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# Correction: On Bayesian modeling of censored data in JAGS

Xinyue Qi<sup>1</sup>, Shouhao Zhou<sup>2\*</sup> and Martyn Plummer<sup>3</sup>

The original article can be found online at https://doi.org/10.1186/s12859-021-04496-8.

\*Correspondence: shouhao.zhou@psu.edu

<sup>1</sup> The University of Texas MD Anderson Cancer Center, Houston, TX, USA <sup>2</sup> Pennsylvania State University, Hershey, PA, USA <sup>3</sup> University of Warwick, Coventry,

# **Correction to: BMC Bioinformatics (2022) 23:102**

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Following the publication of the original article [1], the authors identified errors in the model specifications 1 and 2. The correct models are given below.

```
model{ # Model 1
    for (o in 1:0){ # 0 is the number of observed cases;
        Y[o] ~ f(theta[o]) # f need to be specified for JAGS
}

for (j in 1:J){ # J is the number of censored observations;
    # Left censoring (R=0): lim[j,] = c(cut[j], inf);
    # Right censoring (R=2): lim[j,] = c(-inf, cut[j]);
    # Interval censoring (R=1): lim[j,] = c(cut1[j], cut2[j]);
    R[j] ~ dinterval(Y[0+j], lim[j,])
    Y[0+j] ~ f(theta[0+j])
}

# prior for theta's
}
```



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```
model{ # Model 2
      # block 1: fully-observed
      for (o in 1:0){
            Y[o] ~ f(theta[o]) # f need to be specified for JAGS
      # block 2: left/right censoring
      for (c in 1:C){
            Z1[c] ~ dbern(p[c])
            p[c] <- F(cut[c], theta[0+c])</pre>
      }
      # block 3: interval censoring
      for (i in 1:I){
            Z2[i] ~ dbern(p[C+i])
            p[C+i] \leftarrow F(cut2[i], theta[0+C+i]) - F(cut1[i], theta[0+C+i])
      }
      # prior for theta's
}
```

The original article [1] has been corrected.

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### Reference

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