

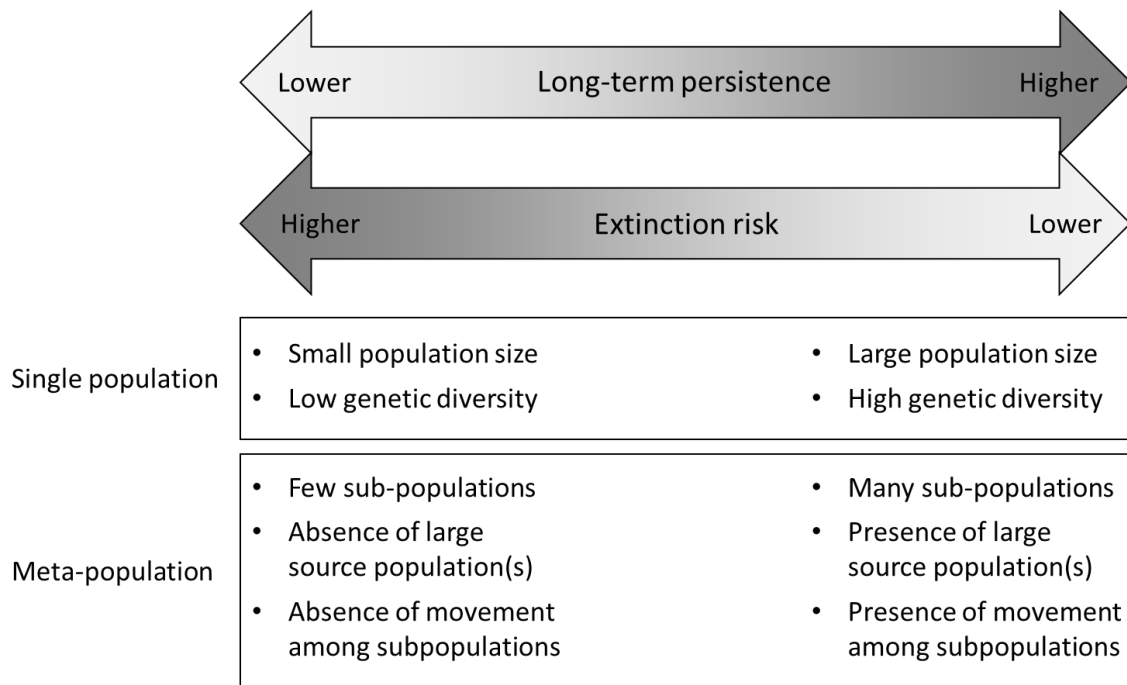
## Connectivity: a primer for Montana grizzly bear conservation

### Theoretical Basis for Connectivity

The best-case scenario for the long-term persistence of grizzly bears in the Lower-48 (and nearby areas of Canada) is the existence of multiple grizzly bear populations that exchange individuals but have somewhat independent dynamics. This complex of interconnected populations is known as a *metapopulation*. Below is an explanation of why connectivity among populations is helpful for their long-term persistence.

Based on both theory and empirical evidence, scientists have identified several factors that influence extinction risk, or conversely, the potential for long-term persistence of species. We know that larger, genetically diverse, and interconnected populations are more resilient to environmental change (providing more assurance of persistence) than smaller, genetically uniform, and/or isolated populations (Figure 1).

To illustrate numerical effects, consider the impact to a species of a weather, disease, or predation event that results in the deaths of 40 individuals (for example a flood). It is easy to understand that a population numbering 500 (8% lost to flood, now numbering 460) would likely fare better than a population numbering 50 (80% lost to flood, now numbering only 10). Now, consider if the population of 50 was not the only such population, but rather was one of 10 similarly sized populations that occurred in reasonably close proximity. As in the scenario of the single, larger population of 500, the impact of the mortality event on the species would be lessened, even if 1 of the 10 populations went extinct. Now, imagine the added benefit if at least 1 of the 10 populations was large, thereby further buffered against local extinction. Finally, suppose that individuals were able to move relatively freely among the various populations on the landscape. These movements might help modulate changes in population size due to environmental factors and would even allow for recolonization of areas where smaller populations may have died out. Simply put, a species consisting of larger, interconnected populations is more resilient to the rigors of an unknown future than a species made up of smaller, isolated populations.



**Figure 1. Factors that may influence the risk of extinction or, conversely, the long-term persistence of populations and metapopulations.**

The size of a population can also influence its overall genetic health and the viability of its members, with both short-term and long-term consequences of small size. One potential consequence of small or isolated populations is increased inbreeding, or the mating between related individuals. The genetic make-up of a population might be described as consisting of “building blocks” (i.e., alleles). As you might recall from your high school biology, these building blocks are organized in pairs. If a gene carries two identical copies of a building block, it is homozygous. If it carries two different copies of a building block, it is heterozygous. Inbreeding increases the frequency of homozygous genes. Severe inbreeding can cause ***inbreeding depression***, which is the reduced ability to reproduce and survive normally resulting from the expression of deleterious traits coded by homozygous pairs. Breeders of domestic livestock or pets are well acquainted with these basic principles, which also apply to wildlife. Species typically possess strategies to avoid inbreeding, however as fewer and fewer individuals are present within a population it becomes more difficult to avoid breeding with relatives. In very small populations, inbreeding effects may be immediately apparent and may influence short-term population viability. In larger populations, inbreeding effects might not be as apparent, but may accumulate over time.

Another impact to small or isolated populations is reduced **genetic diversity**, which might be described as the number and variety of the genetic “building blocks” within a population. Having a wider variety of building blocks allows a population to adapt successfully to a changing environment, because it is more likely that at least some individuals will possess traits suited for the new environment. These are the animals that might survive to produce offspring, allowing the population to persist in the changed environmental conditions. Conversely, populations with fewer of these building blocks may lack the ability to adapt to the changing environment and may eventually perish.

Large or inter-connected populations generally have more of these building blocks than smaller, isolated ones, because they are better at retaining those they already have, and because they are better at creating new ones. In small populations, where fewer individuals mean fewer copies of each building block, it is more likely that some would be lost simply by chance. For example, imagine if only 2 individuals possess copies of a rare building block, and they both happen to die before reproducing. That building block would be forever lost. This random loss of genetic material is known as **genetic drift**. Large populations are less prone to drift, because more individuals mean more copies of each building block and fewer losses. Additionally, new building blocks arise from random mutations, which occur more frequently in larger or inter-connected populations than in smaller or isolated populations. Higher genetic diversity enhances the adaptive capacity of a population in the long-term, however changes in a population’s genetic diversity can happen relatively quickly, especially if the population is very small.

In any population, large or small, loss of genetic diversity and negative effects of inbreeding can be countered by **gene flow**, or the movement of genetic material from one population to another through movement of individuals. Connectivity within a metapopulation is especially important for small populations which are more prone to negative genetic characteristics.

### **Applying the Concept to Grizzly Bears**

As shown above, dispersal movements of individuals from one sub-population to another can provide multiple benefits. When neighboring populations exchange individuals and gene flow is achieved through reproduction of immigrants (and their descendants), this is referred to as **genetic connectivity**. Genetic connectivity helps populations maintain or increase genetic diversity and reduce inbreeding. In grizzly bears, genetic connectivity is most easily achieved through exchange of males, who typically disperse larger distances than females. Of course, these males must not only disperse from one sub-

population to another but breed with a female whose cubs then carry some of his genetic information. Full-time residency of bears in areas between sub-populations is not necessarily needed, however movements between sub-populations are more likely when the distance separating the sub-populations does not exceed male dispersal distances. That is, males are more likely to get to a new sub-population if born to a mother who already lives relatively close by.

When neighboring populations exchange individuals and immigrants (and their descendants) contribute significantly to population dynamics, this is referred to as **demographic connectivity**. Demographic connectivity can produce immediate conservation benefits in small populations where the addition of immigrants can mean the difference between population decline and stability or growth, often referred to as a **rescue effect**. In turn, the long-term maintenance of demographic connectivity provides for stability within a metapopulation complex. In grizzly bears, demographic connectivity is best achieved by maintaining residency of females and males in the areas between sub-populations. This is because female bears most often set up their home range in proximity to their mother's range, and only rarely disperse long distances (although it has been observed). If sub-populations are too distant from one another, they are unlikely to exchange females. By default, demographic connectivity also achieves genetic connectivity.

The Northern Continental Divide Ecosystem) population represents the chief segment of the largest and one of the most genetically diverse populations within the region shared with southern British Columbia and Alberta. We believe the NCDE is large enough, and the habitat is secure enough, to consider it self-sustaining and a likely source for dispersing individuals. Demographic and genetic connectivity exists with neighboring population(s) to the north in Canada and inbreeding is unlikely to be an issue. Still, connectivity to the west and south would enhance its long-term adaptive capacity by minimizing genetic drift and maintaining low levels of inbreeding.

The GYE is numerically large, self-sustaining, and a likely source of dispersers like the NCDE. Levels of inbreeding are low in this population. However, evidence indicates the GYE population has been isolated for about 100 years and exhibits lower genetic diversity than many other populations in the region. Therefore, genetic connectivity with other populations to the north would enhance its long-term adaptive capacity and provide more assurance of long-term persistence.

The populations in the other two occupied Recovery Zones (SE and CYE) are quite small. These two ecosystems hold 3 somewhat distinct populations within the Selkirk, Purcell, and Cabinet Mountains. At

present, there is evidence of some limited natural movements and gene flow among these 3 sub-populations. Additionally, augmentation of the Cabinet Mountain sub-population, through translocation of individuals from Canadian and US portions of the NCDE population, has resulted in demographic contributions and gene flow. Nonetheless, both the SE and CYE populations remain below recovery goals numerically, exhibit lower genetic diversity than many neighboring populations, and are prone to inbreeding. Thus, these small populations would greatly benefit from both demographic and genetic connectivity among themselves and with larger source populations.

How does the Bitterroot ecosystem (BE) fit into the metapopulation concept? If a population were established, the likelihood of long-term persistence of the species in Montana would be substantially increased by the existence of 5 sub-populations instead of 4 sub-populations. The 5 sub-populations would be separate enough that environmental perturbations might act independently on each, minimizing the potential for the metapopulation to go extinct, even under extreme circumstances. The mixture of genetic material among all populations (likely supplemented by populations in Canada) would provide for increased genetic diversity, counteract and eventually minimize inbreeding effects, and increase the capacity for the populations to adapt to potential environmental changes. An established population in the BE could, in the future, act as a stepping-stone between the CYE, NCDE, and GYE populations, making exchange of individuals more effective within the metapopulation.

Currently, there is not an existing population in the BE. Natural recolonization of this ecosystem could be accomplished through demographic connectivity. As such, at least some residency of females would be needed between the BE and the potential source populations (NCDE, GYE, and/or CYE). If the population were reestablished through a reintroduction effort, either genetic or demographic connectivity with neighboring populations would be beneficial, depending on population size.

The support team's view is that, due to population growth and range expansion, the goal of connectivity among sub-populations is achievable and that we are closer to achieving it than at any time during the past 100 years or so. However, little to no genetic or demographic connectivity has been observed to date. Achieving this goal will be a challenge that will require dedicated effort and resources.

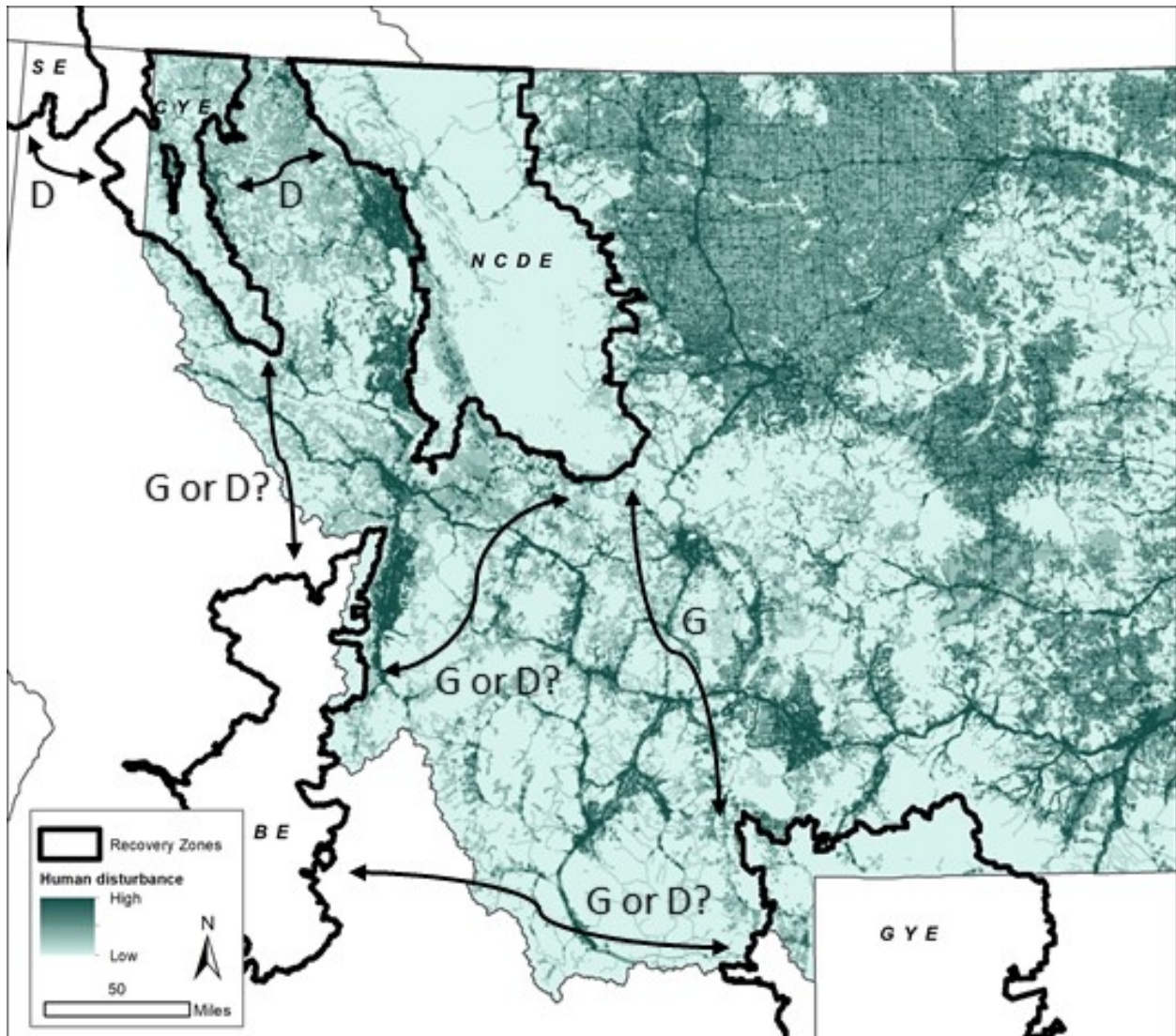


Figure 2. Potential future connectivity among grizzly bear populations in or adjacent to Montana, including the Selkirk Ecosystem (SE), Cabinet-Yaak Ecosystem (CYE), Northern Continental Divide Ecosystem (NCDE), Bitterroot Ecosystem (BE; unoccupied), and Greater Yellowstone Ecosystem (GYE). Arrows are not intended to depict specific routes, but to illustrate the connections between Ecosystems. The types of connectivity, genetic (G) or demographic (D), are referenced in the text. The background map depicts an index of human disturbance based on 6 categories, including development, transportation, agriculture, resource extraction/energy development, introduced vegetation, and forestry practices. Lighter areas are less disturbed and darker areas are more disturbed (Montana Human Disturbance Index, Montana Natural Heritage Program, Montana State Library, 2014).