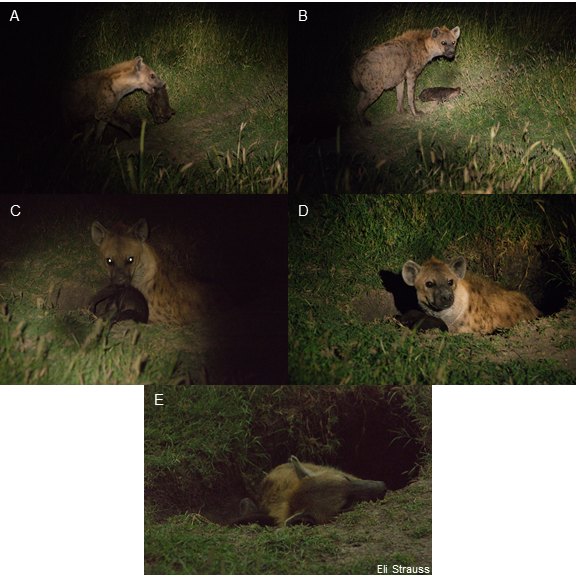
Supplemental Material for Brown et al.

## Photos of mother caring for deceased offspring

In this observation



## Model detail and diagnostic for moratlity ~ age at death

Here we used a multinomial model of mortality source as a function of age at death to understand the contribution of different mortality sources to overall mortality. This model was initialized with weak, uninformative priors, and three chains were run for 15000 iterations each (7500 warmup).

#### Model summary and diagnostic

# Priors  
prior\_summary(fit)

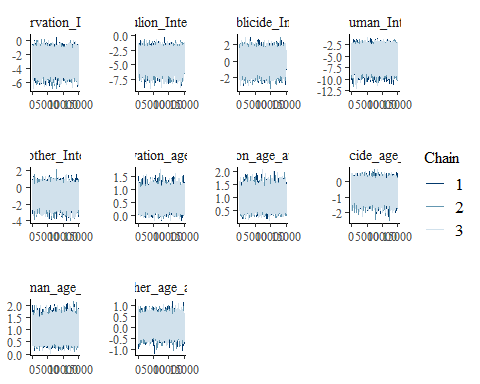
## prior class coef group resp dpar nlpar bound  
## normal(0,3) b muhuman   
## normal(0,3) b age\_at\_death muhuman   
## normal(0,3) b mulion   
## normal(0,3) b age\_at\_death mulion   
## normal(0,3) b muother   
## normal(0,3) b age\_at\_death muother   
## normal(0,3) b musiblicide   
## normal(0,3) b age\_at\_death musiblicide   
## normal(0,3) b mustarvation   
## normal(0,3) b age\_at\_death mustarvation   
## normal(0,3) Intercept muhuman   
## normal(0,3) Intercept mulion   
## normal(0,3) Intercept muother   
## normal(0,3) Intercept musiblicide   
## normal(0,3) Intercept mustarvation   
## source  
## default  
## (vectorized)  
## default  
## (vectorized)  
## default  
## (vectorized)  
## default  
## (vectorized)  
## default  
## (vectorized)  
## default  
## default  
## default  
## default  
## default

summary(fit)

## Family: multinomial   
## Links: mustarvation = logit; mulion = logit; musiblicide = logit; muhuman = logit; muother = logit   
## Formula: y | trials(1) ~ 1 + age\_at\_death   
## Data: known.mortality.mom.alive (Number of observations: 66)   
## Samples: 3 chains, each with iter = 30000; warmup = 15000; thin = 1;  
## total post-warmup samples = 45000  
##   
## Population-Level Effects:   
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS  
## mustarvation\_Intercept -2.86 0.89 -4.77 -1.24 1.00 38698  
## mulion\_Intercept -3.99 1.04 -6.20 -2.14 1.00 35174  
## musiblicide\_Intercept -0.12 0.71 -1.52 1.27 1.00 35245  
## muhuman\_Intercept -5.14 1.40 -8.18 -2.71 1.00 34516  
## muother\_Intercept -1.02 0.68 -2.40 0.28 1.00 40730  
## mustarvation\_age\_at\_death 0.61 0.22 0.20 1.08 1.00 23263  
## mulion\_age\_at\_death 0.93 0.23 0.52 1.41 1.00 22727  
## musiblicide\_age\_at\_death -0.50 0.38 -1.31 0.17 1.00 26268  
## muhuman\_age\_at\_death 0.95 0.26 0.47 1.50 1.00 23409  
## muother\_age\_at\_death 0.10 0.25 -0.40 0.57 1.00 24298  
## Tail\_ESS  
## mustarvation\_Intercept 29948  
## mulion\_Intercept 28205  
## musiblicide\_Intercept 34530  
## muhuman\_Intercept 26108  
## muother\_Intercept 34446  
## mustarvation\_age\_at\_death 25053  
## mulion\_age\_at\_death 24230  
## musiblicide\_age\_at\_death 24351  
## muhuman\_age\_at\_death 25258  
## muother\_age\_at\_death 27849  
##   
## Samples were drawn using sampling(NUTS). For each parameter, Bulk\_ESS  
## and Tail\_ESS are effective sample size measures, and Rhat is the potential  
## scale reduction factor on split chains (at convergence, Rhat = 1).

par(mfrow = c(3, 3))  
mcmc\_plot(fit, type = 'trace') ## Traceplots indicate convergence

## No divergences to plot.



rhat(fit)

## b\_mustarvation\_Intercept b\_mulion\_Intercept   
## 0.9999592 1.0000572   
## b\_musiblicide\_Intercept b\_muhuman\_Intercept   
## 0.9999475 1.0000153   
## b\_muother\_Intercept b\_mustarvation\_age\_at\_death   
## 1.0001175 1.0000540   
## b\_mulion\_age\_at\_death b\_musiblicide\_age\_at\_death   
## 1.0001042 1.0000290   
## b\_muhuman\_age\_at\_death b\_muother\_age\_at\_death   
## 1.0000967 1.0003780   
## lp\_\_   
## 1.0000808

## Model detail and diagnostic for prey density ~ mortality + (1|clan)

Here we built a mixed model of prey density in the month before death as a function of mortality source, including a random effect of clan. This model was initialized with weak, uninformative priors, and four chains were run for 2000 iterations each (1000 warmup).

#### Model summary and diagnostic

# Priors  
prior\_summary(prey\_mod)

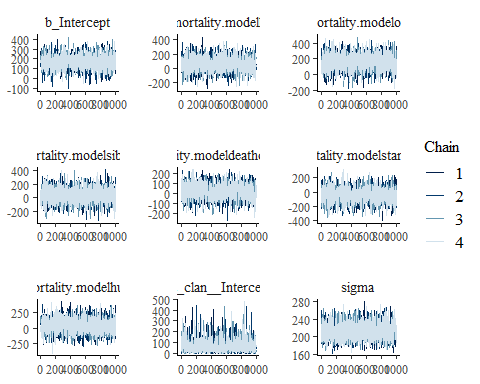
## prior class coef group resp  
## (flat) b   
## (flat) b mortality.modeldeathofmother   
## (flat) b mortality.modelhuman   
## (flat) b mortality.modellion   
## (flat) b mortality.modelother   
## (flat) b mortality.modelsiblicide   
## (flat) b mortality.modelstarvation   
## student\_t(3, 174.7, 147.4) Intercept   
## student\_t(3, 0, 147.4) sd   
## student\_t(3, 0, 147.4) sd clan   
## student\_t(3, 0, 147.4) sd Intercept clan   
## student\_t(3, 0, 147.4) sigma   
## dpar nlpar bound source  
## default  
## (vectorized)  
## (vectorized)  
## (vectorized)  
## (vectorized)  
## (vectorized)  
## (vectorized)  
## default  
## default  
## (vectorized)  
## (vectorized)  
## default

summary(prey\_mod)

## Family: gaussian   
## Links: mu = identity; sigma = identity   
## Formula: prey\_density ~ 1 + mortality.model + (1 | clan)   
## Data: hypothesis.test.dataset[!is.na(hypothesis.test.dat (Number of observations: 85)   
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;  
## total post-warmup samples = 4000  
##   
## Group-Level Effects:   
## ~clan (Number of levels: 4)   
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS  
## sd(Intercept) 63.41 56.85 2.27 205.37 1.00 1297 1630  
##   
## Population-Level Effects:   
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS  
## Intercept 171.48 65.45 34.25 298.39 1.00 1718  
## mortality.modellion 65.63 93.79 -120.08 250.54 1.00 1893  
## mortality.modelother 155.97 94.55 -28.44 339.86 1.00 1954  
## mortality.modelsiblicide 43.91 102.28 -156.20 243.23 1.00 2104  
## mortality.modeldeathofmother 18.43 71.05 -117.15 156.03 1.00 1723  
## mortality.modelstarvation -35.60 96.24 -234.03 152.57 1.00 2162  
## mortality.modelhuman 39.37 111.29 -179.72 252.16 1.00 2344  
## Tail\_ESS  
## Intercept 1569  
## mortality.modellion 2545  
## mortality.modelother 2557  
## mortality.modelsiblicide 2629  
## mortality.modeldeathofmother 2339  
## mortality.modelstarvation 2096  
## mortality.modelhuman 2476  
##   
## Family Specific Parameters:   
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS  
## sigma 212.48 17.12 181.78 249.06 1.00 3416 2852  
##   
## Samples were drawn using sampling(NUTS). For each parameter, Bulk\_ESS  
## and Tail\_ESS are effective sample size measures, and Rhat is the potential  
## scale reduction factor on split chains (at convergence, Rhat = 1).

par(mfrow = c(3, 3))  
mcmc\_plot(prey\_mod, type = 'trace') ## Traceplots indicate convergence

## No divergences to plot.



rhat(prey\_mod)

## b\_Intercept b\_mortality.modellion   
## 1.0007226 1.0003561   
## b\_mortality.modelother b\_mortality.modelsiblicide   
## 0.9995397 1.0009362   
## b\_mortality.modeldeathofmother b\_mortality.modelstarvation   
## 1.0000562 0.9997458   
## b\_mortality.modelhuman sd\_clan\_\_Intercept   
## 0.9999478 1.0017845   
## sigma Intercept   
## 0.9997444 1.0008370   
## r\_clan[happy.zebra,Intercept] r\_clan[serena.n,Intercept]   
## 0.9999492 0.9999367   
## r\_clan[serena.s,Intercept] r\_clan[talek,Intercept]   
## 1.0030681 1.0009977   
## lp\_\_ z\_1[1,1]   
## 1.0009693 0.9996342   
## z\_1[1,2] z\_1[1,3]   
## 1.0002753 1.0019428   
## z\_1[1,4]   
## 1.0002476

## Model detail and diagnostic for cub density ~ mortality + (1|clan)

Here we built a mixed model of prey density in the month before death as a function of mortality source, including a random effect of clan. This model was initialized with weak, uninformative priors, and four chains were run for 2000 iterations each (1000 warmup).

#### Model summary and diagnostic

# Priors  
prior\_summary(cub\_density\_mod)

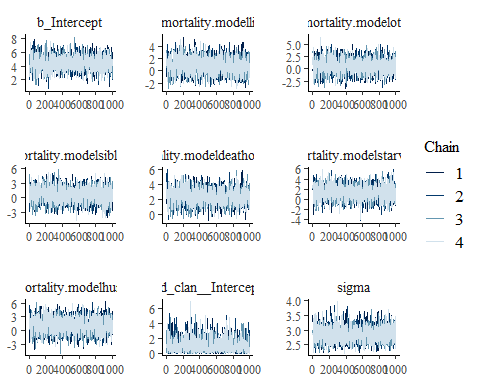
## prior class coef group resp dpar  
## (flat) b   
## (flat) b mortality.modeldeathofmother   
## (flat) b mortality.modelhuman   
## (flat) b mortality.modellion   
## (flat) b mortality.modelother   
## (flat) b mortality.modelsiblicide   
## (flat) b mortality.modelstarvation   
## student\_t(3, 5.3, 2.8) Intercept   
## student\_t(3, 0, 2.8) sd   
## student\_t(3, 0, 2.8) sd clan   
## student\_t(3, 0, 2.8) sd Intercept clan   
## student\_t(3, 0, 2.8) sigma   
## nlpar bound source  
## default  
## (vectorized)  
## (vectorized)  
## (vectorized)  
## (vectorized)  
## (vectorized)  
## (vectorized)  
## default  
## default  
## (vectorized)  
## (vectorized)  
## default

summary(cub\_density\_mod)

## Family: gaussian   
## Links: mu = identity; sigma = identity   
## Formula: cub\_associates ~ 1 + mortality.model + (1 | clan)   
## Data: hypothesis.test.dataset[!is.na(hypothesis.test.dat (Number of observations: 80)   
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;  
## total post-warmup samples = 4000  
##   
## Group-Level Effects:   
## ~clan (Number of levels: 4)   
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS  
## sd(Intercept) 0.90 0.80 0.03 2.98 1.00 1349 1935  
##   
## Population-Level Effects:   
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS  
## Intercept 4.49 0.96 2.54 6.47 1.00 1603  
## mortality.modellion 0.88 1.24 -1.59 3.33 1.00 1910  
## mortality.modelother 0.60 1.40 -2.20 3.39 1.00 1938  
## mortality.modelsiblicide 0.58 1.45 -2.27 3.46 1.00 2228  
## mortality.modeldeathofmother 2.38 0.99 0.46 4.34 1.00 1637  
## mortality.modelstarvation 1.34 1.32 -1.15 3.96 1.00 1990  
## mortality.modelhuman 1.05 1.60 -2.05 4.25 1.00 2267  
## Tail\_ESS  
## Intercept 1988  
## mortality.modellion 2270  
## mortality.modelother 2594  
## mortality.modelsiblicide 2562  
## mortality.modeldeathofmother 2273  
## mortality.modelstarvation 2691  
## mortality.modelhuman 2565  
##   
## Family Specific Parameters:   
## Estimate Est.Error l-95% CI u-95% CI Rhat Bulk\_ESS Tail\_ESS  
## sigma 2.86 0.24 2.43 3.36 1.00 3083 2692  
##   
## Samples were drawn using sampling(NUTS). For each parameter, Bulk\_ESS  
## and Tail\_ESS are effective sample size measures, and Rhat is the potential  
## scale reduction factor on split chains (at convergence, Rhat = 1).

par(mfrow = c(3, 3))  
mcmc\_plot(cub\_density\_mod, type = 'trace') ## Traceplots indicate convergence

## No divergences to plot.



rhat(cub\_density\_mod)

## b\_Intercept b\_mortality.modellion   
## 1.003904 1.001073   
## b\_mortality.modelother b\_mortality.modelsiblicide   
## 1.001814 1.001838   
## b\_mortality.modeldeathofmother b\_mortality.modelstarvation   
## 1.001989 1.002282   
## b\_mortality.modelhuman sd\_clan\_\_Intercept   
## 1.000776 1.002827   
## sigma r\_clan[happy.zebra,Intercept]   
## 1.000621 1.001415   
## r\_clan[serena.n,Intercept] r\_clan[serena.s,Intercept]   
## 1.002030 1.001213   
## r\_clan[talek,Intercept] lp\_\_   
## 1.001291 1.002071