

CORRECTION

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Correction: On Bayesian modeling of censored data in JAGS

Xinyue Qi¹, Shouhao Zhou^{2*} and Martyn Plummer³

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

*Correspondence: shouhao.zhou@psu.edu

¹The University of Texas MD Anderson Cancer Center, Houston, TX, USA

²Pennsylvania State University, Hershey, PA, USA

³University of Warwick, Coventry, UK

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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:O){ # O 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[O+j], lim[j,])
    Y[O+j] ~ f(theta[O+j])
  }

  # prior for theta's
}
```



```

model{ # Model 2
  # block 1: fully-observed
  for (o in 1:O){
    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])
  }

  # block 3: interval censoring
  for (i in 1:I){
    Z2[i] ~ dbern(p[C+i])
    p[C+i] <- 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

1. Qi X, et al. On Bayesian modeling of censored data in JAGS. BMC Bioinform. 2022;23:102. <https://doi.org/10.1186/s12859-021-04496-8>.

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