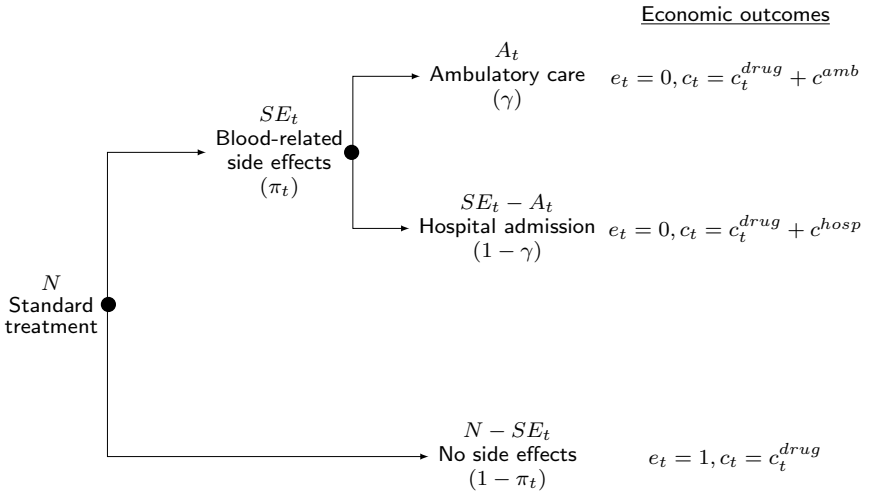

$\Rightarrow$

```
# JAGS model (saved to 'modelChemo.txt')
model {
    pi[1] ~ dbeta(a.pi,b.pi)
    pi[2] <- pi[1]*rho
    rho ~ dnorm(m.rho,tau.rho)
    gamma ~ dbeta(a.gamma,b.gamma)
    c.amb ~ dlnorm(m.amb,tau.amb)
    c.hosp ~ dlnorm(m.hosp,tau.hosp)
    for (t in 1:2) {
        SE[t] ~ dbin(pi[t],N)
        A[t] ~ dbin(gamma,SE[t])
        H[t] <- SE[t] - A[t]
    }
}
```

$\Downarrow$

```
# Calls JAGS in background to run the model
library(R2jags)
data <- list("a.pi","b.pi","a.gamma","b.gamma",
          "m.amb","tau.amb","m.hosp","tau.hosp",
          "m.rho","tau.rho","N")
filein <- "modelChemo.txt"
params <- c("pi","gamma","c.amb","c.hosp",
            "rho","SE","A","H")
inits <- function()
    list(pi=c(runif(1),NA),gamma=runif(1),
         c.amb=rlnorm(1),c.hosp=rlnorm(1),
         rho=runif(1))

chemo <- jags(data,inits,params,n.iter=20000,
  model.file=filein,n.chains=2,n.burnin=9500,
  n.thin=42,DIC=FALSE)
print(chemo,digits=3,intervals=c(0.025, 0.975))
attach.jags(chemo)
```

$\Leftarrow$

```
# Creates the variables of cost & effectiveness
e <- c <- matrix(NA,1000,2)
e <- N - SE
for (t in 1:2) {
   c[,t] <- c.drug[t]*(N-SE[,t]) +
            (c.amb+c.drug[t])*A[,t] +
            (c.hosp+c.drug[t])*H[,t]
}
```