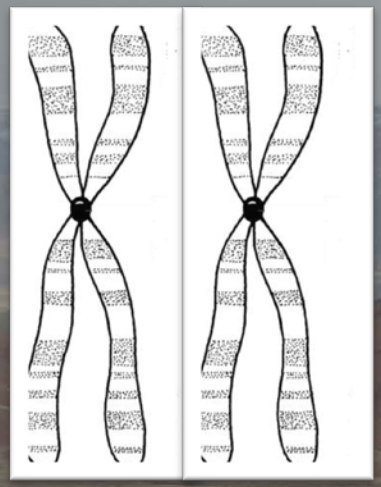
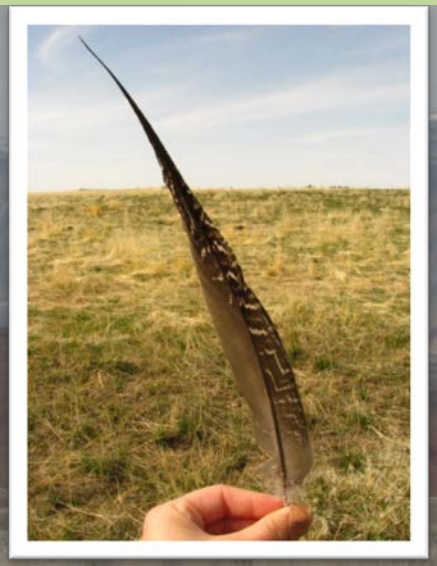
Connectivity and Corridors in Habitat Restoration





Beth Fitzpatrick, Ph.D. Candidate
Melanie Murphy, Assistant Professor
Department of Ecosystem Science and Management
Program in Ecology
University of Wyoming

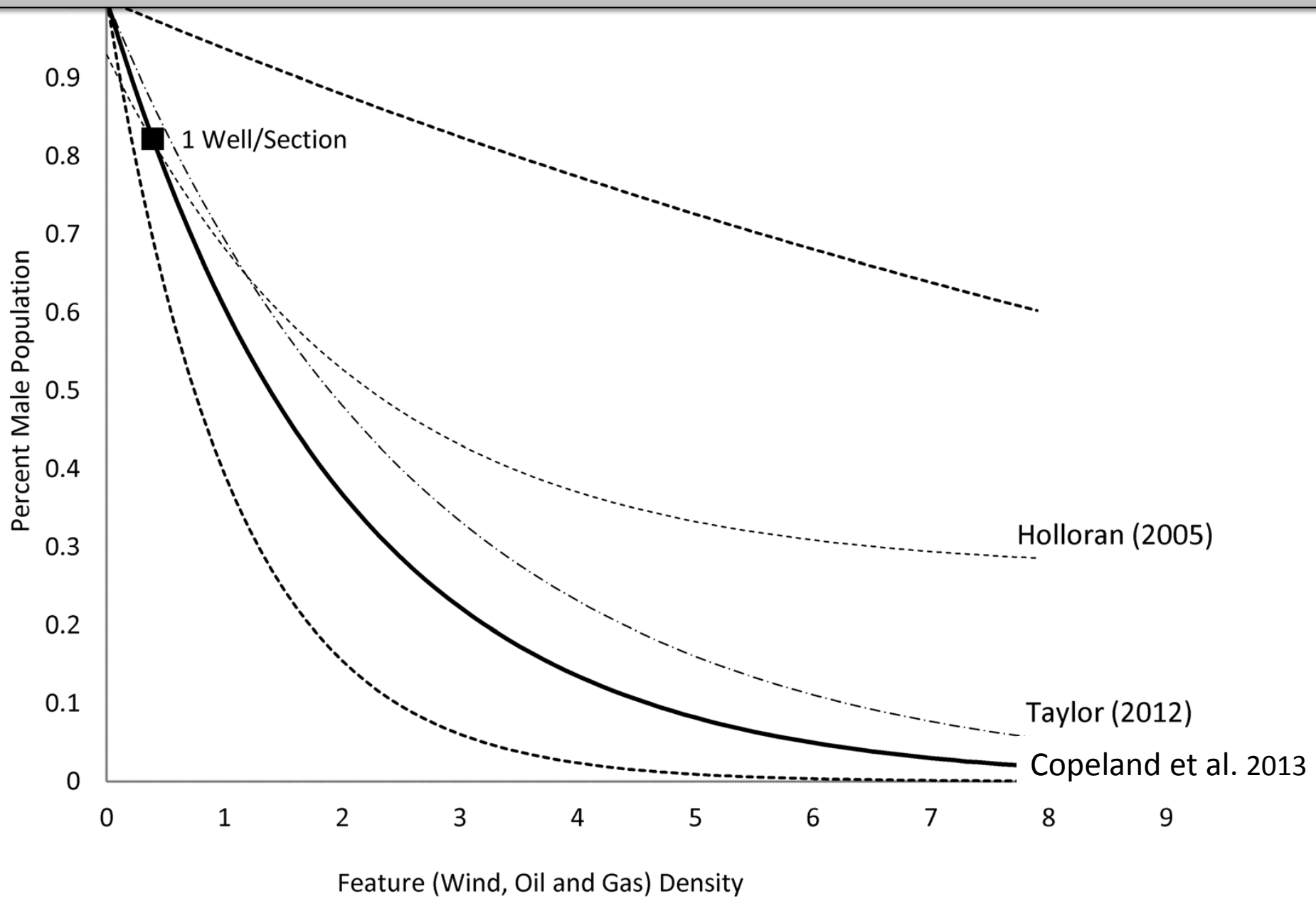
Historical and current distribution

Greater Sage-Grouse

(Photo credit: Kiesecker)

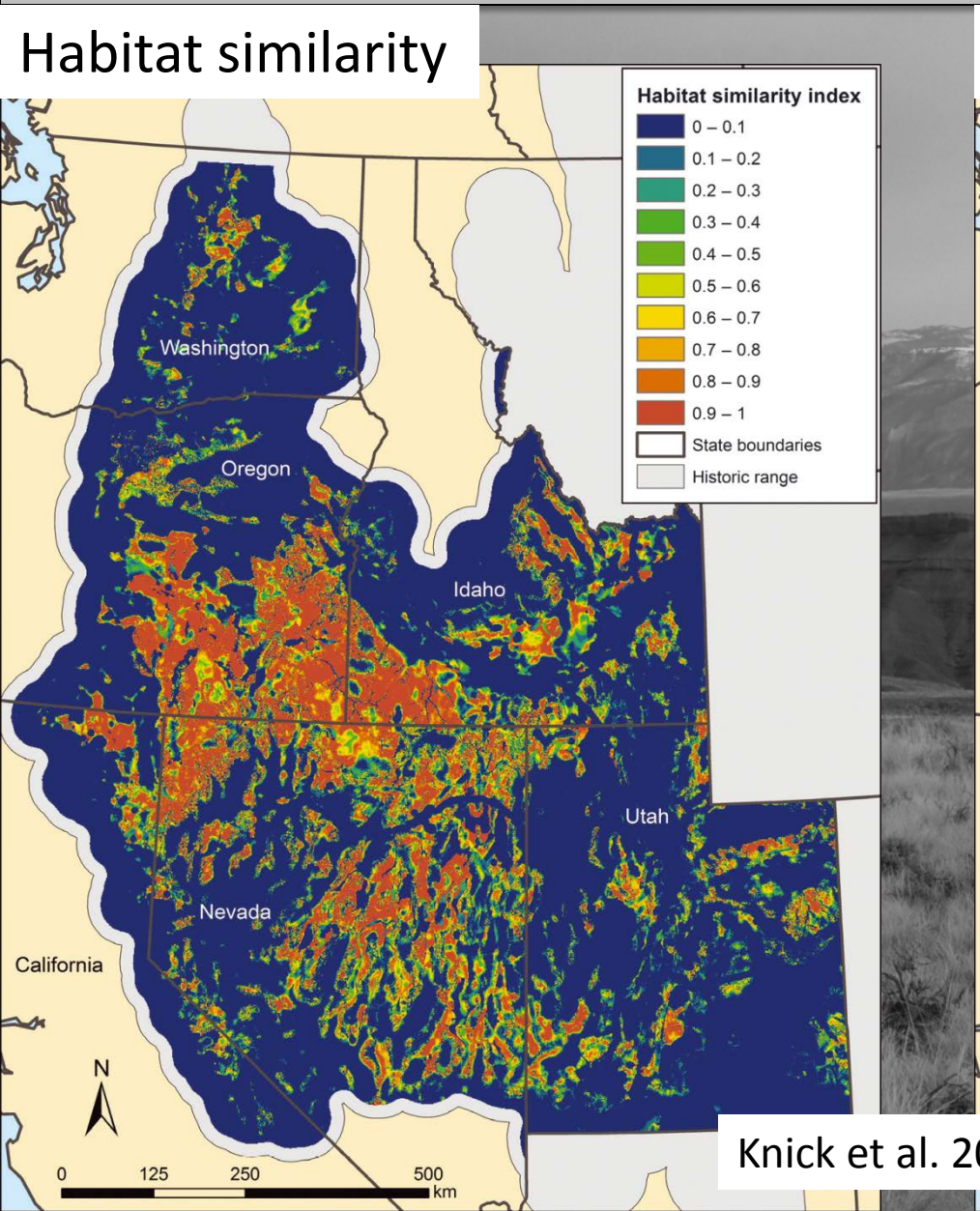
Greater Sage-Grouse: What's Going On?

Example: Oil and Gas Development

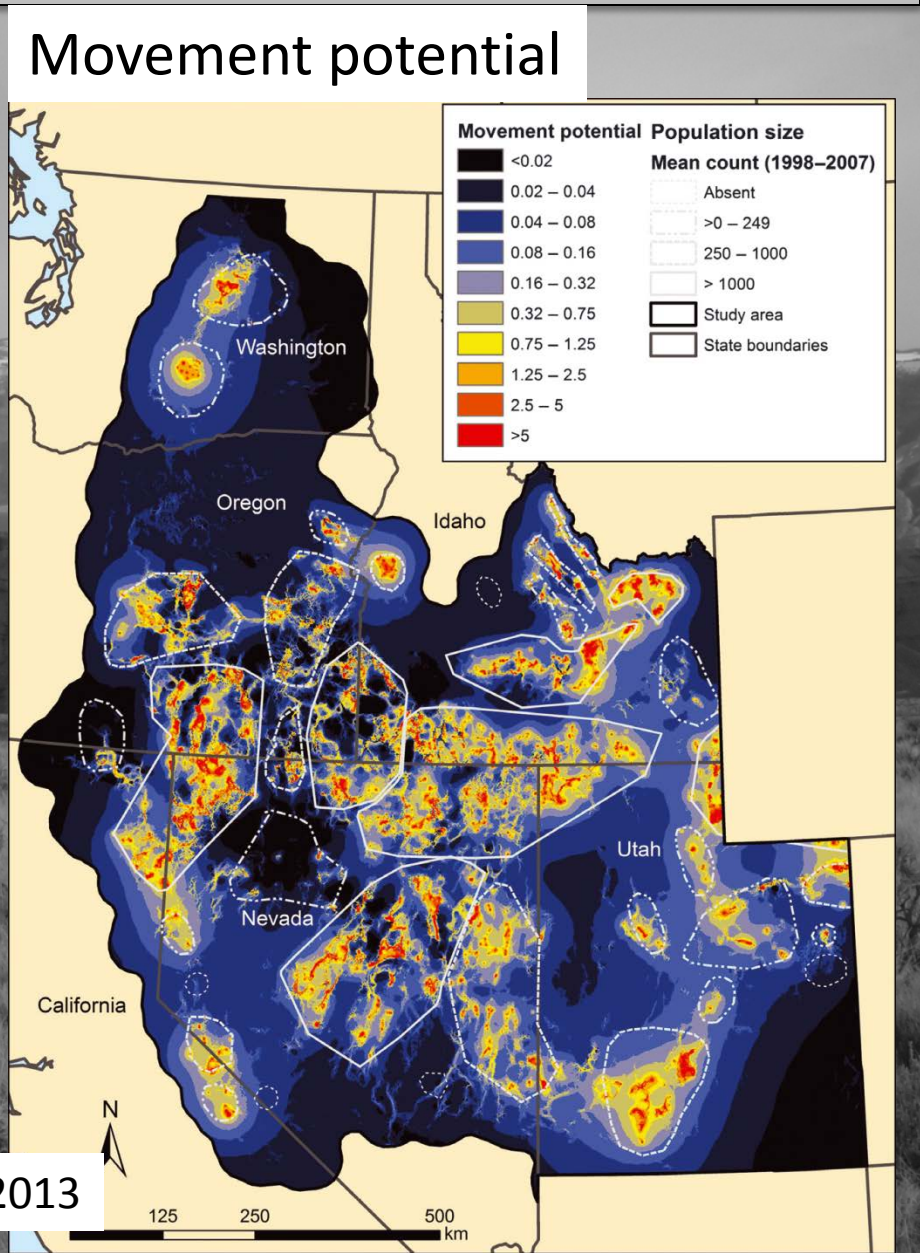


Structural Connectivity

Habitat similarity



Movement potential



Knick et al. 2013

Structural vs. Functional Connectivity

Sex	Movement state	Predictor variable				
		Mesic areas[a]	Slope[b]	Topographic roughness[c]	Road Density[d]	
Female	Encamped	Well Density[e]	Sagebrush[f]	Patchiness of sagebrush[g]		
Male	Traveling					
	Relocating					

Harju et al. 2013

Structural vs. Functional Connectivity

Sex	Movement state	Predictor variable				
		Mesic areas[a]	Slope[b]	Topographic roughness[c]	Road Density[d]	
Female	Encamped	Well Density[e]	Sagebrush[f]	Patchiness of sagebrush[g]		
Male	Traveling					
	Relocating					

Encamped: shortest 25% of movement ~ m:<177.25 and f: < 168.81m
Traveling: 50 % of movement ~m:>177.25 – 800.38m and f: >168.81 - <798.87
Relocating longest 25% m:>800.38 meters, f: >798.87

Harju et al. 2013

Structural vs. Functional Connectivity

Sex	Movement state	Predictor variable			
		Mesic areas[a]	Slope[b]	Topographic roughness[c]	Road Density[d]
Female	Encamped	Well Density[e]	Sagebrush[f]	Patchiness of sagebrush[g]	
Male	Traveling				
	Relocating				

Harju et al. 2013

Structural vs. Functional Connectivity

Sex	Movement state	Predictor variable: Mesic areas[a]	Slope[b]	Topographic roughness[c]	Road Density[d]
Female	Encamped	1.000	**0.929**	**0.942**	1.360
	Traveling	1.000	**0.939**	**0.906**	1.063
	Relocating	**0.999**	**0.947**	**0.952**	1.059

Movement state	Well Density[e]	Sagebrush[f]	Patchiness of sagebrush[g]
Encamped	1.116	1.002	1.178
Traveling	**0.868**	**1.147**	**1.123**
Relocating	**0.749**	**1.115**	**1.173**

Harju et al. 2013

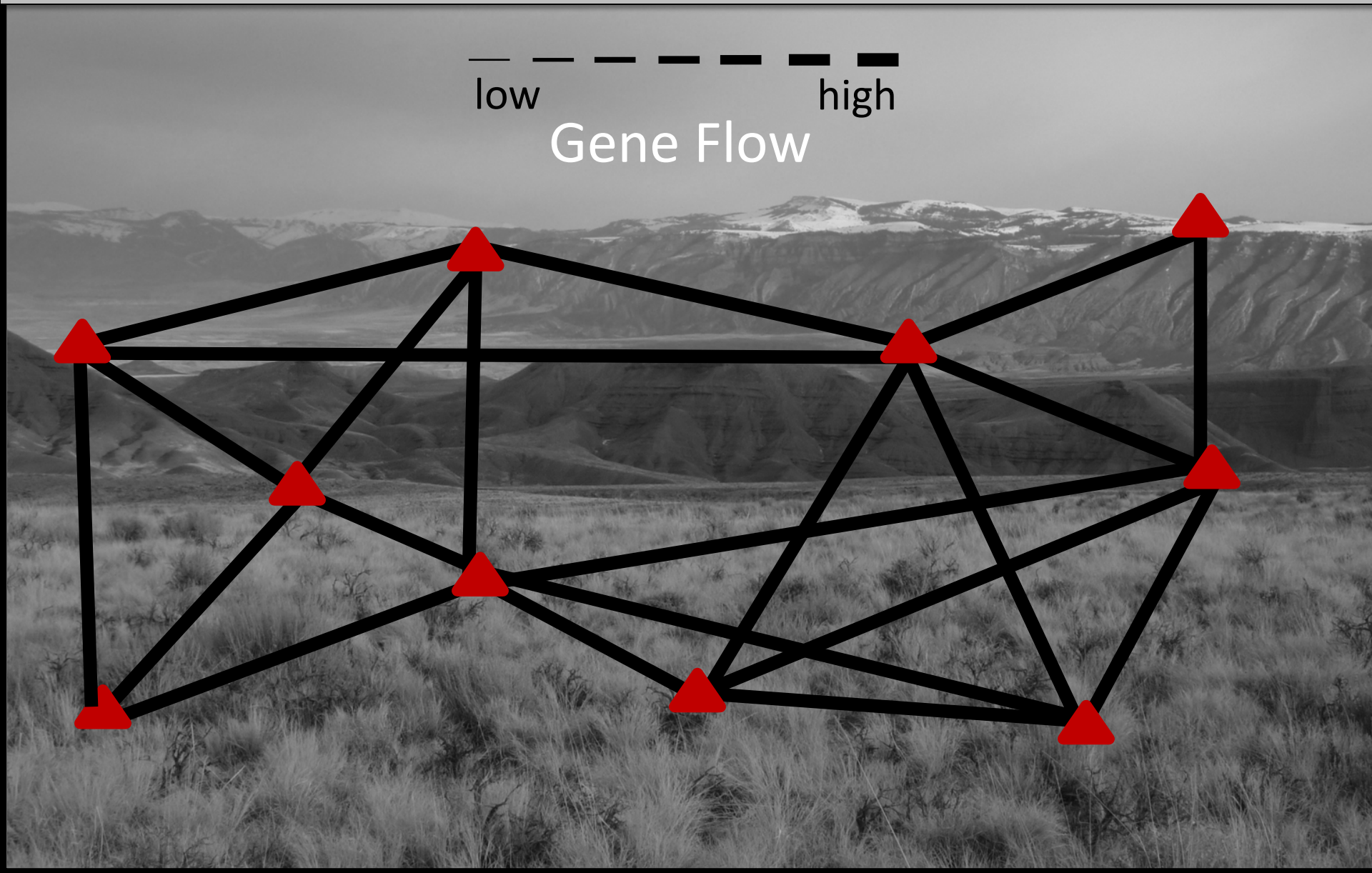
Structural vs. Functional Connectivity

Sex	Movement state	Predictor variable: Mesic areas[a]	Slope[b]	Topographic roughness[c]	Road Density[d]
Male	Encamped	1.001	1.006	0.942	1.670
	Traveling	0.999	**0.951**	**0.924**	**2.417**
	Relocating	1.000	**0.940**	0.983	**1.945**

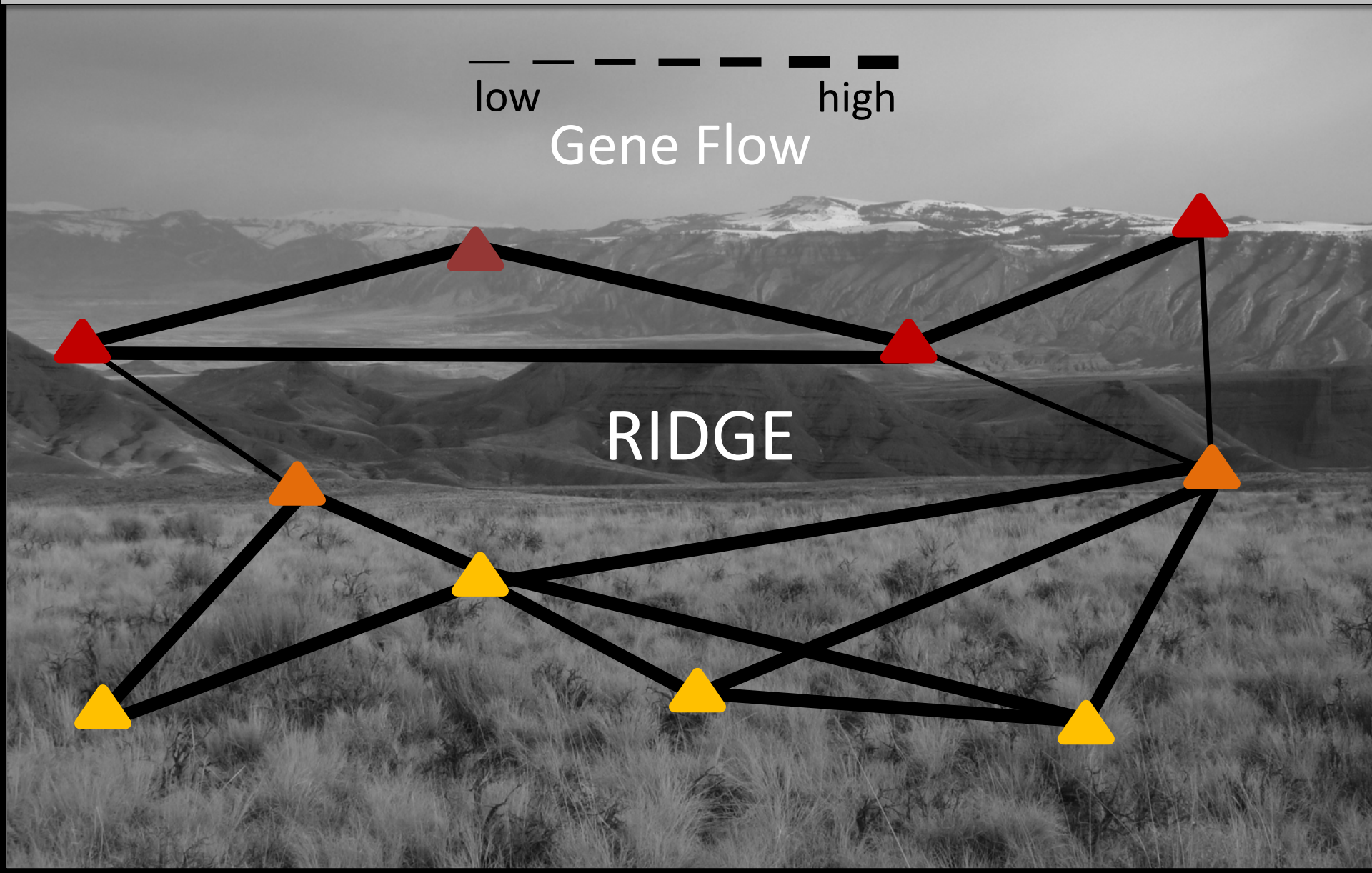
		Well Density[e]	Sagebrush[f]	Patchiness of sagebrush[g]
Male	Encamped	1.140	1.048	1.369
	Traveling	**0.663**	**1.088**	**1.193**
	Relocating	**0.555**	**1.127**	0.988

Harju et al. 2013

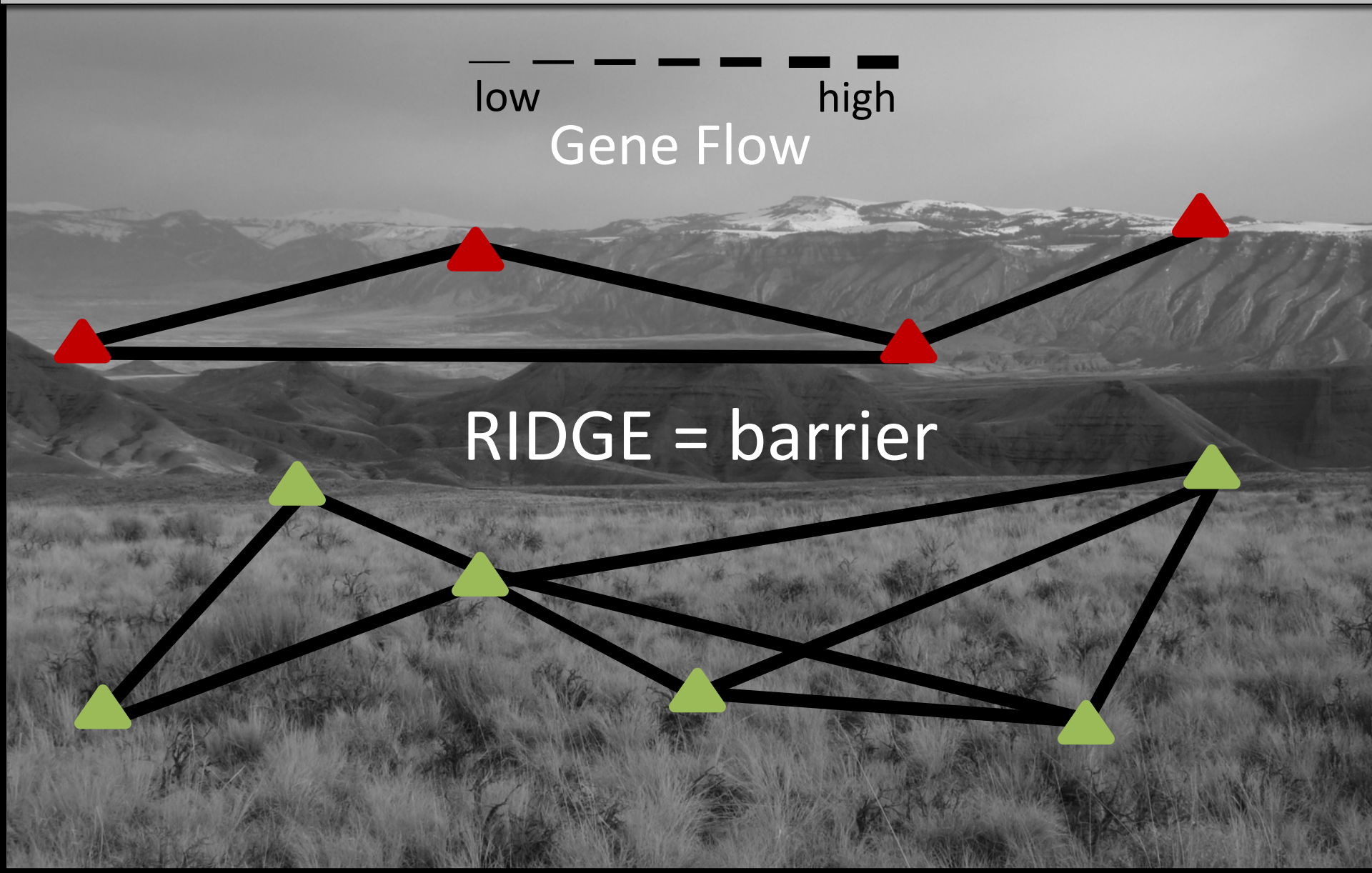
Functional Connectivity



Functional Connectivity



Functional Connectivity



Main objective

To create a tool for managers and developers to prioritize management activities

Objectives

1: Identify features impacting lek distribution

2: Identify features impacting genetic connectivity

3: Problem solving land management

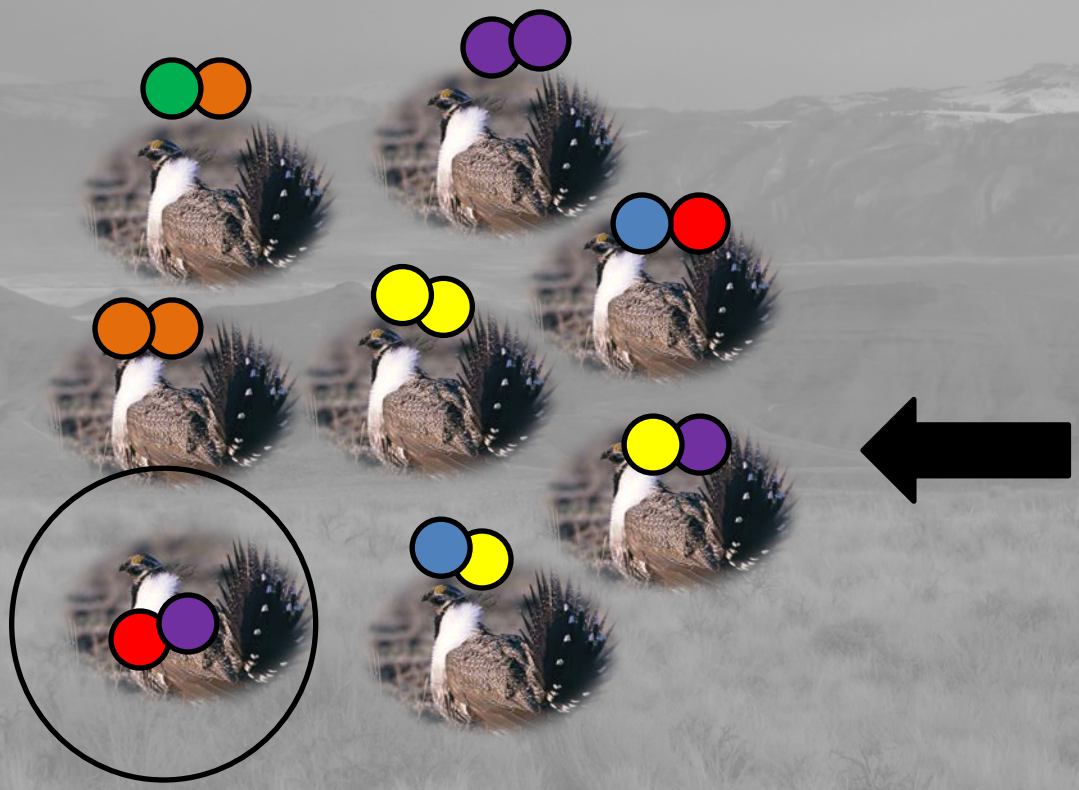
Objectives

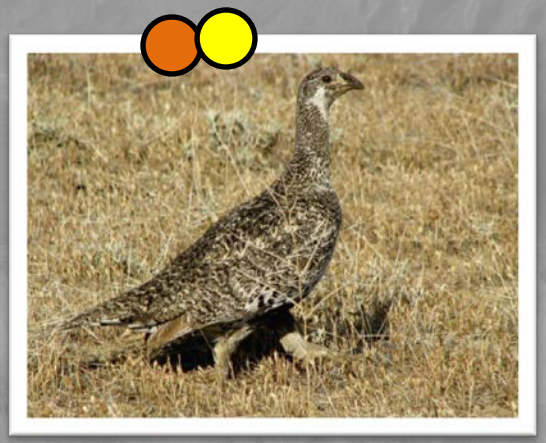
1: Identify features impacting lek distribution

2: Identify features impacting genetic connectivity

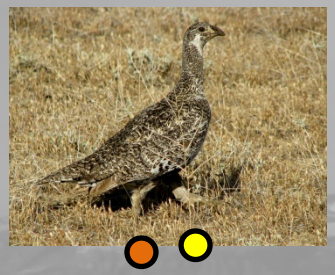
3: Problem solving land management

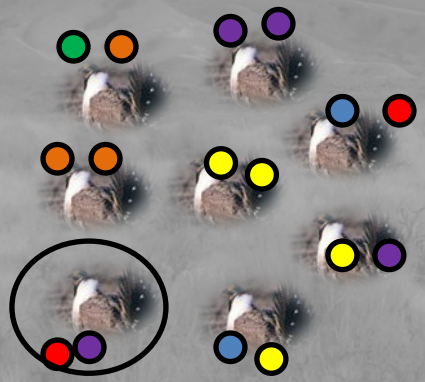
Conceptual Idea: Choosing a mate



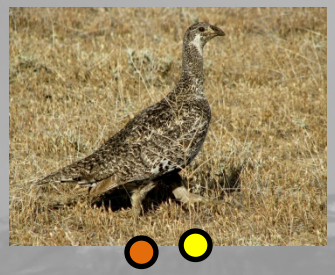


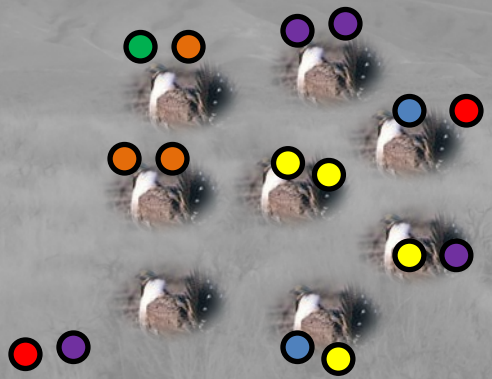
Conceptual Idea: nesting

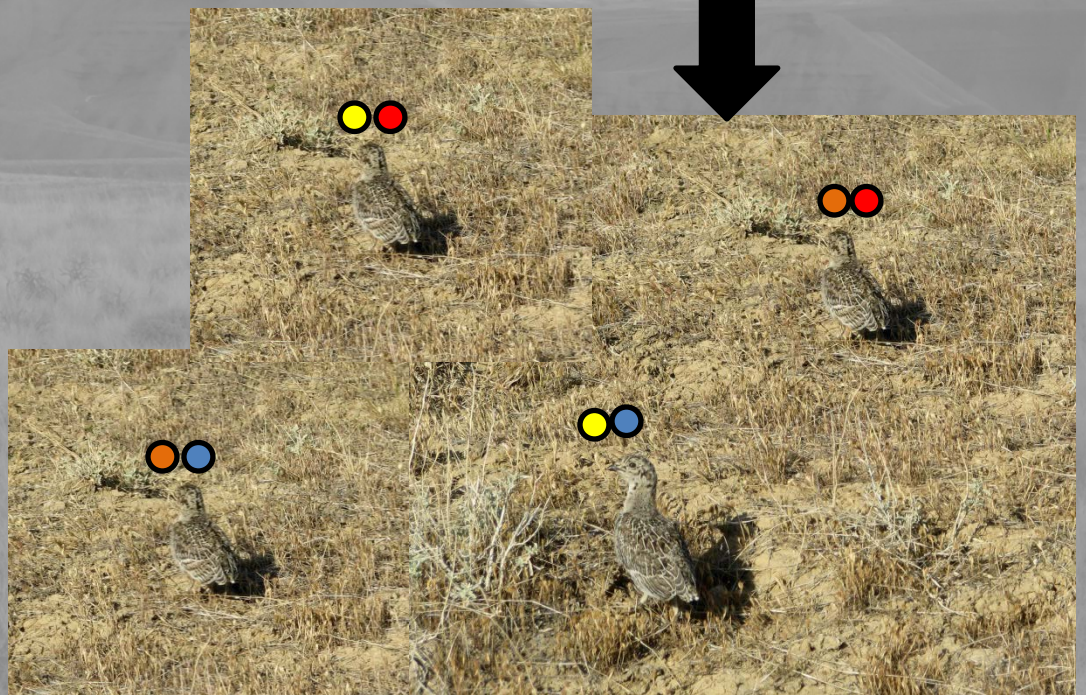




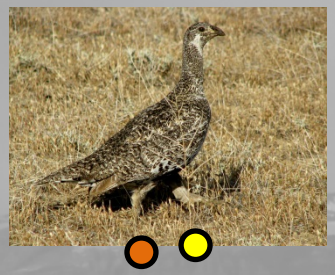
Conceptual Idea: Hatch Success

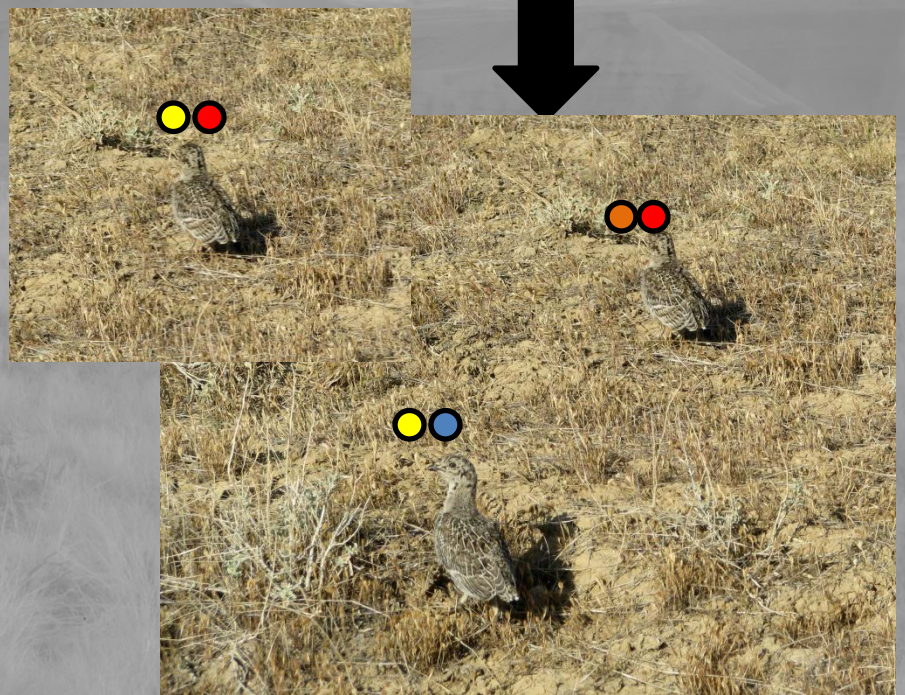


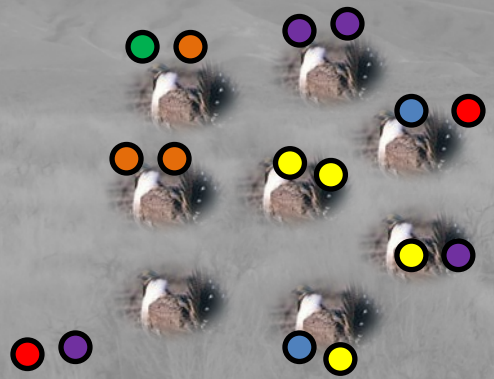




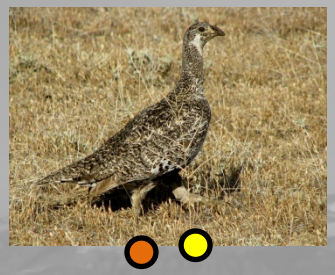
Conceptual Idea: Early Brood

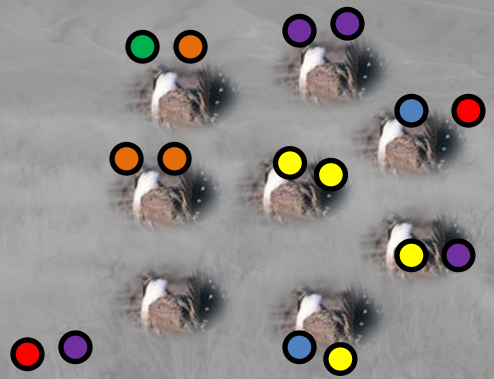




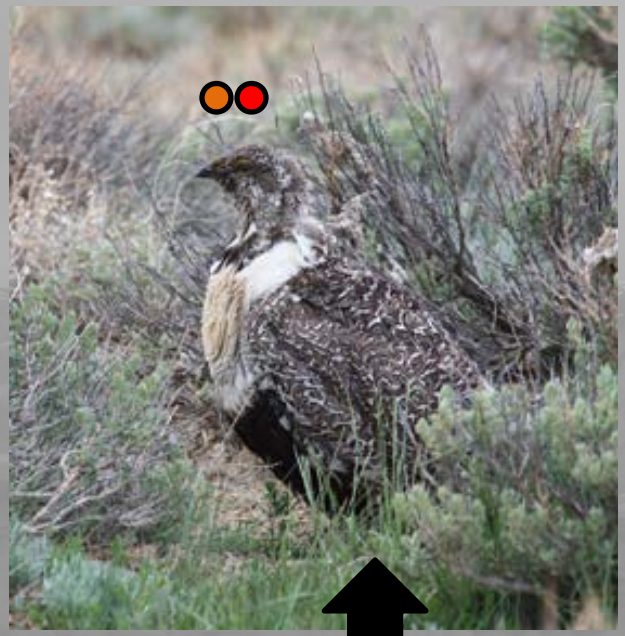


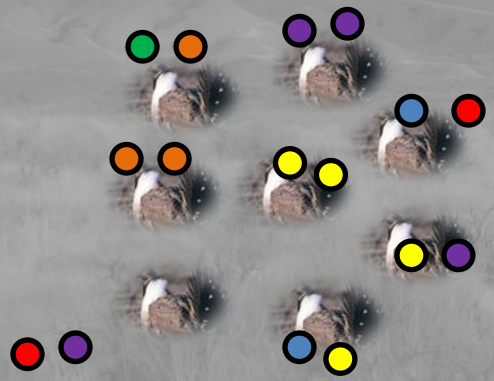
Conceptual Idea: Late Brood





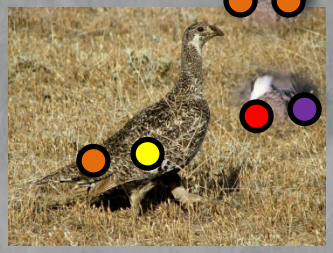
Conceptual Idea: Survive Fall & Winter





Conceptual Idea

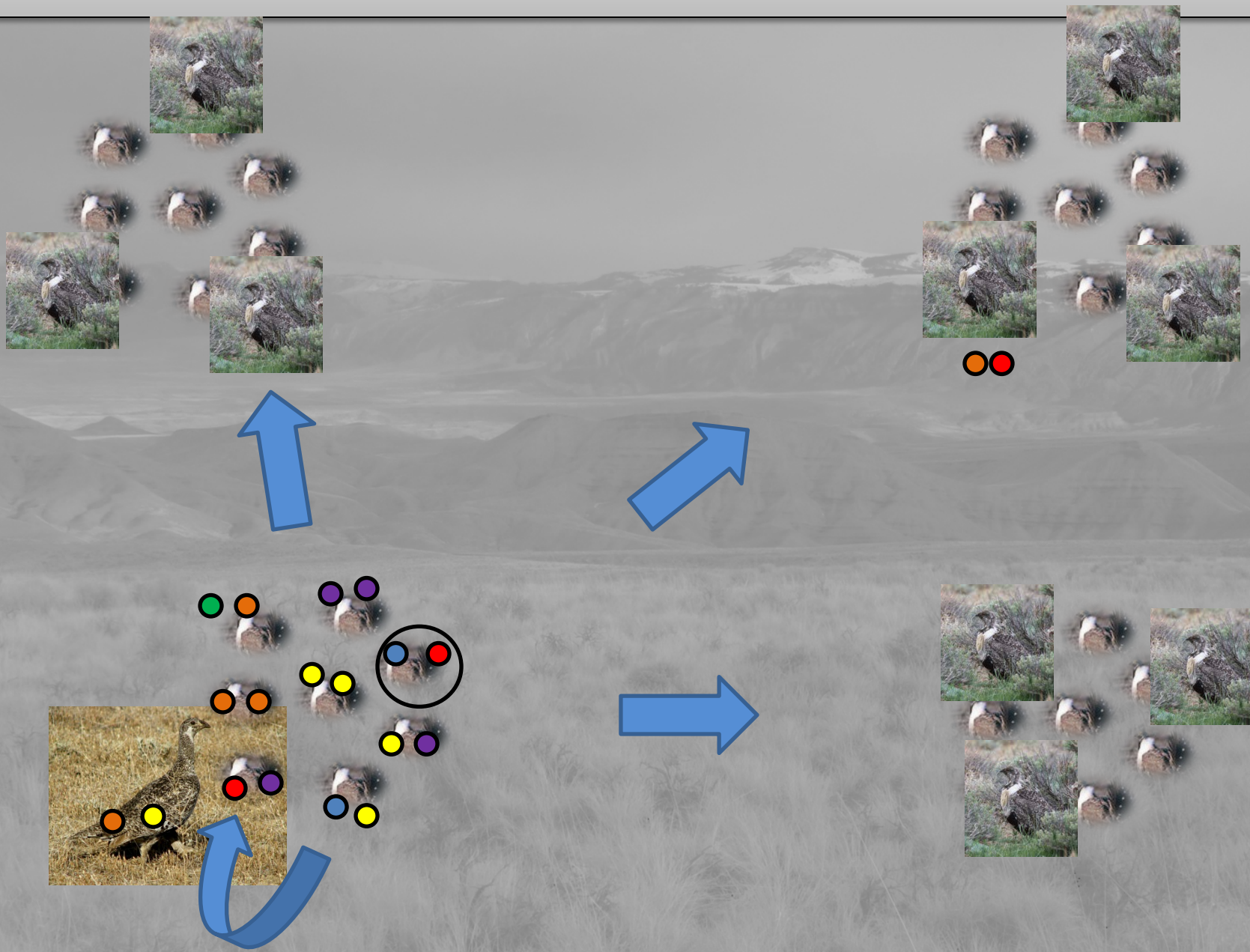
Year 1



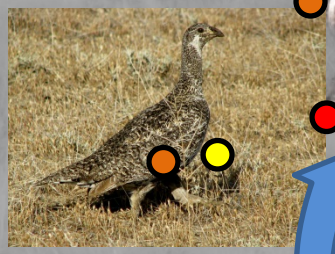
Conceptual Idea

Year 2 +

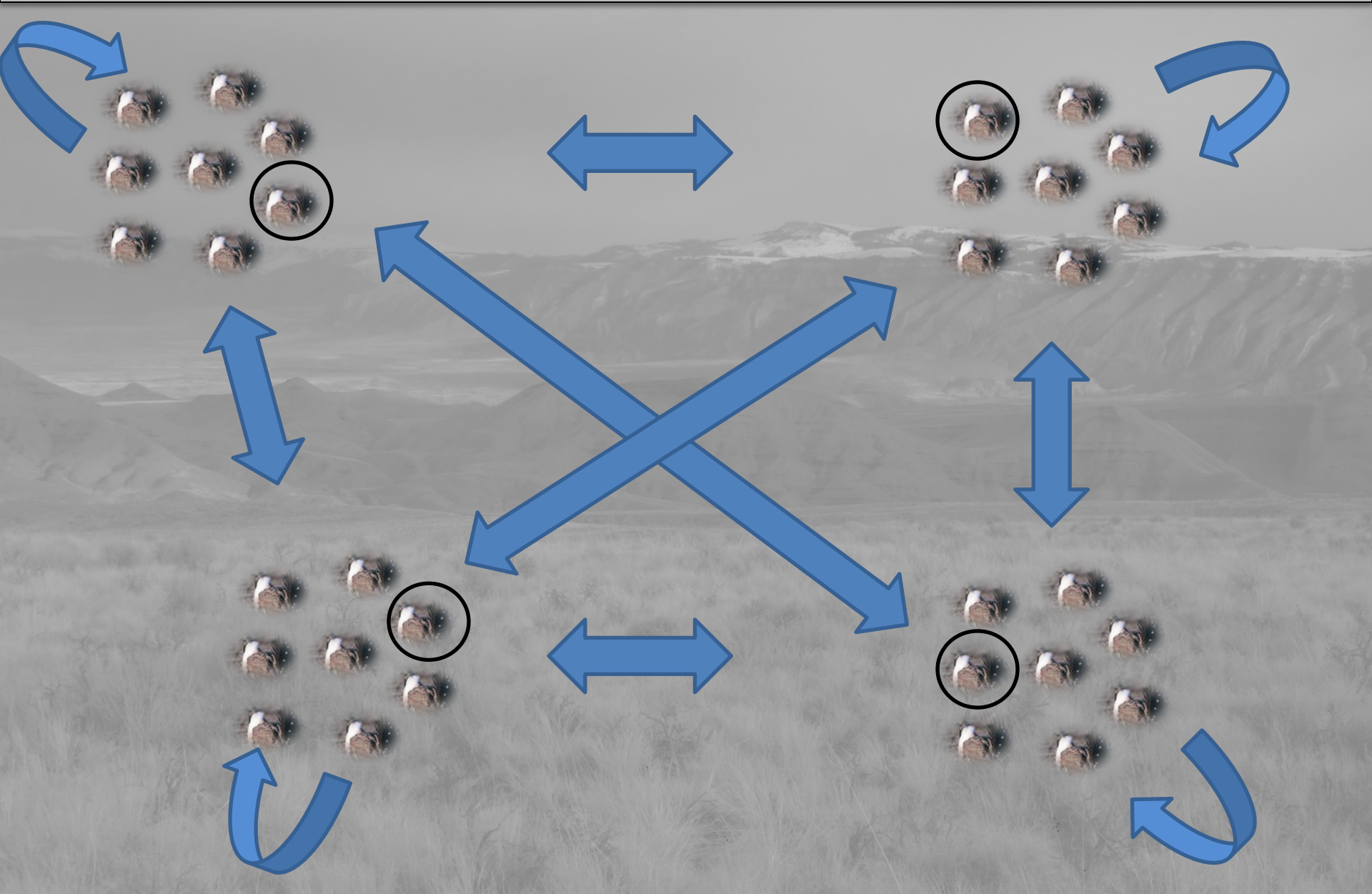
Conceptual Idea



Conceptual Idea



Conceptual Idea



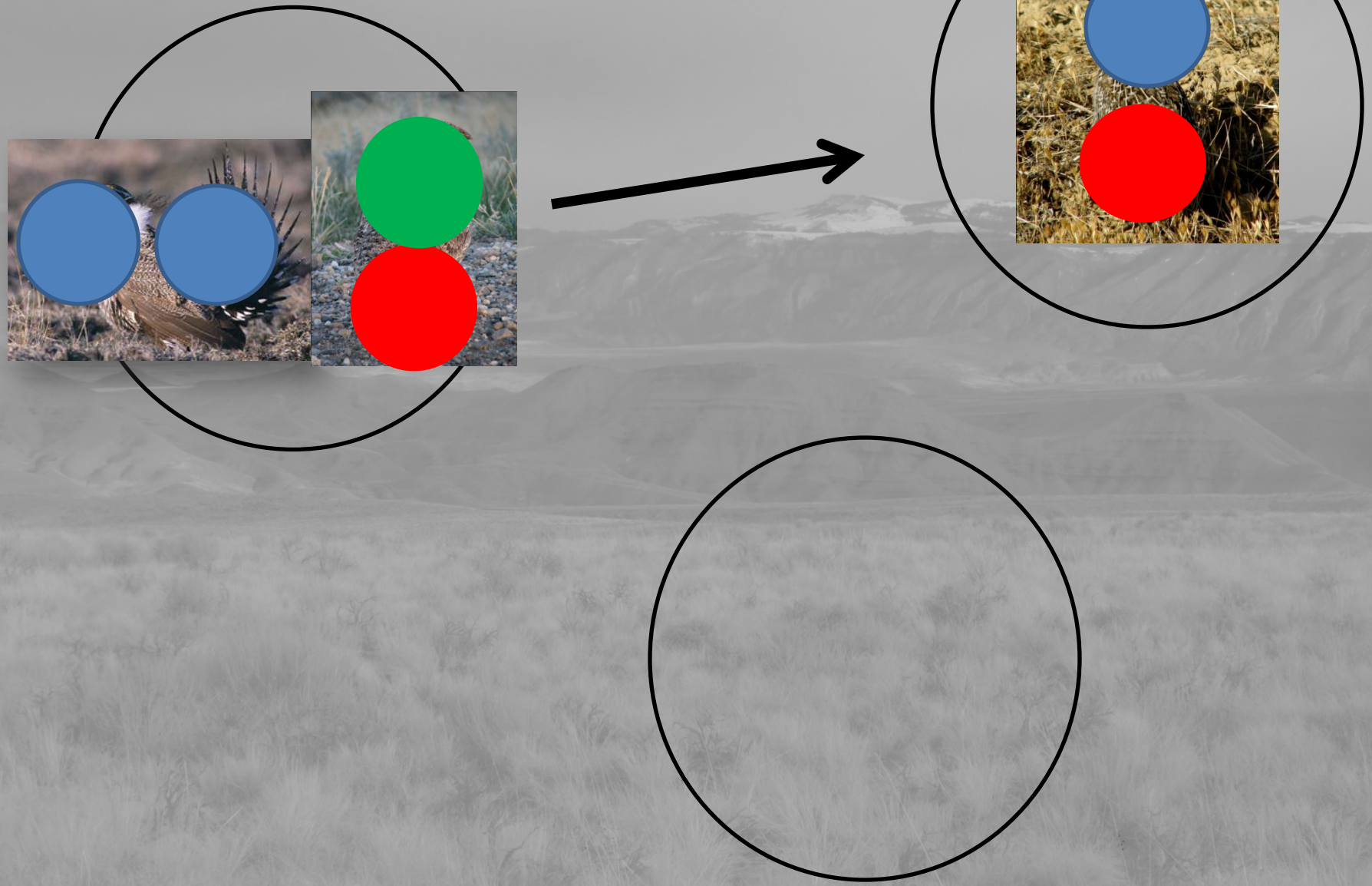
Gene Flow

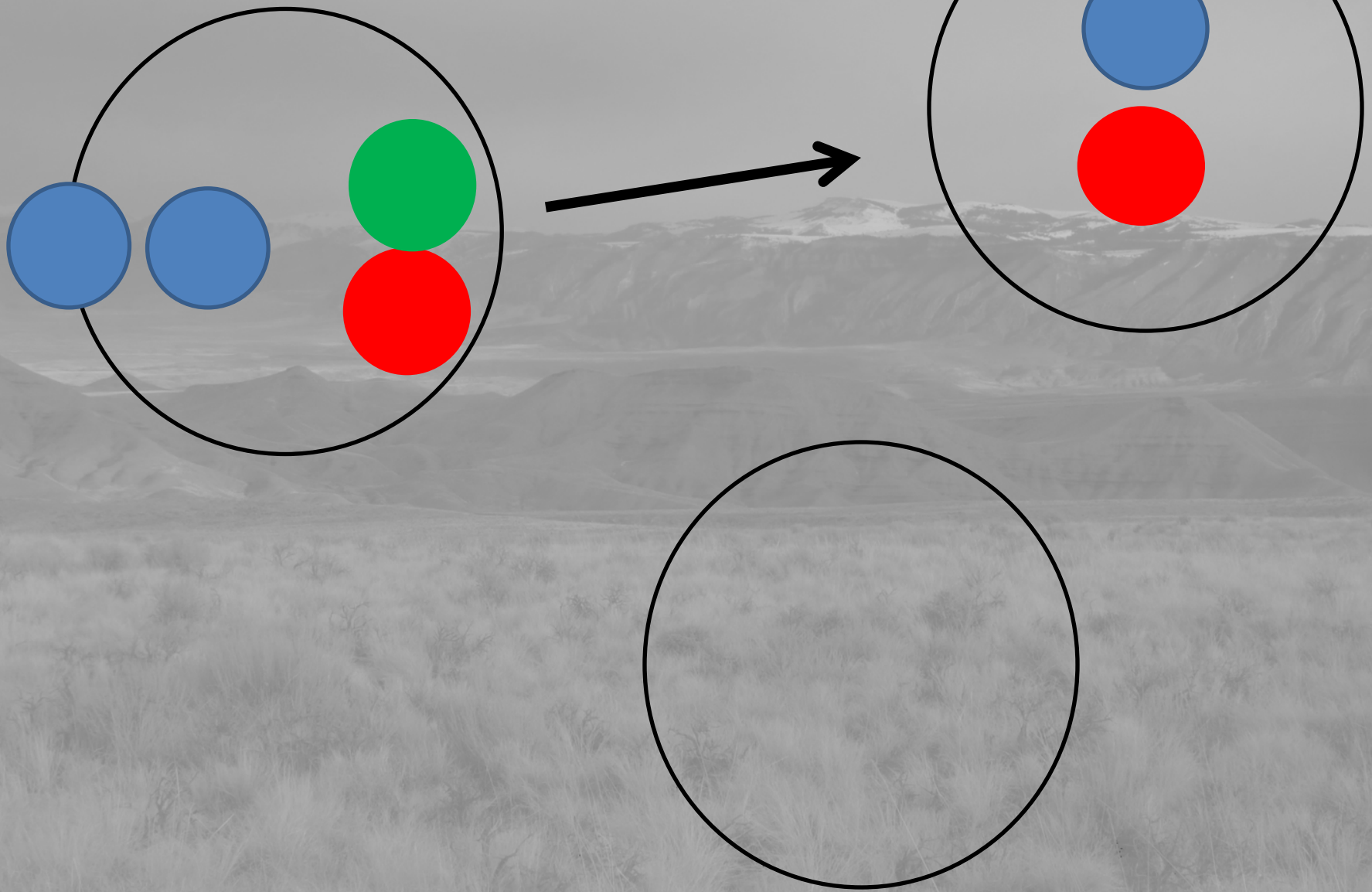
Parents

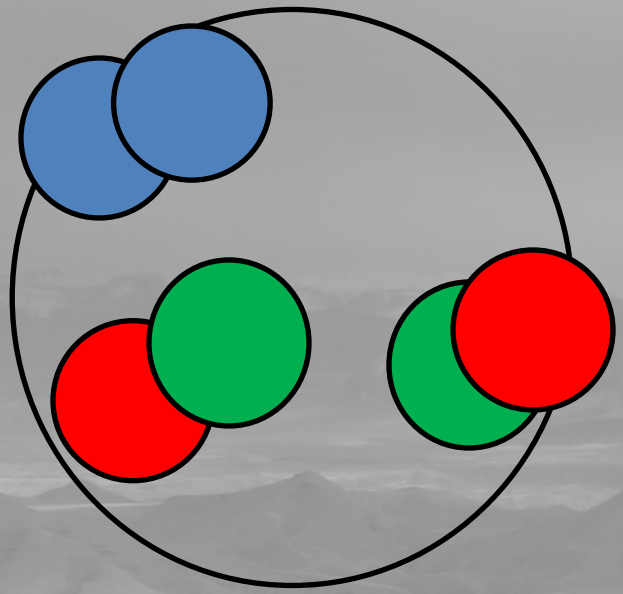
Locus

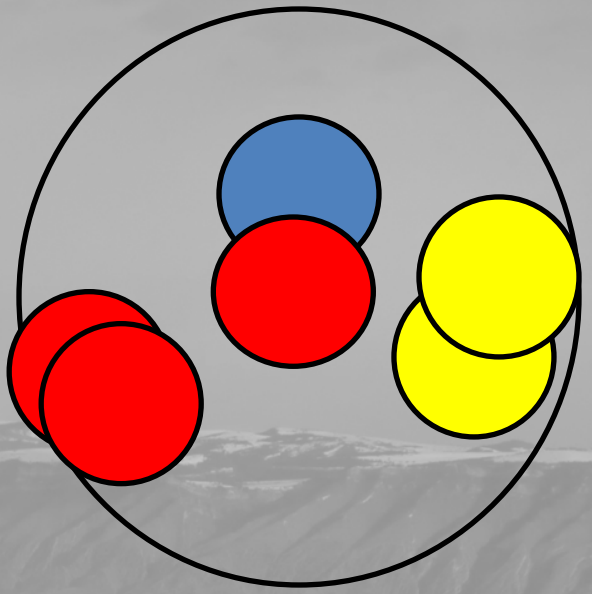
Offspring

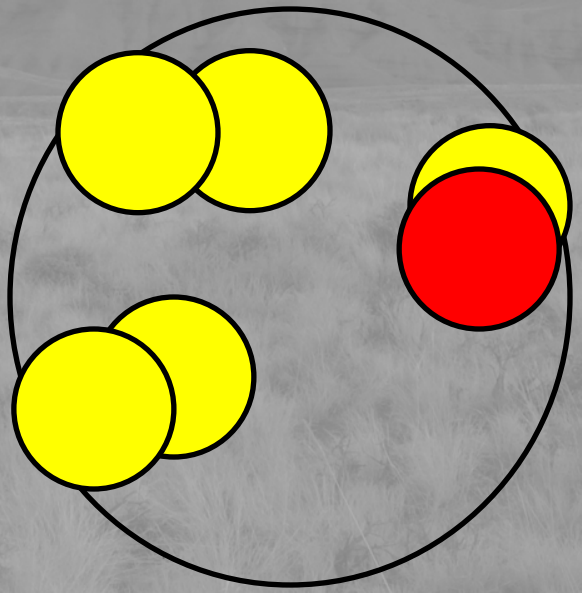
Alleles

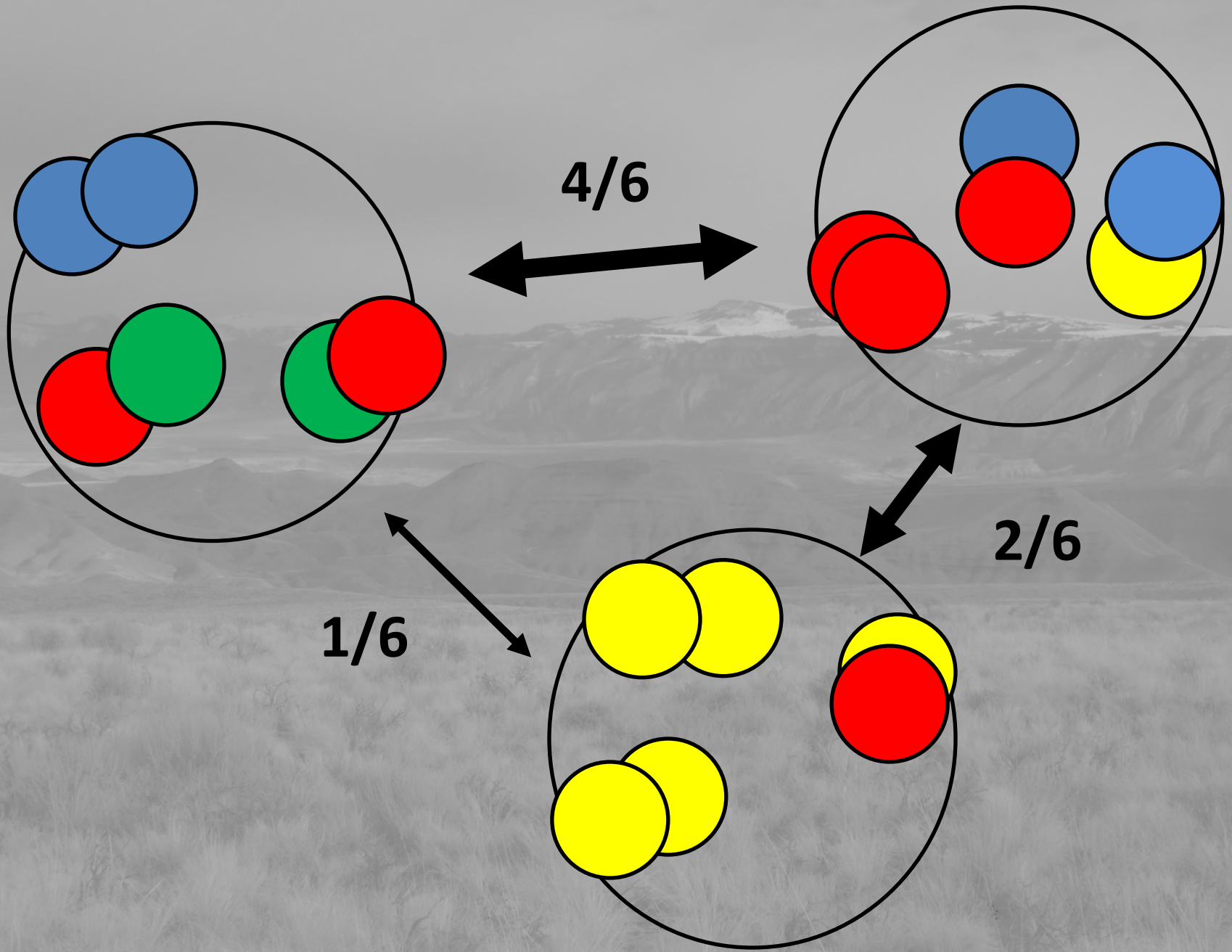




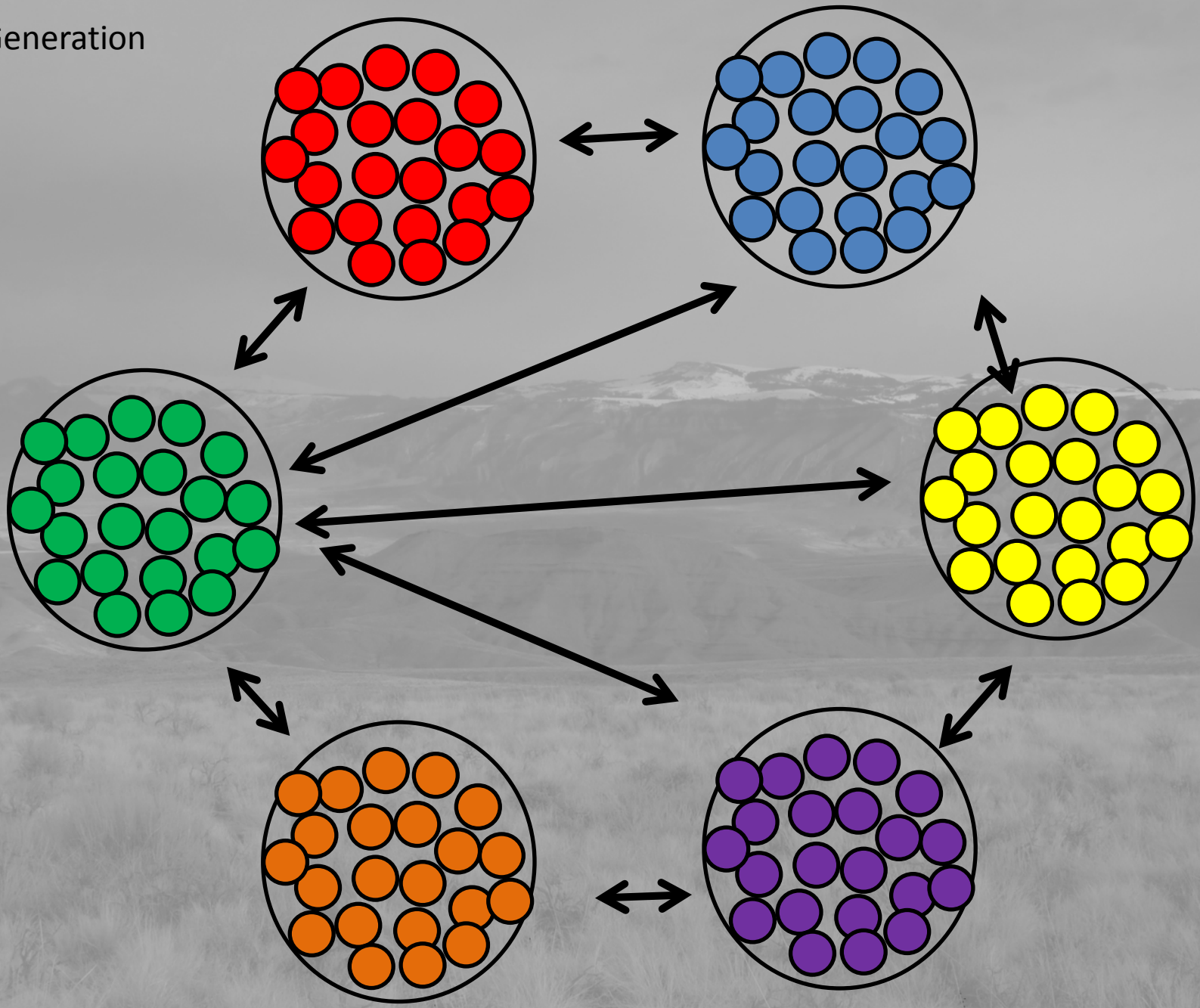


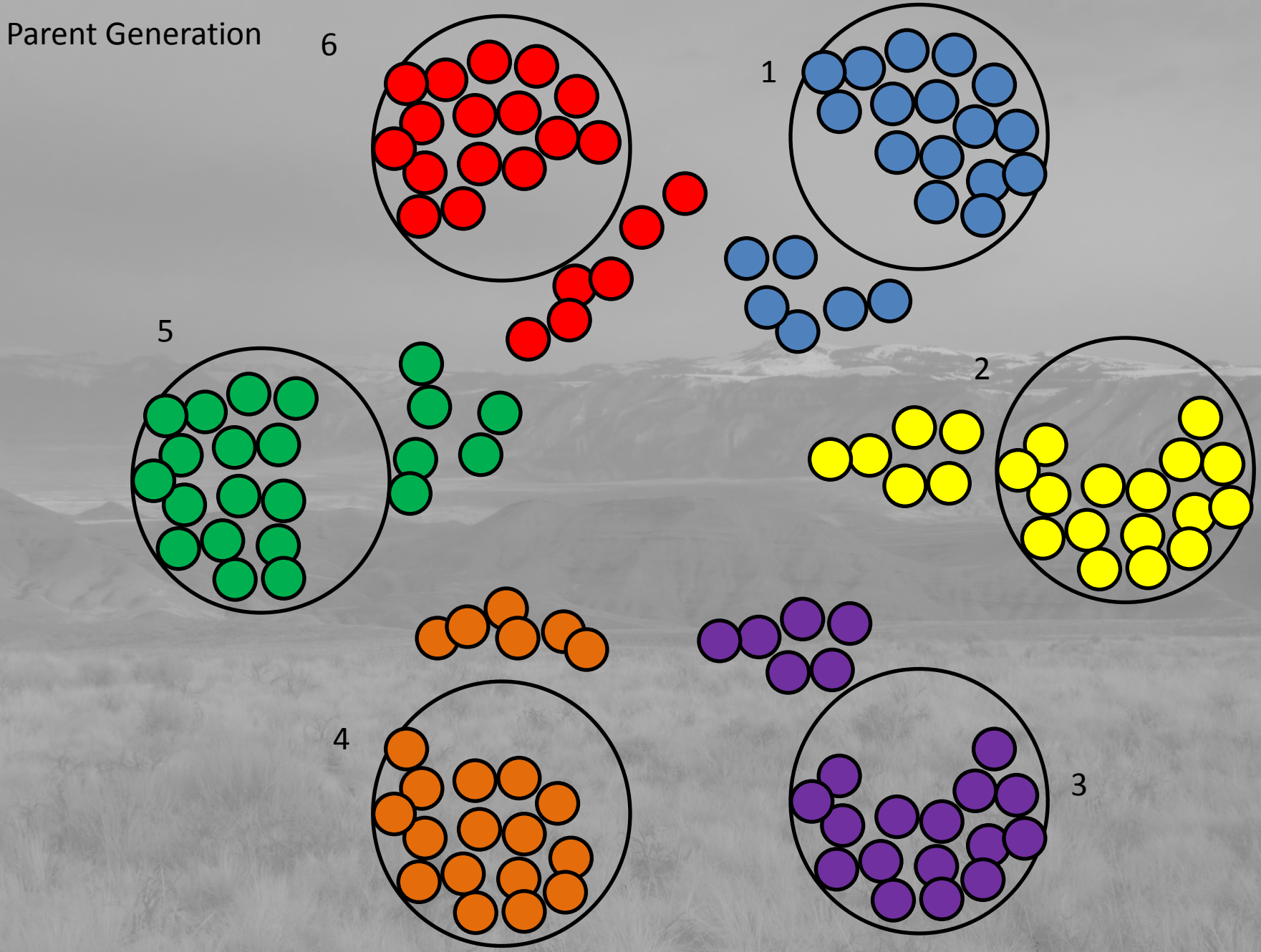


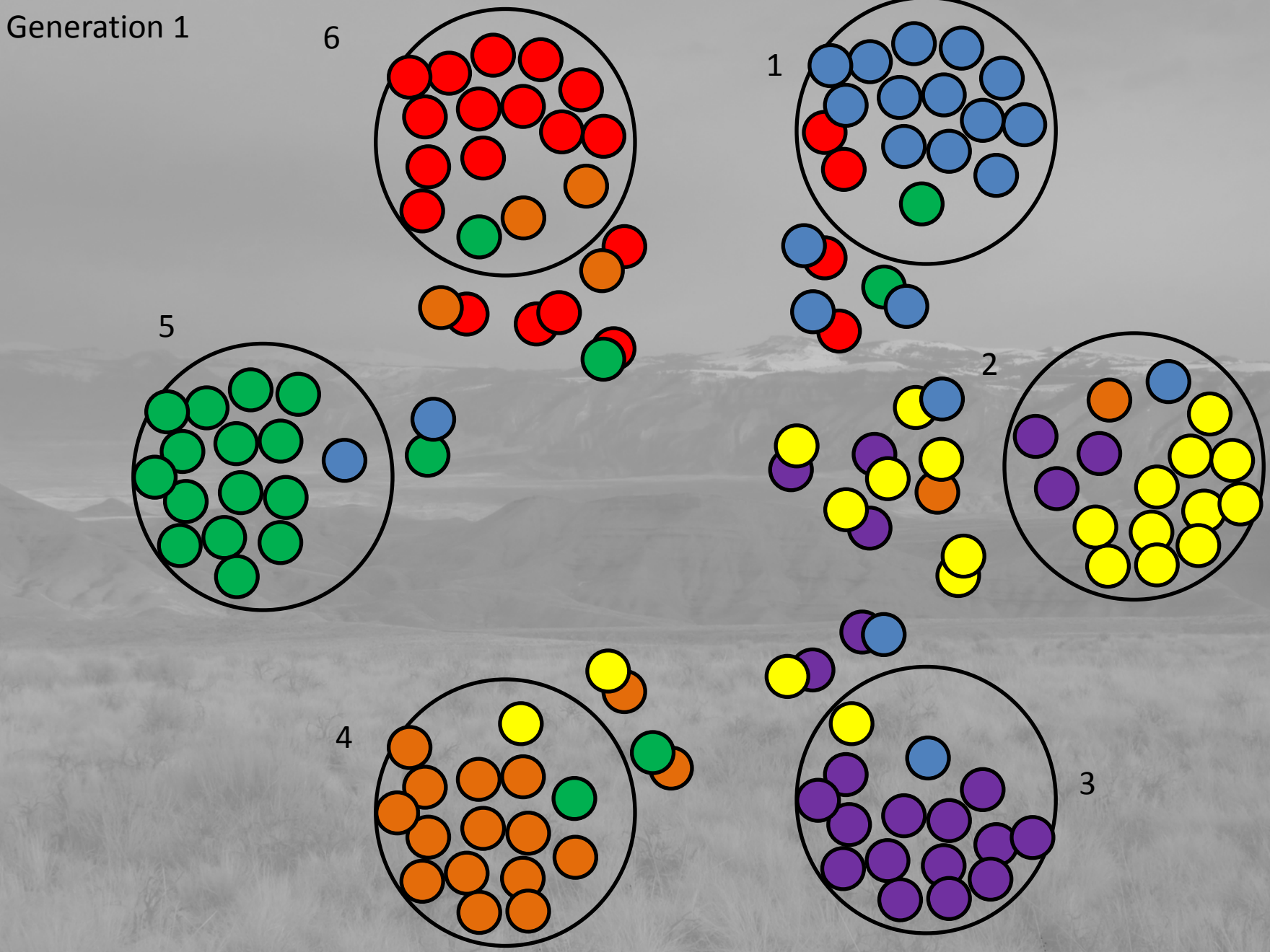


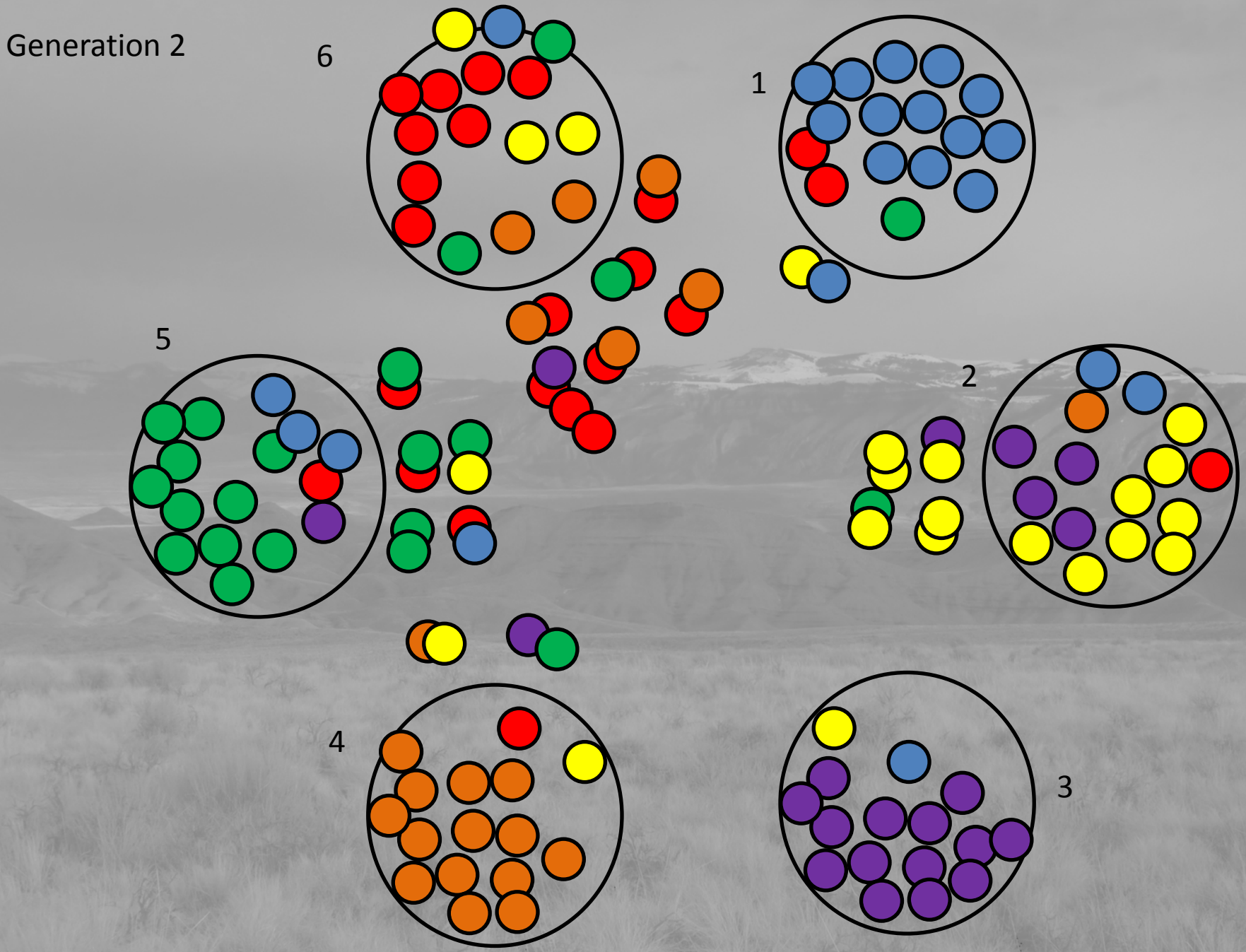

4/6
2/6
1/6

Parent Generation

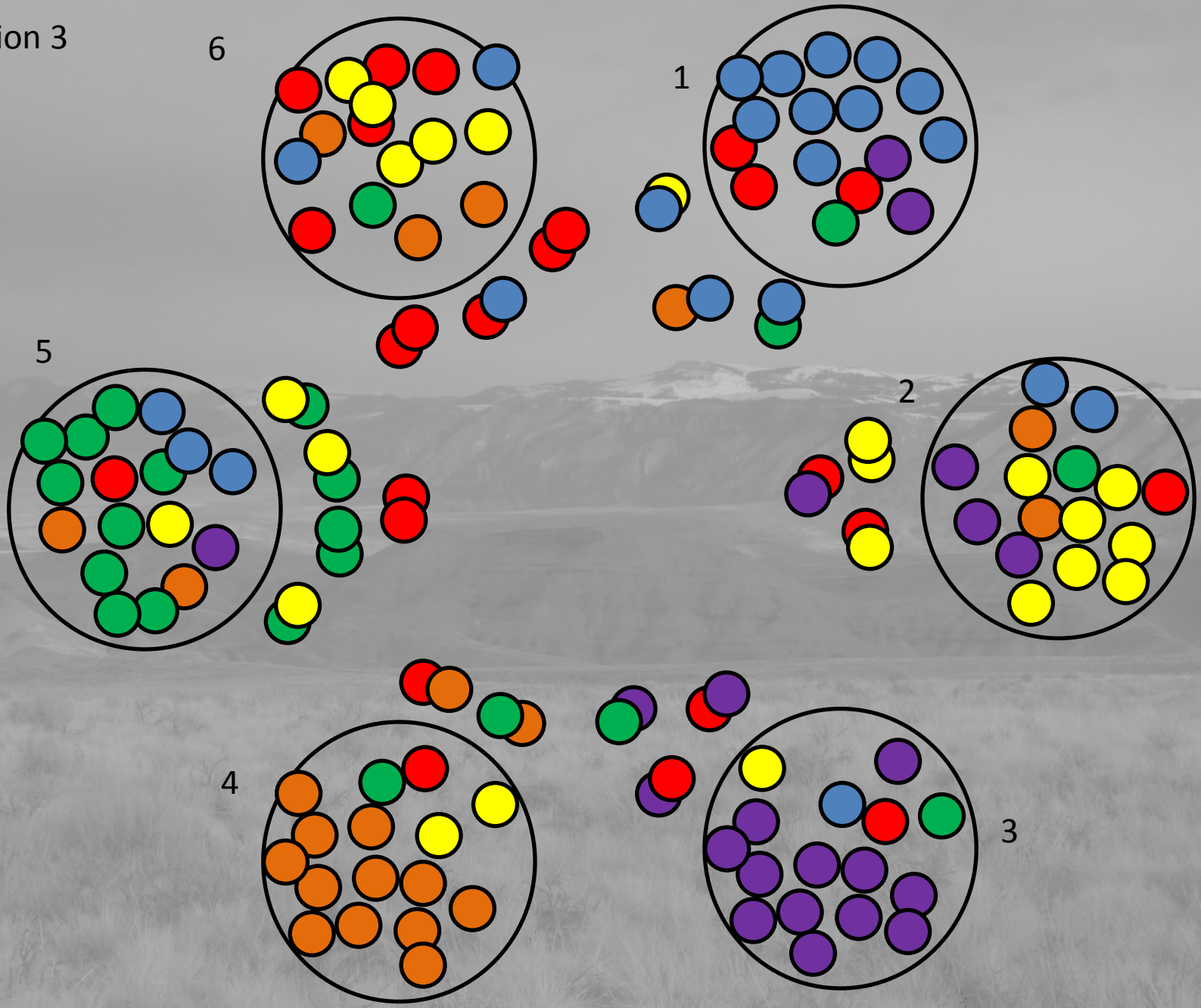



Parent Generation
6
1
5
2
4
3
Equal probability of dispersing to any lek

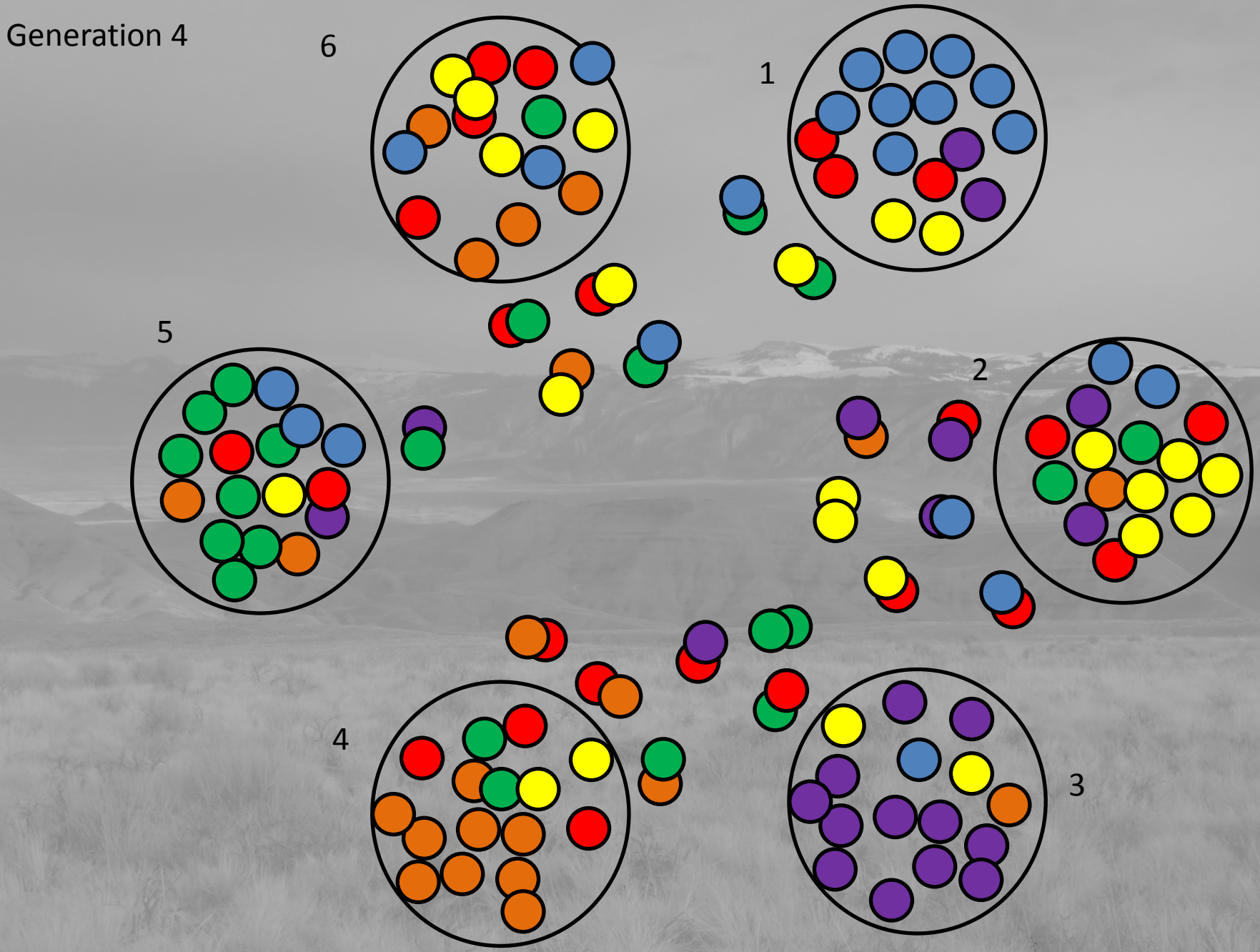

Generation 1
6
1
5
2
4
3
Equal probability of dispersing to any lek

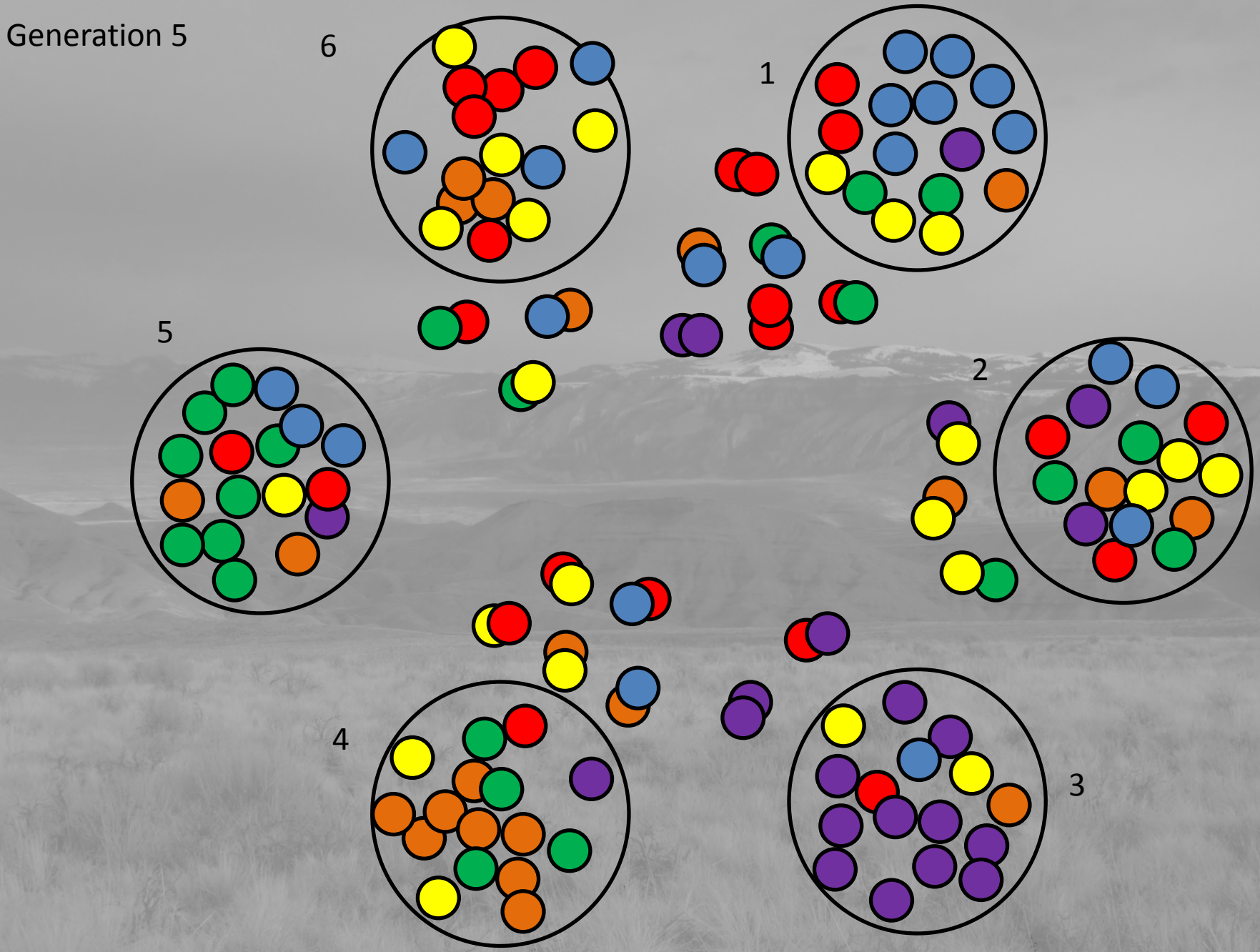

Generation 2
6
1
5
2
4
3
Equal probability of dispersing to any lek

Generation 3

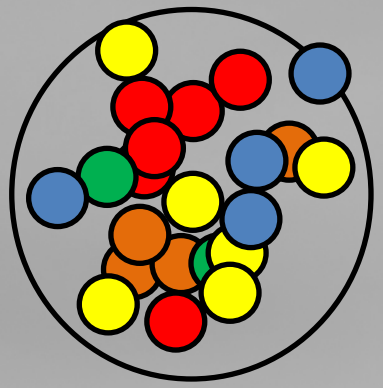


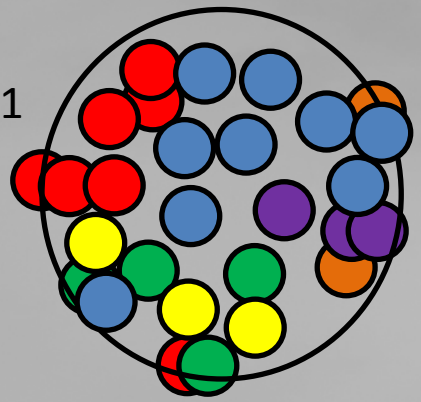
Equal probability of dispersing to any lek

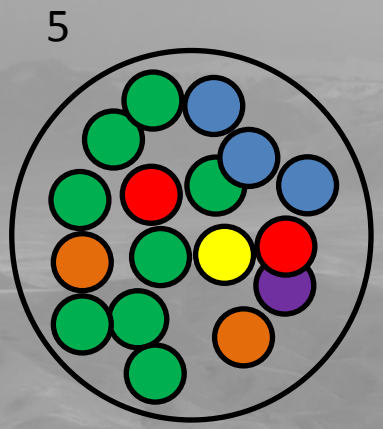

Generation 4
6
1
5
2
4
3
Equal probability of dispersing to any lek

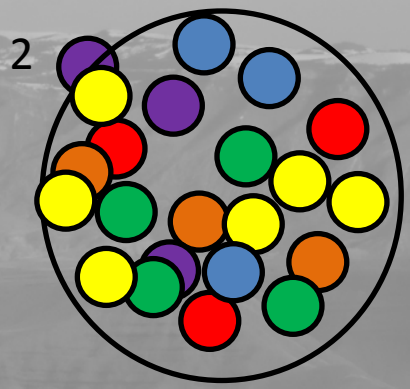

Generation 5
6
1
5
2
4
3
Equal probability of dispersing to any lek

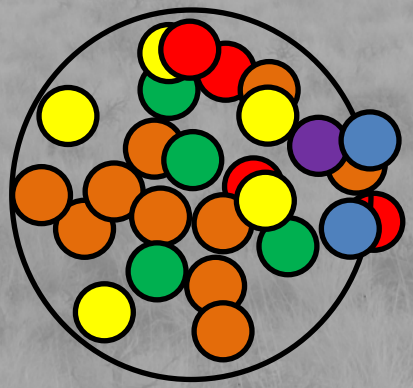
Generation 5

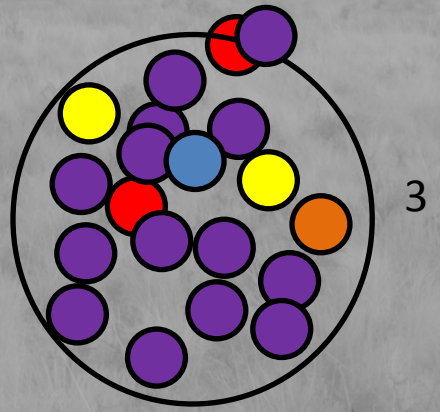




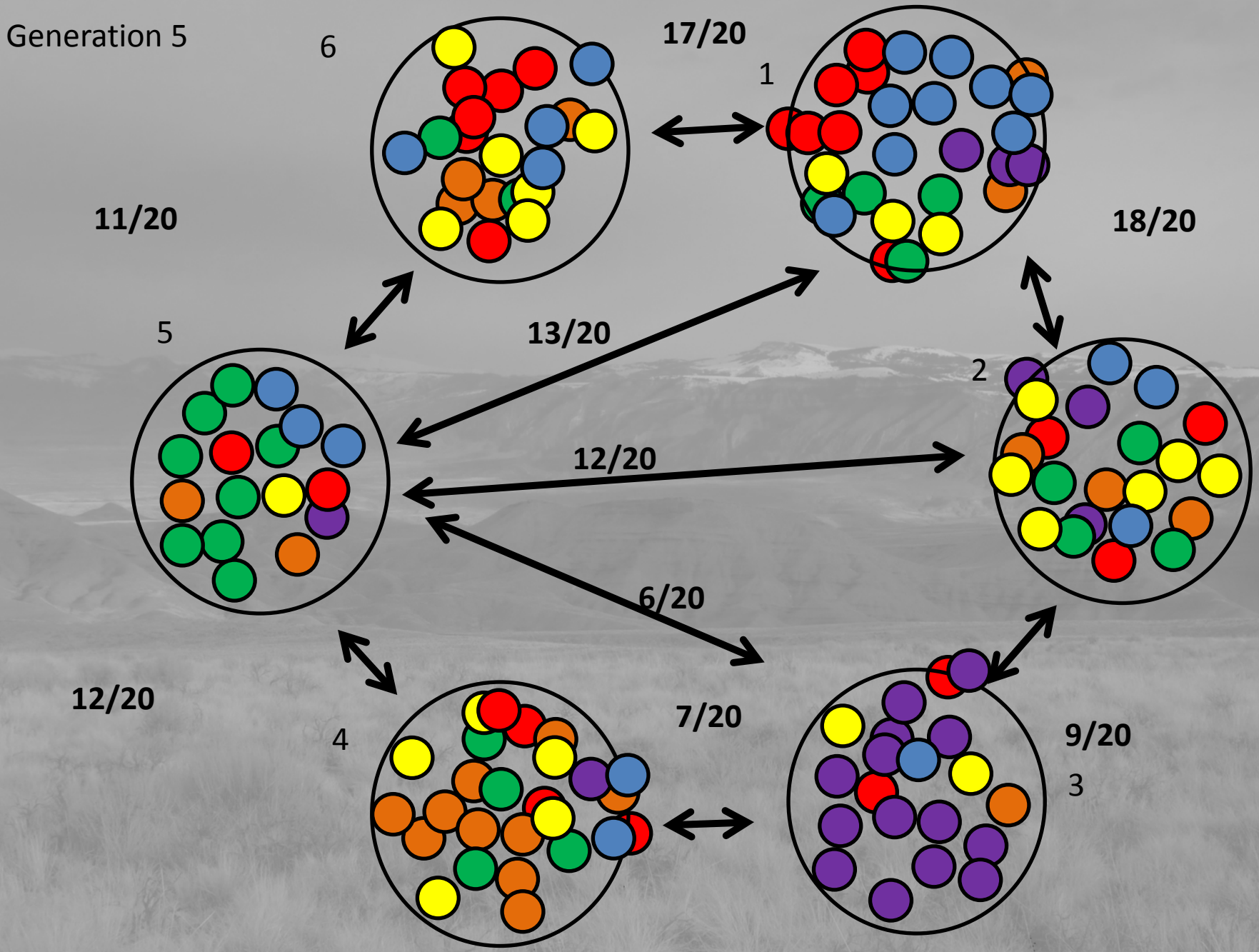


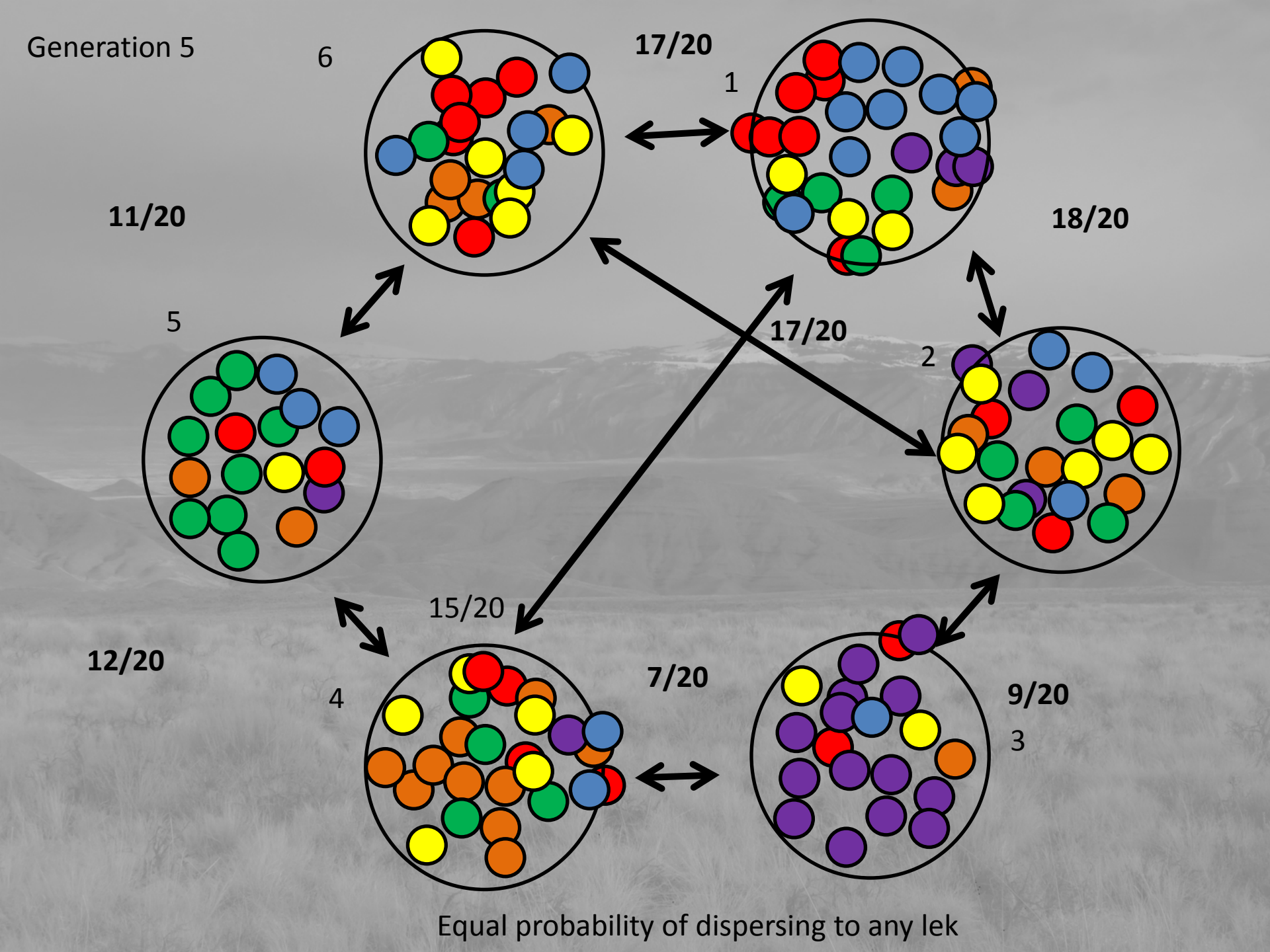




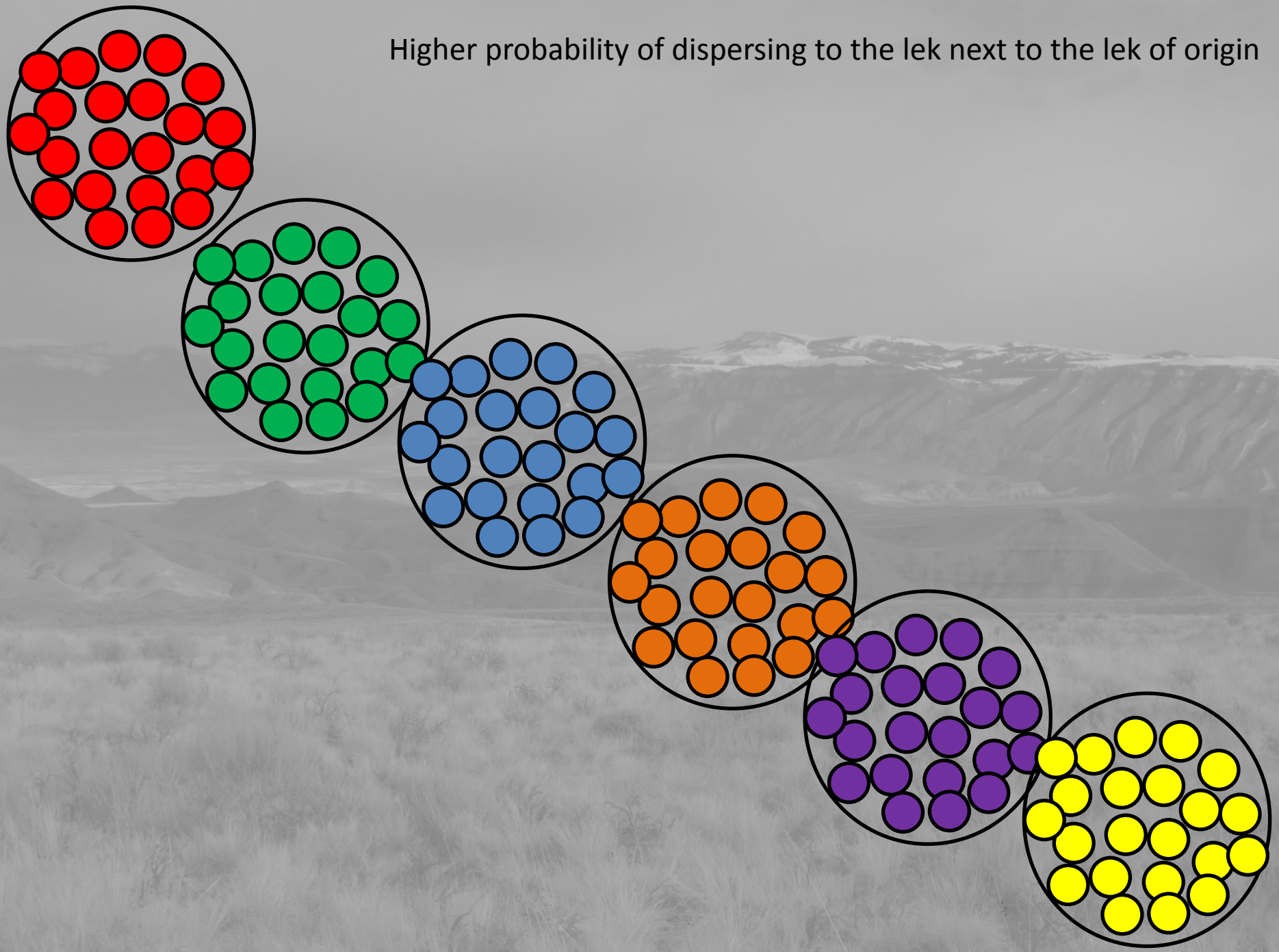


Equal probability of dispersing to any lek


Generation 5
6
17/20
1
11/20
18/20
5
13/20
2
12/20
6/20
12/20
4
7/20
9/20
3
Equal probability of dispersing to any lek


Generation 5
6
17/20
1
11/20
18/20
5
17/20
2
15/20
12/20
4
7/20
9/20
3
Equal probability of dispersing to any lek

Higher probability of dispersing to the lek next to the lek of origin

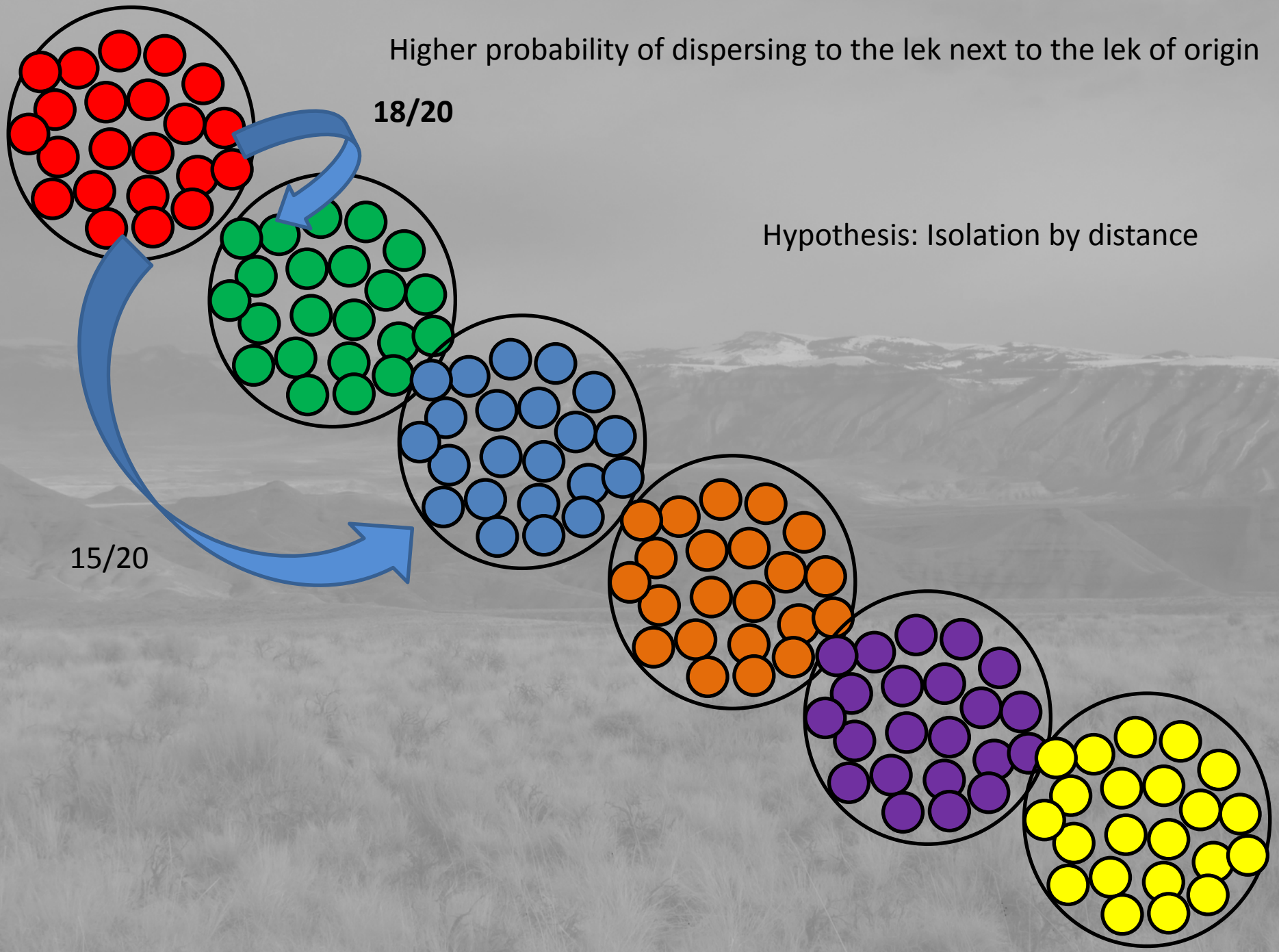


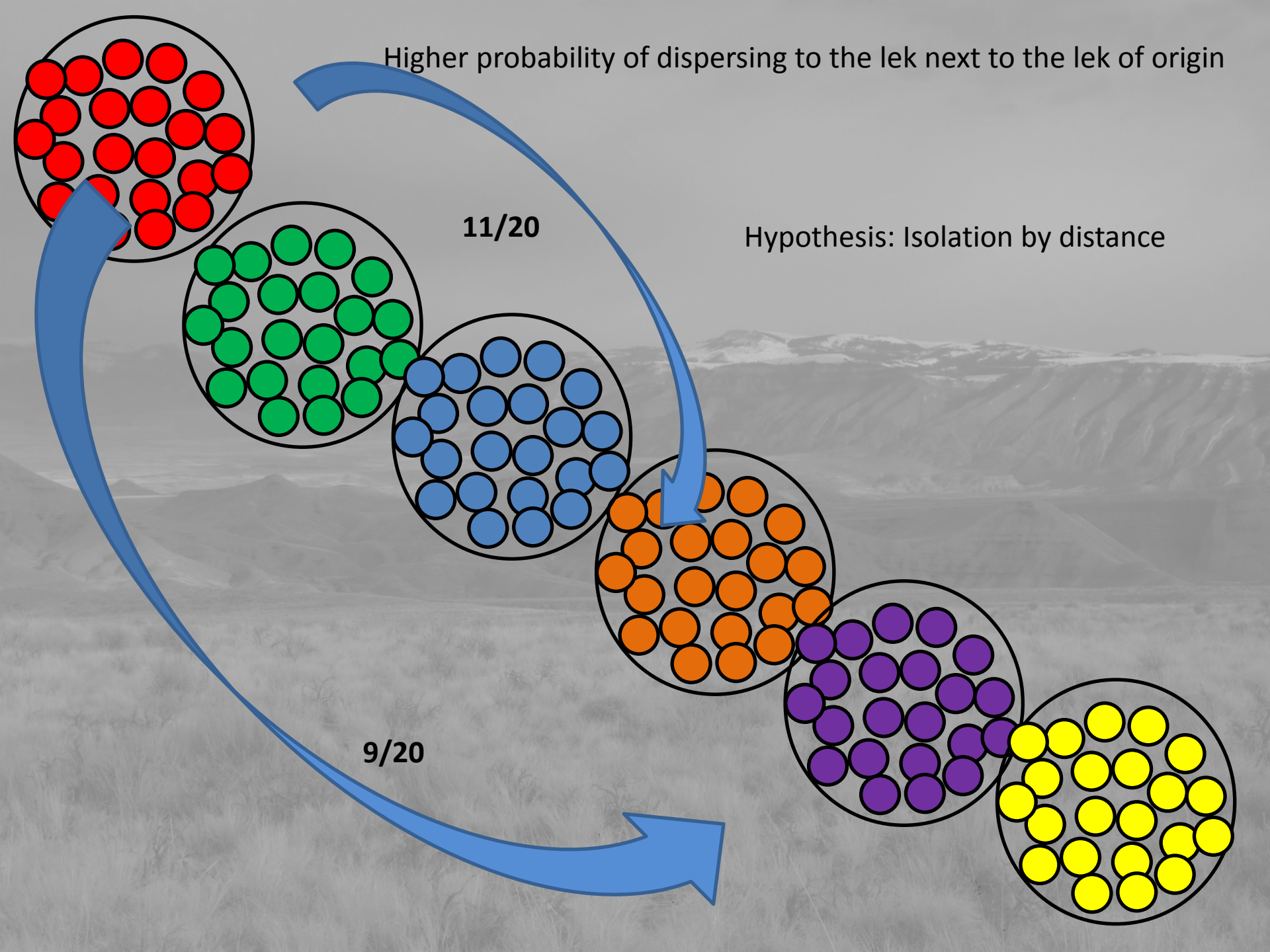
Higher probability of dispersing to the lek next to the lek of origin

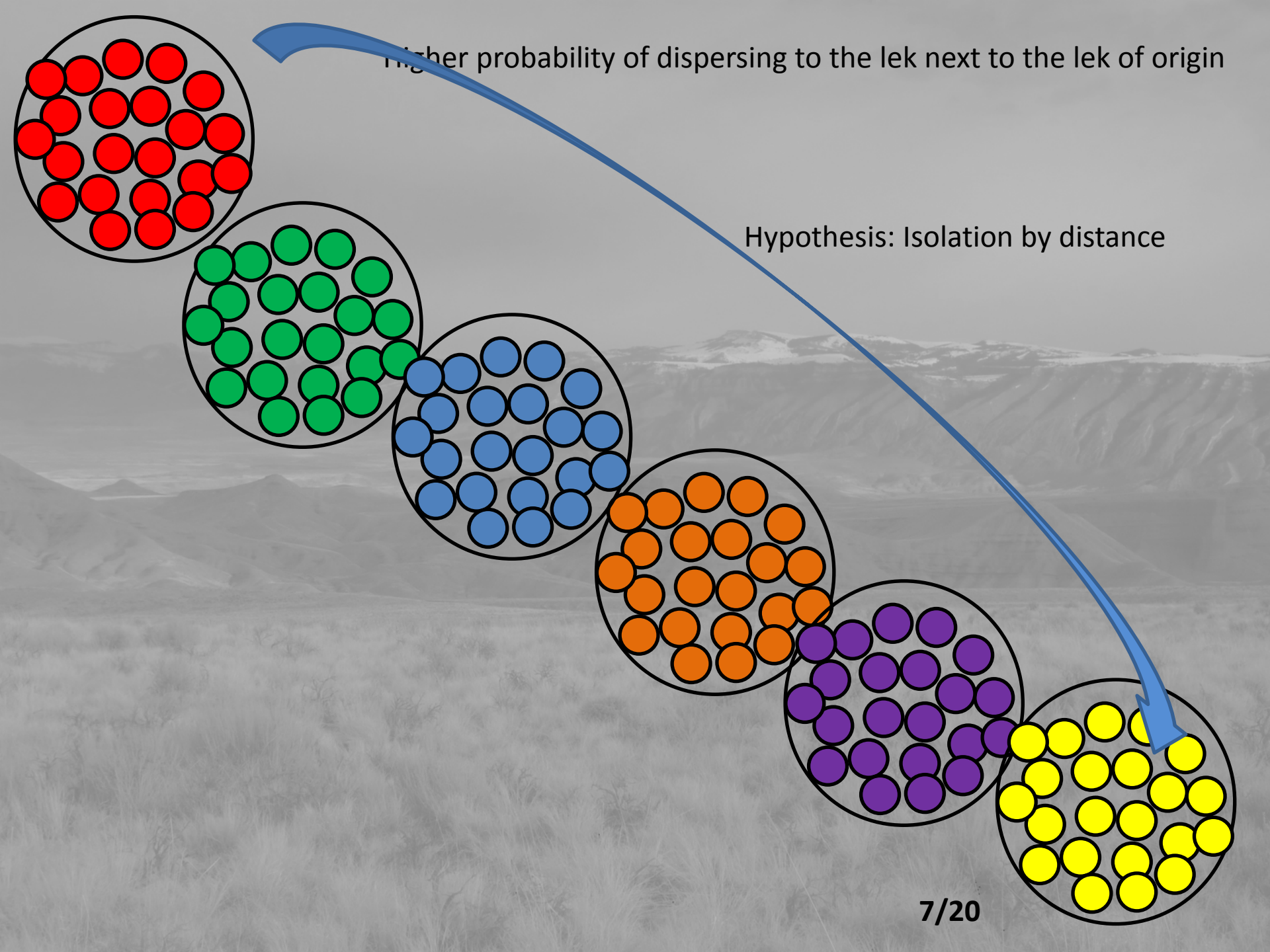
18/20

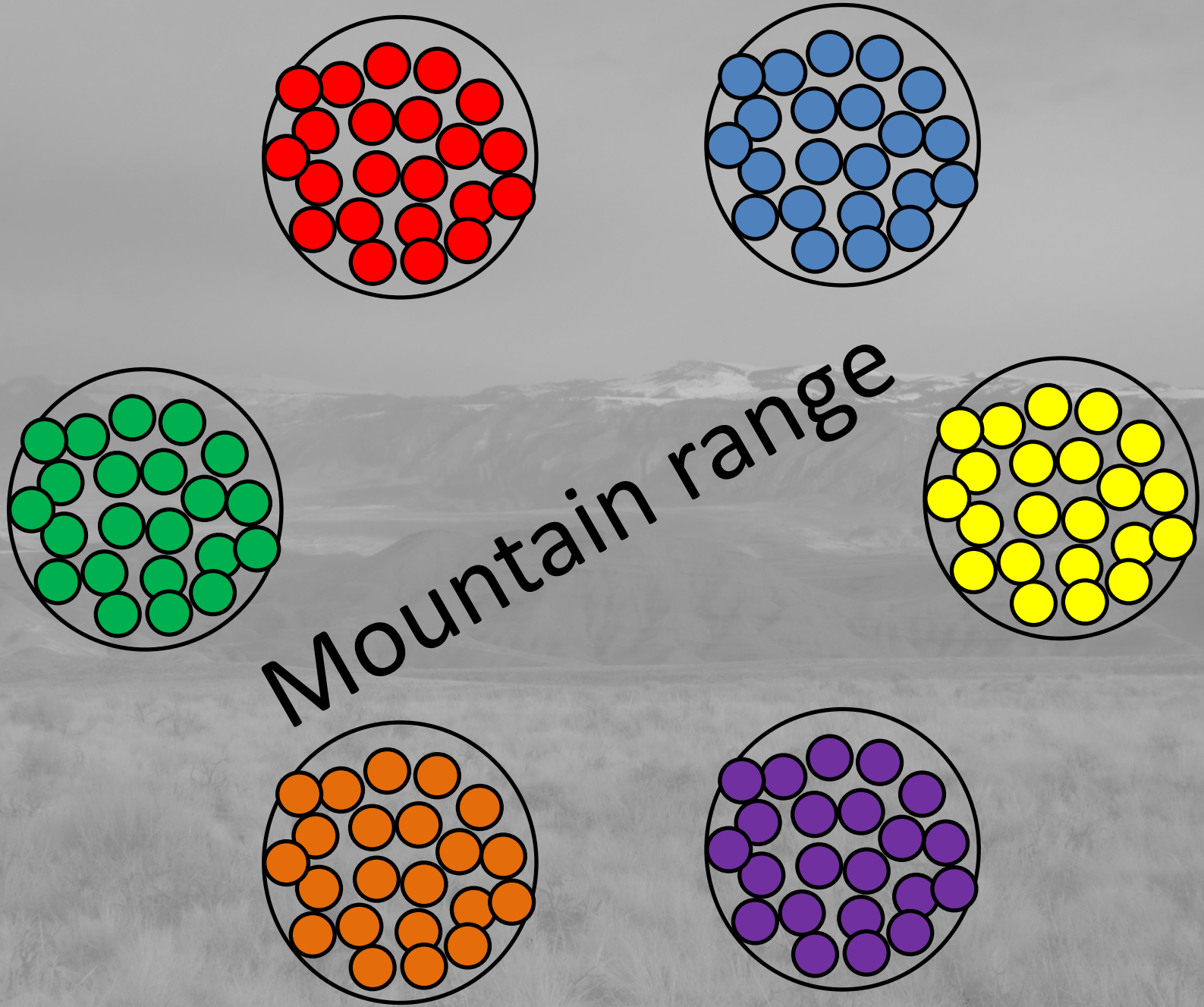
Hypothesis: Isolation by distance

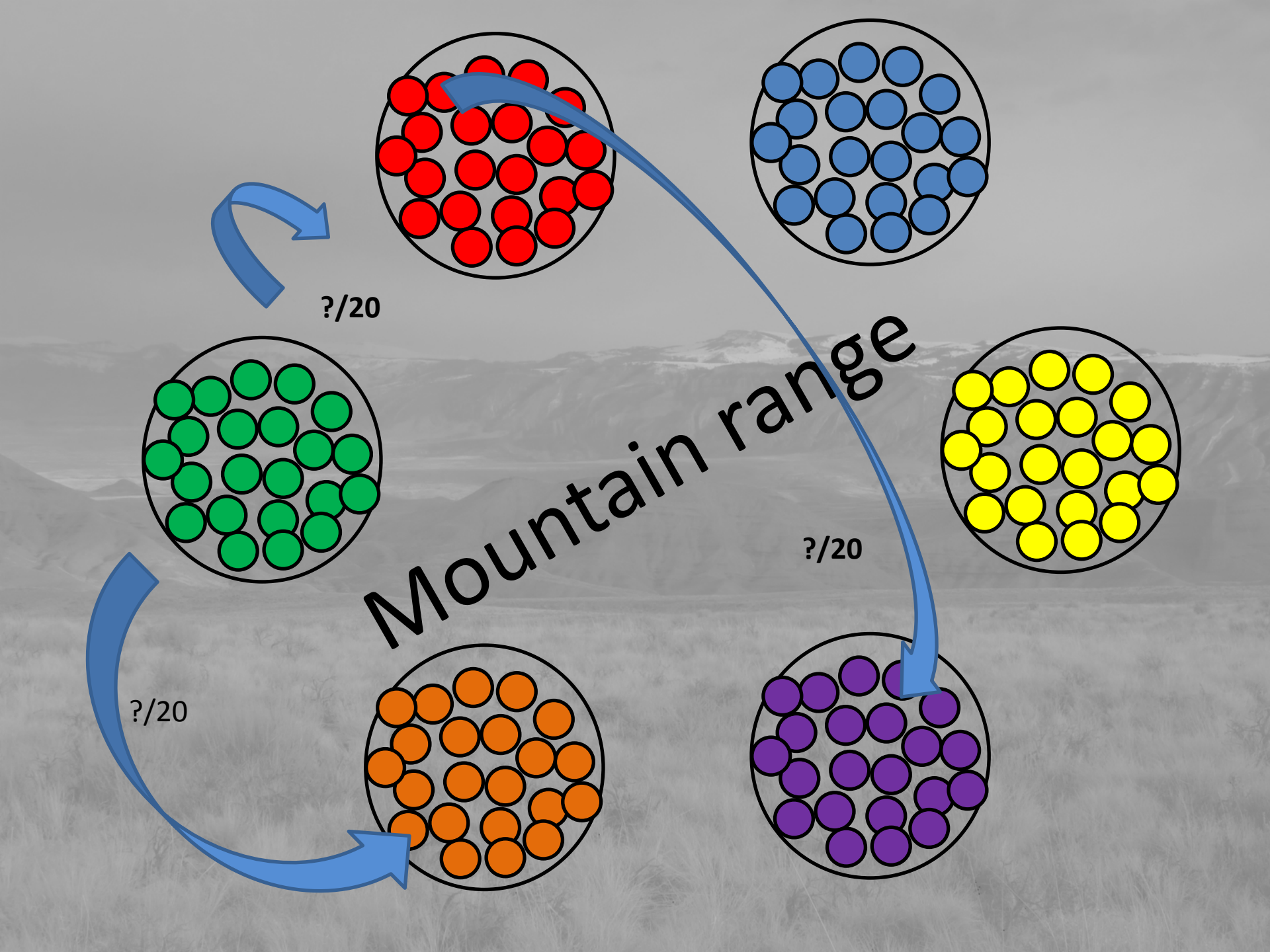
15/20

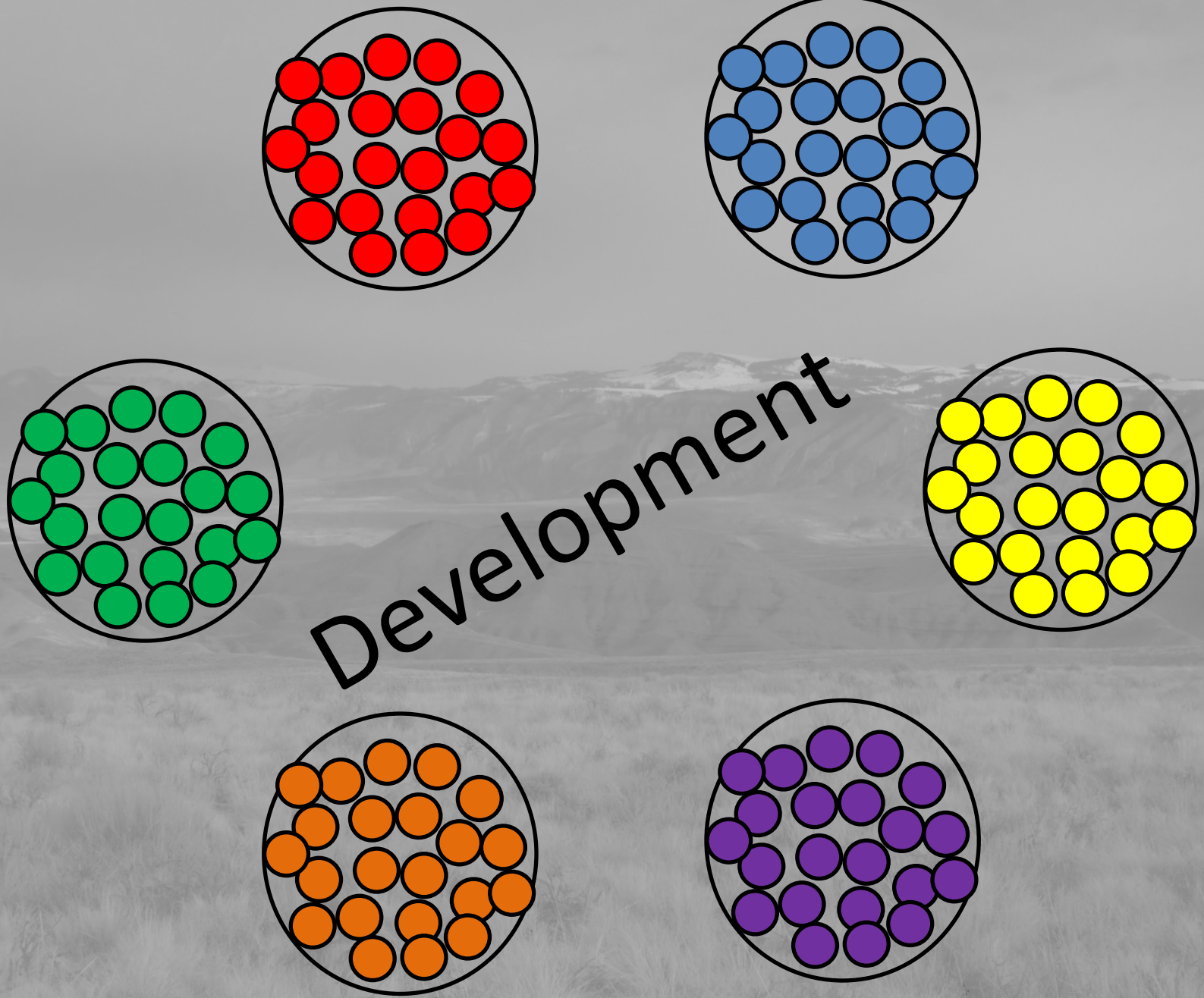


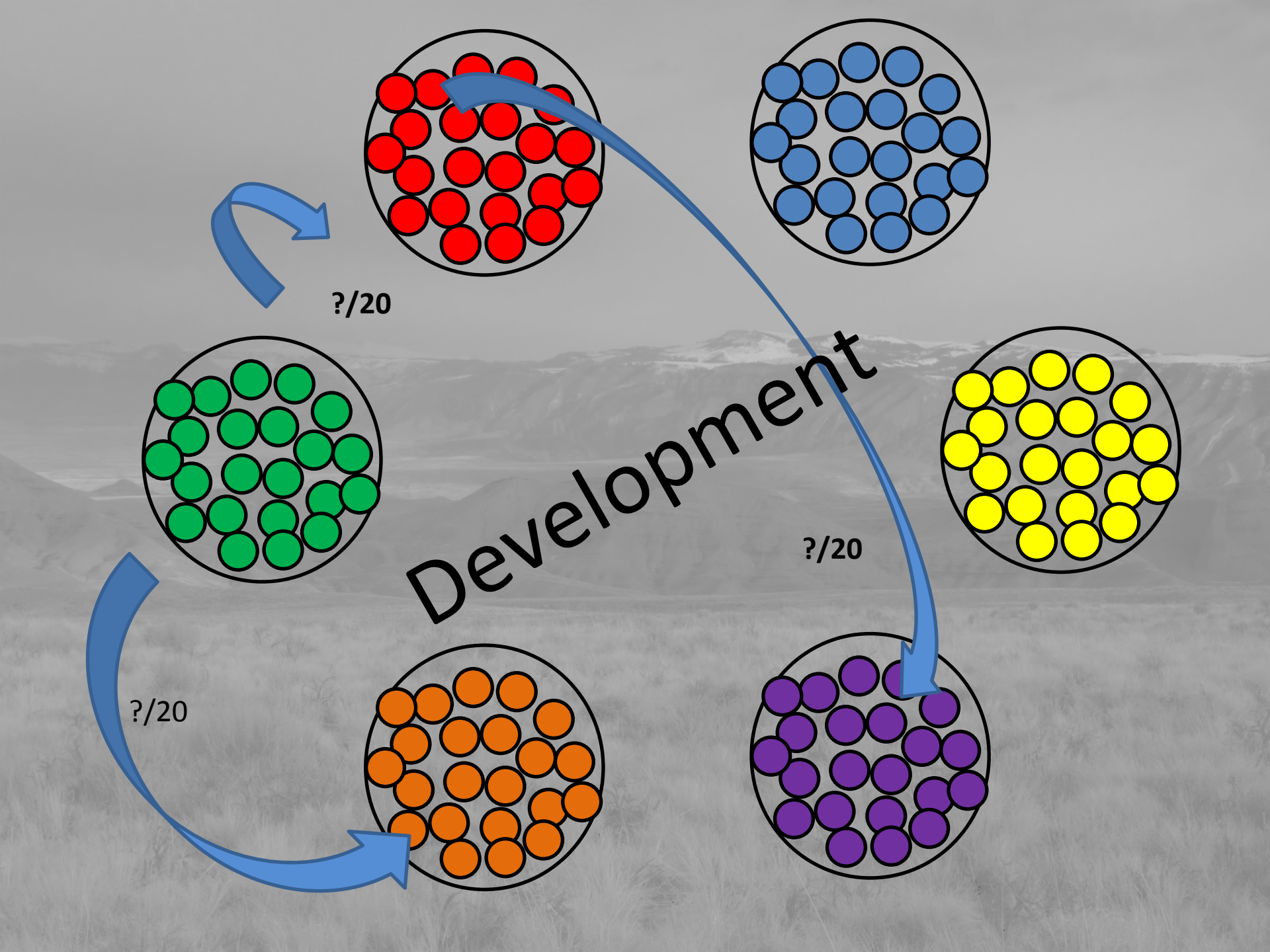

Higher probability of dispersing to the lek next to the lek of origin
11/20
Hypothesis: Isolation by distance
9/20


Higher probability of dispersing to the lek next to the lek of origin
Hypothesis: Isolation by distance

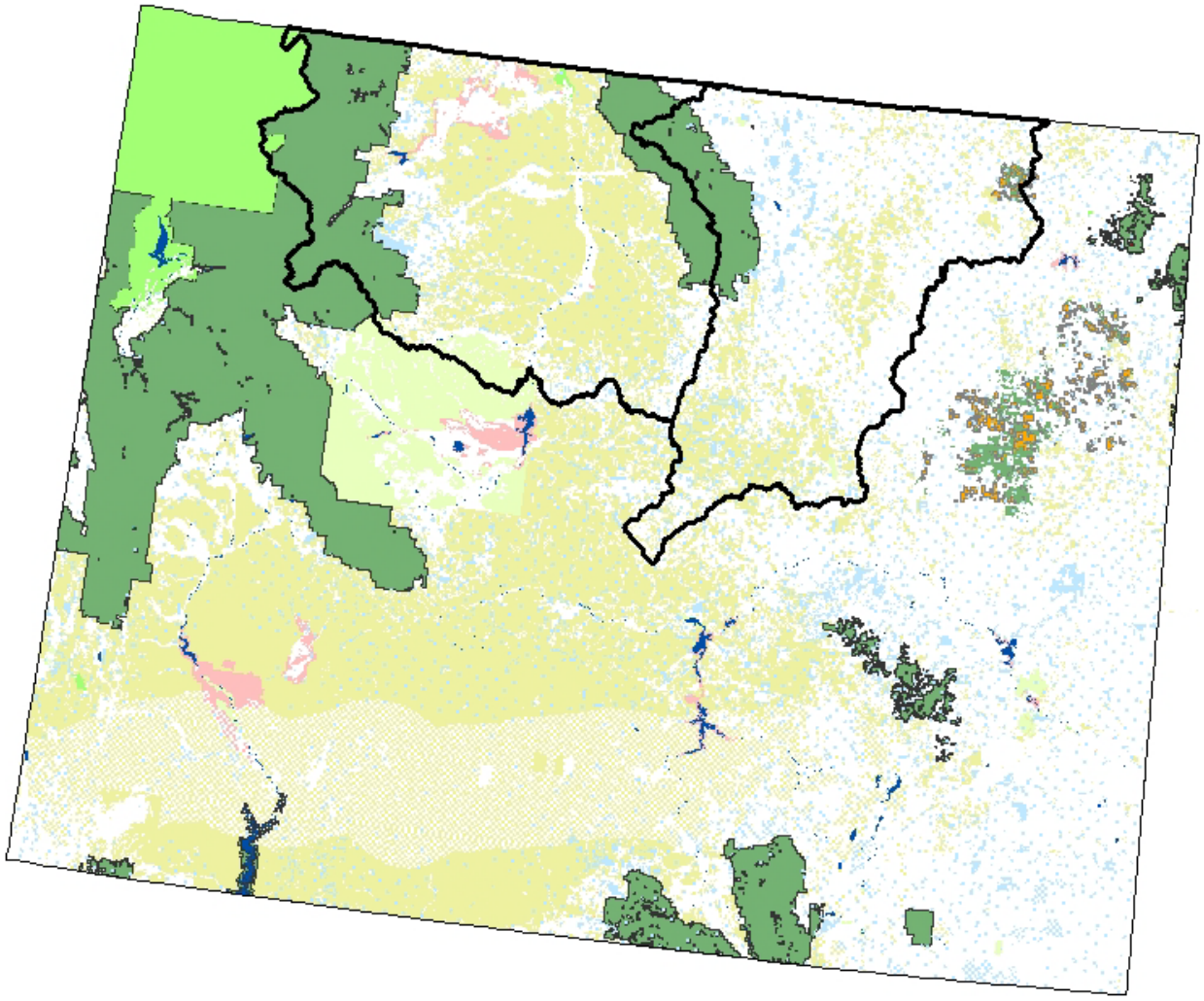

Mountain range


?/20
Mountain range
?/20
?/20

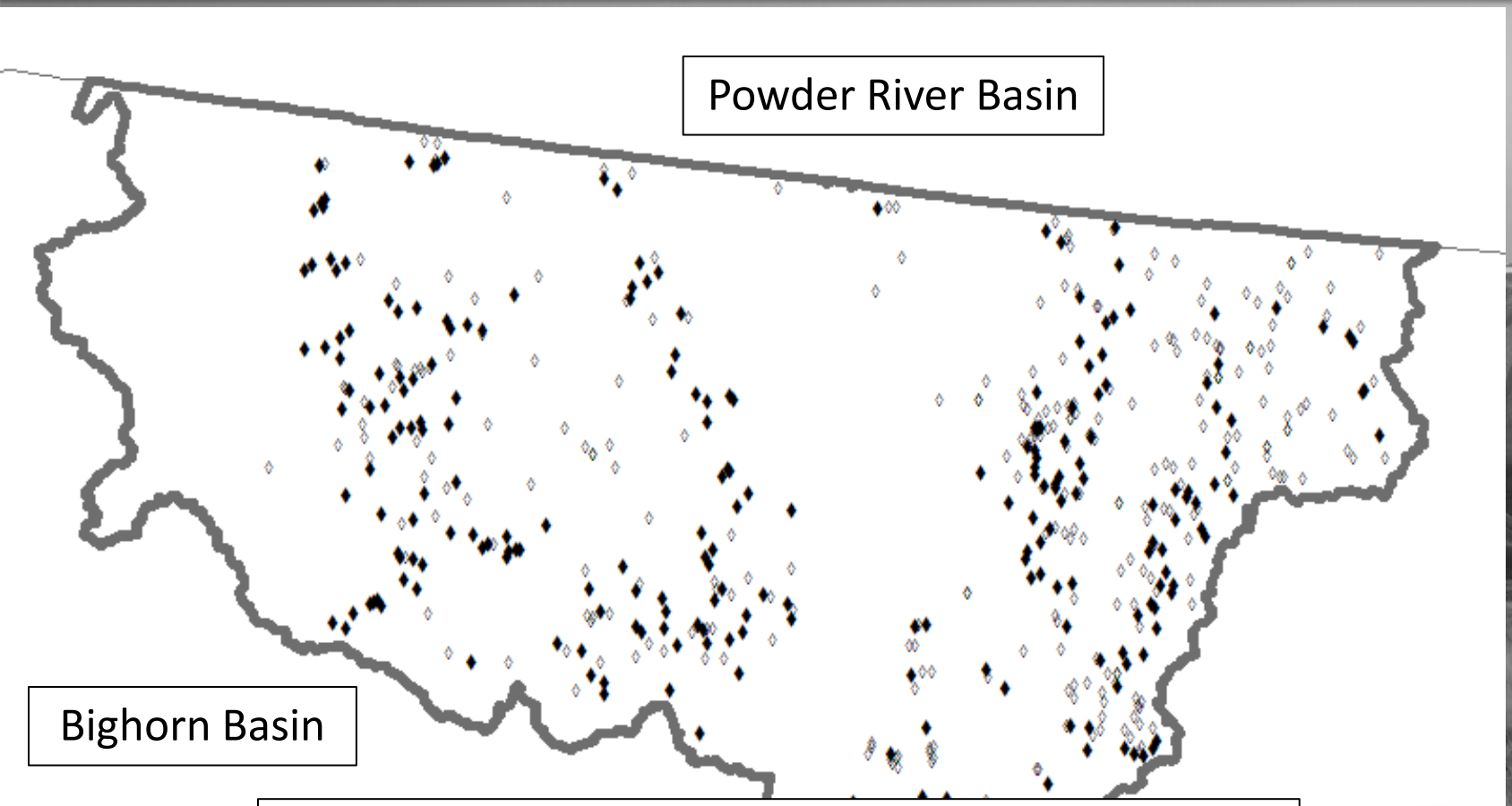

Development

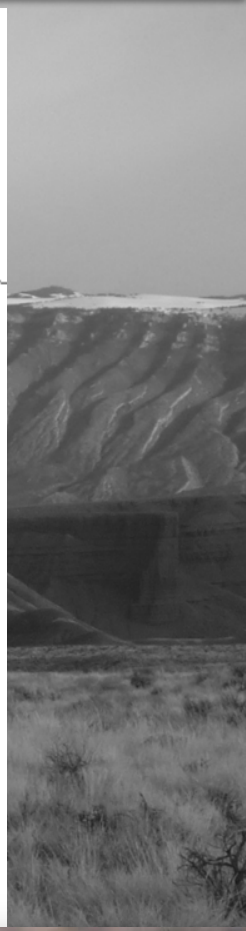

?/20
Development
?/20
?/20

Study Area: Northern Wyoming



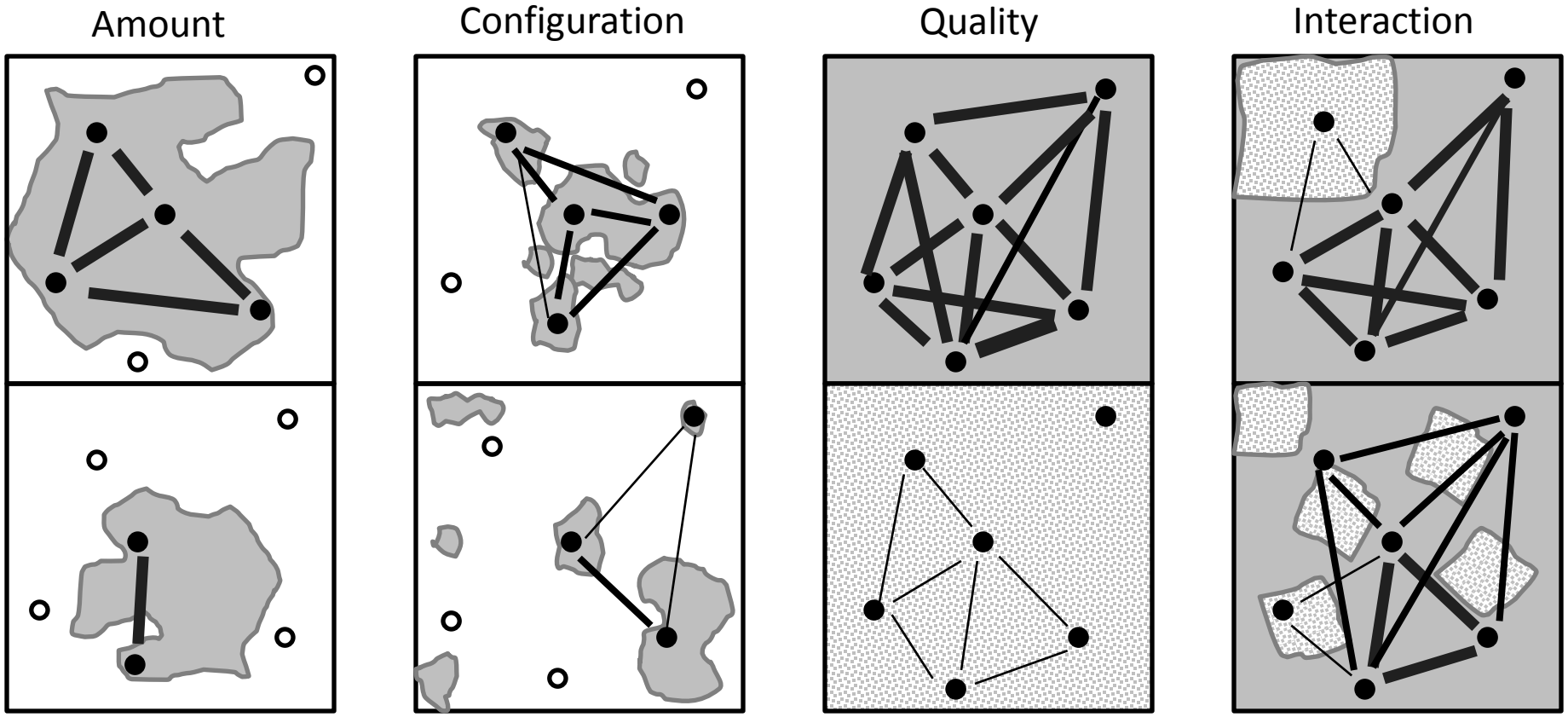
Presence or Absence of Displaying Males





Total: 245 active out of 541 locations
Bighorn Basin: 71%
Powder River Basin: 44%

Gene Flow Hypotheses



Preliminary Analysis: Methods

Genetic Data: 56 leks; 387 samples
Connectivity Model: 35 leks; 340 samples
7 microsatelites + Sex ID used (out of 18)

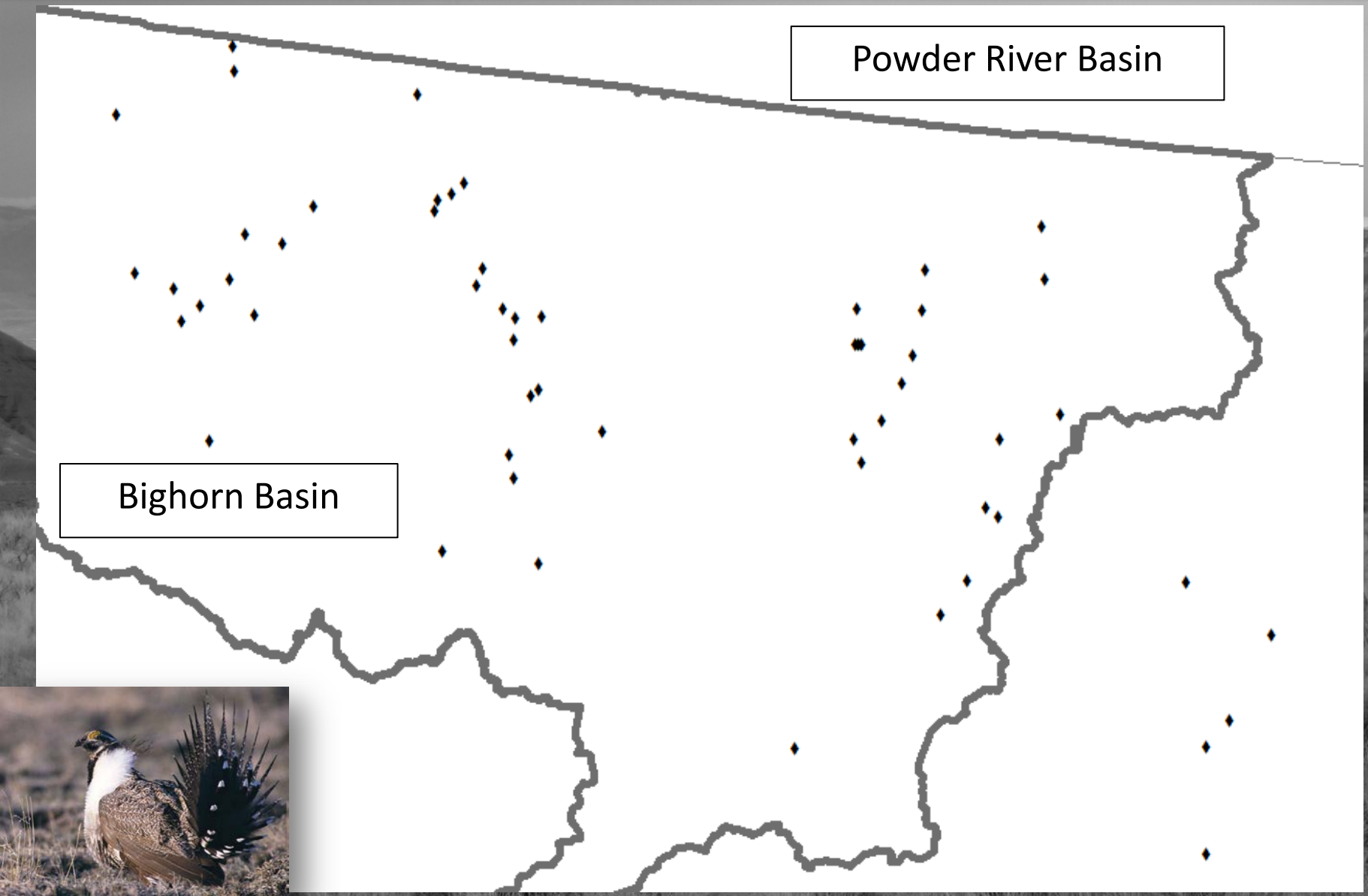
Microsatellites: Caizergues et al. 2001, Caizergues et al. 2003, Piertney & Dallas 1997, Piertney & Höglund 2001, Cheng et al. 1995, Kahn et al. 1998, Burt et al. 2003, Segelbacher et al. 2000, Taylor et al. 2003

Preliminary Analysis: Methods

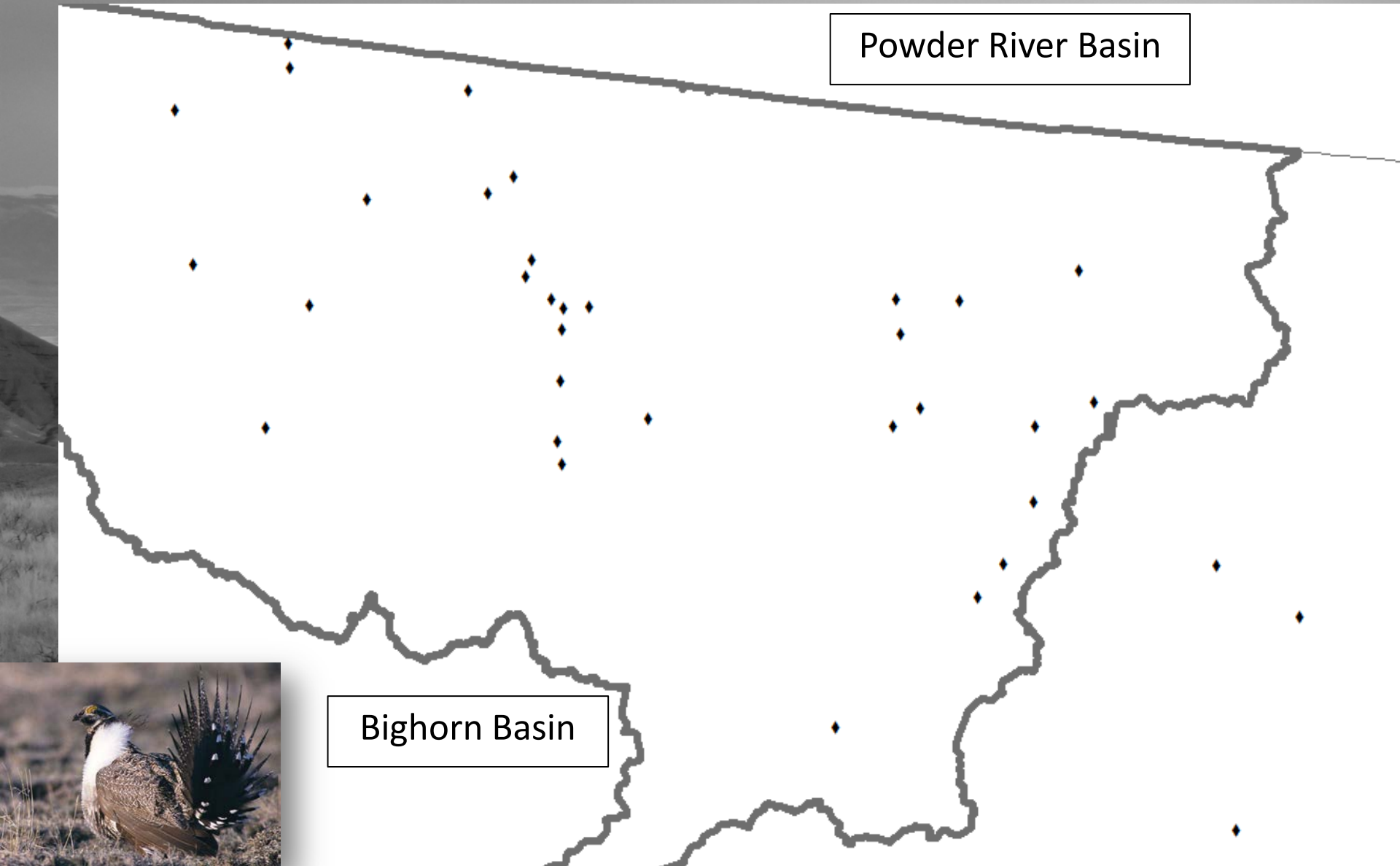
Spatial Data

- Sagebrush (NLCD, Knick et al. 2010)
- Growing Season Precip. (Rehfeldt et al. 2006)
- Mean Annual Precip. (Rehfeldt et al. 2006)
- Development (Kiesecker et al. 2012)
- Well locations (WOGCC & MBOG)
- Elevation relief ratio (topography) (Evans 1972)

Genetic Data Locations



Connectivity Data Locations



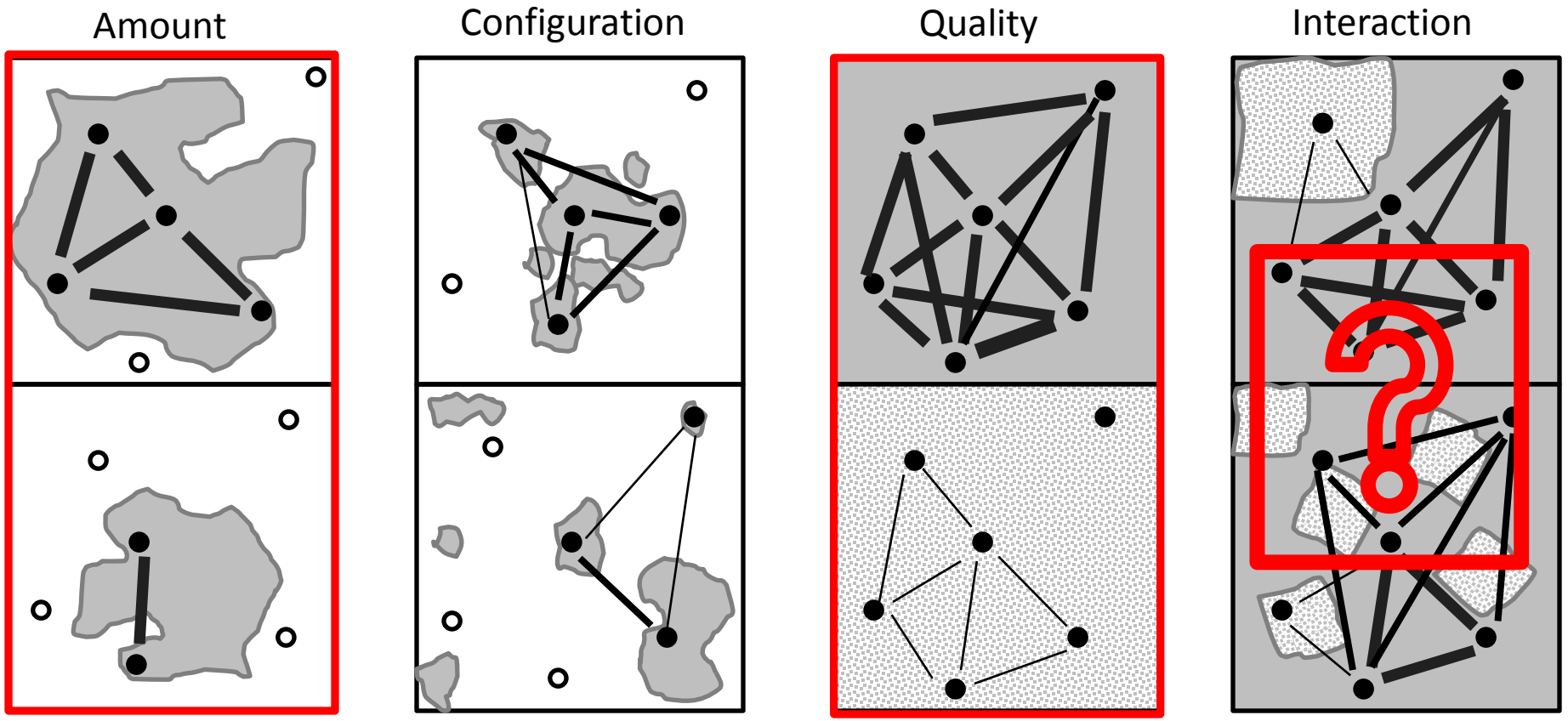
Results: Genetic Data

	Minimum	Maximum	Mean
#Alleles/Locus (n=56)	7	28	13.6
F_{st} (n=35)	0	0.236	------
D_{ps} (n=35)	0.268	0.744	------

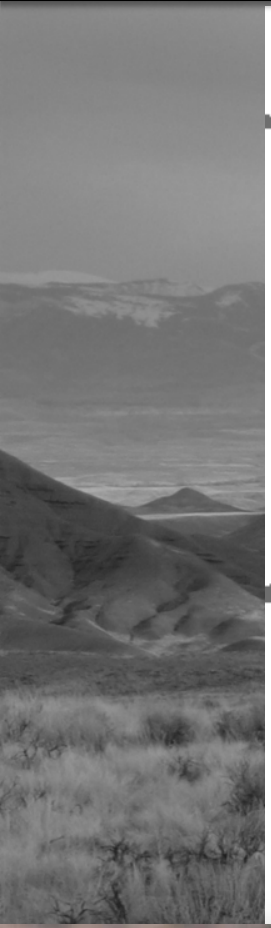
37

299

Gene Flow Hypotheses



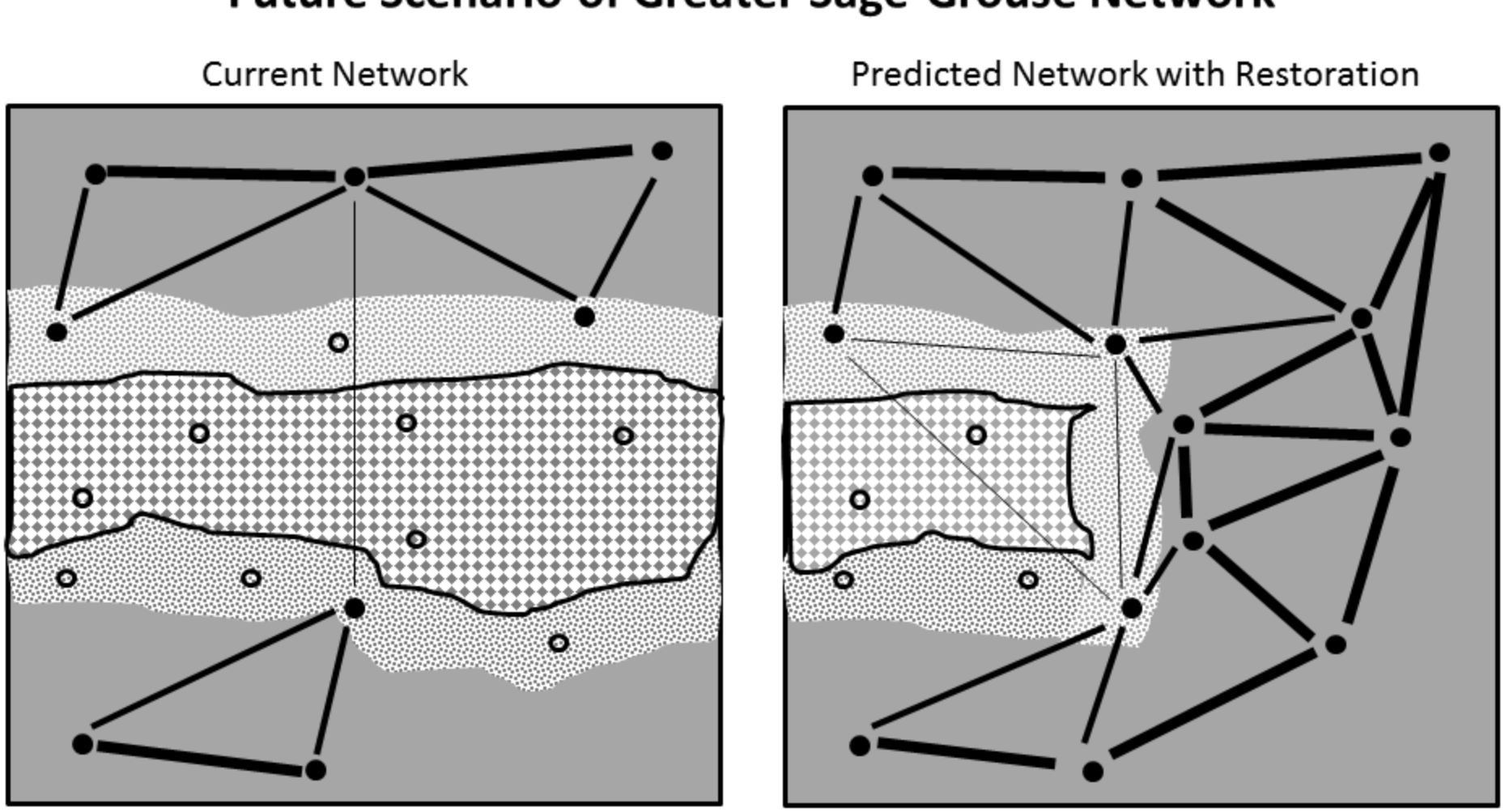
Total Sample Locations



Powder River Basin

Bighorn Basin

Future Scenario of Greater Sage-Grouse Network



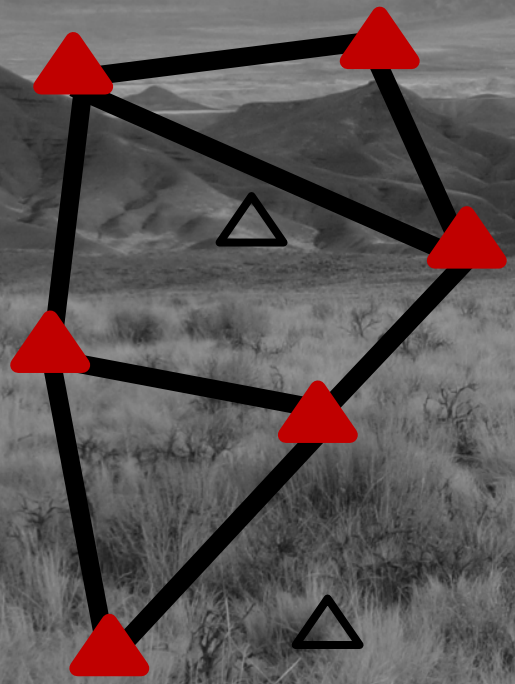
Research Impact

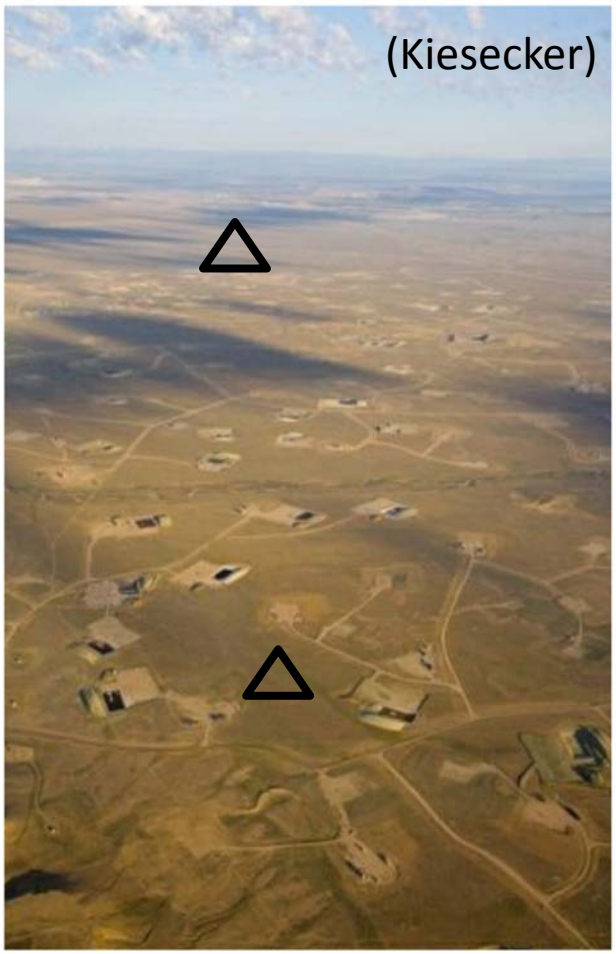
Presence =

Absence =

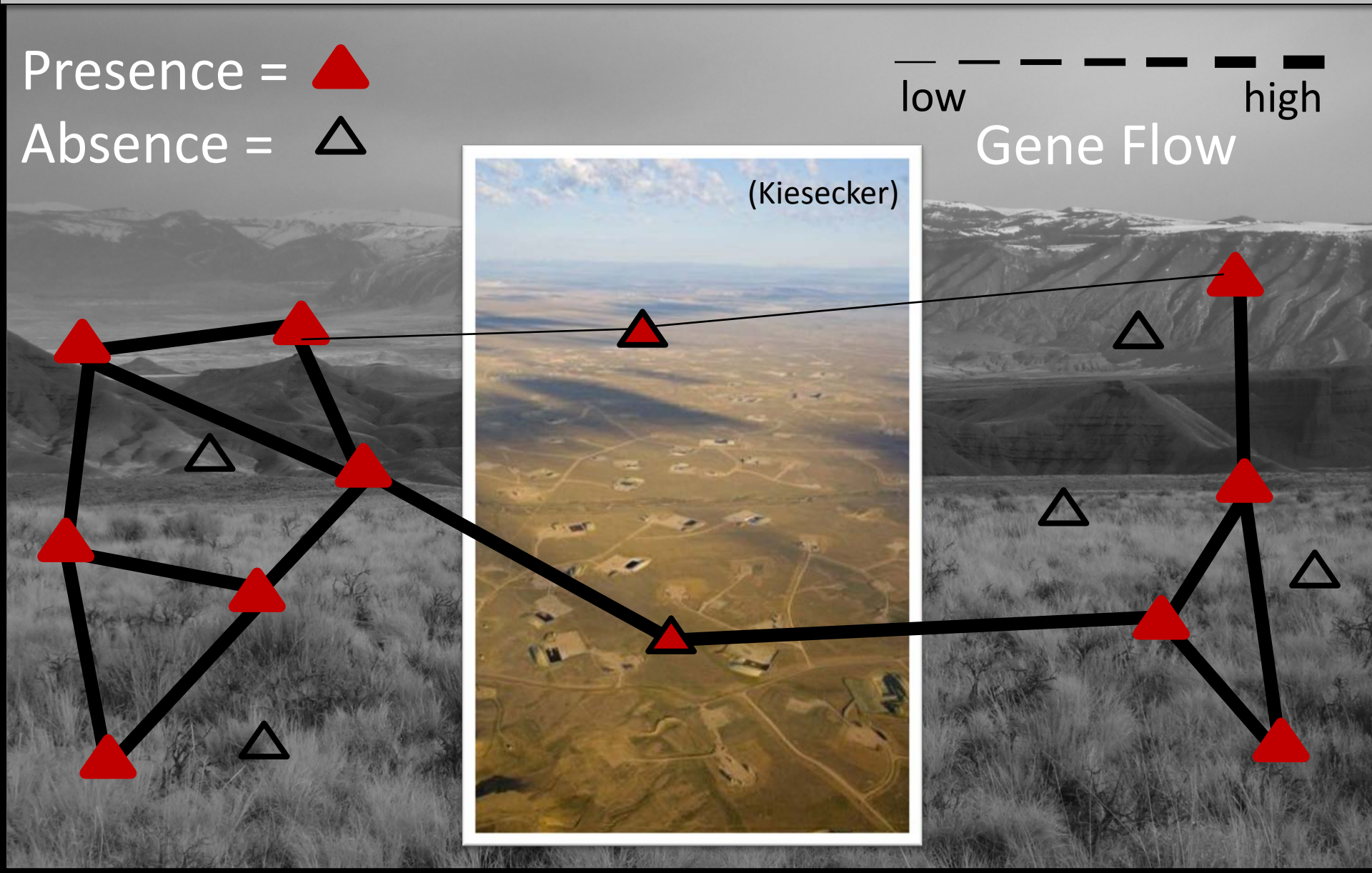
low — high

Gene Flow



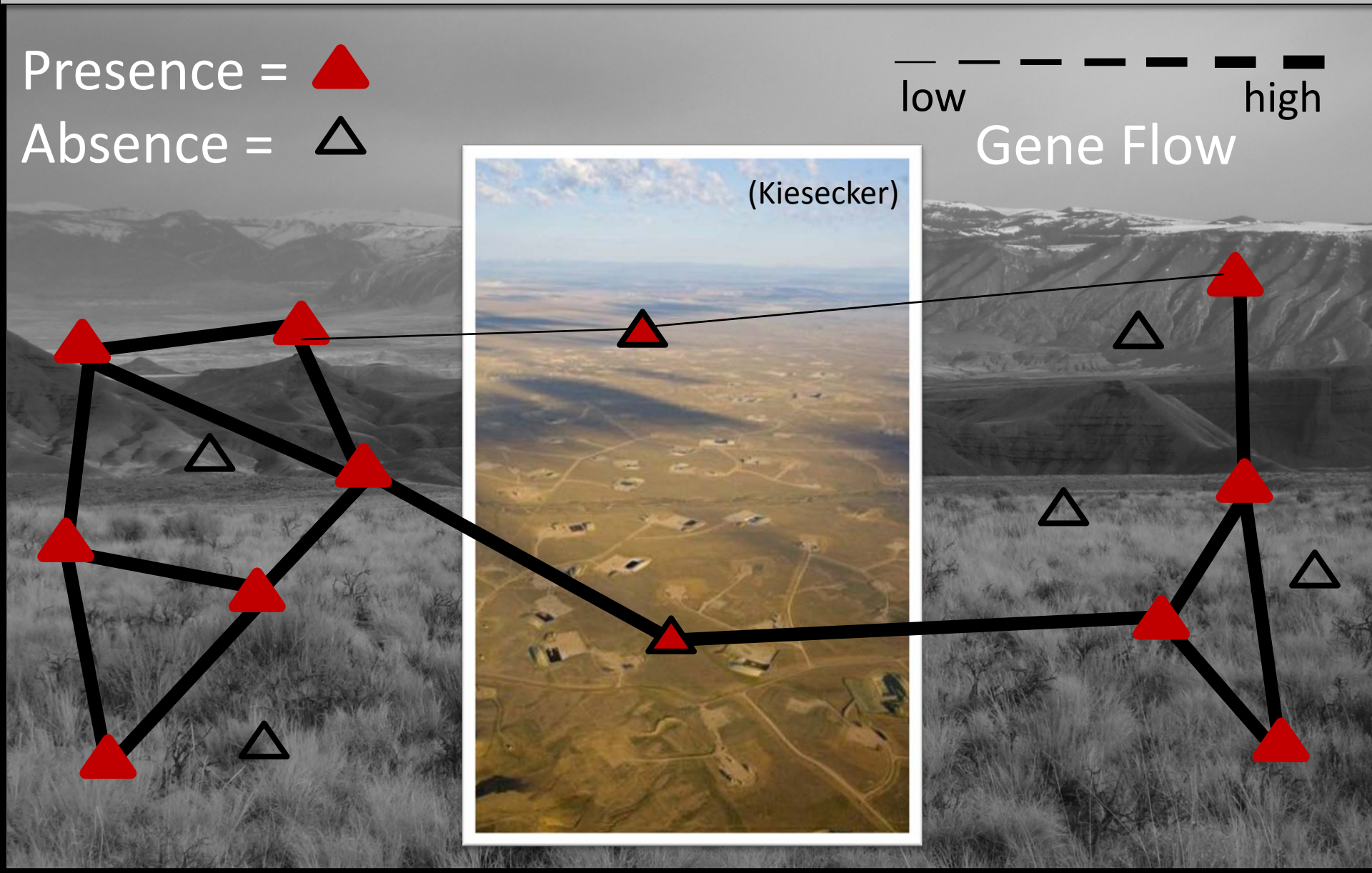


Research Impact



Sagebrush restoration

Research Impact

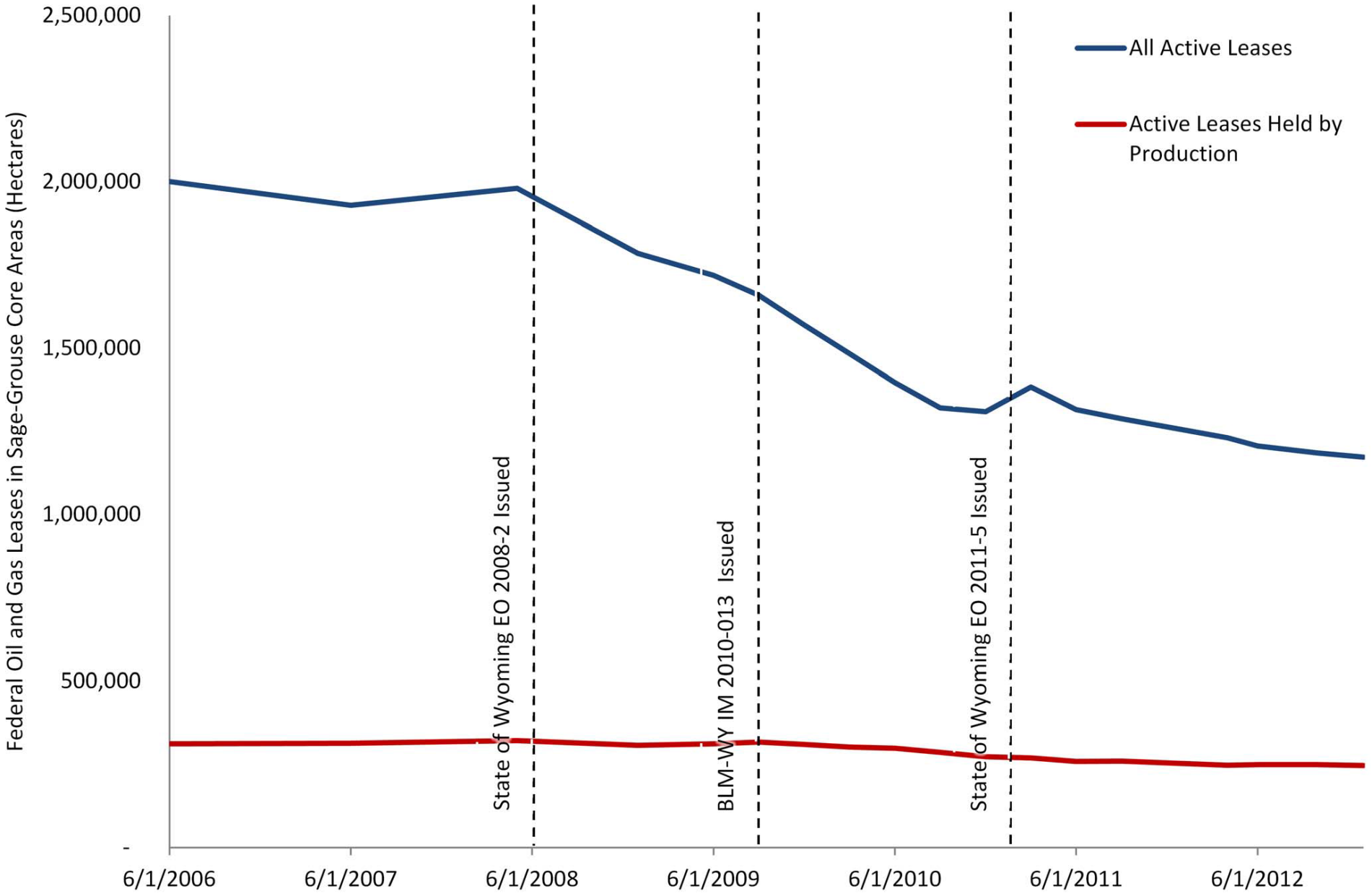


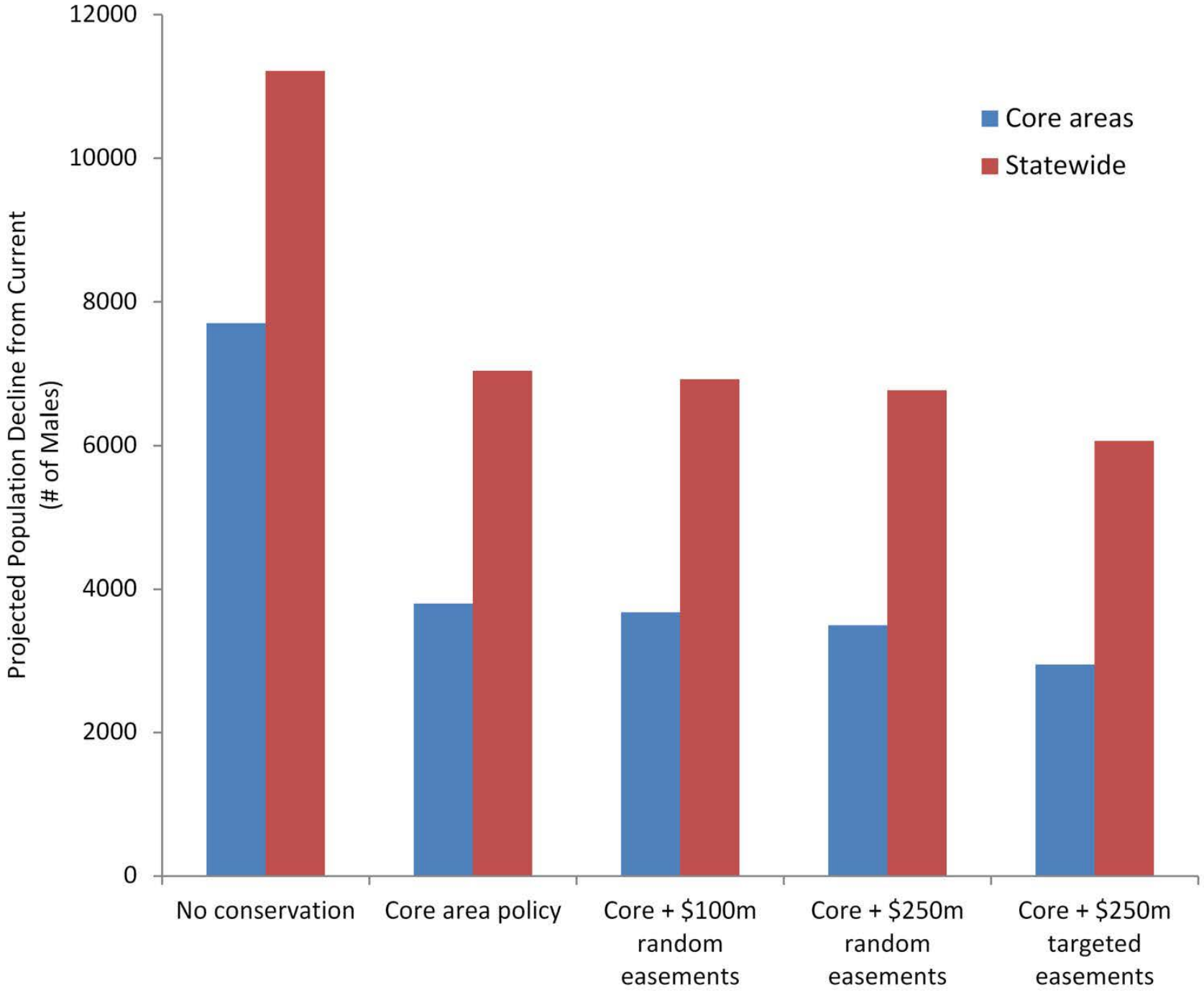
Acknowledgements

Funding: Northeast Wyoming Sage-grouse Working Group, Margaret and Sam Kelly Ornithology Research Fund, Society for Integrative and Comparative Biology GIAR, Wyoming NASA Space Grant, Laramie Audubon Society, National Science Foundation – UW Science Posse, Restoration Scholarship

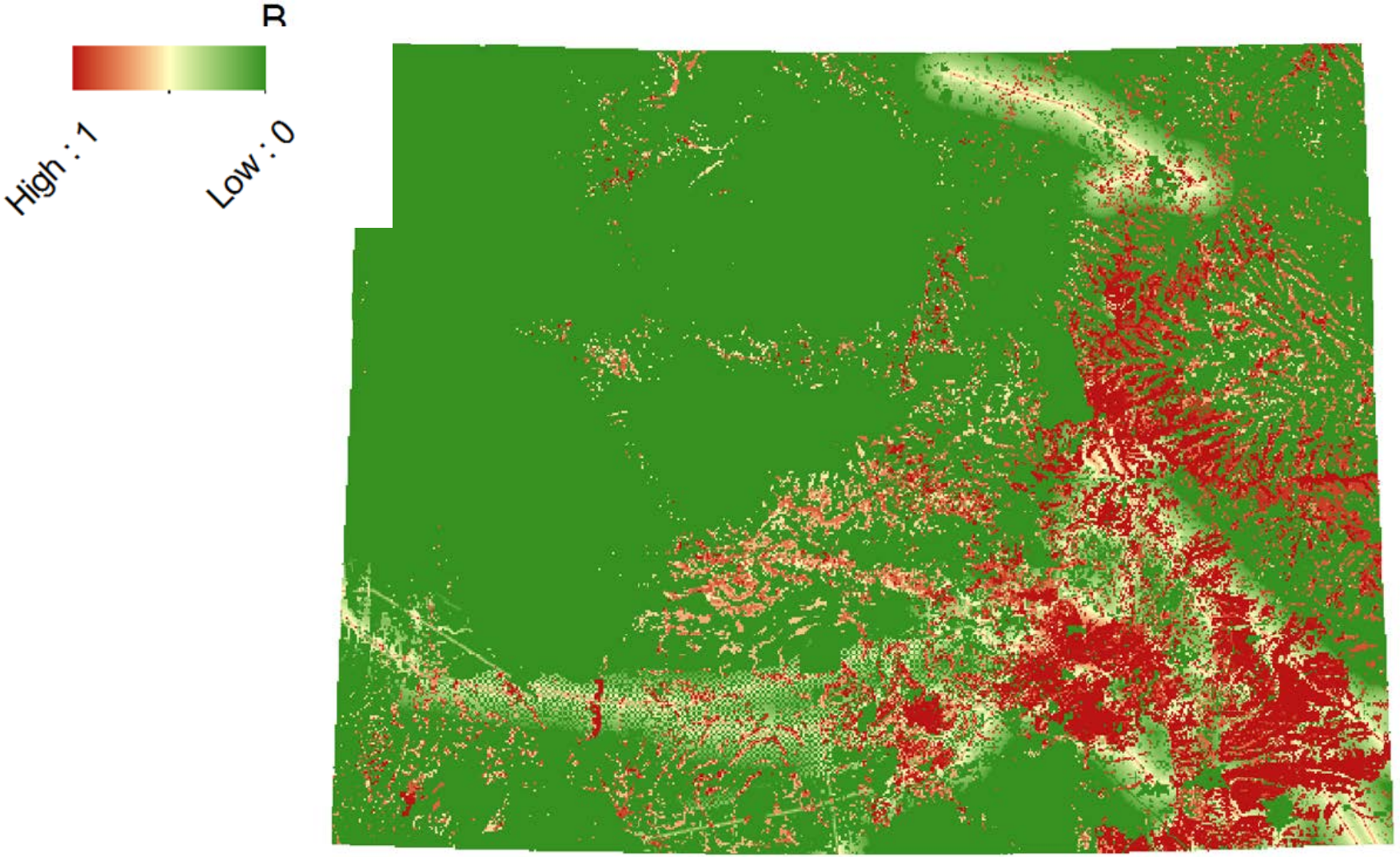
Acknowledgements: Ph.D. Committee: Drs. Jeff Beck, Merav Ben-David, Pete Stahl, Amy Pocewicz: Murphy – Hufford Lab group; USGS: Drs. Sarah Oyler-McCance, Cameron Aldridge, and Brad Fedy; Dr. Jeffrey Evans; Dr. Shannon Albeke; Aaron Pratt; Northeast Wyoming Sage-grouse Working Group; BLM: Bill Ostheimer, Destin Harrell, Tim Stephens, Chuck Swick; Wyoming Game and Fish Department: Tom Easterly and Dan Thiele; NRCS: Allison McKenzie, Kassie Bales, Andrew Cassiday; Lake DeSmet Conservation District: Nikki Lohse; Field Technicians: John Chestnut, Salina Wunderle, Katherine Zarn, Kevin Ryer; MANY Landowners

Questions?


2,500,000
2,000,000
1,500,000
1,000,000
500,000
-
Federal Oil and Gas Leases in Sage-Grouse Core Areas (Hectares)
All Active Leases
Active Leases Held by Production
State of Wyoming EO 2008-2 Issued
BLM-WY IM 2010-013 Issued
State of Wyoming EO 2011-5 Issued
6/1/2006
6/1/2007
6/1/2008
6/1/2009
6/1/2010
6/1/2011
6/1/2012

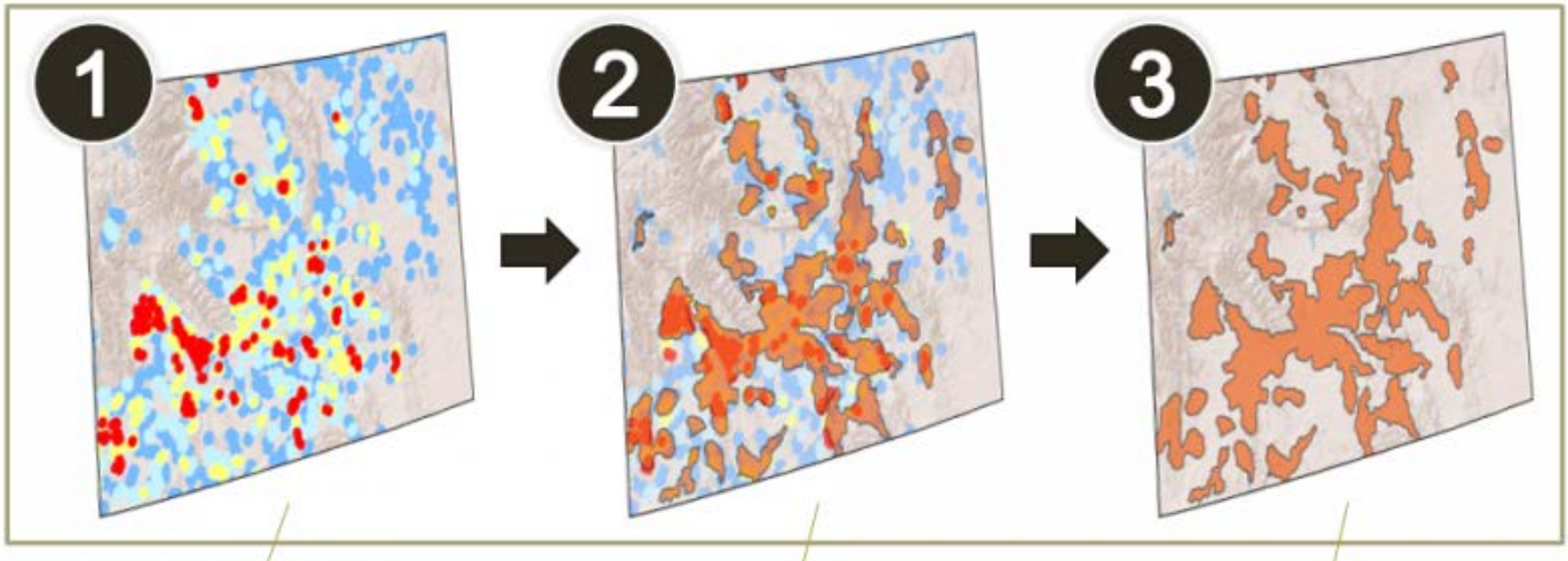

12000
10000
8000
6000
4000
2000
0
Projected Population Decline from Current (# of Males)
Core areas
Statewide
No conservation
Core area policy
Core + $100m random easements
Core + $250m random easements
Core + $250m targeted easements

Wind Development



The creation of Core Areas

Note that while this diagram is hopefully useful, it is a severe oversimplification

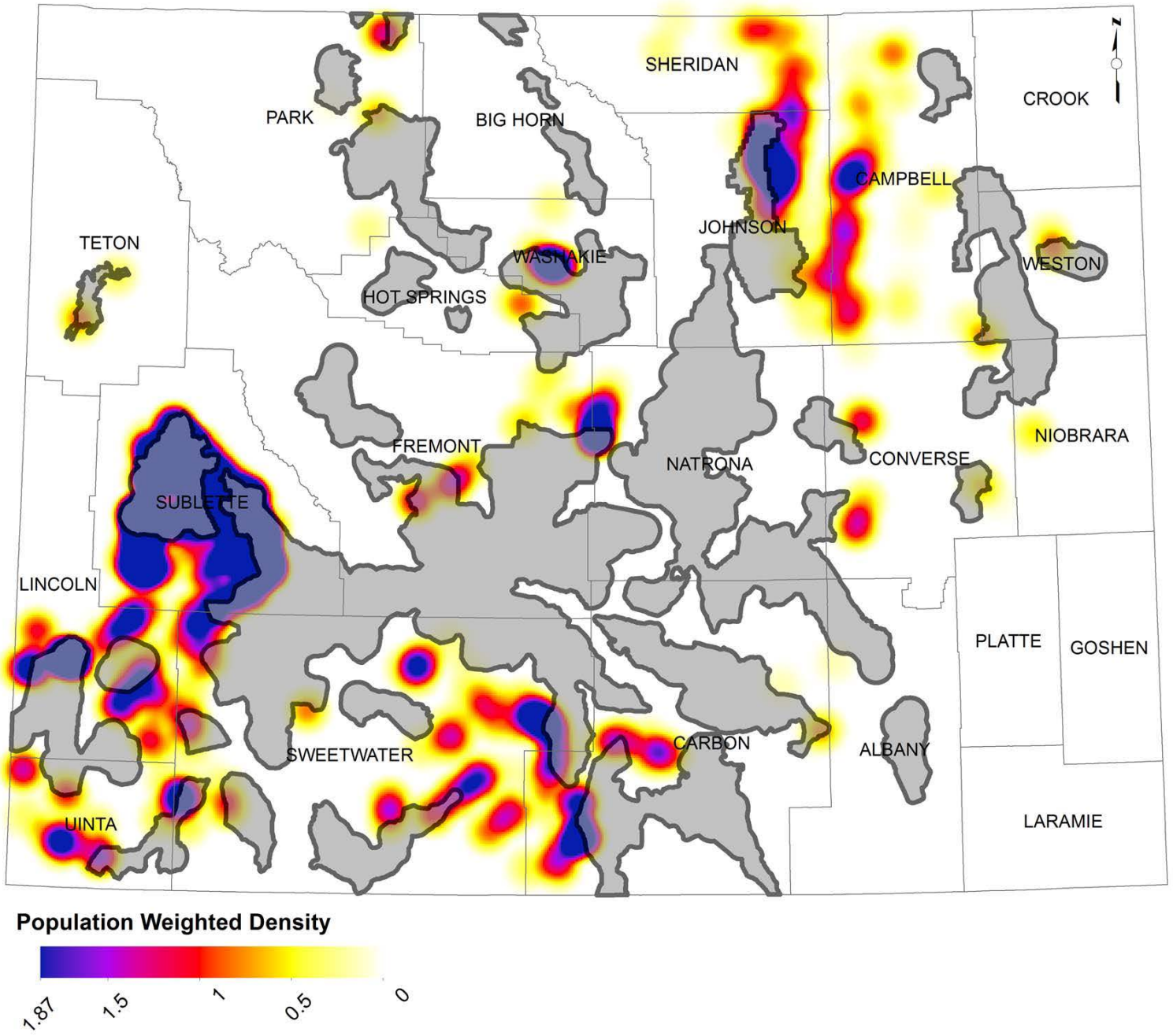


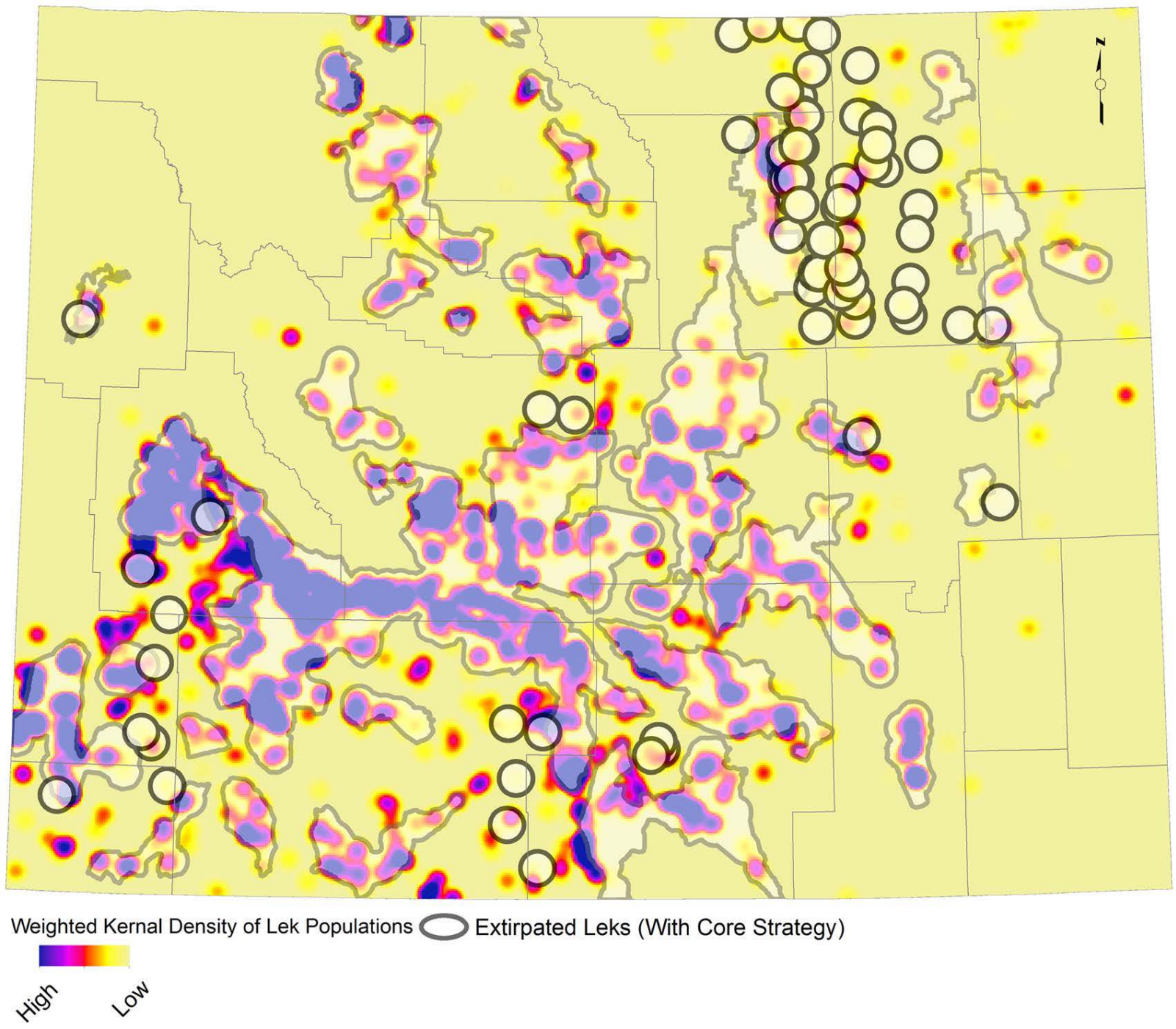
Identify leks of highest use
(buffered to contain likely nesting habitat)

Delineate Core Areas
(taking into account species biology, current land uses, and politics)

Wyoming Greater Sage-grouse Core Areas

Wyoming Cooperative Fish and Wildlife Unit – Jason Carlisle and Anna Chalfoun


SHERIDAN
CROOK
PARK
BIG HORN
CAMPBELL
JOHNSON
TETON
WASHAKIE
WESTON
HOT SPRINGS
FREMONT
NATRONA
CONVERSE
NIOBRARA
SUBLETTE
LINCOLN
PLATTE
GOSHEN
CARBON
ALBANY
SWEETWATER
UINTA
LARAMIE
Population Weighted Density
1.87
1.5
1
0.5
0


N
Weighted Kernal Density of Lek Populations
Extirpated Leks (With Core Strategy)
High
Low

Residential Development

WY Greater Sage Grouse regulations

- Buffers
- Noise regulations
- Surface regulations
- Habitat treatments/ enhancements

Northeast Local Working Group

Big Horn Local Working Group

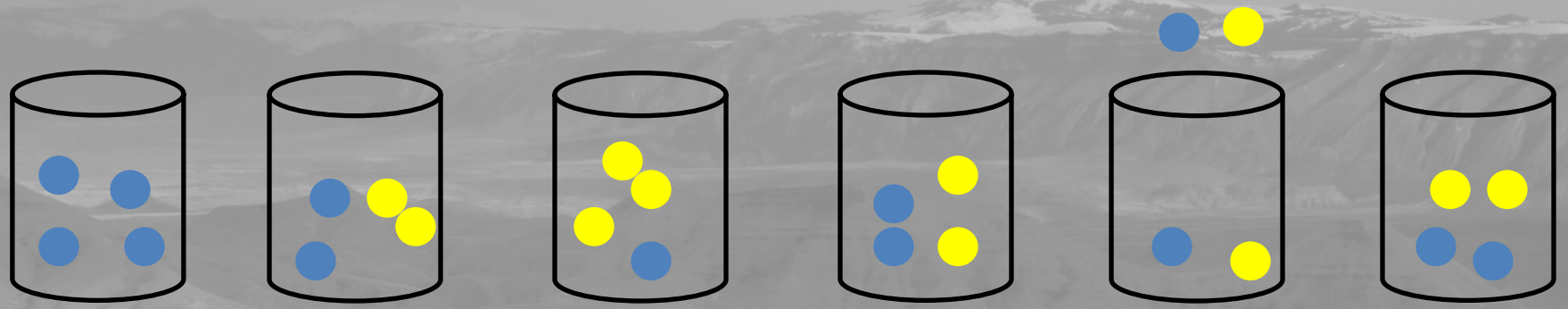
Gene Flow Activity

Jar 1 Jar 2 Jar 3 Jar 4 Jar 5 Jar 6

1. Each person picks a jar, any jar

Gene Flow Activity

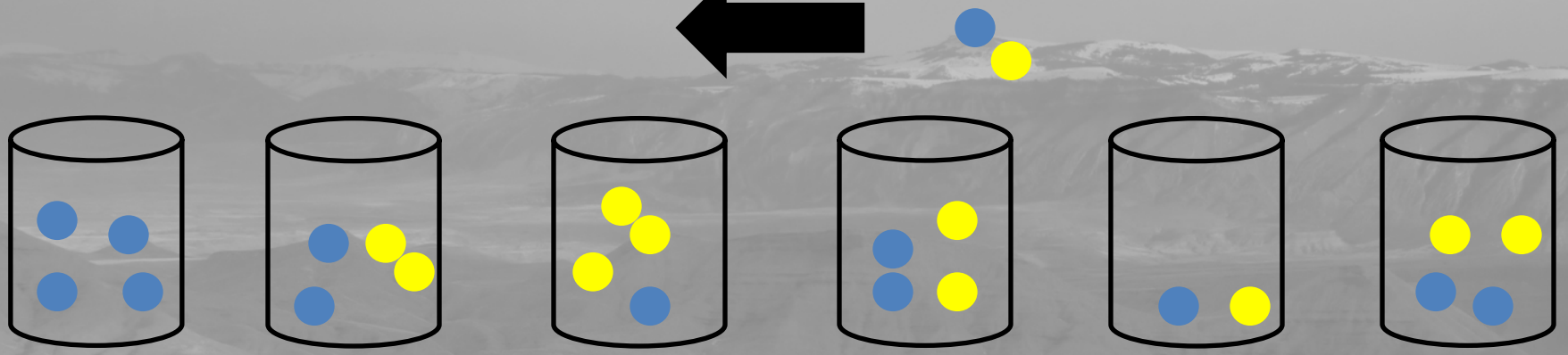
Jar 1 Jar 2 Jar 3 Jar 4 Jar 5 Jar 6



1. Each person picks a jar, any jar
2. Without looking pick 2 beads from the jar

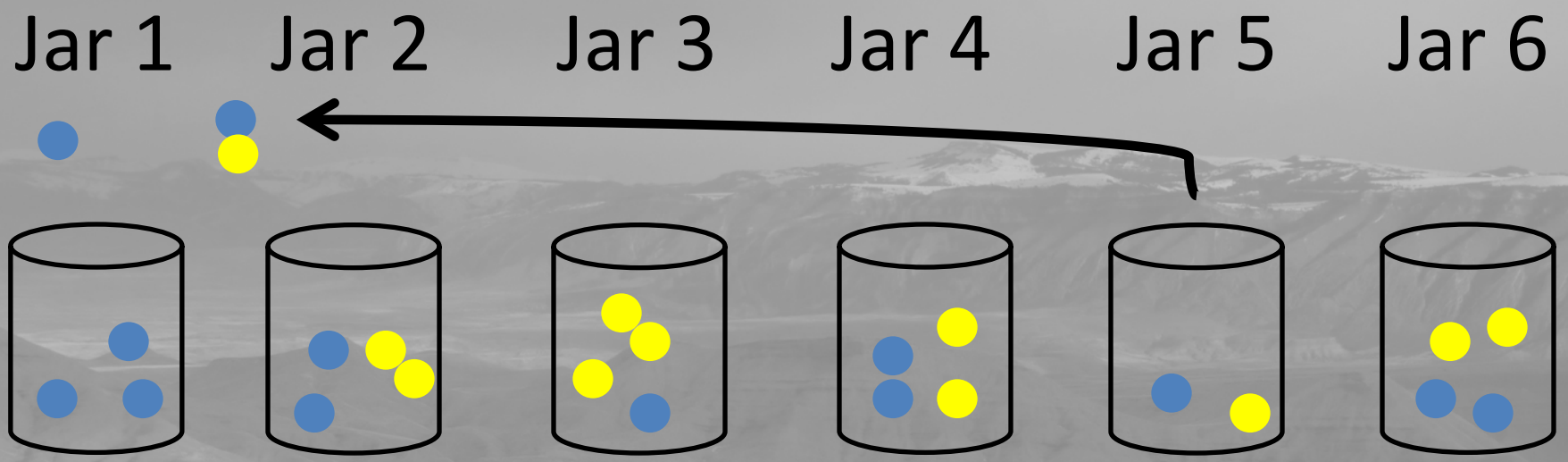
Gene Flow Activity

Jar 1 Jar 2 Jar 3 Jar 4 Jar 5 Jar 6



1. Each person picks a jar, any jar
2. Without looking pick 2 beads from the jar
3. Move to another jar

Gene Flow Activity



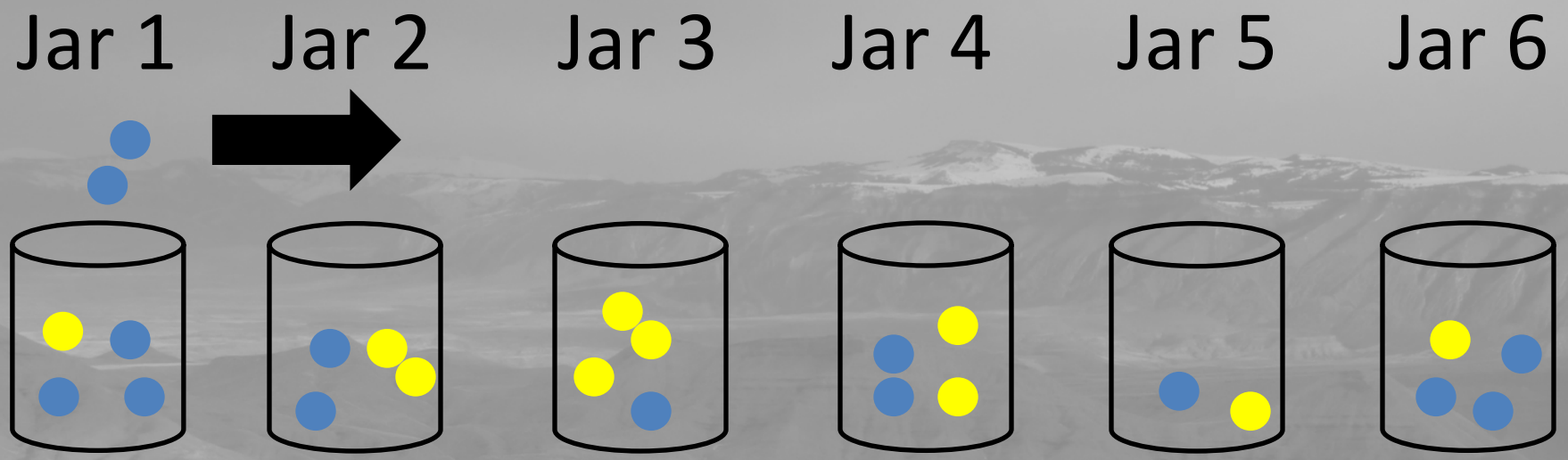
1. Each person picks a jar, any jar
2. Without looking pick 2 beads from the jar
3. Move to another jar
4. Without looking pick up 1 bead with one hand

Gene Flow Activity

Jar 1 Jar 2 Jar 3 Jar 4 Jar 5 Jar 6

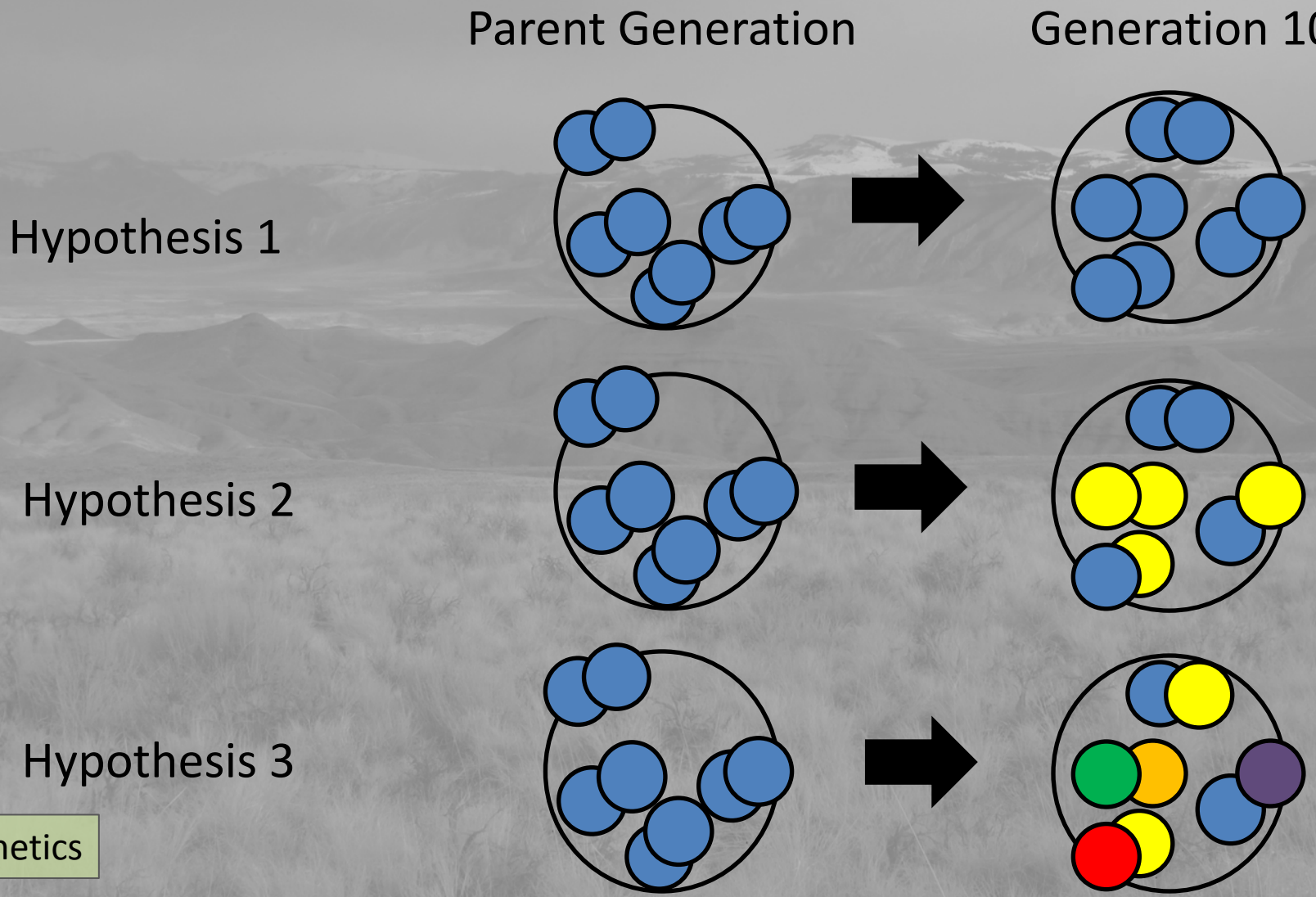
1. Each person picks a jar, any jar
2. Without looking pick 2 beads from the jar
3. Move to another jar
4. Without looking pick up 1 bead with one hand
5. Without looking drop 1 bead from your other hand (original beads)

Gene Flow Activity



1. Each person picks a jar, any jar
2. Without looking pick 2 beads from the jar
3. Move to another jar
4. Without looking pick up 1 bead with one hand
5. Without looking drop 1 bead from your other hand (original beads)
6. Go to a different jar and repeat number 4 and 5

Activity: What will happen in 10 generations?



Rules:

1. When switching out beads pick a bead first then drop a random bead.

2. Can not go to the same jar 2 times in a row, but you can go to individual jars multiple times. You do not have to go to every jar.

3. You will start with a parent generation and then switch beads until you get to your _th generation.

4. Do this as fast as possible.

5. If there are a lot of people at one jar you can move to another if you think it will take less time.