STATE: Montana

AGENCY: Fish, Wildlife & Parks

GRANT: Grouse Food, Pollinator, and Dung Beetle Ecology - Grazing

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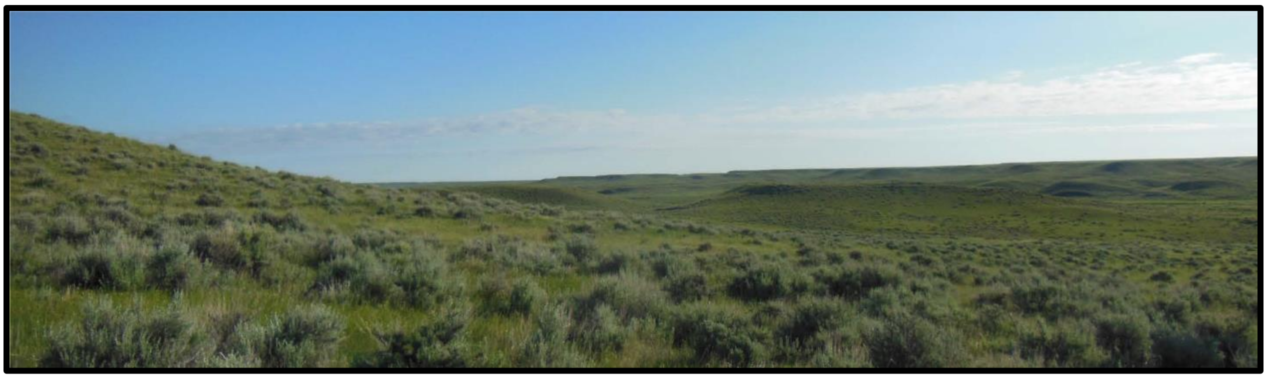

Photo by the Avian Science Center, University of Montana, Missoula

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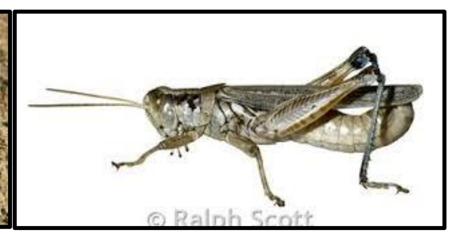
Predictive Spatial Layer of Invertebrate Biomass for Sage-Grouse and Songbird Grazing Studies in Central Montana



3/31/2019

2018 Annual Progress Report

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Predictive Spatial Layer of Invertebrate Biomass for Sage-Grouse and Songbird Grazing Studies in Central Montana

2018 ANNUAL PROGRESS REPORT

Submitted to: Montana Fish, Wildlife, and Parks, and the U.S. Fish and Wildlife Service

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Period of Agreement Date: Apr 1, 2018 – Mar 31, 2019

All information in this report is preliminary and subject to further evaluation.

EXECUTIVE SUMMARY

Previous studies suggest that invertebrates are vital to sage-grouse diets when they are available, composing 10-15% of adult sage-grouse diets during the spring and summer. In particular, invertebrates compose a large part of diets in sage-grouse chicks and may be important for their survival, and also that of hens during the spring/summer. Areas with higher densities of invertebrates are preferred by hens with broods.

Little is known about the foraging habits of songbirds in central Montana. But in general, across their distributions, invertebrates are a mainstay of the diets of several of the songbird species found in central Montana that are of conservation concern including Brewer's Sparrow, Sage Thrasher, McCown's Longspur, Chestnut-collared Longspur, and Lark Bunting. These species eat a combination of ground-dwelling and above-ground invertebrates.

Montana Fish, Wildlife, and Park's (FWP) sage-grouse grazing project (PR grant #F15AF00490 "MT Sage-Grouse Grazing Evaluation") is estimating habitat use and survival for sage-grouse hens and chicks in central Montana, and how these are influenced by grazing and habitat variables. In conjunction, the University of Montana – Avian Science Center is evaluating how grazing impacts songbird diversity, abundance, and reproduction in the same location (PR grant #F16AF00294 "Migratory Songbird Grazing Study"). However, these projects are not measuring invertebrate availability as a food resource for birds. This agreement focuses on measuring this key resource for both projects to help evaluate the effects of grazing management on invertebrates and the implications for conservation of sage-grouse and songbird communities in this area.

Data collected to date focused on evaluating the overall impact of rotational grazing on invertebrate diversity and abundance. This has provided a foundation that describes the structure of invertebrate communities in our study area and the impacts of grazing on these communities. Results to date suggest that invertebrates, particularly those preferred by sage-grouse, respond positively to pasture rest during the early brood-rearing period. But invertebrate sampling has not yet been linked to sage-grouse demographics or songbird communities. For the final three years of the project, under this agreement, the focus will be on evaluating the relationship of invertebrate biomass to songbird communities and sage-grouse demographics, population dynamics, and habitat use.

To this end, field sampling during the reporting period focused on collecting invertebrate biomass data to generate a predictive spatial layer of invertebrate biomass for the entire study area, encompassing both sage-grouse locations and songbird survey locations, and has been used to inform locations that will be sampled in 2019 to improve the model.

This report summarizes progress made during Apr 2018 – Mar 2019 on generating the predictive invertebrate biomass spatial layer for the sage-grouse and songbird study areas. Results to date regarding the impacts of grazing on invertebrates can be found on our website: <http:// http://fwp.mt.gov/fishAndWildlife/diseasesAndResearch/research/nongame/arthropods/default.html>.

BACKGROUND

Greater sage-grouse (*Centrocercus urophasianus*; hereafter 'sage-grouse') populations have been in decline in the western U.S. since the 1950s (Connelly and Braun 1997), and approximately 76% of sagebrush (*Artemisia* spp.) -associated songbird species are declining nationally (Saab and Rich 1997; Paige and Ritter 1999; Dobkin et al. 2008). Sage-grouse conservation is currently a priority, as this species was a candidate for protection under the Endangered Species Act (ESA) in 2010 and 2015. In 2015, the U.S. Fish and Wildlife Service (USFWS 2015) determined that listing the sage-grouse was not warranted, in part, due to collaborative conservation efforts among agencies and private landowners. The status of sage-grouse will be re-evaluated by USFWS in 2020. Information on the impacts of grazing to sage-grouse and their habitat, which includes food sources such as invertebrates, is needed to provide support for conservation efforts.

Sage-grouse share their habitat with several migratory songbird species that breed in Montana's sagebrush systems and are also of conservation concern, including: Brewer's sparrow (*Spizella breweria*), sage thrasher

(*Oreoscoptes montanus*), McCown's longspur (*Calcarius mccownii*), chestnut-collared longspur (*Calcarius ornatus*), and lark bunting (*Calamospiza melanocorys*; Casey 2000, Rich et al. 2004). Sagebrush-nesting species make up the largest number of Species of Continental Importance within the Intermountain West (Rich et al. 2004). Songbirds are often used as indicators for ecosystem health in sagebrush steppe habitat because of their mobile and conspicuous nature (Bradford et al. 1998). More than 600 species of conservation concern that depend upon sagebrush ecosystems have been identified (Rich et al. 2005). Efforts to positively impact sage-grouse conservation are assumed to benefit such species, as sage-grouse are touted as an umbrella species for sagebrush ecosystems. Therefore, it is important to understand the big picture of the status of the sagebrush ecosystem and the several species that rely on it, and how our conservation efforts impact the ecosystem.

Declines in sagebrush-associated avian species are congruent with significant losses of sagebrush habitat (Braun et al. 1976, Knick 1999). Conversion of sagebrush to agriculture (Connelly et al. 2004, Smith et al. 2016); fragmentation resulting from energy (Naugle et al. 2011) or subdivision development (Leu and Hanser 2011); conifer invasion (e.g., in Oregon and western Montana; Crawford et al. 2004, Beck et al. 2012); and modifications, such as prescribed fire, herbicides, and some grazing practices that lead to exotic, annual grass establishment are significant stressors on sagebrush systems (Rich et al. 2005, MTSWAP 2015).

Livestock grazing is a land use that is receiving much scrutiny regarding its impacts on wildlife populations because it is so prevalent in sagebrush systems. It is the largest land management practice in the world (Krausman et al. 2009) and the dominant land management practice in sagebrush habitat, impacting 70% of land in the western United States (Fleischner 1994). Thus, this land use is not likely to disappear, and is one of the many land uses we must learn how to manage for desired stakeholder and wildlife management goals.

Livestock grazing impacts sagebrush habitat by altering its vegetation structure, composition, and productivity (Beck and Mitchell 2000, Hormay 1970, Krausman et al. 2009). There is a growing recognition that livestock grazing can be manipulated to positively affect sagebrush-associated bird habitat (Holechek et al. 1998, Coppedge et al. 2008). However, heavy livestock grazing can decrease invertebrate biomass (Krausman et al. 2009); an important food source for several bird species, including sage-grouse and migratory songbirds.

Chick survival is the most concerning demographic rate in sage-grouse (Aldridge and Boyce 2007, Gregg and Crawford 2009, Dahlgren et al. 2010, Guttery et al. 2013). Chick survival is relatively low compared to adult female (hereafter 'hen') survival and nest success in FWP's central Montana sage-grouse grazing project (PR grant #F15AF00490 "MT Sage-Grouse Grazing Evaluation"; Berkeley et al. 2018). Dahlgren et al. (2016) suggest that invertebrates may be important for sage-grouse chick survival, especially during the early brood-rearing period (<21 days). They are a rich source of protein, particularly during the spring when plants have not begun growing and energetic needs are high for newly hatched chicks and nesting hens. Johnson and Boyce (1990) suggest that invertebrates are vital to sage-grouse chick survival and that invertebrates compose a large part of diets in sage-grouse chicks (see also discussion and references in Drut et al. 1994 and Thompson et al. 2006). Fischer et al. (1996) suggest that areas with higher densities of invertebrates are preferred by hens with broods.

Little is known about the foraging habits of songbirds in central Montana. But in general, across their distributions, invertebrates are a mainstay of the diets of several of the songbird species found in this area including Brewer's Sparrow (*Spizella breweri*), Sage Thrasher (*Oreoscoptes montanus*), McCown's Longspur (*Calcarius mccownii*), Chestnut-collared Longspur (*Calcarius ornatus*), and Lark Bunting (*Calamospiza melanocorys*; Rodewald 2015). These species eat a combination of ground-dwelling and above-ground invertebrates (Rodewald 2015).

FWP's sage-grouse grazing project (PR grant #F15AF00490 "MT Sage-Grouse Grazing Evaluation", Berkeley et al. 2018) is estimating habitat use for sage-grouse hens and chicks and how these are influenced by grazing and habitat characteristics in central Montana, and the University of Montana – Avian Science Center's songbird grazing project (PR grant #F16AF00294 "Migratory Songbird Grazing Study", Dreitz et al. 2019) is evaluating how grazing impacts songbird diversity, abundance, and reproduction in the same location. However, these projects are not measuring invertebrate availability as a food resource for birds. Our main goal is to measure this key resource for both projects to help evaluate the effects of grazing management on invertebrates and the implications for conservation of sage-grouse and songbird communities in this area.

Objective

Our primary objective is to sample the biomass of ground-dwelling and above-ground invertebrates that may be food items for sage-grouse and songbirds in central Montana. Field sampling in 2019 – 2020 will be used to generate the spatial layer predicting invertebrate biomass. We will also be collecting field data during 2019 – 2020 to validate the model. Data processing, spatial layer generation, and reporting will be completed by Jun 30, 2021.

METHODS & RESULTS

Our study is conducted in Golden Valley and Musselshell counties, Montana (Figure 1) in big sagebrush steppe habitat. Big sagebrush steppe is the most widely distributed sagebrush system in Montana, and is typically characterized by Wyoming big sage (*Artemisia tridentata* ssp. *wyomingensis*) with perennial grasses and forbs dominating at least 25% of cover (Montana Natural Heritage Program 2011). To reduce sampling effort, instead of sampling insects at sage-grouse nest and brood locations, we will sample at stratified random sites across the study area to create a spatial layer that predicts insect biomass. This strategy enables us to use a model to predict the biomass of food insects available to sage-grouse and songbirds at locations where we are not able to sample directly because of the unrealistically large amount of effort that would be required to do so. In addition, this effort will make use of the data that has already been collected for the grazing aspect of this project since 2012. We provide a general summary of our methods and results below.

Predictive Invertebrate Biomass Model

ACCOMPLISHMENTS:

Generating Sampling Locations. We included several vegetation metrics when building the first iteration of the predictive spatial model to determine which ones were important and would be kept in the model. Please see the attached report prepared by Claudine Tobalske and Jessica Mitchell from the Montana Natural Heritage Program. Preliminary analyses from this project and the sage-grouse grazing project showed that both invertebrates and sage-grouse chicks have a relationship with percent bare ground cover; thus, we used this variable to stratify our sampling locations across the study area (see Tobalske and Mitchell report, attached). The number of plots sampled will be determined by how many technicians are able to sample during May 2019. We generated 60 random points. As of May 17, 2019, our technicians have been able to sample 19 of these points; we anticipate we will get 30 – 40 plots sampled by the end of May, and these plots will then be repeated each month in June and July and used to continue building the predictive spatial model of invertebrate biomass.

We are also simultaneously sampling invertebrates at sage-grouse locations and songbird survey locations. These samples will be used to validate the predictive spatial model of invertebrate biomass. Sampling sites are determined based on sage-grouse locations and locations surveyed for songbirds the previous week. We try to minimize the time between the location of sage-grouse at a site, or the date when a site was surveyed for songbirds, and the date that we sample invertebrates to no longer than a week between the location and the invertebrate sampling. In other words, we try to sample invertebrates at recent locations without disturbing sage-grouse and songbirds. Our technicians have been able to sample at 14 sage-grouse and songbird locations that will be used to validate the spatial model.

Data Collection. Our methods are based on those outlined in Tronstad et al. (2018). Sampling occurs during the day, when both sage-grouse and songbirds are more likely to be active and foraging. It is important to collect both ground-dwelling and above ground insects, because sage-grouse and songbirds eat both. We also collect a suite of vegetation metrics at each sampling site to analyze how these conditions impact invertebrate biomass.

Vegetation Metrics. Please see the attached report by Tobalske and Mitchell on how they generated the stratified random sampling locations. At each sampling site, we set up a 30m x 30m plot using the site coordinates as the center of the plot, with two metric tapes bisecting the plot in the center. The vegetation metrics we collect are the same as those collected for our sage-grouse grazing study and are summarized in Smith et al. (2018).

Invertebrate Sampling. We estimate invertebrate availability at sampling sites using five methods: counting ant mounds, flushing grasshoppers, collecting shrub samples, sampling litter, and sweep nets. Ant mounds and grasshopper flushes are counted while systematically traversing the plot. Four shrub and litter samples are collected in each plot, at the shrub closest to 5m on the tape measuring the plot in each cardinal direction. We place a mesh enclosure around the shrubs we sample to avoid invertebrates escaping before we sample. We use a hand-held vacuum/aspirator to vacuum invertebrates from the shrub and the ground beneath the shrub, which get collected in a cup attached to the vacuum. Then we transfer the collected invertebrates from the cup and into a ziplock bag. We use a sweep net to take 200 sweeps per plot: 100 sweeps along the North-South tape, and 100 sweeps along the East-West tape. During this process, a net with a 3-ft handle and a 12-in diameter bag is swept back and forth through the vegetation along the tape to collect invertebrates. The invertebrates are then transferred to a ziploc bag. All samples are stored in a freezer until processing. Samples are dried, sorted, and identified and weighed according to the Order taxa.

***Analyses*.** Invertebrate biomass is used as a response variable in models that relate vegetation metrics and weather variables to invertebrate biomass (see attached Tobalske and Mitchell report). We began by modeling the data collected through 2018 and assessing which sites within the study area had the highest uncertainty in predicted invertebrate biomass. We focused field sampling at these sites. For details see the Tobalske and Mitchell report, attached. We are currently sampling some of these areas in 2019 and then we will again identify areas in need of more sampling for 2020. The invertebrate biomass response variable will be used as a covariate in sage-grouse survival and habitat use, and songbird diversity, abundance, and reproduction, respectively, are modeled as functions of habitat and grazing variables.

FUTURE GOALS

We will continue data collection to build the spatial model predicting invertebrate biomass across the study area during 2019-2020. We will also continue to simultaneously sample invertebrate biomass at randomly selected sage-grouse locations and songbird survey locations to validate the predictive layer. Final products including the predictive spatial layer, model validation, and final report will be completed in 2021.

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FIGURES

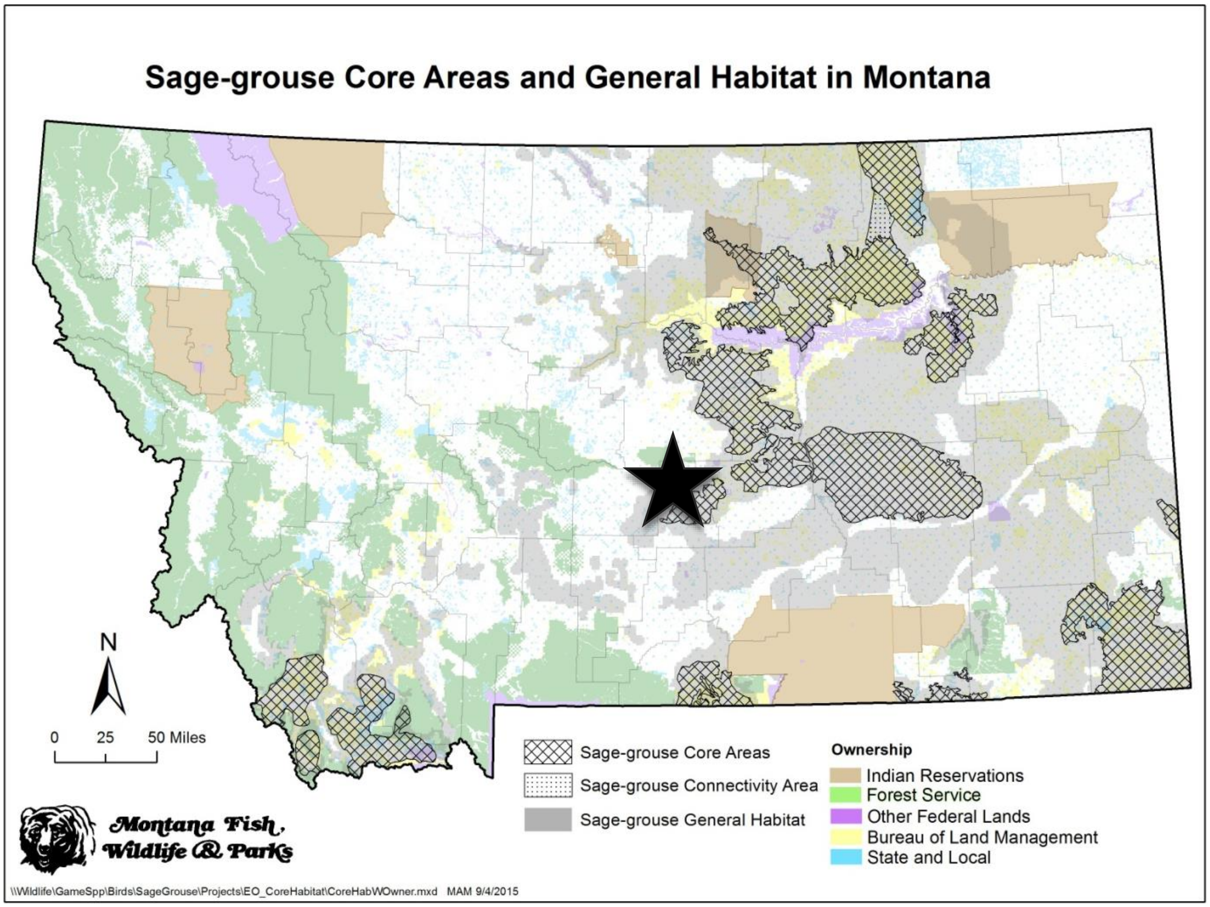

FIGURE 1. Greater sage-grouse core areas as defined by Montana Fish, Wildlife, and Parks. The black star represents the location of the study area for this project in Golden Valley and Musselshell Counties, Montana, USA.

PREDICTING ARTHROPOD BIOMASS DISTRIBUTION IN THE LAKE MASON AREA

Claudine Tobalske and Jessica Mitchell

INTRODUCTION

This is a first attempt at predicting the distribution of arthropod biomass in the Lake Mason study area, Montana, using existing sweeps data (2012-2018) in a Random Forest model. Model results are used to inform arthropod sampling for the 2019 field season, whose data will feed into an updated version of the biomass model.

STUDY AREA

The Lake Mason study area covers 250,389 ha mostly in the Golden Valley and Musselshell counties of central Montana, near the town of Roundup. The study area is dominated by a mixture of sagebrush and grass, as well as privately held agricultural areas (Open Range Consulting 2015; Figure 1).

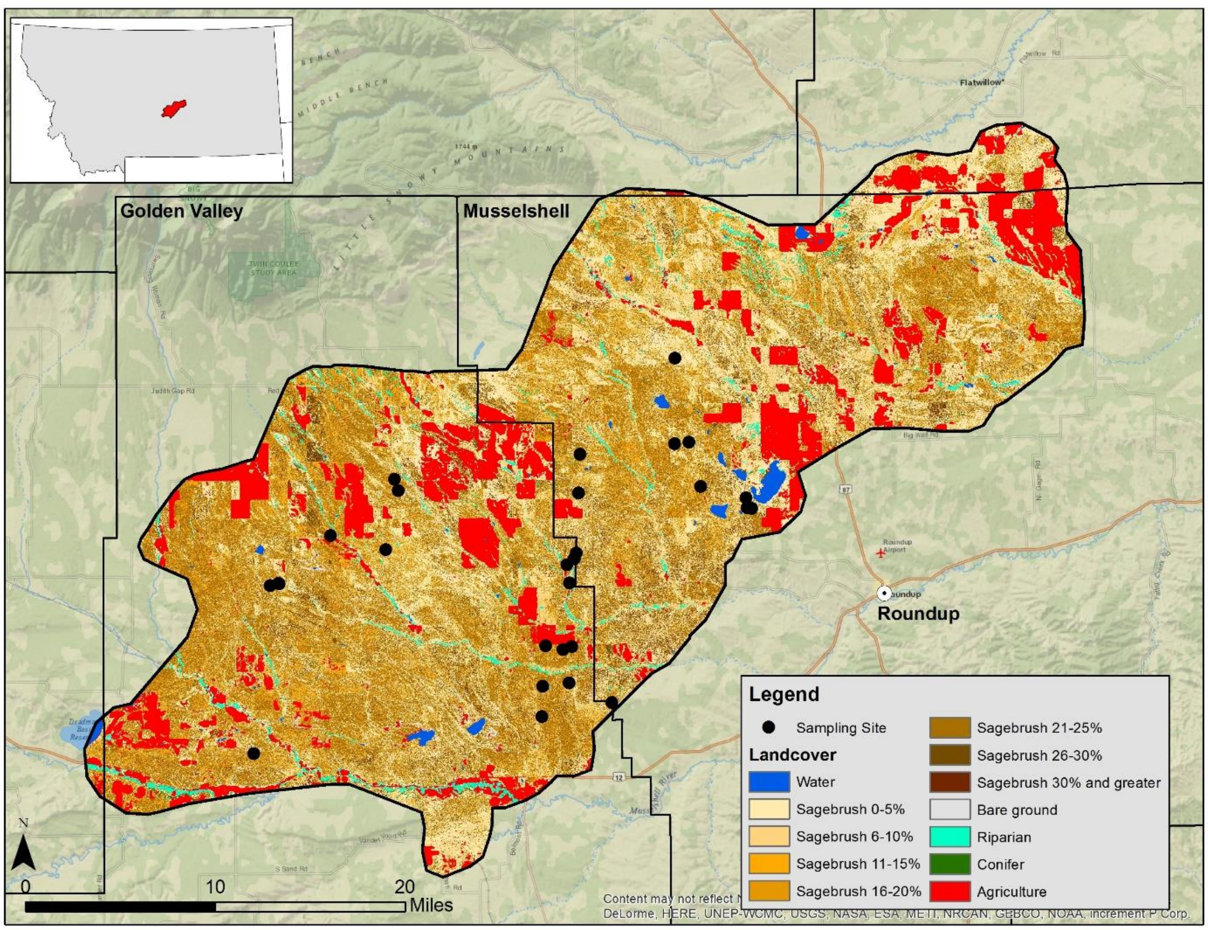

Figure 1. Study area location in Montana and land cover composition.

MODELING DATA

1. Biomass data

A total of 2,541 samples of arthropod biomass (dried, grams) were collected between May 31, 2012 and June 30, 2017 at 30 different geographic locations within the study area; however, one site (Lehfeldt E1N) was eliminated from analysis due to missing x-y coordinates. Arthropod sampling methods included sweeps (all sites) and pitfalls (12 sites), with method also listed as “Not recorded” for some samples at nine sites. Comparison of biomass values from these “Not recorded” samples with those of sweep samples showed no significant difference (Figure 2), so they were considered “sweeps” and used in the analysis. On the other hand, pitfalls samples resulted in much higher biomass values than sweeps samples for the 12 sites where they were also collected at (although with a large standard deviation, Figure 3), so the Random Forest model was run using only sweep samples (n = 1,641).

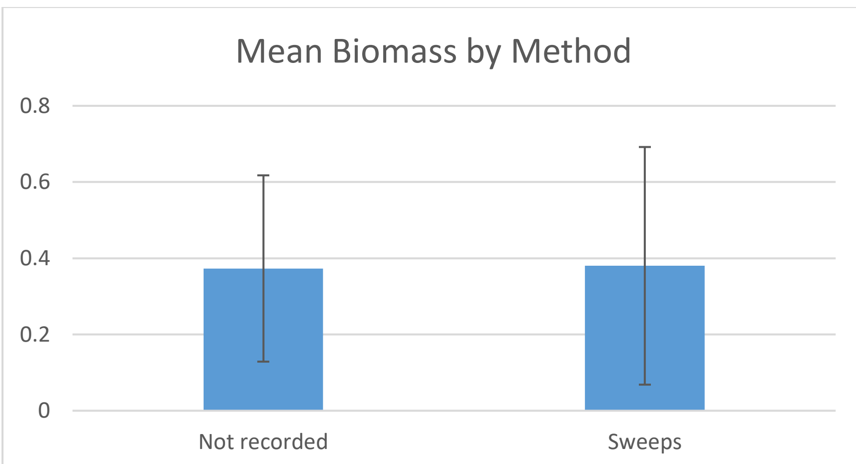

Figure 2. Mean arthropod biomass comparison at nine sites from two different methods.

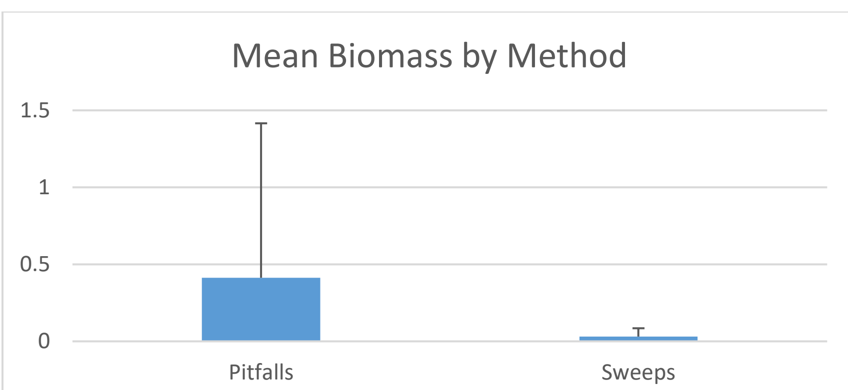

Figure 3. Mean arthropod biomass comparison at twelve sites from two different methods.

An additional 30 new sites were sampled in 2018, using sweeps as well as shrub littler and shrub brushing in a quadrant design. Despite similar biomass between “Shrub” and “Sweep” methods (Figure 4), only those samples collected by the sweep method were included in the analysis.

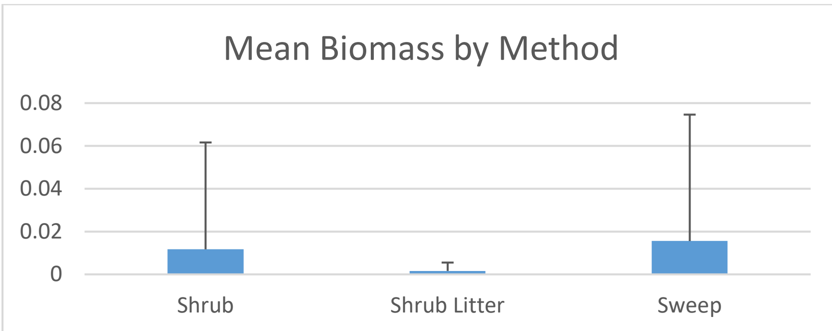

Figure 4. Mean arthropod biomass comparison at 30 sites from three different methods.

Arthropod order was collected for all but 105 samples, 58 of which used the sweep method; a single biomass measurement was provided for each date, most likely the summed biomass at the site for that day. To make biomass data comparable among all sites, the 2012-2017 biomass entries were summed by site ID and collection date, then total average biomass was calculated for each site. Values averaged 0.193 gram/site and ranged from 0.0036 grams at site 32092 to 0.8409 grams at site 33018, with the majority of sites averaging less than 0.1 gram (Figure 5). These biomass averages became the “dependent” variable of the model. Because the largest biomass value was an outlier that influenced model outcome, two versions of the model are considered: one including the outlier, one excluding it. This approach maximized the number of sample sites; there was not a large enough sample size to support grouping by arthropod order, or by early season vs late season biomass.

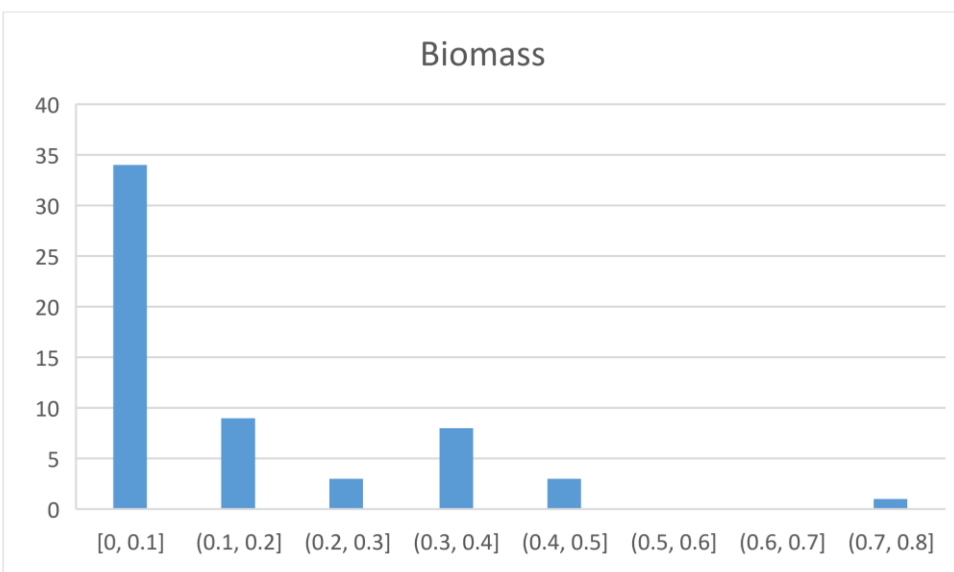

Figure 5. Mean arthropod biomass distribution at 59 sites in the Lake Mason area, 2012-2018.

2. Predictive layers

Four different vegetation layers were generated at 1m pixel resolution by Open Range Consulting (2015) by classifying 2013 NAIP imagery: land cover (categorical variable, Figure 1), percent herbaceous cover, percent ground cover, and percent shrub cover (all three continuous variables). Because most land cover classes were differentiated by percent sagebrush cover, and to simplify the analysis, the land cover layer was treated as a continuous dataset by basing it on percent sagebrush, and assigning 0 to all non sagebrush classes.

Landsat Gross Primary Production data (GPP; Robinson et al. 2018; https://developers.google.com/earth-engine/datasets/catalog/UMT_NTSG_v2_LANDSAT_GPP) (30m pixel resolution) were extracted in Google Earth Engine for May, June, July, August and September 2012 through 2018 and averaged by month. Monthly minimum, maximum and mean temperature rasters (800m pixel resolution) were downloaded from the Montana Climate Office website (http://climate.umt.edu/products/meteorology/temperature.php) for May through September 2002-2012 (the most recent year available) and averaged by month, resulting in 15 variables. Finally, open water and wetlands were extracted from the Montana NWI database (http://geoinfo.msl.mt.gov/home/msdi/wetlands) and rasters of continuous Euclidean distance to the nearest polygon were generated for each. All GIS analyses were conducted using ArcGIS 10.6, unless noted otherwise.

Since the pixel size for the predictive variables varied greatly (1m to 800m), predictive layers were resampled to 30m using the DEGRADE command in Erdas Imagine for the continuous 1m NAIP percent cover rasters and the RESAMPLE command in ArcGIS for all other non-30m rasters (NAIP land cover and temperature rasters). In addition to considerably reducing processing time, this pixel size matched that of field vegetation plots, which are the same type of plot used for arthropod sampling.

METHODS

1. Predictive model

Values for the resampled variables were extracted at each of the 59 sites in ArcGIS and exported to a .csv. For biomass modeling, I used the R package ModelMap (Freeman et al, 2019) in R 3.3.2. This package constructs predictive models of continuous or discrete response variables using Random Forest, allowing for validation with an independent dataset and creation of graphs and tables of basic model validation diagnostics, as well as extrapolation of the model to create prediction surfaces – including map measures of uncertainty such as standard deviation and coefficient of variation for each pixel.

Several versions of the models were run, with and without the outlier biomass, but also with different sets of variables. For example, one run included only mean monthly GPP (5 GPP variables) and another also used individual month/year values (5 + 35 GPP variables).

Other variables were considered (e.g. soil data from SSURGO, Relative Annual Effective Precipitation) but their inclusion did not improve model prediction abilities.

ModelMap offers the possibility of randomly splitting the dataset into training (80%) and validation (20%) sets, based on a user-input seed value. Although this approach gives a better indication of model performance than statistics resulting from within-set substitutions, the small number of samples resulted in quite different outcomes based on what seed number was used. To make sure that both training and validation sets contained similar proportions of smaller and larger biomass values, I split the dataset into training (N = 47) and validation (N = 12) after stratifying by biomass.

The other seed input, for Random Forest proper, also resulted in small variations among models. For each dataset (with and without outlier), I ran models while increasing seed value by 5 (i.e. 5, 10, etc, through 45) and compared model performance and variable importance based on percent increase mean square error (the increase in mse of predictions as a result of the variable being permuted). Model performance was evaluated by percent variance explained and Pearson's and Spearman's correlation coefficients between observed and predicted values of the validation dataset.

2. New sampling sites

A lattice of potential sampling points was automatically generated in ArcGIS, with points regularly spaced by 200m (the minimum distance between two sampling points for the 2018 field season). Cadastral data for Golden Valley and Musselshell counties were downloaded from the Montana Geographic Information Clearinghouse (http://geoinfo.msl.mt.gov/msdi/cadastral) and points overlapping parcels with denied access were deleted. Points falling within the Department of Revenue Final Land Unit agricultural parcels (https://mslservices.mt.gov/Geographic_Information/Data/DataList/datalist_Details.aspx?did={0d715638-eef4-4c69-8d26-a83aff6c7cf2}) were also deleted. Finally, points located within 200m of a site sampled previously (for arthropod biomass and bird data) were deleted, leaving 42,026 to select from. A 1ha circular buffer was centered on each point and percent bare ground (the most important biomass predictor, see results below, also the variable used to stratify sampling in 2018) was extracted for each, along with mean predicted biomass and mean biomass coefficient of variation. Continuous percent bare ground was classified into 4 categories (0-10%, 10-25%, 25-50% and >=50%).

The Sampling Design Tool (NOAA/NOS/NCCOS/CCMA/Biogeography Branch) was used to randomly select 50 points in each of the bottom three bare ground classes; because only 21 points had over 50% bare ground, they were all selected. Mean biomass and mean coefficient of variation (a measure of model uncertainty) were computed at the randomly selected sites and compared to point population values.

RESULTS

1. Predictive models

Models developed without the outlier data yielded better percent variance explained, yet no model explained more than a quarter of the variance in the data (Figure 6).

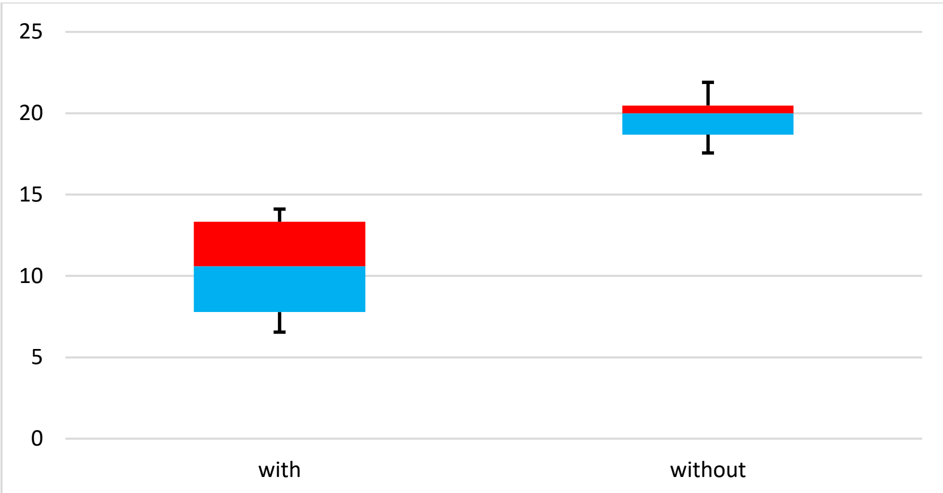

Figure 6. Boxplot comparison of Random Forest models of arthropod biomass generated from nine seed values for data including or excluding an outlier biomass value.

For both datasets, most Pearson and Spearman correlation values between observed and predicted were greater than 0.75. Among the top 6 most important variables regardless of model type, Percent Bare Ground, Percent Shrub Cover, Gross Primary Productivity for 08/2014 and Mean Gross Primary Productivity for June (2012-2018) consistently came at the top (Table 1). Comparing percent variance explained, correlation coefficients and most important variables among the nine models for each dataset, a "best model" was selected then applied to the entire dataset (i.e., no splitting into training and validation). For the dataset with outlier, this full model explained 17.15% of the variance; for the dataset without, it explained 26.7%. Pearson's and Spearman's plotted coefficients for the full models are presented in Figure 7, and percent increase in MSE in Figure 8.

WITH

seed	%Var	Pearson	Spearman	var1	var2	var3	var4	var5	var6
5	10.6	0.79	0.74	bare	shrub	GPP0814	GPP06	GPP0618	GPP05
10	7.72	0.75	0.76	bare	shrub	GPP06	GPP0814	Tmin08	GPP05
15	13.84	0.81	0.75	bare	shrub	GPP0814	GPP06	GPP0618	Tmin08
20	6.55	0.79	0.74	bare	GPP0814	shrub	GPP0618	GPP07	Tmin08
25	13.33	0.81	0.73	bare	shrub	GPP0814	Tmin08	GPP0618	GPP0817
30	7.9	0.78	0.76	shrub	GPP0814	bare	GPP0618	GPP05	GPP0516
35	11.23	0.77	0.73	bare	shrub	GPP06	GPP0814	Tmin08	GPP0618
40	7.78	0.77	0.74	bare	shrub	GPP0814	Tmin08	GPP05	GPP0618
45	14.11	0.84	0.73	bare	shrub	GPP0814	GPP0618	Tmin08	GPP0817

WITHOUT

seed	%Var	Pearson	Spearman	var1	var2	var3	var4	var5	var6
5	20	0.76	0.74	shrub	bare	GPP0814	GPP0618	Tmin08	GPP06
10	19.04	0.78	0.76	GPP0814	bare	shrub	GPP0516	Tmin07	GPP06
15	21.9	0.77	0.78	shrub	bare	GPP0814	Tmin08	GPP0618	GPP06
20	20.48	0.77	0.77	GPP0814	shrub	bare	GPP0618	Tmin09	GPP0918
25	20.72	0.78	0.72	bare	shrub	GPP0814	Tmin08	GPP0618	GPP06
30	17.56	0.79	0.77	GPP0814	bare	GPP06	shrub	GPP07	GPP0918
35	18.29	0.75	76	GPP0814	Tmin08	GPP0618	GPP05	GPP0516	GPP07
40	20.15	0.74	0.77	GPP0814	bare	GPP06	shrub	GPP0618	GPP0918
45	18.69	0.78	0.77	GPP0814	bare	shrub	GPP06	GPP07	GPP0618

Table 1. Comparison of nine Random Forest model characteristics (Percent variance explained, Pearson's and Spearman's coefficients for validation sets, and top 6 most important variables) for two datasets of arthropod biomass, including or excluding an outlier value. The models highlighted in yellow were selected for running on the full datasets.

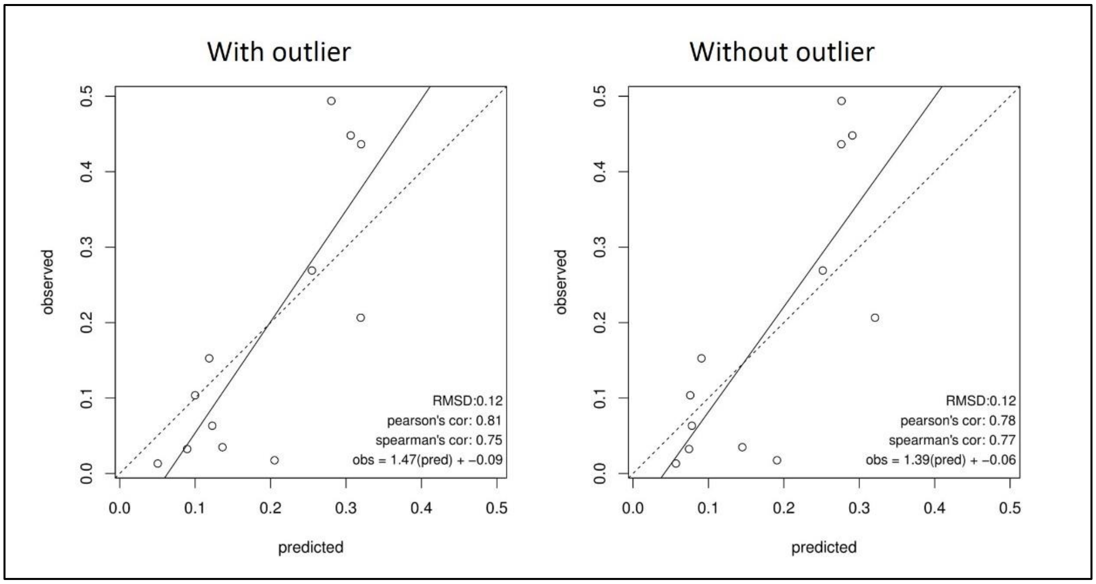

Figure 7. Scatterplot of predicted vs observed values, and Pearson's and Spearman's coefficients, for two models of arthropod biomass from datasets including or excluding an outlier value.

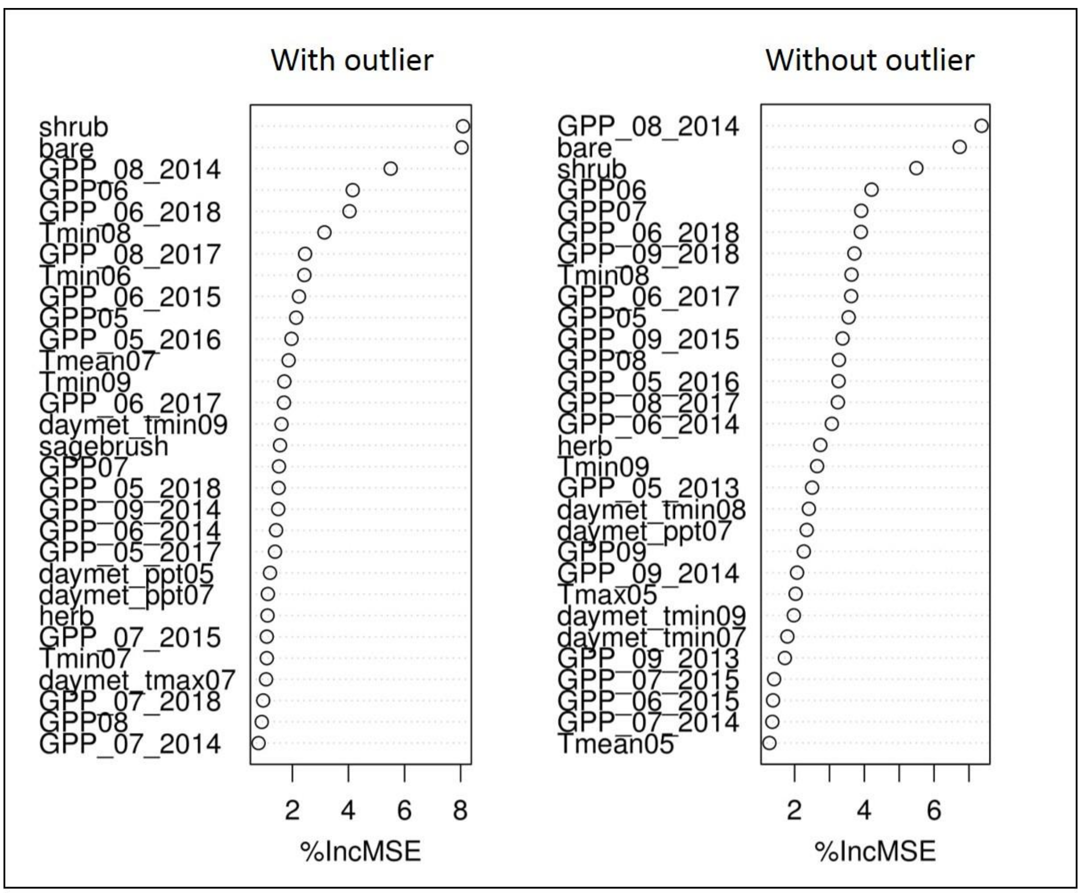

Figure 8. Percent increase in Mean Square Error for the top 30 variables, for two models of arthropod biomass from datasets including or excluding an outlier value.

Extrapolation of both models to continuous surfaces raster allows for visualization and identification of areas predicted to have higher arthropod biomass (Figures 8a and 8b). It is interesting to notice that the inclusion of the outlier with its large biomass value has a strong influence on model output, with a larger proportion of the study area predicted to have higher arthropod biomass.

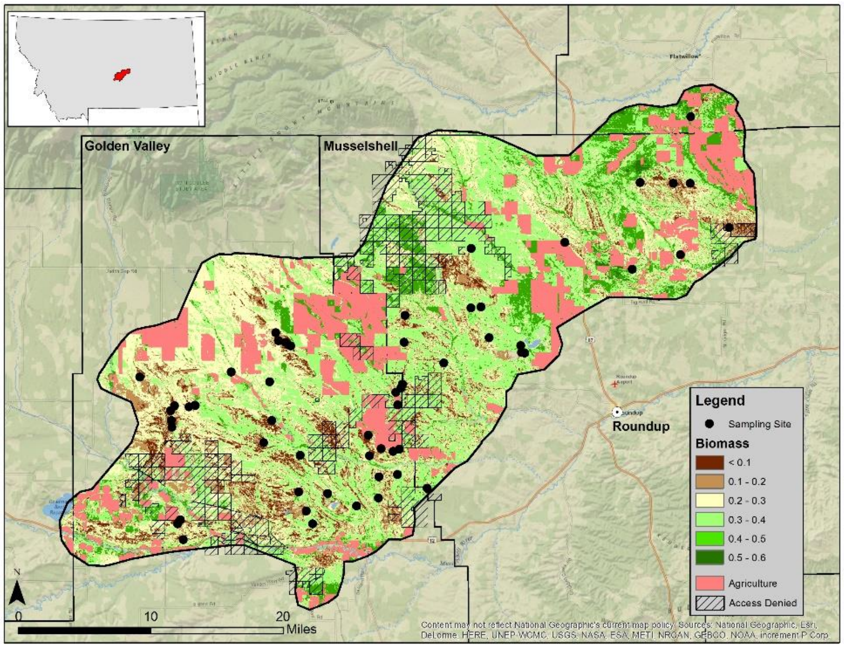

Figure 8a. Predicted arthropod biomass (grams) from dataset including a high value outlier.

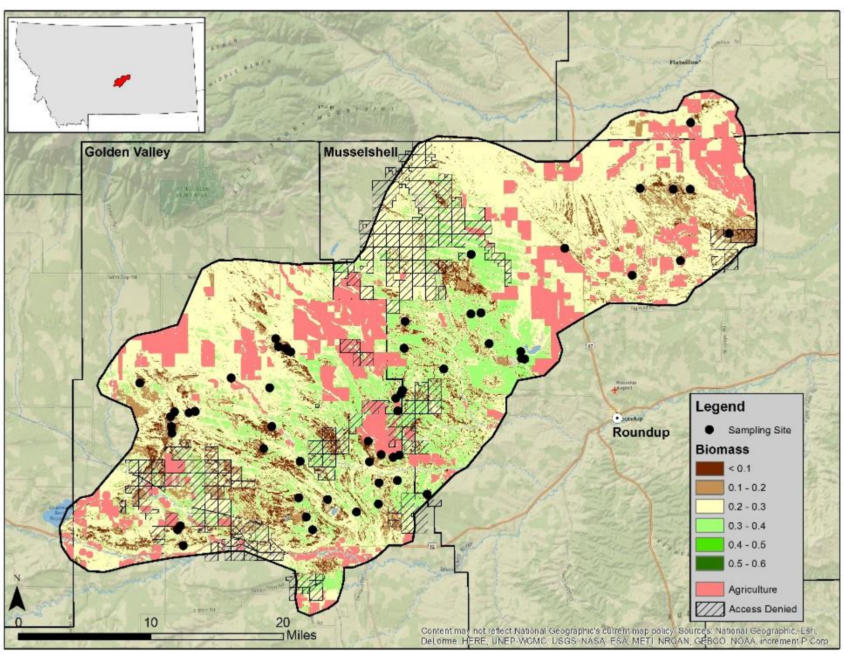

Figure 8b. Predicted arthropod biomass (grams) from dataset excluding a high value outlier.

That said, predicted biomass values at the actual sampling sites did not vary much between models (Figure 9).

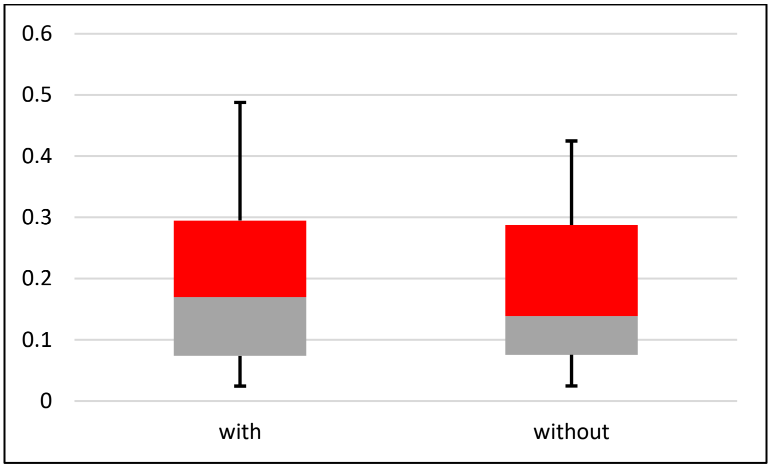

Figure 9. Boxplot comparison of predicted arthropod biomass at 59 (with) and 58 (without) sampling sites based on two Random Forest models, one including a high value outlier, the other excluding it.

Pixels with higher model uncertainty (coefficient of variation greater than 1) were almost five times more numerous for the model including the outlier (N = 55,009 or 2.03% of study area) than for the model excluding it (N = 11,295 or 0.42% of study area), but areas of higher uncertainty overlapped for 4.56% (11,114 ha) of the study area (Figure 10).

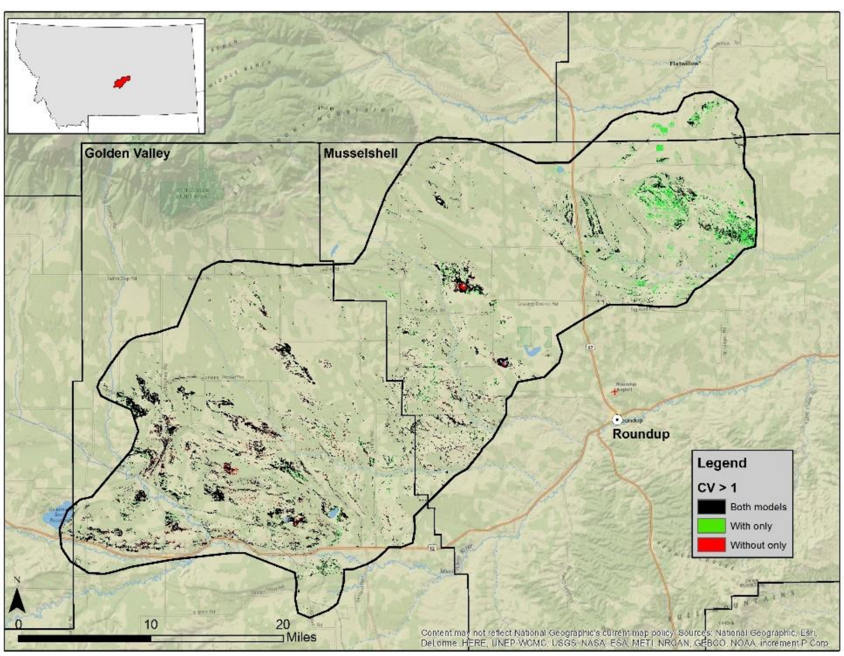

Figure 10. Location of areas of higher model uncertainty (coefficient of variation > 1) for two model of predicted arthropod biomass, including or excluding a high value outlier.

There also appears to be a correlation between model uncertainty and percent bare ground, with higher uncertainty values in areas where bare ground is more prominent; this was visible when looking at the raster datasets, and a moderate positive correlation was obtained when plotting percent bare ground versus coefficient of variation at the sample points (R^2 = 0.4947 for model with outlier, R^2 = 0.5424 for model without outlier; Figure 11).

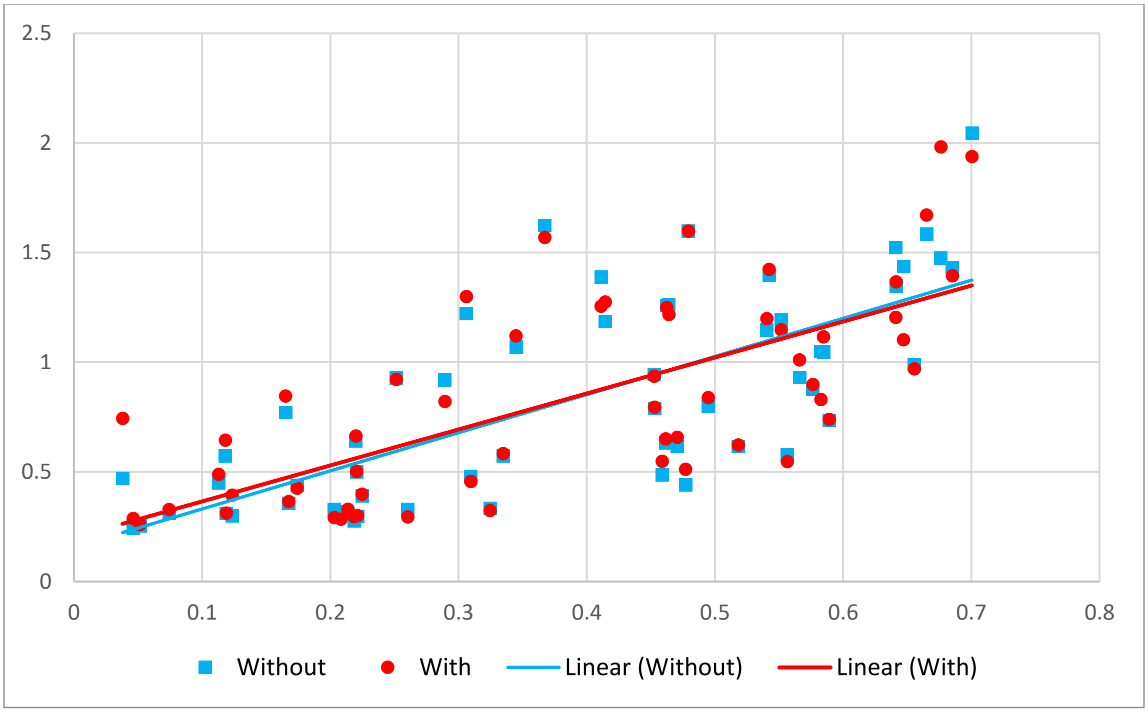

Figure 11. Regression equation of coefficient of variation by percent bare ground for two arthropod biomass models at 59 (with outlier) and 58 (without outlier) sampling points.

2. Random sampling points selection

According to the 1m land cover layer generated from NAIP 2013, the Lake Mason study area is dominated by sagebrush of various density, and is composed of only 1.74% bare ground (Table 2). The 2018 selection of sampling sites was stratified by percent bare ground within 100m square cells (1ha), with more sites assigned to the less common patches of high bare ground cover. Such a stratification works well for the 2019 sampling season, as the biomass models, both with and without the outlier value, were strongly driven by the Percent Bare Ground variable. In addition, selecting sites with higher bare ground cover will result in sampling areas of higher model uncertainty, because of the correlation between these two parameters.

The continuous percent bare ground value within the 42,026 potential sampling circles generated in ArcGIS was reclassified into four categories: 0-10%, 11-25%, 26-50%, and >50%. Only 21 circles contain more than 50% bare ground; all were selected. To these, 60 circles were randomly selected in each bare ground class, for a total of 201 new sampling sites. Of these, 92 (45.8%; with outlier) or 84 (41.8%; without outlier) encompass areas of higher model uncertainty (CV >1). The distribution of predicted arthropod biomass is also well represented, with biomass values ranging from 0.05g to 0.46g per circle (with outlier) and from 0.04g to 0.35g per circle (without outlier). Figure 12 presents the distribution of the potential 2019 sampling sites, along with that of previous sampling sites.

Land cover class	Area (ha)	Percent
Sagebrush 0-5%	64,544	25.83
Sagebrush 6-10%	22,517	9.01
Sagebrush 11-15%	37,960	15.19
Sagebrush 16-20%	11,364	4.55
Sagebrush 21-25%	51,796	20.73
Sagebrush 26-30%	14,020	5.61
Sagebrush 30% and greater	1,802	0.72
Bare ground	4,344	1.74
Riparian	4,289	1.72
Conifer	223	0.09
Water	2,004	14.00
Agriculture	34,970	0.80

Table 2. Composition of the Lake Mason study area based on classification of 1m 2013 NAIP imagery.

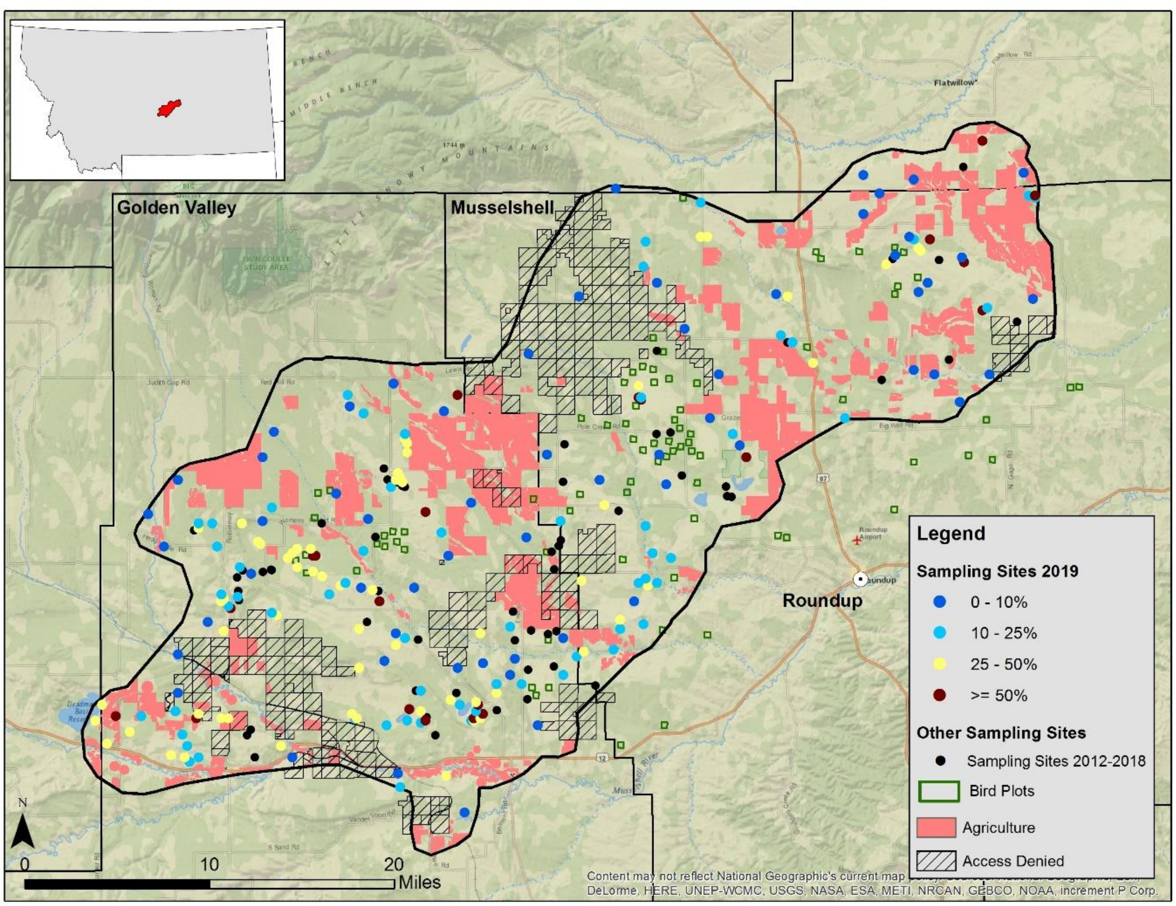

Figure 12. Location of 201 potential arthropod sampling sites for the 2019 field season colored by percent bare ground within a 1-ha circle; and location of previous years' sampling sites, in the Lake Mason study area.

CONCLUSION

Several factors may have contributed to the low percent variance explained by the models. Although Random Forest is known for being well suited to small sample sizes, there were only 59 geographically distinct locations in the whole study area. The 30 samples collected in 2018 did improve percent variance explained, bringing it up from close to zero (for test models developed using 2012-2017 samples only) to the mid-20s; new sample sites in 2019 will hopefully continue this trend. In terms of predictive variables, the main issue is the coarse scale of all the climate variables (800m or 1000m); unfortunately, there are no study-area wide fine-scale climate variables available.

This is a first attempt to model the distribution of arthropod biomass in the Lake Mason area; it will be interesting to see how the 2019 samples conform to model prediction, and to use their data to improve the model. One of the biggest limitations of the current model is the prediction of average biomass over the course of the growing season; if enough data are collected through repeat sampling, it may be possible to run separate models for early vs late growing season.

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