelating steps utilize Matropolis-Hastings sampling routines, which require tuning. All MCMC functions should self-tune during the burnin period (iterations before keep), and they will alert you to the success of tuning. If acceptance rates are too low, "jump" should be decreased, if they are too high, "jump" should be increased. Alternatively, or in addition to adjusting "jump", simply increase the burnin period which will allow the function more time to self-tune.

References

Pratte and Rouder (2010)

dpsdRNSim  

Function dpsdRNSim

description

Simulate data from DPSD model with R a function of N

Usage

dpsdRNSim(NN = 2, NS = 1, I = 30, J = 200, K = 6, muN = c(-0.7, -0.5), s2aN = 0.2, s2bN = 0.2, muS = 0, s2aS = 0.2, s2bS = 0.2, muR = qnorm(0.25), phiA = -1, phiB = -1, crit = matrix(rep(c(-1.6, -0.5, 0, 0.5, 1.6), each = 1), ncol = (K - 1)))
Arguments

- NN: Number of new-item conditions.
- NS: Number of studied-item conditions.
- I: Number of participants.
- J: Number of items.
- K: Number of confidence ratings.
- muN: Mean of new-item distribution.
- s2aN: Variance of participant effects on new-item distribution.
- s2bN: Variance of item effects on new-item distribution.
- muS: Mean of studied-item distribution.
- s2aS: Variance of participant effects on studied-item distribution.
- s2bS: Variance of item effects on studied-item distribution.
- muR: Mean of recollection (on probit space).
- phiA: Linear slope of participant effect on recollection.
- phiB: Linear slope of item effect on recollection.
- crit: Matrix of criteria.

References

See Pratte and Rouder (in review).

dpsdSample

Function to fit hierarchical DPSD model to data.

Description

Runs MCMC estimation for the hierarchical DPSD model.

Usage

dpsdSample(dat, M = 5000, keep = (M/10):M, getDIC = TRUE, freeCrit=TRUE,Hier=TRUE, jump=.01)

Arguments

- dat: Data frame that must include variables Scond, cond, sub, item, lag, resp. Scond indexes studied/new, whereas cond indexes conditions nested within the studied or new conditions. Indexes for Scond, cond, sub, item, and respone must start at zero and have no gaps (i.e., no skipped subject numbers). Lags must be zero-centered.
- M: Number of MCMC iterations.
keep Which MCMC iterations should be included in estimates and returned. Use keep to both get rid of burn-in, and thin chains if necessary
getDIC Logical. Should the function compute DIC value? This takes a while if M is large.
freeCrit Logical. If true then criteria are estimated separately for each participant. Should be set to false if analyzing only one participant (e.g., if averaging over subjects).
Hier Logical. If true then the variances of effects (e.g., item effects) are estimated from the data, i.e., effects are treated as random. If false then these variances are fixed to 2.0 (.5 for recollection effects), thus treating these effects as fixed. This option is there to allow for comparison with more traditional approaches, and to see the effects of imposing hierarchical structure. It should always be set to TRUE in real analysis, and is not even guaranteed to work if set to false.
jump The criteria and decorrelating steps utilize Metropolis-Hastings sampling routines, which require tuning. All MCMC functions should self-tune during the burnin period (iterations before keep), and they will alert you to the success of tuning. If acceptance rates are too low, "jump" should be decreased, if they are too high, "jump" should be increased. Alternatively, or in addition to adjusting "jump", simply increase the burnin period which will allow the function more time to self-tune.

Value The function returns an internally defined "uvsd" structure that includes the following components
mu Indexes which element of blocks contain mu
alpha Indexes which element of blocks contain participant effects, alpha
beta Indexes which element of blocks contain item effects, beta
s2alpha Indexes which element of blocks contain variance of participant effects (alpha).
s2beta Indexes which element of blocks contain variance of item effects (beta).
theta Indexes which element of blocks contain theta, the slope of the lag effect
estN Posterior means of block parameters for new-item means
estS Posterior means of block parameters for studied-item means
estR Posterior means of block for Recollection means.
estCrit Posterior means of criteria
blockN Each iteration for each parameter in the new-item mean block. Rows index iteration, columns index parameter.
blockS Same as blockN, but for the studied-item means
blockR Same as blockN, but for the recollection-parameter means.
s.crit Samples of each criteria.
pD Number of effective parameters used in DIC. Note that this should be smaller than the actual number of parameters, as constraint from the hierarchical structure decreases the number of effective parameters.
DIC DIC value. Smaller values indicate better fits. Note that DIC is notably biased toward complexity.
Number of MCMC iterations run
M

MCMC iterations that were used for estimation and returned
keep

Metropolis-Hastings acceptance rates for decorrelating steps. These should be
between .2 and .6. If they are not, the M, keep, or jump arguments need to be
b0
adjusted.
b0

acceptance rates for criteria.
b0Crit

Author(s)
Michael S. Pratte

References
See Pratte, Rouder, & Morey (2009)

See Also
hbmem

Examples
#In this example we generate data from EVSD, then fit it with both
#hierarchical DPSD and DPSD assuming no participant or item effects.
library(hbmem)
sim=dpsdSim(I=30,J=200)
dat=as.data.frame(cbind(sim@subj,sim@item,sim@cond,sim@Scond,sim@lag,sim@resp))
colnames(dat)=c("sub","item","cond","Scond","lag","resp")
dat$lag[dat$Scond==1]=dat$lag[dat$Scond==1]-mean(dat$lag[dat$Scond==1])

M=10  # Too low for real analysis!
keep=2:M
DPSD=dpsdSample(dat,M=M)

# Look at all parameters
par(mfrow=c(3,3),pch=19,pty='s')

matplot(DPSD@blockN[,DPSD@muN],t='l',
ylab="muN")
abline(h=sim@muN,col="blue")
plot(DPSD@estN[DPSD@alphaN]=sim@alphaN)
abline(0,1,col="blue")
plot(DPSD@estN[DPSD@betaN]=sim@betaN)
abline(0,1,col="blue")

matplot(DPSD@blockS[,DPSD@muS],t='l',
ylab="muS")
abline(h=sim@muS,col="blue")
plot(DPSD@estS[DPSD@alphaS]=sim@alphaS)
abline(0,1,col="blue")
plot(DPSD@estS[DPSD@betaS]=sim@betaS)
abline(0,1,col="blue")
**Function dpsdSim**

**Description**
Simulates data from a hierarchical DPSD model.

**Usage**
```
dpsdSim(NN = 2, NS = 1, I = 30, J = 200, K = 6, muN = c(-.7, -.5), s2aN = .2, s2bN = .2, 
muS = 0, s2aS = .2, s2bS = .2, muR = qnorm(.25), s2aR = .2, s2bR = .2, 
crit = matrix(rep(c(-1.6, -.5, 0, .5, 1.6), each = I), ncol = (K - 1)))
```

**Arguments**
- **NN**: Number of new-item conditions.
- **NS**: Number of studied-item conditions.
- **I**: Number of participants.
- **J**: Number of items.
- **K**: Number of response options.
- **muN**: Mean of new-item distribution. If there are more than one new-item conditions this is a vector of means with length equal to NN.
- **s2aN**: Variance of participant effects on mean of new-item distribution.
- **s2bN**: Variance of item effects on mean of new-item distribution.
- **muS**: Mean of studied-item distribution. If there are more than new-item conditions this is a vector of means with length equal to NN. None studied-item conditions this is a vector of means with length equal to NS.
- **s2aS**: Variance of participant effects on mean of studied-item distribution.
- **s2bS**: Variance of item effects on mean of studied-item distribution.
- **muR**: Mean recollection, on probit space.
- **s2aR**: Variance of participant effects recollection.
- **s2bR**: Variance of item effects on recollection.
- **crit**: Matrix of criteria (not including -Inf or Inf). Columns correspond to criteria, rows correspond to participants.
Value

The function returns an internally defined "dpsdSim" structure.

Author(s)

Michael S. Pratte

References

See Pratte, Rouder, & Morey (2009)

See Also

hbmem

Examples

```r
library(hbmem)
# Data from hiererchial model
sim=dpsdSim()
slotNames(sim)
# Scond indicates studied/new
# cond indicates which condition (e.g., deep/shallow)

table(sim@resp,sim@Scond,sim@cond)

# Useful to make data.frame for passing to functions
dat=as.data.frame(cbind(sim@subj,sim@item,sim@Scond,sim@cond,sim@lag,sim@resp))
colnames(dat)=c("sub","item","Scond","cond","lag","resp")

table(dat$resp,dat$Scond,dat$cond)
```
gammaLikeSample

muN: Object of class "numeric"
muS: Object of class "numeric"
uR: Object of class "numeric"
alphan: Object of class "numeric"
betan: Object of class "numeric"
alphas: Object of class "numeric"
betar: Object of class "numeric"

Function gammaLikeSample

description
Runs MCMC for the hierarchical Gamma Likelihood model

Usage

gammaLikeSample(dat, M = 10000, keep = (M/10):M, getDIC = TRUE, shape=2,jump=.005)

Arguments

dat Data frame that must include variables cond, sub, item, lag, resp. Indexes for cond, sub, item, and response must start at zero and have no gaps (i.e., no skipped subject numbers). Lags must be zero-centered.

M Number of MCMC iterations.

keep Which MCMC iterations should be included in estimates and returned. Use keep to both get ride of burn-in, and thin chains if necessary

getDIC Logical. should the function compute DIC value? This takes a while if M is large.

shape Fixed shape across both new and studied distributions.

jump The criteria and decorrelating steps utilize Matropolis-Hastings sampling routines, which require tuning. All MCMC functions should self tune during the burnin period (iterations before keep), and they will alert you to the success of tuning. If acceptance rates are too low, "jump" should be decreased, if they are too high, "jump" should be increased. Alternatively, or in addition to adjusting "jump", simply increase the burnin period which will allow the function more time to self-tune.
Value

The function returns an internally defined "uvsd" S4 class that includes the following components:

- **mu**: Indexes which element of blocks contain grand means, mu.
- **alpha**: Indexes which element of blocks contain participant effects, alpha.
- **beta**: Indexes which element of blocks contain item effects, beta.
- **s2alpha**: Indexes which element of blocks contain variance of participant effects (alpha).
- **s2beta**: Indexes which element of blocks contain variance of item effects (beta).
- **theta**: Indexes which element of blocks contain theta, the slope of the lag effect.
- **estN**: Posterior means of block parameters for new-item means.
- **estS**: Posterior means of block parameters for studied-item means.
- **estS2**: Not used for gamma model.
- **estCrit**: Posterior means of criteria.
- **blockN**: Each iteration for each parameter in the new-item mean block. Rows index iteration, columns index parameter.
- **blockS**: Same as blockN, but for the studied-item means.
- **blockS2**: Not used for gamma model.
- **s.crit**: Samples of each criteria.
- **pD**: Number of effective parameters used in DIC. Note that this should be smaller than the actual number of parameters, as constraint from the hierarchical structure decreases the number of effective parameters.
- **DIC**: DIC value. Smaller values indicate better fits. Note that DIC is notably biased toward complexity.
- **M**: Number of MCMC iterations run.
- **keep**: MCMC iterations that were used for estimation and returned.
- **b0**: Metropolis-Hastings acceptance rates for new-item distribution parameters. These should be between .2 and .6. If they are not, the M, keep, or jump need to be adjusted.
- **b0S2**: Metropolis-Hastings acceptance rates for studied-item distribution parameters.
- **b0Crit**: Metropolis-Hastings acceptance rates for criteria.

Author(s)

Michael S. Pratte

See Also

hbmem
Examples

# This function is broken, so
# no example that works.
# make data from gamma model
if(1L==0)
{
  library(hbmem)
  sim=gammaLikeSim(I=50, J=400, muS=log(.5), s2aS=0, s2bS=0)
  dat=as.data.frame(cbind(sim@subj, sim@item, sim@cond, sim@Scond, sim@lag, sim@resp))
  colnames(dat)=c("sub", "item", "cond", "Scond", "lag", "resp")
  dat$lag=0

table(dat$resp, dat$Scond)
M=5000
keep=500:M
gamma=gammaLikeSample(dat, M=M, keep=keep, jump=.001)

par(mfrow=c(2,3),pch=19,pty='s')
matplot(exp(gamma@blocks[, gamma@muS]), t='l', xlab="Iteration", ylab="Mu-S")
abline(h=exp(sim@muS), col="blue")
# Estimates of Alpha as function of true values
plot(gamma@ests[gamma@alphaS]~sim@alphaS, xlab="True
Alpha-S", ylab="Est. Alpha-S"); abline(0,1, col="blue")
# Estimates of Beta as function of true values
plot(gamma@ests[gamma@betaS]~sim@betaS, xlab="True
Beta-S", ylab="Est. Beta-S"); abline(0,1, col="blue")

# Look at some criteria
for(i in 1:3){
  matplot(t(exp(gamma@s.crit[i,2:7])),t='l')
  abline(h=sim@crit[i,])
}
gamma@ests[c(gamma@s2alphaS, gamma@s2betaS)]
}

gammaProbs

Function gammaProbs

Description

Returns the probability of making confidence rating responses given parameters of gamma signal detection model.

Usage

gammaProbs(scale, shape, bounds)
**Arguments**

- **scale**  
  Scale of gamma distribution.

- **shape**  
  Shape of gamma distribution, usually fixed to 2.0

- **bounds**  
  Criteria placed on strength axis.

---

**gammaSample**  

*Function gammaSample*

---

**Description**

Runs MCMC for the hierarchical Gamma model

**Usage**

```r
gammaSample(dat, M = 10000, keep = (M/10):M, getDIC = TRUE,
  freeCrit=TRUE,shape=2,jump=.005)
```

**Arguments**

- **dat**  
  Data frame that must include variables cond,sub,item,lag,resp. Indexes for cond, sub, item, and respond must start at zero and have no gaps (i.e., no skipped subject numbers). Lags must be zero-centered.

- **M**  
  Number of MCMC iterations.

- **keep**  
  Which MCMC iterations should be included in estimates and returned. Use keep to both get rid of burn-in, and thin chains if necessary.

- **getDIC**  
  Logical. should the function compute DIC value? This takes a while if M is large.

- **freeCrit**  
  Logical. If TRUE (default) individual criteria vary across people. If false, all participants have the same criteria (but note that overall response biases are still modeled in the means)

- **shape**  
  Fixed shape across both new and studied distributions.

- **jump**  
  The criteria and decorrelating steps utilize Metropolis-Hastings sampling routines, which require tuning. All MCMC functions should self tune during the burnin period (iterations before keep), and they will alert you to the success of tuning. If acceptance rates are too low, "jump" should be decreased, if they are too high, "jump" should be increased. Alternatively, or in addition to adjusting "jump", simply increase the burnin period which will allow the function more time to self-tune.
Value

The function returns an internally defined "uvsd" S4 class that includes the following components:

- **mu**: Indexes which element of blocks contain grand means, mu
- **alpha**: Indexes which element of blocks contain participant effects, alpha
- **beta**: Indexes which element of blocks contain item effects, beta
- **s2alpha**: Indexes which element of blocks contain variance of participant effects (alpha).
- **s2beta**: Indexes which element of blocks contain variance of item effects (beta).
- **theta**: Indexes which element of blocks contain theta, the slope of the lag effect
- **estN**: Posterior means of block parameters for new-item means
- **estS**: Posterior means of block parameters for studied-item means
- **estS2**: Not used for gamma model.
- **estCrit**: Posterior means of criteria
- **blockN**: Each iteration for each parameter in the new-item mean block. Rows index iteration, columns index parameter.
- **blockS**: Same as blockN, but for the studied-item means
- **blockS2**: Not used for gamma model.
- **s.crit**: Samples of each criteria.
- **pD**: Number of effective parameters used in DIC. Note that this should be smaller than the actual number of parameters, as constraint from the hierarchical structure decreases the number of effective parameters.
- **DIC**: DIC value. Smaller values indicate better fits. Note that DIC is notably biased toward complexity.
- **M**: Number of MCMC iterations run
- **keep**: MCMC iterations that were used for estimation and returned
- **b0**: Metropolis-Hastings acceptance rates for new-item distribution parameters. These should be between .2 and .6. If they are not, the M, keep, or jump need to be adjusted.
- **b0S2**: Metropolis-Hastings acceptance rates for studied-item distribution parameters.
- **b0Crit**: Metropolis-Hastings acceptance rates for criteria.

Author(s)

Michael S. Pratte

See Also

hbmem
Examples

# make data from gamma model
library(hbmem)
sim=gammaSim(I=30,J=200)
dat=as.data.frame(cbind(sim@subj,sim@item,sim@cond,sim@scond,sim@lag,sim@resp))
colnames(dat)=c("sub","item","cond","scond","lag","resp")

M=10 # set very small for demo speed
keep=2:M
gamma=gammaSample(dat,M=1,keep=keep,jump=.01)

par(mfrow=c(3,2),pch=19,pty='s')
# Look at chains of MuN and MuS
matplot(gamma@blockN[,gamma@mun],t='l',xlab="Iteration",ylab="Mu-N")
abline(h=sim@mun,col="blue")
matplot(gamma@blockS[,gamma@mus],t='l',xlab="Iteration",ylab="Mu-S")
abline(h=sim@mus,col="blue")

# Estimates of Alpha as function of true values
plot(gamma@estN[gamma@alphaN],sim@alphas,xlab="True Alpha-N",ylab="Est. Alpha-N");abline(0,1,col="blue")
plot(gamma@estS[gamma@alphaS],sim@alphas,xlab="True Alpha-S",ylab="Est. Alpha-S");abline(0,1,col="blue")

# Estimates of Beta as function of true values
plot(gamma@estN[gamma@betaN],sim@betas,xlab="True Beta-N",ylab="Est. Beta-N");abline(0,1,col="blue")
plot(gamma@estS[gamma@betaS],sim@betas,xlab="True Beta-S",ylab="Est. Beta-S");abline(0,1,col="blue")

gamma@estN[c(gamma@s2alphaN,gamma@s2betaN)]
gamma@estS[c(gamma@s2alphaS,gamma@s2betaS)]

# Look at some criteria
par(mfrow=c(2,2))
for(i in 1:4)
matplot(t(gamma@s.crit[i,]),t='l')

---

**gammaSim**  
Function `gammaSim`

**Description**

Simulates data from a hierarchical Gamma model.

**Usage**

```r
gammaSim(NN=1,NS=2,I=30,J=200,K=6,muN=log(.65),s2aN=.2,s2bN=.2,
muS=log(c(8,1.2)),s2aS=.2,s2bS=.2,lagEffect=-.001,shape=2,
crit=matrix(rep(c(.3,.6,1,1.2,1.6),each=1),ncol=(K-1)))
```
**gammaSim**

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>NN</td>
<td>Number of conditions for new words.</td>
</tr>
<tr>
<td>NS</td>
<td>Number of conditions for studied words.</td>
</tr>
<tr>
<td>I</td>
<td>Number of participants.</td>
</tr>
<tr>
<td>J</td>
<td>Number of items.</td>
</tr>
<tr>
<td>K</td>
<td>Number of response options.</td>
</tr>
<tr>
<td>muN</td>
<td>Mean of new-item distribution. If NN is greater than 1, then muN must be a vector of length NN.</td>
</tr>
<tr>
<td>s2aN</td>
<td>Variance of participant effects on mean of new-item distribution.</td>
</tr>
<tr>
<td>s2bN</td>
<td>Variance of item effects on mean of new-item distribution.</td>
</tr>
<tr>
<td>muS</td>
<td>Mean of studied-item distribution. If NS is greater than 1, then muS must be a vector of length NS.</td>
</tr>
<tr>
<td>s2aS</td>
<td>Variance of participant effects on mean of studied-item distribution.</td>
</tr>
<tr>
<td>s2bS</td>
<td>Variance of item effects on mean of studied-item distribution.</td>
</tr>
<tr>
<td>lagEffect</td>
<td>Linear slope of lag effect on log of studied-item scale.</td>
</tr>
<tr>
<td>shape</td>
<td>Common shape for both new and studied distributions.</td>
</tr>
<tr>
<td>crit</td>
<td>Matrix of criteria (not including -Inf or Inf). Columns correspond to criteria, rows correspond to participants.</td>
</tr>
</tbody>
</table>

**Value**

The function returns an internally defined "uvsdSim" structure.

**Author(s)**

Michael S. Pratte

**References**

See Pratte, Rouder, & Morey (2009)

**See Also**

hbmem

**Examples**

```r
library(hbmem)
#Data from hierarchical model
sim=gammaSim()
slotNames(sim)
table(sim@resp,sim@cond,sim@Scond)

#Usefull to make data.frame for passing to model-fitting functions
dat=as.data.frame(cbind(sim@subj,sim@item,sim@cond,sim@Scond,sim@lag,sim@resp))
colnames(dat)=c("sub","item","cond","Scond","lag","resp")
table(dat$resp,dat$cond,dat$Scond)
```
normalSim

Function normalSim

Description

Simulates data from a hierarchical linear normal model.

Usage

```r
normalSim(N=1, I=30, J=300, mu=0, s2a=.2, s2b=.2, muS2=0, s2aS2=0, s2bS2=0)
```

Arguments

- `N` Number of conditions.
- `I` Number of participants.
- `J` Number of items.
- `mu` Grand mean
- `s2a` Variance of subject effect on the mean
- `s2b` Variance of item effect on the mean
- `muS2` Overall variance of data on log scale
- `s2aS2` Variance of subject effect on variance
- `s2bS2` Variance of item effect on variance

Value

The function returns a data frame with subject (subj), item, lag, and response (resp) columns. Lag is a vector of zeros (i.e., no lag effect).

Author(s)

Michael S. Pratte

See Also

hbmem

Examples

```r
library(hbmem)
I=20
J=50
R=I*J
dat=normalSim(I=I, J=J, mu=10, s2a=1, s2b=1, muS2=log(1), s2aS2=0, s2bS2=0)
summary(dat)
```
Description

Confidence ratings data from Pratte, Rouder, \& Morey (2009).

Usage

data(prm09)

Format

A flat-field data frame (each row is a trial) with the following variables

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>cond</td>
<td>0=new; 1=studied</td>
</tr>
<tr>
<td>sub</td>
<td>index of subject starting at 0</td>
</tr>
<tr>
<td>item</td>
<td>index of item starting at 0</td>
</tr>
<tr>
<td>lag</td>
<td>index of lag, zero-centered</td>
</tr>
<tr>
<td>resp</td>
<td>which response was made; 0=&quot;sure new&quot;</td>
</tr>
</tbody>
</table>

Details

Participants studied a list of 240 words, and were then tested on the 240 studied and on 240 new words. At test, participants made one of six confidence ratings ranging from "sure new" to "sure studied". Note that to apply the models to these data the "Scond" variable should be set to "cond", and the "cond" variable should be all zeros. This is a backwards-compatibility issue.

Source


Examples

```r
library(hbmem)
data(prm09)
table(prm09$resp,prm09$cond)
#Turn it into data suitable for
#analysis with HBMEM functions:
newdat=prm09
newdat$Scond=newdat$cond
newdat$cond=0
summary(newdat)
```
Function `rtgamma`

**Description**

Returns random draws from truncated gamma distribution.

**Usage**

```r
d = rtgamma(N, shape, scale, a, b)
```

**Arguments**

- `N`: Number of samples.
- `shape`: Shape of gamma distribution.
- `scale`: Scale of gamma distribution.
- `a`: Lower truncation point.
- `b`: Upper truncation point.

Function `rtnorm`

**Description**

Returns random samples from a truncated normal distribution.

**Usage**

```r
d = rtnorm(N, mu, sigma, a, b)
```

**Arguments**

- `N`: Number of samples to return.
- `mu`: A vector of length N that contains distribution means for each draw.
- `sigma`: A vector of length N that contains distribution standard deviations for each draw.
- `a`: Vector of length N of lower truncation points; may be -Inf.
- `b`: Vector of length N of upper truncation point; may be Inf.

**Details**

This function is currently unstable for drawing from regions with extremely low probabilities. If this happens it should print a warning, and return a draw from a uniform distribution between a and b. See example below for how to break it.
sampleGamma

Value

Returns 'N' random draws.

Author(s)

Michael S. Pratte

See Also

hbmem

Examples

library(hbmem)
# Draw one
rtnorm(1,0,1,0,.2)

# Draw 50
N=500
mu=rep(0,N)
sigma=rep(1,N)
a=rep(1,N)
b=rep(2,N)
x=rtnorm(N,mu,sigma,a,b)
hist(x)

# Break it
rtnorm(1,0,1,1000,1001)

sampleGamma Function sampleGamma

Description

Samples posterior of mean parameters of the hierarchical linear model on the log scale parameter of a gamma distribution. Usually used within an MCMC loop.

Usage

sampleGamma(sample, y, cond, subj, item,
lag,N,I,J,R,ncond,nsub,nitem,s2mu, s2a, s2b, met, shape,
sampLag,pos=FALSE)
Arguments

sample  Block of linear model parameters from previous iteration.
y  Vector of data
cond  Vector fo condition index, starting at zero.
subj  Vector of subject index, starting at zero.
item  Vector of item index, starting at zero.
lag  Vector of lag index, zero-centered.
N  Number of conditions.
I  Number of subjects.
J  Number of items.
R  Total number of trials.
ncond  Vector of length (N) containing number of trials per condition.
nsub  Vector of length (I) containing number of trials per each subject.
nitem  Vector of length (J) containing number of trials per each item.
s2mu  Prior variance on the grand mean mu; usually set to some large number.
s2a  Shape parameter of inverse gamma prior placed on effect variances.
s2b  Rate parameter of inverse gamma prior placed on effect variances. Setting both s2a AND s2b to be small (e.g., .01, .01) makes this an uninformative prior.
met  Vector of tuning parameter for metropolis-hastings steps. Here, all sampling (except variances of alpha and beta) and decorrelating steps utilize the M-H sampling algorithm. This should be adjusted so that .2 < b0 < .6.
shape  Single shape of Gamma distribution.
samplag  Logical. Whether or not to sample the lag effect.
pos  Logical. If true, the model on scale is 1+exp(mu + alpha + beta). That is, the scale is always greater than one.

Value

The function returns a list. The first element of the list is the newly sampled block of parameters. The second element contains a vector of 0s and 1s indicating which of the decorrelating steps were accepted.

Author(s)

Michael S. Pratte

See Also

hbmem
Examples

```r
library(hbmem)
N=2
shape=2
I=30
J=50
R=I*J

# make some data
mu=log(c(1,2))
alpha=rnorm(I,0,.2)
beta=rnorm(J,0,.2)
theta=-.001
cond=sample(0:(N-1),R,replace=TRUE)
subj=rep(0:(I-1),each=J)
item=NULL
for(i in 1:I)
  item=c(item,sample(0:(J-1),J,replace=FALSE))
lag=rnorm(R,0,100)
lag=lag-mean(lag)
resp=1:R
for(r in 1:R)
  {
    resp[r]=rgamma(1,shape,shape,scale=scale)
  }

ncond=table(cond)
nsub=table(subj)
nitem=table(item)
```

```r
M=10
keep=2:M
B=N+I+J+3
s.block=matrix(0,nrow=M,ncol=B)
met=rep(.08,B)
b0=rep(0,B)
jump=.0005
for(m in 2:M)
  {
    tmp=sampleGamma(s.block[m-1,],resp,cond,subj,item,lag,
    N,1,J,R,ncond,nsub,nitem,5,.01,.01,met,2,1,pos=TRUE)
    s.block[m,]=tmp[[1]]
    b0=b0 + tmp[[2]]
  }
  # Auto-tuning of metropolis decorrelating steps
  if(m>20 & m<min(keep))
    {
      met=met+(b0/m<.4)*rep(-jump,B) +(b0/m>.6)*rep(jump,B)
      met[met<jump]=jump
    }
  if(m==min(keep)) b0=rep(0,B)
```
```r
b0/length(keep) # check acceptance rate

hbest=colMeans(s.block[keep,])

par(mfrow=c(2,2),pch=19,pty='s')
matplot(s.block[keep,1:N],t='l')
abline(h=mu,col="green")
acf(s.block[keep,])
plot(hbest[(N+1):((I+N)]-alpha)
abline(0,1,col="green")
plot(hbest[(I+N+1):((I+J+N)]-beta)
abline(0,1,col="green")

# variance of participant effect
mean(s.block[keep,(N+I+J+1)])
# variance of item effect
mean(s.block[keep,(N+I+J+2)])
# estimate of lag effect
mean(s.block[keep,(N+I+J+3)])
```

---

**sampleNorm**

*Function sampleNorm*

**Description**

Samples posterior of mean parameters of the hierarchical linear normal model with a single Sigma2. Usually used within an MCMC loop.

**Usage**

```r
sampleNorm(sample, y, cond, subj, item, lag, N, I, J, R, ncond, nsub, nitem, s2mu, s2a, s2b, meta, metb, sigma2, sampLag=TRUE,Hier=TRUE)
```

**Arguments**

- `sample` : Block of linear model parameters from previous iteration.
- `y` : Vector of data
- `cond` : Vector of condition index, starting at zero.
- `subj` : Vector of subject index, starting at zero.
- `item` : Vector of item index, starting at zero.
- `lag` : Vector of lag index, zero-centered.
- `N` : Number of conditions.
- `I` : Number of subjects.
sampleNorm

J Number of items.
R Total number of trials.
ncond Vector of length (N) containing number of trials per each condition.
nsub Vector of length (I) containing number of trials per each subject.
nitem Vector of length (J) containing number of trials per each item.
s2mu Prior variance on the grand mean mu; usually set to some large number.
s2a Shape parameter of inverse gamma prior placed on effect variances.
s2b Rate parameter of inverse gamma prior placed on effect variances. Setting both s2a AND s2b to be small (e.g., .01, .01) makes this an uninformative prior.
meta Matrix of tuning parameter for metropolis-hastings decorrelating step on mu and alpha. This should be adjusted so that .2 < b0 < .6.
metb Tuning parameter for decorrelating step on alpha and beta.
sigma2 Variance of distribution.
samplag Logical. Whether or not to sample the lag effect.
Hier Logical. If TRUE then effect variances are estimated from data. If FALSE then these values are set to whatever value is in the s2alpha and s2beta slots of sample. This should always be set to TRUE.

Value
The function returns a list. The first element of the list is the newly sampled block of parameters. The second element contains a vector of 0s and 1s indicating which of the decorrelating steps were accepted.

Author(s)
Michael S. Pratte

References
See Pratte, Rouder, & Morey (2009)

See Also
hbmem

Examples
library(hbmem)
N=2
t.mu=c(1,2)
I=20
J=50
R=I*J
#make some data
tmp=normalSim(N=N,I=I,J=J,mu=t.mu,s2a=2,s2b=2,muS2=log(1),s2as2=0,s2bs2=0)
dat=tmp[[1]]
```r

t.alpha = tmp[[2]]  
t.beta = tmp[[3]]

ncond = table(dat$cond)  
nsub = table(dat$sub)  
nitem = table(dat$item)

M = 10  
keep = 2:M  
B = N+I+J+3  
s.block = matrix(0, nrow = M, ncol = B)  
met = c(1, 1); b0 = c(0, 0)  
jump = .001  
for (m in 2:M)  
{  
tmp = sampleNorm(s.block[m-1,], dat$resp, dat$cond, dat$subj, dat$item, dat$lag, 
N, I, 1, R, ncond, nsub, nitem, 5, .01, .01, met[1], met[2], 1, 1, 1)  
s.block[m,] = tmp[[1]]  
b0 = b0 + tmp[[2]]

# Auto-tuning of metropolis decorrelating steps  
if (m>20 & m<min(keep))  
{  
   met = met + (b0/m<.2)*c(-jump, -jump) + (b0/m>.2)*c(jump, jump)  
   met[met < jump] = jump
 }
}

b0/M  # check acceptance rate

hbest = colMeans(s.block[keep,])

par(mfrow = c(2, 2), pch = 19, pty = 's')  
matplot(s.block[keep, 1:N], t = 'l')  
abline(h = t.mu, col = "green")  
abline(h = tapply(dat$resp, dat$cond, mean), col = "orange")  
acf(s.block[keep,])  
plot(hbest[(N+1):(I+1)] - t.alpha)  
abline(0, 1, col = "green")  
plot(hbest[(I+1):(I+J+1)] - t.beta)  
abline(0, 1, col = "green")

# Variance of participant effect  
mean(s.block[keep, (N+I+J+1)])

# Variance of item effect  
mean(s.block[keep, (N+I+J+2)])

# Estimate of lag effect  
mean(s.block[keep, (N+I+J+3)])
```

**Function sampleNormb**

**Description**

Same as sampleNorm, but assumes an additive model on sigma2, and takes the block of sigma2 parameters as argument.

**Usage**

```r
sampleNormb(sample, y, cond, subj, item, lag, N, I, J, R, ncond, nsub, nitem, s2mu, s2a, s2b, meta, metb, blockSigma2, sampLag=1, Hier=1)
```

**Arguments**

- **sample**: Block of linear model parameters from previous iteration.
- **y**: Vector of data.
- **cond**: Vector of condition index, starting at zero.
- **subj**: Vector of subject index, starting at zero.
- **item**: Vector of item index, starting at zero.
- **lag**: Vector of lag index, zero-centered.
- **N**: Number of conditions.
- **I**: Number of subjects.
- **J**: Number of items.
- **R**: Total number of trials.
- **ncond**: Vector of length (N) containing number of trials per each condition.
- **nsub**: Vector of length (I) containing number of trials per each subject.
- **nitem**: Vector of length (J) containing number of trials per each item.
- **s2mu**: Prior variance on the grand mean \( \mu \); usually set to some large number.
- **s2a**: Shape parameter of inverse gamma prior placed on effect variances. Setting both \( s2a \) AND \( s2b \) to be small (e.g., .01, .01) makes this an uninformative prior.
- **s2b**: Rate parameter of inverse gamma prior placed on effect variances. Setting both \( s2a \) AND \( s2b \) to be small (e.g., .01, .01) makes this an uninformative prior.
- **meta**: Matrix of tuning parameter for metropolis-hastings decorrelating step on mu and alpha. This should be adjusted so that \(.2 < b0 < .6\).
- **metb**: Tuning parameter for decorrelating step on alpha and beta.
- **blockSigma2**: Block of parameters for Sigma2 (on log scale). Like all blocks, first element is the overall mean, followed by participant effects and then item effects.
- **sampLag**: Logical. Whether or not to sample the lag effect.
- **Hier**: Logical. If TRUE then effect variances are estimated from data. If false, then these values are fixed to whatever is in the \( s2alpha \) and \( s2beta \) slots of sample. This value should always be TRUE unless you know what you are doing.
Value
The function returns a list. The first element of the list is the newly sampled block of parameters. The second element contains a vector of 0s or 1s indicating which of the decorrelating steps were accepted.

Author(s)
Michael S. Pratte

See Also
hbmem, sampleSig2b

Examples
library(hbmem)
N=2
I=50
J=200
B=N+I+J+3
R = I * J

mu=c(3,5)
mus2=log(c(1,2))
alpha = rnorm(I, 0, sqrt(.2))
beta = rnorm(J, 0, sqrt(.2))
alphas2 = rnorm(I, 0, sqrt(.2))
betas2 = rnorm(J, 0, sqrt(.2))
cond=sample(0:(N-1),R,replace=TRUE)
subj = rep(0:(I - 1), each = J)
item = rep(0:(J - 1), 1)
lag = rep(0, R)
lag=runif(R,-500,500)
lag=lag-mean(lag)
resp = 1:R
for (r in 1:R) {
  sd = sqrt(exp(mus2[cond[r]+1] + alphas2[subj[r] + 1] +
                betas2[item[r] + 1] + .005*lag[r]))
  resp[r] = rnorm(1, mean, sd)
}
sim=(as.data.frame(cbind(cond,subj, item, lag, resp)))
attach(sim)
plot(resp~lag)

###########MCMC SETUP###########
blocksS=blockS2=matrix(0,nrow=10,ncol=B)
b0mean=c(0,0)
b0S2=rep(0,B)
met=rep(.01,B)
jump=.0001
Samples posterior of mean parameters of the hierarchical linear normal model with the effects a linear function of some other variable.
Usage

```r
callNormR(sample, phi, blockD, y, subj, item, lag, I, J, R, nsub, nitem, s2mu, s2a, s2b, meta, metb, sigma2, sampLag)
```

Arguments

- `sample`: Block of linear model parameters from previous iteration.
- `y`: Vector of data
- `phi`: Vector of linear slopes on effects.
- `blockD`: Block of parameters that will serve as the means of random effects
- `subj`: Vector of subject index, starting at zero.
- `item`: Vector of item index, starting at zero.
- `lag`: Vector of lag index, zero-centered.
- `I`: Number of subjects.
- `J`: Number of items.
- `R`: Total number of trials.
- `nsub`: Vector of length (I) containing number of trials per each subject.
- `nitem`: Vector of length (J) containing number of trials per each item.
- `s2mu`: Prior variance on the grand mean mu; usually set to some large number.
- `s2a`: Shape parameter of inverse gamma prior placed on effect variances.
- `s2b`: Rate parameter of inverse gamma prior placed on effect variances. Setting both `s2a` AND `s2b` to be small (e.g., .01, .01) makes this an uninformative prior.
- `meta`: Matrix of tuning parameter for metropolis-hastings decorrelating step on mu and alpha. This should be adjusted so that .2 < b0 < .6.
- `metb`: Tunning parameter for decorrelating step on alpha and beta.
- `sigma2`: Variance of distribution.
- `sampLag`: Logical. Whether or not to sample the lag effect.

Value

The function returns a list. The first element of the list is the newly sampled block of parameters. The THIRD element contains a vector of 0s and 1s indicating which of the decorrelating steps were accepted.

Author(s)

Michael S. Pratte

References

Not published yet.
See Also

hbmem

Examples

```r
library(hbmem)

I=50
J=100
M=10
B=I+J+4
mu=.5
mus2=0
s2a=.2
s2b=.2
s2as2=0
s2bs2=0

phi=c(.2,.08)
blockD=rep(0,B)
blockD[2:2:(I+1)]=rnorm(I,0,.5)
blockD[(I+2):(I+J+1)]=rnorm(J,0,.5)

R = I * J
alpha = rnorm(I, phi[1]*blockD[2:(I+1)], sqrt(s2a))
beta = rnorm(J, phi[2]*blockD[(I+2):(I+J+1)], sqrt(s2b))
alphaS2 = rnorm(I, 0, sqrt(s2as2))
betaS2 = rnorm(J, 0, sqrt(s2bs2))
subj = rep(0:(I - 1), each = J)
item = rep(0:(J - 1), I)
lag = rep(0, R)
resp = 1:R
for (r in 1:R) {
  mean = mu + alpha[subj[r] + 1] + beta[item[r] + 1]
  sd = sqrt(exp(mus2 + alphaS2[subj[r] + 1] + betaS2[item[r] + 1]))
  resp[r] = rnorm(1, mean, sd)
}
sim=as.data.frame(cbind(subj, item, lag, resp))

blockR=matrix(0,M,B)
blockR[1,c(I+J+2,I+J+3)]=c(.1,.1)
met=c(.1,.1)
b0=c(0,0)

for(m in 2:M)
{
  tmp=sampleNormR(blockR[m-1],phi,blockD,sim$resp,sim$subj,sim$itemsim$lag,
  I,J,I*J,table(sim$subj),table(sim$itemsim$lag),I,J,I*J,table(sim$subj),table(sim$itemsim$lag),10,.01,.01,met[1],met[2],1,1)
  blockR[m]=tmp[[1]]
  b0=b0+tmp[[3]]
}
```
Function `samplePosNorm`

**Description**

Samples posterior of mean parameters of the positive hierarchical linear normal model with a single Sigma2 \( (x = N(exp(mu+alpha_i+beta_j),sigma2)) \).

**Usage**

```r
callPosNorm(sample, y, cond, sub, item, lag, N, I, J, R, sig2mu, a, b, met, sigma2, sampLag)
```
Arguments

```
sample  Block of linear model parameters from previous iteration.
y      Vector of data
cond    Vector of condition index.
sub     Vector of subject index, starting at zero.
item    Vector of item index, starting at zero.
lag     Vector of lag index, zero-centered.
N       Number of conditions.
I       Number of subjects.
J       Number of items.
R       Total number of trials.
sig2mu  Prior variance on the grand mean mu; usually set to some large number.
a       Shape parameter of inverse gamma prior placed on effect variances.
b       Rate parameter of inverse gamma prior placed on effect variances. Setting both
       s2a AND s2b to be small (e.g., .01, .01) makes this an uninformative prior.
met     Vector of tuning parameter for metropolis-hastings sampling. There is one tun-
       ing parameter for mu, each of I alphas, each of J betas, s2alpha,s2beta,and theta.
       Those for s2alpha and s2beta are placeholders, as these parameters are sampled
       with gibbs.
sigm2   Variance of distribution.
sampLag Logical. Whether or not to sample the lag effect.
```

Value

The function returns a list. The first element of the list is the newly sampled block of parameters.
The second element contains a vector of 0s and 1s indicating which of the decorrelating steps were accepted.

Author(s)

Michael S. Pratte

References

Not Published yet

See Also

hbmem
Examples

```r
library(hbmem)

N=3
I=50
J=100
R=N*I+J
t.sigma2=3
t.mu=c(-1,0,1)
t.sig2alpha=.2
t.sig2beta=.6
t.alpha=rnorm(I,0,sqrt(t.sig2alpha))
t.beta =rnorm(J,0,sqrt(t.sig2beta))
t.theta=-.5
cond=sample((0:(N-1)),R,replace=TRUE)
sub=rep(rep(0:(I-1),each=J),N)
item=rep(rep(0:(J-1),I),N)
lag=scale(rnorm(R,0,sqrt(t.sigma2)/10))

t.mean=1:R
y=rnorm(R,t.mean,sqrt(t.sigma2))

M=10 #Way too low for real analysis!
B=N*I+J+3
block=matrix(0,nrow=M,ncol=B)
met=rep(.1,B);jump=.0001
b0=rep(0,B)
keep=2:M
for(m in 2:M)
{
 tmp=samplePosNorm(block[m-1,],y,cond,sub,item,lag,N,I,J,R,1,.01,.01,met,t.sigma2,1)
 block[m,]=tmp[[1]]
 b0=b0+tmp[[2]]

 if(m<keep[1])
 |
 met=met+(b0/m<.3)*jump +(b0/m>.5)*jump
 met[met<jump]=jump
 |
 #if(m%100==0) print(m)
 |

 est=colMeans(block[keep,])
b0/M

 par(mfrow=c(3,2))
est.mu=est[1:N]
 matplot(exp(block[keep,1:N]),t='l',main="Mu",ylab="Mu")
 abline(h=exp(t.mu),col="blue")
 #abline(h=tapply(y,cond,mean),col="green")
 acf(block[keep,1],main="ACF of Mu")
```
Function `sampleSig2`  

**Description**  
Samples posterior of the variance of a normal distribution which has an additive structure on the mean, and a single variance for all values. Usually used within MCMC loop.

**Usage**  
sampleSig2(sig2, block, y, cond, sub, item, lag, N, ncond, I, J, a, b)

**Arguments**  
- `sig2`: Sample of `sig2` from previous iteration.  
- `block`: Vector of parameters for mean of distribution.  
- `y`: Vector of data.  
- `cond`: Vector that indexs condition (e.g., deep vs. shallow).  
- `sub`: Vector of subject index, starting at zero.  
- `item`: Vector of item index, starting at zero.  
- `lag`: Vector of lag index, zero-centered.  
- `N`: Number of conditions.  
- `ncond`: Number of trials per condition.  
- `I`: Number of subjects.  
- `J`: Number of items.  
- `a`: Shape parameter for inverse gamma prior on `Sigma2`.  
- `b`: Rate parameter for inverse gamma prior on `Sigma2`. Setting ’a’ and ’b’ to small values (e.g., .01, .01) makes the prior non-informative.
Value

The function returns a new sample of Sigma2.

Author(s)

Michael S. Pratte

See Also

hbmem

Examples

library(hbmem)
true.mean=c(0,0)
true.sigma2=c(10,20)
N=2
l=1
j=1
R=1000
cond=rep(0:1,R/2)
ncond=table(cond)
sub=rep(0,R)
item=rep(0,R)
lag=rep(0,R)

#make some data
dat=rnorm(R,true.mean[cond+1],sqrt(true.sigma2[cond+1]))
true.block=c(true.mean,rep(0,(I+J+3)))
a=b=.01
M=10
s.sigma2=matrix(1,M,N)

for(m in 2:M)
{
  s.sigma2[m,]=sampleSig2(s.sigma2[m-1,],true.block,dat,cond,sub,item,lag,N,ncond,I, J,a,b)
}

par(mfrow=c(1,1),pty='s')
matplot(s.sigma2,t='1')
abline(h=true.sigma2,col="blue")
abline(h=colMeans(s.sigma2),col="green") #post mean
Function sampleSig2b

Description

Samples posterior of the variance of a normal distribution which has the same additive structure on the mean and the log of variance. Usually used within MCMC loop.

Usage

```r
sampleSig2b(sample, y, cond, sub, item, lag, N, I, J, R, ncond, nsub, nitem, s2mu, s2a, s2b, met, blockMean, sampLag = 1, Hier = 1)
```

Arguments

- `sample`: Previous sample of block variances.
- `y`: Vector of data.
- `cond`: Vector of condition index, starting at zero.
- `sub`: Vector of subject index, starting at zero.
- `item`: Vector of item index, starting at zero.
- `lag`: Vector of lag index, zero-centered.
- `N`: Number of conditions.
- `I`: Number of subjects.
- `J`: Number of items.
- `R`: Total number of trials.
- `ncond`: Vector of length (N) containing number of trials per each condition.
- `nsub`: Vector of length (I) containing number of trials per each subject.
- `nitem`: Vector of length (J) containing number of trials per each item.
- `s2mu`: Prior variance on the grand mean mu; usually set to some large number.
- `s2a`: Shape parameter of inverse gamma prior placed on effect variances.
- `s2b`: Rate parameter of inverse gamma prior placed on effect variances. Setting both s2a AND s2b to be small (e.g., .01, .01) makes this an uninformative prior.
- `met`: Vector of metropolis-hastings tuning parameters.
- `blockMean`: Block of parameters for the mean of the distribution.
- `sampLag`: Logical. Whether or not to sample the lag effect.
- `Hier`: Logical. If TRUE then effect variances are estimated from data. If FALSE then these values are set to whatever value is in the s2alpha and s2beta slots of sample. This should always be set to TRUE.
Details

This function is for a model with an additive structure on the log of the variance of a normal distribuion. This model is under development, the code is buggy, and it might not even work in the end.

Value

The function returns a new sample of a block of Sigma2 paramters.

Author(s)

Michael S. Pratte

See Also

hbmem,sampleNormb

Examples

#See sampleNormb for example

---

uvsd-class     Class "uvsd"

Description

This class holds objects that are returned from uvsdSample.

Slots

muN: Object of class "numeric" ~
alphaN: Object of class "numeric" ~
betaN: Object of class "numeric" ~
s2alphaN: Object of class "numeric" ~
s2betaN: Object of class "numeric" ~
thetaN: Object of class "numeric" ~
muS: Object of class "numeric" ~
alphaS: Object of class "numeric" ~
betaS: Object of class "numeric" ~
s2alphaS: Object of class "numeric" ~
s2betaS: Object of class "numeric" ~
thetaS: Object of class "numeric" ~
estN: Object of class "numeric" ~
estS: Object of class "numeric" ~~  
estS2: Object of class "numeric" ~~  
estCrit: Object of class "matrix" ~~  
blockN: Object of class "matrix" ~~  
blockS: Object of class "matrix" ~~  
blockS2: Object of class "matrix" ~~  
s.crit: Object of class "array" ~~  
pD: Object of class "numeric" ~~  
DIC: Object of class "numeric" ~~  
M: Object of class "numeric" ~~  
keep: Object of class "numeric" ~~  
bØ: Object of class "matrix" ~~  
bØS2: Object of class "numeric" ~~  
bØCrit: Object of class "numeric" ~~  

---

**uvsdLogLike**  
*Function uvsdLogLike*

**Description**

Computes log likelihood for UVSD model

**Usage**

`uvsdLogLike(R, NN, NS, I, J, K, dat, cond, Scond, subj, item, lag, blockN, blockS, blockS2, crit)`

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>R</code></td>
<td>Total number of trials.</td>
</tr>
<tr>
<td><code>NN</code></td>
<td>Number of new-item conditions.</td>
</tr>
<tr>
<td><code>NS</code></td>
<td>Number of studied-item conditions.</td>
</tr>
<tr>
<td><code>I</code></td>
<td>Number of subjects.</td>
</tr>
<tr>
<td><code>J</code></td>
<td>Number of items.</td>
</tr>
<tr>
<td><code>K</code></td>
<td>Number of response options.</td>
</tr>
<tr>
<td><code>dat</code></td>
<td>Vector of responses, ranging from 0:(K-1).</td>
</tr>
<tr>
<td><code>cond</code></td>
<td>Vector of condition index.</td>
</tr>
<tr>
<td><code>Scond</code></td>
<td>Vector of new/studied condition index; 0=new, 1=studied.</td>
</tr>
<tr>
<td><code>subj</code></td>
<td>Vector of subject index, starting at 0 with no missing subject numbers.</td>
</tr>
<tr>
<td><code>item</code></td>
<td>Vector of item index, starting at 0 with no missing item numbers.</td>
</tr>
<tr>
<td><code>lag</code></td>
<td>Vector of lag index.</td>
</tr>
</tbody>
</table>
Block of parameters for new-item means.

Block of parameters for studied-item means.

Block of parameters for Sigma2 values. If there is only one Sigma2 for all participants and items, then the first element of blockS2 should contain this value, and the other elements fo blockS2 should be zero.

VECTOR of criteria including -Inf and Inf for top and bottom criteria, respectively. Vector contains the (K+1) criteria for the first subjects, followed by those for the second subject, etc.

Value

The function returns the log likelihood.

Author(s)

Michael S. Pratte

References

See Pratte, Rouder, & Morey (2009)

See Also

hbmem

Function uvsdProbs

Description

Returns the probability of making confidence ratings given parameters of UVSD.

Usage

uvsdProbs(mean, sd, bounds)

Arguments

mean Mean of the signal-detection distribution. In the common parameterization of the model, this would be zero for new-item trials, and d’ for studied-item trials. In the PRM09 parameterization, these are dn and ds for new and studied-item trials, respectively.

sd Standard deviation of the distribution

bounds Criteria (not including -Inf or Inf).
Value
The function returns the probability of making each response for the parameters given.

Author(s)
Michael S. Pratte

References
See Pratte, Rouder, & Morey (2009)

See Also
hbmem

Examples
uvsdProbs(-1,1,c(-1,-.5,0,.5,1)) #New condition
uvsdProbs(1,1.3,c(-1,-.5,0,.5,1)) #Studied condition

uvsdSample Function uvsdSample

Description
Runs MCMC estimation for the hierarchical UVSD model.

Usage
uvsdSample(dat, M = 10000, keep = (M/10):M, getDIC = TRUE,
freeCrit=TRUE, equalVar=FALSE, freeSig2=FALSE, Hier=TRUE,jump=.001)

Arguments
dat Data frame that must include variables Scond,cond,sub,item,lag,resp. Scond indexes studied/new, whereas cond indexes conditions nested within the studied or new conditions. Indexes for Scond,cond, sub, item, and response must start at zero and have no gaps (i.e., no skipped subject numbers). Lags must be zero-centered.
M Number of MCMC iterations.
keep Which MCMC iterations should be included in estimates and returned. Use keep to both get ride of burn-in, and thin chains if necessary
getDIC Logical. should the function compute DIC value? This takes a while if M is large.
freeCrit Logical. If TRUE (default) individual criteria vary across people. If false, all participants have the same criteria. This should be set to false if there is only one participant, e.g., if averaging data over subjects.
equalVar Logical. If FALSE (default), unequal-variance model is fit. If TRUE, equal-variance model is fit.

freeSig2 Logical. If FALSE (default), one sigma is fit for all participants and items (as in Pratte, et al., 2009). If TRUE, then an additive model is placed on the log of sigma2 (as in Pratte and Rouder (2010).

Hier Logical. If TRUE then the variances of effects (e.g., item effects) are estimated from the data, i.e., effects are treated as random. If FALSE then these variances are fixed to 2.0 (.5 for recollection effects), thus treating these effects as fixed. This option is there to allow for comparison with more traditional approaches, and to see the effects of imposing hierarchical structure. It should always be set to TRUE in real analysis, and is not even guaranteed to work if set to false.

jump The criteria and decorrelating steps utilize Metropolis-Hastings sampling routines, which require tuning. All MCMC functions should self tune during the burnin period (iterations before keep), and they will alert you to the success of tuning. If acceptance rates are too low, "jump" should be decreased, if they are too high, "jump" should be increased. Alternatively, or in addition to adjusting "jump", simply increase the burnin period which will allow the function more time to self-tune.

Value

The function returns an internally defined "uvsd" S4 class that includes the following components:

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>mu</td>
<td>Indexes which element of blocks contain grand means, mu</td>
</tr>
<tr>
<td>alpha</td>
<td>Indexes which element of blocks contain participant effects, alpha</td>
</tr>
<tr>
<td>beta</td>
<td>Indexes which element of blocks contain item effects, beta</td>
</tr>
<tr>
<td>s2alpha</td>
<td>Indexes which element of blocks contain variance of participant effects (alpha).</td>
</tr>
<tr>
<td>s2beta</td>
<td>Indexes which element of blocks contain variance of item effects (beta).</td>
</tr>
<tr>
<td>theta</td>
<td>Indexes which element of blocks contain theta, the slope of the lag effect</td>
</tr>
<tr>
<td>estN</td>
<td>Posterior means of block parameters for new-item means</td>
</tr>
<tr>
<td>estS</td>
<td>Posterior means of block parameters for studied-item means</td>
</tr>
<tr>
<td>estS2</td>
<td>Posterior means of block for studied-item variances.</td>
</tr>
<tr>
<td>estCrit</td>
<td>Posterior means of criteria</td>
</tr>
<tr>
<td>blockN</td>
<td>Each iteration for each parameter in the new-item mean block. Rows index iteration, columns index parameter.</td>
</tr>
<tr>
<td>blockS</td>
<td>Same as blockN, but for the studied-item means</td>
</tr>
<tr>
<td>blockS2</td>
<td>Same as blockN, but for variances of studied-item distribution. If equalVar=TRUE, then these values are all zero. If UVSD is fit but freeSig2=FALSE, then only the first element is non-zero (mu).</td>
</tr>
<tr>
<td>s.crit</td>
<td>Samples of each criteria</td>
</tr>
<tr>
<td>pD</td>
<td>Number of effective parameters used in DIC. Note that this should be smaller than the actual number of parameters, as constraint from the hierarchical structure decreases the number of effective parameters.</td>
</tr>
</tbody>
</table>
DIC
DIC value. Smaller values indicate better fits. Note that DIC is notably biased toward complexity.

M
Number of MCMC iterations run

keep
MCMC iterations that were used for estimation and returned

b0
Metropolis-Hastings acceptance rates for decorrelating steps. These should be between .2 and .6. If they are not, the M, keep, or jump need to be adjusted.

b0S2
If additive model is placed on Sigma2 (i.e., freeSigma2=TRUE), then all parameters on S2 must be tuned. b0S2 are the acceptance probabilities for these parameters.

Author(s)
Michael S. Pratte

References
See Pratte, Rouder, & Morey (2009)

See Also
hbmem

Examples
In this example we generate data from UVSD with a different muN,muS, and Sigma2 for every person and item. These data are then fit with a hierarchical UVSD allowing participant or item effects on log(Sigma2).

library(hbmem)
sim=uvsdSim(NN=1,mun=-.5,NS=2,mus=c(.5,1),J=30,J=300,s2aN = .2, s2bN = .2,
mus2=log(c(1,3,1.5)),s2aS= .2, s2bS= .2,s2aS2 = .2,s2bS2 = .2)
dat=as.data.frame(cbind(sim@subj,sim@item,sim@cond,sim@Scond,sim@lag,sim@resp))
colnames(dat)=c("sub","item","cond","Scond","lag","resp")
M=10 #Way too low for real analysis
keep=2:M
uvsd=uvsdSample(dat,M=M,keep=keep,equalVar=FALSE,freeSig2=TRUE,jump=.0001,Hier=1)

par(mfrow=c(3,2),pch=19,pty='s')
#Look at chains of MuN and MuS
matplot(uvsvd@blockN[uvsvd@muN],t='l',xlab="Iteration",ylab="Mu-N")
abline(h=sim@muN,col="blue")
matplot(uvsvd@blockS[uvsvd@muS],t='l',xlab="Iteration",ylab="Mu-S")
abline(h=sim@muS,col="blue")

#Estimates of strength effects as function of true values
plot(uvsvd@estN[uvsvd@alphaN]-sim@alphaN,xlab="True Alpha-N",ylab="Est. Alpha-N");abline(0,1,col="blue")
plot(uvsvd@estS[uvsvd@alphaS]-sim@alphaS,xlab="True Alpha-S",ylab="Est. Alpha-S");abline(0,1,col="blue")
Function `uvsdSim`

Simulates data from a hierarchical UVSD model.

**Usage**

```
uvsdSim(NN = 2, NS = 1, I = 30, J = 200, K = 6, muN = c(-0.5, -0.2), s2aN = 0.2, s2bN = 0.2, muS = 0.5, s2aS = 0.2, s2bS = 0.2, muS2 = log(1), s2aS2 = 0, s2bS2 = 0, lagEffect = -0.001, crit = matrix(rep(c(-1.5,-0.5, 0, 0.5, 1.5), each = I), ncol = (K - 1)))
```

**Arguments**

- **NN**: Number of conditions for new words.
- **NS**: Number of conditions for studied words.
- **I**: Number of participants.
- **J**: Number of items.
- **K**: Number of response options.
- **muN**: Mean of new-item distribution. If NN is greater than 1, then muN must be a vector of length NN.
s2aN  Variance of participant effects on mean of new-item distribution.
s2bN  Variance of item effects on mean of new-item distribution.
muS  Mean of studied-item distribution. If NS is greater than 1, then muS must be a
      vector of length NS.
s2aS  Variance of participant effects on mean of studied-item distribution.
s2bS  Variance of item effects on mean of studied-item distribution.
lagEffect Magnitude of linear lag effect on both studied-item distribution and log(sigma2).
muS2  Mean variance of studied-item distribution, sigma2
s2aS2 Variance of participant effects sigma2.
s2bS2 Variance of item effects on sigma2.
crit  Matrix of criteria (not including -Inf or Inf). Columns correspond to criteria,
      rows correspond to participants.

Value

The function returns an internally defined "uvsdSim" structure.

Author(s)

Michael S. Pratte

References

See Pratte, Rouder, & Morey (2009)

See Also

hbmem

Examples

library(hbmem)
#Data from hiererchial model
sim=uvsdSim()
slotNames(sim)
table(sim@resp,sim@Scond,sim@cond)

#Usefull to make data.frame for passing to model-fitting functions
dat=as.data.frame(cbind(sim@subj,sim@item,sim@cond,sim@Scond,sim@lag,sim@resp))
colnames(dat)=c("sub","item","cond","Scond","lag","resp")
table(dat$resp,dat$Scond,dat$cond)
Class “uvsdSim”

Description

Class that holds objects from function `uvsdSim()`

Slots

- `scond`: Object of class "numeric"
- `cond`: Object of class "numeric"
- `subj`: Object of class "numeric"
- `item`: Object of class "numeric"
- `lag`: Object of class "numeric"
- `resp`: Object of class "numeric"
- `muN`: Object of class "numeric"
- `muS`: Object of class "numeric"
- `muS2`: Object of class "numeric"
- `alphaN`: Object of class "numeric"
- `betaN`: Object of class "numeric"
- `alphaS`: Object of class "numeric"
- `betaS`: Object of class "numeric"
- `alphaS2`: Object of class "numeric"
- `betaS2`: Object of class "numeric"
- `crit`: Object of class "matrix"
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