

## PROJECT PROPOSAL TEMPLATE

**Project Category:** Forest Ecosystems

**Project Title:** The North Pacific Forest Landscape Corridor and Connectivity Project: Assessing Landscape and Species Vulnerability

**Principal Investigator responsible for completion of project:**

Erin L. Landguth, Computational Ecologist, Division of Biological Sciences, University of Montana, erin.landguth@mso.umt.edu, 406-243-2393

**Cooperators/Partners:**

**Project Summary:**

The North Pacific Forest Landscape Corridor and Connectivity Project will utilize a landscape connectivity simulator (UNICOR) and a genetic simulation program (CDPOP) to model the functional (dispersal and genetic) connectivity in the North Pacific Landscape. The outputs from these programs will indicate areas with high potential for landscape and genetic isolation and low probability of dispersal and colonization. Data delivery and visualization tools will be provided through dynamic interactive web map applications. This project will provide land managers and researchers with spatial corridor and connectivity pathway products that can be used to assist in conservation and management decisions.

**Project Proposal:**

**Background and Need:** Increasing human population has fueled urban growth, leading to rapid habitat loss and fragmentation due to conversion of natural landscapes for anthropocentric uses (Riitters et al. 2000; FAO 2006). Climate change is expected to drive large-scale, geographic shifts in ecological conditions and vegetation types (Dale et al. 2001; Schwartz et al. 2009). The synergy of the anthropogenic effects of climate change and land conversion will likely result in complex patterns of habitat loss and fragmentation for many native species.

The potential impact of climate change on the connectivity of habitats has become an area of concern among scientists and land managers. Key questions include how to identify and prioritize corridors for maintaining and enhancing population connectivity, identification of vulnerable species and populations, and identification of those populations that may require habitat restoration or assisted migration to maintain viability. These research threads have been identified as high priority for incorporation into research by most U.S. Federal agencies.

Land and resource managers in the North Pacific Landscape Conservation Cooperative (NPLCC) currently lack conservation planning tools that can directly feed into the planning, design, delivery, and monitoring of ecosystems across all levels of biodiversity from genes to ecosystems. The purpose of this proposal is to model the functional (dispersal and genetic) connectivity for two habitat-specific groups across the NPLCC under three projected climate regime shifts. The modeling effort will predict movement corridors for different connectivity threshold distances to reflect species-specific dispersal abilities. We will integrate the most current understandings of expected future change in vegetation patterns across the North Pacific, and use state-of-the-art spatial analysis and modeling approaches to predict effects of these changes on habitat area, fragmentation, and functional connectivity. The approach will build off of the corridor modeling approach introduced by Landguth et al. (2011b), which has been successfully applied to a number of projects (Landguth et al. 2011c; Landguth et al. 2011d), including the Great Plains Landscape Conservation Cooperative (Cushman et al 2011). In addition, we will assess the potential for genetic isolation associated with increased habitat fragmentation and changes in ecosystem connectivity using CDPOP v1.0 (Landguth et al. 2011a). This project is designed to provide spatially-explicit predictions of current and potential future patterns of fragmentation, prioritization of keystone corridors for protection and enhancement, and identification of places that may require habitat restoration or assisted migration to maintain viability. Results will be presented in a dynamic interactive web-based application and will be valuable to natural resources

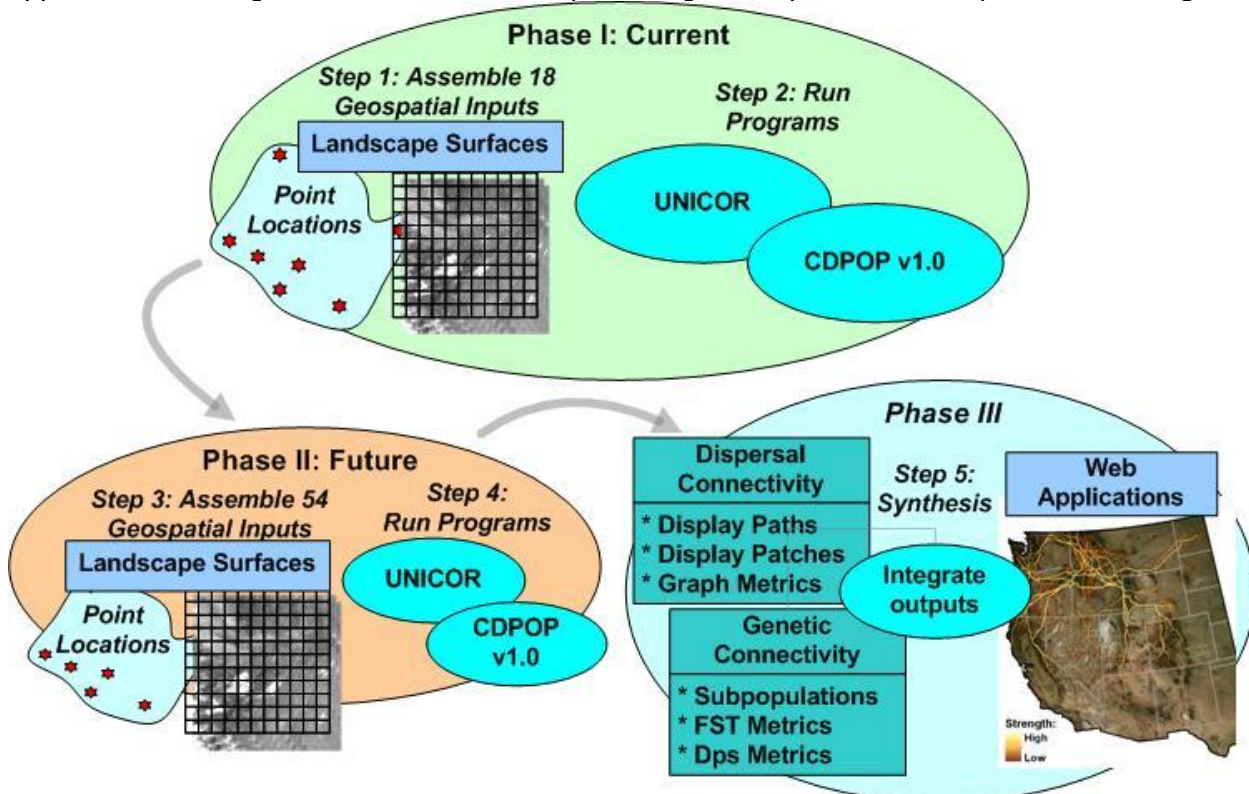
managers, planners, decision makers, and scientists with a stake in maintaining biodiversity across the NPLCC.

### Objectives:

- (1) Estimate habitat area, fragmentation, and corridor connectivity under current climate for montane conifer and subalpine habitat associated species expressing a range of habitat requirements and dispersal abilities.
- (2) Identify key geographical locations that are most important to maintaining population connectivity and facilitating movement for each group of species.
- (3) Predict changes to habitat area, fragmentation, and corridor connectivity for species groups under potential future scenarios involving a combination of climate change, and environmental features to help with landscape restoration and assisted migration.
- (4) Provide a web-based decision support system and data repository that will allow for interactive exploration of potential changes in landscape connectivity.

### Methods:

*Experimental Design:* The proposed project will be completed in three phases. Phase I is designed to focus on simulations of functional connectivity for prediction of habitat area, fragmentation, and patch/corridor identification for the current pattern of habitat area and land use activities for two generic species based on biome-level habitat association across a range of dispersals for the full NPLCC extent. In Phase II of the project, we will evaluate future functional connectivity by comparing predicted landscape and genetic changes stemming from projected climatic change. Phase III will synthesize and present current and future patterns of connectivity in an interactive web-based application. See Figure 1 below for a conceptual diagram of phases and experimental design.



*Landscape Surfaces:* Our analysis will focus on two habitat types (forest and subalpine) across the NPLCC extent. Species associated with these habitat types have varying sensitivities to fragmentation and landscape changes. We will address this potential variation by defining 18 potential movement resistance models reflecting the hypothetical costs associated with crossing pixels (see Spear et al. 2010) for each habitat-specific species group based on a combination of biome-level

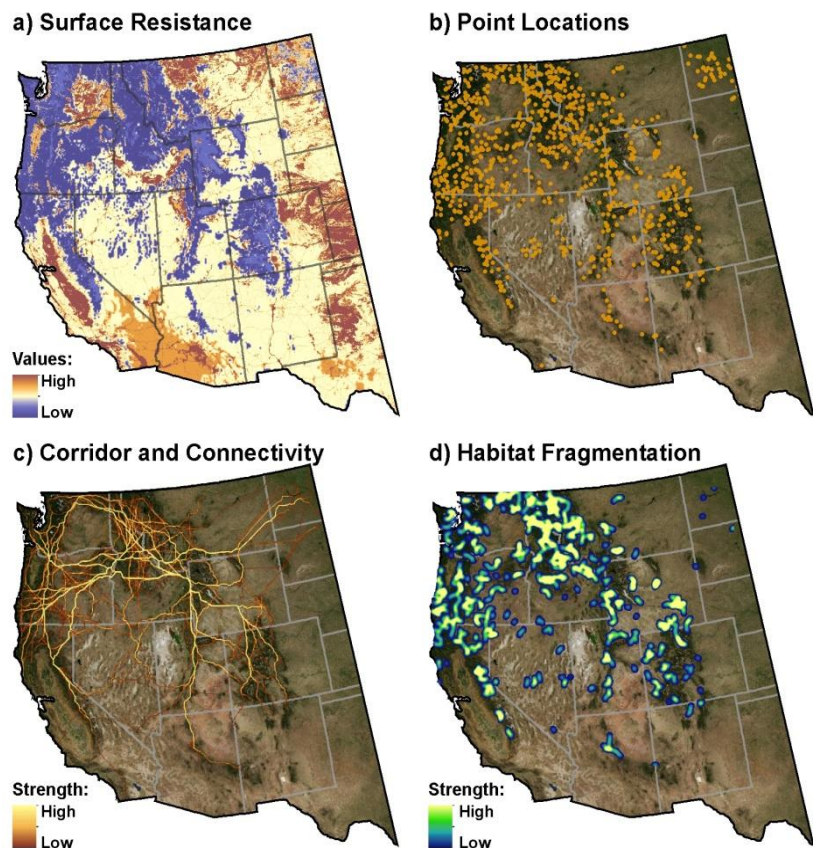
vegetation (2000 data from the Mapped Atmosphere-Plant-Soil System Study, <http://www.fs.fed.us/pnw/mdr/mapss/>), urban activity (Socioeconomic Data and Applications Center Human Footprint, Last of the Wild Data Version 2, <http://sedac.ciesin.columbia.edu/wildareas/>), and elevation (Shuttle Radar Topography Mission, USGS, <http://www.glcf.umd.edu/data/srtm/>). The 18 resistance models will consist of a 3-way factorial of relative sensitivity to (1) 2 levels of biome-level vegetation (forest and subalpine), (2) 3 levels of urban influence (low, medium, and high), and (3) 3 levels of elevation (low, medium, and high). This enables evaluation of the sensitivity of results to variation in the nature of the functional response to landscape composition and allow us to quantify the degree of uncertainty in our predictions. The climate change component will involve creating 54 potential future landscape surfaces that will assess connectivity for 3 levels of carbon emission scenarios (A1B, A2, and B1) for the Global Circulation Model (GCM, MIROC) for the year 2080 and include the projected habitat-specific species group (2080 data from the Mapped Atmosphere-Plant-Soil System Study).

**Dispersal Connectivity:** We will assess the connectivity of our 72 landscape surfaces (current plus future) using UNICOR (Landguth et al. 2011b), a species connectivity and corridor identification tool, to identify and characterize dispersal networks and habitat fragmentation. Specifically, we will produce maps of predicted connected habitat for each of the landscape resistance models across a range of five dispersal abilities resulting in 360 simulation scenarios. UNICOR is the only individual-based program that allows a user to simulate different movement strategies of each species in a spatially structured setting involving different dispersal functions and connectivity thresholds.

We illustrate UNICOR as a tool for evaluating current habitat area, fragmentation, and corridor connectivity with two example simulations for a resistance surface of a montane conifer associated

species across the full extent of the western United States at 1km spatial resolution (Figure 2 above). 1,000 initial starting locations for individuals were placed in the conifer vegetation biome occurrence class (Figure 2b). A connectivity threshold of 100km was used as an estimate for dispersal distance in (Figure 2d) and a maximum connectivity threshold was used in Figure 2c. The Gaussian kernel density estimation produced gradients of the common area connections. This example illustrates how UNICOR can be used to designate movement corridors, identify isolated populations, and identify species and subpopulations at risk due to habitat fragmentation.

**Genetic Connectivity:** The recently developed model CDPOP (Landguth and Cushman 2010; Landguth et al. 2011) simulates the influences of landscape structure on emergence of spatial patterns in population genetic data as functions of individual-based movement, breeding, and dispersal. Its realistic representation of the spatial environment and population genetic processes provide a powerful framework to investigate the impact of ecological factors on the genetic structure of populations (e.g., isolation or connectivity). The program provides spatially located genotypes that can then be related to population substructure by either assigning spatial regions to different populations and calculating





classical population genetic parameters (e.g.,  $F_{ST}$ ) or by analyzing pair-wise genetic distances among individuals with Mantel and partial Mantel tests (Mantel 1967). This approach has already advanced knowledge of the patterns of genetic variation in spatially-explicit contexts (Landguth et al. 2010a; Landguth et al. 2010b; Cushman and Landguth 2010; Landguth et al. 2011e; Hand et al. 2011).

*Functional Connectivity:* Current and future landscape surfaces will be used as input in both UNICOR and CDPOP. Both programs will be used to prioritize areas of greatest concern for forest and subalpine habitat associated species on the landscapes with regard to future changing surfaces. Specifically, UNICOR will identify landscape locations that are spatially isolated. CDPOP will be used to simulate the change in gene flow across the changing future surfaces and will address how shrinking habitat and species isolation will influence genetic diversity of fragmented populations. UNICOR will identify *a priori* knowledge about subpopulation connectivity that will in turn be related to population substructure through CDPOP (e.g., through population genetic parameter changes, such as  $F_{ST}$ ).

*Web-based Application:* Our analysis will be made available to the public through the Computational Ecology Laboratory website <http://cel.dbs.umt.edu>. In addition to the content available on the website, a series of interactive online web mapping applications will be available to users (see <http://cel.dbs.umt.edu/webapp> for a prototype). Our web mapping applications will be intuitive, easy to use, and will be explicated by an accompanying series of video tutorials on how to use these maps. The maps will also provide quick visualization capabilities for non-scientific audiences to whom conservation needs are still of great importance. In addition to visualization, our interactive maps will also function as a decision support system. This decision support system will provide online geospatial tools to help end-users prioritize areas of conservation concern. These tools will also provide end-users with the ability to download output files from geospatial databases for a user-defined extent viewable in commercial or open-source GIS software packages.

*Contributions:* University of Montana. – Dr. Erin Landguth will provide overall project coordination and supervise its completion. She will employ Ross Carlson as a GIS analyst and he will work closely with her in efforts to apply tools to predict current and future population fragmentation and movement corridors. She will also employ John Lucotch (<http://ntsg.umt.edu/user/65>) to provide his expertise on web-based interactive mapping (see <http://rap.ntsg.umt.edu/tools> as an example of John's work). All will take roles in preparing manuscripts for delivery to the NPLCC.

### **Geographic Extent:**

The analysis will encompass the entire geographic extent of the NPLCC, as well as a buffer of 50km inland to ensure accurate corridor identification along the edges of the NPLCC extent.

### **Timeline of Schedules, Products and Outcomes:**

Assuming a start date of July 1, 2011, we will complete the analysis and modeling of current habitat area and fragmentation by Nov 1, 2011. We will complete the analysis and modeling of future climate change and scenarios by Feb 1, 2012. We will identify conservation hot-spots under current and future scenarios for each species group by April 1, 2012. We will complete web-based applications and final manuscripts by July 1, 2012.

Deliverables will include 1) maps of current habitat under each landscape resistance hypothesis for each species group, 2) maps of future habitat under each climate change scenario, 3) identification of locations in the NPLCC that are important to maintain connectivity across future scenarios or areas where habitat restoration would enhance current population connectivity, 4) a detailed project web site which will provide extensive information on the purpose, objectives, and methods of analysis, as well as provide a central portal for downloading all data products produced by the project, 5) web-based interactive maps, and 6) a peer reviewed publication, target submission date of Sept 1, 2012.

### **Disclaimer regarding Data Sharing:**

There will be no known restrictions on sharing the data expected to be generated by this project. All finished products will be available to view and download through the Computational Ecology Laboratory website <<http://cel.dbs.umt.edu>>.

## Citations:

- Cushman SA, Landguth EL (2010) Spurious correlations and inferences in landscape genetics. *Molecular Ecology*, 19, 3592-3602.
- Cushman SA, Landguth EL, Flather CH (2011) Climate Change and Connectivity: Assessing Landscape and Species Vulnerability across the Great Plains. GPLCC report.
- Dale VH, et al. (2001) Climate change and forest disturbances. *BioScience*, 51, 723-734.
- FAO (2006) Global Forest Resources Assessment 2005, Main report. *Progress towards sustainable forest management*, FAO Forestry Paper 147, Rome, p 320.
- Hand BK, et al. (2011) Dispersal and genetic connectivity: how a changing climate alters patterns. In prep.
- Landguth EL, Cushman SA (2010) CDPOP: a spatially explicit cost distance population genetics program. *Molecular Ecology Resources*, 10, 156-161.
- Landguth EL, et al. (2010a) Quantifying the lag time to detect barriers in landscape genetics. *Molecular Ecology*, 19, 4179-4191.
- Landguth EL, et al. (2010b) Relationships between migration rates and landscape resistance assessed using individual-based simulations. *Molecular Ecology Resources*, 10, 854-862.
- Landguth EL, Hand BK, Glassy JM (2011a) CDPOP v1.0: An individual-based adaptive landscape genetics program. *Bioinformatics*, in review.
- Landguth EL, Hand BK, Glassy JM, Cushman SA (2011b) UNICOR: A species connectivity and corridor network simulator. *Ecography*. In review.
- Landguth et al. (2011c) Assessing Landscape and Species Vulnerability across the Western United States. In prep.
- Landguth EL, Sawaya MS, Carlson RT (2011d) Highway crossing structures: challenges and opportunities to reestablishing gene flow. In prep.
- Landguth EL, et al. (2011e) Effects of sample size, number of markers, and allelic richness on landscape genetic inference. *Molecular Ecology*, submitted.
- Last of the Wild Data Version 2 (2005) Global Human Footprint data set (HF). Wildlife Conservation (WCS) and Center for International Earth Science Information Network (CIESIN). <http://sedac.ciesin.columbia.edu/wildareas/>.
- Mantel N (1967) The detection of disease clustering and a generalized regression approach. *Cancer Res.*, 27, 209-220.
- Opdam P, Wascher D (2003) Climate change meets habitat fragmentation: linking landscape and biogeographical scale levels in research and conservation. *Biological Conservation*, 117, 285-297.
- Pacific Northwest Research Station (2008) Mapped Atmosphere-Plant-Soil System Study. <http://www.fs.fed.us/pnw/mdr/mapss/index.shtml>.
- Riitters K, et al. (2000) Global scale patterns of forest fragmentation. *Conservation Ecology*, 4, <http://www.consecol.org/vol4/iss2/art3/>.
- Schwartz MK, et al. (2009) Wolverine gene flow across a narrow climatic niche. *Ecology*, 90, 3222-3232.
- Spear SF, et al. (2010) Use of resistance surfaces for landscape genetic studies: Considerations for parameterization and analysis. *Molecular Ecology*, 17, 3576-3591.
- U.S. Geological Survey (2009) Shuttle Radar Topography Mission (SRTM): U.S. Geological Survey Fact Sheet 2009-3087. <http://www.glcf.umd.edu/data/srtm/>.

**Budget:**

	Phase 1, 2011	Phase 2, 2012	Phase 3, 2012	Totals
Personnel				
P.I.: Erin Landguth	\$3,350	\$3,350	\$3,350	\$10,050
GIS Analyst	\$3,350	\$3,350	\$3,350	\$10,050
Interactive Web Support	\$0	\$0	\$4,000	\$4,000
Equipment	\$0	\$5,000	\$0	\$5,000
Publication Costs	\$0	\$0	\$1,000	\$1,000
Computers	\$5,000	\$0	\$0	\$5,000
Indirect Costs (%41.5)	\$8,300	\$8,300	\$8,300	\$24,900
Total	\$20,000	\$20,000	\$20,000	<b>\$60,000</b>

*Budget Summary:* The total budget will be for \$60,000. This project will require 720 simulations between 2 programs; therefore we request financial assistance with the purchase of a multi-core high performance computer (~24 cores and 48GB RAM). We can build an equivalent machine for ~\$5,000. \$5,000 is requested for equipment that will include data storage and web server licensing (Windows Server 2008). \$1,000 is requested in anticipation of color figure costs with publications. The University of Montana will take 41.5% for indirect costs leaving \$22,400 left for salary, fringe, and insurance for Landguth (~221 hours), Carlson (~402 hours), and Lucotch (~160 hours).

## Erin L. Landguth

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### Professional Preparation

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Ph.D.	2010	University of Montana (Mathematical/Computational Ecology)
M.S.	2004	SD School of Mines and Technology (Atmospheric Sciences)
B.S.	2002	SD School of Mines and Technology (Mathematics)

### Professional Experience

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2010 – Pres. University of Montana. Research Assistant Professor. Division of Biological Sciences.  
2009 – 2010 NCEAS Landscape Genetics DGS. Research Assistant. Dr. Wagner, U of Toronto.  
2008 – 2010 RMRS-USDA-FS. Research Assistant. Dr. Cushman, Landscape Ecology.  
2008 University of Auckland. NSF EAPSI Fellowship. Dr. Kirk, Mathematics Department.  
2006 – 2008 University of Montana. NSF IGERT Trainee. Montana Ecology of Infectious Diseases.  
2007 University of California-Davis. MEID Internship. Dr. Crutchfield, CS Department.  
2000 – 2006 SD School of Mines and Technology. Research/Teaching Assistant. Rapid City, SD.  
2006 Walter Reed AIR. Outreach GEMS Coordinator. Washington D.C. & Polson, MT.  
2005 – 2006 RESPEC, Inc. Professional Engineering Associate. Rapid City, SD.  
2004 Santa Fe Institute Complex Systems Summer School. Research Scholar. Santa Fe, NM.

### Publications

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Landguth EL, Johnson T, (2011) Modeling temporally-forced disease dynamics in a host-vector community. *Bulletin of Mathematical Biology*, in preparation.

Landguth EL, Cushman SA, Johnson NA (2011) Natural selection in landscape genetics. *Ecology and Evolution*, submitted.

Landguth EL, Muhlfeld CC, Luikart G (2011) A tool for understanding gene flow in riverscapes. *Conservation Genetics Resources*, submitted.

Landguth EL, Fedy BC, Oyler-McCance S, Garey AL, Emel SL, Mumma M, Wagner HH, Fortin M-J, Cushman SA (2011) Effects of sample size, number of markers, and allelic richness on landscape genetic inference. *Molecular Ecology*, submitted.

Landguth EL, Hand BK, Glassy J, (2011) CDPOP v1.0: An individual-based adaptive landscape genetics program. *Bioinformatics*, in review.

Landguth EL, Hand BK, Glassy J, Cushman SA (2011) UNICOR: a species corridor, connectivity, and colonization network simulator. *Ecography*, in review.

Shirk A, Cushman SA, Landguth EL (2011) Deductive inferences in landscape genetics. *Landscape Ecology*, in review.

Balkenhol N, Landguth EL (2011) Simulation modeling in landscape genetics: on the need to go further. *Molecular Ecology*, **20**, 667-670.

Short Bull R, Cushman SA, Mace R, Chilton T, Kendall K, Landguth EL, Schwartz MK, McKelvey K, Allendorf FW, Luikart G (2011) Why replication is important in landscape genetics: case of the American black bear in the Rocky Mountains. *Molecular Ecology*, **20**, 1092-1107.

Landguth EL, Cushman SA, Schwartz MK, Murphy M, McKelvey KS, Luikart G (2010) Quantifying the lag time to detect barriers in landscape genetics. *Molecular Ecology*, **19**, 4179-4191.

Landguth EL, Cushman SA, Murphy M, Luikart G (2010) Relationships between migration rates and landscape resistance assessed using individual-based simulations. *Molecular Ecology Resources*, **10**, 854-862.

Cushman SA, Landguth EL (2010) Spurious correlations and inferences in landscape genetics.

*Molecular Ecology*, **19**, 3592-3602.

Cushman SA, Landguth EL (2010) Scaling landscape genetics. *Landscape Ecology*, **25**, 967-979.

Landguth EL, Cushman SA (2010) CDPOP: a spatially explicit cost distance population genetics program. *Molecular Ecology Resources*, **10**, 156-161.

## Teaching Experience

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- Guest Lecturer, *Computation Biology*, Montana Integrative Learning Experience for Students, University of Montana, Spring 2011.
- Instructor, *Landscape Genetics: developing best practices for testing landscape effects on gene flow*, NCEAS Distributed Graduate Seminar, University of Montana, Spring 2010.
- Guest Lecturer, CONGEN, *The role of simulation modeling in landscape genetics*, University of Montana Biological Station, August 2009.
- Instructor, BIOL495, *Spatial epidemiology applications in GIS*, University of Montana, Fall 2009.
- Guest Lecturer, CS577: *Computer Simulations CS577*, Spring 2008.
- Guest Lecturer, MATH414: *Ordinary Differential Equations*, University of Montana, Fall 2007.
- Instructor, *Introduction to GIS*, Department of Geology, SDSM&T, Spring 2005.
- Graduate TA, ATM594: *Atmospheric Physics*, Dept. of Atmospheric Sciences, SDSM&T, Spring 2004.
- Graduate TA, GEOL516: *Geographic Information Systems*, Dept. of Geology, SDSM&T, Fall 2003.
- Graduate TA, ATM510: *Environmental Remote Sensing*, Dept. of Atmospheric Sciences, SDSM&T, Spring 2003.

## Funding, Grants, and Awards

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| 2011         | USGS CESU Agreement. Developing and applying an agent-based gene flow model for salmonids in complex and nonequilibrium stream environments. University of Montana.                               |
| 2010 – Pres. | USDA-Forest Service Joint Venture Agreement. Modeling habitat connectivity for wildlife species across the western United States under alternative future climate regimes. University of Montana. |
| 2010 – Pres. | USDA-Forest Service Joint Venture Agreement. Conifer genomics and climate changes. University of Montana.   |
| 2010 – Pres. | USDA-Forest Service Cooperative Agreement. Developing methods for detecting ADS data using multi-temporal Landsat data. University of Montana.  |
| 2010 – Pres. | USDA-Forest Service Cooperative Agreement. Developing and applying an agent based model for adaptive evolution in complex and nonequilibrium environments. University of Montana.                 |
| 2010 – Pres. | USDA-Forest Service Cooperative Agreement. Effects of climate change on wildlife populations, habitat & connectivity. University of Montana.  |
| 2009 – 2010  | USDA-Forest Service Joint Venture Agreement. Developing and applying an agent-based cost distance model. University of Montana.   |
| 2009 – 2010  | NCEAS DGS Research Assistant. Developing best practices for testing landscape effects on gene flow. NCEAS/University of Santa Barbara.  |
| 2008         | NSF EAPSI. Modeling temporally-forced disease dynamics in a host-vector community. University of Auckland.  |
| 2008         | Bertha Morton Scholarship. University of Montana.   |
| 2006 – 2008  | NSF IGERT Fellowship. University of Montana. Ecology of Infectious Disease.   |
| 2004 – 2005  | South Dakota NASA Space Grant Fellowship. SD School of Mines and Technology.  |
| 2002 – 2005  | Graduate Research Assistance NSF/EPSCoR #EPS-0091948. SD School of Mines and Technology.  |