

# Generalized linear mixed effects model

## Sow culling time

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# Outline

- Mixed effect Poisson regression
  - Modeling
  - Estimation via Stan
  - Posterior
- Decision making
  - Maximize utility

# Sow culling time

From Caitlyn Abell:

*I have attached the data file with 2,868 records from one farm. The contemporary group (cg) is farm, year and season. There are columns for number born alive (nba), number born dead (nbd), and parity. One thing you could look at would be improvement over time or differences of performance between the parities [litters]. I think determining the optimal culling time for a sow given her past history would be interesting.*

Primary question of interest: when should a sow be removed from breeding?

```
d = read.table("Ch16b-farm62.txt", header=T)
d$cg = d$farm = d$yearmo = d$nbd = d$dam = NULL
d = plyr::rename(d, c("sire"="grandsire")) |>
  mutate(sowid = factor(sowid), grandsire = factor(grandsire))
```

```
head(d)
```

	sowid	nba	parity	grandsire
1	985120010234800	3	1	C61LW4846
2	985120011536089	11	1	C60LX1975
3	985120011536089	6	2	C60LX1975
4	985120011537054	8	1	C63LW10719
5	985120011537054	11	2	C63LW10719
6	985120011537120	12	1	C60LX3542

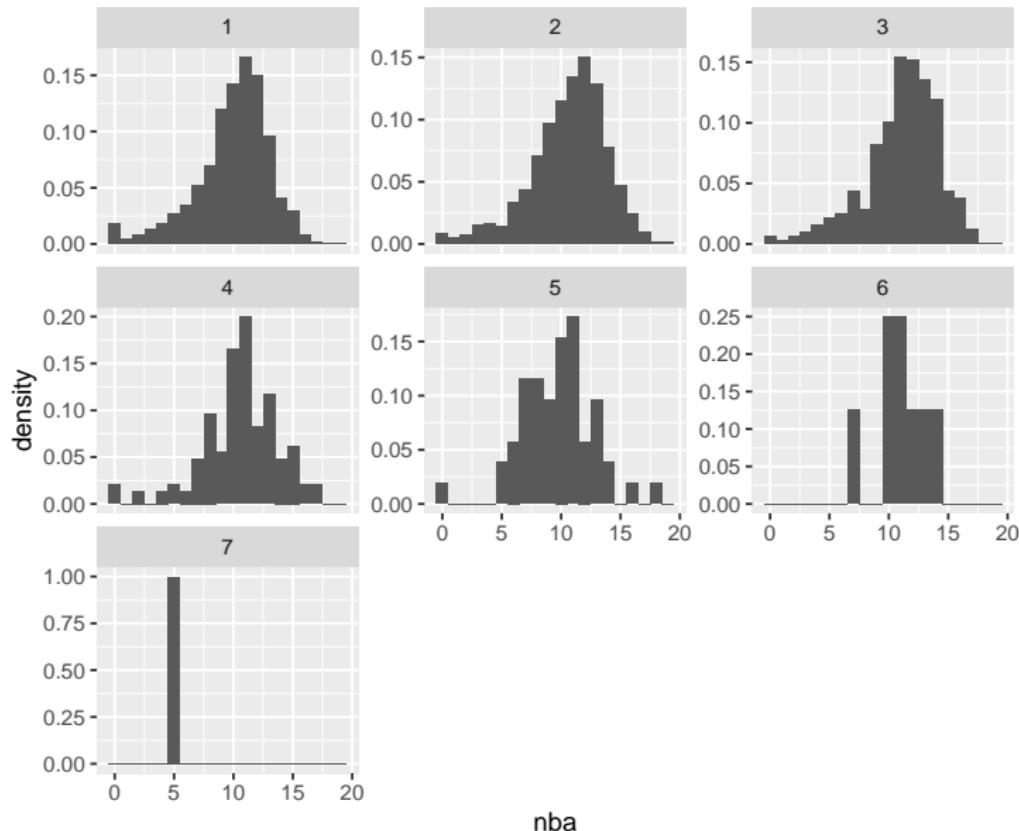
```
summary(d)
```

	sowid	nba	parity	grandsire
985152000271505:	7	Min. : 0.00	Min. :1.000	103086 : 238
985120011545841:	6	1st Qu.: 9.00	1st Qu.:1.000	376475 : 105
985120025398712:	6	Median :11.00	Median :1.000	514976 : 91
985152000271655:	6	Mean :10.28	Mean :1.714	572703 : 87
985152002194887:	6	3rd Qu.:12.00	3rd Qu.:2.000	019800 : 84
985152002429483:	6	Max. :19.00	Max. :7.000	376770 : 79
(Other)	:2831			(Other):2184

```
dim(d); nlevels(d$sowid); nlevels(d$grandsire)
```

```
[1] 2868     4
[1] 1621
[1] 182
```

1	2	3	4	5	6	7
1621	724	317	145	52	8	1



# Model

Let  $y_i$  be the number born alive for the  $i^{th}$  litter. Assume

$$\begin{aligned} y_i &\stackrel{ind}{\sim} Po(e^{\mu_i}) & i = 1, \dots, n \\ \mu_i &= \rho_p[i] + \alpha_{s[i]} + \beta_{g[i]} \end{aligned}$$

where

- $p[i]$  is the parity for the  $i^{th}$  litter,
- $s[i]$  is the sow for the  $i^{th}$  litter, and
- $g[i]$  is the grandsire for the  $i^{th}$  litter.

The hierarchical structure treats  $\alpha$  and  $\beta$  as random effects, i.e.

$$\begin{aligned} \alpha_s &\stackrel{iid}{\sim} N(0, \sigma_\alpha^2) & s = 1, \dots, n_{sows} \\ \beta_g &\stackrel{iid}{\sim} N(0, \sigma_\beta^2) & g = 1, \dots, n_{grandssires}. \end{aligned}$$

The prior is

$$p(\rho_1, \dots, \rho_6, \sigma_\alpha, \sigma_\beta) \propto Ca^+(\sigma_\alpha; 0, 0.1) Ca^+(\sigma_\beta; 0, 0.1)$$

```
model = "
data {
    int<lower=1> n;
    int<lower=1> np;
    int<lower=1> ns;
    int<lower=1> ng;
    int<lower=0> y[n];
    int<lower=1, upper=np> parity[n];
    int<lower=1, upper=ns> sow[n];
    int<lower=1, upper=ng> grandsire[n];
}

parameters {
    real rho[np];      // implicit prior over whole real line
    real alpha[ns];
    real beta[ng];
    real<lower=0> sigma_alpha;
    real<lower=0> sigma_beta;
}

model {
    for (i in 1:n) {
        y[i] ~ poisson(exp(rho[parity[i]] + alpha[sow[i]] + beta[grandsire[i]]));
    }

    // Random effects
    alpha ~ normal(0, sigma_alpha);
    beta ~ normal(0, sigma_beta);

    // Priors
    sigma_alpha ~ cauchy(0,0.1);
    sigma_beta ~ cauchy(0,0.1);
}"
```

```

d = d[d$parity!=7,]
dat = list(y = d$nba,
           parity = d$parity,
           sow = as.numeric(d$sowid),
           grandsire = as.numeric(d$grandsire))
dat$n = length(dat$y)
dat$np = max(dat$parity)
dat$ns = max(dat$sow)
dat$ng = max(dat$grandsire)

time = system.time(r <- sampling(object = m,
                                    data = dat,
                                    pars = c("rho", "alpha", "beta", "sigma_alpha", "sigma_beta"),
                                    iter = 10000,
                                    thin = 5))

```

SAMPLING FOR MODEL 'anon\_model' NOW (CHAIN 1).

Chain 1:

Chain 1: Gradient evaluation took 0.000235 seconds

Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 2.35 seconds.

Chain 1: Adjust your expectations accordingly!

Chain 1:

Chain 1:

Chain 1: Iteration: 1 / 10000 [ 0%] (Warmup)

Chain 1: Iteration: 1000 / 10000 [ 10%] (Warmup)

Chain 1: Iteration: 2000 / 10000 [ 20%] (Warmup)

Chain 1: Iteration: 3000 / 10000 [ 30%] (Warmup)

Chain 1: Iteration: 4000 / 10000 [ 40%] (Warmup)

Chain 1: Iteration: 5000 / 10000 [ 50%] (Warmup)

Chain 1: Iteration: 5001 / 10000 [ 50%] (Sampling)

Chain 1: Iteration: 6000 / 10000 [ 60%] (Sampling)

Chain 1: Iteration: 7000 / 10000 [ 70%] (Sampling)

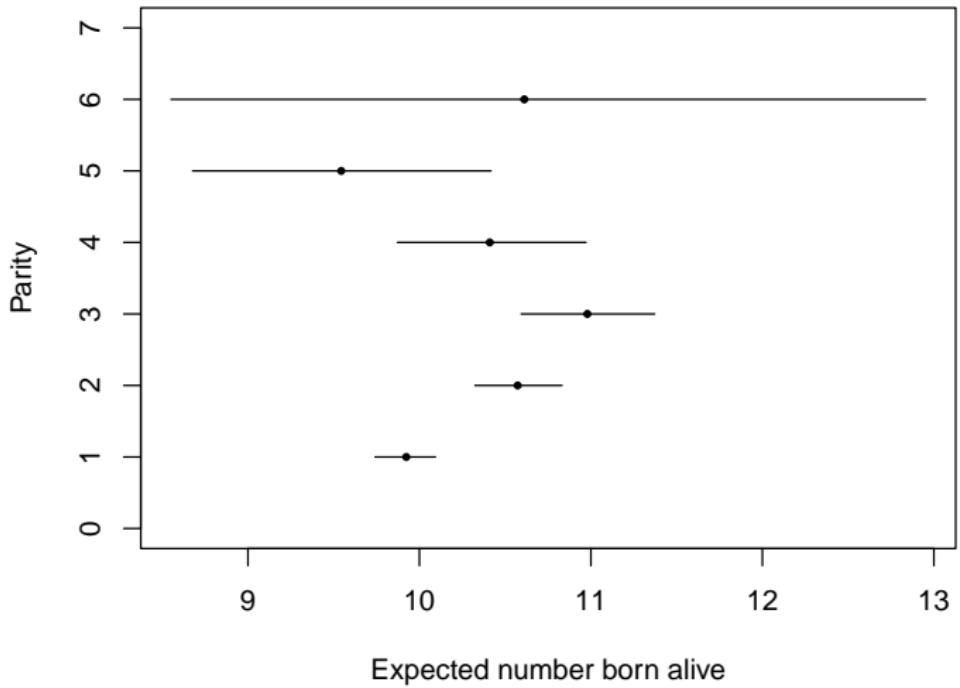
Chain 1: Iteration: 8000 / 10000 [ 80%] (Sampling)

Chain 1: Iteration: 9000 / 10000 [ 90%] (Sampling)

# Run time and summary

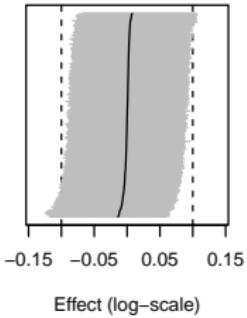
```
time  
user  system elapsed  
517.128  3.807 523.881
```

```
s = summary(r)$summary
```

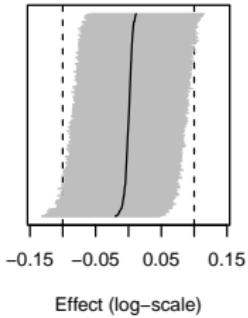


**Max parity 1**

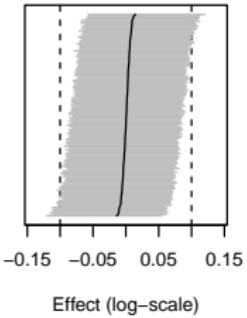
Ordered dams

**Max parity 2**

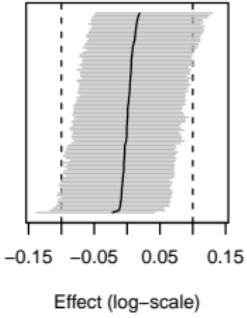
Ordered dams

**Max parity 3**

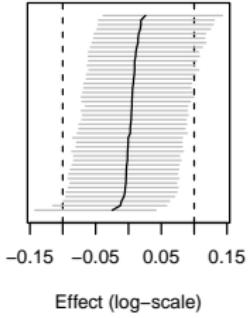
Ordered dams

**Max parity 4**

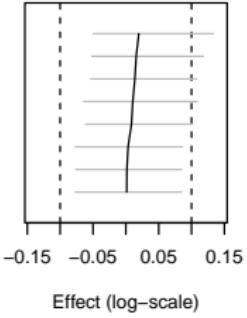
Ordered dams

**Max parity 5**

Ordered dams

**Max parity 6**

Ordered dams



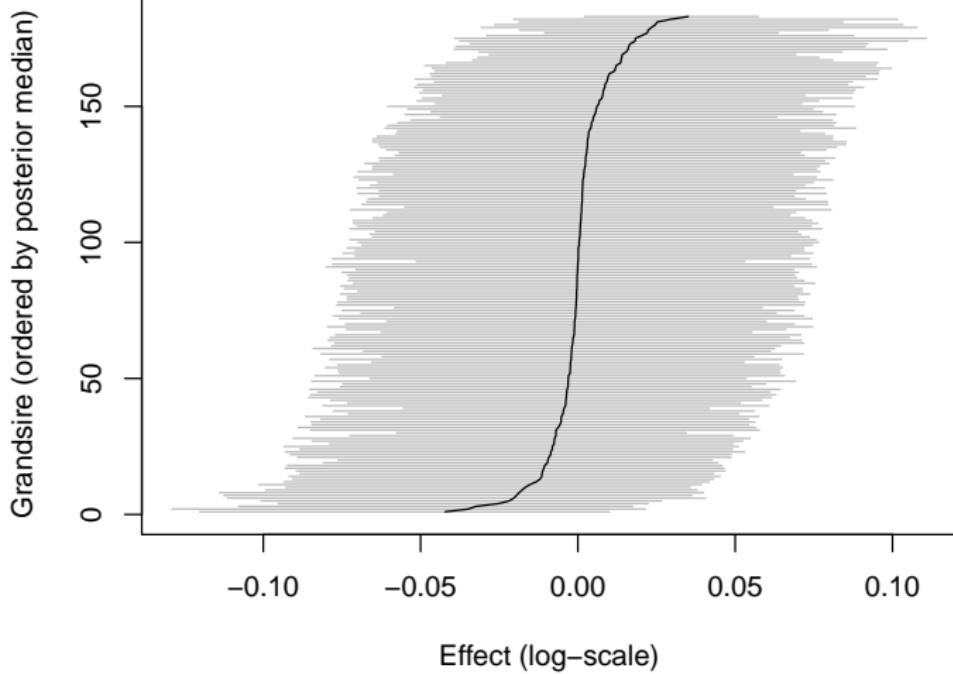
## Best and worst performing sows with max parity 4 and 5

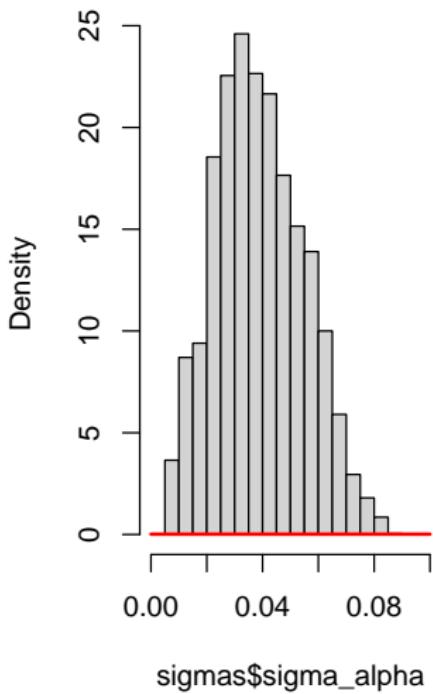
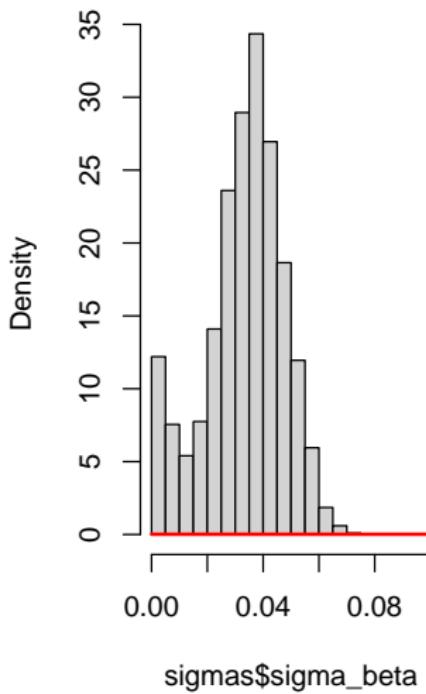
NBA for best and worst performing sows with max parity of 4

	sowid	1	2	3	4
1	985152000271823	7	6	5	5
2	985152000856299	15	17	13	13

NBA for best and worst performing sows with max parity of 5

	sowid	1	2	3	4	5
1	985120012076420	13	14	15	14	18
2	985120026637130	1	7	2	10	10



**Sow sd****Grandsire sd**

# Culling time

Primary question of interest: when should a sow be removed from breeding?

Who is expected to have more number born alive:

- a current sow  $s$
- a new sow

Current sow (for parity  $p$  and average grandsire):

$$\begin{aligned} E[\tilde{y}_s|y] &= E[E[\tilde{y}_s|\rho, \alpha, \beta]|y] \\ &= E[e^{\rho_p + \alpha_s}|y] \\ &\approx \frac{1}{K} \sum_{k=1}^K e^{\rho_p^{(k)} + \alpha_s^{(k)}} \end{aligned}$$

New sow (for parity 1 and average grandsire):

$$E[\tilde{y}_{new}|y] \approx \frac{1}{K} \sum_{k=1}^K e^{\rho_1^{(k)} + \alpha_{new}^{(k)}}$$

where  $\alpha_{new}^{(k)} \sim N(0, [\sigma_\alpha^{(k)}]^2)$ .

## Simulated answer

For MCMC iterations  $k = 1, \dots, K$ ,

1. Obtain the  $k^{th}$  joint draw from the posterior for  $\rho_p^{(k)}$ ,  $\rho_1^{(k)}$ ,  $\alpha_s^{(k)}$ , and  $\sigma_\alpha^{(k)}$ .
2. Calculate  $\mu_s^{(k)} = e^{\rho_p^{(k)} + \alpha_s^{(k)}}$ .
3. Calculate  $\mu_{new}^{(k)} = e^{\rho_p^{(k)} + \alpha_{new}^{(k)}}$  where  $\alpha_{new}^{(k)} \sim N\left(0, \left[\sigma_\alpha^{(k)}\right]^2\right)$ .
4. Calculate  $\delta^{(k)} = \mu_{new}^{(k)} - \mu_s^{(k)}$ .

So  $\delta^{(k)}$  is a realization of the expected difference in the number born alive between a new sow and current sow  $d$ .

```
sow_summary <- d |>
  group_by(sowid) |>
  summarize(
    max_parity = max(parity),
    sum_nba    = sum(nba),
    mean_nba   = sum_nba/max_parity
  )

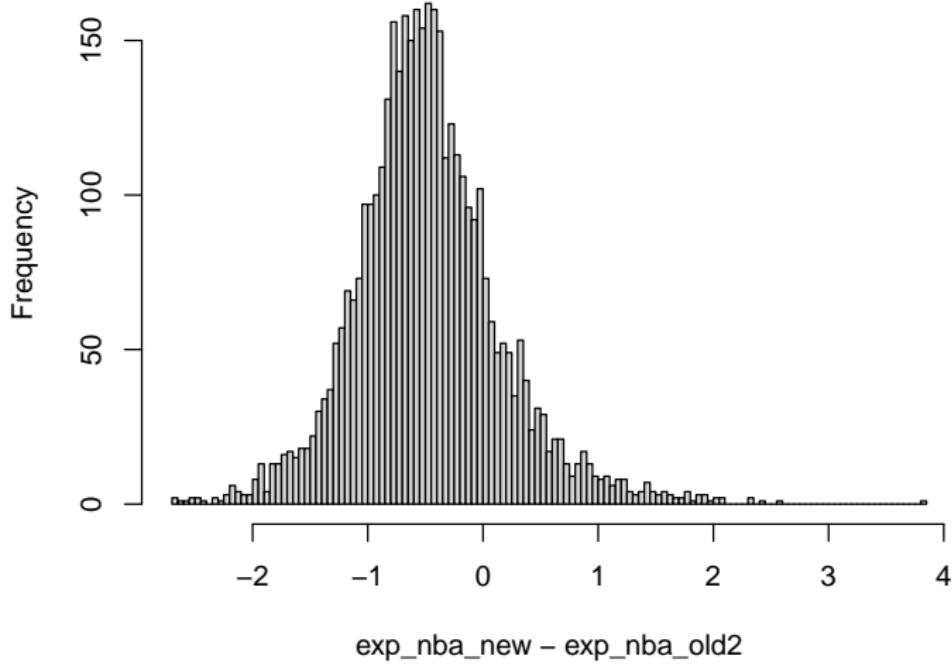
# Find a sow with 0 born alive in parity 1 (and no other data)
sow = which(sow_summary$max_parity==1 & sow_summary$sum_nba==0)[1]

# Expected nba in parity 2 for sow with 0 born alive in first parity
alphas <- extract(r, "alpha")$alpha
rhos   <- extract(r, "rho")$rho
exp_nba_old2 <- exp(rhos[, 2] + alphas[, sow])

# Expected nba in parity 1 for random sow
alpha_new   <- rnorm(nrow(rhos), 0, sigmas$sigma_alpha)
exp_nba_new <- exp(rhos[, 1] + alpha_new)
```

```
hist(exp_nba_new - exp_nba_old2, 100, main=expression(paste(delta, " (new-old)")))
```

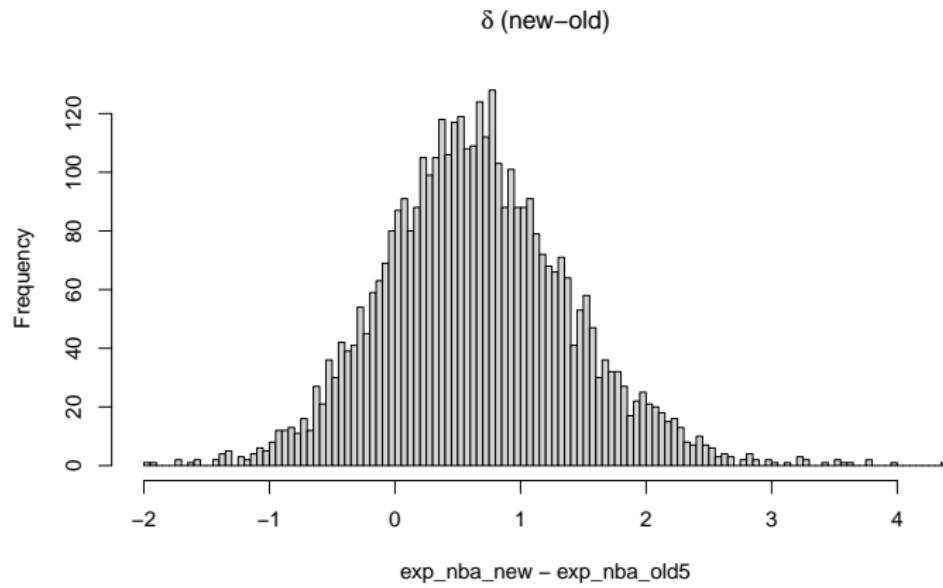
$\delta$  (new-old)



```
# Replace sow with 23 born alive after 4 parities?
sow = which(sow_summary$max_parity==4 & sow_summary$sum_nba==23) [1]

# Expected nba in parity 3 for sow with 0 born alive in first parity
exp_nba_old5 = exp(rhos[,5] + alphas[,sow])

# Difference in expected nba
hist(exp_nba_new-exp_nba_old5, 100, main=expression(paste(delta, " (new-old)")))
```



# Estimated number born alive

Estimates of the expected number born alive for each sow with Monte Carlo uncertainty:

```
rbind(
  new = as.data.frame(mcse(exp_nba_new)),
  old2 = as.data.frame(mcse(exp_nba_old2)),
  old5 = as.data.frame(mcse(exp_nba_old5))
) |> round(2)

      est    se
new   9.93 0.01
old2 10.41 0.01
old5  9.28 0.01
```

Estimates of the expected difference with Monte Carlo uncertainty:

```
rbind(
  `parity2 - new` = as.data.frame(mcse(exp_nba_old2 - exp_nba_new)),
  `parity5 - new` = as.data.frame(mcse(exp_nba_old5 - exp_nba_new)),
  `parity5 - parity2` = as.data.frame(mcse(exp_nba_old5 - exp_nba_old2))) |>
  round(2)

      est    se
parity2 - new     0.48 0.01
parity5 - new    -0.65 0.01
parity5 - parity2 -1.13 0.01
```

## Utility functions

Suppose the only cost difference is in the number born alive, then  
 $U(\tilde{y}_i) = u_1 \tilde{y}_i$  and want

$$\max_{i \in \{d, new\}} E[U(\tilde{y}_i)|y]$$

or, equivalently, pick *new* if

$$E[U(\tilde{y}_{new})|y] - E[U(\tilde{y}_s)|y] > 0$$

But, since expectation is a linear operator,

$$\begin{aligned} E[U(\tilde{y}_{new})|y] - E[U(\tilde{y}_s)|y] &= E[U(\tilde{y}_{new}) - U(\tilde{y}_s)|y] \\ &= E[u_1 \tilde{y}_{new} - u_1 \tilde{y}_s | y] \\ &= u_1 E[\tilde{y}_{new} | y] - u_1 E[\tilde{y}_s | y] \\ &= u_1 E[\delta | y] \end{aligned}$$

So  $u_1$  just scales our posterior expectation for the difference.

## Utility functions

Suppose the utility function also involves moving a new sow in, then  $U(\tilde{y}_i) = u_1 \tilde{y}_i - u_2 I(i = \text{new})$  and you should pick *new* if

$$E[U(\tilde{y}_{\text{new}})|y] - E[U(\tilde{y}_s)|y] = u_1 E[\delta|y] - u_2 > 0.$$

Now suppose an older sow (or this particular sow) needs more medications, then  $U(\tilde{y}_i) = u_1 \tilde{y}_i - u_2 I(i = \text{new}) - u_3 I(i = d)$  and you should pick *new* if

$$E[U(\tilde{y}_{\text{new}})|y] - E[U(\tilde{y}_s)|y] = u_1 E[\delta|y] - u_2 + u_3 > 0.$$

Now, the decision will depend on the individual utilities  $u_1$ ,  $u_2$ , and  $u_3$ .

## Cost functions

So far, all cost functions have been linear in  $\tilde{y}$ , but suppose  $U(\tilde{y}_i)$  is a complicated function of  $\tilde{y}_i$ . Then to pick *new*, we want

$$E[U(\tilde{y}_{\text{new}})|y] - E[U(\tilde{y}_s)|y] > 0$$

This may be analytically intractable, but we can easily simulate from it.  
Suppose

$$U(\tilde{y}_i) = \tilde{y}_i + 0.1(\tilde{y}_i - 10)\mathbf{I}(\tilde{y}_i > 10) - 0.2\mathbf{I}(i = \text{new}).$$

## New data realizations

To estimate these utility functions, we will need predictive simulations  $\tilde{y}$  for the old sow and the new sow.

We can obtain these simulations via

- Old sow (parity  $p$  and average grand-sire):

$$\tilde{y}_s^{(k)} \sim Po\left(e^{\rho_p^{(k)} + \alpha_s^{(k)}}\right)$$

- New sow (average grand-sire):

$$\tilde{y}_{new}^{(k)} \sim Po\left(e^{\rho_1^{(k)} + \alpha_{new}^{(k)}}\right)$$

where  $e^{\rho_p^{(k)} + \alpha_s^{(k)}}$  and  $e^{\rho_1^{(k)} + \alpha_{new}^{(k)}}$  are simulations previously drawn.

# Summary

Lecture demonstrated

- mixed effect Poisson regression model,
- implementation in Stan,
- posterior summaries, and
- using the analysis to make a decision regarding sow culling time.