

R2 R2WinBUGS CODE

Regression Code

#predictand is the log transformed flows matrix

#predictor is the tree chronology matrix

#npred is the number of predictors

#ntimes is the number of years of Y data

nsites is the number of streamflow stations

Wp <- diag(npred)

#.....#

Running WinBugs from R

#.....#

library("MCMCpack")

library("arm")

library("R2WinBUGS")

Model 1 : Simple Regression on all sites separately.

Run in the Bayesian set up under no pool scenario: Run in Bayesian setup to compare the Regression Coefficients

data <- list("npred", "nsites", "ntimes", "predictand", "predictor")

parameters <- c("mu.predictand.np", "sigma.predictand.np", "alpha.np", "betas.np", "predictand.rep.np")

delaware.nopool <-

bugs(data, inits=NULL, parameters, "model_nopool.bug", n.chains=3, n.iter=5000, debug=TRUE, bugs.directory="C:/Program Files (x86)/WinBUGS14")

attach.bugs(delaware.nopool)

Model 2 : Single Level Hierarchical Model Bayesian Partial Pooling

```
data <- list("npred", "ntimes", "nsites", "predictand", "predictor", "Wp")

parameters <- c("mu.predictand.pp", "sigma.predictand.pp", "alpha.pp", "betas.pp", "mu.betas.pp",
"sigma.betas.pp", "rho.betas.pp", "predictand.rep.pp")

inits <- function () {
list(betas.pp = array(rnorm(nsites*npred),c(nsites,npred)), mu.betas.pp = rnorm(npred),
tau.betas.pp = rwish(npred + 1, diag(npred)))
}
delaware.parpool <-
bugs(data,inits,parameters,"model_mvparpool.bug",n.chains=3,n.iter=5000,debug=TRUE,bugs.directory=
"C:/Program Files (x86)/WinBUGS14")
attach.bugs(delaware.parpool)
```