

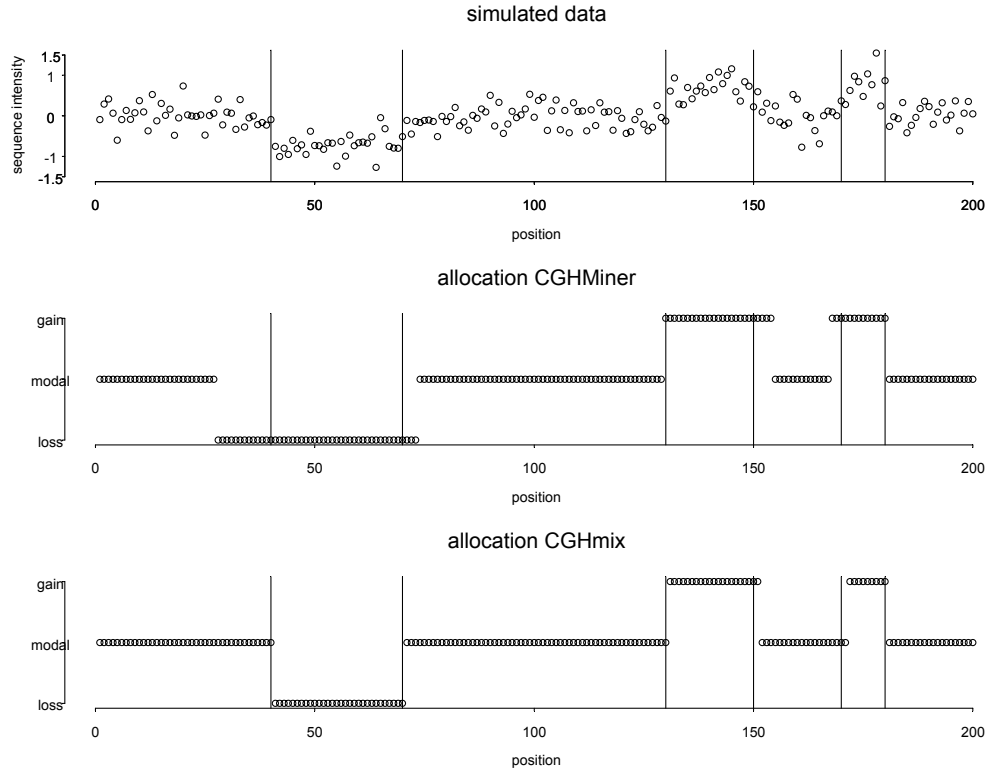


Figure I: Comparative results between CGHMiner (panel 2) and CGHmix (panel 3) on one dataset simulated under configuration 1 (panel 1). The vertical bars indicate the breakpoint between the true different states.

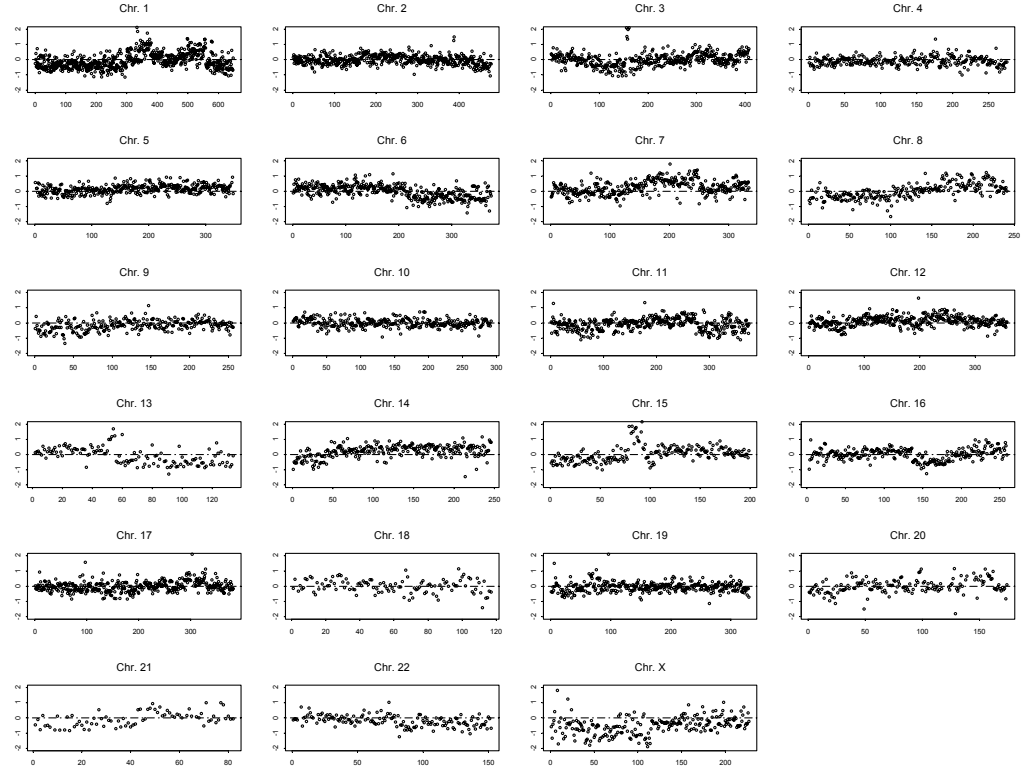


Figure II: Genomic sequence measurements of the MCF7 cell line ordered along the 23 chromosomes (Chr.). The dotted horizontal bar indicates the value zero.

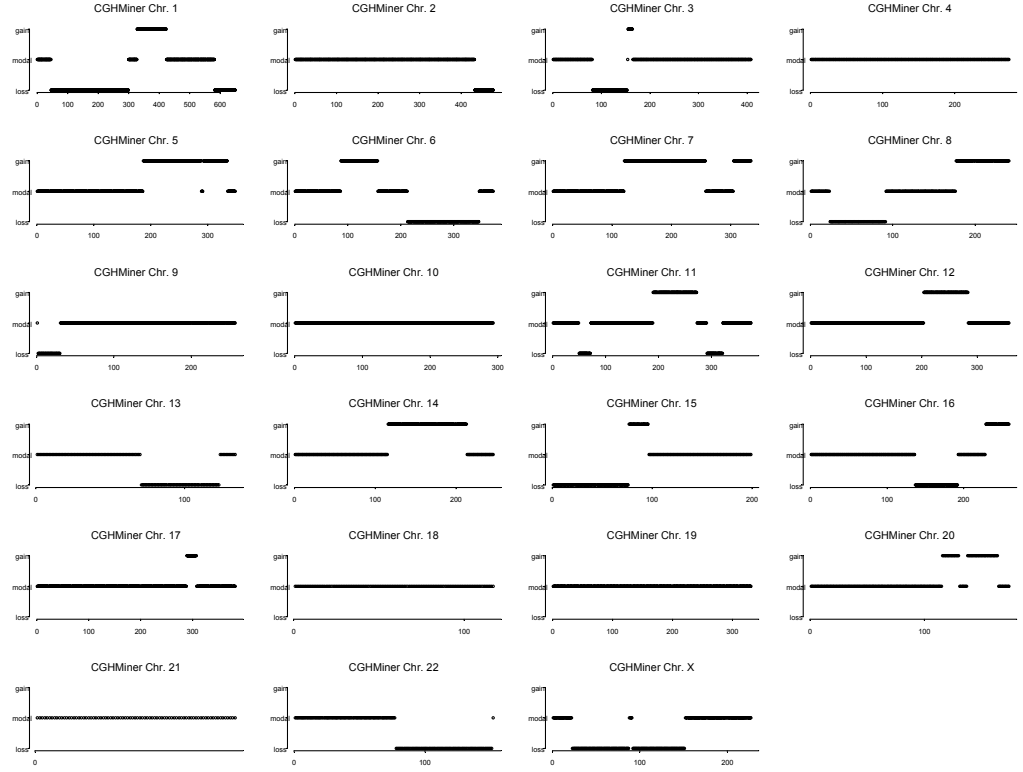


Figure III: Results for CGH-Miner for the MCF7 dataset. The 23 panels display the results for each chromosome (Chr.).

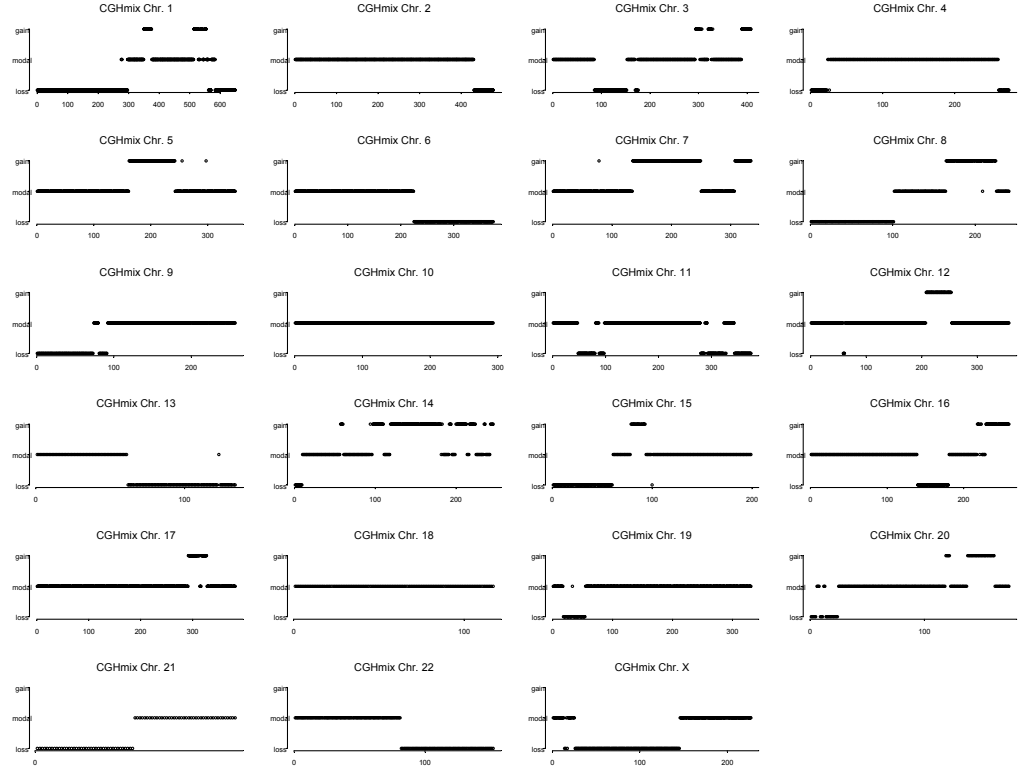


Figure IV: Results for CGHmix for the MCF7 dataset. The 23 panels display the results for each chromosome (Chr.).

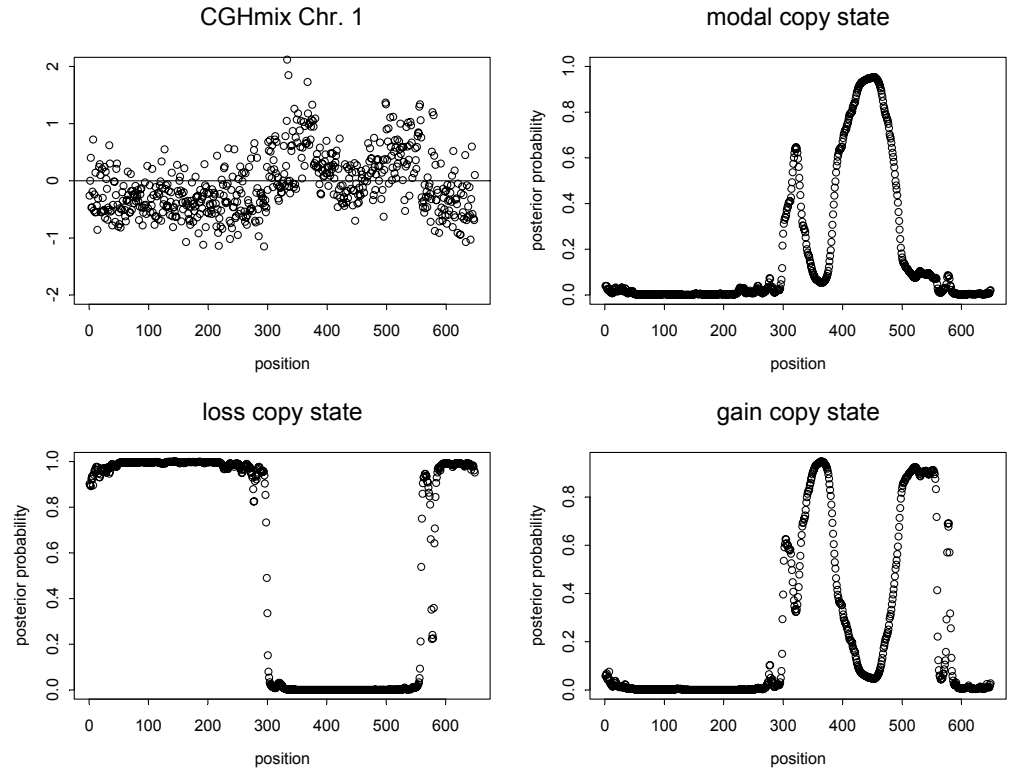


Figure V: Posterior probabilities for the structured model for chromosome 1 (Chr. 1) of the MCF7 breast cancer cell line.

Code

This is the WinBUGS (Spiegelhalter et al., 1999) code for the Bayesian spatially structured mixture (three components) model considered in the article but presented (for simplicity) for one chromosome. The code shown here is for the model. It can easily be modified to include more than one chromosome. We used version 1.4 of WinBUGS to run this model.

```

model
{
  for( i in 1 : N ) {Y[i] ~dnorm(mu[i], tauR[i]) # genomic sequence measure-
ments
    mu[i] <- lambda[T[i]]
    tauR[i] <- tau[T[i]]
    p[i,1] <-exp(alpha1[i])/(exp(alpha1[i])+exp(alpha2[i])+exp(alpha3[i]))
    p[i,2] <-exp(alpha2[i])/(exp(alpha1[i])+exp(alpha2[i])+exp(alpha3[i]))
    p[i,3] <-exp(alpha3[i])/(exp(alpha1[i])+exp(alpha2[i])+exp(alpha3[i]))
    T[i] ~dcat(p[i,1:3]) # latent variable (deletion/gain/modal)
    T1[i] <-equals(T[i],1) ;T2[i] <-equals(T[i],2) ;T3[i] <-equals(T[i],3) # latent
variables}

  # Fields specification
  alpha1[1:N] ~car.normal(adj[], weights[], num[], tauC[1])
  alpha2[1:N] ~car.normal(adj[], weights[], num[], tauC[2])
  alpha3[1:N] ~car.normal(adj[], weights[], num[], tauC[3])
  # weights specification
  for(i in 1:1){weights[i] <- 1;adj[i] <- i+1 ;num[i]<- 1}
  for(i in 2:(N-1)) {weights[2+(i-2)*2] <- 1;adj[2+(i-2)*2] <- i-1
  weights[3+(i-2)*2] <- 1; adj[3+(i-2)*2] <- i+1;num[i] <- 2}
  for(i in N:N){weights[(N-2)*2 + 2] <- 1;adj[(N-2)*2 + 2] <- i-1;num[i] <- 1}
  # prior (precision/variance spatial field)
  sig2C[1] ~dgamma(0.01, 0.01)I(0.0001, )
  sig2C[2] ~dgamma(0.01, 0.01)I(0.0001, )
  sig2C[3] ~dgamma(0.01, 0.01)I(0.0001, )
  tauC1[1] <- 1/sig2C[1]; tauC1[2] <- 1/sig2C[2]; tauC1[3] <- 1/sig2C[3]
  # prior (range [a-b])
  lambda[1] <- 0 # modal copy
  lambda[3] ~dnorm(0, 1.0E-6)I(a,0.0 ) # loss copy
  lambda[2] ~dnorm(0, 1.0E-6)I(0.0,b) # gain copy
  # precision/variance (density)
  tau[1] ~dgamma(0.1, 0.1)
  tau[2]~dgamma(0.1, 0.1)
  tau[3]~dgamma(0.1, 0.1)
  sigma[1] <- 1/sqrt(tau[1]) ;sigma[2] <- 1/sqrt(tau[2]) ;sigma[3] <- 1/sqrt(tau[3])
}

```