Final Report

Phase I:
Climate Change and Connectivity:
Assessing Landscape and
Species Vulnerability

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Great Plains Landscape Conservation Cooperative

U.S. FOREST SERVICE ROCKY MOUNTAIN RESEARCH STATION

Climate Change and Connectivity: Assessing Landscape and Species Vulnerability

Phase 1

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Table 14. Percentages of the total study area in connected habitat (All), core habitat (Core), and fracture zone (Fracture), broken down by species intersection. Core habitat is defined as being predicted as occupied in at least three out of the nine relative resistance X dispersal ability combinations. Fracture zones are defined as being outside of the core but within the range of connected habitat in at least one of the nine relative resistance X dispersal ability combinations. For example, 0.35% of the study area is jointly core area for both swift fox and

INTRODUCTION

This project is addressing some of the most important emerging conservation issues in the American Great Plains region by studying the interaction of climate change and human development on habitat for native wildlife species. We are integrating the most current understandings of expected future change in vegetation and land use patterns across the Great Plains, and using state-of-the-art spatial analysis and modeling approaches to predict effects of these changes on habitat area, fragmentation and corridor network connectivity. Our products provide practical, detailed and specific management recommendations at scales relevant to population viability for a selected set of focal species.

Increasing human population nationally and regionally fuel urban development and affect land use conversions generally, leading to habitat loss and fragmentation due to conversion of natural land cover to uses dominated by human activities. Simultaneously, climate change is expected to drive large-scale shifts in ecological conditions and geographic shifts in vegetation types. The interaction of these two major ecological stressors is expected to result in complex patterns of habitat loss and fragmentation for many native wildlife species. Predicting the synergistic effects of these multiple stressors at broad geographical scales on habitat area, fragmentation, and connectivity is critical to informed management and perseveration of healthy, functioning, and intact ecosystems.

Climate induced changes in ecosystems coupled with rapidly increasing habitat loss and fragmentation will likely interact in ways that amplify their individual negative effects on biodiversity. It is essential to provide managers with rigorous information on how these dominant stressors will impact a range of native wildlife species across broad landscapes that encompass a substantial proportion of their geographic ranges. This project was designed to provide quantitative and spatially explicit predictions of current and potential future patterns of fragmentation, prioritization of keystone corridors for protection and enhancement, and identification of which species in which places may require habitat restoration or assisted migration to maintain viability. These outcomes will be valuable to natural resources managers, planners, and scientists with a stake in maintaining biodiversity across the Great Plains Landscape Conservation Cooperative (GPLCC).

The research includes a number of components that address common themes identified as high priority for incorporation into research by most Federal agencies and found in the U.S. Fish and Wildlife Strategic Habitat Conservation Plan, the USGS NCCWSC Climate Change Report, and the Forest Service Global Change Research Strategy. The products from this research will include forecasts and scenarios for landuse/climate change impacts, simulation of species response to these changes by linking the change models to dispersal processes for species with different vagilities, and identification and prioritization of specific conservation/restoration areas for on-the-ground conservation implementation. We selected three focal species from the species of greatest conservation concern lists specified in the State Wildlife Action Plans. In addition, the connectivity modeling provides broad understandings that will contribute to the diversity of knowledge required to manage landscapes for the benefit of all native taxa. The project is particularly useful to increasing knowledge of understudied taxonomic groups such as reptiles

and amphibians, invertebrates and non-game mammals. The project provides analysis for the entire GPLCC geographic area, providing broadly relevant management applications.

The research was intended to be completed in two phases. Phase I was designed to focus on developing modeling tools to predict habitat area, fragmentation, and corridor connectivity for the current pattern of habitat area and land use activities. Resistant kernel (Compton et al. 2007; Cushman et al. 2010a) and least-cost path approaches (Cushman et al. 2008; Cushman et al. 2010b) coupled with landscape pattern analysis were used to evaluate *current* habitat area, fragmentation, and corridor connectivity for 3 terrestrial animals of particular conservation concern, as well as a suite of generic species based on biome-level habitat association, dispersal ability and sensitivity to habitat fragmentation. In Phase II of the project, we will evaluate *future* changes to habitat area, fragmentation and corridor connectivity by comparing predicted landscape changes stemming from climate regime shifts, urban development, and their interactions. The climate change component will involve quantifying connectivity for each group of species across dispersal threshold distances for 2 carbon emission scenarios across 2 downscaled Global Circulation Models (GCMs). The urban development component will quantify connectivity across 4 potential future development patterns, based on spatially contagious and network expansion from current development patterns. We will combine climate change and development effects in a third set of analyses to quantify the potential amplification of effects in the combined action of these two important ecological stressors.

This report is focused on Phase I (current funding) findings and the following specific objectives: (1) estimate habitat area, fragmentation and corridor connectivity under current climate and landuse/road network patterns for a large number of native wildlife species expressing a range of habitat requirements and dispersal abilities; and (2) identify key geographical locations that are most important to maintaining population connectivity and facilitating movement for each group of species. Future reports (conditioned on funding) will address Phase II (conditioned on future funding) objectives, including: (3) predict changes to habitat area, fragmentation, and corridor connectivity for selected focal species under six potential future scenarios involving a combination of climate change, urban development, and road network expansion; and (4) develop spatially explicit strategies for adaptation to future climate and development patterns by combining landscape restoration (to facilitate natural movement of species) and assisted migration (when natural movement has a high probability of failure).

METHODS

Study Area and Focal Species
The GPLCC is an applied conservation partnership that will provide science and decision-support tools for the full complement of plant, fish and wildlife resources in the Great Plains geographical area. The geographic area of the GPLCC encompasses parts of eight states: New Mexico, Texas, Oklahoma, Colorado, Kansas, Nebraska, South Dakota, and Wyoming (Figure 1). Some of the most endangered habitats in the U.S. are found in this area, along with a number of imperiled species. In this extent, we have identified two out of the six habitat types as priority: forests and grasslands and model generic forestland- and grassland-associated species with varing degrees of fragmentation sensitivities and dispersal abilities. In addition to these

habitat generalists, we also selected three focal species from the species of greatest conservation concern lists specified in the State Wildlife Action Plans. These species include the swift fox (*Vulpes velox*), lesser prairie-chicken (*Tympanuchus pallidicinctus*), and massasauga (*Sistrurus catenatus*).

Experimental Design

We evaluated current habitat area, fragmentation, and corridor connectivity for our selected focal species (3 terrestrial species of conservation concern) and 2 general habitat associates. To accomplish this we defined a series of landscape resistance models (see Cushman et al. 2006) which reflect the hypothetical costs associated with crossing pixels of each land cover type. We defined a series of movement resistance models for each focal species and species group based on a combination of current biome-level vegetation at an 8km scale (Neilson and Draypek 2009), roads, landuse and landcover. For each species and species group we defined 6 potential resistance models consisting of a 2-way factorial of relative sensitivity to (1) biome-level vegetation (2 levels), and (2) roads and landuse/landcover (3 levels).

For grassland associated species we parameterized resistance to landcover classes to reflect preference for moving through grassland habitat and avoidance of non-grassland cover types. Similarly, for forestland associated species, we parameterized resistance to reflect preference for moving through forest and avoidance of non-forest cover types. We created six resistance layers for forestland biome associated species and six resistance layers for grassland biome associated species. These six resistance layers reflected variation in the relative influence of the combined effects of roads and landuse on resistance to organism movement. Road effects were varied across three levels, from relatively weak to relatively strong effects of roads as movement barriers. Likewise, landcover effects varied across three levels, from relatively strong to relatively weak. We combined these through addition into six different resistance layers for each of the forestland and grassland associated species groups. This resulted in 12 different resistance layers. We replicated all spatial modeling analyses on all 12 of these resistance layers to quantify the degree to which predictions of population connectivity depended on the particular resistance values chosen. Figure 2 shows a workflow diagram of the landscape resistance model creation. Table 1 shows the resistance parameterization for each of the cover classes in the 6 resistance models. Evaluating habitat extent and connectivity across this range of resistance parameters enabled quantitative evaluation of the sensitivity of results to variation in the nature of the functional response to landscape composition (as in Cushman et al. 2006) and allowed us to quantify the degree of uncertainty in our predictions. Figure 3 shows the 3 potential resistance models for grassland associated species defined by roads high/landcover high (grhlh), roads medium/landcover medium (grmlm), and roads low/landcover low (grlll). Figure 4 shows the 3 potential resistance models for forest associated species defined by frhlh, frmlm, and frlll. The differences between these maps primarily are in relation to the relative resistance of crossing the focal habitat (grassland or forest) compared to crossing suboptimal habitat (agriculture, residential, urban) and roads. Contrast is highest in the GRHLH and FRHLH and lowest in the GRLLL and FRLLL.

For Phase I we evaluated current connectivity across a range of dispersal abilities using connectivity thresholds for each species and species group across the full GPLCC extent. We evaluated connectivity across each of the 12 resistance maps described above for each of the 3

focal species and 2 animal groups across a range of dispersal abilities. These dispersal abilities were expressed as distances the organism can move through optimal habitat. The actual modeled dispersal distances are attenuated by cumulative cost of the resistant kernel modeling approach, as in Compton et al. (2007). We chose three dispersal thresholds for each of the three focal species that best reflect the range of uncertainty in the literature regarding their dispersal distances (Table 2). For the grassland and forestland species groups we chose five levels of dispersal ability to reflect the range of dispersal ability that encompassed the vast majority of native wildlife (5km, 10km, 15km, 20km, 25km).

We used two different connectivity modeling approaches to map population core areas, fracture zones and predicted corridors. In our analysis we define core areas as portions of the landscape expected to be occupied by a study species and that experience high internal rates of movement. Fracture zones are defined as areas expected to be sparsely or intermittently occupied, with relatively low internal movement rates due to effects of habitat fragmentation. In our analysis, we define corridors as potentially optimal paths that connect isolated core populations through unoccupied habitat. These are therefore not predicted to be currently functioning habitat corridors, but rather the routes dispersing animals through unoccupied portions of the landscape would optimally take to move from one occupied patch to another. This provided spatially explicit identification of where on the landscape conservation actions may be warranted to maintain, enhance, or create connectivity for species of particular conservation concern. Moreover, this approach allowed us to identify which species or species groups appeared to be most vulnerable to habitat loss and fragmentation caused by climate change.

Connectivity Modeling Approaches

This project has expanded an ongoing project funded through the U.S. Forest Service RMRS Climate Change proposal program. The Forest Service Team has successfully developed tools to predict habitat area, fragmentation, and map corridors based on resistant kernel least-coast path approaches and landscape pattern analysis (e.g. Compton et al. 2007; Cushman et al. 2010a; Cushman et al. 2010b). The resistant kernel approach to modeling landscape connectivity has a number of advantages as a robust approach to assessing current population connectivity for multiple wildlife species under climate change scenarios. First, unlike most corridor prediction efforts, it is spatially synoptic and provides prediction and mapping of expected migration rates for every pixel in the study area extent, rather than only for a few selected "linkage zones" (e.g. Compton et al. 2007). Second, scale dependency of dispersal ability can be directly included to assess how species of different vagilities will be affected by landscape change and fragmentation under a range of scenarios (e.g. Cushman et al. 2010a). Third, it is computationally efficient, enabling simulation and mapping across the entire GPLCC for a large combination of species (e.g. Cushman et al. 2010b).

In addition, the team has developed UNICOR, a species connectivity and corridor identification tool. UNICOR applies Dijkstra's shortest path algorithm to individual-based simulations. We used the UNICOR outputs to designate movement corridors, identify isolated populations, and identify species and subpopulations at risk due to habitat fragmentation. As such, UNICOR provided information needed to develop spatially-explicit conservation and restoration strategies to promote species persistence. The program's key features include a driver-module framework, connectivity mapping with thresholding and buffering, and graph theory metrics. Through

parallel-processing computational efficiency is greatly improved allowing analysis of larger geographic extents and populations. Previous approaches were limited by prolonged computational times and poor algorithmic efficiency that restricted the size of the conservation problem that could be analyzed, or required artificial subsamples of target populations.

Details of the Resistant Kernel Connectivity Modeling Approach

The resistant kernel approach to connectivity modeling is based on least-cost dispersal from some defined set of sources. The sources in our case are the locations of pixels of suitable habitat (for the grassland and forestland analyses) or NATURESERV records of occurrence (for the three focal species). A resistance value is given to each class in the land-cover and roads maps. The resistance value is in the form of the cost of crossing that cover type relative to the least-cost cover type. These costs are used as weights in the dispersal function, such that the expected density in a pixel is down-weighted by the cumulative cost from the source, following the least-cost route (Compton et al. 2007). The initial expected density in each cell for our general grassland and forestland species was set to 1 in each source cell. The initial expected density for our three focal species was set to 1 in each cell containing a NATURESERV record. The predicted density in each surrounding cell in each kernel therefore is density relative to the maximum at a source cell. As described above in the Experimental Design section, we produced six different resistance maps to assess landscape connectivity for species associated with forestlands or grasslands.

The model calculates the expected relative density of each species or species group in each pixel around the source, given the dispersal ability of the species, the nature of the dispersal function, and the resistance of the landscape (Compton et al. 2007; Cushman et al. 2010). We wrote an ESRI ArcGrid script to calculate the resistant kernel (R_k) density. The script uses the ArcGrid COSTDISTANCE function to produce a map of the movement cost from each source up to a specified dispersal threshold. These costdistance grids are inverted and scaled such that the maximum value for each individual kernel is one. Once the expected density around each source cell is calculated, the kernels surrounding all sources are summed to give the total expected density at each pixel. The results of the model are surfaces of expected density of dispersing organisms at any location in the landscape.

We wished to bracket the range of dispersal abilities of animal species breeding in the GPLCC landscape. Accordingly, for forestland and grassland associated species we ran the models over five levels of dispersal ability (D), corresponding to maxima of the COSTDISTANCE function of 5000, 10000, 15000, 20000, and 25000 cost units. These reflect dispersal abilities in optimal habitat that range from 5 to 25 kilometers. We also chose a range of dispersal abilities for each of the three focal species that varied in their inherent dispersal capability (Table 2). The dispersal distance settings for each species were based on careful review of published dispersal distance data in the scientific literature. For the lesser prairie-chicken, Hagen and Giesen (2005) reported that 7% of 348 movements by individuals of this species in sw. Kansas exceeded 30 km. Robb and Schroeder (2005) report that lesser prairie-chicken individuals are capable of long distance movements. They believe there are no natural barriers impeding the connectivity of lesser prairie-chicken populations throughout most of their range. Based on the observed frequency of dispersal greater than 30 kilometers, we chose three dispersal distances to model for the lesser prairie-chicken which likely bracket the functional range of dispersal in this species. These were

20000, 40000, and 80000 cost units, reflecting a range of 20 to 80 kilometers of dispersal ability in optimal habitat. For the massasauga, Mackessy (2005) reports that over the course of the active season, massasaugas moved a considerable distances. Data from three individuals indicated that total distance movements may be 2 to 4 km. Clark et al. (2008) report that massasaugas exhibit population genetic structure over very short distances (1-2 km), indicating either extremely limited natal dispersal, reduced movement associated with mating, or both. Accordingly, we chose dispersal thresholds for massasauga of 2000, 4000, and 6000 cost units, corresponding to dispersal ability in optimal habitat of between 2 and 6 kilometers. For swift fox, Dark-Smiley and Keinath (2003) reported dispersal distances for adult swift foxes averaging 11 km, with an observed maximum distance of 64 km (Mercure et al. 1993). Kamler et al. (2004) report movement of one female swift fox as far as 20 km, before returning to her natal range where she remained philopatric. Based on these published movement abilities we chose dispersal thresholds for swift fox of 10000, 30000, and 60000 cost units, corresponding to dispersal ability of 10 to 60 kilometers in optimal habitat.

Analysis of Kernel Connectivity Maps

The analyses above produced 57 connectivity maps. Nine maps were produced for each focal species (lesser prairie-chicken, swift fox, massasauga), corresponding to the factorial combination of the three dispersal abilities described above and the three levels of relative landscape resistance (Low, Med, High) described in the Experimental Design section above. There were 15 connectivity maps produced for each of the grassland and forestland associated analyses. These comprised the factorial of the five dispersal abilities described above (50000, 10000, 15000, 20000, 25000) and the three levels of relative landscape resistance (Low, Med, High). These output grids provide the basis for several further analyses of population connectivity. In their raw form (Figure 5) these maps depict the expected distribution of connected populations (where the cells are expected to contain non zero occupancy rates for each species) and the variation in expected densities. These two attributes are the foundation for analyses of population distribution, identification of core areas, fracture zones and barriers to dispersal.

Analyzing Extent and Connectivity of Core Habitat

To quantify the extent and connectivity of core habitat, the maps were reclassified into binary form for analysis in FRAGSTATS. We recoded the output grids into binary maps showing the areas predicted to be core habitat for each species and species group. We defined core habitat as all cells in the landscape predicted to have over 10% of the maximum value of the input resistant kernel map. In other words, core areas are all cells that have greater than 10% of the maximum predicted occupancy rates. We analyzed the extent and pattern of core habitat using FRAGSTATS. We used FRAGSTATS (McGarigal et al. 2002) to calculate the percentage of the landscape, correlation length, largest patch index and number of patches of predicted core habitat for focal species and species group. The percentage of the landscape is the simplest metric of landscape composition, and quantifies how much of the study area is covered by potentially occupied habitat for each species and species group. The percentage of the landscape, however, does not quantify any information about the configuration of that potential habitat. Population connectivity is a function of the ability of organisms to traverse continuously through connected habitat. We calculated two additional landscape metrics to provide a view of the degree of connectivity and fragmentation of these core habitats for each species group and focal species.

Correlation length provides a measure of the average distance an organism can move within a patch before encountering the patch boundary from a random starting point. When aggregated at the land type class or landscape level, the correlation length represents the average traversability of habitat within the GPLCC. It gives a global measure of the connectivity within habitat in the GPLCC landscape and is a more relevant functional measure of habitat availability than more basic measures such as patch size, nearest neighbor distance and percentage of the landscape in occupied habitat (McGarigal et al. 2002). Third, we calculated the largest patch index (McGarigal et al. 2002) of connected core habitat. This index reports the extent, as a proportion of the size of the study area, of the largest patch of connected core habitat. Fourth, we calculated the number of patches of internally connected habitat for each species and species group across the combination of dispersal ability and relative landscape resistance.

We analyzed the results of this FRAGSTATS analysis in several ways to quantify the extent and fragmentation of core habitat. First, we use the percentage of the landscape index as a measure of how much potential habitat there is in the study area for each species. Species and species groups predicted to have very low areas of potential core habitat will be at risk of extirpation regardless of the configuration of that habitat. Second, we compare the relative values of correlation length and largest patch index with the percentage of the landscape for each species and species group. This provides a means to assess how connected the predicted core habitat is. For species and species groups in which core habitat is highly fragmented by roads and landuse barriers there will be relatively small values of correlation length and largest patch index, indicating that predicted habitat is highly fragmented into small isolated patches.

We formally evaluated changes in the four FRAGSTATS metrics (percentage of the landscape, correlation length, largest patch index and number of patches) across each factorial described above (combinations of dispersal ability and relative landscape resistance). It is extremely important to evaluate how different plausible combinations of landscape resistance and dispersal ability affect predictions of habitat area and fragmentation. We formally evaluated the full range of all combinations of these for each species and species group for each FRAGSTATS metric to identify thresholds in dispersal ability where fragmentation of connected populations increased greatly, and to quantify the relative importance of dispersal ability in comparison to relative landscape resistance in driving population connectivity for each species and species group.

Identifying Barriers and Fracture Zones
The FRAGSTATS analyses described above provide quantitative evaluation of the extent and fragmentation of core habitat for each species and species group. However, to be most useful to managers within the GPLCC analyses need to provide spatially explicit predictions of the location of barriers breaking up populations and of fracture zones where connectivity is reduced to limited functionality (Figure 6). Mapping barriers and fracture zones provides the information needed for managers to identify the most critical locations in the landscape for conservation or restoration. For example, seeing a barrier caused by a highway between two habitat patches would help guide managers perhaps in siting overpass/underpass structures. Likewise, seeing an attenuated degree of connectivity across a fracture zone of agricultural land between two substantial core populations may help conservationists prioritize land acquisition or easements for restoration to promote enhanced movement through that portion of the landscape.

We mapped barriers and fracture zones for each species and species group across the full factorial of levels of relative landscape resistance and dispersal ability. We identified barriers as locations where the resistant kernel predictions became zero between patches of core habitat. We identified fracture zones as locations where the resistant kernel predictions were

$$0 < R_k < 10\% \text{ of maximum.}$$

This produced definition of patches between core habitat where occupancy and internal movement rates were at least 90% less than the highest recorded for the species or species group. The upper limit of R_k that defines a fracture zone is arbitrary and represents the area of the landscape in which the expected density of individuals is less than 10% of the maximum density. We created barrier and fracture zone maps for each species and species group across the full factorial of landscape resistance and dispersal ability for use by managers in spatially explicit conservation planning and restoration. We also conducted further analyses to identify the areas that are predicted to be barriers and fracture zones simultaneously for the three focal species. Management actions will likely have larger overall benefit if they simultaneously address the ecological needs of multiple species of concern.

Details of the UNICOR Corridor Modeling Approach

The UNICOR simulator uses Dijkstra's algorithm (Dijkstra 1959) to solve the single source shortest path problem from every potential species location on a landscape to every other potential species location. The analysis produces predicted least-cost path routes from each source point to each destination point. These are then combined through summation (as in Cushman et al. 2009) to produce maps of connectivity networks among all pairs of sources and destinations. UNICOR requires two input files: (1) a landscape resistance surface, and (2) point locations for each population or individual's location.

Point locations define starting and ending nodes of individuals. 50 and 100 points were referenced on the landscape resistance surface at a random point placement pattern. From graph theory and network analysis, we can then represent the landscape resistance surface as a graph with nodes and edges. Every pixel is considered to be a node. The graph edges, which represent possible movement paths between each node are weighted by the resistance value of the cell, times the distance to the next pixel center, which gives the total edge length in terms of raster cell units (resistance distance). Dijkstra's algorithm is then implemented to find optimal paths of movement, which is computed for every paired combination of starting and ending nodes. All shortest connections are then combined to produce a connectivity graph.

The maps that are produced by the program show the optimal paths that are buffered based on kernel density estimations (see Silverman 1986; Scott 1992:125-194) following a distribution around frequency of common connections. A choice of a Gaussian function was used for the kernel density estimations (as in Li & Racine 2007). Outputs include maps of paths among habitat patches that can be used to display expected species movement routes and provide managers with visual guidance on identifying corridors that are likely critical for maintaining network connectivity. Quantification of changes to habitat area, fragmentation, and corridor connectivity is enabled through outputs of graph theory metrics (e.g., density, number of nodes,

radius, etc.) and connectivity maps that can directly input into popular landscape ecology programs (e.g., FRAGSTATS (McGarigal *et al.* 2002).

Analysis of UNICOR Connectivity Maps
The analyses above produced 54 connectivity maps. Six maps were produced for each focal species (lesser prairie-chicken, swift fox, massasauga) and each animal group (grasslands and forestlands), corresponding to the factorial combination of the two point placements (50 and 100) and the three levels of relative landscape resistance (Low, Med, High) described in the Experimental Design section above.

RESULTS

Connected habitat
We predicted connected habitat for each species and species group using the resistant kernel analysis across a combination of multiple levels of relative landscape resistance and dispersal ability. The three levels of landscape resistance were Low, Med, and High as defined in Table 1. There were three levels of dispersal ability for each of the three focal species, chosen to bracket the true dispersal ability of each species. There were five levels of dispersal ability for each species group, chosen to cover a broad range from species with limited to high vagility. Connected habitat predictions are areas in the study area that are expected to be joined into patches where kernel predictions of expected density are above 0.1 in every connected pixel. We mapped and analyzed the extent and pattern of connected habitat for each species and species group across the full combination of relative resistance and dispersal ability. Core habitat is predicted to have very high rates of internal movement, and is likely core source habitat for the species. Fracture zones are areas of connected habitat in which movement rates are at least 90% lower than the maximum in the landscape, and are likely areas with attenuated gene flow and partial isolation. However, at the level of analyzing connected habitat, both core and fracture zones are combined.

Lesser prairie-chicken –
We mapped nine different alternative models for lesser prairie-chicken habitat connectivity. These consisted of the factorial of relative landscape resistance (Low, Med, High) and dispersal ability (20km, 40km, 80km). Medium relative landscape resistance and 40km dispersal ability is shown in Figure 7. We chose to illustrate this combination as it reflects the median prediction that we feel best reflects the probable true population connectivity of the species. Maps of predicted connected habitat for all nine combinations of connected relative landscape resistance and dispersal ability for lesser prairie chicken are available for download. In this figure, connected habitat is the area in the center panel occupied by the colored predicted density surface, and in the right panel that is contained in either "core" or "fracture zone" patches.

The figure depicts the pattern of expected distribution of connected habitat and the expected rate of internal movement across each pixel (Figure 7b). The figure shows that connected lesser prairie-chicken habitat at the Med x 40km combination of relative landscape resistance and dispersal ability is concentrated in two regions of the study area, one in the southwest, and another in the north-central. The southwest population exists in a single connected patch with

large core area and high internal migration rates. The north-central populations are broken up into five patches that are predicted to be isolated from one another and from the southwestern population. There is a relatively large core area with high internal migration rate in the central patch in this north-central group. However, the eastern patches in this group are predicted to have weak internal migration rates due to low number of lesser prairie-chicken location records from that area in the NATURESERV database used to populate the model.

We calculated four FRAGSTATS metrics of landscape composition and configuration on the connected habitat maps for all nine combinations for relative landscape resistance and dispersal ability for lesser prairie chicken connected habitat (Table 3) and core connected habitat (Table 4). The metrics are percentage of the landscape occupied by connected habitat (PLAND), number of isolated patches of internally connected habitat (NP), correlation length of connected habitat (CL), and largest patch of connected habitat percentage of the landscape (LPI). At all levels of dispersal ability and relative landscape resistance, there was a very large decrease in the FRAGSTATS metrics between analysis of all connected habitat (Table 3) and only the core connected habitat (Table 4). Specifically, core habitat comprises about 1/3 the total area of connected habitat, and has roughly half the connectivity as measured by correlation length and largest patch index. The percentage of the landscape, correlation length and largest patch index of connected habitat increase greatly, and the number of patches decreases, with changes in dispersal ability (Figure 8). In contrast, extent and connectivity of connected habitat is largely independent of the relative values of landscape resistance used in our analysis. Table 5 quantifies the relative importance of dispersal ability compared to landscape resistance for each of the landscape metrics calculated. For all four landscape metrics dispersal ability had more than a ten times greater effect than variation in relative landscape resistance.

Swift fox –
We mapped the same nine different alternative models of habitat connectivity, consisting of the factorial of relative landscape resistance (Low, Med, High) and dispersal ability (10km, 30km, 60km). The Medium relative resistance and 30km dispersal ability scenario is shown in Figure 9. In this figure, connected habitat is the area in the left panel occupied by the colored predicted density surface, and in the right panel that is contained in either "core" or "fracture zone" patches. Maps of predicted connected habitat for all nine combinations of connected relative landscape resistance and dispersal ability for Swift fox are available for download.

Figure 9b depicts the pattern of expected distribution of connected habitat and the expected rate of internal movement across each pixel. The figure shows that connected Swift fox habitat at the Med x 30km combination of relative landscape resistance and dispersal ability is relatively wide spread across the northwestern 2/3 of the study area, with four large core concentrations. The northernmost populations are broken up into two major centers and several smaller isolated subpopulations predicted to be isolated from one another. The large west-central concentration area is largely connected into a single large patch containing several large core areas predicted to have high rates of internal movement linked across fracture zones of attenuated movement. Finally, there are several isolated subpopulations in the southwestern corner of the study area, including one core area predicted to a relatively high density of internal movement based on the records in the NANTURESERV database used to populate the model.

We calculated the same four FRAGSTATS metrics of landscape composition and configuration on the connected habitat maps for all nine combinations for relative landscape resistance and dispersal ability for swift fox (Table 6; Table 7). At all levels of dispersal ability and relative landscape resistance, there was a very large decrease in the FRAGSTATS metrics between analysis of all connected habitat and only the core connected habitat. Specifically, core habitat comprises about ¼ to 1/2 the total area of connected habitat, and has roughly 1/3 to ½ the connectivity as measured by correlation length and largest patch index. As for the lesser prairie-chicken, the percentage of the landscape, correlation length and largest patch index of connected habitat increase greatly, and the number of patches decreases, with changes in dispersal ability (Figure 10). Also consistent with the lesser prairie chicken, extent and connectivity of connected swift fox habitat is largely independent of the relative values of landscape resistance used in our analysis. For all four landscape metrics dispersal ability had more than 20 times greater effect than variation in relative landscape resistance Table 5.

Massasauga –
We mapped the same nine different alternative models of habitat connectivity, consisting of the factorial of relative landscape resistance (Low, Med, High) and dispersal ability (2km, 4km, 6km) for the massasuaga. One of those combinations is shown in Figure 11. This figure shows the strong effect of the limited dispersal ability of this species, with connected habitat concentrated in close proximity to the occurrence records taken from the NATURESERV database. Maps of predicted connected habitat for all nine combinations of connected relative landscape resistance and dispersal ability for massasauga are available for download.

Figure 9b depicts the pattern of expected distribution of connected habitat and the expected rate of internal movement across each pixel for the Med x 4km combination of relative landscape resistance and dispersal ability. The figure shows that the population of this species is concentrated in the west-central area of the study area. Most of the predicted occurrence is united by dispersal into a single patch, with a number of apparently isolated satellite subpopulations. There are also several small and isolated subpopulations in the central and northeast parts of the study area.

We calculated the same four FRAGSTATS metrics of landscape composition and configuration on the connected habitat maps for all nine combinations for relative landscape resistance and dispersal ability for massasauga (Table 8; Table 9). In contrast to the previous focal species, there was a relatively small decrease in the FRAGSTATS metrics between analysis of all connected habitat and only the core connected habitat. This reflects the limited dispersal ability of the species, which concentrates patches into core area with limited fracture zone area. As in the previous cases, the percentage of the landscape, correlation length and largest patch index of connected habitat increase greatly, and the number of patches decreases, with changes in dispersal ability (Figure 12). Also consistent with the previous two species, extent and fragmentation of connected massasauga habitat is largely independent of the relative values of landscape resistance used in our analysis. For all four landscape metrics dispersal ability had more than 10 times greater effect than variation in relative landscape resistance Table 5.

Grassland associated species –
We mapped 15 different alternative models for grassland associated species habitat connectivity. These consisted of the factorial of relative landscape resistance (Low, Med, High) and dispersal ability (5km, 10km, 15km, 20km, 25km). We chose a broader range and more levels of dispersal ability because, unlike in the previous cases of particular focal species, we wished to depict habitat connectivity conditions for a broad range of species which depend on grassland for habitat. One of those combinations is shown in Figure 13. Maps of predicted connected habitat for all 15 combinations of connected relative landscape resistance and dispersal ability for grassland associated species are available for download. In this figure, connected habitat is the area in the center panel occupied by the colored predicted density surface, and in the right panel that is contained in either "core" or "fracture zone" patches.

The figure depicts the pattern of expected distribution of connected habitat and the expected rate of internal movement across each pixel (Figure 13b). The figure shows that connected grassland associated species habitat at the Med x 20km combination of relative landscape resistance and dispersal ability is distributed broadly in the study area, with four major concentrations in different regions of the study area. The north-northcentral connected habitat exists in a largely connected block containing numerous core areas of predicted high internal connectivity linked by fracture zones of predicted lower movement and migration rates. Similarly, the large area of habitat in the south-central portion of the study area in predicted to be dominated by a large patch of connected habitat, partly or completely broken in places by narrow bands of high resistance, associated with major highways and urban/residential development. In contrast, habitat in the south-central portion of the study area is predicted to comprise a network of complex patches partly or completely isolated by agriculture and urban/residential development.

The four FRAGSTATS metrics of landscape composition and configuration on the connected habitat maps for all 15 combinations for relative landscape resistance and dispersal ability for grassland associated species are shown in Table 10 (all connected) and Table 11 (core). At all levels of dispersal ability and relative landscape resistance, there was a very large decrease in the FRAGSTATS metrics between analysis of all connected habitat and only the core connected habitat. Specifically, core habitat comprises about 1/10 to 1/2 the total area of connected habitat, and has roughly 1/3 the connectivity as measured by correlation length and largest patch index. The percentage of the landscape, correlation length, and largest patch index of connected habitat increase greatly with changes in dispersal ability, while number of patches decreases (Figure 14). As for the focal species described above, extent and connectivity of connected habitat for grassland associated species is largely independent of the relative values of landscape resistance used in our analysis. Table 5 quantifies the relative importance of dispersal ability compared to landscape resistance for each of the landscape metrics calculated. For all four landscape metrics dispersal ability had greater effect than variation in relative landscape resistance. However, this difference in effects size was much weaker for correlation length, largest patch index and number of patches than was seen in the three focal species. For correlation length and largest patch index, the effect of dispersal ability was approximately twice as large as the impact of variation in relative landscape resistance, while for number of patches of internally connected habitat the effects were approximately equal.

Forestland associated species –

One of the combinations 15 different alternative models for forestland associated species habitat connectivity is shown in Figure 15. Maps of predicted connected habitat for all 15 combinations of connected relative landscape resistance and dispersal ability for grassland associated species are available for download. The figure depicts the pattern of expected distribution of connected habitat and the expected rate of internal movement across each pixel (Figure 15b) for forestland associated species habitat at the Med x 20km combination of relative landscape resistance and dispersal ability. Internally connected forest habitat is largely restricted to the extreme west-northwestern part of the study area, mostly outside the boundaries of the GPLCC proper. There is also some highly fragmented forestland habitat in the south eastern corner of the study area.

At all levels of dispersal ability and relative landscape resistance, there was a very large decrease in the FRAGSTATS metrics between analysis of all connected habitat (Table 12) and only the core connected habitat (Table 13). Specifically, core habitat comprises about 1/5 the total area of connected habitat, and has roughly 1/4 the connectivity as measured by correlation length and largest patch index. The percentage of the landscape, correlation length, and largest patch index of connected habitat increase greatly with changes in dispersal ability, while number of patches decreases (Figure 16). The extent and connectivity of connected habitat for grassland associated species is largely independent of the relative values of landscape resistance used in our analysis. Table 5 shows that for all four landscape metrics, dispersal ability had much greater effect than variation in relative landscape resistance.

Corridor

We predicted corridor habitat for each species and species group using UNICOR across a combination of multiple levels of relative landscape resistance and point densities. The three levels of landscape resistance were Low, Med, and High as defined in Table 1. There were two levels of random point placement, 50 and 100 points. Corridor habitat predictions are areas in the study area that are expected to be joined from shortest-path connections or easiest movement through the resistance surface. We mapped and analyzed the extent and pattern of corridor habitat for each species and species group across the full combination of relative resistance and two point densities. Corridor habitats are areas of connection in which movement rates are expected to be highest, and are likely areas with increased gene flow.

Lesser prairie chicken –

We mapped six different alternative models for lesser prairie-chicken corridors. These consisted of the factorial of relative landscape resistance (Low, Med, High) and point placement (50, 100). The 100 point placement across the landscape resistances is shown in Figure 7a. Maps of predicted corridors for all six combinations of relative landscape resistance and point placements for lesser prairie-chicken are available for download. In this figure, corridor habitat is the area occupied by the colored predicted Guassian kernel density surface.

The figure depicts the pattern of expected corridors and the expected rate of internal movement across each landscape resistance surface. The figure shows that corridors of lesser prairie-chicken across each relative landscape resistance are concentrated in the southwest with two major paths (dark gold) leading to the central region.

Swift fox –

We mapped six different alternative models for swift fox corridors. These consisted of the factorial of relative landscape resistance (Low, Med, High) and point placement (50, 100). The 100 point placement across the landscape resistances is shown in Figure 9a. Maps of predicted corridors for all six combinations of relative landscape resistance and point placement for Swift fox are available for download. In this figure, corridor habitat is the area occupied by the colored predicted Guassian kernel density surface.

The figure depicts the pattern of expected corridors and the expected rate of internal movement across each landscape resistance surface. The figure shows the corridors of swift fox across each relative landscape resistance that are concentrated in the southwest with major paths leading to the northwest region.

Massasauga –

We mapped six different alternative models for massasauga corridors. These consisted of the factorial of relative landscape resistance (Low, Med, High) and point placement (50, 100). The 100 point placement across the landscape resistances is shown in Figure 11a. Maps of predicted corridors for all six combinations of relative landscape resistance and point placement for massasauga are available for download. In this figure, corridor habitat is the area occupied by the colored predicted Guassian kernel density surface.

The figure depicts the pattern of expected corridors and the expected rate of internal movement across each landscape resistance surface. The figure shows the corridors of massasauga across each relative landscape resistance that are concentrated in the central with paths leading to the northeast region.

Grassland associated species –

We mapped six different alternative models for grassland associated species corridors. These consisted of the factorial of relative landscape resistance (Low, Med, High) and point placement (50, 100). The 100 point placement across the landscape resistances is shown in Figure 13a. Maps of predicted corridors for all six combinations of relative landscape resistance and point placement for grassland associated species are available for download. In this figure, corridor habitat is the area occupied by the colored predicted Guassian kernel density surface.

The figure depicts the pattern of expected corridors and the expected rate of internal movement across each landscape resistance surface. The figure shows the corridors of grassland associated species across each relative landscape.

Forestland associated species –

We mapped six different alternative models for forest associate species corridors. These consisted of the factorial of relative landscape resistance (Low, Med, High) and point placement (50, 100). The 100 point placement across the landscape resistances is shown in Figure 15a. Maps of predicted corridors for all six combinations of relative landscape resistance and point placement for forest associate species are available for download. In this figure, corridor habitat is the area occupied by the colored predicted Guassian kernel density surface.

The figure depicts the pattern of expected corridors and the expected rate of internal movement across each landscape resistance surface. The figure shows the corridors of forest associated species across each relative landscape.

Multiple-species Patterns

One of the key objectives of this project is to evaluate the degree to which conservation strategies can be designed to meet the needs of multiple species or species simultaneously. To assess this we computed the intersection of core areas, fracture zones and corridors for each of the three focal species.

Multiple-species Core –

We intersected the core areas for each species to depict areas that are predicted to be highly important centers of internally connected habitat patches for multiple species. To do this intersection we needed to produce a single core map for each species. We collapsed the core maps across the factorial of relative landscape resistance dispersal ability for each species by taking as core the area that was predicted as core in at least 7 of the 9 core maps of the factorial for each species. The intersection map for predicted core areas is shown in Figure 17. In the figure blue areas are core for swift fox and no other species, yellow for prairie chicken only and red for snake only. Green are core for both fox and snake, purple for fox and chicken, orange for snake and chicken and brown for all three species simultaneously. We computed the percentage of the landscape in each of these intersection classes (Table 14). 92% of the study area is not inside any core area. About 4.5% of the study area is fox only core, and about 2.3% is prairie chicken only core. Interestingly, none of the multiple-species intersections totaled even 0.5% of the study area, with the intersection of Swift fox and prairie chicken core areas by far the greatest. There was virtually zero three-way overlap between core area of Swift fox, prairie chicken and massasauga.

Multiple-species Fracture –

Similarly to the intersection of core areas, we intersected the fracture zones for each species to depict areas that are predicted to be peripheral dispersal habitat for multiple species simultaneously. To do this intersection we needed to produce a single core map for each species. We collapsed the core maps across the factorial of relative landscape resistance dispersal ability for each species by taking as fracture the area that was predicted as connected habitat 3 of the 9 combinations of the factorial, but not core area, for each species. The intersection map for predicted fracture zones is shown in Figure 17b. In the figure blue areas are core for swift fox and no other species, yellow for prairie chicken only and red for snake only. Green are core for both fox and snake, purple for fox and chicken, orange for snake and chicken and brown for all three species simultaneously. We computed the percentage of the landscape in each of these intersection classes (Table 14). In contrast to core area, which exhibited very little intersection, there was considerable overlap among fracture zone habitat for swift fox and lesser prairie chicken. 76% of the study area is not inside fracture zone for any species. About 13% of the study area is fox only fracture zone, and about 6.11% is prairie chicken only core. The intersection of Swift fox and prairie chicken core areas by far the greatest, amounting to 3.7% of the study area. The other intersections were very small.

DISCUSSION

Measuring current species vulnerability and mapping current habitat connectivity are identified as core needs in the GPLCC. Landscape connectivity is critical to species viability at several scales. Mobile animals engage in movement behavior to maximize fitness by increasing access to critical resources and minimizing risk of predation. As organisms move through spatially complex landscapes, they respond to the conditions of multiple ecological attributes, expressing movement paths that optimize fitness benefits while minimizing fitness costs. At the population level, connectivity is centrally important to regional viability of animal populations (Hanski 1998; Flather & Bevers 2002; Cushman 2006). Habitat loss and fragmentation have been identified as perhaps the most important drivers of the global biodiversity crisis (Fahrig 2003) and there is a wide consensus that studies of the effects of habitat fragmentation are especially urgent and should receive special priority (Lubchenko et al. 1991, Cushman 2006). Habitat fragmentation decreases dispersal (Gibbs 1998), increases mortality (Fahrig et al.1995) and reduces genetic diversity (Reh & Seitz 1990; Wilson & Provan 2003; Keyghobadi et al. 2005). Populations may decline if immigration is prevented (Brown & Kodric-Brown 1977; Harrison 1991) and may not be recolonized following local extinction (Semlitsch & Bodie 1998). Thus, the ability of individual animals to move across complex landscapes is critical for maintaining regional populations (Fahrig 2003; Cushman 2006).

Connectivity is also critical at the level of species ranges. Projected climate over the next few centuries is expected to substantially displace the geographic range of many species. Anticipating how current landscape conditions, including landscape permeability, will affect future species immigration patterns (rates and direction) is a very complex problem. If conservation practitioners are to address individual species dispersal constraints, then reliable and robust spatially-explicit models of how species will respond to climate and landuse change are needed. Such models are required to evaluate which species are likely able to accommodate future shifts in suitable habitat; which species may need assistance; what kind of landscape management can be employed to facilitate range shift; and where in the landscape would management be best applied. Despite the clear importance of habitat connectivity for population persistence, specific factors mediating connectivity are largely unknown for most species (With et al. 1997, Bowne and Bowers 2004, Cushman 2006). There have been hundreds of theoretical and empirical studies of the ecological effects of habitat fragmentation conducted over the past 20 years (Saunders et al. 1991, Andre´n 1994, Debinski and Holt 2000, McGarigal and Cushman 2002). The knowledge gained from these studies has come from a variety of approaches, including field observations, experiments, as well as spatially-explicit mathematical models. In spite of these efforts, very little is yet known about the mechanisms that link ecosystem population responses to changes in habitat patterns that result from fragmentation.

Our analysis estimated habitat area, fragmentation, and corridor connectivity under current climate and landuse/road network patterns for a large number of native wildlife species whose life histories span a range of habitat requirements and dispersal abilities. Our analysis relied on both resistant kernel and least-cost corridor modeling approaches. The resistant kernel approach to modeling landscape connectivity has a number of major advantages as a robust approach to assessing current and future population connectivity for multiple wildlife species under climate change scenarios. First, unlike most corridor prediction efforts, it is spatially synoptic and

provides prediction and mapping of expected migration rates for every pixel in the study area extent, rather than only for a few selected "linkage zones" (e.g. Compton et al. 2007). Second, scale dependency of dispersal ability can be directly included to assess how species of different vagilities will be affected by landscape change and fragmentation under a range of scenarios (e.g. Cushman et al. 2010a). The least-cost corridor analyses used a species connectivity and corridor identification tool called UNICOR developed by the project team. UNICOR applies Dijkstra's (1959) shortest path algorithm to individual-based simulations to designate movement corridors, identify isolated populations, and identify species and subpopulations at risk due to habitat fragmentation. The combination of kernel and path-based approaches enables a full assessment of species specific, scale-dependent population core areas, fracture zones, and movement corridors across the GPLCC. This enables the identification of key geographical locations that are most important to maintaining population connectivity and facilitating movement for each group of species in the current landscape conditions, and to develop spatially explicit strategies for maintaining current population connectivity for multiple species of conservation concern. The approach is a further development of that proposed by Cushman et al. (2008), who used a similar corridor modeling approach to identify over 20 key locations that should receive focus in efforts to preserve or enhance connectivity of bear populations in the U.S. Northern Rocky Mountains.

Quantifying Current Habitat Area, Fragmentation, and Corridor Connectivity for Focal Species

Our maps and statistical analyses (Tables 3-14, Figures 7-17) provide a basis to assess current habitat area, fragmentation, and corridor connectivity across the full extent of the GPLCC for three focal species of conservation concern. This enables identification of key geographical locations that are most important to maintaining population connectivity and facilitating movement for each species in the current landscape conditions, and to develop spatially explicit strategies for maintaining current population connectivity for multiple species of conservation concern.

Lesser prairie-chicken: key locations for maintaining connectivity –

The combination of scale-dependent predictive mapping of core, fracture, and corridors for lesser prairie chicken enable us to identify key geographical locations for maintaining population connectivity for this species. Full detail and spatial data on the predicted core areas, fracture zones, and corridors for this species are available for download. The analysis provides a comprehensive assessment of population connectivity which accounts for the uncertainty in the response of the species to landscape composition and uncertainty in the dispersal ability of the species. We evaluated nine combinations of relative landscape resistance and dispersal ability. We identified locations in the GPLCC predicted to be important core, fracture, and corridors for this species in all of the nine combinations. This provides a consensus prediction of areas that are important for maintaining population connectivity in the current landscape context.

Core Areas – Core areas for prairie-chicken occur in two distinct metpopulations (Figure 18). The largest and most well-connected population occurs in the extreme southwest portion of the GPLCC (southeastern NM). The other core area complex is less well-connected and occurs as a set of diffuse subpopulations in the central portion of the GPLCC. Maintaining existing core areas is the single most important means to maintain viable populations of the lesser prairie-

chicken. Thus, we recommend conservation efforts focus on maintaining and expanding all existing predicted lesser prairie-chicken core population areas.

Fracture Zones – We identified two key fracture zones that lay between major core areas. These are the subset of fracture zones for lesser prairie-chicken that should receive the largest focus for conservation or restoration, as they are the expected linkages between existing core areas (Figure 18). The key fracture zone in the northern most patch results in near isolation of the northern cluster of lesser-prairie chicken subpopulations. Long-term viability of these small and isolated groups probably will depend on maintaining gene flow and demographic rescue through this fracture zone. The southern key fracture zone is a predicted area of greatly attenuated connectivity between the two largest patches of core habitat of this species in the GPLCC. As such, maintaining and enhancing connectivity through both of these fracture zones is of very high priority.

Corridors – We identified four key corridors that predict the optimal movement routes among isolated core areas (Figure 19). Long-term viability of the lesser prairie-chicken may depend on gene flow and demographic rescue among the metapopulation of core areas. The four key corridors may provide optimal routes for dispersal among the large isolated clusters of population core areas. These key corridors are substantially longer than the estimated dispersal ability of the species. Therefore, for the predicted corridors to be effective at spanning these gaps, additional habitat restoration or establishment of stepping stone populations may be necessary. This is particularly the case for the gap between the large southern core populations and the smaller and more scattered northern populations. This gap is many times larger than the dispersal ability of the species, meaning that demographic or genetic rescue of the northern populations by the southern population is unlikely. Enhancing connectivity among the full network of core areas is potentially critical for long-term viability. This is especially the case for the lesser prairie chicken in the GPLCC, which is predicted to exist in three distinct and largely mutually-isolated metapopulations. Enhancing movement and gene flow among these metapopualtions may be critical to provide flexibility necessary for population response to climate change. Conservation efforts should target habitat protection and restoration in the northern three corridor areas, as these have potential to help link several isolated core areas through dispersal. The extensively long corridor linking the southern core complex to the northern populations is probably too long to be mitigated through conservation actions.

Swift fox: key locations for maintaining connectivity –

Full detail and spatial data on the predicted core areas, fracture zones and corridors for swift fox are available for download. The analysis provides a comprehensive assessment of population connectivity which accounts for the uncertainty in the response of the species to landscape composition and uncertainty in the dispersal ability of the species. We evaluated nine combinations of relative landscape resistance and dispersal ability, producing consensus prediction of areas that are important for maintaining population connectivity in the current landscape context.

Core Areas –Predicted swift fox core population areas are found in three clusters of core habitat (Figure 20). All three clusters occur in the western half of the GPLCC, with the two largest clusters occurring the in the northwestern quadrant. Maintaining existing core areas is the

single most important means to maintain viable populations of the swift fox. Thus, we recommend conservation efforts focus on maintaining and expanding all existing predicted swift fox core population areas.

Fracture Zones – We identified three key fracture zones that lay between core areas for swift fox across the full extent of the GPLCC. These are the subset of fracture zones for the swift fox that should receive the largest focus for conservation or restoration, as they are the expected linkages between existing core areas that likely have the greatest conservation benefit for swift fox. The southern two key fracture zones we predicted potentially represent serious impediments to potential dispersal and gene flow. Our fracture zone analysis predicts these areas experience greatly attenuated movement rates, which probably results in nearly complete isolation of the core areas separated on either side of these fracture zones. This may result in near isolation of the large core population clusters in the south from those in the northern part of the study area. In addition, these fracture zones may break the large, central complex of swift fox core populations into three isolated subpopulations. This subdivision of the population could have detrimental effects on long-term viability. Enhancing connectivity across these fracture zones through a combination of preservation of existing habitat and restoration and enhancement of degraded habitat, therefore, is of high priority for swift fox conservation. In contrast, our predicted northernmost fracture zone is relatively modest in effect, with the cluster of core populations largely interconnected by high predicted rates of movement. Maintaining existing connectivity among core areas is the second most important conservation action and should be focused within the two southernmost key fracture zones (Figure 20). Given the small and fragmented nature of core areas in the south, it is likely that funds directed at restoring habitats in fracture zones here may have limited benefits to maintaining persistence of swift fox across the GPLCC.

Corridors – We identified three corridors that are least cost routes linking isolated swift fox population core areas (Figure 21). Long-term swift fox viability in the GPLCC may depend on gene flow and demographic rescue among the metapopulation of core areas. The three major gaps among the swift fox core areas are substantially wider than the estimated dispersal ability of the species. Therefore, for the predicted corridors to be effective at spanning these gaps, additional habitat restoration or establishment of stepping stone populations may be necessary. This is particularly the case for the gap between the large central core population and the small and highly isolated southern most core population. This gap is many times greater than the maximum dispersal ability of the species. The two northern gaps spanned by predicted corridors are also substantially greater than the dispersal ability of the species, indicating the swift fox population in the GPLCC may be functionally isolated into several distinct metapopulations. This has potentially large implications for long-term viability of swift fox in the GPLCC. Isolation of small metapopulations across large gaps, such as is predicted by our connectivity modeling, suggests relatively high vulnerability of the isolated portions of the swift fox population to genetic drift and demographic stochasticity. This is particularly true for the core swift fox populations in the southern part of the GPLCC are extremely isolated by distances many times greater than the maximum dispersal ability of the species. This gap is probably too large to mitigate through active management. However, mitigating the potential isolation between the large central population and the northern populations by protecting and restoring habitat in the two northern corridors should receive high priority. Improving connectivity across these gaps will greatly enhance connectivity among the full network of core areas, which is

potentially critical for long-term viability, and will provide flexibility necessary for population response to climate change.

Massasauga: key locations for maintaining connectivity –
Full detail and spatial data on the predicted core areas, fracture zones and corridors for massasauga are available for download. The analysis provides a comprehensive assessment of population connectivity which accounts for the uncertainty in the response of the species to landscape composition and uncertainty in the dispersal ability of the species. We evaluated nine combinations of relative landscape resistance and dispersal ability, producing consensus prediction of areas that are important for maintaining population connectivity in the current landscape context.

Core Areas – Maintaining existing core areas is the single most important means to maintain viable populations of massasuaga. Key core areas for massasauga are of a limited spatial extent and are concentrated in the west-central portion of the GPLCC (Figure 22). Owing to the species' limited dispersal capability, core areas are small and highly fragmented. Given the critical role existing core populations play in species viability, we recommend conservation efforts focus on maintaining and expanding all existing predicted massasauga core population areas.

Fracture Zones – We identified key fracture zones that lay between consensus core areas for swift fox across the full extent of the GPLCC (Figure 22). These are the subset of fracture zones for the massasauga that should receive the largest focus for conservation or restoration, as they are the expected linkages between existing core areas. The NATURESEV database suggested a relatively limited distribution of this species in the study area, clustered largely in the west-central area. This population cluster was predicted to have relatively high internal connectivity, with relatively few fracture zones within it. However, given the very limited dispersal ability of this species, the southern two of the three key fracture zones we identified appear to represent near complete barriers isolating core areas. In contrast, northernmost key fracture zone is predicted to experience relatively high movement and migration. Therefore, we recommend efforts at enhancing connectivity to focus on the southern two key fracture zones, while maintaining habitat connectivity in the northern key fracture zone..

Corridors – We identified three key corridors that predict the optimal movement routes among isolated massasauga population core areas (Figure 23). Long-term massasauga viability in the GPLCC may depend on gene flow and demographic rescue among the metapopulation of core areas. Given the very limited dispersal ability of this species, all these gaps are predicted to result in isolation of core populations separated across them. The westernmost two predicted corridors are relatively short and plausibly could function to a limited degree. In contrast the eastern predicted corridor is immensely long, spanning several states, while linking several small and disjunct populations. This corridor is not likely to provide any practical conservation service to this species. Maintenance of the isolated eastern populations will likely require local habitat enhancement, conservation and, when necessary, population augmentation to increase genetic diversity and bolster population size. Habitat protection and enhancement in the western two key corridor areas, coupled with establishing stepping stone populations, are high priority actions to help maintain viable populations of the massasauga in the GPLCC.

Spatially Explicit Strategies for Maintaining Connectivity for Multiple Species

The identification of consensus core, fracture, and corridor areas for each focal species provides means to develop optimized single-species conservation applications. However, efficiency of conservation outcomes in the contexts of limited budgets will depend on effective strategies to address connectivity needs of multiple species simultaneously. We addressed this in two ways. First, we evaluated the degree to which the geographic footprint of core areas, fracture zones, and corridors intersected among each species. Full detail and spatial data on the intersection of core, fracture and corridor among species is available for download. We identified the core, fracture, and corridor intersection among species that are also identified as key consensus areas for each species, as described above (Figure 17). This subset would be considered high priority for conservation action if the goal is to protect critical core and connectivity habitat for several of our focal species simultaneously.

Quantifying Current Habitat Area, Fragmentation, and Corridor Connectivity for Species Groups

The analyses for our three focal species incorporate the best available information on their actual distribution with quantitative modeling of core and connectivity areas. However, there are many additional species which are not addressed in our analyses for these three focal species. To provide a broad assessment of core and connectivity habitat conditions we also assessed core areas, fracture zones and movement corridors for broadly defined habitat associated species groups. These are grassland and forestland associated species. We assessed core, fracture and core areas for these species across 15 combinations of dispersal ability (Tables 10 and 11). These 15 combinations are intended to provide a broad net that will represent the range of dispersal ability and response to landscape conditions for most native species associated with these ecosystems.

Grassland associated species: key locations for maintaining connectivity –

Full detail and spatial data on the predicted core areas, fracture zones and corridors for grassland associated species are available for download at. The analysis provides a comprehensive assessment, which accounts for the uncertainty in the response of the species to landscape composition and uncertainty in the dispersal ability of the species. We evaluated 15 combinations of relative landscape resistance and dispersal ability, producing consensus prediction of areas that are important for maintaining population connectivity in the current landscape context.

Core Areas – Maintaining existing core areas is the single most important means to maintain viable populations of grassland associated species. Core areas across the 15 combinations of relative landscape resistance and dispersal ability for grassland associated species are identified in Figure 23.

Fracture Zones – We identified 15 key fracture zones that lay between core areas for grassland associated across the full extent of the GPLCC. These are the subset of fracture zones for grassland associated species that should receive the largest focus for conservation or restoration, as they are the expected linkages between existing core areas. Maintaining existing connectivity among core areas is the second most important conservation action. Figures 23, 24

and 25 show the locations and structure of these fracture zones. Many of them are associated with narrow bands of impacted habitat and interstate highways, making them good candidates for structural projects, such as overpasses/underpasses on highways, coupled with habitat restoration and conservation. Others are a result of more diffuse and fragmenting habitat loss by agricultural and urban development, and will require a more broad-scale effort at habitat conservation and restoration in a spatially optimized design to increase the functional connectivity of the core areas separated across them. The three northernmost fracture zones fall into this category. These are particularly important, because, along with the northernmost corridors, these fracture zones potentially are the key to linkage between the large group of population core areas in the northern portion of the GPLCC and those in the central and southern parts of the study area. Therefore, habitat protection and restoration in these three northernmost fracture zones may be the second most important conservation objective for grassland associated species, after protecting and expanding existing core population areas.

Corridors –Long-term viability of a range of grassland associated species in the GPLCC may depend on gene flow and demographic rescue among the metapopulation of core areas. We identified key corridors that predict the optimal movement routes among isolated grassland associated species population core areas (Figure 26). The northernmost two of the five identified corridors linking core populations are most important for maintaining regional connectivity of grassland habitat. These northern two corridors provide the only links between the extensive core populations in the northern part of the GPLCC and the rest of the study area. As such, regional connectivity of grassland associated species habitat may depend on movement through these predicted corridors. Therefore, we believe these areas should receive high priority for conservation actions aimed at enhancing movement and survivorship. In contrast, the southern three corridors provide alternative routes between core areas that are linked through additional pathways that pass through fracture zones and other core areas. Therefore we suggest focus on the northern two corridors, while maintaining habitat connectivity in the regions occupied by the southern corridors. Enhancing connectivity among the full network of core areas is potentially critical for long-term viability, and is likely critical to provide flexibility necessary for population response to climate change.

Forestland associated species: key locations for maintaining connectivity –
Full detail and spatial data on the predicted core areas, fracture zones and corridors for forestland associated species are available for download. The analysis provides a comprehensive assessment, which accounts for the uncertainty in the response of the species to landscape composition and uncertainty in the dispersal ability of the species. We evaluated 15 combinations of relative landscape resistance and dispersal ability, producing consensus prediction of areas that are important for maintaining population connectivity in the current landscape context.

Core Areas – Maintaining existing core areas is the single most important means to maintain viable populations of forestland associated species. Core forest habitat is clustered in a band that runs north to south in the far western edge of the study area, mostly outside of the boundary of the GPLCC proper. Key core areas across the 15 combinations of relative landscape resistance and dispersal ability for grassland associated species are identified in Figure 27.

Fracture Zones – We identified five key fracture zones that lay between consensus core areas for forestland associated across the full extent of the GPLCC (Figure 27). These are the subset of fracture zones for forestland associated species that should receive the largest focus for conservation or restoration, as they are the expected linkages between existing core areas. The southernmost of the five identified key fracture zones is predicted to have relatively high connectivity. Maintaining current habitat in this fracture zone is the best strategy. The most important fracture zones for forest associated species are the second, third and fourth from the northernmost. The second is predicted to be a nearly complete gap, associated with Interstate 70 west of Denver. The third and fourth fracture zones are probably the most important, as they provide key connection points that link the northern and southern complexes of forestland associated species core population areas. Maintaining existing connectivity among core areas these core areas is the second most important conservation action, after maintaining the core populations themselves. Therefore, we recommend actions to protect and restore connectivity within the third and fourth fracture zones identified for forestland associated species as the highest priority conservation actions, following preservation of existing core areas, for the conservation of species associated with forest habitat.

Corridors – We identified key corridors that predict the optimal movement routes among isolated forestland associated species population core areas (Figure 28). Core areas for grassland associated species are highly restricted within the GPLCC, concentrated in a north-south band at the extreme western boundary, and also spread in a sparse pattern in the southeastern corner. Our corridor modeling approach predicted the least cost routes between all these core areas. However, given the immense distances among these, most of the predicted corridors for forestland associated species are not biologically relevant. Even for the most highly mobile avian species, the dispersal distances between the western and southeastern core areas are likely too great to be feasible. Therefore, we present only two corridors that we feel do have biological relevance to forestland associated species. The first of these is in the extreme northwestern part of the study area, and predicts a least cost dispersal route between the main band of forestland core habitat and an isolated patch of forest core area to the north. This corridor is predicted to be quite long relative to the dispersal abilities of even the most mobile forestland associated species, but may be important for long term viability in providing low rates of gene flow and intermittent immigration to the northern patch. The second corridor we highlight is in the southeastern corner of the GPLCC and represents low cost movement routes among the sparse distribution of forest habitat patches in that portion of the study area.

Scientific Decision Support for Measurable Outcomes in Fragmented Systems
The mapping and prioritization of core areas, fracture zones, and corridors for focal species and species groups described above provides scientific decision support for measurable outcomes. The analysis and mapping of core areas, fracture zones and putative corridors for focal species and species groups provides the foundation for optimal conservation strategies to mitigate the effects of landscape fragmentation. The prioritization of fracture zones and corridors for targeted conservation action helps focus limited resources where they will be most effective. These actions will be important in the GPLCC to mitigate the relatively severe effects of habitat loss and fragmentation on population connectivity of multiple species of native wildlife.

Area Sensitivity and the GPLCC –

The geographical area covered by the GPLCC is one of the regions of the United States that has suffered the most extensive habitat loss as a result of agriculture and associated economic development. Habitat loss has consistently negative effects on biodiversity (Fahrig 2003), including reductions in species richness (Findaly and Houlahan 1997, Gurd et al. 2001, Schmiegelow and Monkkonen 2002, Steffan-Dewenter et al. 2002), population declines and changes in distribution (Gibbs 1998, Sanchez-Zapata and Calvo 1999, Donovan and Flather 2002). Habitat loss changes the distribution of resources and can affect individual behavior and spatial activity patterns, changing the ability of the organism to acquire the resources needed to survive and reproduce (Mangel and Clark 1986, Wiens et al. 1993). For example, from an energetics perspective, if food resources become more patchily distributed, it may be more costly to acquire them (Mahan and Yahner 1999). In addition, moving between disjunct resource patches to acquire food resources may involve moving through sub-optimal habitats that require higher energetic expenditures and expose individuals to higher rates of predation (Bergin et al. 2000) and reduce breeding (Kurki et al. 2000) and dispersal success (Belisle et al. 2001, With and Crist 1995, With and King 1999).

Most species require at least a minimum area of habitat in order to meet all life history requirements (e.g., Robbins et al. 1989). Theoretical studies predict a threshold habitat level below which the population cannot sustain itself (Fahrig 2001, Flather and Bevers 2002, Hill and Caswell 1999, Fahrig 2003). The amount of habitat required for species persistence depends on species-specific behavioral and life-history characteristics (Gibbs 1998, Vance et al. 2003), and the effects of habitat loss on each species will depend on the interaction of its ecological requirements and capabilities with the degree of habitat loss in the surrounding landscape (McGarigal and Cushman 2002, Schmiegelow and Monkkonen 2002, Fahrig 2003). For example, large bodied, high trophic-level species appear to be particularly vulnerable to local extinction due to habitat loss (Gibbs and Stanton 2001).

Some species require that their minimum area requirements be fulfilled in contiguous habitat patches; in other words, the individual habitat patch must be larger than the species' minimum area requirement for a species to occupy the patch. These species are sometimes referred to as "area-sensitive" species. For example, many neotropical migratory bird species display a marked area-sensitivity whereby their probability of occurrence in a forest patch increases non-linearly with the size of the patch (Freeemark and Merriam 1986, Robbins et al. 1989, Whitcomb et al. 1981, Trzcincski et al. 1999). Some other species, however, can tolerate the subdivision of habitat patches within their home range. For example, northern spotted owls have minimum area requirements for late-seral forest that varies geographically; yet, individual spotted owls use late-seral forest that may be distributed among many patches (Lehmkuhl and Raphael 1993, Forsman et al. 1984). In either case, habitat fragmentation reduces the size of suitable habitat patches and makes it increasingly difficult for these species to meet their minimum area requirements. As the habitat undergoes fragmentation, the most area-sensitive species will be lost first. As the habitat is further fragmented, other species will drop out according to their minimum area requirements (e.g., Robbins et al. 1989, Bender and Fahrig 1998, Flather and Bevers 2002). Thus, smaller patches generally contain fewer species than larger patches (Debinski and Holt 2000), and the set of species remaining in small patches is often a predictable subset of those found in large patches in the same region (Ganzhorn and Eisenbeib 2001, Vallan 2000, Fahrig 2003).

In the context of the GPLCC, our core area mapping for the three focal species provides the foundation for evaluating habitat area requirements for each species. The extent and pattern of our predicted core areas allows assessment of which species may be vulnerable due to limited population size and distribution. A simple assessment based on the percentage of the landscape occupied by core area habitat identifies all three species as potentially highly vulnerable based on habitat loss. FRAGSTATS analysis evaluated extent of core habitat for each species across a factorial of relative landscape resistance and dispersal ability. At the median dispersal ability, which best reflects the expected functional dispersal of each species, none of the three species were predicted to have population core areas that covered over 13% of the study area. Swift fox was predicted to have the largest area of occupied core area, followed by lesser prairie chicken (6.1%) and massasauga (0.5%). If the distribution of massasauga is correct, then this extremely low habitat area is cause of immediate and grave conservation concern. Protecting and expanding the size and distribution of the massasauga population is critical. Lesser prairie chicken distribution data are likely more reliable, given its high conservation profile and charismatic nature. A level of occupied population core areas of only 6.1% of the GPLCC study area is alarming and calls for strong actions to protect and expand these core populations. Even the swift fox, which had the largest core habitat areas of the three, has quite limited distribution and small occupied habitat area in the study landscape, which puts it at potential risk due to habitat loss alone.

Analysis of the extent of potential population core areas based on habitat availability gives a substantially different picture than the analysis of the actual occurrence data of the focal species. We evaluated two species groups based on coarse habitat associations and across a range of dispersal abilities. For grassland associated species, the amount of available core habitat in the study area varied greatly, by over an order of magnitude, depending on dispersal ability. For very highly mobile animals, such as swift fox and lesser prairie chicken, the extent of potential habitat core areas is quite large (over 40% of the study area). In contrast, for animals with limited dispersal ability, such as the massasauga and other herptiles and small mammals, the extent of expected connected core habitat is very small, given the limited ability of these species to integrate patches separated by barriers. These results suggest that there may be potential for substantial success in expanding and integrating the distributions of swift fox and lesser prairie chicken given careful management to reduce mortality, and protect and enhance habitat in the key fracture zones and corridors we identified to maximize net effect on improving population connectivity. The results also suggest that it may not be feasible to develop broad-scale connectivity strategies for the large portion of biodiversity with limited dispersal abilities, given the extremely patch and fragmented nature of their populations, resulting from dispersal limitations relative to the scale of habitat loss and fragmentation in the GPLCC.

Fragmentation Sensitivity and the GPLCC –
One of the ultimate consequences of habitat fragmentation is the disruption of movement patterns and the resulting isolation of individuals and local populations. As habitat is fragmented, it is broken up into separate fragments that are isolated to varying degrees. Because habitat fragments are relatively small and therefore support fewer individuals (than the original contiguous habitat), there will be fewer local (within-patch) opportunities for intra-specific interactions. This may not present a problem for individuals (and the persistence of the

population) if movement among patches is largely unimpeded by intervening habitats in the surrounding landscape and connectivity across the landscape can be maintained. However, if movement among habitat patches is significantly impeded, then individuals (and local populations) in remnant habitat patches may become functionally isolated (Rukke 2000, Virgos 2001, Tischendorf et al. 2003). The degree of isolation for any fragmented habitat distribution will vary among species depending on how they perceive and interact with landscape patterns (Dale et al. 1994, With and Crist 1995, Pearson and Gardner 1997, With et al. 1997, With 2000); less vagile species with very restrictive habitat requirements and limited gap-crossing ability will likely be most sensitive to isolation effects (e.g. Marsh and Trenham 2001, Rothermel and Semlitsch 2002). Habitat patches can become functionally isolated in several ways. First, the patch edge may act as a filter or barrier that impedes or prevents movement, thereby disrupting emigration and dispersal from the patch (Wiens et al. 1985). Second, the distance from remnant habitat patches to other neighboring habitat patches may influence the likelihood of successful movement of individuals among habitat patches. A 100 m-wide agricultural field may be a complete barrier to dispersal for small organisms such as invertebrates (e.g., Mader 1984) or amphibians (Rothermel and Semlitsch 2002, Marsh et al. 2004), yet be quite permeable for larger and more vagile organisms such as birds. Lastly, the composition and structure of the intervening landscape mosaic may determine the permeability of the landscape to movements. Each habitat may differ in its "viscosity" or resistance to movement, facilitating movement through certain elements of the landscape and impeding it in others (e.g., Cushman 2006). Again, the degree to which a given landscape structure facilitates or impedes movement will vary among organisms.

Reduction in movement among habitat patches can have dire consequences for individuals and populations. The population-level consequences of such spatially-structured populations, often referred to as metapopulations (after Levin 1974), has received considerable attention in the scientific literature (Hanski and Gilpin 1991). These so-called "metapopulations" are literally populations of populations connected by dispersal. The theory has been formalized in a number of models representing variations on the metapopulation theme (Harrison 1991, 1994; Harrison and Taylor 1997), which largely differ in the rate and direction of individual movement among habitat patches. At its simplest, the theory holds that within each habitat patch the population has a finite probability of extinction, and likewise each patch has a particular colonization rate based on the number of occupied patches in the metapopulation, among other things. Populations in particular patches continually go extinct, but the metapopulation as a whole persists so long as colonization rate is equal to extinction rate. Metapopulations subject to high extinction rates, but with correspondingly high rates of recolonization, have high population turnover, but persist as long as the opposing rates are equal. Metapopulation dynamics reflect the rates of local extinctions and recolonizations as determined by inter-patch movement, and factors affecting these processes. Individual movement between patches is perhaps the most important defining feature of a metapopulation. The theory predicts that subdivision and isolation of populations caused by fragmentation can lead to reduced dispersal success and patch colonization rates, which may result in a decline in the persistence of the local populations and an enhanced probability of regional extinction for the entire metapopulation (e.g., Lande 1987, With and King 1999, With 2000). Specifically, increased population isolation increases extinction risk by reducing demographic and genetic input from immigrants and reducing the chance of recolonization after extinction (Lande 1987, Schoener and Spiller 1992, Sjogren-Gulve 1994).

Our mapping of core, fracture and corridor areas in the GPLCC for the three focal species clearly indicates that the populations of all three species are fragmented. The massasauga would appear to be the most vulnerable to fragmentation given its highly limited dispersal ability. However, the apparently aggregated distribution of this species may reduce this effect (Figure 11). The main core population appears to be relatively well connected, with a few internal fracture zones and gaps spanned by potentially important corridors. We believe, therefore, that the main risks to massasauga are related to limited population size and area of occupied habitat, and conservation actions should focus primarily on protecting and expanding core areas, and only secondarily on mitigating the key fracture zones and corridors. Lesser prairie chicken and swift fox have relatively large dispersal abilities, which should help mitigate the effects of habitat fragmentation. However, the scale at which the populations of these species are broken into patches results in potentially severe fragmentation effects (Figures 18, 19, 20, 21). For both species, the main core areas of occupied habitat are separated by large gaps into at least four nearly isolated metapopulations. This isolation may increase local extinction risk to each subpopulation and for the full metapopulation. For these species mitigating connectivity issues in the identified fracture zones and potential linkage corridors may be nearly as important as protecting core habitat. Protecting core habitat we feel is always the first priority, but for these species increasing connectivity between the isolated or nearly isolated core patches could be critical for long-term viability.

Scope and Limitations

There are a number of limitations to the scope of this analysis that managers should be aware of as they incorporate these analyses into their decision-making process. These include the importance of empirically validating predicted corridors, uncertainty in species responses to landscape composition, uncertainty in species dispersal abilities, uncertainty in species distributions, and uncertainty in fragmentation thresholds.

Validating Predicted Corridors –

Predicted core areas, fracture zones and corridors provided by models have sometimes been criticized because they lack supporting movement data (Simberloff et al. 2002; Rosenberg et al. 1997) and because they may contain errors in model parameters or incorrect assumptions (Spear et al. 2010). Therefore, additional vetting of modeled corridors in the field is recommended. We recommend further investment of resources to test and validate our predictions of core, fracture, and corridor areas using movement (e.g. Cushman et al. 2010c; Cushman and Lewis 2010) and molecular landscape genetic methods (e.g. Cushman et al. 2006)

Uncertainty in Landscape Resistance –

Most current methods to predict population connectivity and map movement corridors, including those used in this analysis, begin with landscape resistance maps. Landscape resistance maps depict the putative cost of movement through any location in the landscape. These resistance surfaces that assign different resistance-to-movement values to different landscape features (e.g., a high resistance-to-movement might be assigned to a known road or a body of water). Cells are given weights or 'resistance values' reflecting the presumed influence of each variable on movement of the species. The resistance values in the cells reflect the step-wise cost of moving through that cell, and degree of isolation, or its inverse connectivity, is a function of cumulative cost across the landscape from sources to destinations.

Human landuse and climate change alter the composition and configuration of landscapes. Whether these changes result in the loss and fragmentation of suitable habitat for a particular organism depends on the scale and nature of those changes in relation to how that organism perceives and interacts with landscape patterns (With and Crist 1995, Pearson et al. 1996, With 1997, With et al. 1997). For example, changes in the size and isolation of mature forest patches at a particular scale may have little or no detectable impact on species that perceive and respond to landscape patterns at a different scale or that select habitat on the basis of other environmental variables (e.g., shrub cover, litter depth) or that utilize a broad range of habitats (i.e., generalist or multi-habitat species).

Most of the published studies using landscape resistance maps have utilized expert opinion to estimate resistance to movement due to landscape features given the lack of detailed information on animal movement or gene flow (e.g. Compton et al. 2007). This is not surprising given the difficulty in gathering sufficient sample sizes of reliable data on relationships between animal movement and multiple landscape features at broad spatial scales (McGarigal & Cushman 2002; Cushman 2006). Basing analyses on unvalidated expert opinions is not desirable (Seoane et al. 2005). Landscapes are perceived by particular species in ways that may not correspond to our assumptions concerning connectivity and habitat quality (With et al. 1997, Wiens 2001). Using expert opinion to develop resistance maps has been a major weakness of most past landscape resistance modeling efforts.

We sought to mitigate this uncertainty by evaluating a range of potential landscape resistance parameterizations for each focal species and species group. For example, we repeated all analyses on six different resistance maps, three for grassland associated species and three for forestland associated species. These reflect different relative resistance of roads, human development, agriculture, forest and grassland habitat types. The purpose was to explicitly evaluate uncertainty due to variability in functional landscape resistance among species and species groups. Our analysis shows a very small affect of differential functional landscape resistance (Table 5). Specifically, prediction of core areas, fracture zones and corridors was relatively unaffected by the choice of which landscape resistance parameterization to use.

Uncertainty in Dispersal Ability –
What constitutes functional connectedness is highly dependent on the dispersal behaviour of the particular species in question. For example, patches that are connected for one species may be completely isolated for another. Thus, habitat connectivity is affected by population distribution and habitat continuity, but the magnitude and nature of the affect depends on the dispersal ability of the particular species. The cumulative cost distances organisms are able to traverse, and the probability distributions of movements as function of cost distances between sources and potential destinations vary greatly among species. Generally, larger organisms can travel longer distances. Therefore, a 100 m-wide agricultural field may be a complete barrier to dispersal for small organisms such as invertebrates (e.g., Mader 1984) or amphibians (Rothermel and Semlitsch 2002, Marsh et al. 2004), yet be quite permeable for larger and more vagile organisms such as birds. There is much uncertainty in dispersal ability of wildlife species in the GPLCC. We sought to explicitly quantify this uncertainty by evaluating a range of potential dispersal abilities for the three focal species and species groups. We extensively reviewed the literature on

the dispersal abilities of the three focal species, and chose to evaluate three different dispersal thresholds for each (Table 2). The goal of this was to evaluate a "low end", "middle" and "high end" estimate of dispersal ability to quantify the effects of differential mobility on predictions of the extent and connectivity of habitat in the GPLCC. For the grassland and forestland species groups we evaluated five different dispersal abilities (5km, 10km, 15km, 20km, 25km). We chose this range of dispersal abilities to evaluate a broad range that would reflect a large proportion of native plant and animal species. Our results indicate that predictions of the extent and pattern of core areas, and the degree to which they are linked by dispersal is extremely sensitive to dispersal ability. In our analysis, variation in dispersal ability was generally 5 to 10 times more impactful on our predictions than variation in landscape resistance parameterization.

Uncertainty in Species Distributions – The methods we employ are based on predicting population cores, fracture and corridors based on quantitative modeling of dispersal from a collection of source locations in the landscape. These sources reflect expected locations occupied by the species. Therefore, the analysis is completely dependent on knowledge of species distribution. Analysis based on incorrect species distribution information may be highly misleading. Accurate information on the occurrence and distribution of species is fundamental to reliable predictions. Obtaining reliable and consistent information of spatial patterns of species distributions is very challenging. At the scale of the full extent of the GPLCC there are very few consistent data products describing the spatial distribution of species of conservation concern.

We addressed this uncertainty in two ways. First, for the three focal species we utilized all element occurrences recorded since 1970 in the NATURESERV database. This arguably is the best synoptic database of distribution and occurrence across the full GPLCC. However, it is limited, as it is not based on consistent and systematic inventory methods, is subject to observation error, and geographic variation in survey/collecting effort. Therefore, our predictions may not reflect the true pattern of occurrence and relative abundance of our focal species, and the degree to which this departure affects the reliability of our predictions is not known. To mitigate this uncertainty in the distribution of the focal species, we conducted a habitat-based species-group analysis. We analyzed core, fracture, and corridor for grassland and forestland associated species groups. This species group analysis does not reflect actual species distributions. Rather, it predicts the connectivity of habitats, regardless of whether they are occupied by particular species. The advantage of this is that we have substantially better knowledge of landuse and landcover than of the distributions of particular species. Therefore, the habitat-based connectivity predictions are reliable measures of potential connectivity of the landscape based on habitat conditions. The major limitation is that potential connectivity of habitat may not reflect the actual connectivity of populations, which are often limited in range, variable in density, and patchy in distribution. We feel the combination of focal-species analysis using the best available distribution data and species-group analysis based on connectivity of habitat provide a broad perspective to assist managers and conservationists design effective actions.

Uncertainty in Critical Fragmentation Thresholds –

A critical threshold is an abrupt, nonlinear change that occurs in an organism response (e.g., dispersal success, productivity, patch occupancy, etc.) across a small range of habitat loss and/or fragmentation (With and King 1999). Both empirical data (Carlson and Stenberg 1995,

Doncaster et al. 1996, Jansson and Angelstam 1999) and theoretical models predict critical thresholds of habitat where ecological relationships change abruptly (Turner and Gardner 1991, O'Neil et al. 1988, With and Crist 1995, Bascompte and Sole 1996, Flather and Bevers 2002). For example, neutral landscape models, derived from percolation theory as applied in the field of landscape ecology (Gardner et al. 1987, Gardner et al. 1989, Gardner and O'Neill 1991, Pearson and Gardner 1997, With 1997, With and King 1997) have been used to characterize habitat loss and fragmentation as a threshold phenomenon (With and King 1999). Above the so-called percolation threshold, habitat loss results in a simple additive loss of habitat. At the threshold, a qualitative change in landscape structure occurs. A small additional loss of habitat at this point produces a physically disconnected landscape in which the organism's habitat no longer maintains continuity across the landscape. Further habitat loss merely leads to greater discontinuity. The existence, nature and severity of critical thresholds in the population response to fragmentation among wildlife species inhabiting the GPLCC is largely unknown. Our analysis quantifies location, size and connectivity of core patches, fracture zones and corridors. Full interpretation of the biological implications of these patterns would require knowledge of how incremental change in core areas, fracture zones and corridors would affect demographic and genetic processes affecting viability. This is an area which would deserve additional investment and research.

FUTURE ANALYSIS (PHASE II)

The next phase of the project will predict changes to habitat area, fragmentation, and corridor connectivity for these species under six potential future scenarios involving a combination of climate change, urban development and road network expansion, identify key geographical locations that are most important to maintaining population connectivity and facilitating movement for each group of species under future landscape conditions, and develop spatially explicit strategies for adaptation to future climate and development patterns by combining landscape restoration (to facilitate natural movement of species) and assisted migration (when natural movement has a high probability of failure).

Future Landscape Change Driven by Climate and Landuse Change
Global climate is expected to change rapidly over the next century (Thompson and others 1998, IPPC 2001), affecting forest ecosystems both directly by altering biophysical conditions (Neilson 1995, Neilson and Drapek 1998, Bachelet and others 2001b) and indirectly through changing disturbance regimes (Baker 1995, McKenzie and others 1996, Keane and others 1999, Dale and others 2001, He and others 2002). Changes in biophysical conditions could lead to species replacement in communities and latitudinal and altitudinal migrations. Expected increases in the size, severity, and frequency of disturbance (Mearns and others 1984, Overpeck and others 1990, Solomon and Leemans 1997, IPCC 2001) will lead to changes in vegetation structure, species composition, and diversity (Christensen 1988, McKenzie and others 2004). The changes in distributions of plant species caused by changing climate, and associated changes in disturbance regimes, may have large impacts on many aspects of ecological diversity and function (Peters and Lovejoy 1992, Miller 2003).

Simultaneously, increasing human population nationally and regionally drive urban development, expansion of road networks, and landuse conversions. These changes lead to rapid habitat loss and fragmentation due to conversion of natural landscapes to uses dominated by human activities. The interaction of climate change and expansion of the human footprint are likely to result in synergistic increases in impacts greater than the sum of either alone. There is considerable uncertainty in the extent and effect of future climate change, and similar uncertainty in the extent and pattern of future human population and landuse change.

This document presents results from Phase I of this project, which is limited to evaluating core, fracture and corridor connectivity under the current landscape condition. Phase II, if funded, will evaluate future changes to habitat area, fragmentation and corridor connectivity by comparing change predicted due to climate regime shifts, and land use change. The climate change component will involve quantifying connectivity for species and species-group for 2 carbon emission scenarios across 2 Global Circulation Models. The 2 carbon emission scenarios will be IPCC: (1) B2 representing a future which emphasizes local solutions to economic, social, and environmental sustainability and has intermediate levels of economic development (relatively less warming); and (2) A2 representing a very heterogeneous world that emphasizes self-reliance and regional economic development (relatively more warming). The GCMs are chosen to represent a relatively "cool" model (CCSM3.0) and a relatively "hot" model (UKMO-HadCM3). Together, the combination of 2 GCM and 2 emissions scenarios bracket the range of uncertainty in current climate change and vegetation predictions. The land use change component will quantify connectivity across 4 potential future development patterns, based on spatially contagious and network expansion from current development patterns. We will combine climate change and land use effects in a third set of analyses to quantify the potential amplification of effects in the combined action of these two important ecological stressors.

This combination of multiple carbon emissions scenarios and multiple GCM predictions will provide explicit quantification of uncertainty and the range of plausible climate impacts. Likewise, the combination of 4 potential future development patterns provides a quantification of the range of realistic future changes in the human footprint. The combination of these will provide a means to evaluate the synergistic effects an range of potential future patterns of habitat and connectivity. This will enable development of conservation and restoration strategies that provide detailed and specific recommendations that are predicted to be effective under both current and likely future landscape conditions.

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TABLES

Table 1. Classification of resistance values in each of the 12 resistance maps used in our analysis.

Land Attribute	Assigned Resistance Level		
	Low	Medium	High
Land Cover†			
Natural: Perennial Ice/Snow; Barren Land; Deciduous Forest; Evergreen Forest; Mixed Forest; Scrub/Shrub; Herbaceous; Emergent Herbaceous Wetlands	1	1	1
Agricultural: Hay/Pasture; Cultivated Crops	5	10	15
Water: Open water	5	10	15
Residential: Developed, Open Space; Developed, Low Intensity	10	15	20
Urban: Developed, Medium Intensity; Developed, High Intensity	15	20	25
Roads‡			
Primary Highway With Limited Access: Interstate highways and some toll highways are in this category and are distinguished by the presence of interchanges.	200	400	600
Primary Road Without Limited Access : This category consists mainly of US highways, but may include some state highways and county highways that connect cities and larger towns.	50	100	150
Secondary and Connecting Road: This category includes mostly state highways, but may include some county highways that connect smaller towns, subdivisions, and neighborhoods.	50	100	150
Local, Neighborhood, and Rural Road: A road in this category is used for local traffic and usually has a single lane of traffic in each direction.	10	10	10

Vehicular Trail: A road in this category is usable only by four-wheel drive vehicles, is usually a one- lane dirt trail, and is found almost exclusively in very rural areas.	10	10	10
Road with Special Characteristics: This category includes roads, portions of a road, intersections of a road, or the ends of a road that are parts of the vehicular highway system and have separately identifiable characteristics.	10	10	10
Road as Other Thoroughfare: This category includes foot and hiking trails located on park and forest land, as well as stairs or walkways that follow a road right-of-way and have names similar to road names.	10	10	10

Biome§	Forestland Species	Grassland Species
Mixed Conifer: Temperate Cool Mixed Forest; Temperate Evergreen Needleleaf Woodland; Temperate Cool Mixed Woodland	1	10
Grass/Shrub: Subtropical Grassland; Subtropical Shrubland; Temperate Grassland; Temperate Shrubland	10	1
Desert: Subtropical Desert	15	5
Subalpine: Tundra; Subalpine	5	15

†Categorical land cover classes from the 2001 National Land Cover database (http://www.mrlc.gov/nlcd.php).

‡Line dataset of roads in the United States from the 2000 Census TIGER line features (http://www.icpsr.umich.edu/cocoon/TIGER/2000ua/states.xml).

§Predicted vegetation cover from 2000 Nielson/Drapek vegetation cover (http://www.fs.fed.us/pnw/corvallis/mdr/mapss)

Table 2. Range of dispersal distances for three focal species used to examine connectivity in the GPLCC.

Species	Dispersal Distance Settings	Sources
Lesser prairie-chicken (*Tympanuchus pallidicinctus*)	20 km; 40 km; 80 km	Hagen and Giesen (2005) Robb and Schroeder (2005)
Massasauga (*Sistrurus catenatus*)	2 km; 4 km; 6 km	Mackessy (2005) Clark et al. (2008)
Swift fox (*Vulpes velox*)	10 km; 30 km; 60 km	Mercure et al. (1993) Dark-Smiley and Keinath (2003) Kamler et al. (2004)

Table 3. FRAGSTATS results for percentage of landscape in connected habitat (PLAND), largest patch of connected habitat percentage of study area (LPI), correlation length of connected habitat (CL), and number of individual patches of connected habitat (NP) across factorial combination of three levels of relative landscape resistance (Low, Med, High) and three levels of dispersal ability (20,000; 40,000; 80,000) for the lesser prairie-chicken.

		20,000	40,000	80,000
PLAND	High	2.3924	5.1272	10.7409
	Med	2.5275	5.4978	11.5517
	Low	2.7581	6.1111	12.7718
NP	High	25	12	4
	Med	25	12	3
	Low	22	10	3
CL	High	37269.38	53830.22	127731.1
	Med	37122.96	54081.76	127936.5
	Low	39961.27	58962.21	127535.4
LPI	High	1.1692	2.1976	6.7096
	Med	1.1946	2.2746	7.3368
	Low	1.3091	2.3763	8.2982

Table 4. FRAGSTATS results for percentage of landscape in core habitat, largest patch of core habitat percentage of study area, correlation length of core habitat, and number of individual patches of core habitat across factorial combination of three levels of relative landscape resistance (Low, Med, High) and three levels of dispersal ability (20,000; 40,000; 80,000) for the lesser prairie-chicken.

		20,000	40,000	80,000
PLAND	High	0.6819	1.2999	2.5067
	Med	0.714	1.3834	2.6601
	Low	0.7748	1.5045	2.9002
NP	High	31	24	18
	Med	28	22	18
	Low	26	21	16
CL	High	21129.95	30371.5	56664.74
	Med	21205.94	30807.03	57089.12
	Low	21180.72	31417.42	57552.61
LPI	High	0.3398	0.8133	2.0292
	Med	0.3467	0.8377	2.1092
	Low	0.3562	0.8693	2.2135

Table 5. Relative effect size of landscape resistance and dispersal ability on FRAGSTATS results for percentage of landscape in connected habitat, largest patch of connected habitat percentage of study area, correlation length of connected habitat, and number of individual patches for the three focal species and two species groups.

	PLAND		CL		LPI		NP	
	Landscape Resistance	Dispersal Ability	Landscape Resistance	Dispersal Ability	Landscape Resistance	Dispersal Ability	Landscape Resistance	Dispersal Ability
Lesser Prairie-Chicken	0.085442	1.13663	0.030007	0.87969	0.070306	1.56102	0.08944	0.61702
Swift Fox	1.129048	0.08031	0.082296	1.39325	0.112608	4.29312	0.194557	0.61218
Massasauga	0.038748	0.42811	0.027731	0.18015	0.071573	0.62098	0.036311	0.22154
Grassland Species	0.080809	0.14751	0.261036	0.53501	0.176073	0.31667	0.346598	0.36043
Forestland Species	0.026235	0.34933	0.035752	0.72719	0.036544	0.49293	0.022412	0.14181

Table 6. FRAGSTATS results for percentage of landscape in connected habitat, largest patch of connected habitat percentage of study area, correlation length of connected habitat, and number of individual patches of connected habitat across factorial combination of three levels of relative landscape resistance (Low, Med, High) and three levels of dispersal ability (10,000; 30,000; 60,000) for the swift fox.

		10,000	30,000	60,000
PLAND	High	4.3969	11.1103	18.7446
	Med	4.6114	11.8443	20.001
	Low	5.0103	13.1437	22.0791
NP	High	114	52	22
	Med	112	41	15
	Low	95	30	12
CL	High	22280.2	76067.72	109790.7
	Med	22165.44	77680.42	111916.6
	Low	27465.05	80848.34	130739.7
LPI	High	0.5893	5.1481	9.1118
	Med	0.6013	5.521	9.91
	Low	0.7343	6.1922	11.4212

Table 7. FRAGSTATS results for percentage of landscape in core habitat, largest patch of core habitat percentage of study area, correlation length of core habitat, and number of individual patches of core habitat across factorial combination of three levels of relative landscape resistance (Low, Med, High) and three levels of dispersal ability (10,000; 30,000; 60,000) for the swift fox.

		10,000	30,000	60,000
PLAND	High	1.2841	2.7136	6.0366
	Med	1.3136	2.8844	6.4867
	Low	1.378	3.1661	7.2152
NP	High	148	120	84
	Med	144	112	85
	Low	140	108	75
CL	High	8990.677	32729.71	67448.92
	Med	9931.553	35700.49	68799.49
	Low	11783.55	39240.69	71451.68
LPI	High	0.1315	1.1771	3.6961
	Med	0.1332	1.2667	3.942
	Low	0.2081	1.3797	4.3711

Table 8. FRAGSTATS results for percentage of landscape in connected habitat, largest patch of connected habitat percentage of study area, correlation length of connected habitat, and number of individual patches of connected habitat across factorial combination of three levels of relative landscape resistance (Low, Med, High) and three levels of dispersal ability (2,000; 4,000; 6,000) for the massasuaga.

		2,000	4,000	6,000
PLAND	High	0.3535	0.4919	0.6565
	Med	0.3237	0.4996	0.6742
	Low	0.3282	0.5185	0.7105
NP	High	29	22	19
	Med	34	21	19
	Low	34	21	19
CL	High	16159.06	18969.24	19879.41
	Med	13612.7	18994.64	19855.07
	Low	13617.15	18953.08	19781.07
LPI	High	0.1761	0.261	0.3296
	Med	0.121	0.2644	0.3371
	Low	0.1221	0.2719	0.3517

Table 9. FRAGSTATS results for percentage of landscape in core habitat, largest patch of core habitat percentage of study area, correlation length of core habitat, and number of individual patches of core habitat across factorial combination of three levels of relative landscape resistance (Low, Med, High) and three levels of dispersal ability (2,000; 4,000; 6,000) for the massasuaga.

		2,000	4,000	6,000
PLAND	High	0.2291	0.2664	0.326
	Med	0.2122	0.2672	0.3294
	Low	0.2123	0.2707	0.3409
NP	High	30	30	21
	Med	31	30	21
	Low	31	30	20
CL	High	13966.87	13970.47	18293.45
	Med	13501.83	13983.17	18300.92
	Low	13498.96	13890.8	18768.55
LPI	High	0.0934	0.107	0.1838
	Med	0.0787	0.1073	0.1857
	Low	0.0787	0.1079	0.1971

Table 10. FRAGSTATS results for percentage of landscape in connected habitat, largest patch of connected habitat percentage of study area, correlation length of connected habitat, and number of individual patches of connected habitat across factorial combination of three levels of relative landscape resistance (Low, Med, High) and five levels of dispersal ability (5,000; 10,000; 15,000; 20,000; 25,000) for grassland associated species.

		5,000	10,000	15,000	20,000	25,000
PLAND	High	44.0722	57.4442	62.1783	68.4119	72.8777
	Med	44.9524	62.3116	66.8726	72.472	76.8896
	Low	49.1479	69.6529	73.9493	79.7584	84.2691
NP	High	5391	2258	1742	1257	956
	Med	5141	1590	1184	823	629
	Low	3943	779	594	476	344
CL	High	152050.3	236020.1	248575.6	409537.5	417883.5
	Med	156353.4	384473.5	387918.2	408208.9	425609.2
	Low	210215.1	402750.7	421613	423492.5	423558.4
LPI	High	15.4049	34.4021	38.7604	63.4477	69.8113
	Med	15.9277	53.2057	57.2673	67.3913	75.3171
	Low	26.8939	64.0406	71.8796	78.2577	83.06

Table 11. FRAGSTATS results for percentage of landscape in core habitat, largest patch of core habitat percentage of study area, correlation length of core habitat, and number of individual patches of core habitat across factorial combination of three levels of relative landscape resistance (Low, Med, High) and five levels of dispersal ability (5,000; 10,000; 15,000; 20,000; 25,000) for grassland associated species.

		5,000	10,000	15,000	20,000	25,000
PLAND	High	3.7286	13.3045	27.9425	35.1842	39.899
	Med	3.7553	13.797	29.5756	37.2878	42.3587
	Low	3.8048	14.9143	32.3268	40.8812	46.4459
NP	High	733	463	287	207	207
	Med	821	473	247	170	170
	Low	814	477	262	171	171
CL	High	11487.57	18525.31	68657.28	130974.4	156859.3
	Med	11459.55	26568.1	84720.33	149078.1	235664.3
	Low	11711.84	53699.77	121867.3	187667.6	241970.7
LPI	High	0.2463	0.515	6.7483	10.8119	14.1075
	Med	0.2461	1.687	7.8242	13.0143	25.7596
	Low	0.2457	4.5717	10.0547	13.9931	28.9394

Table 12. FRAGSTATS results for percentage of landscape in connected habitat, largest patch of connected habitat percentage of study area, correlation length of connected habitat, and number of individual patches of connected habitat across factorial combination of three levels of relative landscape resistance (Low, Med, High) and five levels of dispersal ability (5,000; 10,000; 15,000; 20,000; 25,000) for forestland associated species.

		5,000	10,000	15,000	20,000	25,000
PLAND	High	2.0742	3.9862	4.4548	5.2117	6.0183
	Med	2.0949	4.0481	4.5358	5.3335	6.1917
	Low	2.126	4.1863	4.6993	5.5515	6.4429
NP	High	1871	1379	1263	1108	1017
	Med	1861	1359	1230	1079	991
	Low	1851	1320	1200	1034	965
CL	High	17255.18	33456.81	41405.13	76930.1	72832.75
	Med	18771.63	33377.66	41424.9	76364.9	72342.26
	Low	19500.96	39388.27	40976.52	74882.76	73172.17
LPI	High	0.4001	1.0367	1.3507	2.558	2.7166
	Med	0.4029	1.0492	1.3764	2.5824	2.7394
	Low	0.4238	1.2619	1.3985	2.6122	2.7923

Table 13. FRAGSTATS results for percentage of landscape in core habitat, largest patch of core habitat percentage of study area, correlation length of core habitat, and number of individual patches of core habitat across factorial combination of three levels of relative landscape resistance (Low, Med, High) and five levels of dispersal ability (5,000; 10,000; 15,000; 20,000; 25,000) for forestland associated species.

		5,000	10,000	15,000	20,000	25,000
PLAND	High	0.0581	0.225	0.7631	1.1259	1.4586
	Med	0.1201	0.227	0.7852	1.1911	1.513
	Low	0.1218	0.2371	0.8361	1.258	1.5992
NP	High	40	39	24	22	19
	Med	79	40	29	20	19
	Low	77	41	29	19	23
CL	High	3260.348	8392.992	16446.09	20008.09	28153.1
	Med	3721.751	8407.381	16494.7	23926.82	30850.48
	Low	3708.452	8451.82	18569.89	26784.48	31877.54
LPI	High	0.0152	0.0765	0.1936	0.3373	0.5399
	Med	0.0203	0.0774	0.1981	0.4139	0.5561
	Low	0.0203	0.082	0.2257	0.4309	0.5744

Table 14. Percentages of the total study area in connected habitat (All), core habitat (Core), and fracture zone (Fracture), broken down by species intersection. Core habitat is defined as being predicted as occupied in at least three out of the nine relative resistance X dispersal ability combinations. Fracture zones are defined as being outside of the core but within the range of connected habitat in at least one of the nine relative resistance X dispersal ability combinations. For example, 0.35% of the study area is jointly core area for both swift fox and lesser prairie chicken, and 0.8% of the study area is a shared fracture zone between the three species.

	All	Core	Fracture
none	71.93%	92.46%	76.61%
Fox only	15.08%	4.49%	13.18%
Snake only	0.01%	0.18%	0.08%
Chicken only	5.90%	2.34%	6.11%
Fox Snake	0.21%	0.14%	0.09%
Fox Chicken	6.38%	0.35%	3.74%
Chicken Snake	0.07%	0.04%	0.10%
Fox Chicken Snake	0.42%	0.00%	0.08%

FIGURES
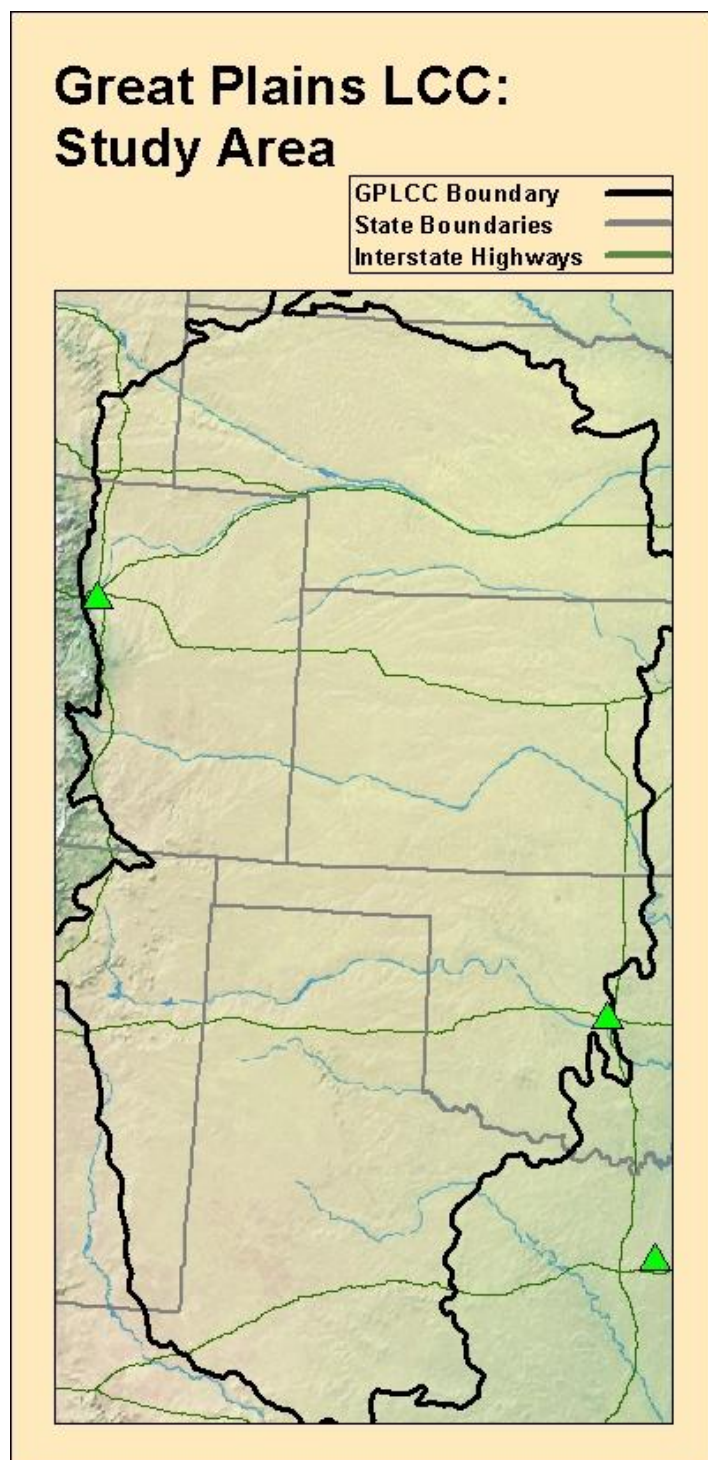
FIGURES

Figure 1. Analysis area extent.
The area of analysis for all results reported in this report is the extent of the rectangle inside the beige border. The GPLCC extent is demarcated by a bold black line. State boundaries are shown in gray, and interstate highways in green.
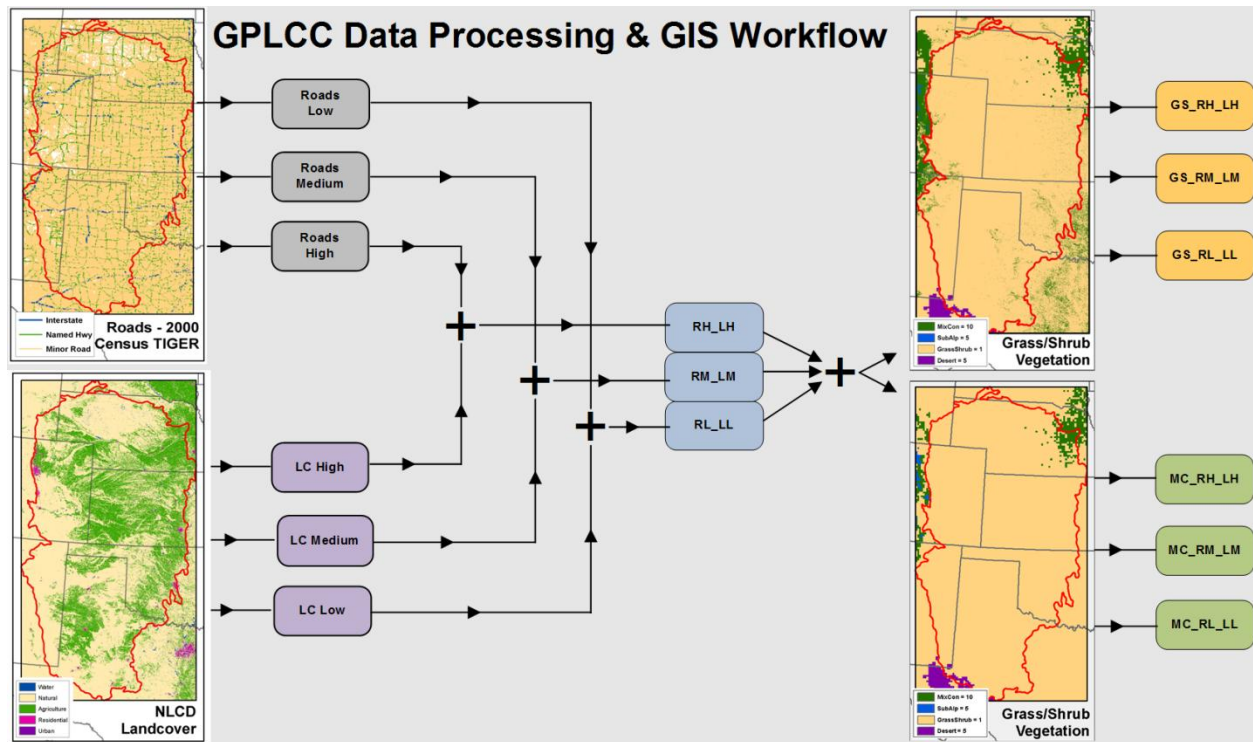
Figure 2. Landscape resistance model workflow.
We created several resistance maps to evaluate population connectivity for selected focal species and species groups. These consisted of a factorial combination of road, landcover and biome vegetation type effects. For grassland associated species we parameterized resistance to landcover classes to reflect preference for moving through grassland habitat and avoidance of non-grassland cover types. Similarly, for forestland associated species, we parameterized resistance to reflect preference for moving through forest and avoidance of non-forest cover types. We created six resistance layers for forestland biome associated species and six resistance layers for grassland biome associated species. These six resistance layers reflected variation in the relative influence of the combined effects of roads and landuse on resistance to organism movement. Road effects were varied across three levels, from relatively weak to relatively strong effects of roads as movement barriers. Likewise, landcover effects varied across three levels, from relatively strong to relatively weak. We combined these into six different resistance layers for each of the forestland and grassland associated species groups. This resulted in 12 different resistance layers. We replicated all spatial modeling analyses on all 12 of these resistance layers to quantify the degree to which predictions of population connectivity depended on the particular resistance values chosen.
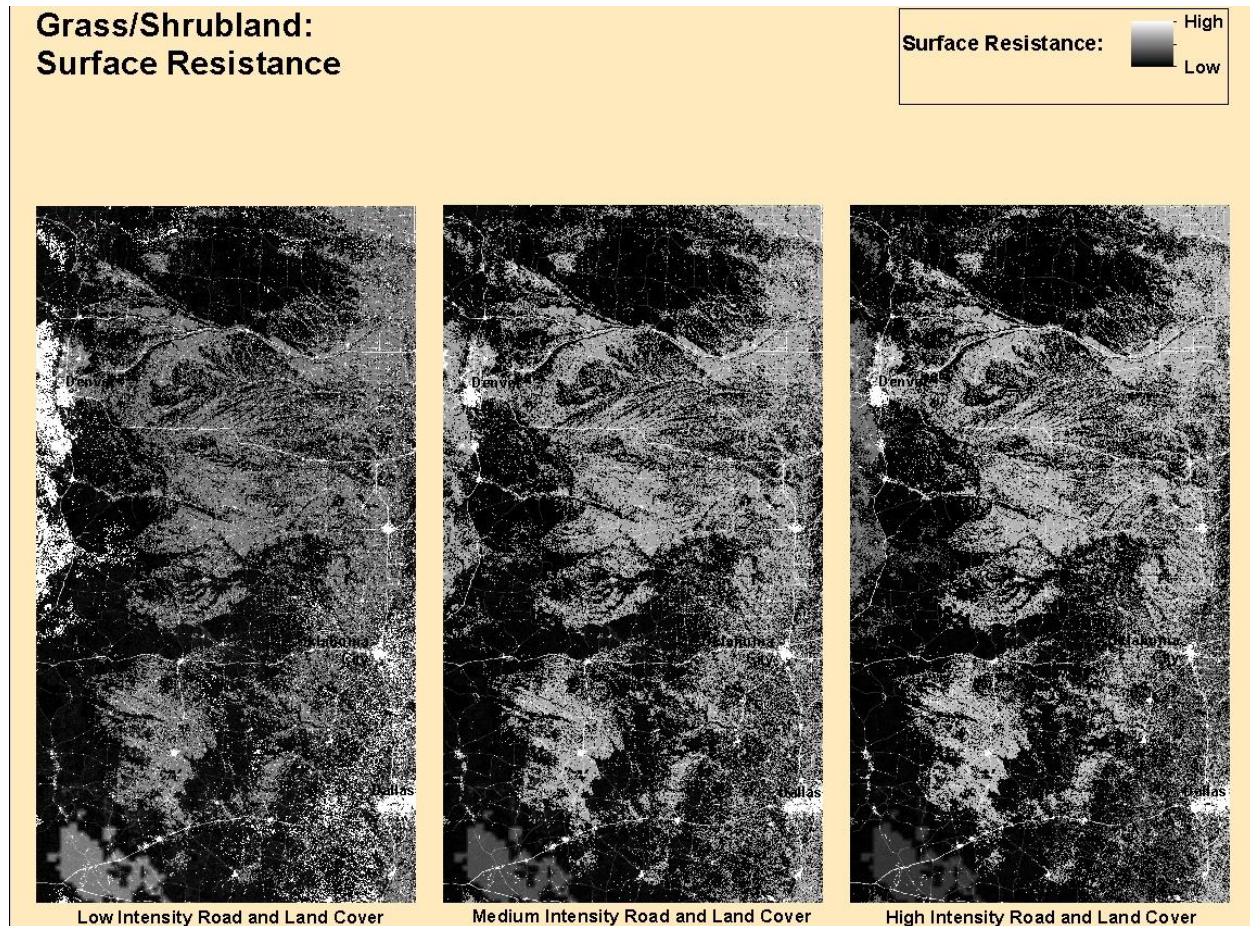
Figure 3. Landscape resistance models for grassland associated species.
a) GRLLL – Grassland associated species, with low relative effects of roads and landcover, b) GRMLM – Grassland associated species, with medium relative effects of roads and landcover, c) GRHLH – Grassland associated species, with high relative effects of roads and landcover. The differences between these maps primarily are in relation to the relative resistance of crossing the focal habitat (grassland) compared to crossing suboptimal habitat (agriculture, forest, residential, urban) and roads. Contrast is highest in the GRHLH and lowest in the GRLLL.
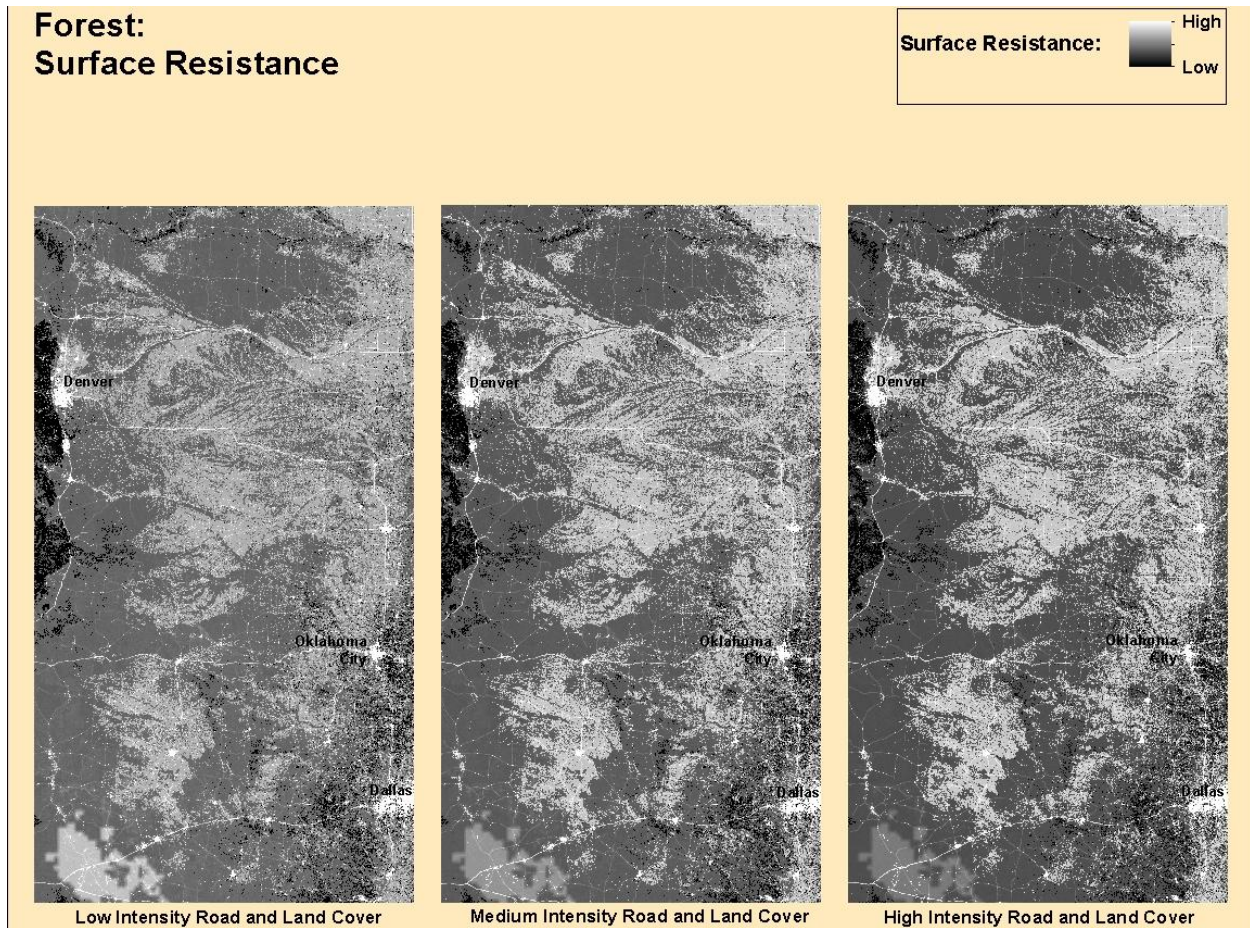
Figure 4. Landscape resistance models for forest associated species.
a) FRLLL – Forestland associated species, with low relative effects of roads and landcover, b) FRMLM – Forestland associated species, with medium relative effects of roads and landcover, c) FRHLH – Forestland associated species, with high relative effects of roads and landcover. The differences between these maps primarily are in relation to the relative resistance of crossing the focal habitat (forestland) compared to crossing suboptimal habitat (agriculture, grassland, residential, urban) and roads. Contrast is highest in the FRHLH and lowest in the FRLLL.
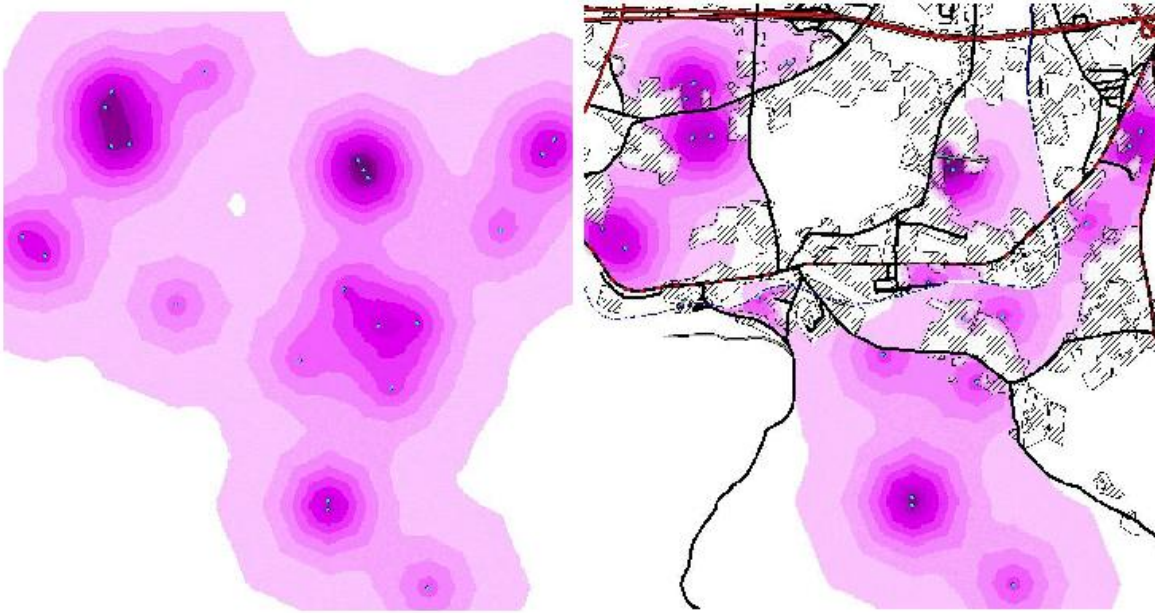
Figure 5. Raw maps of kernel expected density

(a) sources in a uniformly suitable landscape, (b) the same sources in a landscape fragmented by roads and human land uses. The colormap ranges from high predicted density and movement rates per pixel (dark purple) to low predicted occupancy and movement rates (pink).
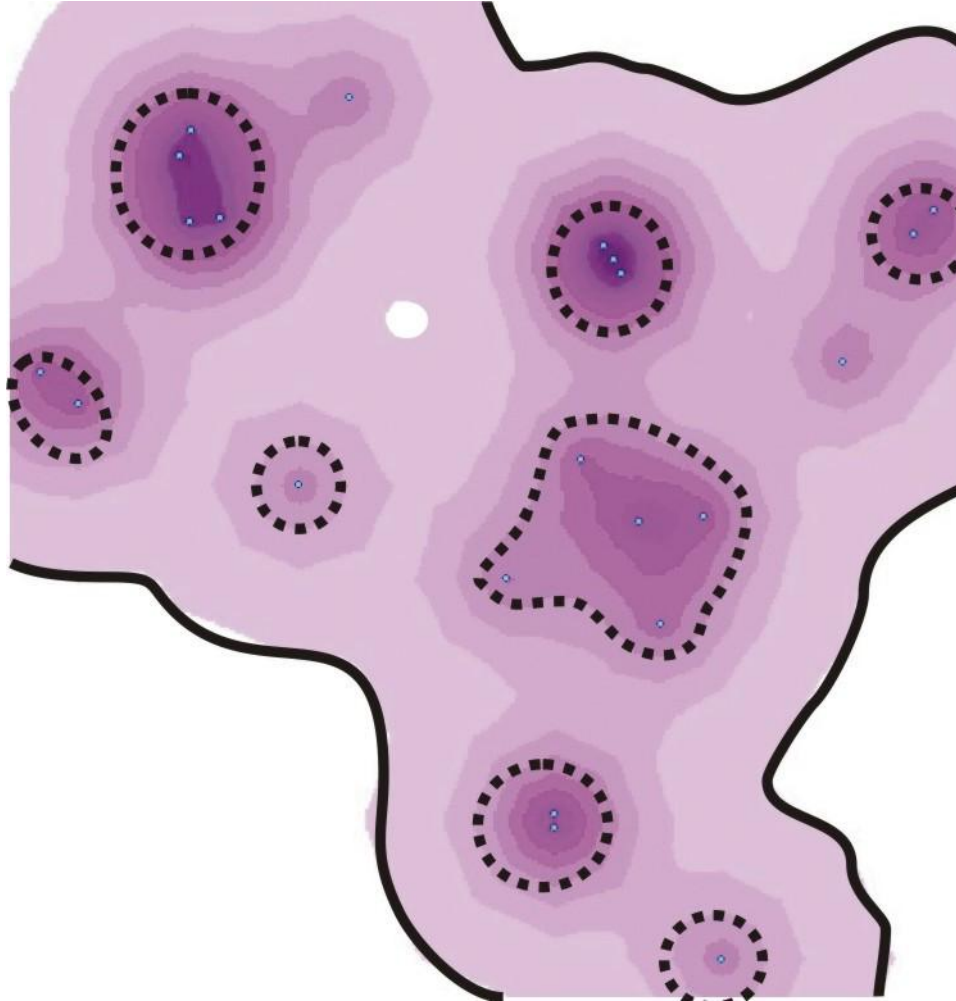
Figure 6. Illustration of defining core areas and fracture zones from cumulative resistant kernel surfaces.
In shaded color are the areas predicted to have positive density of individuals of a given species at a certain level of dispersal ability and on a particular resistance landscape. The core areas are defined as the regions in the map with density between the above 10% of the maximum density in the map. In this figure core areas are enclosed inside dotted line boundaries. Fracture zones are areas predicted to have density above zero but below 10% of the maximum density in the map. In this figure the fracture zone is represented by the area that lies outside of core areas and inside the solid line boundary. The area outside the solid line boundary is predicted to have zero occupancy rates and is a barrier to the extent of the population.
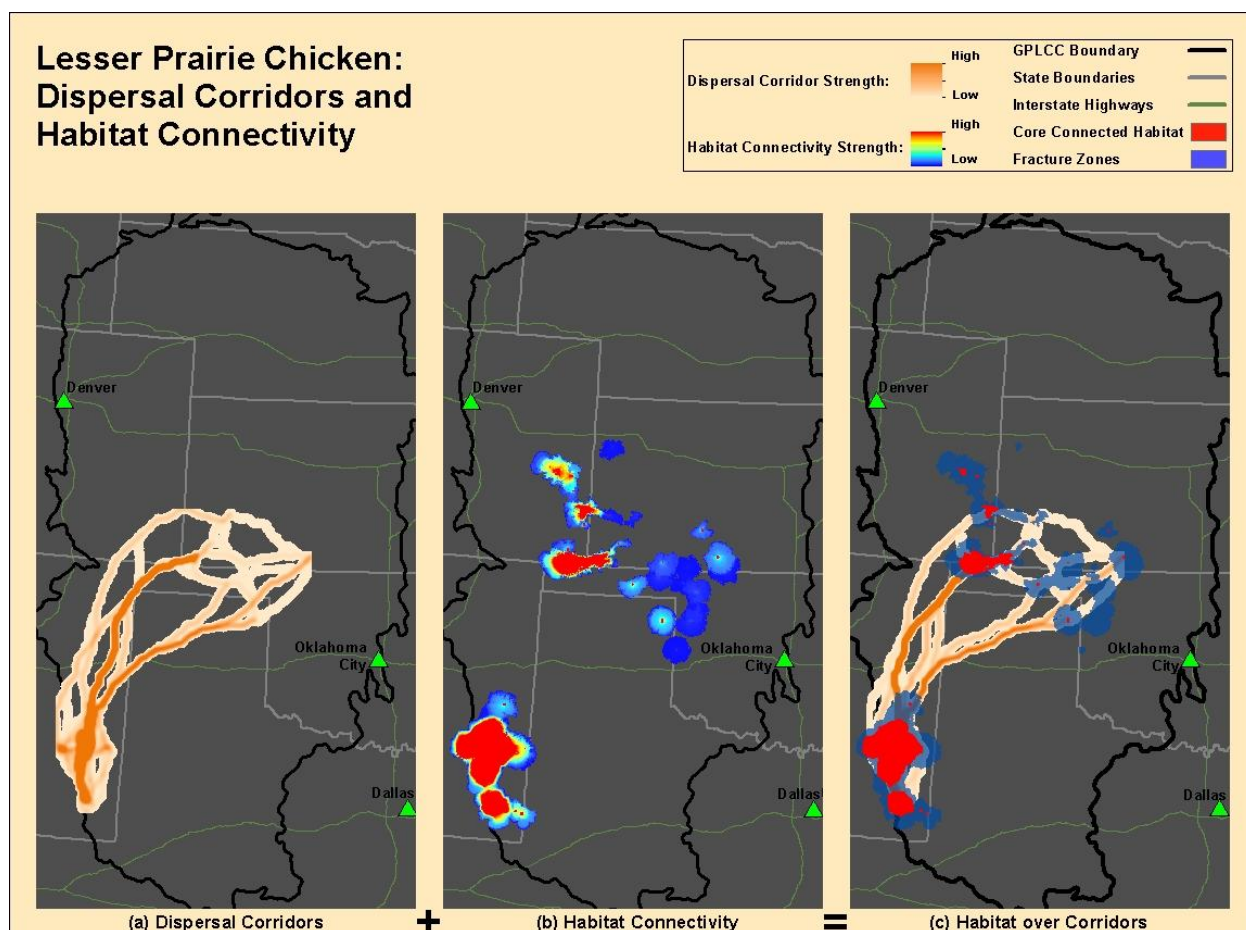
Figure 7. Lesser prairie-chicken dispersal corridors and habitat connectivity for the resistance map GHRMLM, corresponding to grassland associated species with medium relative resistance due to roads and landuse. (a) UNICOR corridor predictions among NATURESERV records of lesser prairie chicken occurrence; (b) resistant kernel density predictions based on a 40km maximum dispersal distance; (c) resistant kernel core areas (red) and fracture zones (blue) overlaying the UNICOR corridor pathways.
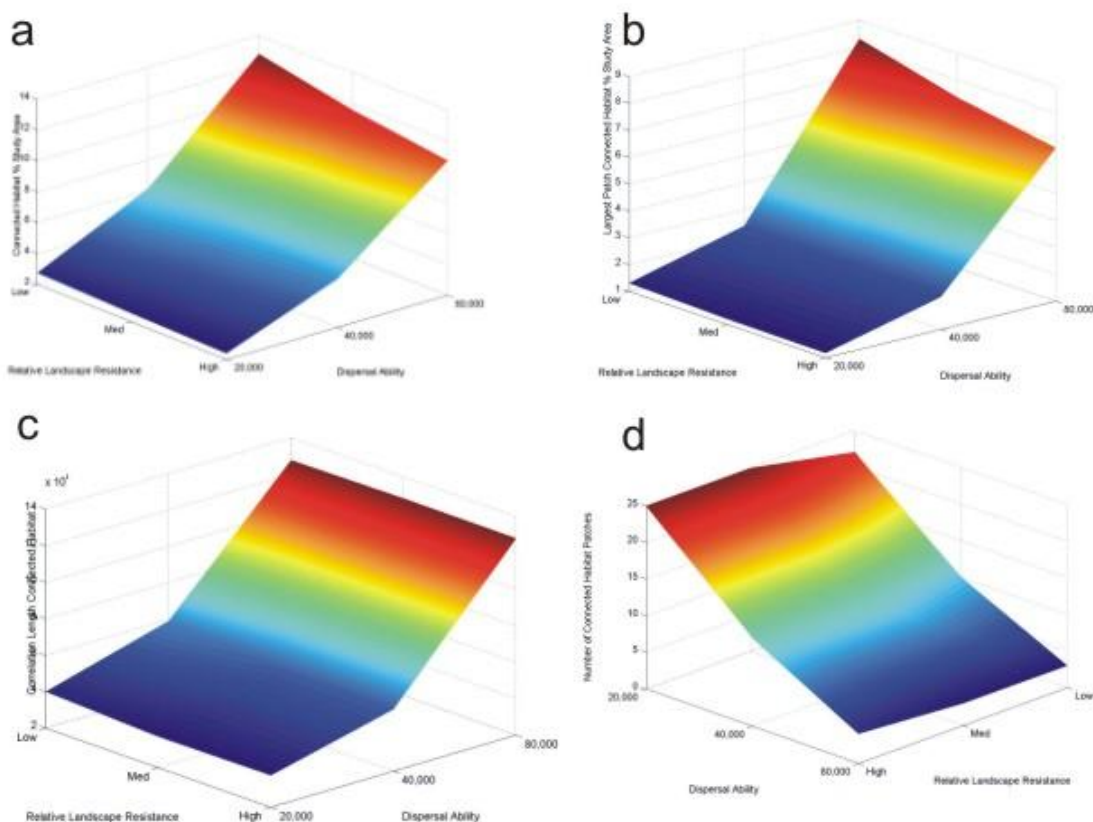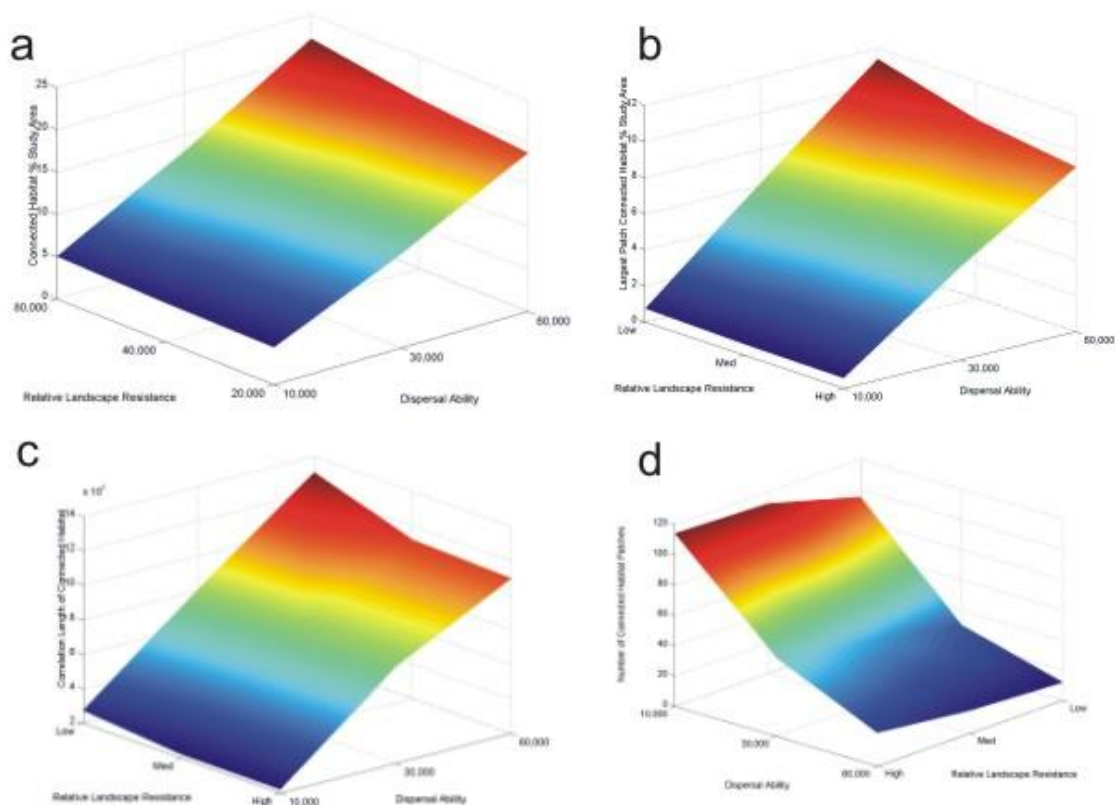
Figure 8. FRAGSTATS results for lesser prairie chicken.
Percentage of landscape in connected habitat (a; PLAND), largest patch of connected habitat percentage of study area (b; LPI), correlation length of connected habitat (c, CL), and number of individual patches of connected habitat (d, NP) across factorial combination of three levels of relative landscape resistance (Low, Med, High) and three levels of dispersal ability (20,000; 40,000; 80,000) for the lesser prairie-chicken.
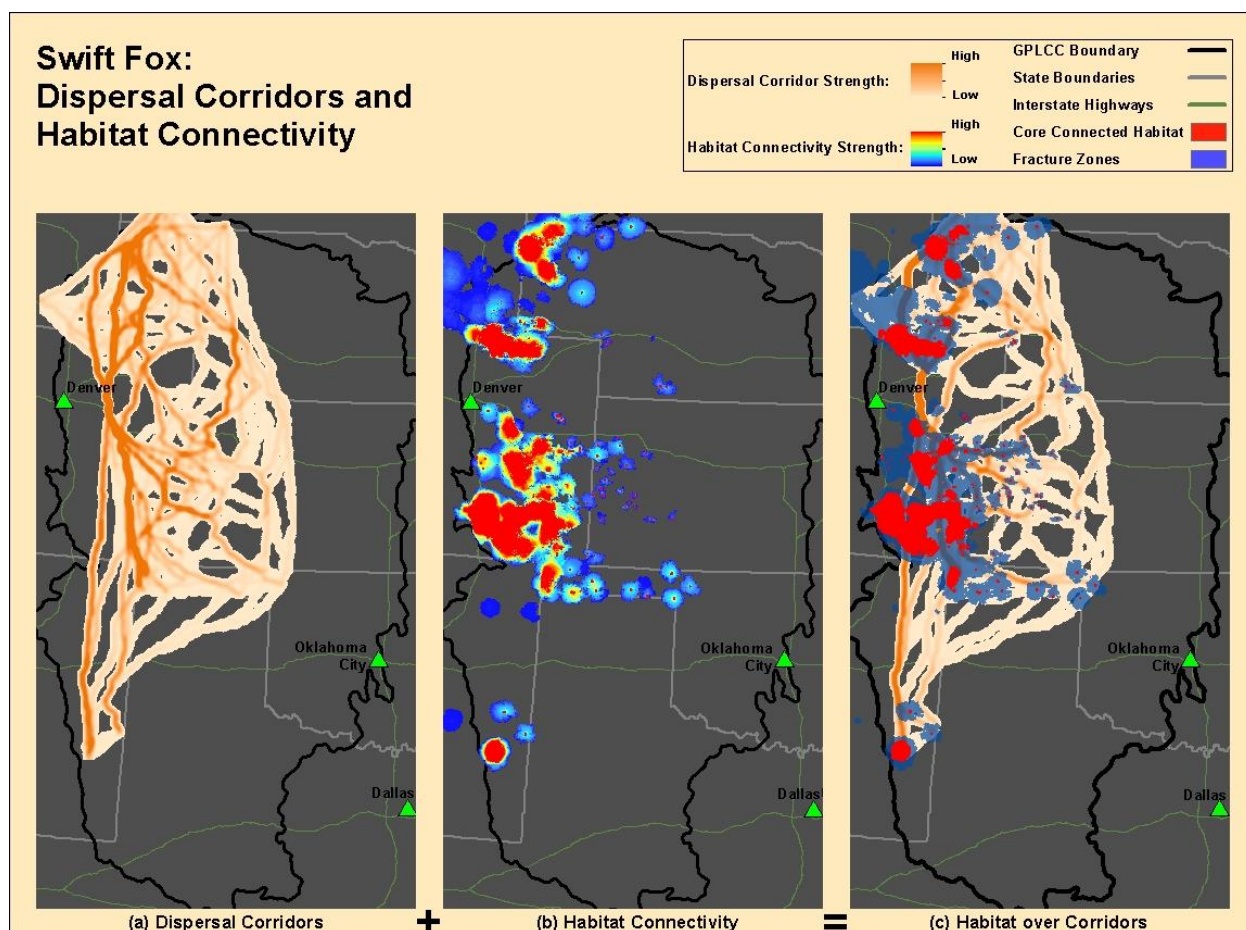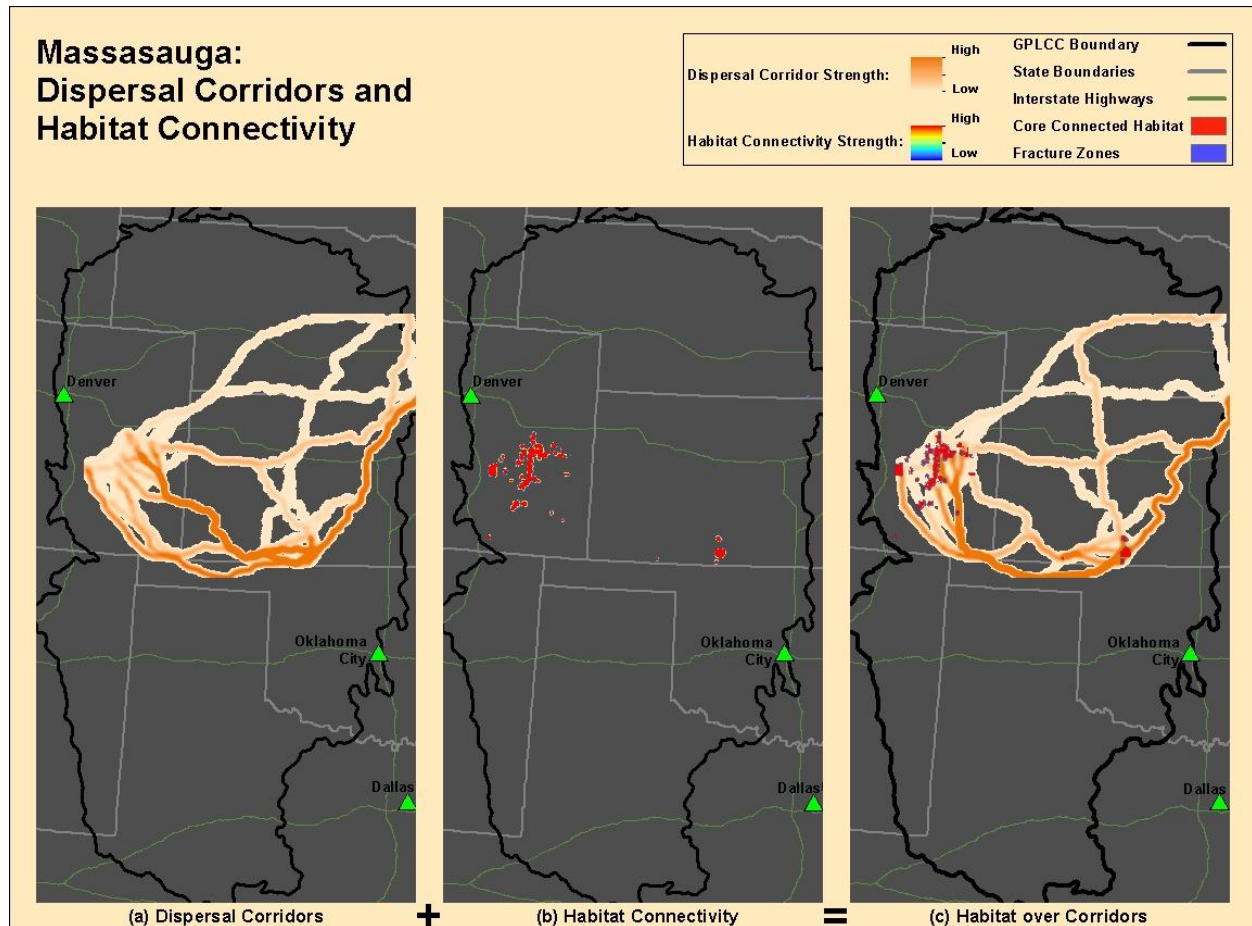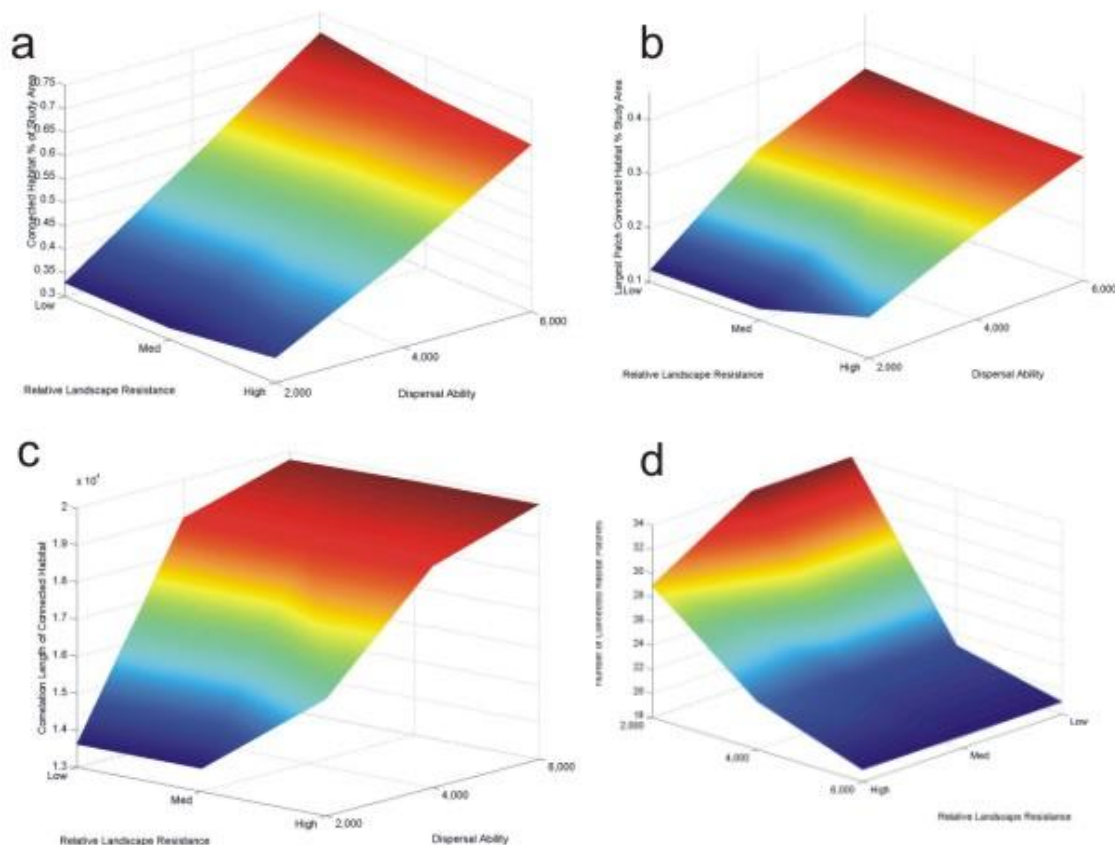
Figure 9. Swift fox dispersal corridors and habitat connectivity for the resistance map GHRMLM, corresponding to grassland associated species with medium relative resistance due to roads and landuse.

(a) UNICOR corridor predictions among NATURESERV records of swift fox occurrence; (b) resistant kernel density predictions based on a 30km maximum dispersal distance; (c) resistant kernel core areas (red) and fracture zones (blue) overlaying the UNICOR corridor pathways.

Figure 10. FRAGSTATS results for swift fox.
a) percentage of landscape in connected habitat, b) largest patch of connected habitat percentage of study area, c) correlation length of connected habitat, and d) number of individual patches of connected habitat across factorial combination of three levels of relative landscape resistance (Low, Med, High) and three levels of dispersal ability (10,000; 30,000; 60,000) for the swift fox.
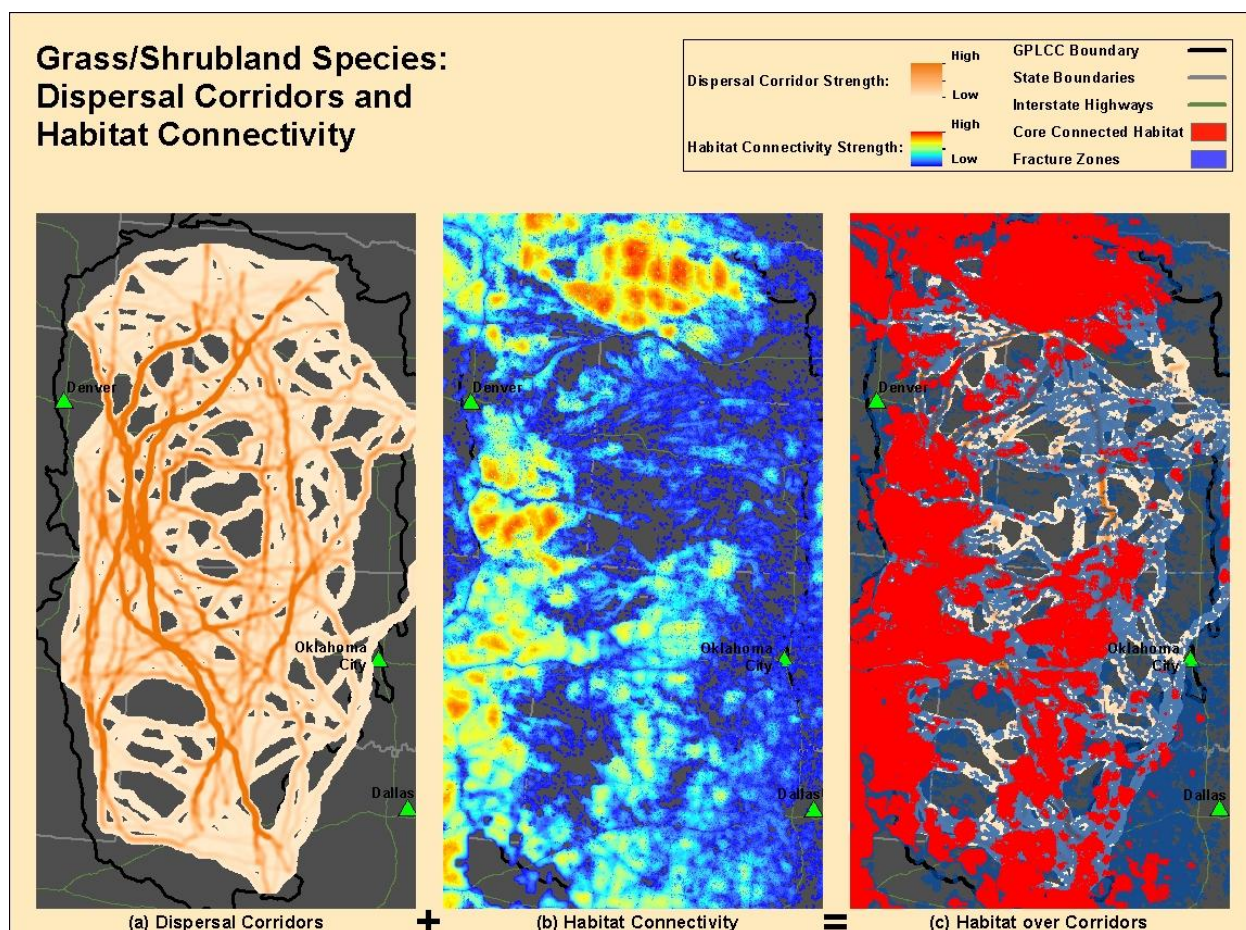
Figure 11. Massasauga dispersal corridors and habitat connectivity for the resistance scenario GHRMLM, corresponding to grassland associated species with medium relative resistance due to roads and landuse.
(a) UNICOR corridor predictions among NATURESERV records of lesser prairie chicken occurrence; (b) resistant kernel density predictions based on a 4km maximum dispersal distance; (c) resistant kernel core areas (red) and fracture zones (blue) overlaying the UNICOR corridor pathways.
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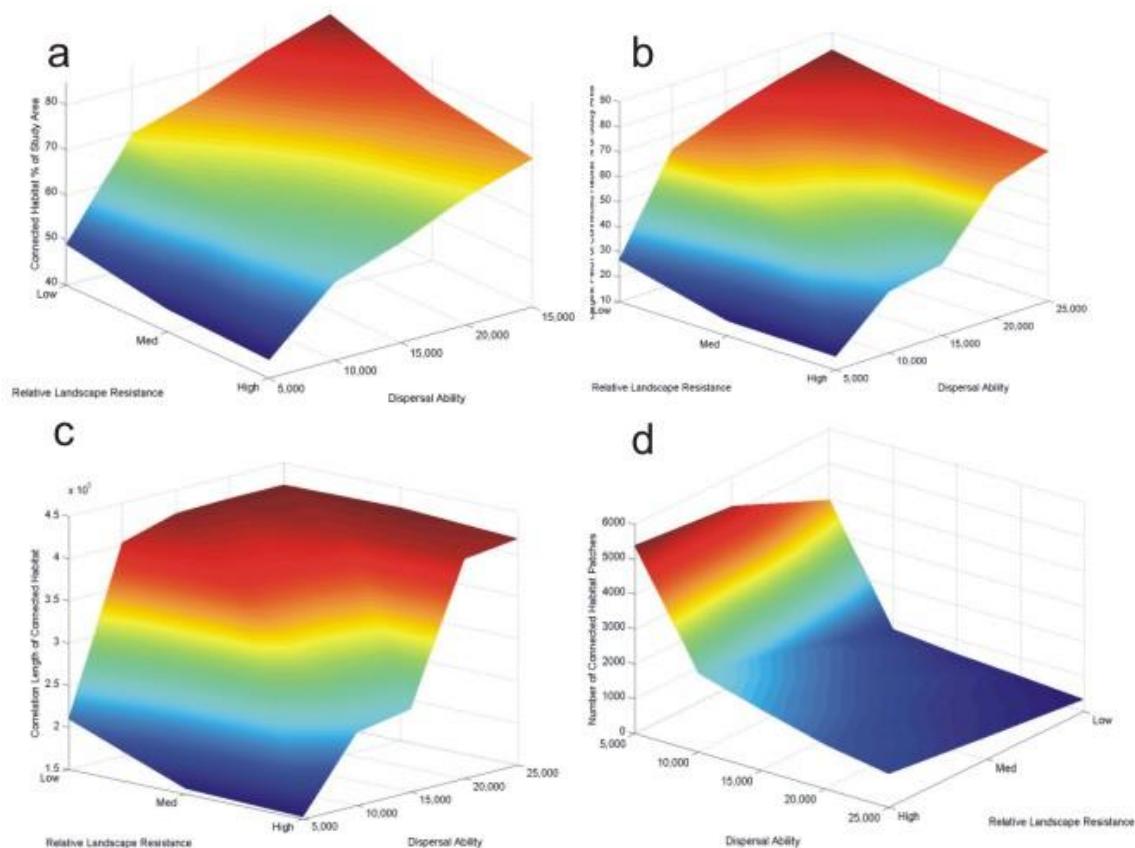**Figure 12. FRAGSTATS results for massasauga.**
a) percentage of landscape in connected habitat, b) largest patch of connected habitat percentage of study area, c) correlation length of connected habitat, and d) number of individual patches of connected habitat across factorial combination of three levels of relative landscape resistance (Low, Med, High) and three levels of dispersal ability (2,000; 4,000; 6,000) for the massasuaga.

Figure 13. Grassland associated species dispersal corridors and habitat connectivity for the resistance scenario GHRMLM, corresponding to grassland associated species with medium relative resistance due to roads and landuse.
(a) UNICOR corridor predictions among 100 points uniformly distributed among grassland pixels; (b) resistant kernel density predictions based on a 20km maximum dispersal distance based on the summation of over 36,000 source kernels originating in grassland pixels; (c) resistant kernel core areas (red) and fracture zones (blue) overlaying the UNICOR corridor pathways.
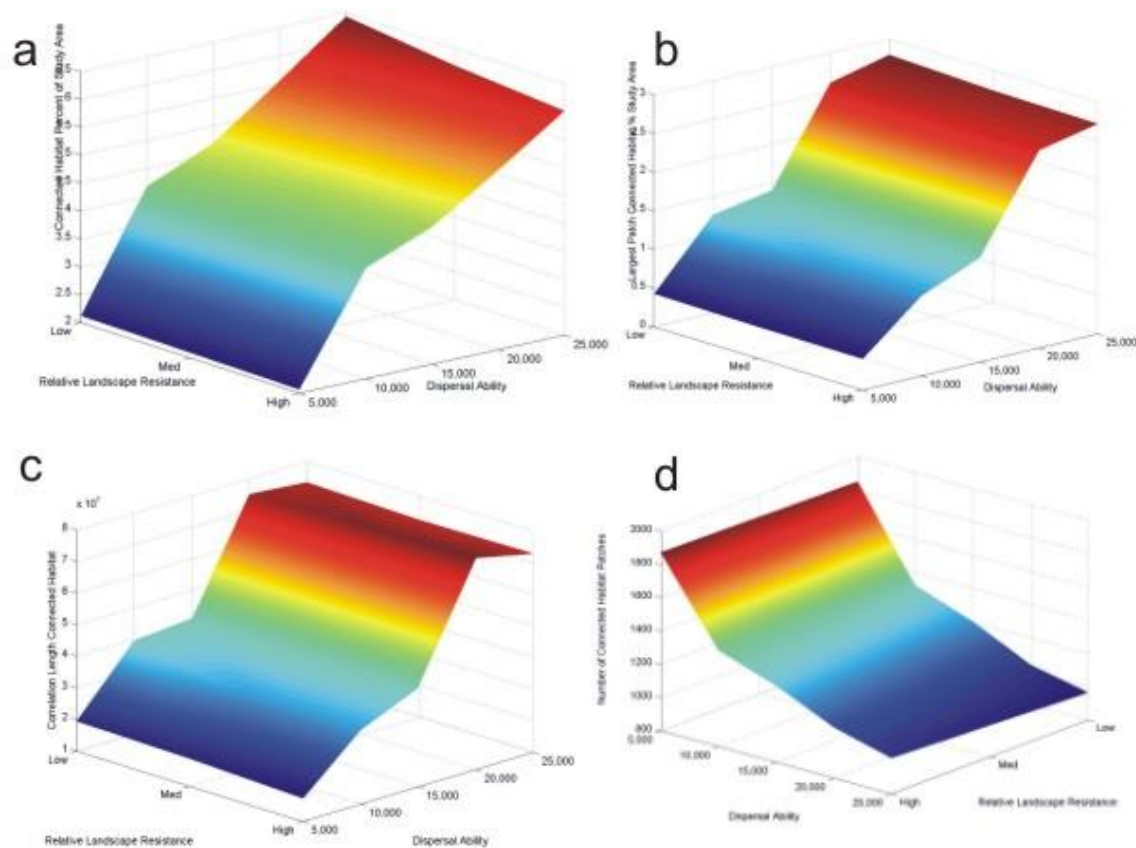.

Figure 14. FRAGSTATS results for grassland associated species.
 a) percentage of landscape in connected habitat, b) largest patch of connected habitat percentage of study area, c) correlation length of connected habitat, and d) number of individual patches of connected habitat across factorial combination of three levels of relative landscape resistance (Low, Med, High) and five levels of dispersal ability (5,000; 10,000; 15,000; 20,000; 25,000) for grassland associated species.
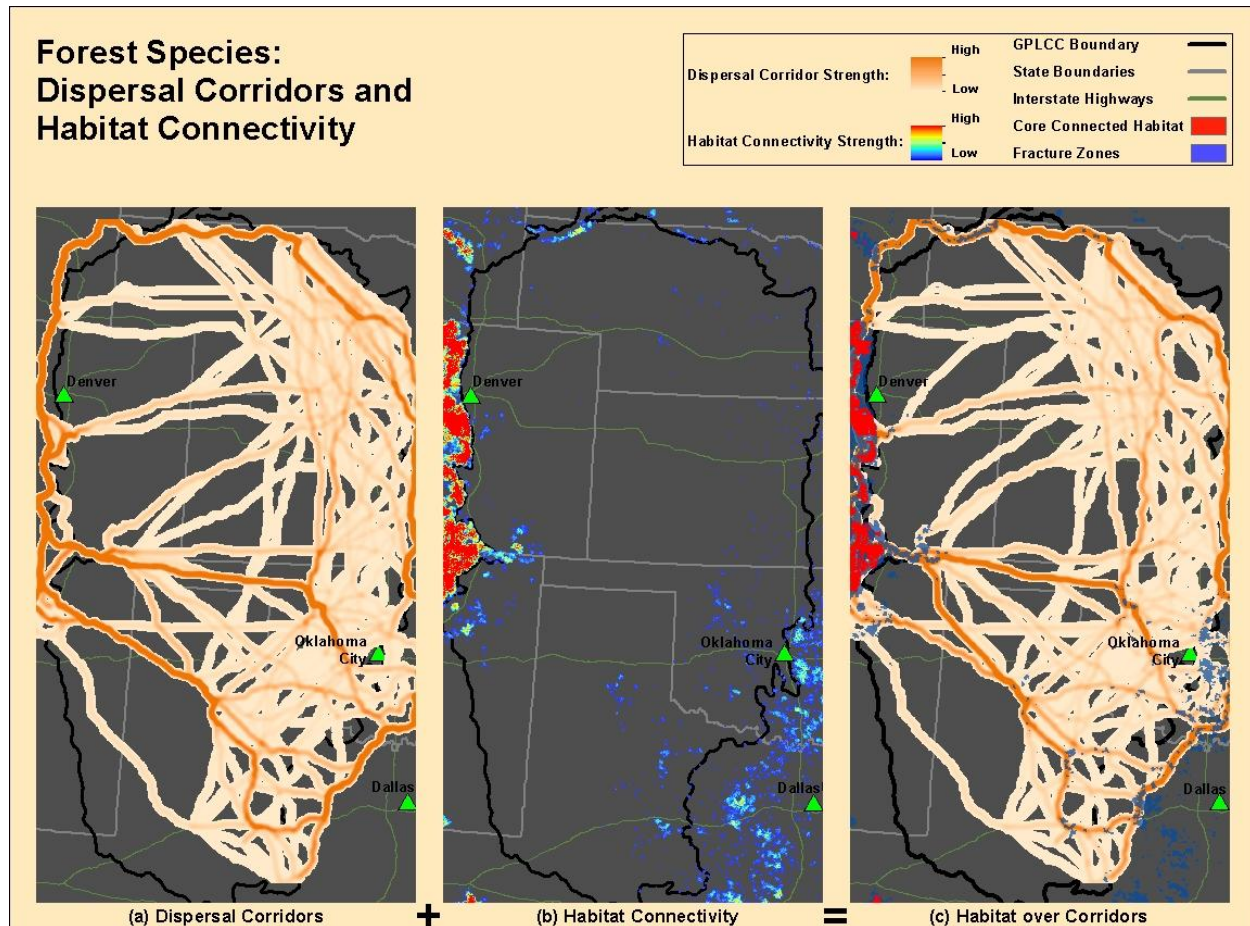
Figure 15. Forestland associated species dispersal corridors and habitat connectivity FRMLM, corresponding to forestland associated species with medium relative resistance due to roads and landuse.
(a) UNICOR corridor predictions among 100 points uniformly distributed among forestland pixels; (b) resistant kernel density predictions based on a 20km maximum dispersal distance based on the summation of over18,000 source kernels originating in grassland pixels; (c) resistant kernel core areas (red) and fracture zones (blue) overlaying the UNICOR corridor pathways.

Figure 16. FRAGSTATS results for forestland associated species.
a) percentage of landscape in connected habitat, b) largest patch of connected habitat percentage of study area, c) correlation length of connected habitat, and d) number of individual patches of connected habitat across factorial combination of three levels of relative landscape resistance (Low, Med, High) and five levels of dispersal ability (5,000; 10,000; 15,000; 20,000; 25,000) for forestland associated species.
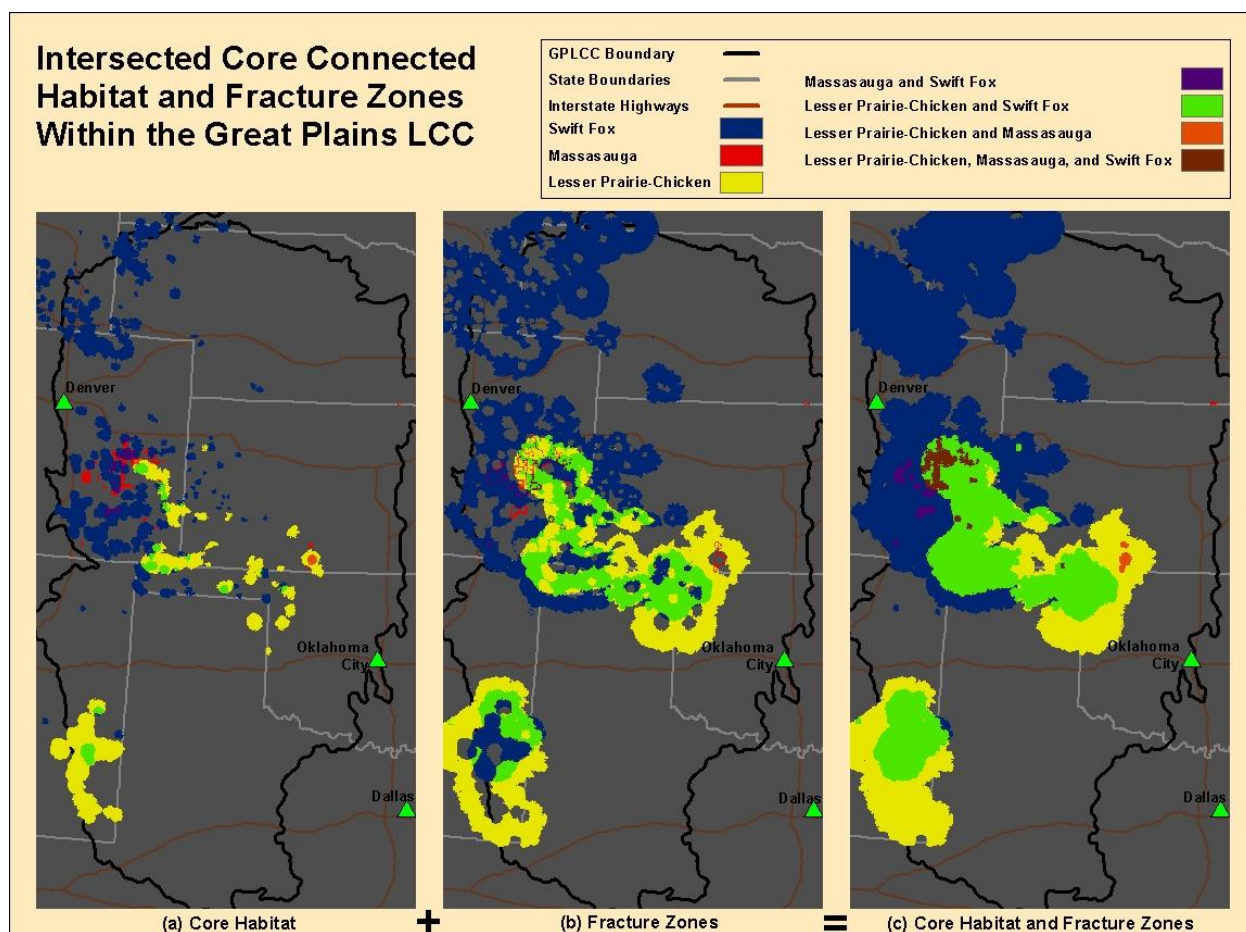
Figure 17. Intersection map for predicted (a) core areas, (b) fracture zone, and (c) full connected habitat.

The colors depict different species combinations: blue – swift fox only; yellow – lesser prairie chicken only; red massasauga only; green – swift fox and prairie chicken; purple – swift fox and massasauga; orange – prairie chicken and massasauga; brown – all three species.
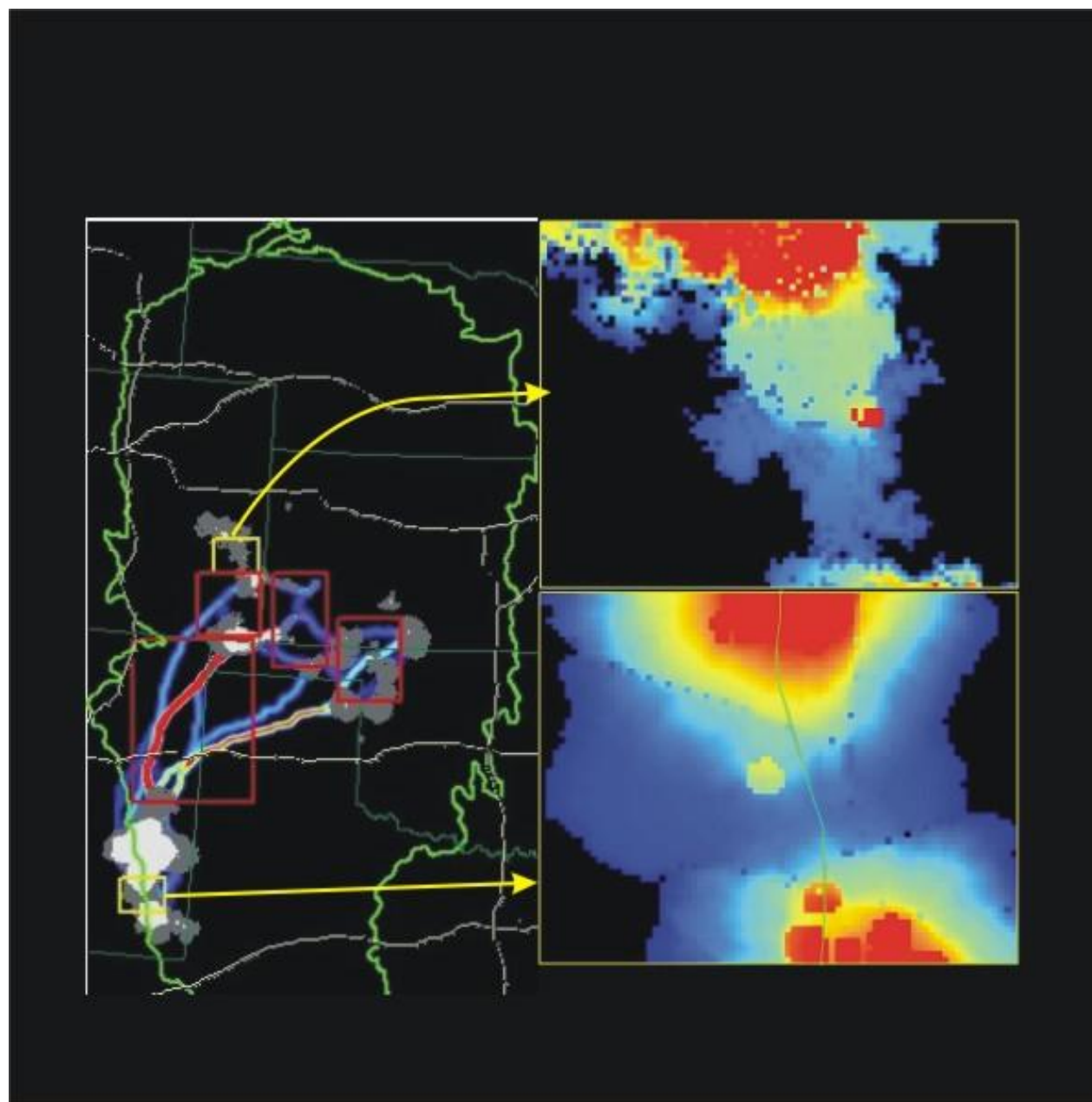
Figure 18. Key consensus fracture zones for lesser prairie-chicken.

The panel at left shows the extent of the GPLCC specified by a green outline. State boundaries are shown in dark green and intersate highways are shown as gray lines. Population core areas are shown as white patches. Gray patches are predicted fracture zones, where the expected rate of movement is at at least 90% less than the maximum predicted rate of movement for the species in the study area. These fracture zones are areas of critically attenuated movement that constitute partial barriers. The yellow boxes show the locations of the key fracture zones we identified as being particularly important to regional connectivity. The red boxes show the location of key potential movement corridors between isolated populations. The panel at right shows the key fracture zones we identified as most important to maintaining regional connectivity of the lesser prairie chicken. The colormap ranges from red (high predicted movement rate) to dark blue (low predicted movement rate). Black areas are predicted to nave zero occupancy. There are two critical fracture zones separating predicted lesser prairie chicken core populations. The fracture zone separating the two core areas in the southern population is of particular importance to maintaining long-term population viability
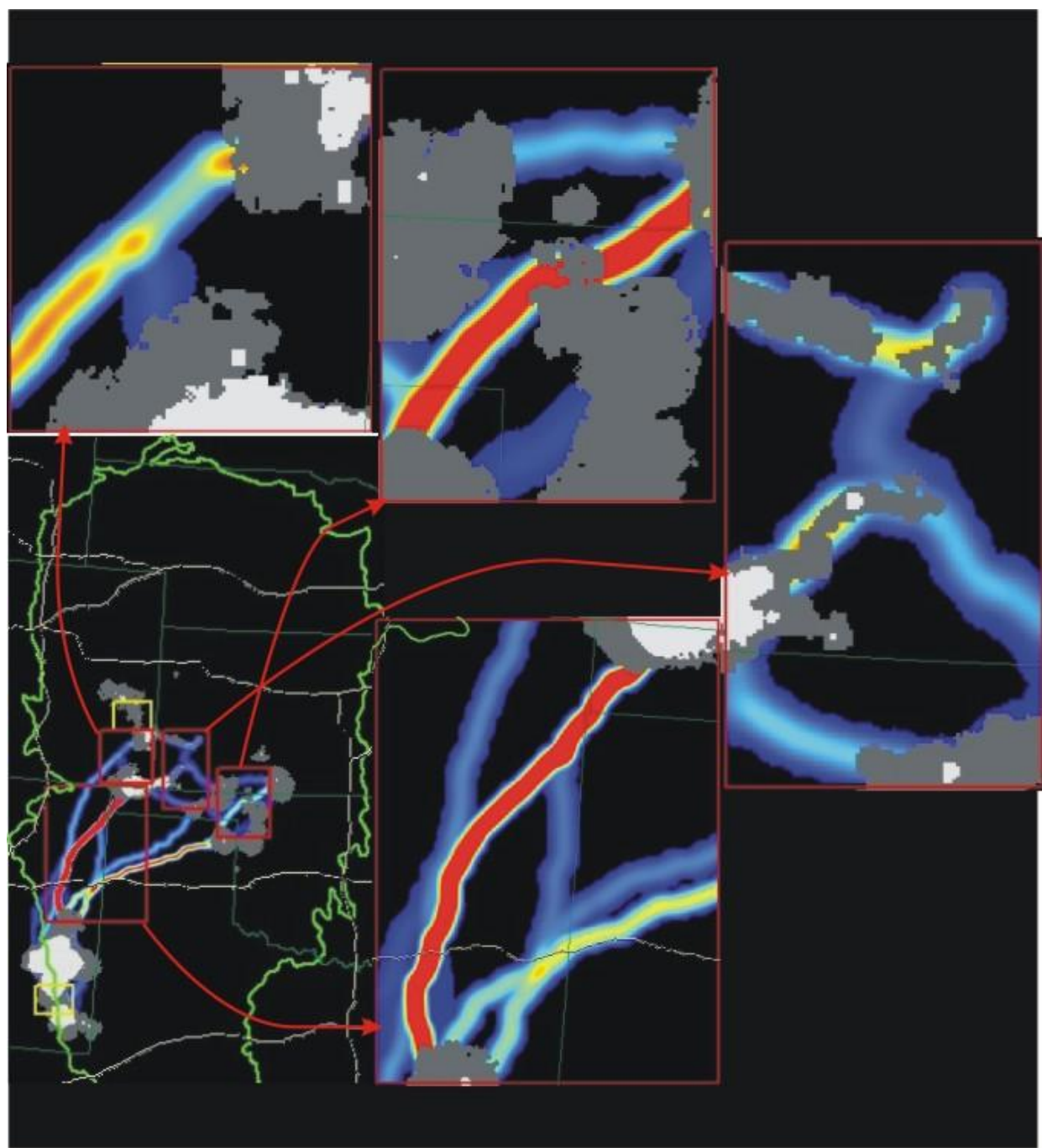
Figure 19. Key corridors for lesser prairie-chicken.

The panel at lower left shows the extent of the GPLCC specified by a green outline. State boundaries are shown in dark green and interstate highways are shown as gray lines. Population core areas are shown as white patches, and fractures zones as gray patches . The yellow boxes show the locations of the key fracture zones we identified as being particularly important to regional connectivity. The red boxes show the location of key potential movement corridors between isolated populations. The inset panels at right and above show the key corridors we identified as most important to maintaining regional connectivity of the lesser prairie-chicken. The colormap ranges from red (high corridor strength) to dark blue (low corridor strength). Black areas are predicted to not be part of the predicted corridor. There are four major gaps among the lesser prairie chicken core areas. These are predicted to be wider than the dispersal ability of the species. Therefore, for the predicted corridors to be effective at spanning these gaps, additional habitat restoration or establishment of stepping stone populations may be necessary. This is particularly the case for the gap between the large southern core populations and the smaller and more scattered northern populations. This gap is many times larger than the dispersal ability of the species, meaning that demographic or genetic rescue of the northern populations by the southern population is unlikely.
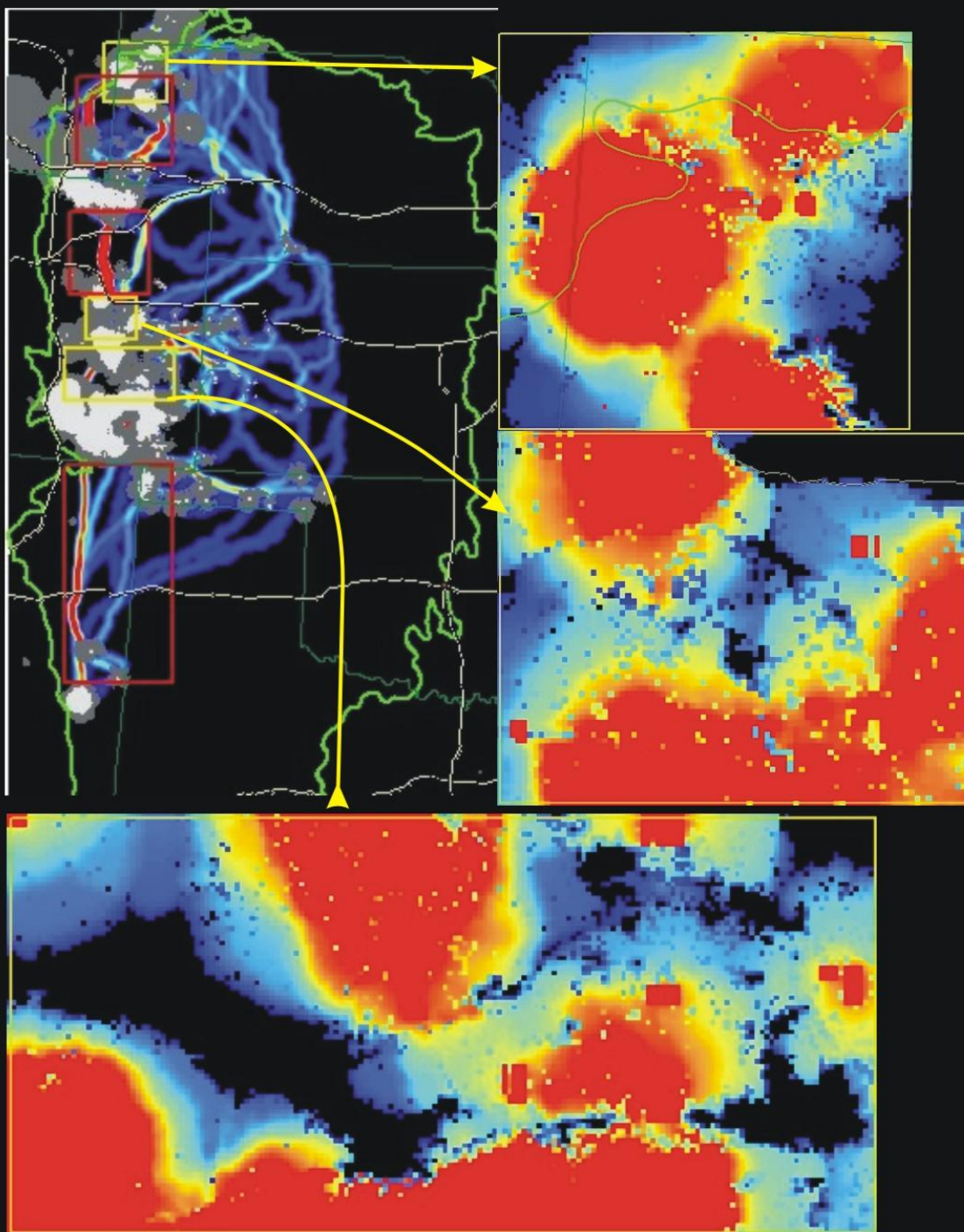
Figure 20. Key consensus fracture zones for swift fox.

The panel at upper left shows the extent of the GPLCC specified by a green outline. State boundaries are shown in dark green and interstate highways are shown as gray lines. Population core areas are shown as white patches. Gray patches are predicted fracture zones, where the expected rate of movement is at at least 90% less than the maximum predicted rate of movement for the species in the study area. These fracture zones are areas of critically attenuated movement that constitute partial barriers. The yellow boxes show the locations of the key fracture zones we identified as being particularly important to regional connectivity. The red boxes show the location of key potential movement corridors between isolated populations. The other inset panels at right and below show the key fracture zones we identified as most important to maintaining regional connectivity of the swift fox in the GPLCC. The colormap ranges from red (high predicted movement rate) to dark blue (low predicted movement rate). Black areas are predicted to nave zero occupancy. There are three critical fracture zones separating swift fox core populations. The northernmost fracture zone is relatively modest in effect, with the cluster of core populations largely interconnected by high predicted rates of movement. In contrast, the southern two identified key fracture zones pose a much more serious impediment to potential dispersal and gene flow. Our fracture zone analysis predicts these areas experience greatly attenuated movement rates, which probably results in nearly complete isolation of the core areas separated on either side of these fracture zones.
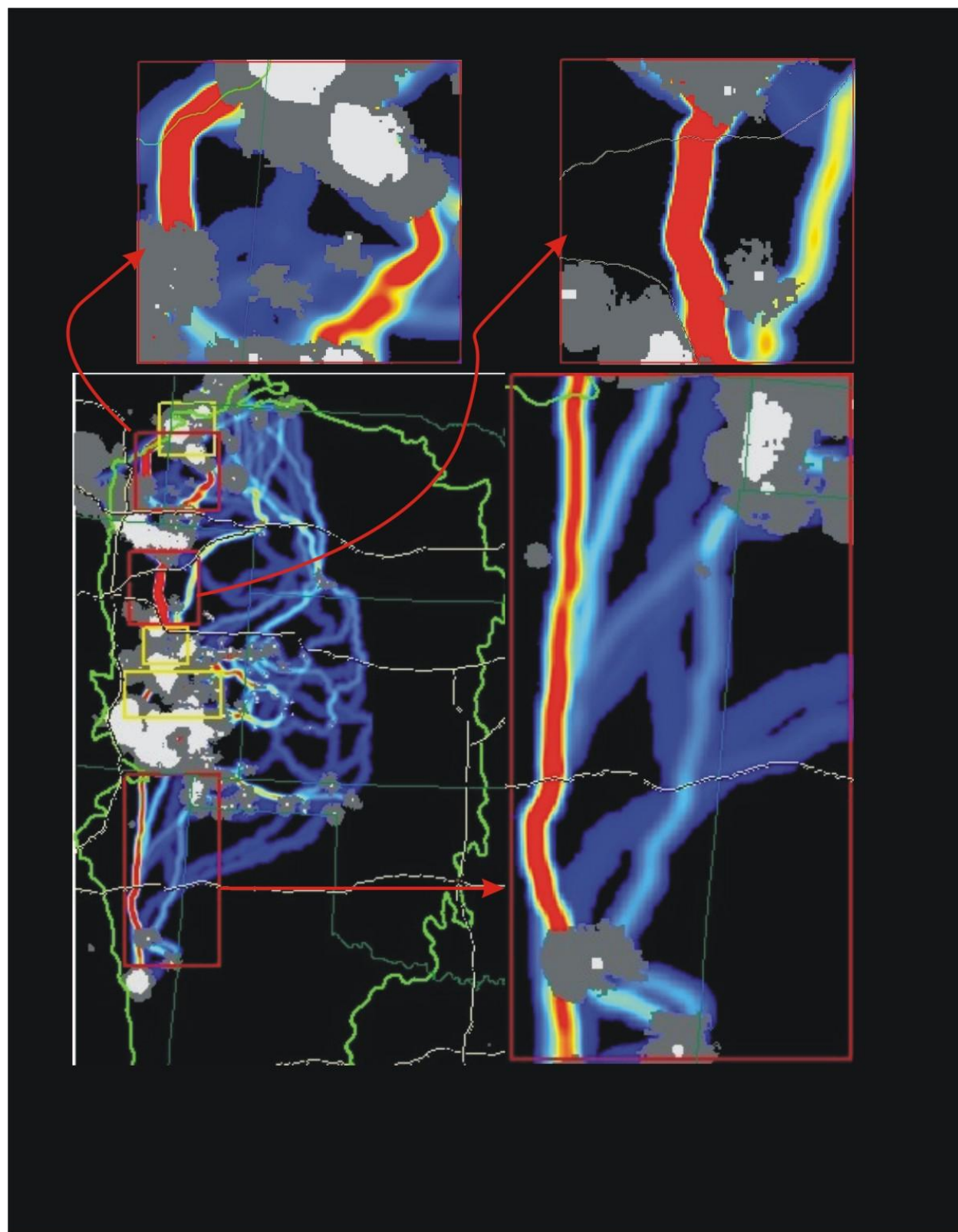
Figure 21. Key consensus corridors for swift fox.
The panel at lower left shows the extent of the GPLCC specified by a green outline. State boundaries are shown in dark green and interstate highways are shown as gray lines. Population core areas are shown as white patches, and fractures zones as gray patches . The yellow boxes show the locations of the key fracture zones we identified as being particularly important to regional connectivity. The red boxes show the location of key potential movement corridors between isolated populations. The inset panels at right and above show the key corridors we identified as most important to maintaining regional connectivity of the swift fox. The colormap ranges from red (high corridor strength) to dark blue (low corridor strength). Black areas are predicted to not be part of the predicted corridor.There are three major gaps among the swift fox core areas. These are predicted to be wider than the dispersal ability of the species. Therefore, for the predicted corridors to be effective at spanning these gaps, additional habitat restoration or establishment of stepping stone populations may be necessary. This is particularly the case for the gap between the large central core population and the small and highly isolated southern most core population. This gap is many times greater than the maximum dispersal ability of the species. The two northern gaps spanned by predicted corridors are also substantially greater than the dispersal ability of the species, indicating the swift fox population in the GPLCC may be functionally isolated into several distinct metapopulations.
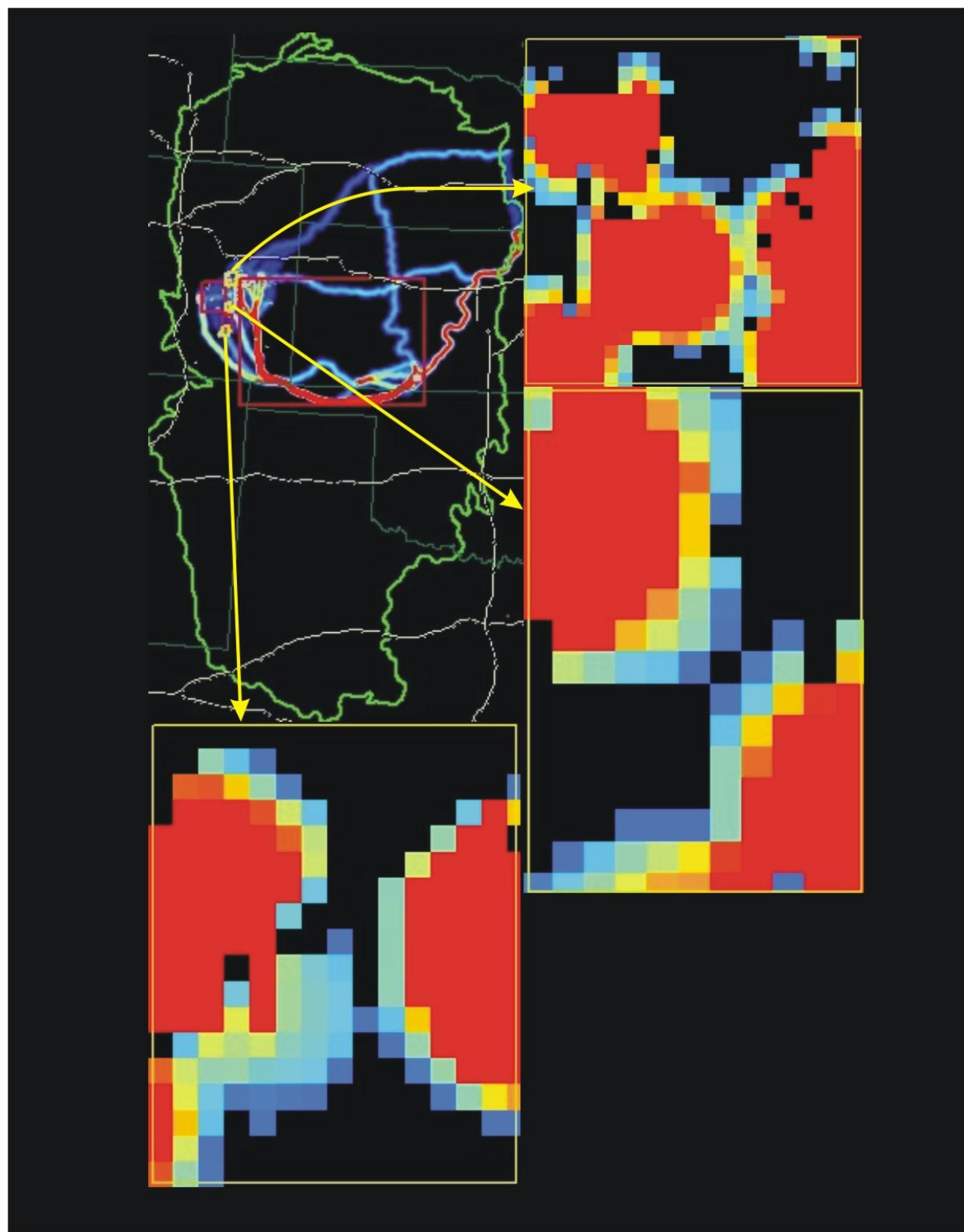
Figure 22. Key fracture zones for massasauga focal species.

The panel at upper left shows the extent of the GPLCC specified by a green outline. State boundaries are shown in dark green and interstate highways are shown as gray lines. Population core areas are shown as white patches. Gray patches are predicted fracture zones, where the expected rate of movement is at at least 90% less than the maximum predicted rate of movement for the species in the study area. These fracture zones are areas of critically attenuated movement that constitute partial barriers. The yellow boxes show the locations of the key fracture zones we identified as being particularly important to regional connectivity. The red boxes show the location of key potential movement corridors between isolated populations. The other inset panels at right and below the key fracture zones we identified as most important to maintaining regional connectivity of the massasauga. The colormap ranges from red (high predicted movement rate) to dark blue (low predicted movement rate). Black areas are predicted to nave zero occupancy. We identified three key fracture zones that separate core population areas for the massasauga. Given the very limited dispersal ability of this species, the southern two of these fracture zones appear to represent near complete barriers isolating core areas. In contrast, the fracture zone analysis predicts relatively high movement and migration across the northernmost key fracture zone.
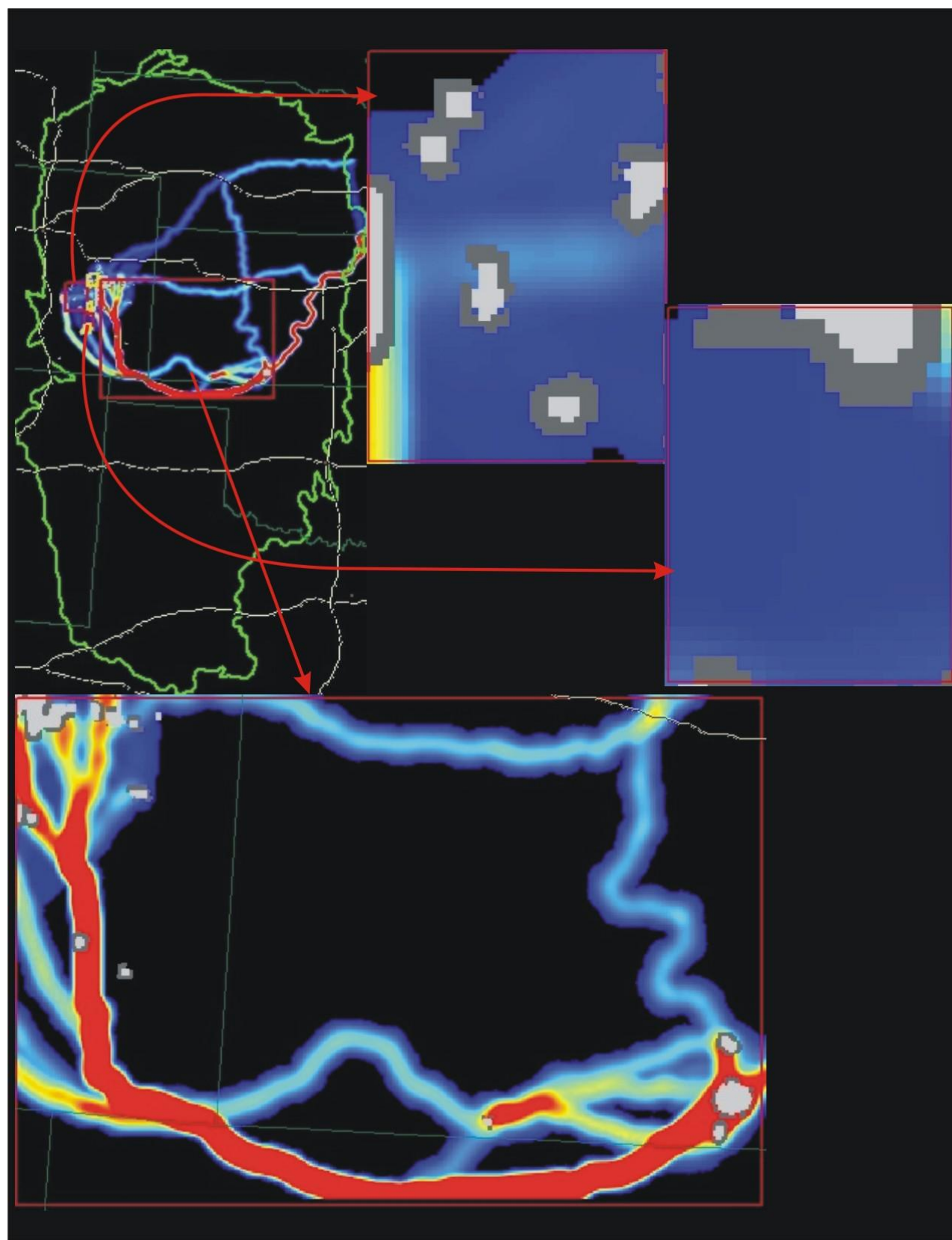
Figure 23. Key corridors for the massasauga.

The panel at upper left shows the extent of the GPLCC specified by a green outline. State boundaries are shown in dark green and interstate highways are shown as gray lines. Population core areas are shown as white patches, and fractures zones as gray patches . The yellow boxes show the locations of the key fracture zones we identified as being particularly important to regional connectivity. The red boxes show the location of key potential movement corridors between isolated populations. The inset panels at right and below show the key corridors we identified as most important to maintaining regional connectivity of the massasauga. The colormap ranges from red (high corridor strength) to dark blue (low corridor strength). Black areas are predicted to not be part of the predicted corridor. We identified three key corridors that could link currently isolated core populations. Given the very limited dispersal ability of this species, all these gaps are predicted to result in isolation of core populations separated across them. The westernmost two predicted corridors are relatively short and plausibly could function to a limited degree. In contrast the eastern predicted corridor is immensely long, spanning several states, while linking several small and disjunct populations. This corridor is not likely to provide any practical conservation service to this species. Maintenance of the isolated eastern populations will likely require local habitat enhancement, conservation and, when necessary, augmentation to increase genetic diversity and bolster population size.
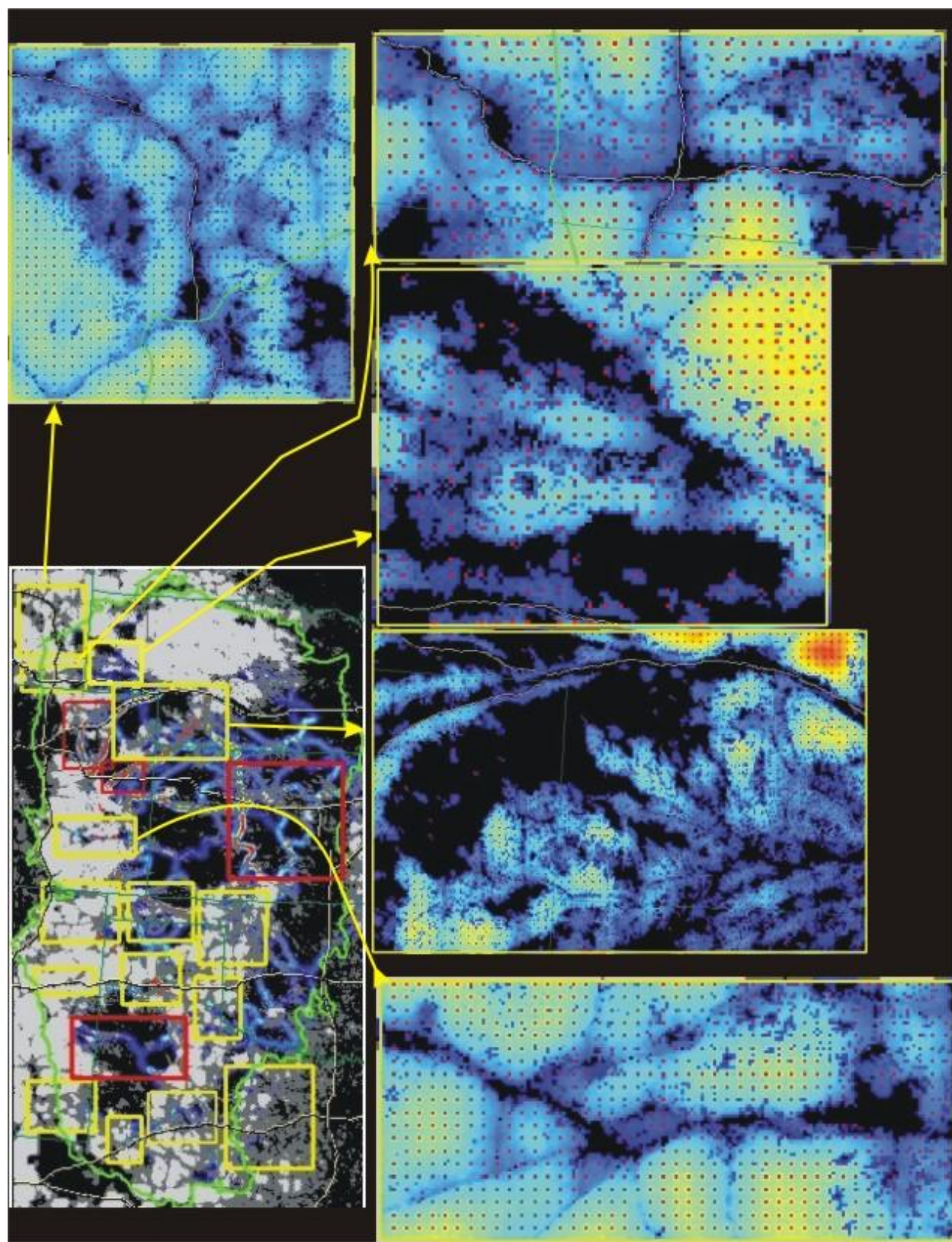
Figure 23. The northernmost five key fracture zones for grassland associated species.

The panel at lower left shows the extent of the GPLCC specified by a green outline. State boundaries are shown in dark green and intersate highways are shown as gray lines. Population core areas are shown as white patches. Gray patches are predicted fracture zones, where the expected rate of movement is at at least 90% less than the maximum predicted rate of movement for the species in the study area. These fracture zones are areas of critically attenuated movement that constitute partial barriers. The yellow boxes show the locations of the key fracture zones we identified as being particularly important to regional connectivity. The red boxes show the location of key potential movement corridors between isolated populations. The inset panels at right and above show the key fracture zones we identified as most important to maintaining regional connectivity of the grassland associated species. The colormap ranges from red (high predicted movement rate) to dark blue (low predicted movement rate). Black areas are predicted to nave zero occupancy. The red dots indicate the locations of dispersal sources used in the resistant kernel analysis.
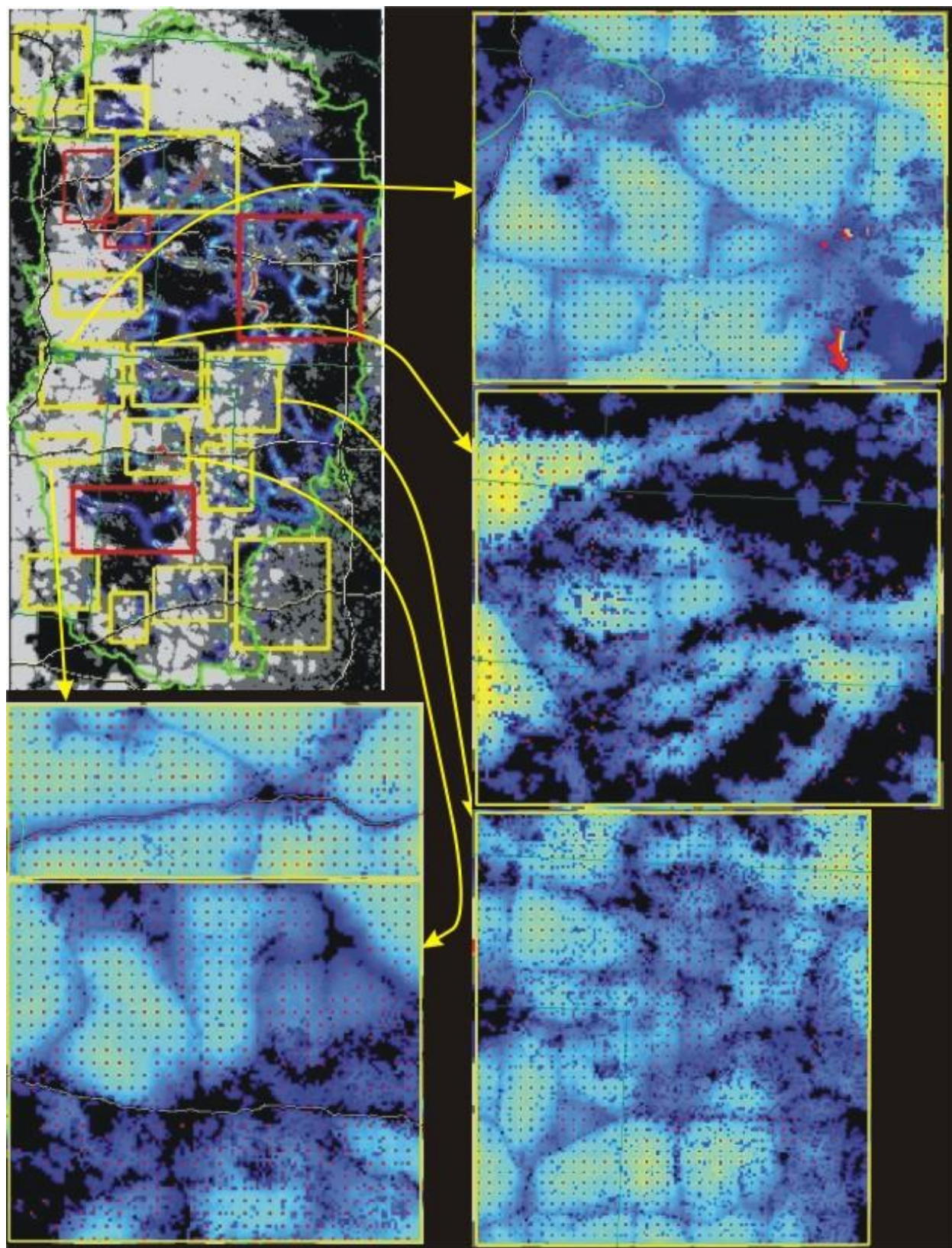
Figure 24. The central five key fracture zones for grassland associated species.
The panel at lower left shows the extent of the GPLCC specified by a green outline. State boundaries are shown in dark green and intersate highways are shown as gray lines. Population core areas are shown as white patches. Gray patches are predicted fracture zones, where the expected rate of movement is at at least 90% less than the maximum predicted rate of movement for the species in the study area. These fracture zones are areas of critically attenuated movement that constitute partial barriers. The yellow boxes show the locations of the key fracture zones we identified as being particularly important to regional connectivity. The red boxes show the location of key potential movement corridors between isolated populations. The inset panels at right and above show the key fracture zones we identified as most important to maintaining regional connectivity of the grassland associated species. The colormap ranges from red (high predicted movement rate) to dark blue (low predicted movement rate). Black areas are predicted to nave zero occupancy. The red dots indicate the locations of dispersal sources used in the resistant kernel analysis.
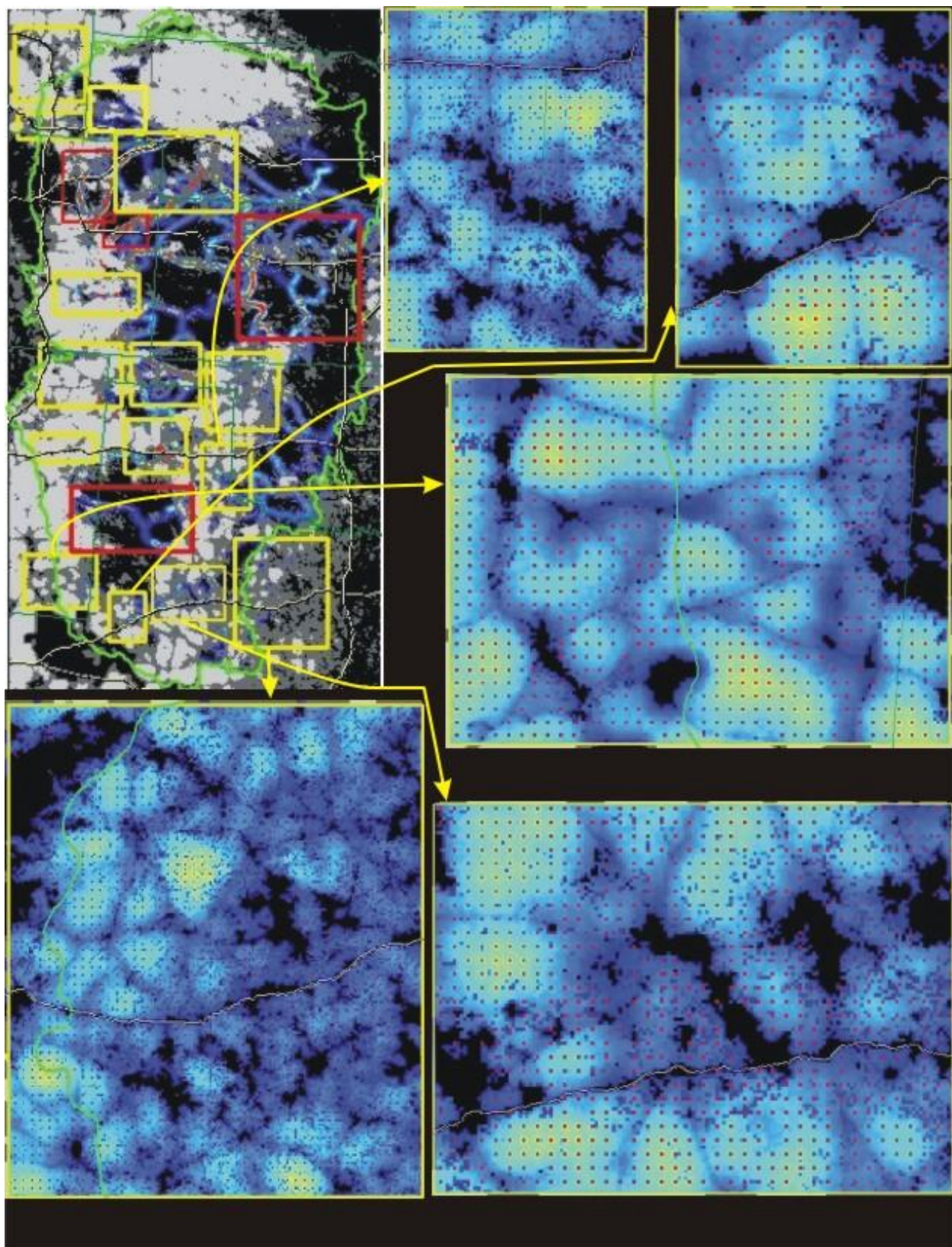
Figure 25. The southern five key fracture zones for grassland associated species.

The panel at lower left shows the extent of the GPLCC specified by a green outline. State boundaries are shown in dark green and intersate highways are shown as gray lines. Population core areas are shown as white patches. Gray patches are predicted fracture zones, where the expected rate of movement is at at least 90% less than the maximum predicted rate of movement for the species in the study area. These fracture zones are areas of critically attenuated movement that constitute partial barriers. The yellow boxes show the locations of the key fracture zones we identified as being particularly important to regional connectivity. The red boxes show the location of key potential movement corridors between isolated populations. The inset panels at right and above show the key fracture zones we identified as most important to maintaining regional connectivity of the grassland associated species. The colormap ranges from red (high predicted movement rate) to dark blue (low predicted movement rate). Black areas are predicted to nave zero occupancy. The red dots indicate the locations of dispersal sources used in the resistant kernel analysis.
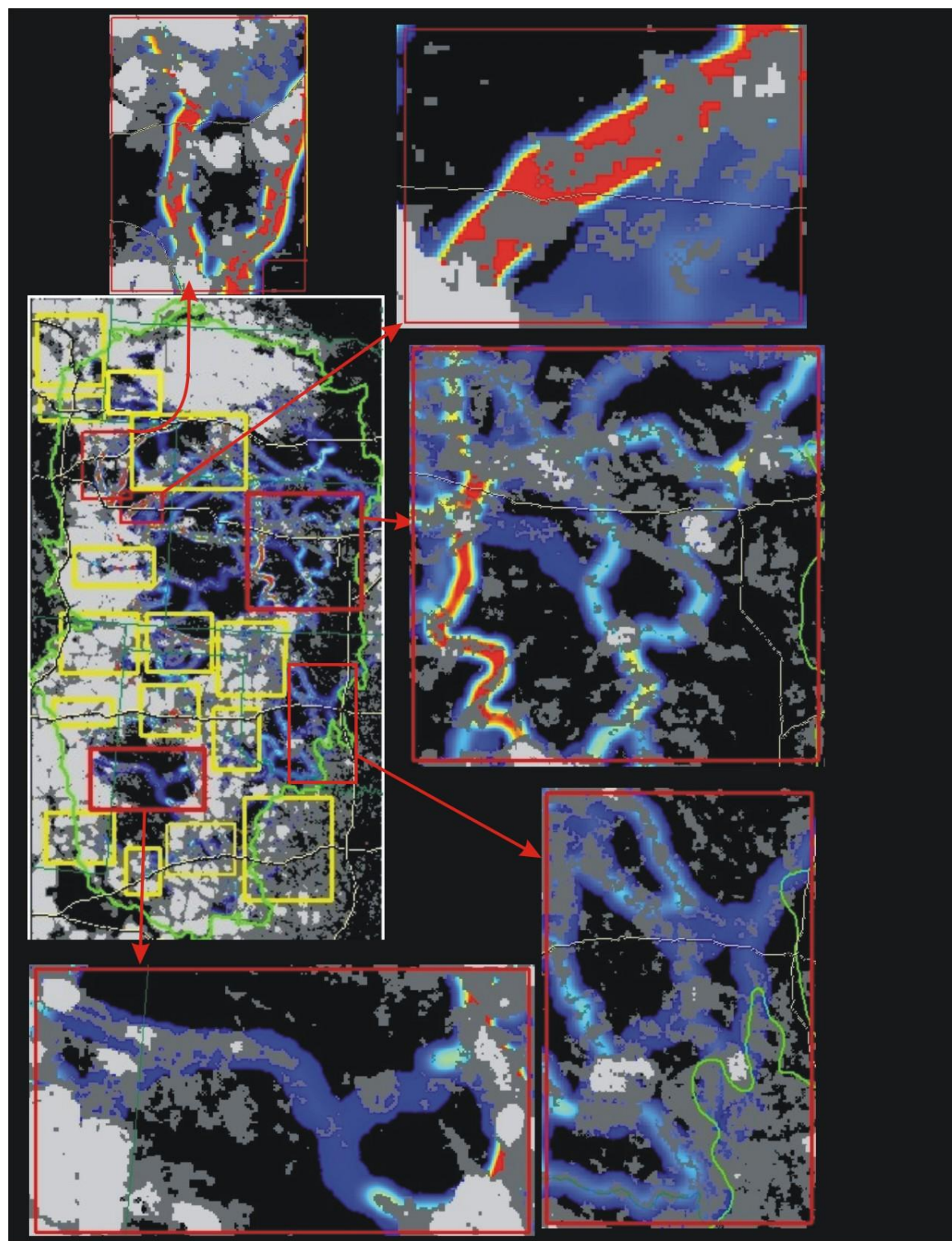
Figure 26 –Key corridors for grassland focal species.

The panel at lower left shows the extent of the GPLCC specified by a green outline. State boundaries are shown in dark green and intersate highways are shown as gray lines. Population core areas are shown as white patches, and fractures zones as gray patches . The yellow boxes show the locations of the key fracture zones we identified as being particularly important to regional connectivity. The red boxes show the location of key potential movement corridors between isolated populations. The inset panels at right and above show the key corridors we identified as most important to maintaining regional connectivity of grassland associated species. The colormap ranges from red (high corridor strength) to dark blue (low corridor strength). Black areas are predicted to not be part of the predicted corridor. The northernmost two of the five identified corridors linking core populations are by far the most important for maintaining regional connectivity of grassland habitat. The southern three corridors provide alternative routes between core areas that are linked through additional pathways that pass through fracture zones and other core areas. In contrast, the northern two corridors provide the only links between the extensive core populations in the northern part of the GPLCC and the rest of the study area. As such, these areas should receive high priority for conservation actions aimed at enhancing movement and survivorship through these predicted corridors.
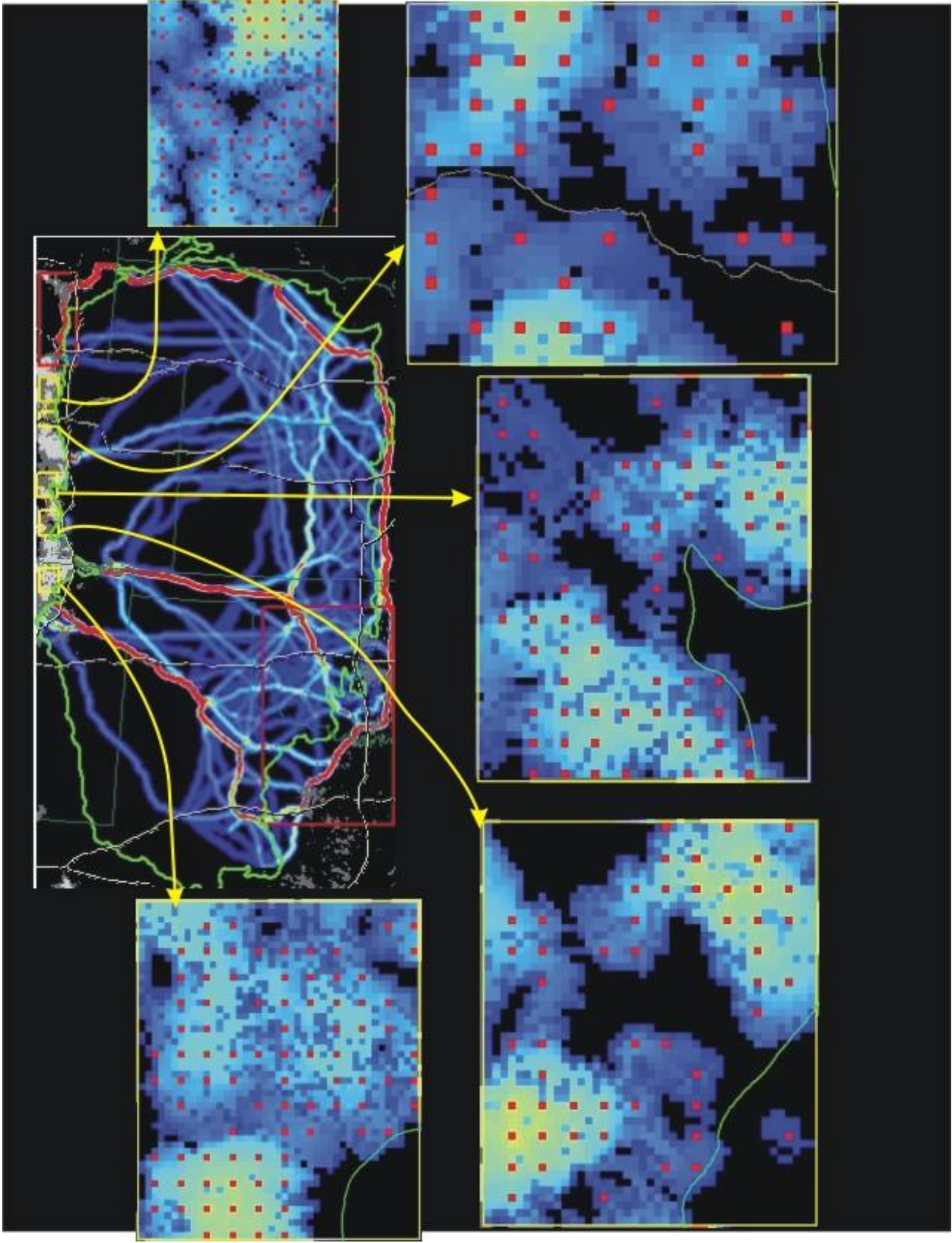
Figure 27. Key fracture zones for forestland associated species.
The panel at upper left shows the extent of the GPLCC specified by a green outline. State boundaries are shown in dark green and intersate highways are shown as gray lines. Population core areas are shown as white patches. Gray patches are predicted fracture zones, where the expected rate of movement is at least 90% less than the maximum predicted rate of movement for the species in the study area. These fracture zones are areas of critically attenuated movement that constitute partial barriers. The yellow boxes show the locations of the key fracture zones we identified as being particularly important to regional connectivity. The red boxes show the location of key potential movement corridors between isolated populations. The inset panels at right and above show the key fracture zones we identified as most important to maintaining regional connectivity of the forestland associated species. The colormap ranges from red (high predicted movement rate) to dark blue (low predicted movement rate). Black areas are predicted to have zero occupancy. The red dots indicate the locations of dispersal sources used in the resistant kernel analysis.
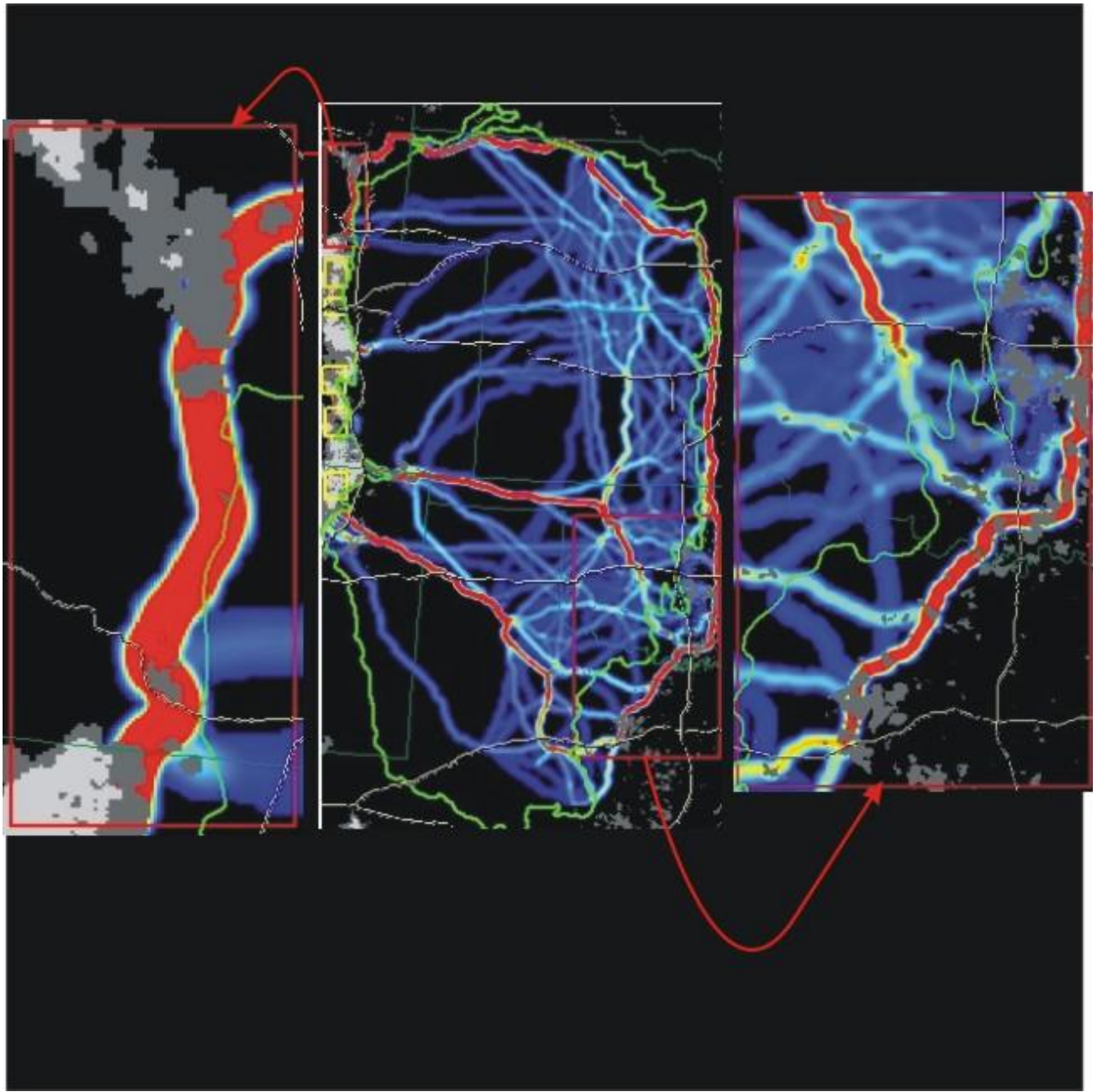
Figure 28. Key corridors for forestland associated species.

The panel at lower left shows the extent of the GPLCC specified by a green outline. State boundaries are shown in dark green and intersate highways are shown as gray lines. Population core areas are shown as white patches, and fractures zones as gray patches. The yellow boxes show the locations of the key fracture zones we identified as being particularly important to regional connectivity. The red boxes show the location of key potential movement corridors between isolated populations. The inset panels at right and above show the key corridors we identified as most important to maintaining regional connectivity of forestland associated species. The colormap ranges from red (high corridor strength) to dark blue (low corridor strength). Black areas are predicted to not be part of the predicted corridor.