

Help file for R function Bayes.DR(), which implements the dimension reduction method in:

Reich BJ, Bondell HD, Li L. Sufficient dimension reduction via Bayesian mixture modeling. In press, Biometrics.

The inputs (default values) are:

y	An n-vector of responses.
X	An nxp matrix of covariates (should not include the intercept).
slices (7)	The number of slices in the probit probabilities.
d (1)	The dimension of the central subspace. Currently, d must be either 1, 2, 3, or 4.
iterations (5000)	Number of MCMC samples to generate.
burnin (1000)	Number of MCMC samples to discard.
update (100)	Number of iterations between displaying the current iteration.

The outputs are:

A	The estimate of the pxd basis for the sufficient dimension.
A.samples	Posterior samples of A.
P	The posterior mean projection matrix, i.e., the posterior mean of $A(A'A)^{-1}A'$.
in.prob	The p-vector of inclusion probabilities. In.prob[j] is the posterior probability that the jth covariate is included in at least one direction.