Version 2: 2 clusters; Fix cluster label switching u,v; 1 chain

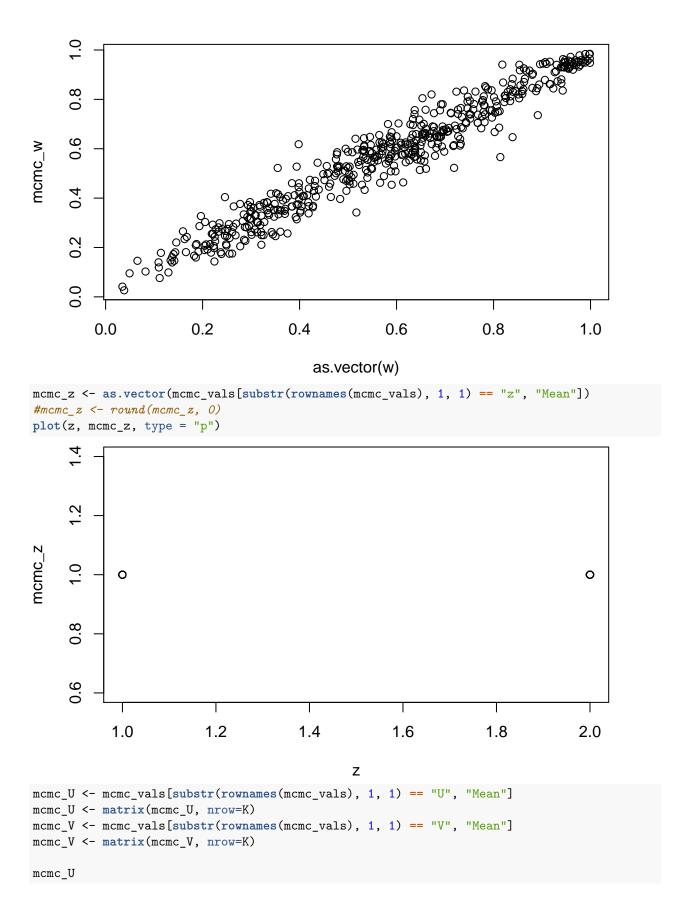
Simulate data

```
I <- 50
K <- 2
S <- 10
# choose diffuse priors for gamma
a_gamma <- 2
b_gamma <- 10
avrg <- a_gamma * b_gamma
std.dv <- sqrt(a_gamma*b_gamma^2)</pre>
g_range = seq(0, avrg + 5*std.dv, 0.01)
g_y = dgamma(g_range, a_gamma, rate = 1/b_gamma)
\#plot(g\_range, g\_y, type = "l", ylim=c(0, max(g\_y) + 0.01))
set.seed(123)
a <- matrix(NA, nrow=K, ncol=S)
b <- matrix(NA, nrow=K, ncol=S)
for (s in 1:S) {
 a[, s] <- rgamma(K, a_gamma, rate = 1/b_gamma)
  b[, s] <- rgamma(K, a_gamma, rate = 1/b_gamma)
pi <- as.vector(rdirichlet(1, rep(1, K)))</pre>
z <- sample(1:K, size = I, replace = T, prob = pi)
w <- matrix(NA, nrow=I, ncol=S)
for (s in 1:S) {
  w[, s] \leftarrow rbeta(I, a[,s][z], b[,s][z])
tcn <- matrix(2, nrow=I, ncol=S)</pre>
m <- matrix(rep(sample(1:2, size = I, replace = T), S), nrow=I, ncol=S)
calcTheta <- function(m, tcn, w) {</pre>
  (m * w) / (tcn * w + 2*(1-w))
theta <- calcTheta(m, tcn, w)</pre>
n <- replicate(S, rpois(I, 100))</pre>
y <- matrix(NA, nrow=I, ncol=S)
for (i in 1:I) {
 for (s in 1:S) {
    y[i, s] <- rbinom(1, n[i, s], theta[i,s])
```

}

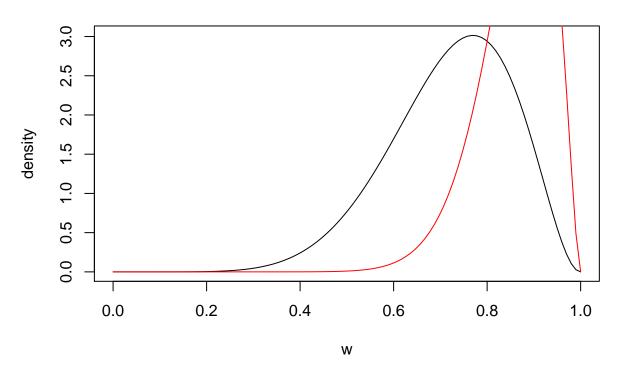
JAGS

```
jags.file <- file.path(models.dir, "v2_uv_unif_fix.jags")</pre>
test.data <- list("I" = I, "S" = S, "K" = K,
                   "y" = y, "n" = n,
                   "m" = m, "tcn" = tcn)
jags.m <- jags.model(jags.file, test.data,</pre>
                       n.chains = numChains)
## Compiling model graph
      Resolving undeclared variables
##
##
      Allocating nodes
## Graph information:
##
      Observed stochastic nodes: 500
##
      Unobserved stochastic nodes: 591
##
      Total graph size: 8450
##
## Initializing model
params <- c("z", "w", "a", "b", "U", "V")
update(jags.m, n.iter=1000)
samps <- coda.samples(jags.m, params, n.iter=1000)</pre>
s <- summary(samps)</pre>
#effectiveSize(window(samps, start=5001))
pdf(file.path(trace.dir, paste0(runName, "_trace.pdf")))
plot(samps)
dev.off()
## pdf
##
mcmc_vals <- s$statistics</pre>
mcmc_w <- mcmc_vals[substr(rownames(mcmc_vals), 1, 1) == "w", "Mean"]</pre>
plot(as.vector(w), mcmc_w, type = "p")
```

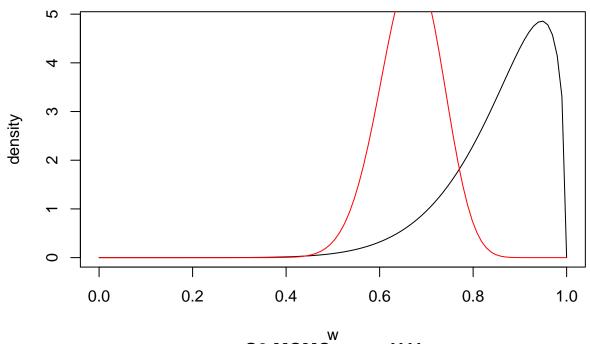


```
[,1]
                        [,2]
                                  [,3]
                                            [,4]
                                                       [,5]
                                                                 [,6]
## [1,] 0.7202845 0.9420078 0.5825985 0.5452757 0.5625535 0.2411650 0.3087352
## [2,] 0.8587357 0.9708146 0.7905685 0.7737616 0.7793115 0.6324905 0.6559683
             [,8]
                        [,9]
##
                                 [,10]
## [1,] 0.7084000 0.5603281 0.4763288
## [2,] 0.8555612 0.7812279 0.7340869
p \leftarrow seq(0, 1, length = 100)
for (s in 1:S) {
  for (k in 1:K) {
    if (k == 1) {
      plot(p, dbeta(p, mcmc_U[k,s] * mcmc_V[k,s], (1-mcmc_U[k,s])*mcmc_V[k,s]),
           main = paste0("S", s, " MCMC mean U,V"),
           ylab = "density", xlab = "w", type = "l", col = k)
    } else {
      lines(p, dbeta(p, mcmc_U[k,s] * mcmc_V[k,s], (1-mcmc_U[k,s])*mcmc_V[k,s]),
            type = "l", col = k)
    }
  }
  for (k in 1:K) {
    if (k == 1) {
      plot(p, dbeta(p, a[k,s], b[k,s]),
           main = paste0("S", s, " truth"),
           ylab = "density", xlab = "w", type = "l", col = k)
    } else {
      lines(p, dbeta(p, a[k,s], b[k,s]), type = "l", col = k)
    }
  }
}
```

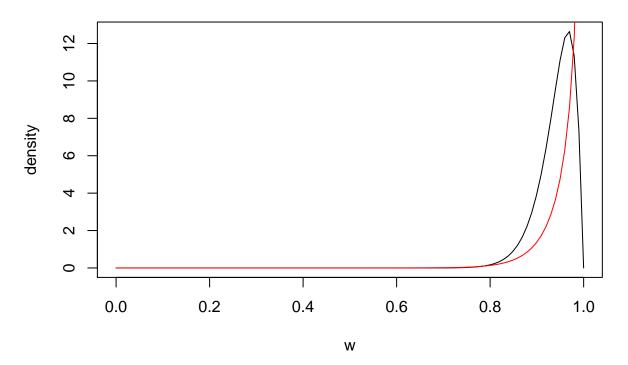
S1 MCMC mean U,V



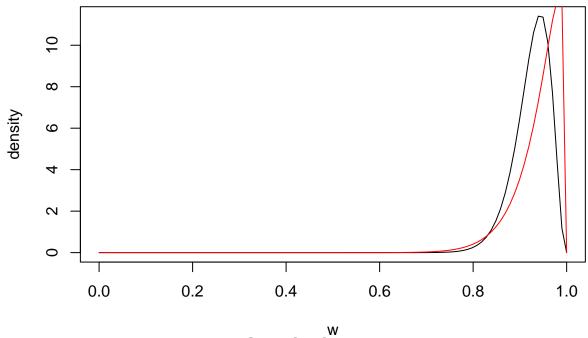




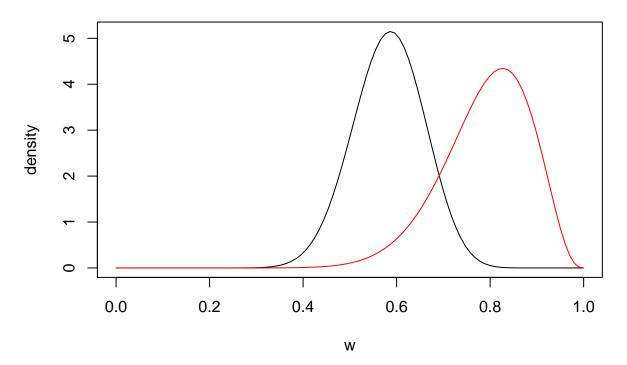
S2 MCMC mean U,V



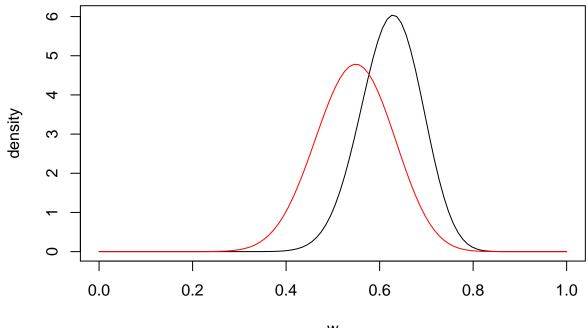




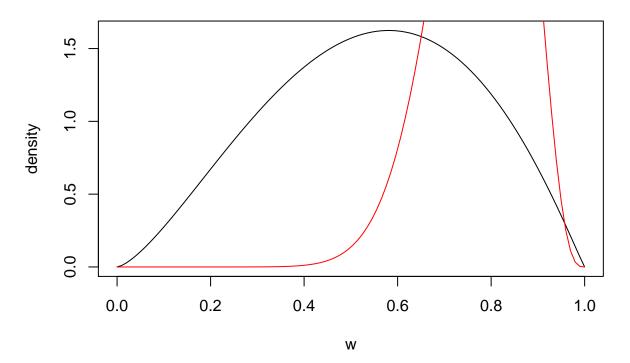
S3 MCMC mean U,V



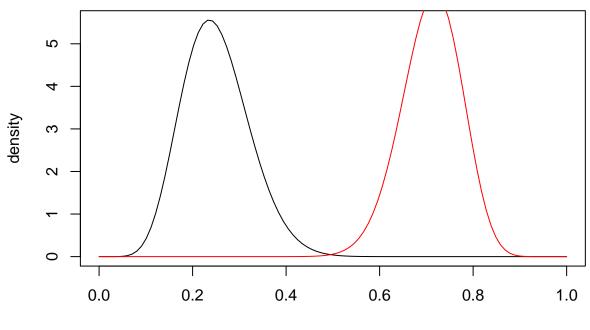




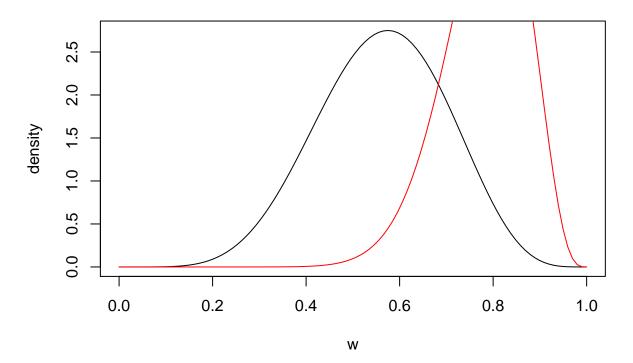
S4 MCMC mean U,V



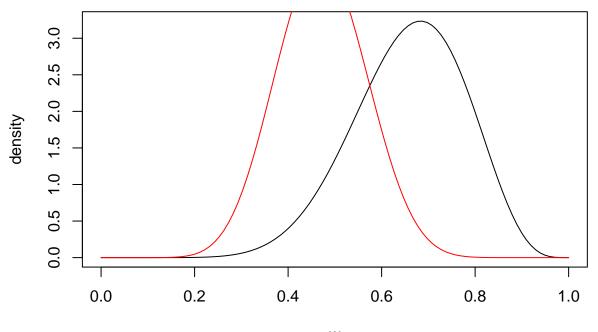




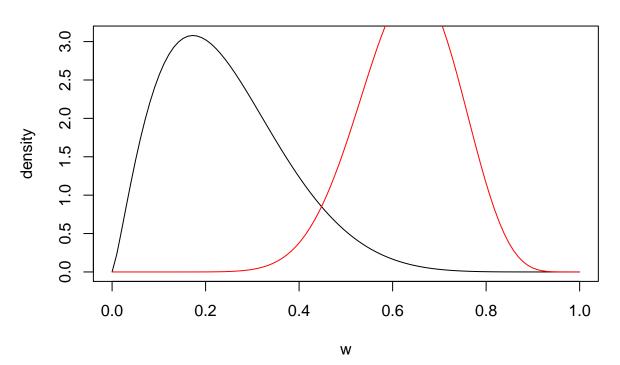
S5 MCMC mean U,V



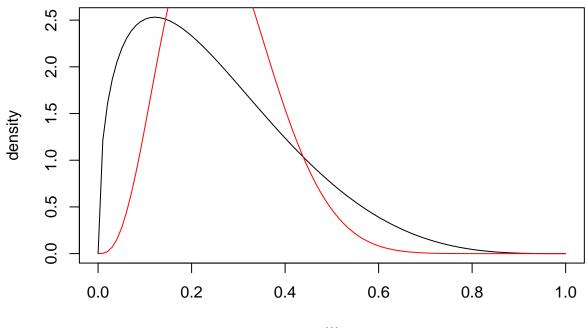




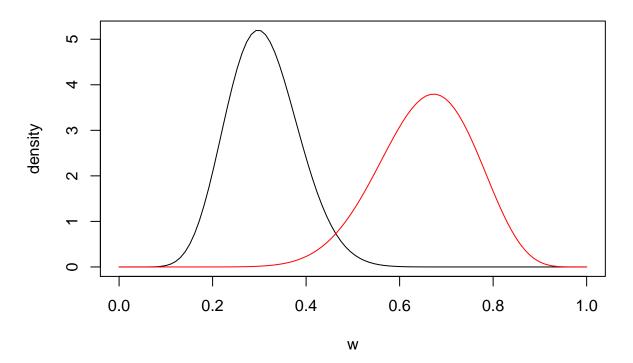
S6 MCMC mean U,V



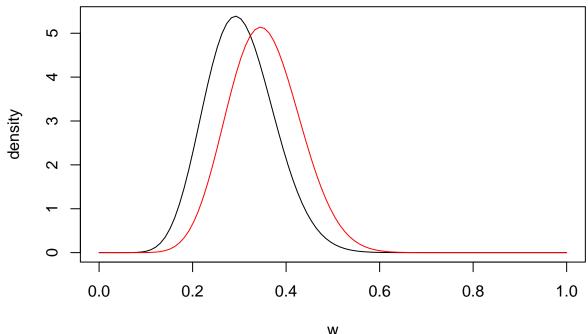




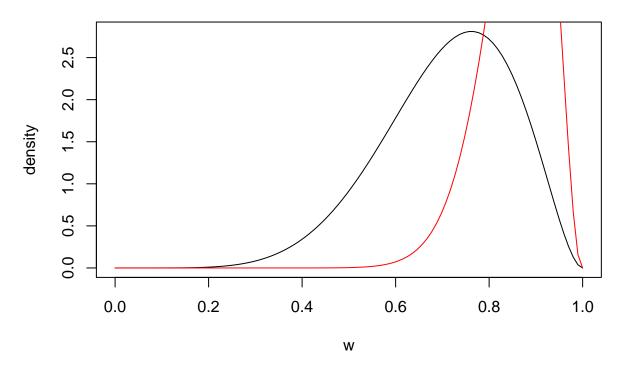
S7 MCMC mean U,V



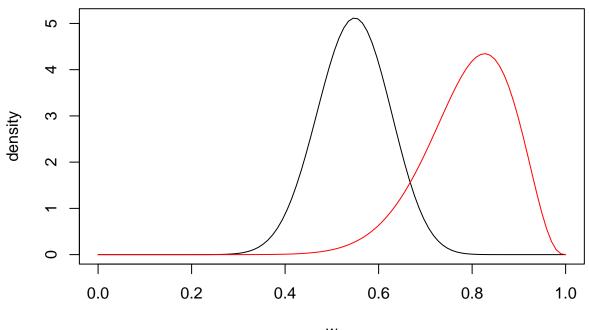




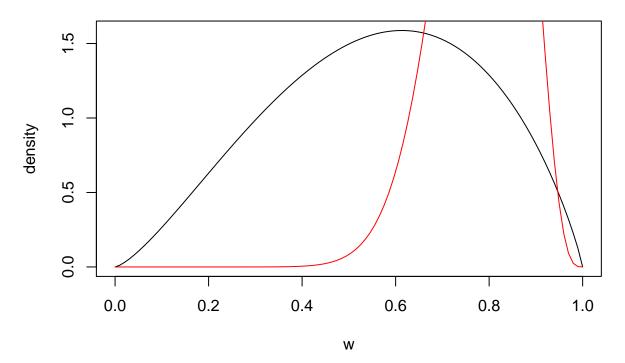
S8 MCMC mean U,V



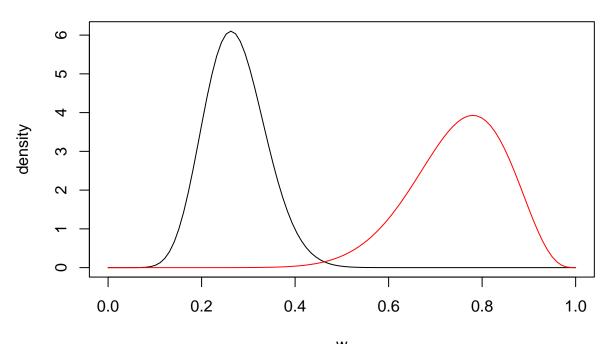




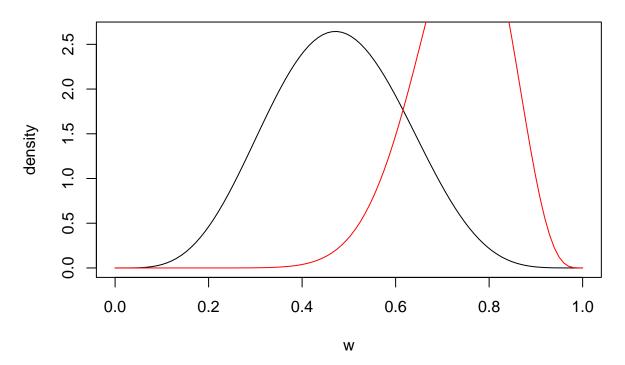
S9 MCMC mean U,V







S10 MCMC mean U,V



S10 truth

