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“Web-based Supplementary Materials for *A Survival Analysis Approach to Modeling Human Fecundity* by Rajeshwari Sundaram*, Alexander McLain and Germaine M. Buck Louis.”

1. WEB APPENDIX A

R code for the likelihood based biologically valid discrete survival modeling approach.

```
TTPlike<-function(par, q, p, r, TTP, CEN, cov, tcov, covt=999,
frail=TRUE) {

##Usage:
#TTPlike(par, q, p, r, TTP, CEN, cov, tcov, covt=999, frail=TRUE)

##Arguments:
#par: A vector of q regression parameters (may include 1
```

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```
#time dependent parameter), r regression parameters for
#day-level covs, p time dependent intercepts, and 1 nu
#(log variance of the frailty omitted if frail=FALSE).

#TTP: Time to pregnancy in menstrual cycles.
#CEN: Indicator that an observation was censored.

#cov: A qxn matrix of covariates (q-1 x n if covt!=999).
#tcov: A nx(p*r) matrix of day-level intercourse behavior.
#The 1st r columns are for cycle 1, the next r are for
#cycle 2, etc.
#covt: A nxp matrix of time-dependent covariates.
#frail: Logical, should frailty be included in model?
##Defining the parameters##
beta = par[1:q]
      #Defining the last beta as the parameter for a
      #time-dependent cov.
if(covt[1]!=999){tbeta = beta[q]
beta  = beta[-q]}
      #regression coefficient for day-level cov.
betat = par[(q+1):(q+r)]
      #time dependent intercepts#
alpha = par[(q+r+1):(q+r+p)]
      #variance of the frailty
```

```
if(frail){nu = exp(par[q+r+p+1])}
n = length(TTP)

#Calculating the F().
fecimp = matrix(0,n,p)
find = matrix(0,n,p)
rvec = rep(1,r)

for(k in 1:p){
i1 = (k-1)*r +1
i2 = k*r
fecimp[,k] = tcov[,i1:i2]*%betat
find[,k] = tcov[,i1:i2]*%rvec
}
fi = I(find==0)

bsq=0
if(covt[1]!=999){bsq = rep(tbeta,p)}
if(covt[1]==999){covt= matrix(0,n,p)}

Fil = exp(t(t(cov*%beta*%t(rep(1,p)))+alpha
+t(covt)*bsq)+fecimp)

#Correcting for 0-risk periods.
```

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```
Fi1[fi]=0
Fit=NULL
Fitm1=NULL
PNI = NULL
for(i in 1:length(TTP)){
Fit[i] = sum(Fi1[i,1:TTP[i]])
Fitm1[i] = 0
if(TTP[i]>1){Fitm1[i] = sum(Fi1[i,1:(TTP[i]-1)])}
}
#Log likelihood contribution for all individuals.
if(frail){
indlike=log((1-CEN)*h(Fitm1,nu)+(2*CEN-1)*h(Fit,nu))
}
if(!frail){
indlike=log((1-CEN)*exp(-Fitm1)+(2*CEN-1)*exp(-Fit))
}

#Full likelihood
fulllike = sum(indlike)
return(-fulllike)
}
h<-function(F,nu){(1/(nu*F+1))^(1/nu)}
```