

## Supplementary information

### Using Bayesian state-space models to understand the population dynamics of the dominant malaria vector, *Anopheles funestus* in rural Tanzania

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S1: JAGS code

```
##### 1. Jags model#####
```

```
popMod2<-"model{
```

```
  #Multiple trajectory
```

```
  for(i in 1:Ntr){
```

```
    ###MAIN LOOP###
```

```
    #Supply the initial values
```

```
    Ieggs[i,1]~dunif(0,3000)
```

```
    ILarvae[i,1]~dunif(0,3000)
```

```
    Ipupae[i,1]~dunif(0,3000)
```

```
    Iadult[i,1]~dunif(0,1000)
```

```
    Iblood_fed[i,1]~dunif(0,1000)
```

```
    Igravid[i,1]~dunif(0,100)
```

```
    IgraG[i,1]~dunif(0,100)
```

```
    eggs[i,1]<-round(Ieggs[i,1])
```

```
    larvae[i,1]<-round(ILarvae[i,1])
```

```
    pupae[i,1]<-round(Ipupae[i,1])
```

```
    adult[i,1]<-round(Iadult[i,1])
```

```
    blood_fed[i,1]<-round(Iblood_fed[i,1])
```

```
    gravid[i,1]<-round(Igravid[i,1])
```

```
    graG[i,1]<-round(IgraG[i,1])
```

```
    ####Start of the time loop####
```

```
    for(t in 2:(tmax))
```

```
    {
```

```
      LarE[i,t]~dnorm(0,precLE+1)
```

```
      pupE[i,t]~dnorm(0,precPE+1)
```

```
      aduE[i,t]~dnorm(0,precAE+1)
```

```
      bLoE[i,t]~dnorm(0,precAE+1)
```

```
      graE[i,t]~dnorm(0,precAE+1)
```

```
      breE[i,t]~dnorm(0,precBE+1)
```

```
      #Effect of density dependence, rainfall and temperature on Larvae survival
```

```
      Logit(spv[i,t])<-sLInv + PrTempLs*Temp[i,t-1] + PrTemps*Temp[i,t-1]^2 - Pr  
_dd*prec[i,t-1] - larvae[i,t-1]*Ldd*(1 - Pr_dd3*prec3[i,t-1]/max(prec3))+LarE[i,  
t]
```

```
      LarS[i,t] ~ dbin(spv[i,t], larvae[i,t-1])
```

```
      Logit(spu[i,t])<-sp0+pupE[i,t]
```

```
      pupS[i,t] ~ dbin(spu[i,t], pupae[i,t-1])
```

```
      #seasonality into adult-unfed
```

```
      Logit(sav[i,t])<-saInv + 0*Temp[i,t-1] + 0*Temp[i,t-1]^2+aduE[i,t]
```

```
      aduS[i,t] ~ dbin(sav[i,t], adult[i,t-1])
```

```

#seasonality into adult-bloodfed
Logit(sbv[i,t])<-sbInv + 0*Temp[i,t-1] + 0*Temp[i, t-1]^2+bloE[i,t]
bloS[i,t] ~ dbin(sbv[i,t], blood_fed[i,t-1])

#seasonality into adult-gravid
Logit(sgv[i,t])<-sgInv + 0*Temp[i,t-1] + 0*Temp[i, t-1]^2+graE[i,t]
graS[i,t] ~ dbin(sgv[i,t], gravid[i,t-1])

#Growth for each stage
eggG[i,t] ~ dbin(lambda, eggs[i,t-1])

#Positive effect of temp on Larval growth
Logit(lgv[i,t]) <- lrInv + PrTempLg*(Temp[i,t-1]-27)
larG[i,t] ~ dbin(lgv[i,t], larS[i,t])

pupG[i,t] ~ dbin(pr, pupS[i,t])

aduG[i,t] ~ dbin(ar, aduS[i,t])

bloG[i,t] ~ dbin(bfr, bloS[i,t])

graG[i,t] ~ dbin(gr, graS[i,t])

#fecundity penalised by egg survival
Log(bre[i,t])<-bre0+breE[i,t]
fec[i,t] ~ dpois(se*0.5*bre[i,t]*graG[i,t-1])

# Propagation of population classes through time (no class is allowed to go
extinct, hence the +1)
eggs[i,t] <-eggs[i,t-1]-eggG[i,t]+fec[i,t]+1
larvae[i,t] <- larS[i,t]-larG[i,t]+eggG[i,t]+1
pupae[i,t] <- pupS[i,t]-pupG[i,t]+larG[i,t]+1
adult[i,t] <- aduS[i,t]-aduG[i,t]+pupG[i,t] + graG[i,t]+1
blood_fed[i,t] <- bloS[i,t]-bloG[i,t]+aduG[i,t]+1
gravid[i,t] <- graS[i,t]-graG[i,t]+bloG[i,t]+1

#Observation process model
# Observaton likelihoods against real data
adultD[i,t] ~ dnorm(ef0[i,efLev[t]]*adult[i,t], 1/(seAd[i,t])^2)T(0,)
blood_fedD[i,t] ~ dnorm(ef0[i,efLev[t]]*blood_fed[i,t]*ef1, 1/(seBf[i,t])^2
)T(0,)
gravidD[i,t] ~ dnorm(ef0[i,efLev[t]]*gravid[i,t]*ef2, 1/(seGr[i,t])^2)T(0,)

# Predictions (no data) used to generate prediction intervals for plotting
Later
adultd[i,t] ~ dnorm(ef0[i,efLev[t]]*adult[i,t], 1/(seAd[i,t])^2)T(0,)
blood_fedd[i,t] ~ dnorm(ef0[i,efLev[t]]*blood_fed[i,t]*ef1, 1/(seBf[i,t])^2
)T(0,)

```

```

gravidd[i,t] ~ dnorm(ef0[i,efLev[t]]*gravid[i,t]*ef2, 1/(seGr[i,t])^2)T(0,)

# Modelling the standard errors for the weekly mean counts.
seAd[i,t]<-1e-6+ef0[i,efLev[t]]*adult[i,t]*cva[i]
seBf[i,t]<-1e-6+ef0[i,efLev[t]]*blood_fed[i,t]*ef1*cva[i]
seGr[i,t]<-1e-6+ef0[i,efLev[t]]*gravid[i,t]*ef2*cva[i]

} #End of time loop

} #End of trajectory loop

#Density dependence at Larval stage (Determines carrying capacity)
Ldd ~ dgamma(0.5,1)T(0.0001,10)

# Precisions for stochasticity in survival rates
precLE~dgamma(10,1)
precPE~dgamma(10,1)
precAE~dgamma(10,1)
precBE~dgamma(10,1)

# Scaling parameters for all beta priors
b1<-100
b2<-100
b3<-2
b4<-2

#Prior for coefficient of variation in trapping
mu.cva<-0.5
sd.cva<-0.4/b3
cvamax<-mu.cva+b4*sd.cva
cvamin<-max(0, mu.cva-b4*sd.cva)
cvae[1]~dbeta(b1, b2)
cva[1]<-cvamin+cvae[1]*(cvamax-cvamin)
cvae[2]~dbeta(b1, b2)
cva[2]<-cvamin+cvae[2]*(cvamax-cvamin)

ef0[1,1]<-0.5

dev[2,1]~dnorm(0,10)
ef0[2,1]<-0.1*exp(dev[2,1])/(1+exp(dev[2,1]))

for( day in 2:7)
{
  dev[1,day]~dnorm(0,10)
  Logit(ef0[1,day])<-dev[1,day]
  dev[2,day]~dnorm(0,10)
}

```

```
ef0[2, day]<-0.1*exp(dev[2, day])/(1+exp(dev[2, day]))
}
```

```
# CDC trap effectiveness for blood fed
```

```
mu.ef1<-0.1
sd.ef1<-0.05/b3
efmax1<-min(1, mu.ef1+b4*sd.ef1)
efmin1<-max(0, mu.ef1-b4*sd.ef1)
efe1~dbeta(b1, b2)
ef1<-efmin1+efe1*(efmax1-efmin1)
```

```
ef2<-0.505*ef1
```

```
#Proportion eggs survived (literature)
```

```
mu.se<- 0.7940
sd.se<- 0.101/b3
semax<-min(1, mu.se+b4*sd.se)
semin<-max(0, mu.se-b4*sd.se)
see~dbeta(b1, b2)
se<-semin+see*(semax-semin)
```

```
#Hatching period
```

```
mu.Lam<- 0.5
sd.Lam<- 0.1/b3
Lamax<-min(1, mu.Lam+b4*sd.Lam)
Lammin<-max(0, mu.Lam-b4*sd.Lam)
Lamm~dbeta(b1, b2)
Lambda<-Lammin+Lamm*(Lamax-Lammin)
```

```
#Survival rates pupae
```

```
mu.sp<-0.9414
sd.sp<-0.0339/b3
spmax<-min(1, mu.sp+b4*sd.sp) #spmax goes to 1.0092
spmin<-max(0, mu.sp-b4*sd.sp)
spp~dbeta(b1, b2)
sp<-spmin+spp*(spmax-spmin)
sp0<-Log(sp/(1-sp))
```

```
#Survival rates adults/unfed
```

```
mu.sa<-0.9348
sd.sa<-0.0288/b3
samax<-min(1, mu.sa+b4*sd.sa)
samin<-max(0, mu.sa-b4*sd.sa)
saa~dbeta(b1, b2)
sa<-samin+saa*(samax-samin)
saInv0<-Log(sa/(1-sa))
```

```
#Survival rates blood-fed
```

```

mu.sb<-0.8074
sd.sb<-0.0766/b3
sbmax<-min(1, mu.sb+b4*sd.sb)
sbmin<-max(0, mu.sb-b4*sd.sb)
sbb~dbeta(b1, b2)
sb<-sbmin+sbb*(sbmax-sbmin)
sbInv0<-Log(sb/(1-sb))

#Survival rates gravid
mu.sg<-0.9041
sd.sg<-0.0282/b3
sgmax<-min(1, mu.sg+b4*sd.sg)
sgmin<-max(0, mu.sg-b4*sd.sg)
sgg~dbeta(b1, b2)
sg<-sgmin+sgg*(sgmax-sgmin)
sgInv0 <-Log(sg/(1-sg))

#Seasonality in adult survival (Temperature)
ATopt<-27 # Optimal temperature for adult survival
PrTempa~dgamma(25,0.5) # Linear term coefficient
PrTempas<- -PrTempa/(2*ATopt) # Quadratic term coefficient
saInv <-saInv0-PrTempa*ATopt/2 # Ensures that the maximum survival is mu.sa
sbInv <-sbInv0-PrTempa*ATopt/2 # Ensures that the maximum survival is mu.sb
sgInv <-sgInv0-PrTempa*ATopt/2 # Ensures that the maximum survival is mu.sg

#Survial rates Larvae
mu.sl<-0.9226
sd.sl<-0.0610/b3
slmax<-min(1, mu.sl+b4*sd.sl)
slmin<-max(0, mu.sl-b4*sd.sl)
sll~dbeta(b1, b2)
sl<-slmin+sll*(slmax-slmin)
slInv0<-Log(sl/(1-sl))

#Seasonality in Larvae (Temperature)
LTopt<-27 # Optimal temperature
PrTempls~dgamma(10,10) # Linear term coefficient
PrTempls<- -PrTempls/(2*LTopt) # Quadratic term coefficient
slInv<-slInv0-PrTempls*LTopt/2 # Ensures that the maximum survival is mu.sl

#Growth rates Larvae
mu.lr<-0.0629
sd.lr<-0.0038/b3
lrmax<-min(1, mu.lr+b4*sd.lr)
lrmin<-max(0, mu.lr-b4*sd.lr)
lrr~dbeta(b1, b2)
lr<-lrmin+lrr*(lrmax-lrmin)
lrInv<-Log(lr/(1-lr))

```

```

# Temperature dependence of Larval growth rate
PrTempLg~dgamma(1,1000) #

#Growth rates pupae
mu.pr<-0.5222
sd.pr<-0.1347/b3
prmax<-min(1, mu.pr+b4*sd.pr)
prmin<-max(0, mu.pr-b4*sd.pr)
prr~dbeta(b1, b2)
pr<-prmin+prr*(prmax-prmin)

#Growth rates adult
mu.ar<- 0.2
sd.ar<-0.01/b3
armax<- min(1, mu.ar+b4*sd.ar) #1
armin<- max(0, mu.ar-b4*sd.ar) #6 days=0.1667
arr~dbeta(b1, b2)
ar<-armin+arr*(armax-armin)

#Growth rates blood-fed
mu.bfr<-0.25
sd.bfr<-0.1/b3
bfrmax<-min(1, mu.bfr+b4*sd.bfr)
bfrmin<-max(0, mu.bfr-b4*sd.bfr)
bfr~dbeta(b1, b2)
bfr<-bfrmin+bfr*(bfrmax-bfrmin)

#Growth rates gravid
mu.gr<-0.3333
sd.gr<-0.1/b3
grmax<-min(1, mu.gr+b4*sd.gr)
grmin<-max(0, mu.gr-b4*sd.gr)
grr~dbeta(b1, b2)
gr<-grmin+grr*(grmax-grmin)

#Number of eggs
mu.b<-80
sd.b<-20/b3
bmax<-mu.b+b4*sd.b
bmin<-max(0, mu.b-b4*sd.b)
br~dbeta(b1, b2)
breed<-bmin+br*(bmax-bmin)
bre0<-Log(breed)

#Effect of precipitation on Larvae
Pr_dd~dgamma(5.382, 46.4)

#Density dependence of Larvae at lag time 3 days rainfall
Pr_dd3~dbeta(7.2,0.8) # Upward-biased prior, towards 1

```

```

#data# blood_fedD, gravidD, adultD, prec, prec3, Temp, tmax, Ntr, efLev

#monitor# breed, se, sp, sa, sb, sg, sl, lr, pr, ar, bfr, gr, lambda, Pr_dd,
Pr_dd3, Ldd, ef1, ef0, precLE, precAE, precBE, precPE
#monitor# PrTempls, PrTemps, PrTemplg, PrTempa, PrTempas, cva
#monitor# eggs, larvae, pupae, adult, blood_fed, gravid
#monitor# spv, sgv, sav, sbv, lgv, lrInv, saInv, sgInv, slInv, sbInv, bre,
bre0
#monitor# adultd, blood_fedd, gravidd

#inits# Ldd

}" #End of the model loop ,

#Data
adultD<-rbind(po$adult, p1$adult)
blood_fedD<-rbind(po$blood_fed, p1$blood_fed)
gravidD<-rbind(po$gravid, p1$gravid)
prec<-rbind(po$Rainfall, p1$Rainfall)
prec3<-rbind(po$RainCuWeek, p1$RainCuWeek)

tmax<-365
Ntr<-2

# Weekly index
efLev<-c(rep(1:7, 52),1)

#Temperature
Temp<-rbind(po$Temp, p1$Temp)

#standard error
seAd<-rbind(po$seAd, p1$seAd)/1
seBf<-rbind(po$seBf, p1$seBf)/1
seGr<-rbind(po$seGr, p1$seGr)/1

##### 2. Model running #####
n.chains=6
Ldd<-list(chain1=c(0.01), chain2=c(0.03),
          chain3=c(0.5), chain4=c(0.05),
          chain5=c(0.01), chain6=c(0.02))

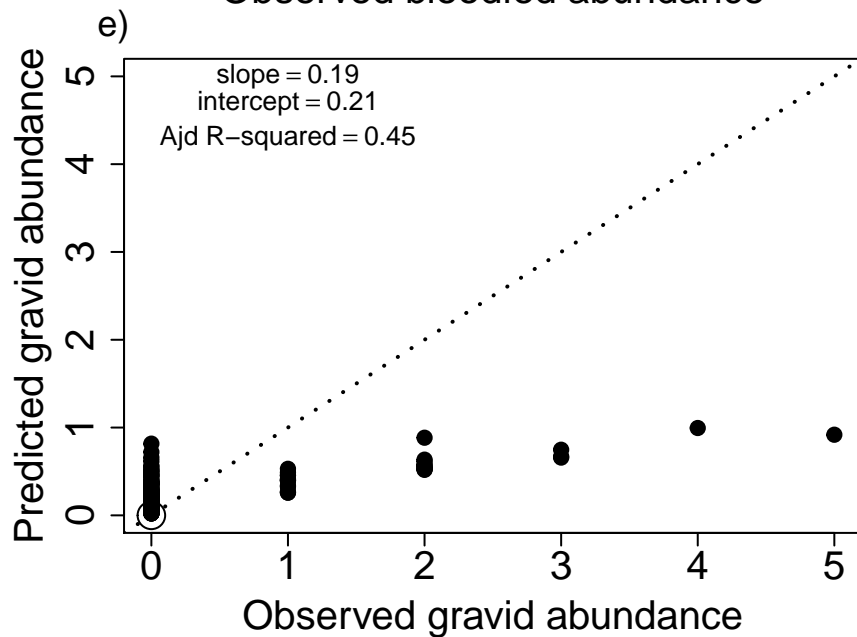
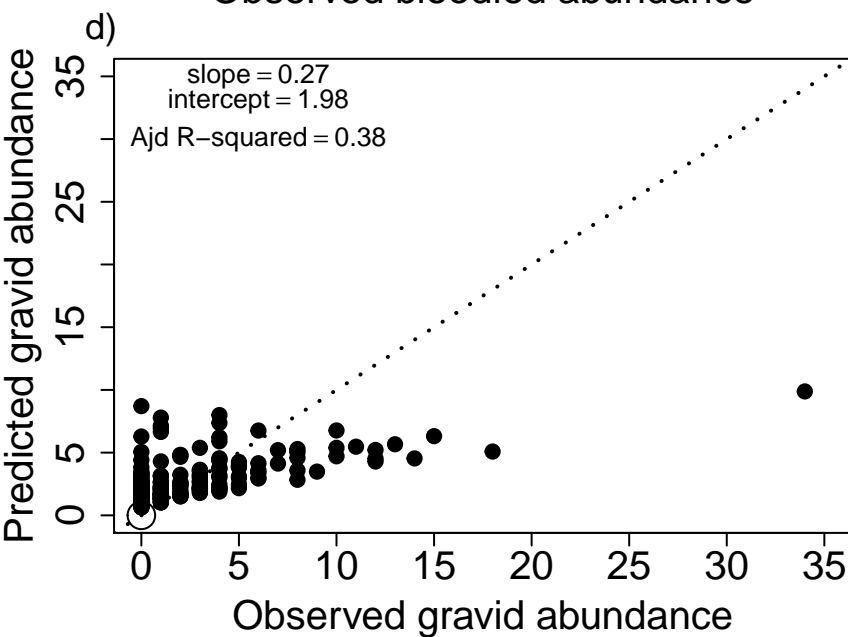
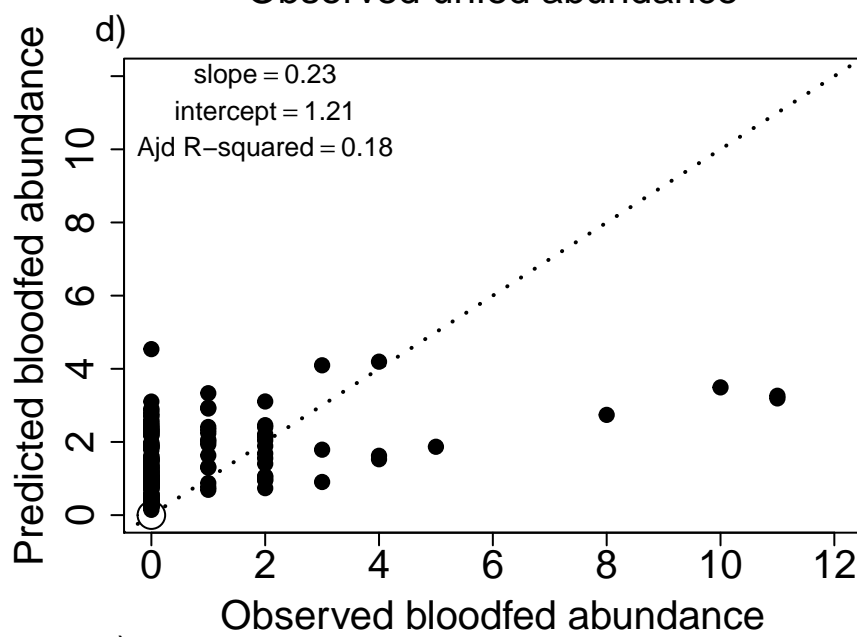
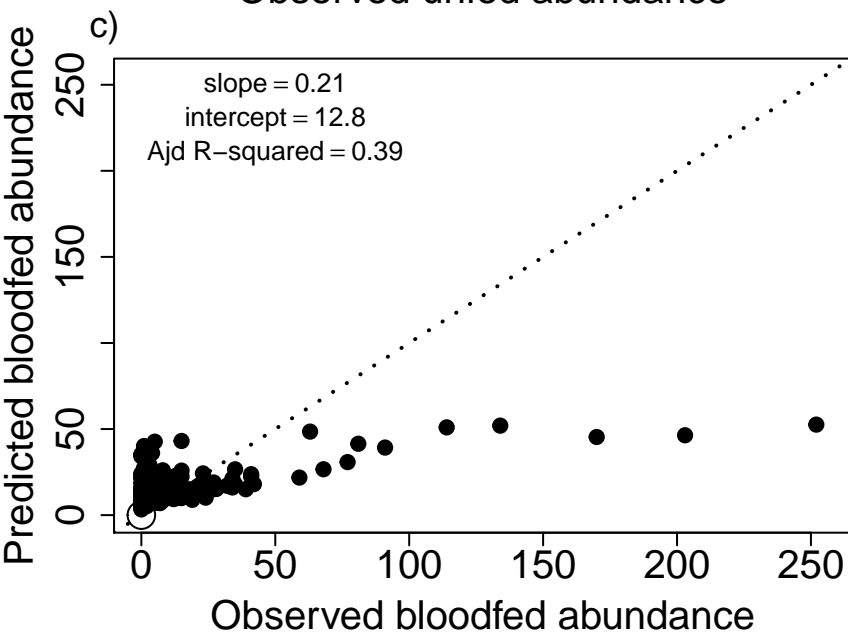
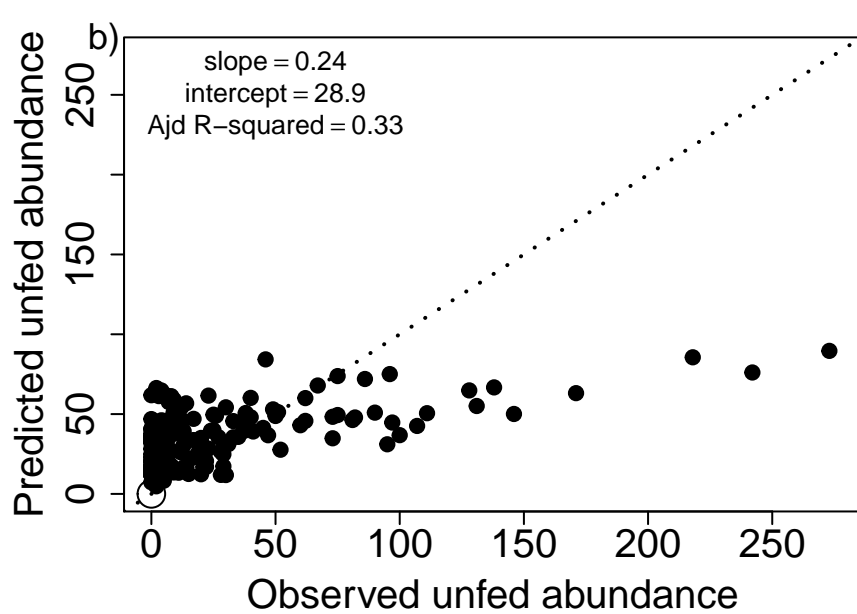
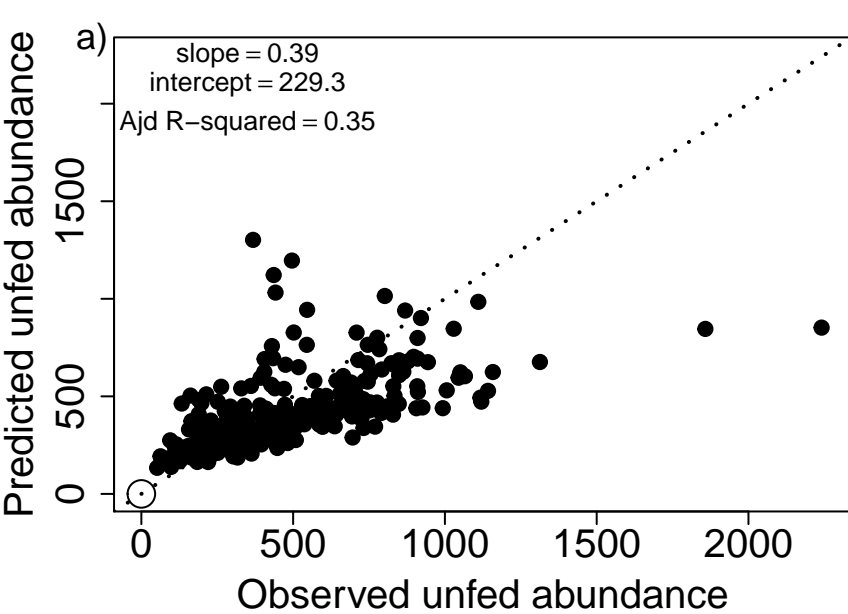
brn=100000 # Burn-in
spl=10000 # Sampling

results <- run.jags(popMod2, n.chains=n.chains, adapt = 1000,
                   burnin=brn, sample=spl, thin=10,
                   method = "parallel")

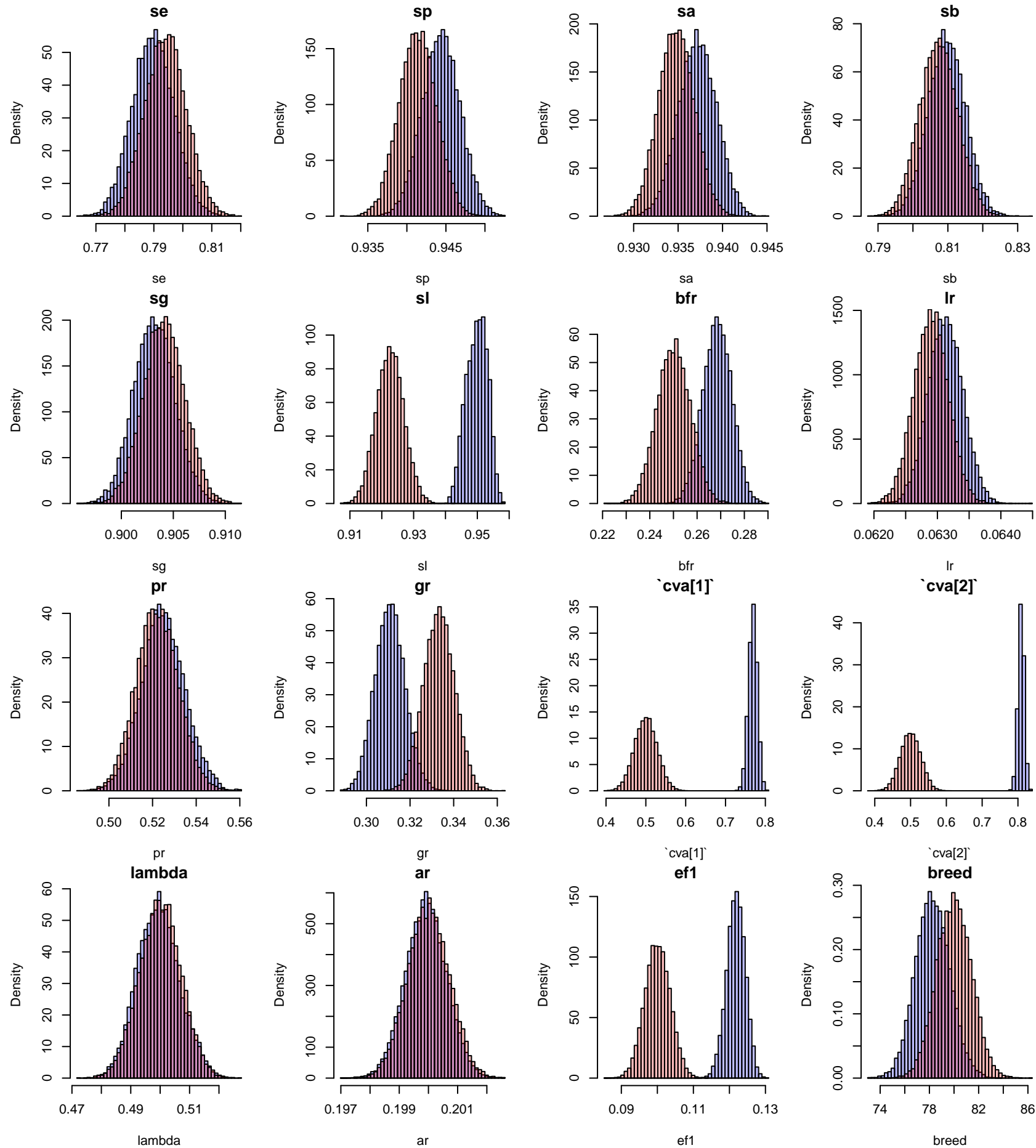
```



**Figure S2:** Goodness-of-fit: Observed versus predicted unfed, bloodfed and gravid densities across all populations. Adjusted R-squared, intercept and slope values are from a linear model of the predicted against observed values. Dotted lines correspond to 1:1 line. Left column (a,c,d) is data collected from June 2018 to May 2019 and right column (b,d,e) is data from Jan-Dec 2015. Grey area is the period with rainfall.



**Figure S3.1:** Prior (orange histogram) and posterior (blue histogram) distribution of the main baseline and observational parameters in the state-space model.



**Figure S3.2:** Prior (orange histogram) and posterior (blue histogram) distribution of the main environmental covariates parameters in the state-space model.

