SUPPLEMENTAL INFORMATION

USE OF RESTORED URBAN HABITAT BY LONG-TOED SALAMANDERS (*AMBYSTOMA MACRODACTYLUM*) IN SEATTLE, WASHINGTON, USA

JULIANNA C. HOZA AND JONATHAN D. BAKKER

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Spatial.—Surveys in the Union Bay Natural Area (UBNA) found American Bullfrogs (*Lithobates catesbeianus*) as well as Long-toed Salamanders (*Ambystoma macrodactylum*). American Bullfrogs could pose a significant threat to native species such as Long-toed Salamanders if they were able to breed in the same ponds that the salamanders primarily use. However, permanent ponds are necessary for American Bullfrog breeding because tadpoles take two years to mature before metamorphosing (Corkran and Thoms 2006). Long-toed Salamanders, on the other hand, can breed in vernal ponds such as Shoveler's Pond and the Forested Creek, because their larvae metamorphose in one season (Corkran and Thoms 2006). This means that Long-toed Salamanders primarily use ponds on the east side of UBNA while American Bullfrogs primarily use ponds on the west side of UBNA (Fig. S1). This could be because the east side of UBNA has more ponds that are permanent such as the E5 Parking Area North Pond and is closer to Lake Washington and the University Canal. This separation could allow Long-toed Salamanders and American Bullfrogs to coexist within the same park, but it could also exclude other native amphibian species that would overlap with American Bullfrog breeding territory to a greater extent. For example, Northwestern Salamanders (*Ambystoma gracile*) and Northern Red-legged Frogs (*Rana aurora*) are not present in UBNA. These species breed in permanent ponds, but UBNA's permanent ponds are occupied by American Bullfrogs, which may outcompete native amphibian species that require permanent ponds (like Northwestern Salamanders and Northern Red-legged Frogs) (Corkran and Thoms 2006).

Temporal.—American Bullfrogs were infrequently sighted earlier in the season, with frequency increasing greatly toward the end of March. This could indicate a temporal difference in activity between American Bullfrogs and Long-toed Salamanders in UBNA, which are most active

between December and March. This could allow for coexistence between the two species if their breeding seasons do not overlap temporally in UBNA.

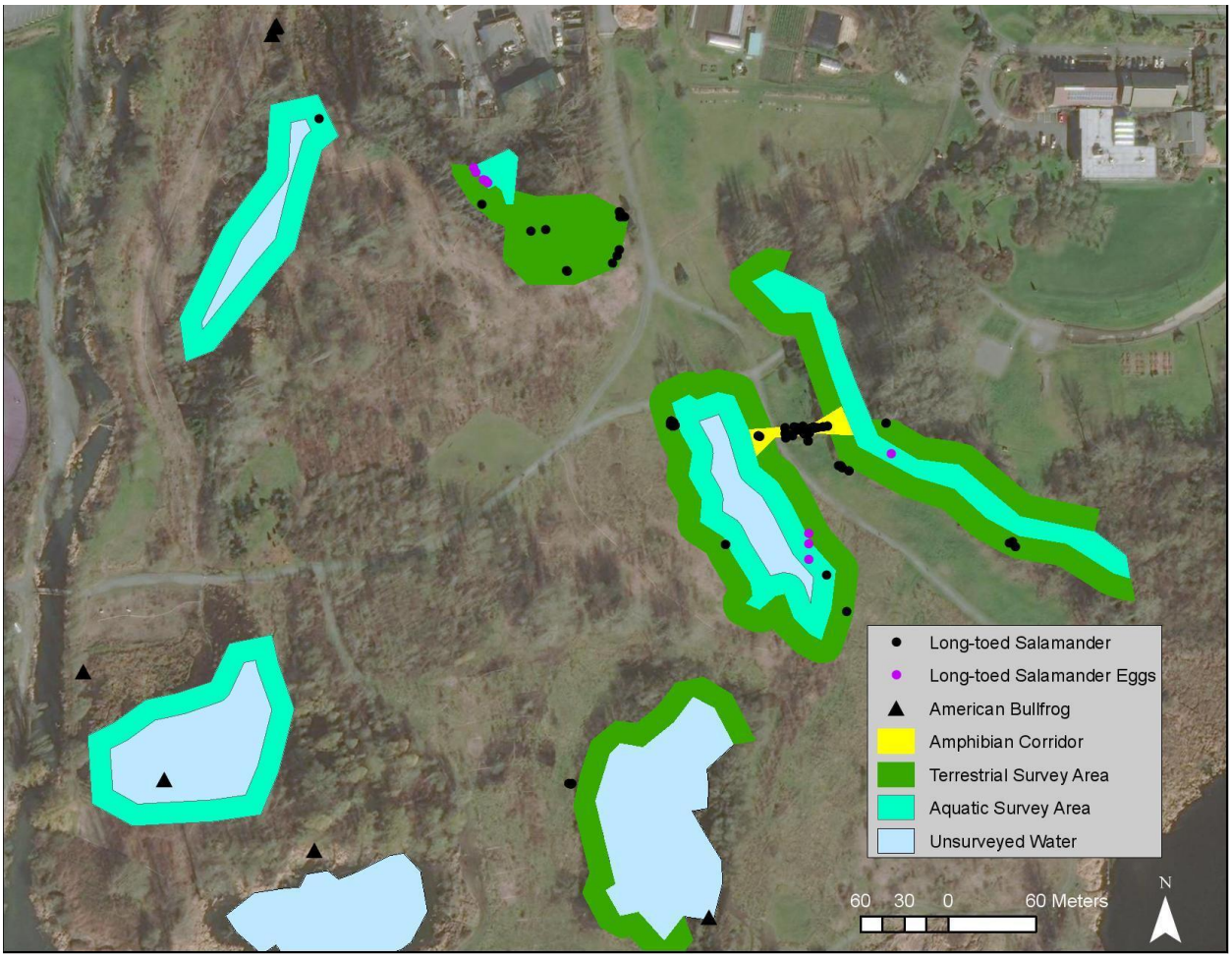

Figure S1. Locations at which American Bullfrogs (*Rana catesbeiana*) (black triangles; n = 6 locations, many sightings) and Long-toed Salamanders (*Ambystoma macrodactylum*) were captured (black dots; n = 113 captures) and Long-toed Salamander egg masses were found (purple dots; n = 9 masses observed). Surveys were conducted in the Union Bay Natural Area (Seattle, WA) between December 2020 and April 2021, with one terrestrial survey each week and one aquatic survey each week. Yesler Swamp was also surveyed but no amphibians were

detected there. Data source information: Service layer credits: Source: Esri, Maxar, GeoEye, Earthstar Graphics, CNES/Airbus DS, USDA, USGS, AeroGRID, IGN, and the GIS User Community.

SPOT-PATTERN MAPPING: WILD-ID

Wild-ID is software developed to allow researchers to identify individual animals based on their unique spot patterns (Bolger et al. 2012), as we did with Long-toed Salamanders. One Long-toed Salamander photo from each capture event was input into Wild-ID to test its efficacy in identifying individual Long-toed Salamanders. To use Wild-ID, photos are processed by the software, and the user is presented with a given photo along with the 20 photos that Wild-ID selects as the most similar to that photo. Next, the user must decide whether any of the 20 photos actually match the given photo. Thus, Wild-ID uses software to narrow down the selection of possible individual matches but still ultimately relies on by-eye identification.

We compared Wild-ID results (with the lead author as the user) to the lead author's conclusions and to a collective of volunteers, via the website capture-match.hoza.us. Unlike in Wild-ID, the lead author and the volunteers each compared every photo to every other photo that had potential to be a recaptured individual. Pattern mapping techniques were compared in terms of the number of individuals identified and the number of captures per individual. We found that Wild-ID was not as accurate as the lead author's or the volunteers' individual identifications: assuming that volunteer and the lead author's by-eye matching was 100% accurate, Wild-ID results misidentified ~23% of captures as unique individuals rather than recaptures. This indicates that by-eye identification is more effective than software for this type of study with low quality

photos. Low-quality photography did not appear to pose an issue for by-eye matching, where assessing spot patterns was straight-forward. By-eye matching by volunteers and the lead author both showed that 40 individuals were found out of 88 captures during the focal period (January–April). Since both the collective volunteer assessment and the lead author assessment agreed exactly on the number of individuals and recaptures per individual, we concluded that by-eye matching was an effective means of identifying individuals, while Wild-ID likely missed recaptures and therefore identified extra individuals.

Previous research showed that Wild-ID software is highly accurate in identifying individual newts (Mettouris et al. 2016), but this research was conducted with anesthetized newts and much higher quality photos. In our study, Wild-ID software did not perform as well, but could be more efficient if higher quality images and stationary subjects are available. It is also worth noting that Wild-ID never misidentified two salamanders as recaptures that were actually unique individuals; rather, it only misidentified multiple recaptures as being separate individuals. This is because Wild-ID ultimately relies on by-eye confirmation in its matching, so the user must confirm that no images selected by Wild-ID are matches, even if an image not selected but present in the image set is a match.

MICROHABITAT ANALYSIS CODE AND DATA

Analysis.—We used the following code to analyze likelihood of finding a salamander under a piece of woody debris given woody debris size and distance to the center of the Amphibian Corridor:

```
data <- read.csv(file = "WoodyDebrisData.csv")
head(data)
size <- data$debris_size
cd <- data$corridor_center_distance
present <- data$Present

library(MuMIn)

## assumptions
hist(size)
hist(cd)
resids <- residuals(sizeonly)
hist(resids)

## debris size
summary(glm.size <- glm(present ~ size, family = binomial))
confint(glm.size)
AICc(glm.size)

plot(present ~ size, type = "p", data = data, las = 1)
pred.data <- data.frame(size = seq(from = min(size), to = max(size), by = 1))
fitted.glm <- predict(glm.size, newdata = pred.data, type = "link", se.fit = TRUE)

pred.data$fit.bi <- fitted.glm$fit
pred.data$lwr.bi <- fitted.glm$fit + qt(.025, df = nrow(pred.data) - 2)*fitted.glm$se.fit
pred.data$upr.bi <- fitted.glm$fit + qt(.975, df = nrow(pred.data) - 2)*fitted.glm$se.fit

pred.data$fit.prob <- exp(pred.data$fit.bi)/(1+ exp(pred.data$fit.bi))
pred.data$lwr.prob <- exp(pred.data$lwr.bi)/(1+ exp(pred.data$lwr.bi))
pred.data$upr.prob <- exp(pred.data$upr.bi)/(1+ exp(pred.data$upr.bi) )

windowsFonts(A = windowsFont("Times New Roman"))

par(mar = c(6, 6, 4.1, 1.9), xaxs = "i", yaxs = "i")

plot(present ~ size, type = "p", data = data,
```

```
    xlab = "Woody Debris Size (cm)",  ylab = "Probability of Presence", pch = 19,
    cex.lab = 2, las = 1, cex.axis = 1.5, family = "A",
    xlim = c(5,60), ylim = c(-.1, 1.1))
lines(fit.prob ~ size, data = pred.data, type = "l", col = 1, lwd = 2)
lines(lwr.prob ~ size, data = pred.data, type = "l", col = 1, lty = 2, lwd = 2)
lines(upr.prob ~ size, data = pred.data, type = "l", col = 1, lty = 2, lwd = 2)


 ## size at diff probabilities

# log(presence/(1 - presence)) = -3.55512 + 0.08683*size
# log(.25/(1 - .25)) = -3.55512 + 0.08683*size
# (-1.098612 + 3.55512)/0.08683 = size
# 28.29101 = size

# log(presence/(1 - presence)) = -3.55512 + 0.08683*size
# log(.5/(1-.5)) = -3.55512 + 0.08683*size
# 3.55512 = 0.08683*size
# 40.94345 = size

# log(presence/(1-presence)) = -3.55512 + 0.08683*size
# log(.75/(1-.75)) = -3.55512 + 0.08683*size
# (1.098612 + 3.55512)/0.08683 = size
# 52.59586 = size

# log(presence/(1-presence)) = -3.55512 + 0.08683*size
# log(.95/(1-.95)) = -3.55512 + 0.08683*size
# (2.944439 + 3.55512)/0.08683 = size
# 74.85384 = size

## debris size with polynomials
summary(glm <- glm(present ~ size, family = binomial))
AICc(glm)

summary(poly2 <- glm(present ~ size + I(size^2), family = binomial))
AICc(poly2)

summary(poly3 <- glm(present ~ size + I(size^2) + I(size^3)), family = binomial)
AICc(poly3)

## other link functions

summary(glm.probit <- glm(present ~ size, family = binomial(link = "probit")))
AICc(glm.probit)

summary(glm.cauchit <- glm(present ~ size, family = binomial(link = "cauchit")))
```

```
AICc(glm.cauchit)

AICc(glm)

fitted.glm$fit
fitted.glm.probit <- predict(glm.probit, newdata = pred.data, type = "response")
fitted.glm.cauchit <- predict(glm.cauchit, newdata = pred.data, type = "response")

plot(present ~ size, type = "p", data = data,
    xlab = "Woody Debris Size (cm)", ylab = "Probability of Presence", main = "Presence as a
Function of Woody Debris Size", font.main = 1)

lines(fitted.glm.probit ~ size, data = pred.data, type = "l", col = 4)
lines(fit.prob ~ size, data = pred.data, type = "l", col = 2)
lines(fitted.glm.cauchit ~ size, data = pred.data, type = "l", col = 3)

## distance to center
summary(glm.cd <- glm(present ~ cd, family = binomial))
AICc(glm.cd)

plot(present ~ cd, type = "p", data = data)
pred.data.cd <- data.frame(cd = seq(from = min(cd), to = max(cd), by = 1))
fitted.glm.cd <- predict(glm.cd, newdata = pred.data.cd, type = "link", se.fit = TRUE)

pred.data.cd$fit.bi <- fitted.glm.cd$fit
pred.data.cd$lwr.bi <- fitted.glm.cd$fit + qt(.025, df = nrow(pred.data.cd) -
2)*fitted.glm.cd$se.fit
pred.data.cd$upr.bi <- fitted.glm.cd$fit + qt(.975, df = nrow(pred.data.cd) -
2)*fitted.glm.cd$se.fit

pred.data.cd$fit.prob.cd <- exp(pred.data.cd$fit.bi)/(1+ exp(pred.data.cd$fit.bi))
pred.data.cd$lwr.prob.cd <- exp(pred.data.cd$lwr.bi)/(1+ exp(pred.data.cd$lwr.bi))
pred.data.cd$upr.prob.cd <- exp(pred.data.cd$upr.bi)/(1+ exp(pred.data.cd$upr.bi) )

plot(present ~ cd, type = "p", data = data,
    xlab = "Woody Debris Size (cm)", ylab = "Probability of Presence",
    main = "Presence vs. Distance from Center", font.main = 1)
lines(fit.prob.cd ~ cd, data = pred.data.cd, type = "l", col = 1, lwd = 2)
lines(lwr.prob.cd ~ cd, data = pred.data.cd, type = "l", col = 7, lty =2, lwd = 2)
lines(upr.prob.cd ~ cd, data = pred.data.cd, type = "l", col = 7, lty = 2, lwd = 2)

## distance to center with polynomials
summary(cdglm <- glm(present ~ cd, family = binomial))
AICc(cdglm)

summary(cdpoly2 <- glm(present ~ cd + I(cd^2), family = binomial))
```

```
AICc(cdpoly2)

summary(cdpoly3 <- glm(present ~ cd + I(cd^2) + I(cd^3), family = binomial))
AICc(cdpoly3)

#combine models
summary(glm.combined <- glm(present ~ size + cd, family = binomial))
summary(glm.combined <- glm(present ~ size*cd, family = binomial))

AICc(glm.combined)

#combine models with polynomials
glm.full <- glm(present ~ size + cd + I(size^2) + I(size^3) + I(cd^2) + I(cd^3),
      family = binomial(link = "logit"), na.action = "na.fail")


#dredge function for combined with polynomials
dredged <- dredge(glm.full)
allmodels <- get.models(dredged, subset = TRUE)
dredged

dredgedcomb <- dredge(glm.combined)
allcombmodels <- get.models(dredgedcomb, subset = TRUE)
dredgedcomb


#check assumptions
sizeonly <- allmodels$`9`
summary(sizeonly)
pchisq(37.308, df = 36, lower.tail = FALSE)
```

Data.—We used the following data in the above code. WD_ID refers to the unique identification number assigned to each piece of woody debris (these are not consecutive since we recorded woody debris across the entire study site, but this analysis only contains data from the Amphibian Corridor). Debris_size refers to the diameter of the woody debris log round at its widest point (measured in cm). Corridor_center_distance refers to the distance from the closest edge of the woody debris to the center of the Amphibian Corridor's ditch (measured in cm).

Present is the binary indicator of whether a salamander was ever captured under a given piece of woody debris, where 1 = at least one salamander was caught under the woody debris during the study and 0 = no salamanders were caught under the woody debris at any point during the study.

Table S1. Woody debris data used in R code above.

WD_ID	debris_size	corridor_center_distance	Present
2	31	0	1
4	36	76	1
5	20	170	1
10	26	168	1
17	37	191	1
19	43	0	1
20	43	0	1
21	54	0	1
23	25	0	1
30	40	200	1
100	25	0	1
0	23	280	0
1	21	0	0
3	21	0	0
6	20	0	0
7	38	0	0
8	34	140	0

9	28	180	0
11	35	0	0
12	29	0	0
13	18	73	0
14	14	260	0
15	13	220	0
16	35	200	0
18	39	0	0
22	26	0	0
24	39	170	0
25	23	150	0
26	51	210	0
27	28	300	0
28	19	180	0
29	34	130	0
31	28	252	0
32	12	20	0
33	21	0	0
34	18	180	0
35	25	310	0
96	12	50	0
97	29	230	0

LITERATURE CITED

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