

# QPAD offset correction factor calculation

Peter Solymos

April 4, 2025

In QPAD, we have the expected value of the counts ( $Y$ ) defined as  $E[Y] = DApq$ . We use the following settings for density ( $D$ ) and the detectability correction ( $Apq$ ). The *old* (biased due to TZ offset issue) and *new* (fixed) corrections are used here as follows:

```
D <- 1
Apq_old <- 0.94
Apq_new <- 1.12
```

These numbers were taken from the actual offsets (mean of the means) from the BAM data.

Let's assume that the *new* correction is right, so we simulate under:

```
n <- 1000
Y <- rpois(n, lambda = D * Apq_new)
```

Now we estimate density as if our detectability offset estimate would be correct. We can see that the estimate of  $D$  is correct, as expected:

```
off_new <- log(rep(Apq_new, n))
m1 <- glm(Y ~ 1 + offset(off_new), family=poisson)
(D_new <- exp(coef(m1)))
```

```
## (Intercept)
##      0.9696429
```

Now what happens if we use the biased offset estimate?  $D$  is overestimated:

```
off_old <- log(rep(Apq_old, n))
m2 <- glm(Y ~ 1 + offset(off_old), family=poisson)
(D_old <- exp(coef(m2)))
```

```
## (Intercept)
##      1.155319
```

The question now: how can we correct the *old* density estimate using the *old* and *new* offsets without having to re-estimate density using the *new* offsets.

$Y = D_{old}C_{old}$  and  $Y = D_{new}C_{new}$ , therefore  $D_{new} = D_{old}C_{old}/C_{new}$ . On the log scale:  $\log(D_{new}) = \log(D_{old}) + \log(C_{old}) - \log(C_{new})$ .

```
adj <- log(Apq_old) - log(Apq_new)
exp(log(D_old) + adj)
```

```
## (Intercept)
## 0.9696429
```

Which is the same as:

```
alpha <- exp(adj)
D_old * alpha
```

```
## (Intercept)
## 0.9696429
```

Applying the adjustment to tabular population summaries:

- calculate the exponentiated adjustment value as  $\alpha = C_{old}/C_{new}$
- apply the  $\alpha$  value on density so that  $D_{adj} = D_{unadjusted}\alpha$
- calculate  $N_{adj}$  as  $D_{adj}A$
- do this for every spatial unit using the adjustment that applies in that particular region (the BCR subunit that the region is nested inside)
- same applies to land cover classes within that BCR subunit
- note that this needs to be repeated for all impacted species independently because the corrections vary by species

For maps:

- use  $D_{adj} = D_{unadjusted}\alpha$  at the pixel level
- for this we can make a raster with adjustment values added for the cells matching the cell's BCR subunit designation
- take the adjustment layer and multiply with the density layer
- note that this needs to be repeated for all impacted species independently because the corrections vary by species