

Genetic data suggest limited bumble bee dispersal into Canadian Rockies from foothills

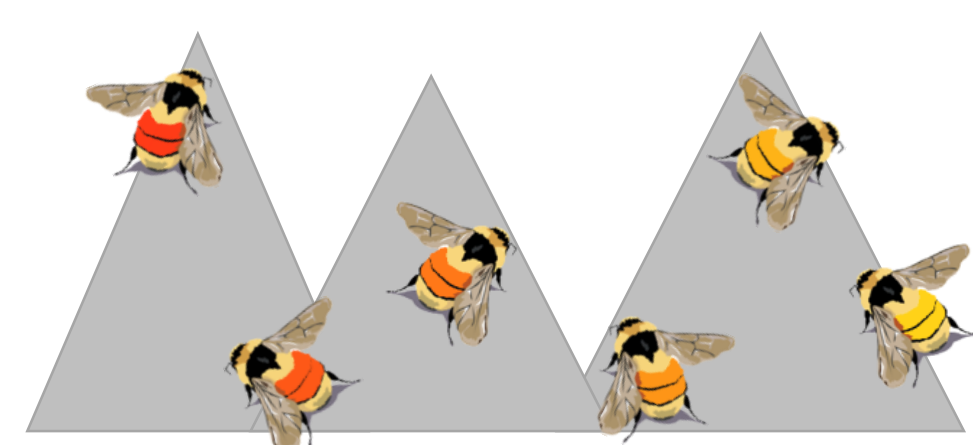
Introduction:

Predicted and observed range shifts associated with climate change, including elevation gradients

- ▶ Are bumble bee populations going to be able to track these climatic changes?
- ▶ What happens to existing high elevation populations if new populations are successful at colonizing upslope?

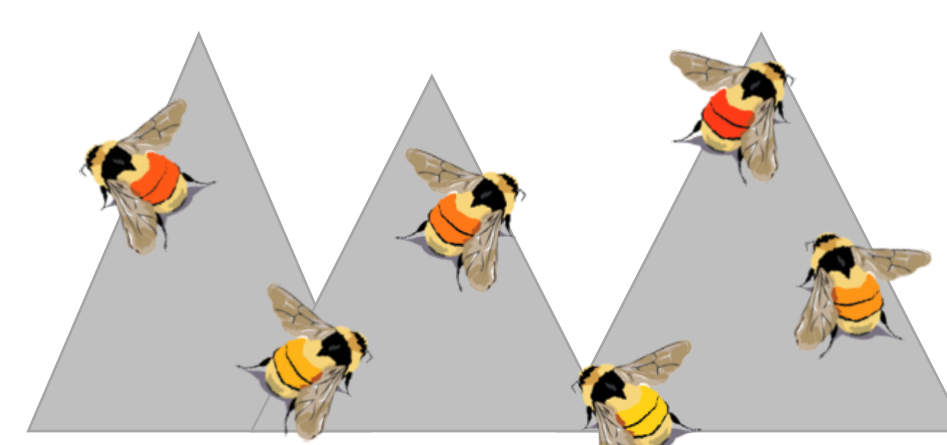
Hypotheses:

Isolation By Distance (IBD)



Use both high and low elevation sites due to close geographic proximity

Isolation By Elevation (IBE)

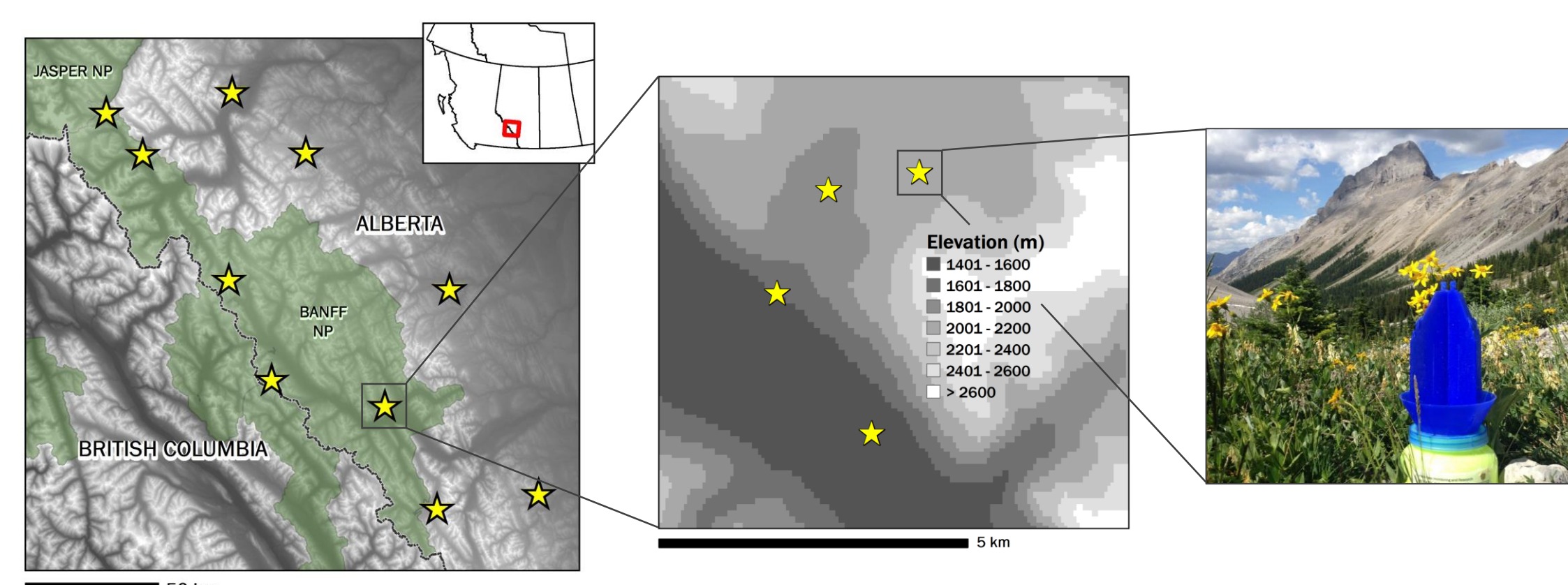


Specialize in either high or low elevation habitats

Methods:

- 1) Sample bumble bees at sites across elevation gradients

- ▶ Minimize correlations between geographic distance and difference in elevation



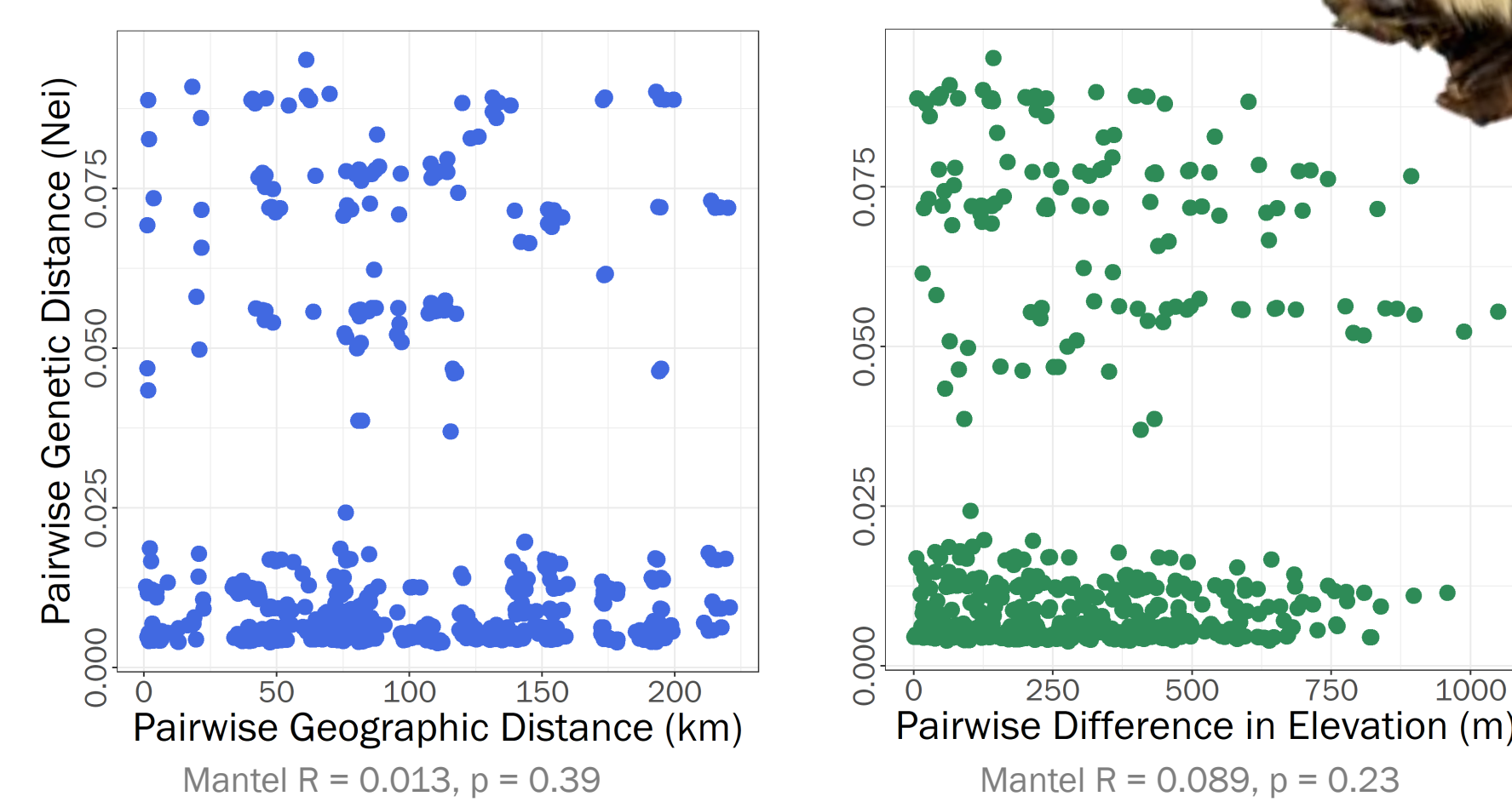
- 2) Extract DNA and prepare ddRADseq library

- 3) 150 bp Paired-End sequencing

Results:

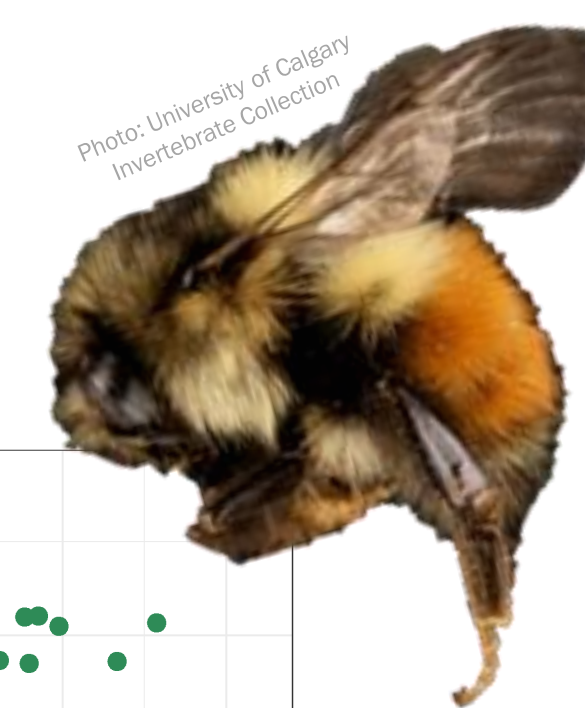
Bombus melanopygus

- ▶ Generalist species



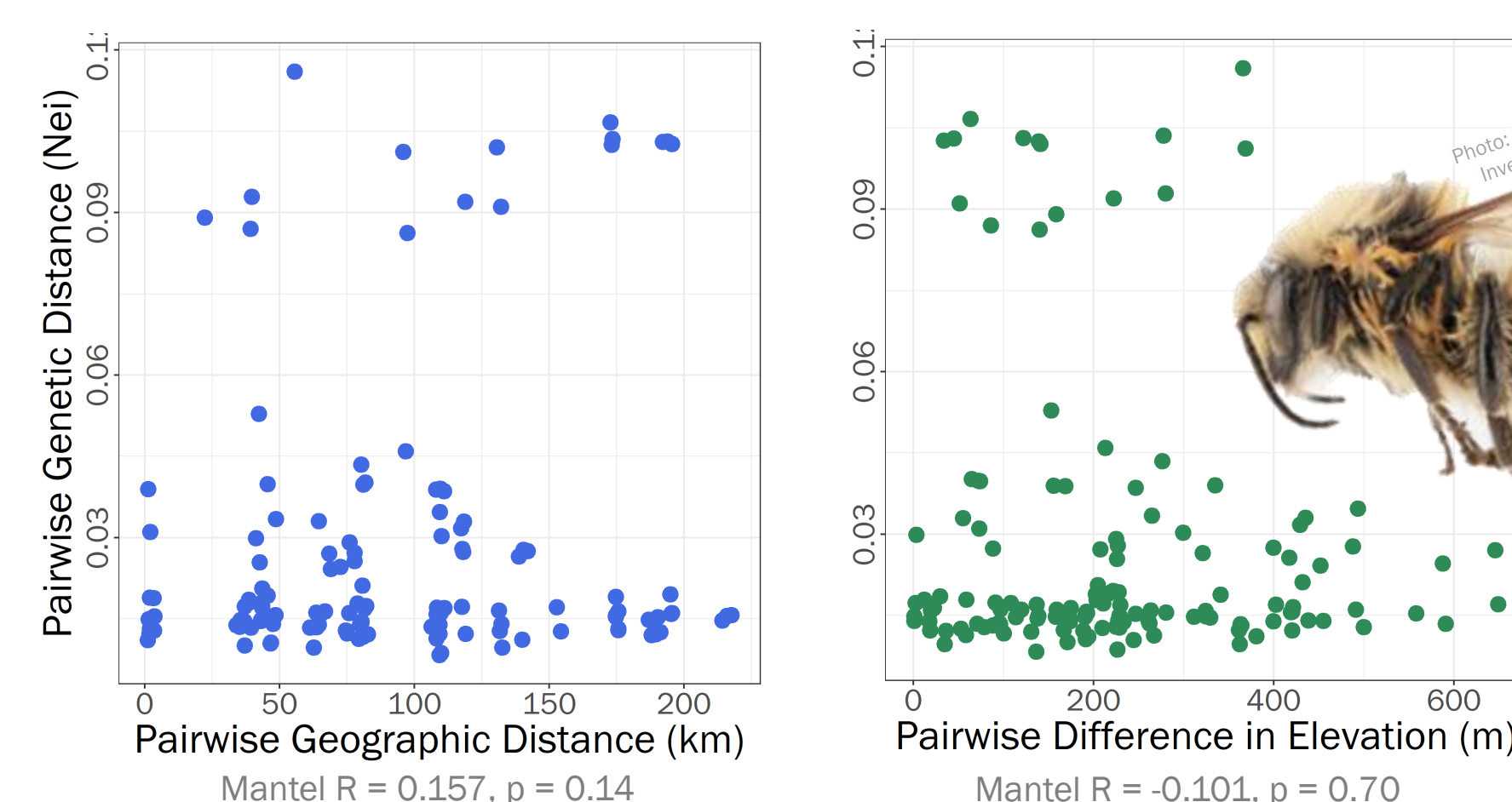
	Estimate	Std. Error	t value	p value
Intercept	0.017	0.003	6.308	<0.01
Elevation	1.1 e-05	5.3 e-06	2.128	0.034
Geographic Distance	7.7 e-09	2.0 e-08	0.392	0.695

lm(Genetic Distance ~ Elevation Difference + Geographic Distance)
Residual standard error: 0.03 on 558 DF
Multiple R²: 0.008, Adjusted R²: 0.005
F-statistic: 2.3 on 2 and 558 DF, p-value: 0.1



Bombus sylvicola

- ▶ Alpine specialist

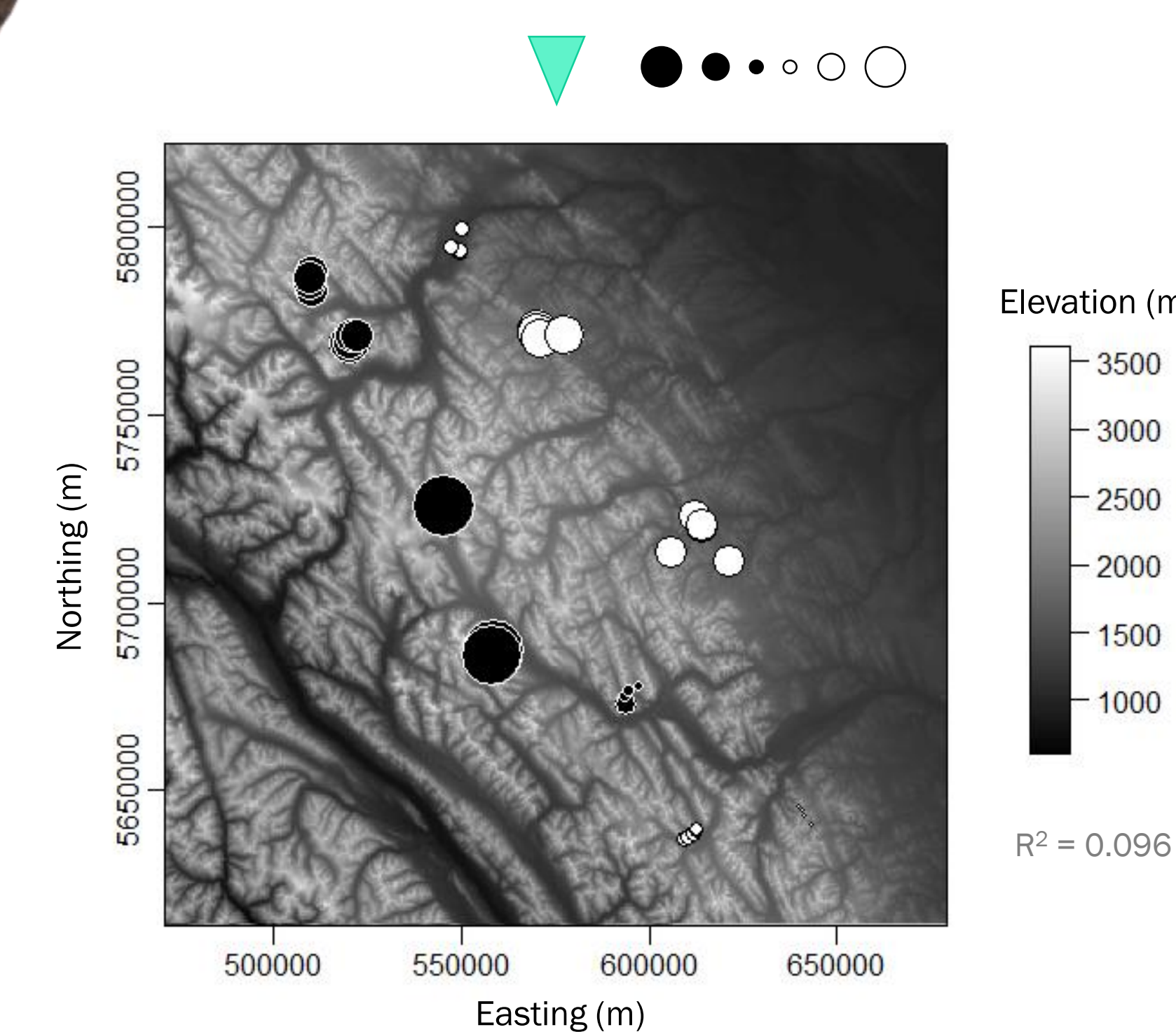


	Estimate	Std. Error	t value	p value
Intercept	0.025	0.005	4.632	<0.01
Elevation	7.2 e-08	3.9 e-08	1.841	0.068
Geographic Distance	-1.8 e-05	1.5 e-05	-1.189	0.236

lm(Genetic Distance ~ Elevation Difference + Geographic Distance)
Residual standard error: 0.026 on 113 DF
Multiple R²: 0.0263, Adjusted R²: 0.0203
F-statistic: 2.398 on 2 and 113 DF, p-value: 0.09

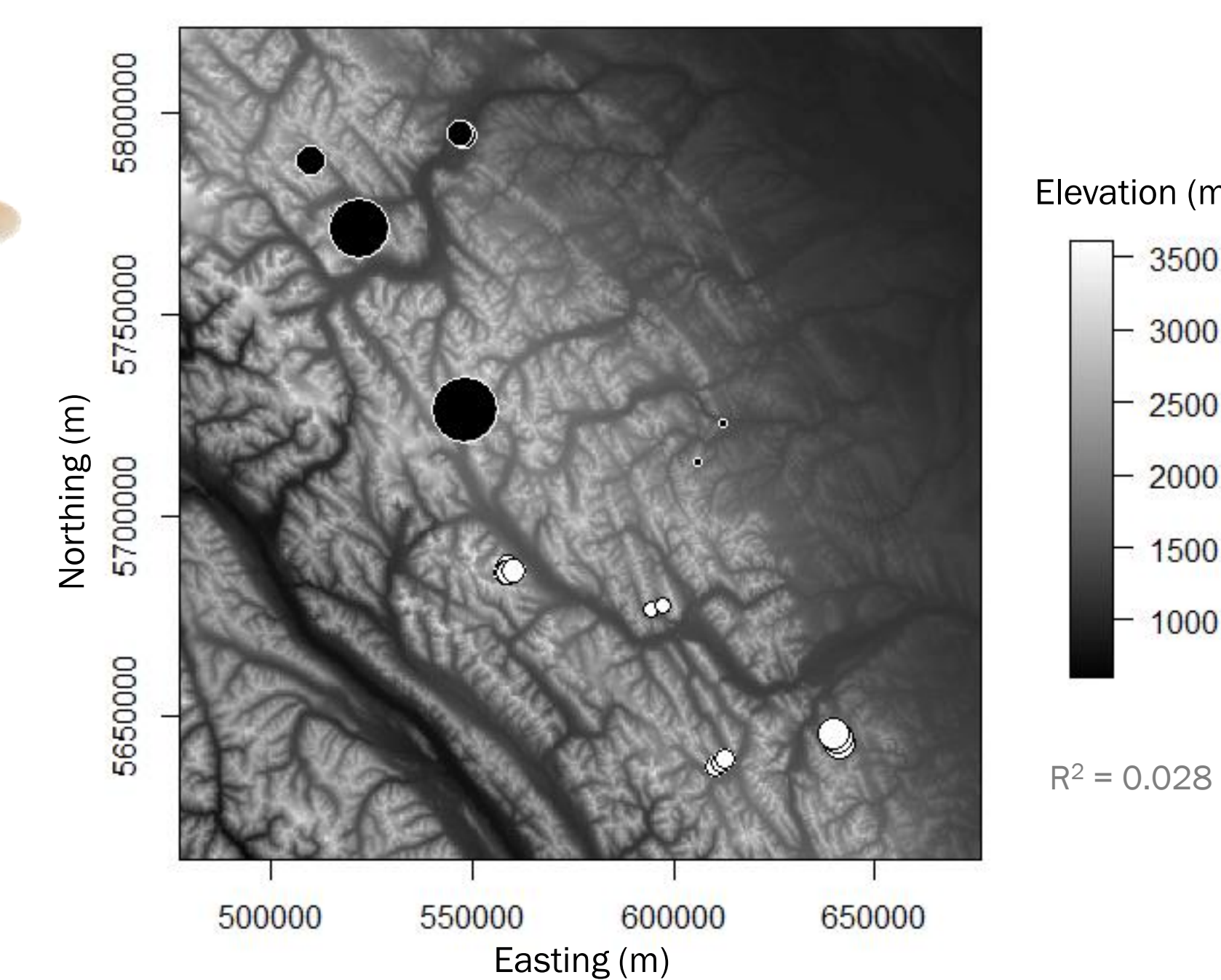


MEMGENE results



Elevation (m)
3500
3000
2500
2000
1500
1000

R² = 0.096

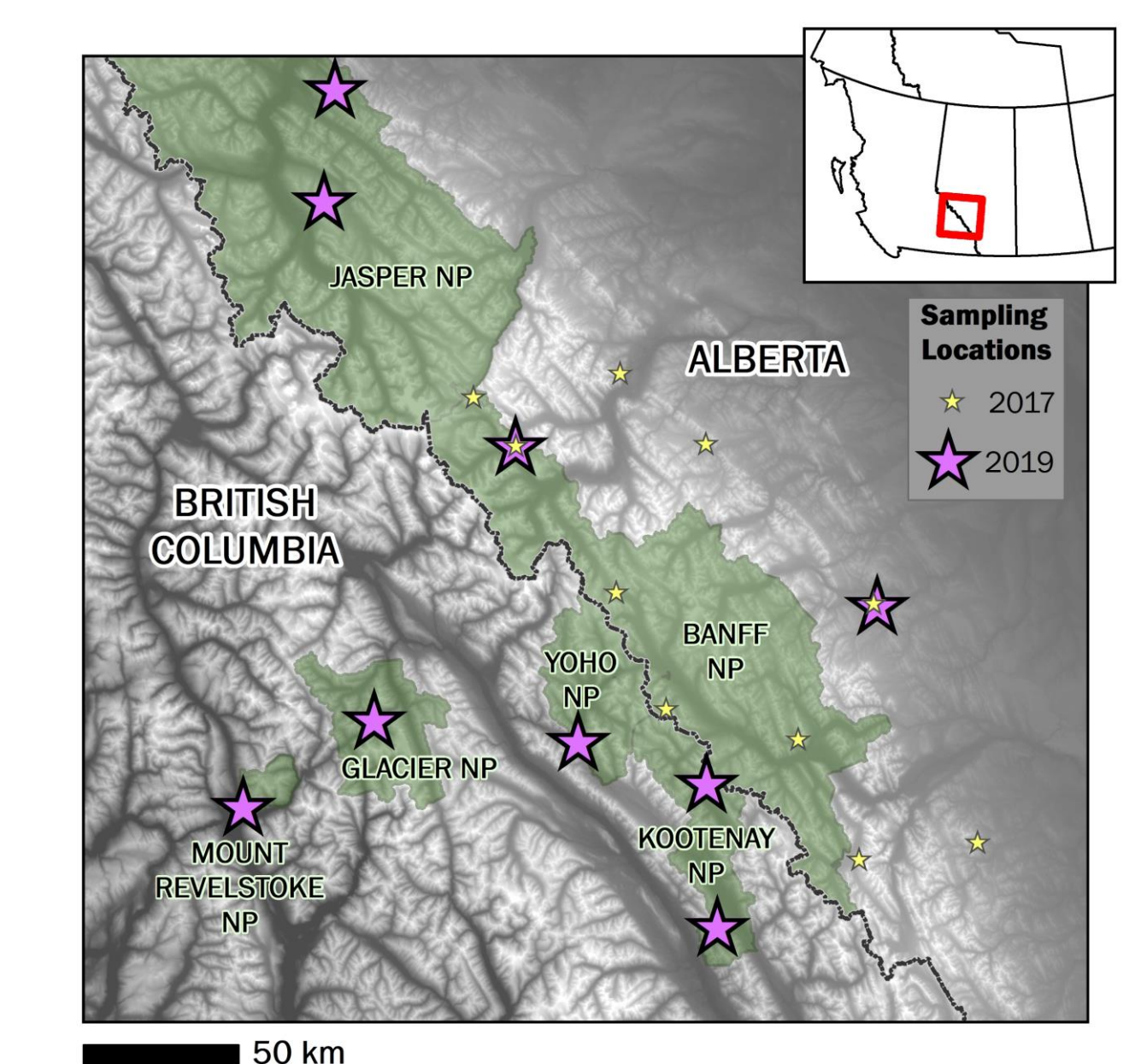


Elevation (m)
3500
3000
2500
2000
1500
1000

R² = 0.028

Next Steps:

Process samples from additional sampling into mountain range



Design probes to target differences in expressed regions of genome

- ▶ Using expressed exome capture sequencing (EecSeq)

(Puritz and Lotterhos 2018)

