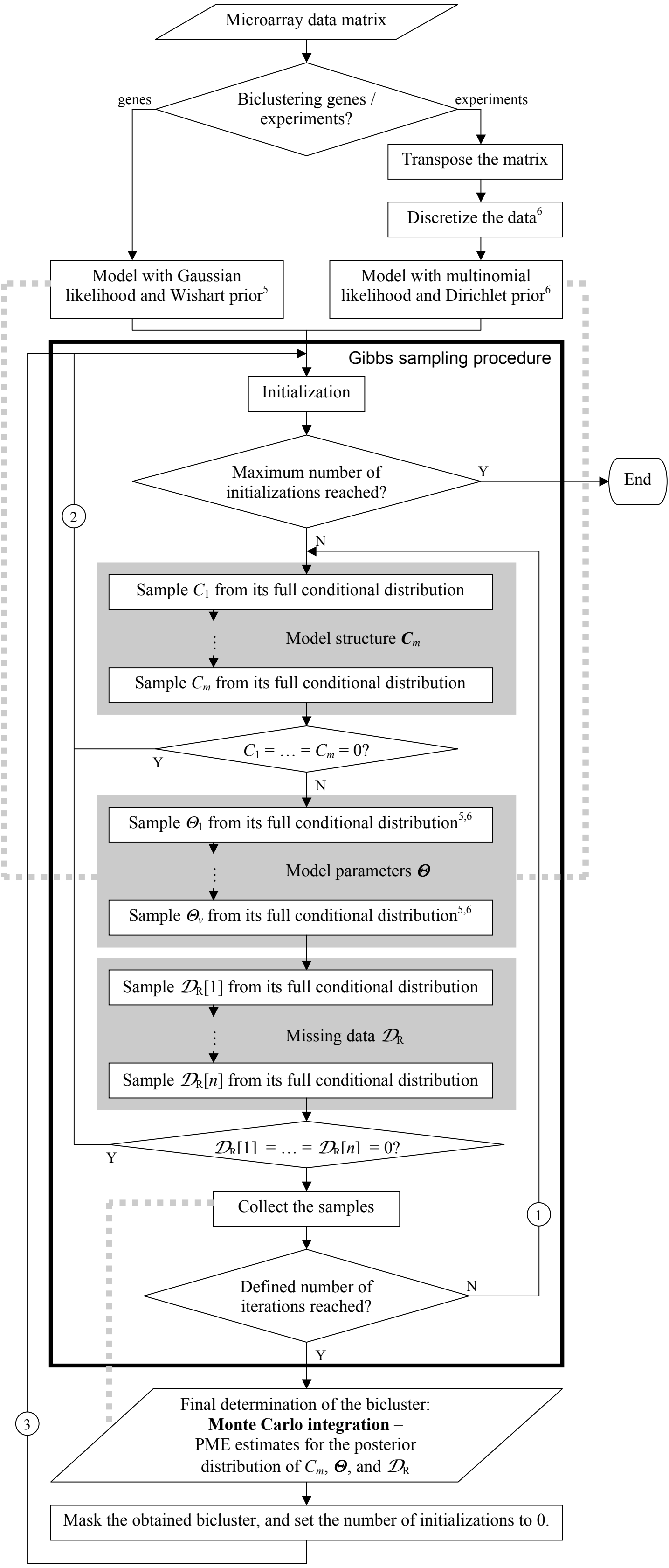
Microarray data matrix
Biclustering genes / experiments?
genes
experiments
Transpose the matrix
Discretize the data[6]
Model with Gaussian likelihood and Wishart prior[5]
Model with multinomial likelihood and Dirichlet prior[6]
Gibbs sampling procedure
Initialization
Maximum number of initializations reached?
Y
End
N
2
Sample C_1 from its full conditional distribution
Model structure $\boldsymbol{C}_m$
Sample C_m from its full conditional distribution
$C_1 = \ldots = C_m = 0$?
Y
N
Sample Θ_1 from its full conditional distribution[5,6]
Model parameters $\boldsymbol{\Theta}$
Sample Θ_v from its full conditional distribution[5,6]
Sample $\mathcal{D}_R[1]$ from its full conditional distribution
Missing data $\mathcal{D}_R$
Sample $\mathcal{D}_R[n]$ from its full conditional distribution
$\mathcal{D}_R[1] = \ldots = \mathcal{D}_R[n] = 0$?
Y
Collect the samples
1
Defined number of iterations reached?
N
Y
3
Final determination of the bicluster:
Monte Carlo integration –
PME estimates for the posterior
distribution of C_m, $\boldsymbol{\Theta}$, and $\mathcal{D}_R$
Mask the obtained bicluster, and set the number of initializations to 0.