

Bitterroot Mountain Lion Project Report

January 2014

Background Wildlife managers need reliable methods to monitor mountain lion population abundance in order to manage harvest, minimize conflicts with humans and balance lion populations with ungulate management objectives. Montana Fish, Wildlife and Parks liberalized mountain lion harvest regulations within the Bitterroot Watershed during winter 2012-2013 with goals of reducing mountain lion abundance by approximately 30% over a three year period. One of the goals of the liberalized mountain lion harvest regulations is to reduce elk calf mortality, and thus, enhance elk populations. However, there is uncertainty in whether these new mountain lion harvest prescriptions will result in a biologically significant reduction in mountain lion abundance. First, without reliable estimates of starting mountain lion population abundance, prescribing harvest regulations to achieve a 30% reduction is difficult. Recently, mountain lion abundance estimates across Montana were generated based on radiocollaring research efforts conducted in the Garnets (Robinson et al. 2013). These estimates were used to generate harvest prescriptions to reduce mountain lion abundance in the Bitterroot Watershed. However, the estimates of mountain lion abundance based on radiocollaring, which were used to develop harvest prescriptions within the Bitterroot Watershed, have not been validated with independent estimates of mountain lion abundance. A DNA-based mark-recapture study in the Blackfoot Watershed of western Montana suggests that mountain lion abundance may be higher than predicted from radiocollaring studies (Russell et al. 2012). Secondly, immigration of mountain lions from adjacent areas may rapidly return a harvested population to pre-harvest levels, and increases in harvest may or may not result in lasting changes in mountain lion abundance (Lindzey et al. 1992, Robinson et al. 2008). Thus, liberalized harvest regulations may or may not reduce mountain lion abundance as targeted.



The purpose of the winter 2012-2013 mountain lion research in the southern Bitterroot was to estimate the abundance of independent mountain lions in HD 250 and HD 270. Concurrent with this effort, we monitored elk calf survival rates throughout the winter of 2012-2013, and are continuing to monitor elk calf survival in 2013-2014. Our long-term goal is to return to HD 250 and HD 270 several years after the liberalized mountain lion regulations are implemented and again estimate mountain lion abundance to evaluate the extent to which mountain lion abundance is controlled by harvest management prescriptions. At that time, we would also estimate cause-specific elk calf mortality to evaluate how potential changes in mountain lion abundance affect elk calf survival and recruitment.



Traditional approaches to estimate mountain lion abundance have focused on radiocollaring and counting individual lions, a method that is labor intensive and expensive. The resource-intensive nature of these methods has limited the spatial scope and utility of the resulting estimates for population management, while depending on the unlikely assumption of achieving a true census. Recent use of biopsy darting on mountain lions has showed promise for obtaining spatially-explicit capture-recapture estimates from DNA identification of individual mountain lions (Russell et al. 2012). In this project, we use a DNA-based spatial capture-recapture approach to estimate mountain lion abundance in the Bitterroot Watershed. We extend the methods developed by Russell et al. (2012) to include the integration of a previously existing mountain lion habitat quality model that was developed using data from 9 radiocollaring projects in Montana (Robinson et al. 2013).

Study Area and Sampling

The 2,625 km² study area was located in the southern Bitterroot watershed in western Montana, primarily within Ravalli County and included portions of HD 250, HD 270, and HD 240. We overlaid a 5 km x 5 km grid across the study area and assigned each cell a grid identification number. We randomly generated a list of grid cells and started search effort each day in the randomly assigned grid cell.

Mountain lion hair, scat, and muscle samples were collected by trackers and houndsmen for genetic analysis to identify individual mountain lions. When a fresh mountain lion track was located, the houndsmen released trained hounds to locate and tree the mountain lion. Tracks were inspected to determine if the mountain lion was independent or associated with a family group, and group size was recorded. We defined mountain lions as independent if they were travelling alone, and we considered the adult female of each family group as an independent animal. Dependent offspring, including both juveniles and kittens, were excluded from the analysis and abundance estimates. Muscle samples were collected from treed animals using biopsy darts fired from a CO₂-powered dart rifle. We used a 3 cc dart with a 1.5 cm punched biopsy tip and yarn tail. When older mountain lion tracks were located, a tracker or houndsmen would backtrack the tracks and collect any hair or scat samples along the tracks. All field crews used a Global Positioning System to record the length and location of their search effort. Samples were also collected from lions that were harvested, removed or handled for management purposes during the sampling period. Harvest samples were collected from within the study area, as well as all adjacent hunting districts in Montana and Idaho. Genetic analysis of all muscle, hair and scat samples was conducted at the United States Forest Service Rocky Mountain Research Station in Missoula, MT.



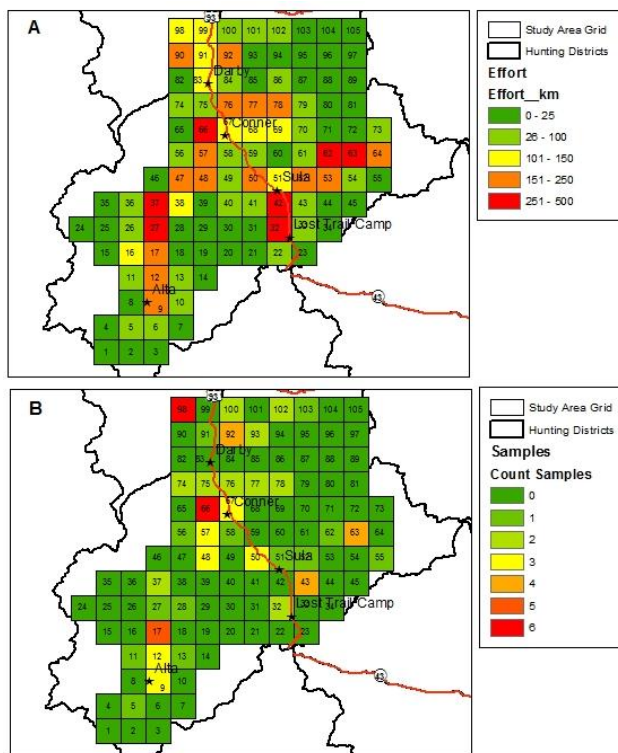


Figure 1. The mountain lion study area showing the 5 km x 5 km sampling grid and the spatial distribution of search effort (Panel A, measured in km) and the spatial locations of mountain lion samples (Panel B).

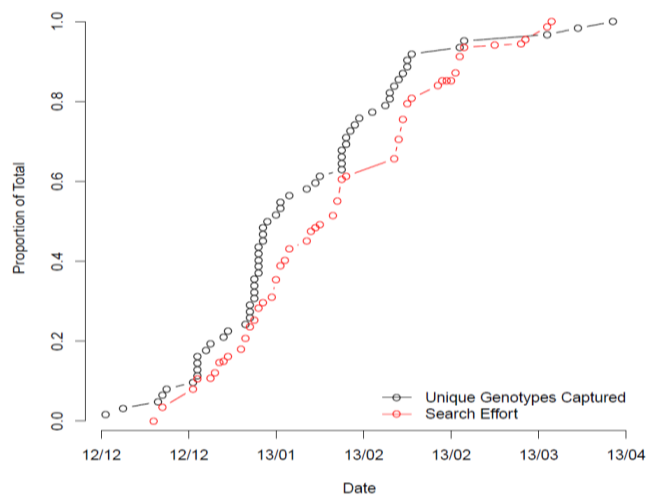


Figure 2. The number of unique genotypes (i.e. individual mountain lions, black line) identified increased with increasing search effort (red line) throughout the sampling period which ranged from Dec. 12, 2012 – April 1, 2013.

Results

We searched for lion sign over a total of 8,382 km during 98 person-days. Search effort was distributed across 85 of 105 grid cells. Animals were sampled in 35 of 105 grid cells, and individual grid cells contained 0 – 6 samples (Figure 1).

We sampled a total of 88 lions from 84 groups, and 80 of the sampled individuals were classified as independent animals and included in the analysis. In 4 cases, only the juvenile member of the group was sampled and these animals and these family units were censored from the analysis because the adult member was not sampled and identified.

From the 80 samples included in the analysis, 62 unique individuals were identified by their DNA. There were 25 male lions identified and 37 female lions identified. Fifteen individuals were recaptured 2-4 times during the sampling period (13 animals captured 2 times, 1 animal captured 3 times, and 1 animal captured 4 times). Catch per unit effort (CPUE) was 1.58 days, meaning that on average a new mountain lion was identified every 1.58 days searched. This is a very low CPUE, and a very high encounter rate, compared to other mountain lion studies.

The overall recapture rate was 24%. New genotypes (i.e. individual mountain lions) were detected throughout the entire sampling period (Figure 2). We continued to obtain new genotypes in a near linear fashion over the winter, correcting for effort, with no saturation of new genotypes over our 4 month sampling window. This suggests we were encountering new mountain lions regularly, supporting the ecological interpretation of high densities. If our field teams had identified most of the mountain lions present, we would then expect the number of new genotypes detected to level off while search effort continued to increase and individuals were recaptured.



We used a spatial capture-recapture (SCR) model to develop spatially explicit mountain lion abundance estimates, and we used this model to estimate abundance in HD 250 and HD 270. SCR models accommodate the heterogeneity of encounter probability due to the spatial arrangement of individuals across the study area. We incorporated existing information regarding mountain lion habitat quality (Robinson et al. 2013) into the SCR model to account for spatial variations in mountain lion encounter probability as a function of habitat quality. The best model estimating spatially-explicit mountain lion abundances included the effects of animal sex, search effort, and habitat quality (Figure 3). Male mountain lions were less likely to be detected than females. Male mountain lions were more likely to be detected further from their estimated activity range centers than female mountain lions, indicating male lions had larger activity ranges than female mountain lions. The probability of detection increased with search effort and the probability of an area being an activity center increased with increasing habitat quality.

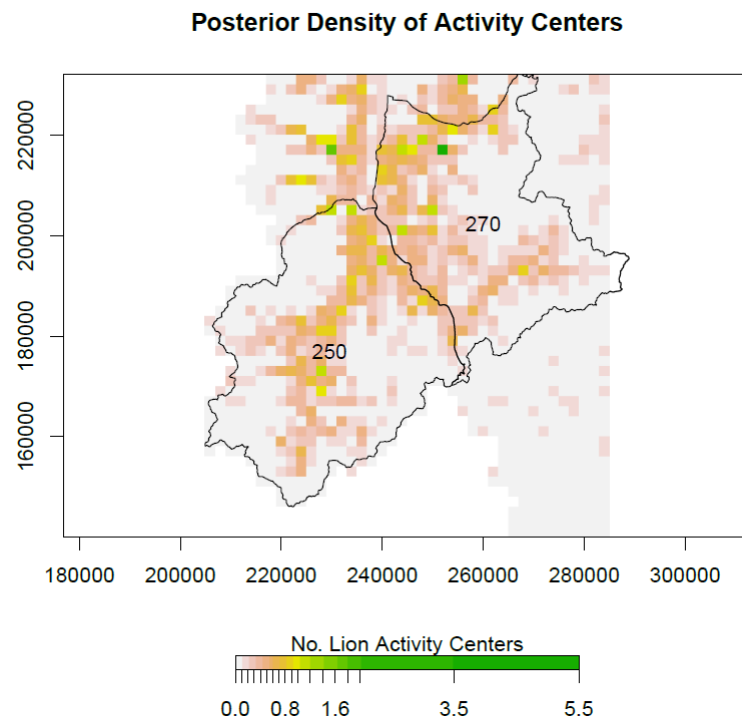


Figure 3. Spatially explicit mountain lion density predictions within the study area. The number of activity centers is the number estimated per 4 km².

The SCR model estimated a total of 85 (95% CI = 54, 141) independent (>15 month old) mountain lions in HD 250 and 82 (95% CI = 51, 137) mountain lions in HD 270. The upper 95% confidence interval is large because with so few recaptures of individuals, the upper limit on abundance was imprecisely estimated. However, across all models the lower 95% confidence interval and mean abundance estimates were stable. These abundances translate into a density of 4.6 mountain lions per 100 km² in HD 250 and 5.4 mountain lions per 100 km² in HD 270. Our abundance estimates for HD 250 and HD 270 are substantially higher than estimates from Robinson et al. (2013, Table 1), but similar to estimates of mountain lion abundance extrapolated from results of Russell et al. (2012, Table 2).

	Hunting district	Low Adult Female	Mean Adult Female	High Adult Female	Low Adult Male	Mean Adult Male	High Adult Male
Robinson et al. 2013	250	9	12	16	4	8	13
Bitterroot - Top Model	250	29	49	80	18	36	73
Robinson et al. 2013	270	9	12	16	3	7	12
Bitterroot - Top Model	270	28	48	79	17	35	71

Table 1. The predicted abundance of mountain lions in HD 250 and 270 based on extrapolated abundance results from the Garnet mountain lion study (Robinson et al. 2013) and results of this study conducted in the southern Bitterroot Watershed (Bitterroot – Top Model).



Discussion The number of different, independent mountain lions that were verified by DNA in this study was much higher than expected, and the estimated mountain lion density in HD 250 and HD 270 is at the higher end of reported mountain lion densities (see Hornocker and Negri 2010). Several factors may contribute to higher than average mountain lion abundance in this area. First, this study was conducted after a 10-year period of no or low female harvest, which would contribute to potentially higher population levels relative to the past. Second, this area contains abundant high quality mountain lion habitat (Robinson et al. 2013). Third, there is an abundant prey base in the study area, including healthy populations of white tailed deer, mule deer, bighorn sheep, and elk. The combination of low harvest during the past 10 years, good quality habitat and abundant prey likely result in a high density mountain lion population. Additionally, the methods we employed included both resident and transient mountain lions in the density estimates, include information about harvested animals, and represent estimates that account for imperfect detection of individual animals rather than minimum counts, as do traditional radiocollaring studies.



The 2012-2013 mountain lion harvest regulations were developed based on minimum counts of lions from a recent mountain lion study conducted in the Garnet Mountains area of west-central Montana extrapolated onto predicted mountain lion habitat quality (Robinson et al. 2013). We identified more unique individuals with DNA sampling than the mountain lion abundance estimates reported in Robinson et al. (2013). The Robinson et al. (2013) estimates therefore undoubtedly underestimate actual abundance, and our model based estimates of mountain lion abundance suggest the actual population is substantially larger than anticipated. The management goal for HD 250 and HD 270 is to reduce the mountain lion population by 30%. The current harvest regulations are compatible with sustaining and conserving mountain lion populations but will likely not result in the targeted 30% reduction in mountain lion population abundance.

	Hunting district	Lower 95% CI	Mean Total	Upper 95% CI	Lower 95% CI	Mean Female	Upper 95% CI	Lower 95% CI	Mean Male	Upper 95% CI
Russell et al. 2012 - Low	250	42	68	104	26	42	64	16	26	40
Russell et al. 2012 - High	250	57	123	201	42	91	149	15	32	52
Bitterroot - Top Model	250	54	85	141	29	49	80	18	36	73
Russell et al. 2012 - Low	270	35	56	86	22	35	53	13	21	33
Russell et al. 2012 - High	270	47	101	165	35	75	122	12	26	43
Bitterroot - Top Model	270	51	82	137	28	48	79	17	35	71

Table 2. The predicted abundance of mountain lions in HD 250 and 270 based on results extrapolated from a SCR model developed in the Blackfoot Watershed (Russell et al. 2012) and results of this study conducted in the southern Bitterroot Watershed (Bitterroot – Top Model). The Russell et al. 2012 – Low model estimated 3.7 mountain lions/100 km² (95% CI 2.3 – 5.7) and 38% of the population was male. The Russell et al. 2012 - High model estimated 6.7 mountain lions/100 km² (95% CI 3.1 – 11.0) and 26% of the population was male. Russell et al. (2012) estimated the total number of mountain lions. The Bitterroot – Top Model (this study) estimated the number of independent mountain lions. The lower and upper 95% CI represent the 95% credible intervals.



The DNA-based SCR methodology applied here differs substantially from traditional mountain lion research approaches that rely on long-term radiocollaring data. We found both strengths and weaknesses to the SCR approach, as well as to the long-term radiocollaring approach. The SCR approach requires only one winter of sampling effort, does not require animals to be handled or radiocollared, and substantially reduces the time and costs associated with estimating mountain lion density. Analytically, the SCR approach employs objective, repeatable methods that account for imperfect detection probability within the sampling area, incorporates potentially heterogeneous lion distribution within a given area, clearly define the extent of the area surveyed, and account for animals whose activity ranges overlap the periphery of the area surveyed. Few decisions need to be made subjectively, and SCR methods provide a reasonable method to standardize density estimates for comparison across studies. However, there are several major limitations of the SCR approach. First, the SCR method provides minimal ecological information about the mountain lion population. The sampled population included only the independent, legally harvestable segment of the population and the method produces limited information about the kitten or juvenile segment of the population. In contrast, radiocollaring studies typically provide detailed information about habitat utilization, vital rates, and dispersal patterns, each of which may be relevant to the management and conservation of mountain lions. Additionally, the SCR method does not distinguish between resident and transient animals. Depending on the application for which information is needed, distinguishing between resident and transient animals may be necessary. We suggest that for the purpose of managing mountain lion density with harvest regulations, including transient animals in the population estimate is appropriate because these animals are present, likely affect the dynamics of local ungulate populations, and are legally harvestable during the hunting season. Regardless, mountain lion density estimates between studies that either include or exclude transients are not comparable.

Please note: The results presented here are considered complete and a manuscript related to this work will be peer-reviewed during 2014. During the peer-review period, some details and numbers may be revised.

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