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Description Model-based clustering using Bayesian parsimonious Gaussian mixture models. MCMC (Markov chain Monte Carlo) are used for parameter estimation. The RJMCMC (Reversible-jump Markov chain Monte Carlo) is used for model selection. GREEN et al. (1995) <[doi:10.1093/biomet/82.4.711](https://doi.org/10.1093/biomet/82.4.711)>.

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Suggests testthat

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Contents

CalculateProposalLambda	2
CalculateProposalPsy	6
calculateRatio	9
calculateVarList	10
changeConstraintFormat	11
clearCurrentThetaYlist	12
combineClusterPara	14
evaluatePrior	16
evaluatePriorLambda	17
evaluatePriorPsi	18
EvaluateProposalLambda	19
EvaluateProposalPsy	22
generatePriorLambda	25
generatePriorPsi	27
generatePriorThetaY	27
getIndThetaY	28
getmode	30
getRemovedIndThetaY	31
getThetaYWithEmpty	32
getZmat	34
Hparam-class	35
likelihood	35
listToStrVec	37
MstepRJMCMCupdate	38
pgmmRJMCMC	40
stayMCMCupdate	42
sumerizeZ	44
summerizePgmmRJMCMC	44
ThetaYList	45
toEthetaYlist	46
toNEthetaYlist	48
updatePostThetaY	49
updatePostZ	52
VstepRJMCMCupdate	53

Index

57

CalculateProposalLambda

CalculateProposalLambda

Description

CalculateProposalLambda

Usage

```
CalculateProposalLambda(hparam, thetaYList, CxyList, constraint, m, p,
  qVec)
```

Arguments

hparam	hparam
thetaYList	thetaYList
CxyList	CxyList
constraint	constraint
m	the number of clusters
p	the number of features
qVec	the vector of the number of factors in each clusters

Examples

```
set.seed(100)
n <- 10
p <- 2
q <- 1
K <- 2
X <- t(
  fabMix::simData(
    sameLambda = TRUE,
    sameSigma = TRUE,
    K.true = K,
    n = n,
    q = q,
    p = p,
    sINV_values = 1 / ((1:p))
  )$data
)
m <- 1
muBar <- c(0, 0)

hparam <- new(
  "Hparam",
  alpha1 = 0.567755037123148,
  alpha2 = 1.1870201935945,
  delta = 2,
  ggamma = 2,
  bbeta = 3.39466184520673
)
qVec <- c(1, 1)
constraint <- c(0, 0, 0)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
thetaYList <-
  new(
    "ThetaYList",
```

```

tao = 0.366618687752634,
psy = list(structure(
  c(
    4.18375613018654,
    0, 0, 5.46215996830771
  ),
  .Dim = c(2L, 2L)
)),
M = list(structure(
  c(
    3.27412045866392,
    -2.40544145363349
  ),
  .Dim = 1:2
)),
lambda = list(structure(
  c(
    2.51015961514781,
    -0.0741189919182549
  ),
  .Dim = 2:1
)),
Y = list(structure(
  c(
    -0.244239011725104,
    -0.26876172736886,
    0.193431511203083,
    0.41624466812811,
    -0.54581548068437,
    -0.0479517628308146,
    -0.633383997203325,
    0.856855296613208,
    0.792850576988512,
    0.268208848994559
  ),
  .Dim = c(1L, 10L)
))
)
CxyList <-
list(
  A = list(structure(
    c(0.567755037123148, 0, 0, 1.1870201935945),
    .Dim = c(2L, 2L)
  )),
  nVec = structure(10, .Dim = c(1L, 1L)),
  Cxxk = list(structure(
    c(
      739.129405647622,
      671.040583460732,
      671.040583460732,
      618.754338945564
    ),
    .Dim = c(2L, 2L)
  )
)

```

```

)),
Cxyk = list(structure(
  c(-18.5170828875512, -16.5748393456787),
  .Dim = 2:1
)),
Cyyk = list(structure(2.4786991560888, .Dim = c(
  1L,
  1L
))),
Cxytk = list(structure(
  c(
    10, 0.787438922114998, 0.787438922114998,
    2.4786991560888
  ),
  .Dim = c(2L, 2L)
)),
Cxtyk = list(structure(
  c(
    -57.5402230447872,
    -54.6677145995824,
    -18.5170828875512,
    -16.5748393456787
  ),
  .Dim = c(
    2L,
    2L
  )
)),
CxL1k = list(structure(
  c(-59.5168204264758, -54.6093504204781),
  .Dim = 2:1
)),
Cxmyk = list(structure(
  c(
    -21.0952527723962,
    -14.6807011202188
  ),
  .Dim = 2:1
)),
sumCxmyk = structure(c(
  -21.0952527723962,
  -14.6807011202188
), .Dim = 2:1),
sumCyyk = structure(3.6657193496833, .Dim = c(
  1L,
  1L
))
)

```

CalculateProposalLambda(hparam, thetaYList, CxyList, constraint, m, p, qVec)

CalculateProposalPsy *CalculateProposalPsy*

Description

CalculateProposalPsy

Usage

```
CalculateProposalPsy(hparam, thetaYList, CxyList, constraint, m, p, qVec)
```

Arguments

hparam	hparam
thetaYList	thetaYList
CxyList	CxyList
constraint	constraint
m	the number of clusters
p	the number of features
qVec	the vector of the number of factors in each clusters

Examples

```
set.seed(100)
n <- 10
p <- 2
q <- 1
K <- 2
m <- 1
muBar <- c(0, 0)
qVec <- c(1, 1)
constraint <- c(0, 0, 0)
X <- t(
  fabMix::simData(
    sameLambda = TRUE,
    sameSigma = TRUE,
    K.true = K,
    n = n,
    q = q,
    p = p,
    sINV_values = 1 / ((1:p))
  )$data
)
hparam <- new(
  "Hparam",
  alpha1 = 0.567755037123148,
  alpha2 = 1.1870201935945,
```

```

delta = 2,
ggamma = 2,
bbeta = 3.39466184520673
)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
thetaYList <-
new(
  "ThetaYList",
  tao = 0.366618687752634,
  psy = list(structure(
    c(
      4.18375613018654,
      0, 0, 5.46215996830771
    ),
    .Dim = c(2L, 2L)
  )),
  M = list(structure(
    c(
      3.27412045866392,
      -2.40544145363349
    ),
    .Dim = 1:2
  )),
  lambda = list(structure(
    c(
      2.51015961514781,
      -0.0741189919182549
    ),
    .Dim = 2:1
  )),
  Y = list(structure(
    c(
      -0.244239011725104,
      -0.26876172736886,
      0.193431511203083,
      0.41624466812811,
      -0.54581548068437,
      -0.0479517628308146,
      -0.633383997203325,
      0.856855296613208,
      0.792850576988512,
      0.268208848994559
    ),
    .Dim = c(1L, 10L)
  ))
)
constraint <- c(0, 0, 0)
CxyList <-
list(
  A = list(structure(
    c(0.567755037123148, 0, 0, 1.1870201935945),
    .Dim = c(2L, 2L)
  )),

```

```

nVec = structure(10, .Dim = c(1L, 1L)),
Cxxk = list(structure(
  c(
    739.129405647622,
    671.040583460732,
    671.040583460732,
    618.754338945564
  ),
  .Dim = c(2L, 2L)
)),
Cxyk = list(structure(
  c(-18.5170828875512, -16.5748393456787),
  .Dim = 2:1
)),
Cyyk = list(structure(2.4786991560888, .Dim = c(
  1L,
  1L
))),
Cytyk = list(structure(
  c(
    10, 0.787438922114998, 0.787438922114998,
    2.4786991560888
  ),
  .Dim = c(2L, 2L)
)),
Cxtyk = list(structure(
  c(
    -57.5402230447872,
    -54.6677145995824,
    -18.5170828875512,
    -16.5748393456787
  ),
  .Dim = c(
    2L,
    2L
  )
)),
CxL1k = list(structure(
  c(-59.5168204264758, -54.6093504204781),
  .Dim = 2:1
)),
Cxmyk = list(structure(
  c(
    -21.0952527723962,
    -14.6807011202188
  ),
  .Dim = 2:1
)),
sumCxmyk = structure(c(
  -21.0952527723962,
  -14.6807011202188
), .Dim = 2:1),
sumCyyk = structure(3.6657193496833, .Dim = c(

```



```
    1L,  
    1L  
  ))  
 )  
 #'
```

```
CalculateProposalPsy(hparam, thetaYList, CxyList, constraint, m, p, qVec)
```

calculateRatio *Log scale ratio calculation*

Description

Log scale ratio calculation

Usage

```
calculateRatio(deno, nume)
```

Arguments

deno	denominator.
nume	numerator.

Value

result of ratio

Examples

```
deno <- log(1)  
nume <- log(2)  
#'  
  
calculateRatio(deno, nume)
```

calculateVarList	<i>calculateVarList</i>
------------------	-------------------------

Description

calculateVarList

Usage

```
calculateVarList(psyList, lambdaList)
```

Arguments

psyList	psyList
lambdaList	lambdaList

Examples

```
set.seed(100)
n <- 10
p <- 2
q <- 1
K <- 2
m <- 1
muBar <- c(0, 0)
qVec <- c(1, 1)
constraint <- c(0, 0, 0)
X <- t(
  fabMix::simData(
    sameLambda = TRUE,
    sameSigma = TRUE,
    K.true = K,
    n = n,
    q = q,
    p = p,
    sINV_values = 1 / ((1:p))
  )$data
)
hparam <- new(
  "Hparam",
  alpha1 = 0.567755037123148,
  alpha2 = 1.1870201935945,
  delta = 2,
  ggamma = 2,
  bbeta = 3.39466184520673
)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
thetaYList <-
  new(
    "ThetaYList",
```

```

tao = 0.366618687752634,
psy = list(structure(
  c(
    4.18375613018654,
    0, 0, 5.46215996830771
  ),
  .Dim = c(2L, 2L)
)),
M = list(structure(
  c(
    3.27412045866392,
    -2.40544145363349
  ),
  .Dim = 1:2
)),
lambda = list(structure(
  c(
    2.51015961514781,
    -0.0741189919182549
  ),
  .Dim = 2:1
)),
Y = list(structure(
  c(
    -0.244239011725104,
    -0.26876172736886,
    0.193431511203083,
    0.41624466812811,
    -0.54581548068437,
    -0.0479517628308146,
    -0.633383997203325,
    0.856855296613208,
    0.792850576988512,
    0.268208848994559
  ),
  .Dim = c(1L, 10L)
))
)
#'

calculateVarList(thetaYList@psy, thetaYList@lambda)

```

changeConstraintFormat

changeConstraintFormat

Description

changeConstraintFormat

Usage

```
changeConstraintFormat(strNum)
```

Arguments

```
strNum      strNum
```

Examples

```
#'
changeConstraintFormat(c(0, 0, 0))
```

```
clearCurrentThetaYlist
      clearCurrentThetaYlist
```

Description

```
clearCurrentThetaYlist
```

Usage

```
clearCurrentThetaYlist(thetaYList, clusInd, mMax)
```

Arguments

```
thetaYList  thetaYList
clusInd     clusInd
mMax       mMax
```

Examples

```
set.seed(100)
n <- 10
p <- 2
q <- 1
K <- 2
m <- 1
muBar <- c(0, 0)
qVec <- c(1, 1)
constraint <- c(0, 0, 0)
X <- t(
  fabMix::simData(
    sameLambda = TRUE,
    sameSigma = TRUE,
    K.true = K,
```

```

    n = n,
    q = q,
    p = p,
    sINV_values = 1 / ((1:p))
  )$data
)
hparam <- new(
  "Hparam",
  alpha1 = 0.567755037123148,
  alpha2 = 1.1870201935945,
  delta = 2,
  ggamma = 2,
  bbeta = 3.39466184520673
)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
thetaYList <-
  new(
    "ThetaYList",
    tao = 0.366618687752634,
    psy = list(structure(
      c(
        4.18375613018654,
        0, 0, 5.46215996830771
      ),
      .Dim = c(2L, 2L)
    )),
    M = list(structure(
      c(
        3.27412045866392,
        -2.40544145363349
      ),
      .Dim = 1:2
    )),
    lambda = list(structure(
      c(
        2.51015961514781,
        -0.0741189919182549
      ),
      .Dim = 2:1
    )),
    Y = list(structure(
      c(
        -0.244239011725104,
        -0.26876172736886,
        0.193431511203083,
        0.41624466812811,
        -0.54581548068437,
        -0.0479517628308146,
        -0.633383997203325,
        0.856855296613208,
        0.792850576988512,
        0.268208848994559
      ),

```

```

        .Dim = c(1L, 10L)
      ))
    )
    clusInd <- rep(1, m)
    mMax <- 1
    #'

    clearCurrentThetaYlist(thetaYList, clusInd, mMax)

```

combineClusterPara *combineClusterPara*

Description

combineClusterPara

Usage

```
combineClusterPara(oldList, newList, ind)
```

Arguments

oldList	oldList
newList	newList
ind	ind

Examples

```

set.seed(100)
n <- 10
p <- 2
q <- 1
K <- 2
m <- 1
muBar <- c(0, 0)
qVec <- c(1, 1)
constraint <- c(0, 0, 0)
X <- t(
  fabMix::simData(
    sameLambda = TRUE,
    sameSigma = TRUE,
    K.true = K,
    n = n,
    q = q,
    p = p,
    sINV_values = 1 / ((1:p))
  )$data
)

```

```

hparam <- new(
  "Hparam",
  alpha1 = 0.567755037123148,
  alpha2 = 1.1870201935945,
  delta = 2,
  ggamma = 2,
  bbeta = 3.39466184520673
)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
newList <- oldList <-
  new(
    "ThetaYList",
    tao = 0.366618687752634,
    psy = list(structure(
      c(
        4.18375613018654,
        0, 0, 5.46215996830771
      ),
      .Dim = c(2L, 2L)
    )),
    M = list(structure(
      c(
        3.27412045866392,
        -2.40544145363349
      ),
      .Dim = 1:2
    )),
    lambda = list(structure(
      c(
        2.51015961514781,
        -0.0741189919182549
      ),
      .Dim = 2:1
    )),
    Y = list(structure(
      c(
        -0.244239011725104,
        -0.26876172736886,
        0.193431511203083,
        0.41624466812811,
        -0.54581548068437,
        -0.0479517628308146,
        -0.633383997203325,
        0.856855296613208,
        0.792850576988512,
        0.268208848994559
      ),
      .Dim = c(1L, 10L)
    ))
  )
#'
combineClusterPara(oldList, newList, 1)

```

evaluatePrior	<i>evaluate Prior</i>
---------------	-----------------------

Description

evaluate prior value for parameter Theta and Y.

Usage

```
evaluatePrior(m, p, muBar, hparam, thetaYList, ZOneDim, qVec, constraint,
             clusInd)
```

Arguments

m	m	
p	p	
muBar	mu_bar	
hparam	hyper parameter class	
thetaYList	theta Y list	
ZOneDim	one dim of z	
qVec	q vector	
constraint	type of constraint	
clusInd	cluster indicator vector	

Examples

```
m <- 20
n <- 500
p <- 10
muBar <- c(
  -33.1342706763595, -35.2699639183419, 48.276928009445, 16.2370659601218,
  19.0023163870536, -23.4900965314972, 37.1081269873873, 4.74944562930846,
  4.6918997353449, -4.55088073255655
)
hparam <- new("Hparam",
  alpha1 = 0.567755037123148, alpha2 = 1.1870201935945,
  delta = 2, ggamma = 2, bbeta = 3.39466184520673
)
qVec <- c(4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
constraint <- c(0, 0, 0)
thetaYList <- generatePriorThetaY(m, n, p, muBar, hparam, qVec, ZOneDim, constraint)
clusInd <- rep(1, m)
#'
```



```

evaluatePrior(
  m,
  p,
  muBar,
  hparam,
  thetaYList,
  ZOneDim,
  qVec,
  constraint,
  clusInd
)

```

evaluatePriorLambda *evaluatePriorLambda*

Description

evaluate prior value for parameter Lambda

Usage

```
evaluatePriorLambda(p, m, alpha2, qVec, psy, lambda, constraint, clusInd)
```

Arguments

p	the number of features
m	the number of clusters
alpha2	hyper parameter
qVec	the vector of the number of factors in each clusters
psy	parameter
lambda	parameter
constraint	the pgmm constraint, a vector of length three with binary entry. For example, c(1,1,1) means the fully constraint model
clusInd	cluster indicator vector

Examples

```

p <- 10
m <- 20
alpha2 <- 1.18
qVec <- rep(4, m)
delta <- 2
bbeta <- 2
constraint <- c(0, 0, 0)
psy <- generatePriorPsi(
  p,

```

```

    m,
    delta,
    bbeta,
    constraint
  )
  lambda <- generatePriorLambda(
    p,
    m,
    alpha2,
    qVec,
    psy,
    constraint
  )
  clusInd <- rep(1, m)
  #'

  evaluatePriorLambda(
    p,
    m,
    alpha2,
    qVec,
    psy,
    lambda,
    constraint,
    clusInd
  )

```

evaluatePriorPsi *evaluatePriorPsi*

Description

evaluate prior value for parameter Psi

Usage

```
evaluatePriorPsi(psy, p, m, delta, bbeta, constraint, clusInd)
```

Arguments

psy	parameter
p	the number of features
m	the number of clusters
delta	parameter
bbeta	parameter
constraint	parameter
clusInd	cluster indicator vector

Examples

```
p <- 10
m <- 20
delta <- 2
bbeta <- 2
constraint <- c(0, 0, 0)
psy <- generatePriorPsi(
  p,
  m,
  delta,
  bbeta,
  constraint
)
clusInd <- rep(1, m)
#'

evaluatePriorPsi(
  psy,
  p,
  m,
  delta,
  bbeta,
  constraint,
  clusInd
)
```

EvaluateProposalLambda

EvaluateProposalLambda

Description

EvaluateProposalLambda

Usage

```
EvaluateProposalLambda(hparam, thetaYList, CxyList, constraint, newlambda,
  m, qVec, p)
```

Arguments

hparam	hparam
thetaYList	thetaYList
CxyList	CxyList
constraint	constraint
newlambda	newlambda

m the number of clusters
 qVec the vector of the number of factors in each clusters
 p the number of features

Examples

```

set.seed(100)
n <- 10
p <- 2
q <- 1
K <- 2
m <- 1
muBar <- c(0, 0)
qVec <- c(1, 1)
constraint <- c(0, 0, 0)
X <- t(
  fabMix::simData(
    sameLambda = TRUE,
    sameSigma = TRUE,
    K.true = K,
    n = n,
    q = q,
    p = p,
    sINV_values = 1 / ((1:p))
  )$data
)
hparam <- new(
  "Hparam",
  alpha1 = 0.567755037123148,
  alpha2 = 1.1870201935945,
  delta = 2,
  ggamma = 2,
  bbeta = 3.39466184520673
)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
thetaYList <-
  new(
    "ThetaYList",
    tao = 0.366618687752634,
    psy = list(structure(
      c(
        4.18375613018654,
        0, 0, 5.46215996830771
      ),
      .Dim = c(2L, 2L)
    )),
    M = list(structure(
      c(
        3.27412045866392,
        -2.40544145363349
      ),
      .Dim = 1:2
    ))
  )

```

```

)),
lambda = list(structure(
  c(
    2.51015961514781,
    -0.0741189919182549
  ),
  .Dim = 2:1
)),
Y = list(structure(
  c(
    -0.244239011725104,
    -0.26876172736886,
    0.193431511203083,
    0.41624466812811,
    -0.54581548068437,
    -0.0479517628308146,
    -0.633383997203325,
    0.856855296613208,
    0.792850576988512,
    0.268208848994559
  ),
  .Dim = c(1L, 10L)
))
)
CxyList <-
list(
  A = list(structure(
    c(0.567755037123148, 0, 0, 1.1870201935945),
    .Dim = c(2L, 2L)
  )),
  nVec = structure(10, .Dim = c(1L, 1L)),
  Cxxk = list(structure(
    c(
      739.129405647622,
      671.040583460732,
      671.040583460732,
      618.754338945564
    ),
    .Dim = c(2L, 2L)
  )),
  Cxyk = list(structure(
    c(-18.5170828875512, -16.5748393456787),
    .Dim = 2:1
  )),
  Cyyk = list(structure(2.4786991560888, .Dim = c(
    1L,
    1L
  ))),
  Cytyk = list(structure(
    c(
      10, 0.787438922114998, 0.787438922114998,
      2.4786991560888
    ),

```

```

    .Dim = c(2L, 2L)
 )),
  Cxtytk = list(structure(
    c(
      -57.5402230447872,
      -54.6677145995824,
      -18.5170828875512,
      -16.5748393456787
    ),
    .Dim = c(
      2L,
      2L
    )
 )),
  CxL1k = list(structure(
    c(-59.5168204264758, -54.6093504204781),
    .Dim = 2:1
 )),
  Cxmyk = list(structure(
    c(
      -21.0952527723962,
      -14.6807011202188
    ),
    .Dim = 2:1
 )),
  sumCxmyk = structure(c(
    -21.0952527723962,
    -14.6807011202188
  ), .Dim = 2:1),
  sumCyyk = structure(3.6657193496833, .Dim = c(
    1L,
    1L
  ))
)
#'

```

```
EvaluateProposalLambda(hparam, thetaYList, CxyList, constraint, thetaYList@lambda, m, qVec, p)
```

EvaluateProposalPsy *EvaluateProposalPsy*

Description

EvaluateProposalPsy

Usage

```
EvaluateProposalPsy(hparam, thetaYList, CxyList, constraint, newpsy, m, p,
  qVec, delta)
```

Arguments

hparam	hparam
thetaYList	thetaYList
CxyList	CxyList
constraint	constraint
newpsy	newpsy
m	the number of clusters
p	the number of features
qVec	the vector of the number of factors in each clusters
delta	hyperparameters

Examples

```

set.seed(100)
n <- 10
p <- 2
q <- 1
K <- 2
m <- 1
muBar <- c(0, 0)
qVec <- c(1, 1)
constraint <- c(0, 0, 0)
X <- t(
  fabMix::simData(
    sameLambda = TRUE,
    sameSigma = TRUE,
    K.true = K,
    n = n,
    q = q,
    p = p,
    sINV_values = 1 / ((1:p))
  )$data
)
hparam <- new(
  "Hparam",
  alpha1 = 0.567755037123148,
  alpha2 = 1.1870201935945,
  delta = 2,
  ggamma = 2,
  bbeta = 3.39466184520673
)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
thetaYList <-
  new(
    "ThetaYList",
    tao = 0.366618687752634,
    psy = list(structure(
      c(
        4.18375613018654,

```

```

      0, 0, 5.46215996830771
    ),
    .Dim = c(2L, 2L)
  )),
  M = list(structure(
    c(
      3.27412045866392,
      -2.40544145363349
    ),
    .Dim = 1:2
  )),
  lambda = list(structure(
    c(
      2.51015961514781,
      -0.0741189919182549
    ),
    .Dim = 2:1
  )),
  Y = list(structure(
    c(
      -0.244239011725104,
      -0.26876172736886,
      0.193431511203083,
      0.41624466812811,
      -0.54581548068437,
      -0.0479517628308146,
      -0.633383997203325,
      0.856855296613208,
      0.792850576988512,
      0.268208848994559
    ),
    .Dim = c(1L, 10L)
  ))
)
constraint <- c(0, 0, 0)
CxyList <-
list(
  A = list(structure(
    c(0.567755037123148, 0, 0, 1.1870201935945),
    .Dim = c(2L, 2L)
  )),
  nVec = structure(10, .Dim = c(1L, 1L)),
  Cxxk = list(structure(
    c(
      739.129405647622,
      671.040583460732,
      671.040583460732,
      618.754338945564
    ),
    .Dim = c(2L, 2L)
  )),
  Cxyk = list(structure(
    c(-18.5170828875512, -16.5748393456787),

```



```

        .Dim = 2:1
    )),
  Cyyk = list(structure(2.4786991560888, .Dim = c(
    1L,
    1L
  )),
  Cytyk = list(structure(
    c(
      10, 0.787438922114998, 0.787438922114998,
      2.4786991560888
    ),
    .Dim = c(2L, 2L)
  )),
  Cxtyk = list(structure(
    c(
      -57.5402230447872,
      -54.6677145995824,
      -18.5170828875512,
      -16.5748393456787
    ),
    .Dim = c(
      2L,
      2L
    )
  )),
  CxL1k = list(structure(
    c(-59.5168204264758, -54.6093504204781),
    .Dim = 2:1
  )),
  Cxmyk = list(structure(
    c(
      -21.0952527723962,
      -14.6807011202188
    ),
    .Dim = 2:1
  )),
  sumCxmyk = structure(c(
    -21.0952527723962,
    -14.6807011202188
  ), .Dim = 2:1),
  sumCyyk = structure(3.6657193496833, .Dim = c(
    1L,
    1L
  ))
)

```

EvaluateProposalPsy(hparam, thetaYList, CxyList, constraint, thetaYList@psy, m, p, qVec, delta)

Description

evaluate prior value for parameter Lambda

Usage

```
generatePriorLambda(p, m, alpha2, qVec, psy, constraint)
```

Arguments

p	the number of features
m	the number of clusters
alpha2	hyper parameter
qVec	parameter
psy	parameter
constraint	parameter

Examples

```
p <- 10
m <- 20
alpha2 <- 1.18
qVec <- rep(4, m)
delta <- 2
bbeta <- 2
constraint <- c(0, 0, 0)
psy <- generatePriorPsi(
  p,
  m,
  delta,
  bbeta,
  constraint
)
#'

generatePriorLambda(
  p,
  m,
  alpha2,
  qVec,
  psy,
  constraint
)
```

generatePriorPsi *generatePriorPsi*

Description

generate prior value for parameter Psi

Usage

```
generatePriorPsi(p, m, delta, bbeta, constraint)
```

Arguments

p	the number of features
m	the number of clusters
delta	hyperparameters
bbeta	hyperparameters
constraint	the pgmm constraint, a vector of length three with binary entry. For example, c(1,1,1) means the fully constraint model

Examples

```
p <- 10
m <- 20
delta <- 2
bbeta <- 2
constraint <- c(0, 0, 0)
```

```
generatePriorPsi(
  p,
  m,
  delta,
  bbeta,
  constraint
)
```

generatePriorThetaY *PriorThetaY list*

Description

generate prior value for parameter Theta and Y.

Usage

```
generatePriorThetaY(m, n, p, muBar, hparam, qVec, ZOneDim, constraint)
```

Arguments

m	the number of cluster
n	sample size
p	number of covariates
muBar	parameter
hparam	hyperparameters
qVec	the vector of the number of factors in each clusters
ZOneDim	ZOneDim
constraint	constraint

Examples

```
m <- 20
n <- 500
p <- 10
muBar <- c(
  -33.1342706763595, -35.2699639183419, 48.276928009445, 16.2370659601218,
  19.0023163870536, -23.4900965314972, 37.1081269873873, 4.74944562930846,
  4.6918997353449, -4.55088073255655
)
hparam <- new("Hparam",
  alpha1 = 0.567755037123148, alpha2 = 1.1870201935945,
  delta = 2, ggamma = 2, bbeta = 3.39466184520673
)
qVec <- c(4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
constraint <- c(0, 0, 0)
#'

generatePriorThetaY(m, n, p, muBar, hparam, qVec, ZOneDim, constraint)
```

```
getIndThetaY
```

```
getIndThetaY
```

Description

```
getIndThetaY
```

Usage

```
getIndThetaY(thetaYList, Ind)
```

Arguments

thetaYList	thetaYList
Ind	Ind

Examples

```

set.seed(100)
n <- 10
p <- 2
q <- 1
K <- 2
m <- 2
muBar <- c(0, 0)
qVec <- c(1, 1)
constraint <- c(0, 0, 0)
X <- t(
  fabMix::simData(
    sameLambda = TRUE,
    sameSigma = TRUE,
    K.true = K,
    n = n,
    q = q,
    p = p,
    sINV_values = 1 / ((1:p))
  )$data
)
hparam <- new(
  "Hparam",
  alpha1 = 0.567755037123148,
  alpha2 = 1.1870201935945,
  delta = 2,
  ggamma = 2,
  bbeta = 3.39466184520673
)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
thetaYList <-
  new(
    "ThetaYList",
    tao = 0.366618687752634,
    psy = list(structure(
      c(
        4.18375613018654,
        0, 0, 5.46215996830771
      ),
      .Dim = c(2L, 2L)
    )),
    M = list(structure(
      c(
        3.27412045866392,
        -2.40544145363349
      ),
      .Dim = 1:2
    )
  )

```

```

)),
lambda = list(structure(
  c(
    2.51015961514781,
    -0.0741189919182549
  ),
  .Dim = 2:1
)),
Y = list(structure(
  c(
    -0.244239011725104,
    -0.26876172736886,
    0.193431511203083,
    0.41624466812811,
    -0.54581548068437,
    -0.0479517628308146,
    -0.633383997203325,
    0.856855296613208,
    0.792850576988512,
    0.268208848994559
  ),
  .Dim = c(1L, 10L)
))
)
#'

getIndThetaY(thetaYList, 1)

```

getmode

getmode

Description

getmode

Usage

getmode(v)

Arguments

v v

Examples

```

# '

getmode(c(1, 1, 2, 3))

```

```
getRemovedIndThetaY  getRemovedIndThetaY
```

Description

```
getRemovedIndThetaY
```

Usage

```
getRemovedIndThetaY(thetaYList, Ind)
```

Arguments

thetaYList	thetaYList
Ind	Ind

Examples

```
set.seed(100)
n <- 10
p <- 2
q <- 1
K <- 2
m <- 2
muBar <- c(0, 0)
qVec <- c(1, 1)
constraint <- c(0, 0, 0)
X <- t(
  fabMix::simData(
    sameLambda = TRUE,
    sameSigma = TRUE,
    K.true = K,
    n = n,
    q = q,
    p = p,
    sINV_values = 1 / ((1:p))
  )$data
)
hparam <- new(
  "Hparam",
  alpha1 = 0.567755037123148,
  alpha2 = 1.1870201935945,
  delta = 2,
  ggamma = 2,
  bbeta = 3.39466184520673
)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
thetaYList <-
  new("ThetaYList", tao = c(0.90162050961987, 0.0983794903801295),
```

```

psy = list(structure(c(3.68472841602225, 0, 0, 8.34691978354054),
  .Dim = c(2L, 2L)), structure(c(0.785011896130842, 0, 0, 1.19022383323437),
  .Dim = c(2L, 2L))), M = list(structure(c(
  2.96424305287004,
  1.08454861414306
), .Dim = 1:2), structure(c(
  -0.232625450433964,
  0.984505960868685
), .Dim = 1:2)), lambda = list(structure(c(
  -0.964026624054337,
  0.89378616732449
), .Dim = 2:1), structure(c(
  0.533334148228635,
  -1.80033696090263
), .Dim = 2:1)), Y = list(structure(c(
  -0.15346475266988,
  1.6584112693271, 0.409294936277862, -1.46628591247549, -0.532753243163142,
  -0.332143130316749, 0.307558110800446, -0.525374243612587, 0.527667526535661,
  0.748193650431916
), .Dim = c(1L, 10L)), structure(c(
  0.571325118638535,
  0.542462985882966, 0.559971315637159, -1.73905343105432, -0.583549598471542,
  1.71264245945391, -0.327119395945831, 1.02464651767821, -1.11462280255215,
  0.81095592501554
), .Dim = c(1L, 10L))))
Ind <- 1
#'

getRemovedIndThetaY(thetaYList, Ind)

```

getThetaYWithEmpty *getThetaYWithEmpty*

Description

getThetaYWithEmpty

Usage

```
getThetaYWithEmpty(NEthetaYList, clusInd)
```

Arguments

NEthetaYList	NEthetaYList
clusInd	clusInd

Examples

```

set.seed(100)
n <- 10
p <- 2
q <- 1
K <- 2
m <- 1
muBar <- c(0, 0)
qVec <- c(1, 1)
constraint <- c(0, 0, 0)
X <- t(
  fabMix::simData(
    sameLambda = TRUE,
    sameSigma = TRUE,
    K.true = K,
    n = n,
    q = q,
    p = p,
    sINV_values = 1 / ((1:p))
  )$data
)
hparam <- new(
  "Hparam",
  alpha1 = 0.567755037123148,
  alpha2 = 1.1870201935945,
  delta = 2,
  ggamma = 2,
  bbeta = 3.39466184520673
)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
thetaYList <-
  new(
    "ThetaYList",
    tao = 0.366618687752634,
    psy = list(structure(
      c(
        4.18375613018654,
        0, 0, 5.46215996830771
      ),
      .Dim = c(2L, 2L)
    )),
    M = list(structure(
      c(
        3.27412045866392,
        -2.40544145363349
      ),
      .Dim = 1:2
    )),
    lambda = list(structure(
      c(
        2.51015961514781,
        -0.0741189919182549
      )
    )
  )

```

```
    ),
    .Dim = 2:1
  )),
  Y = list(structure(
    c(
      -0.244239011725104,
      -0.26876172736886,
      0.193431511203083,
      0.41624466812811,
      -0.54581548068437,
      -0.0479517628308146,
      -0.633383997203325,
      0.85685296613208,
      0.792850576988512,
      0.268208848994559
    ),
    .Dim = c(1L, 10L)
  ))
)
clusInd <- rep(1, m)

getThetaYWithEmpty(thetaYList, clusInd)
```

getZmat

Tool for vector to matrix

Description

Tool for vector to matrix

Usage

```
getZmat(ZOneDim, m, n)
```

Arguments

ZOneDim	a vector.
m	the number of cluster.
n	sample size.

Value

adjacency matrix

Examples

```

m <- 20
n <- 500
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
#'

getZmat(ZOneDim, m, n)

```

Hparam-class

An S4 class to represent a Hyper parameter.

Description

An S4 class to represent a Hyper parameter.

Slots

alpha1 A numeric value
alpha2 A numeric value
delta A numeric value
ggamma A numeric value
bbeta A numeric value

Examples

```
new("Hparam", alpha1 = 1, alpha2 = 2, bbeta = 3, delta = 4, ggamma = 5)
```

likelihood

likelihood

Description

likelihood

Usage

```
likelihood(thetaYList, ZOneDim, qqVec, muBar, X)
```

Arguments

thetaYList	thetaYList
ZOneDim	ZOneDim
qqVec	qqVec
muBar	muBar
X	X

Examples

```

set.seed(100)
n <- 10
p <- 2
q <- 1
K <- 2
m <- 1
muBar <- c(0, 0)
qVec <- c(1, 1)
constraint <- c(0, 0, 0)
X <- t(
  fabMix::simData(
    sameLambda = TRUE,
    sameSigma = TRUE,
    K.true = K,
    n = n,
    q = q,
    p = p,
    sINV_values = 1 / ((1:p))
  )$data
)
hparam <- new(
  "Hparam",
  alpha1 = 0.567755037123148,
  alpha2 = 1.1870201935945,
  delta = 2,
  ggamma = 2,
  bbeta = 3.39466184520673
)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
thetaYList <-
  new(
    "ThetaYList",
    tao = 0.366618687752634,
    psy = list(structure(
      c(
        4.18375613018654,
        0, 0, 5.46215996830771
      ),
      .Dim = c(2L, 2L)
    )),
    M = list(structure(
      c(
        3.27412045866392,
        -2.40544145363349
      ),
      .Dim = 1:2
    )),
    lambda = list(structure(
      c(
        2.51015961514781,
        -0.0741189919182549

```

```

    ),
    .Dim = 2:1
  )),
  Y = list(structure(
    c(
      -0.244239011725104,
      -0.26876172736886,
      0.193431511203083,
      0.41624466812811,
      -0.54581548068437,
      -0.0479517628308146,
      -0.633383997203325,
      0.85685296613208,
      0.792850576988512,
      0.268208848994559
    ),
    .Dim = c(1L, 10L)
  ))
)
#'
likelihood(thetaYList, ZOneDim, qVec, muBar, X)

```

listToStrVec	<i>Convert list of string to vector of string</i>
--------------	---

Description

Convert list of string to vector of string

Usage

```
listToStrVec(stringList)
```

Arguments

stringList list of string

Value

vector of string

Examples

```

stringList <- list("abc")
#'

listToStrVec(stringList)

```

MstepRJMCMCupdate *MstepRJMCMCupdate*

Description

MstepRJMCMCupdate

Usage

```
MstepRJMCMCupdate(X, muBar, p, thetaYList, ZOneDim, hparam, hparamInit,
  qVec, qnew, dVec, sVec, constraint, clusInd, mVec, Mind)
```

Arguments

X	X in MstepRJMCMCupdate
muBar	muBar
p	p
thetaYList	thetaYList
ZOneDim	ZOneDim
hparam	hparam
hparamInit	hparamInit
qVec	qVec
qnew	qnew
dVec	dVec
sVec	sVec
constraint	constraint
clusInd	clusInd
mVec	mVec
Mind	Mind

Examples

```
set.seed(100)
n <- 10
p <- 2
q <- 1
K <- 2
m <- 2
muBar <- c(0, 0)
qVec <- c(1, 1)
constraint <- c(0, 0, 0)
X <- t(
  fabMix::simData(
    sameLambda = TRUE,
```

```

    sameSigma = TRUE,
    K.true = K,
    n = n,
    q = q,
    p = p,
    sINV_values = 1 / ((1:p))
  )$data
)
hparam <- new(
  "Hparam",
  alpha1 = 0.567755037123148,
  alpha2 = 1.1870201935945,
  delta = 2,
  ggamma = 2,
  bbeta = 3.39466184520673
)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
thetaYList <-
new(
  "ThetaYList",
  tao = 0.366618687752634,
  psy = list(structure(
    c(
      4.18375613018654,
      0, 0, 5.46215996830771
    ),
    .Dim = c(2L, 2L)
  )),
  M = list(structure(
    c(
      3.27412045866392,
      -2.40544145363349
    ),
    .Dim = 1:2
  )),
  lambda = list(structure(
    c(
      2.51015961514781,
      -0.0741189919182549
    ),
    .Dim = 2:1
  )),
  Y = list(structure(
    c(
      -0.244239011725104,
      -0.26876172736886,
      0.193431511203083,
      0.41624466812811,
      -0.54581548068437,
      -0.0479517628308146,
      -0.633383997203325,
      0.856855296613208,
      0.792850576988512,

```

```

        0.268208848994559
      ),
      .Dim = c(1L, 10L)
    ))
  )
  qnew <- 1
  dVec <- c(1, 1, 1)
  sVec <- c(1, 1, 1)
  constraint <- c(0, 0, 0)
  clusInd <- rep(1, m)
  Mind <- "BD"
  mVec <- c(1, m)

  MstepRJMCMCupdate(
    X,
    muBar,
    p,
    thetaYList,
    ZOneDim,
    hparam,
    hparamInit,
    qVec,
    qnew,
    dVec,
    sVec,
    constraint,
    clusInd,
    mVec,
    Mind
  )

```

pgmmRJMCMC

bpgmm Model-Based Clustering Using Bayesian PGMM Carries out model-based clustering using parsimonious Gaussian mixture models. MCMC are used for parameter estimation. The RJMCMC is used for model selection.

Description

bpgmm Model-Based Clustering Using Bayesian PGMM Carries out model-based clustering using parsimonious Gaussian mixture models. MCMC are used for parameter estimation. The RJMCMC is used for model selection.

Usage

```

pgmmRJMCMC(X, mInit, mVec, qnew, delta = 2, ggamma = 2, burn = 20,
  niter = 1000, constraint = C(0, 0, 0), dVec = c(1, 1, 1),
  sVec = c(1, 1, 1), Mstep = 0, Vstep = 0, SCind = 0)

```


Arguments

X	the observation matrix with size $p * m$
mInit	the number of initial clusters
mVec	the range of the number of clusters
qnew	the number of factor for a new cluster
delta	scaler hyperparameters
ggamma	scaler hyperparameters
burn	the number of burn in iterations
niter	the number of iterations
constraint	the pgmm initial constraint, a vector of length three with binary entry. For example, c(1,1,1) means the fully constraint model
dVec	a vector of hyperparameters with length three, shape parameters for alpha1, alpha2 and bbeta respectively
sVec	sVec a vector of hyperparameters with length three, rate parameters for alpha1, alpha2 and bbeta respectively
Mstep	the indicator of whether do model selection on the number of clusters
Vstep	the indicator of whether do model selection on variance structures
SCind	the indicator of whether use split/combine step in Mstep

Examples

```

library("fabMix")
library("mclust")
library("pgmm")
library("mvtnorm")
library("mcmcse")
library("MASS")
library("gtools")
n <- 500
p <- 10
q <- 4
K <- 10
nsim <- 10
burn <- 20
qnew <- 4
Mstep <- 1
Vstep <- 1
constraint <- c(0, 0, 0)
mInit <- 20
mVec <- c(1, 20)
X <- t(simData(
  sameLambda = TRUE,
  sameSigma = TRUE,
  K.true = K, n = n, q = q, p = p, sINV_values = 1 / ((1:p))
)$data)

```

```
pgmmRJCMC(X,
  mInit, mVec, qnew,
  niter = nsim, burn = burn,
  constraint = constraint, Mstep = Mstep, Vstep = Vstep
)
```

stayMCMCupdate

stayMCMCupdate

Description

stayMCMCupdate

Usage

```
stayMCMCupdate(X, thetaYList, ZOneDim, hparam, qVec, qnew, dVec, sVec,
  constraint, clusInd)
```

Arguments

X	X
thetaYList	thetaYList
ZOneDim	ZOneDim
hparam	hparam
qVec	qVec
qnew	qnew
dVec	dVec
sVec	sVec
constraint	constraint
clusInd	clusInd

Examples

```
##
set.seed(110)
n <- 10
p <- 2
q <- 1
K <- 2
m <- 2
muBar <- c(0, 0)
qVec <- c(1, 1)
constraint <- c(0, 0, 0)
```

```

X <- t(
  fabMix::simData(
    sameLambda = TRUE,
    sameSigma = TRUE,
    K.true = K,
    n = n,
    q = q,
    p = p,
    sINV_values = 1 / ((1:p))
  )$data
)
hparam <- new(
  "Hparam",
  alpha1 = 0.567755037123148,
  alpha2 = 1.1870201935945,
  delta = 2,
  ggamma = 2,
  bbeta = 3.39466184520673
)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
thetaYList <-
new("ThetaYList", tao = c(0.90162050961987, 0.0983794903801295),
psy = list(structure(c(3.68472841602225, 0, 0, 8.34691978354054),
.Dim = c(2L, 2L)), structure(c(0.785011896130842, 0, 0, 1.19022383323437),
.Dim = c(2L, 2L))), M = list(structure(c(
  2.96424305287004,
  1.08454861414306
), .Dim = 1:2), structure(c(
  -0.232625450433964,
  0.984505960868685
), .Dim = 1:2)), lambda = list(structure(c(
  -0.964026624054337,
  0.89378616732449
), .Dim = 2:1), structure(c(
  0.533334148228635,
  -1.80033696090263
), .Dim = 2:1)), Y = list(structure(c(
  -0.15346475266988,
  1.6584112693271, 0.409294936277862, -1.46628591247549, -0.532753243163142,
  -0.332143130316749, 0.307558110800446, -0.525374243612587, 0.527667526535661,
  0.748193650431916
), .Dim = c(1L, 10L)), structure(c(
  0.571325118638535,
  0.542462985882966, 0.559971315637159, -1.73905343105432, -0.583549598471542,
  1.71264245945391, -0.327119395945831, 1.02464651767821, -1.11462280255215,
  0.81095592501554
), .Dim = c(1L, 10L))))
qnew <- 1
dVec <- c(1, 1, 1)
sVec <- c(1, 1, 1)
constraint <- c(0, 0, 0)
clusInd <- rep(1, m)

```

```

stayMCMCupdate(
  X,
  thetaYList,
  ZOneDim,
  hparam,
  qVec,
  qnew,
  dVec,
  sVec,
  constraint,
  clusInd
)

```

summerizeZ

summerizeZ

Description

summerizeZ

Usage

```
summerizeZ(Zlist, index = 1:length(Zlist))
```

Arguments

Zlist	Zlist
index	index

Examples

```

Zlist <- list(c(1, 2, 3), c(3, 2, 1), c(2, 2, 2))
#'
summerizeZ(Zlist)

```

summerizePgmmRJCMC

summerizePgmmRJCMC

Description

summerizePgmmRJCMC

Usage

```
summerizePgmmRJCMC(pgmmResList, trueCluster = NULL)
```

Arguments

pgmmResList result list from pgmmRJCMCMC
 trueCluster true cluster allocation

Examples

```
library("fabMix")
library("mclust")
library("pgmm")
library("mvtnorm")
library("mcmcse")
library("MASS")
library("gtools")
n <- 50
p <- 10
q <- 4
K <- 10
syntheticDataset <- simData(
  sameLambda = TRUE, sameSigma = TRUE, K.true = K, n = n, q = q, p = p,
  sINV_values = 1 / ((1:p))
)
nsim <- 5
burn <- 0
X <- t(syntheticDataset$data)
qnew <- 4
Mstep <- 1
Vstep <- 1
constraint <- c(0, 0, 0)
mInit <- 20
mVec <- c(1, 20)

res <- pgmmRJCMCMC(X, mInit, mVec, qnew,
  niter = nsim, burn = burn, constraint = constraint,
  Mstep = Mstep, Vstep = Vstep
)

summerizePgmmRJCMCMC(res, syntheticDataset$class)
```

 ThetaYList

ThetaYList-class

Description

Definiton of ThetaYList parameter sets

Slots

tao A numeric vector
 psy A list value
 M A list value
 lambda A list value
 Y A list value

toEthetaYlist	<i>Title</i>
---------------	--------------

Description

Title

Usage

```
toEthetaYlist(NEthetaYList, NEZOneDim, qnew, clusInd)
```

Arguments

NEthetaYList	NEthetaYList
NEZOneDim	NEZOneDim
qnew	qnew
clusInd	clusInd

Examples

```

set.seed(100)
n <- 10
p <- 2
q <- 1
K <- 2
m <- 1
muBar <- c(0, 0)
qVec <- c(1, 1)
constraint <- c(0, 0, 0)
X <- t(
  fabMix::simData(
    sameLambda = TRUE,
    sameSigma = TRUE,
    K.true = K,
    n = n,
    q = q,
    p = p,
    sINV_values = 1 / ((1:p))
  )$data

```

```
)
hparam <- new(
  "Hparam",
  alpha1 = 0.567755037123148,
  alpha2 = 1.1870201935945,
  delta = 2,
  ggamma = 2,
  bbeta = 3.39466184520673
)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
thetaYList <-
  new(
    "ThetaYList",
    tao = 0.366618687752634,
    psy = list(structure(
      c(
        4.18375613018654,
        0, 0, 5.46215996830771
      ),
      .Dim = c(2L, 2L)
    )),
    M = list(structure(
      c(
        3.27412045866392,
        -2.40544145363349
      ),
      .Dim = 1:2
    )),
    lambda = list(structure(
      c(
        2.51015961514781,
        -0.0741189919182549
      ),
      .Dim = 2:1
    )),
    Y = list(structure(
      c(
        -0.244239011725104,
        -0.26876172736886,
        0.193431511203083,
        0.41624466812811,
        -0.54581548068437,
        -0.0479517628308146,
        -0.633383997203325,
        0.856855296613208,
        0.792850576988512,
        0.268208848994559
      ),
      .Dim = c(1L, 10L)
    ))
  )
clusInd <- rep(1, m)
qnew <- 1
```

```
toEthetaYlist(thetaYList, ZOneDim, qnew, clusInd)
```

toNEthetaYlist	<i>toNEthetaYlist</i>
----------------	-----------------------

Description

toNEthetaYlist

Usage

```
toNEthetaYlist(thetaYList, ZOneDim, qVec, clusInd)
```

Arguments

thetaYList	thetaYList
ZOneDim	ZOneDim
qVec	qVec
clusInd	clusInd

Examples

```
set.seed(100)
n <- 10
p <- 2
q <- 1
K <- 2
m <- 1
muBar <- c(0, 0)
qVec <- c(1, 1)
constraint <- c(0, 0, 0)
X <- t(
  fabMix::simData(
    sameLambda = TRUE,
    sameSigma = TRUE,
    K.true = K,
    n = n,
    q = q,
    p = p,
    sINV_values = 1 / ((1:p))
  )$data
)
hparam <- new(
  "Hparam",
  alpha1 = 0.567755037123148,
  alpha2 = 1.1870201935945,
  delta = 2,
  ggamma = 2,
  bbeta = 3.39466184520673
```



```

)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
thetaYList <-
  new(
    "ThetaYList",
    tao = 0.366618687752634,
    psy = list(structure(
      c(
        4.18375613018654,
        0, 0, 5.46215996830771
      ),
      .Dim = c(2L, 2L)
    )),
    M = list(structure(
      c(
        3.27412045866392,
        -2.40544145363349
      ),
      .Dim = 1:2
    )),
    lambda = list(structure(
      c(
        2.51015961514781,
        -0.0741189919182549
      ),
      .Dim = 2:1
    )),
    Y = list(structure(
      c(
        -0.244239011725104,
        -0.26876172736886,
        0.193431511203083,
        0.41624466812811,
        -0.54581548068437,
        -0.0479517628308146,
        -0.633383997203325,
        0.856855296613208,
        0.792850576988512,
        0.268208848994559
      ),
      .Dim = c(1L, 10L)
    ))
  )
clusInd <- rep(1, m)

toNEthetaYlist(thetaYList, ZOneDim, qVec, clusInd)

```

Description

Update posterior theta Y list

Usage

```
updatePostThetaY(m, n, p, hparam, thetaYList, ZOneDim, qVec, constraint, X,
  ggamma)
```

Arguments

m	the number of clusters.
n	the number of observations.
p	the number of variables
hparam	hyper parameters
thetaYList	theta Y list
ZOneDim	ZOneDim
qVec	qVec
constraint	constraint
X	X
ggamma	ggamma

Examples

```
set.seed(100)
n <- 10
p <- 2
q <- 1
K <- 2
m <- 1
muBar <- c(0, 0)
qVec <- c(1, 1)
constraint <- c(0, 0, 0)
X <- t(
  fabMix::simData(
    sameLambda = TRUE,
    sameSigma = TRUE,
    K.true = K,
    n = n,
    q = q,
    p = p,
    sINV_values = 1 / ((1:p))
  )$data
)
hparam <- new(
  "Hparam",
  alpha1 = 0.567755037123148,
  alpha2 = 1.1870201935945,
  delta = 2,
```

```

    ggamma = 2,
    bbeta = 3.39466184520673
  )
  ZOneDim <- sample(seq_len(m), n, replace = TRUE)
  thetaYList <-
  new(
    "ThetaYList",
    tao = 0.366618687752634,
    psy = list(structure(
      c(
        4.18375613018654,
        0, 0, 5.46215996830771
      ),
      .Dim = c(2L, 2L)
    )),
    M = list(structure(
      c(
        3.27412045866392,
        -2.40544145363349
      ),
      .Dim = 1:2
    )),
    lambda = list(structure(
      c(
        2.51015961514781,
        -0.0741189919182549
      ),
      .Dim = 2:1
    )),
    Y = list(structure(
      c(
        -0.244239011725104,
        -0.26876172736886,
        0.193431511203083,
        0.41624466812811,
        -0.54581548068437,
        -0.0479517628308146,
        -0.633383997203325,
        0.856855296613208,
        0.792850576988512,
        0.268208848994559
      ),
      .Dim = c(1L, 10L)
    ))
  )
  constraint <- c(0, 0, 0)
  #'

```

```

updatePostThetaY(m, n, p, hparam, thetaYList, ZOneDim, qVec, constraint, X, ggamma)

```

updatePostZ	<i>updatePostZ</i>
-------------	--------------------

Description

updatePostZ

Usage

updatePostZ(X, m, n, thetaYList)

Arguments

X	X
m	m
n	n
thetaYList	thetaYList

Examples

```

set.seed(100)
n <- 10
p <- 2
q <- 1
K <- 2
m <- 1
muBar <- c(0, 0)
qVec <- c(1, 1)
constraint <- c(0, 0, 0)
X <- t(
  fabMix::simData(
    sameLambda = TRUE,
    sameSigma = TRUE,
    K.true = K,
    n = n,
    q = q,
    p = p,
    sINV_values = 1 / ((1:p))
  )$data
)
hparam <- new(
  "Hparam",
  alpha1 = 0.567755037123148,
  alpha2 = 1.1870201935945,
  delta = 2,
  ggamma = 2,
  bbeta = 3.39466184520673
)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)

```

```

thetaYList <-
  new(
    "ThetaYList",
    tao = 0.366618687752634,
    psy = list(structure(
      c(
        4.18375613018654,
        0, 0, 5.46215996830771
      ),
      .Dim = c(2L, 2L)
    )),
    M = list(structure(
      c(
        3.27412045866392,
        -2.40544145363349
      ),
      .Dim = 1:2
    )),
    lambda = list(structure(
      c(
        2.51015961514781,
        -0.0741189919182549
      ),
      .Dim = 2:1
    )),
    Y = list(structure(
      c(
        -0.244239011725104,
        -0.26876172736886,
        0.193431511203083,
        0.41624466812811,
        -0.54581548068437,
        -0.0479517628308146,
        -0.633383997203325,
        0.856855296613208,
        0.792850576988512,
        0.268208848994559
      ),
      .Dim = c(1L, 10L)
    ))
  )

updatePostZ(X, m, n, thetaYList)

```

VstepRJMCMCupdate

VstepRJMCMCupdate

Description

VstepRJMCMCupdate

Usage

```
VstepRJMCMCupdate(X, muBar, p, thetaYList, ZOneDim, hparam, hparamInit,
  qVec, qnew, ggamma, dVec, sVec, constraint, clusInd)
```

Arguments

X	X
muBar	muBar
p	p
thetaYList	thetaYList
ZOneDim	ZOneDim
hparam	hparam
hparamInit	hparamInit
qVec	qVec
qnew	qnew
ggamma	ggamma
dVec	dVec
sVec	sVec
constraint	constraint
clusInd	clusInd

Examples

```
set.seed(100)
n <- 10
p <- 2
q <- 1
K <- 2
m <- 1
muBar <- c(0, 0)
qVec <- c(1, 1)
constraint <- c(0, 0, 0)
X <- t(
  fabMix::simData(
    sameLambda = TRUE,
    sameSigma = TRUE,
    K.true = K,
    n = n,
    q = q,
    p = p,
    sINV_values = 1 / ((1:p))
  )$data
)
hparam <- new(
  "Hparam",
  alpha1 = 0.567755037123148,
```

```

alpha2 = 1.1870201935945,
delta = 2,
ggamma = 2,
bbeta = 3.39466184520673
)
ZOneDim <- sample(seq_len(m), n, replace = TRUE)
thetaYList <-
new(
  "ThetaYList",
  tao = 0.366618687752634,
  psy = list(structure(
    c(
      4.18375613018654,
      0, 0, 5.46215996830771
    ),
    .Dim = c(2L, 2L)
  )),
  M = list(structure(
    c(
      3.27412045866392,
      -2.40544145363349
    ),
    .Dim = 1:2
  )),
  lambda = list(structure(
    c(
      2.51015961514781,
      -0.0741189919182549
    ),
    .Dim = 2:1
  )),
  Y = list(structure(
    c(
      -0.244239011725104,
      -0.26876172736886,
      0.193431511203083,
      0.41624466812811,
      -0.54581548068437,
      -0.0479517628308146,
      -0.633383997203325,
      0.856855296613208,
      0.792850576988512,
      0.268208848994559
    ),
    .Dim = c(1L, 10L)
  ))
)
qnew <- 1
dVec <- c(1, 1, 1)
sVec <- c(1, 1, 1)
constraint <- c(0, 0, 0)
clusInd <- rep(1, m)

```

```
VstepRJMCMCupdate(  
  X,  
  muBar,  
  p,  
  thetaYList,  
  ZOneDim,  
  hparam,  
  hparamInit,  
  qVec,  
  qnew,  
  ggamma,  
  dVec,  
  sVec,  
  constraint,  
  clusInd  
)
```


Index

CalculateProposalLambda, [2](#)
CalculateProposalPsy, [6](#)
calculateRatio, [9](#)
calculateVarList, [10](#)
changeConstraintFormat, [11](#)
clearCurrentThetaYlist, [12](#)
combineClusterPara, [14](#)

evaluatePrior, [16](#)
evaluatePriorLambda, [17](#)
evaluatePriorPsi, [18](#)
EvaluateProposalLambda, [19](#)
EvaluateProposalPsy, [22](#)

generatePriorLambda, [25](#)
generatePriorPsi, [27](#)
generatePriorThetaY, [27](#)
getIndThetaY, [28](#)
getmode, [30](#)
getRemovedIndThetaY, [31](#)
getThetaYWithEmpty, [32](#)
getZmat, [34](#)

Hparam-class, [35](#)

likelihood, [35](#)
listToStrVec, [37](#)

MstepRJMCMCupdate, [38](#)

pgmmRJMCMC, [40](#)

stayMCMCupdate, [42](#)
sumerizeZ, [44](#)
summerizePgmmRJMCMC, [44](#)

ThetaYList, [45](#)
toEthetaYlist, [46](#)
toNthetaYlist, [48](#)

updatePostThetaY, [49](#)
updatePostZ, [52](#)

VstepRJMCMCupdate, [53](#)