

Landscape Epigenetics



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Quest for Adaptive Variation

Expression Profiles

F_{ST} Outliers

microRNA

McDonald–Kreitman test

Selective Sweeps

Allele Frequency Correlations



A close-up photograph of a man with a full, reddish-brown beard and short, light-colored hair. He is wearing thin-framed glasses and a blue t-shirt. He is holding a clear glass filled with a golden-yellow liquid, likely beer, with a thick white head of foam. The background is dark and out of focus, showing what appears to be a bar or restaurant interior.

There doesn't
seem to be as
much adaptive
variation as I think
there should be.



Methylation,
Fitness without
inheritance.

Meh.

Reference Genome

ACTTCGACGCTACAATCGACGACTCATACATCATACTCGCTA
ACTTCGACGCTACAATCG
CTTCGACGCTACAATCGAC
GACGCTACAATCGACGAC
CGCTACAATCGACGACTCAT
CGCTACAATCGACGACTCATA
GCTACAATCGACGACTCATA
CTACAATCGACGACTCATA
ACAATCGACGACTCATACATC
CAATCGACGACTCATACATCATA
ATCGACGACTCATACATCATACTCGCTA

(Epi) and Genetic Similarity

		Reference Genetic Structure	
		Low	High
Reference Spatial Structure	High		
	Low		Locally Induced

(Epi) and Genetic Similarity

Reference
Genetic Structure

		Low	High
		Low	Long-Term Stable Inheritance
Reference Spatial Structure	High		
	Low		Locally Induced

(Epi) and Genetic Similarity

		Reference Genetic Structure	
		Low	High
Reference Spatial Structure	High	Some Inheritance	Long-Term Stable Inheritance
	Low	Other	Locally Induced

A close-up photograph of a man's face. He has light blue eyes, wears thin metal-rimmed glasses, and has a well-groomed, dark brown beard and mustache. He is looking upwards and slightly to his right with a contemplative expression. His hand is resting against his chin, supporting his head.

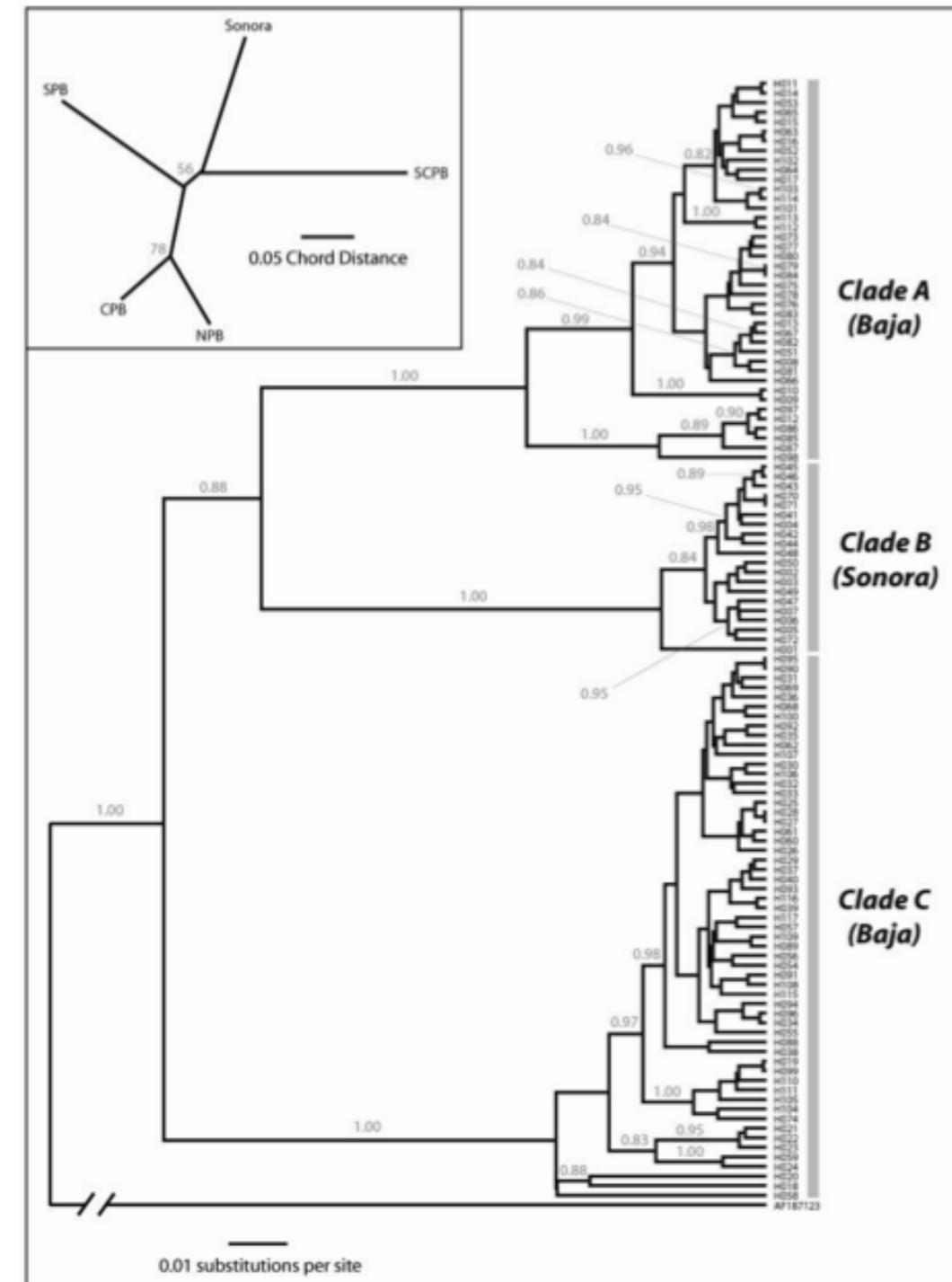
So I said to myself,

“Self, are all methylation
‘markers’ induced or do some
persist along **evolutionarily**
relevant timescales?

Arapthus attenuatus

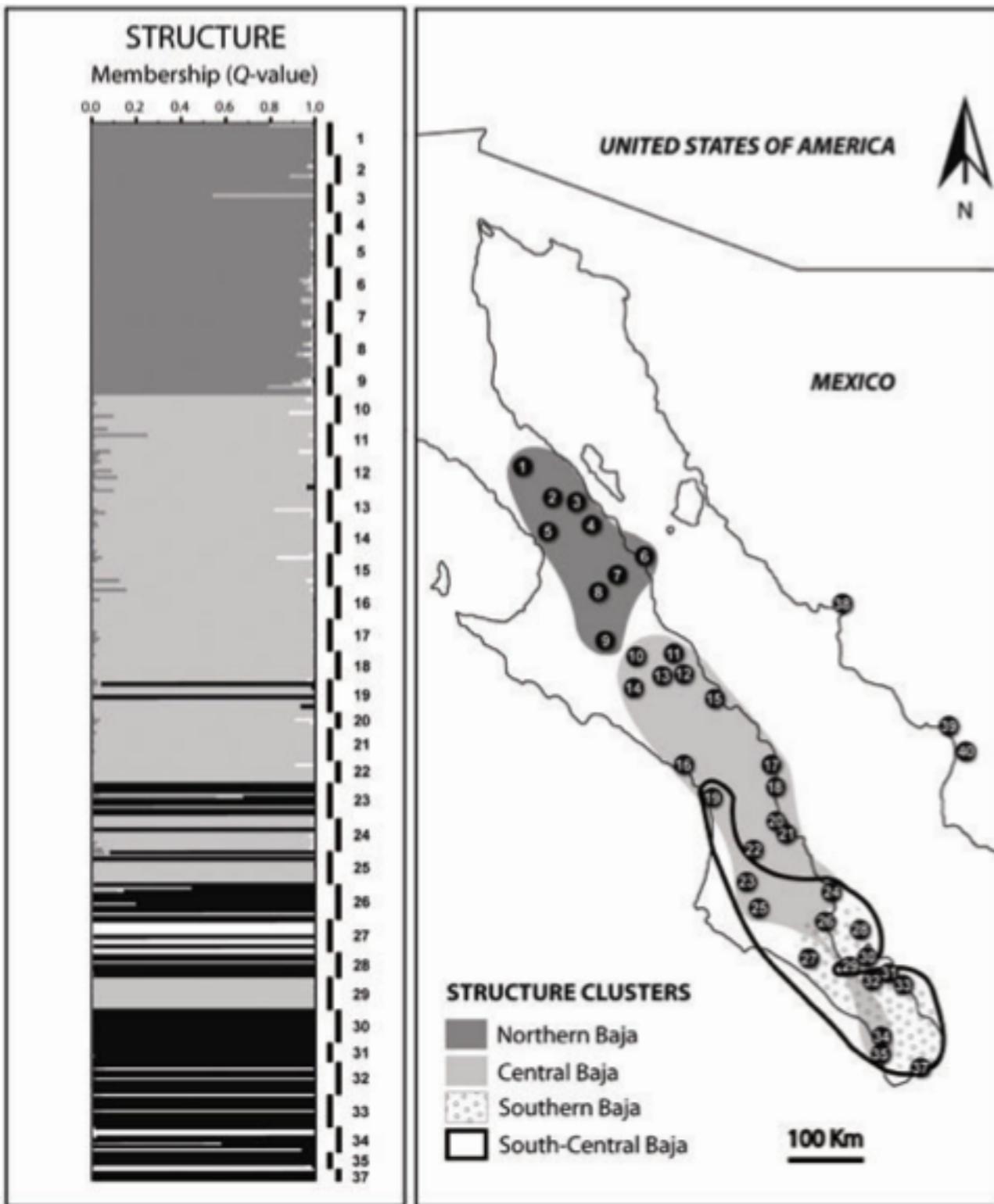
40 Populations
Baja California & Sonora

500 bp mtDNA
COI



8-12% Sequence Divergence
2 Groups in Baja California & Sonora

Nested Structure

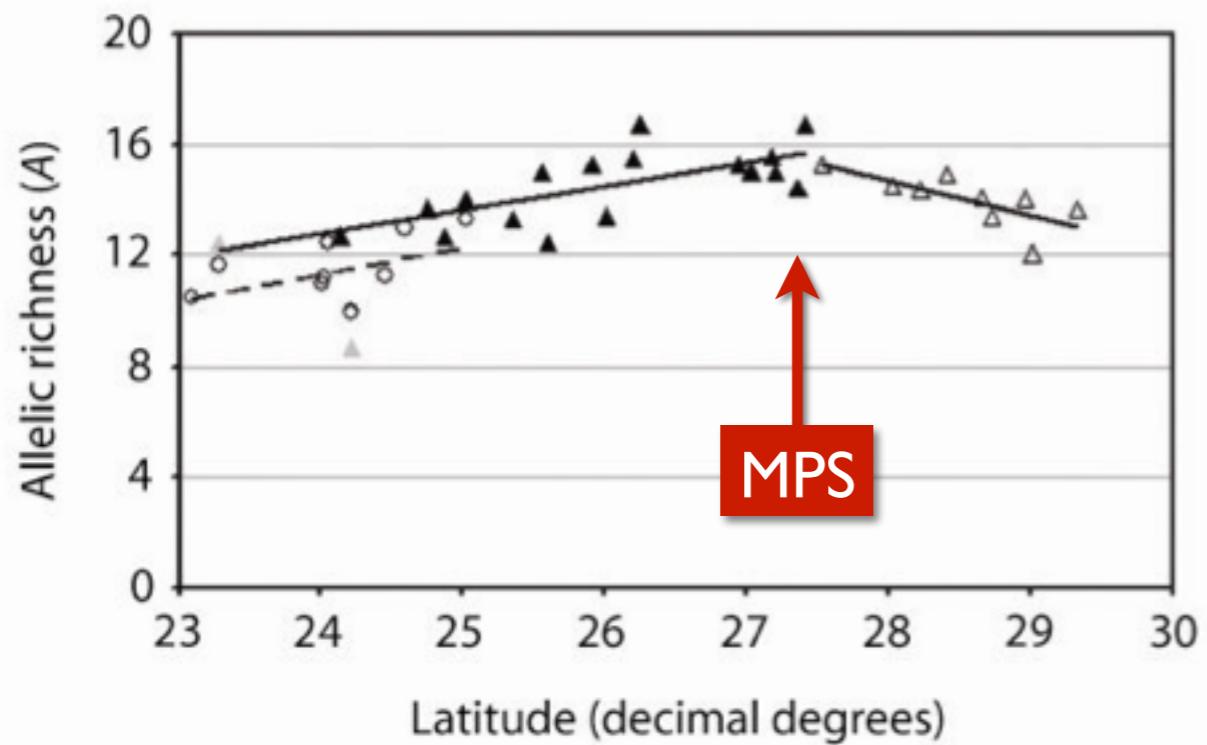


Nested Structure



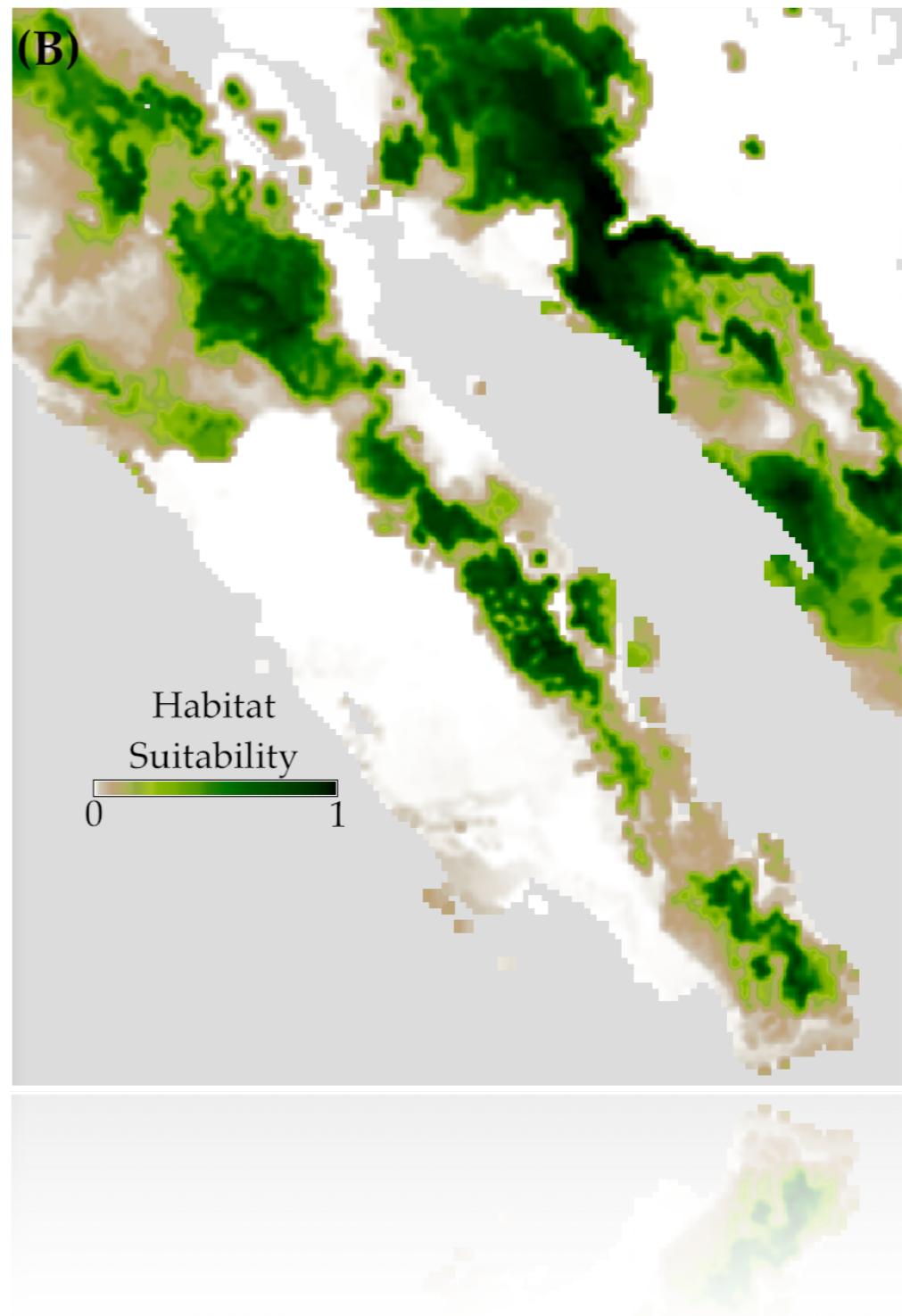
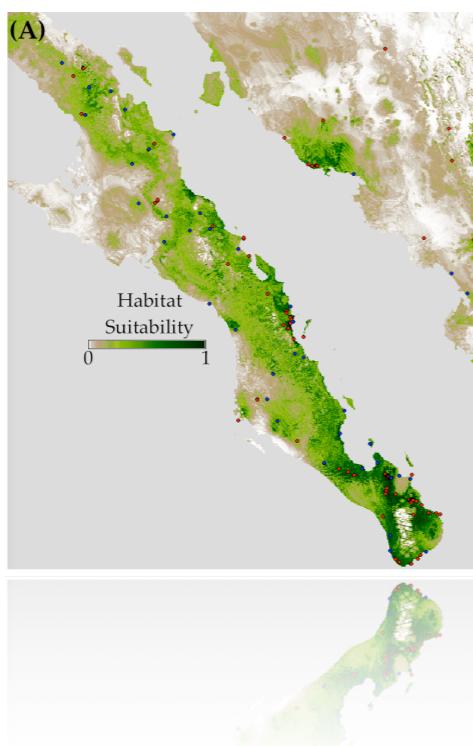
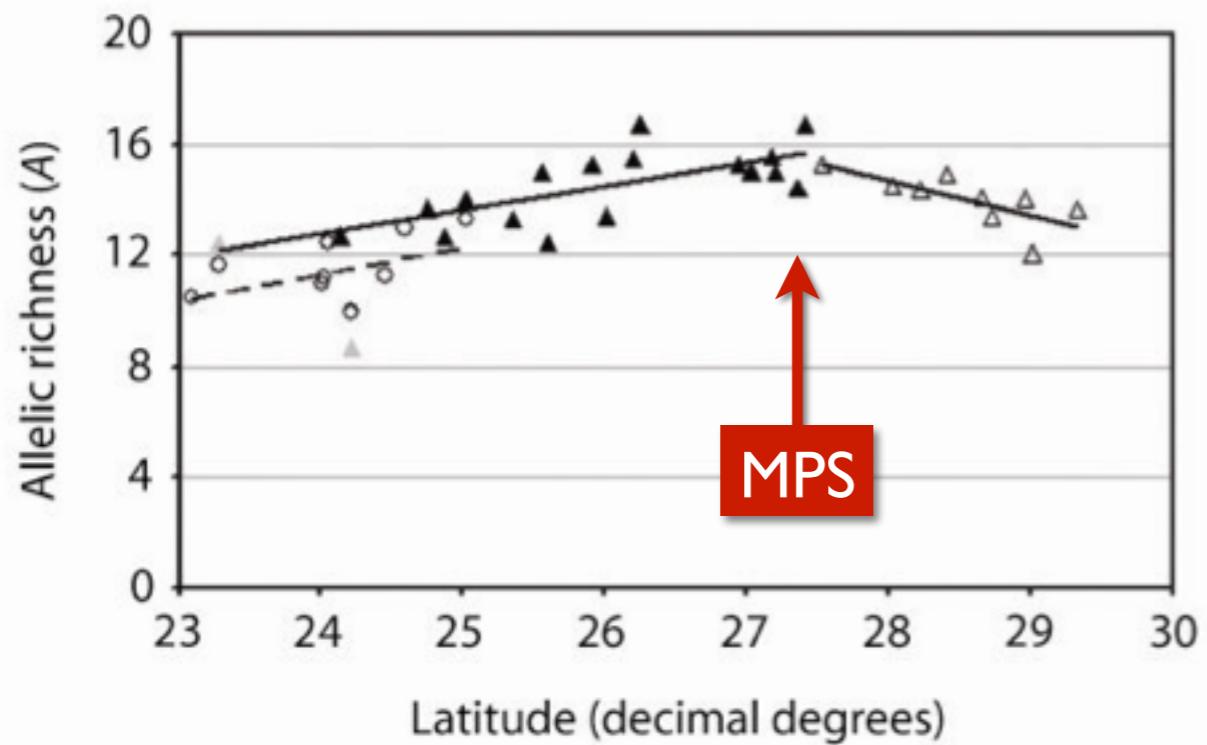
Frequency Gradients

Nuclear markers



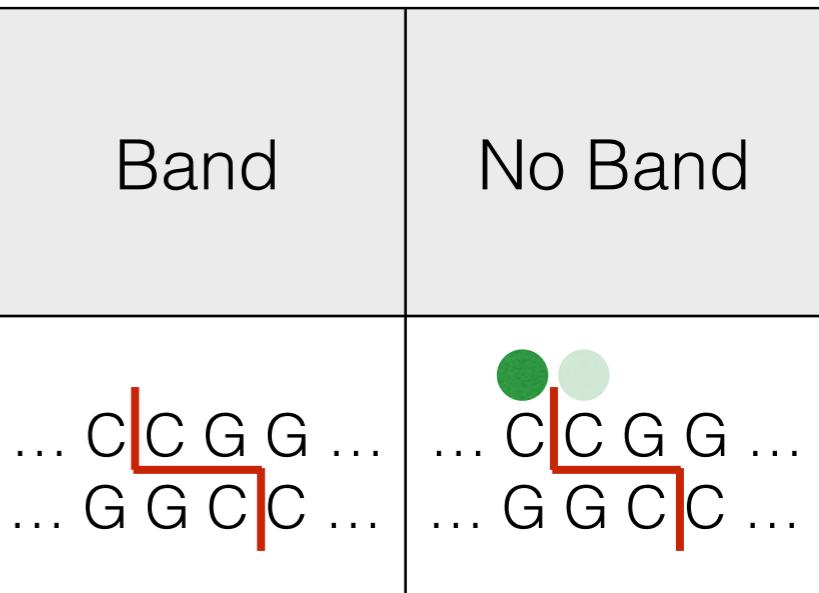
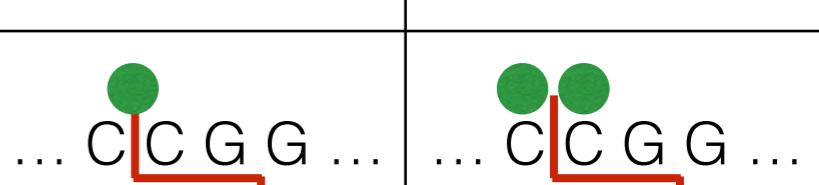
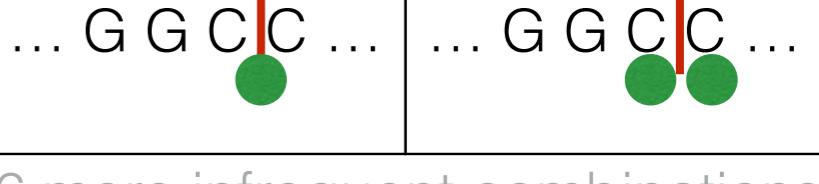
Frequency Gradients

Nuclear markers



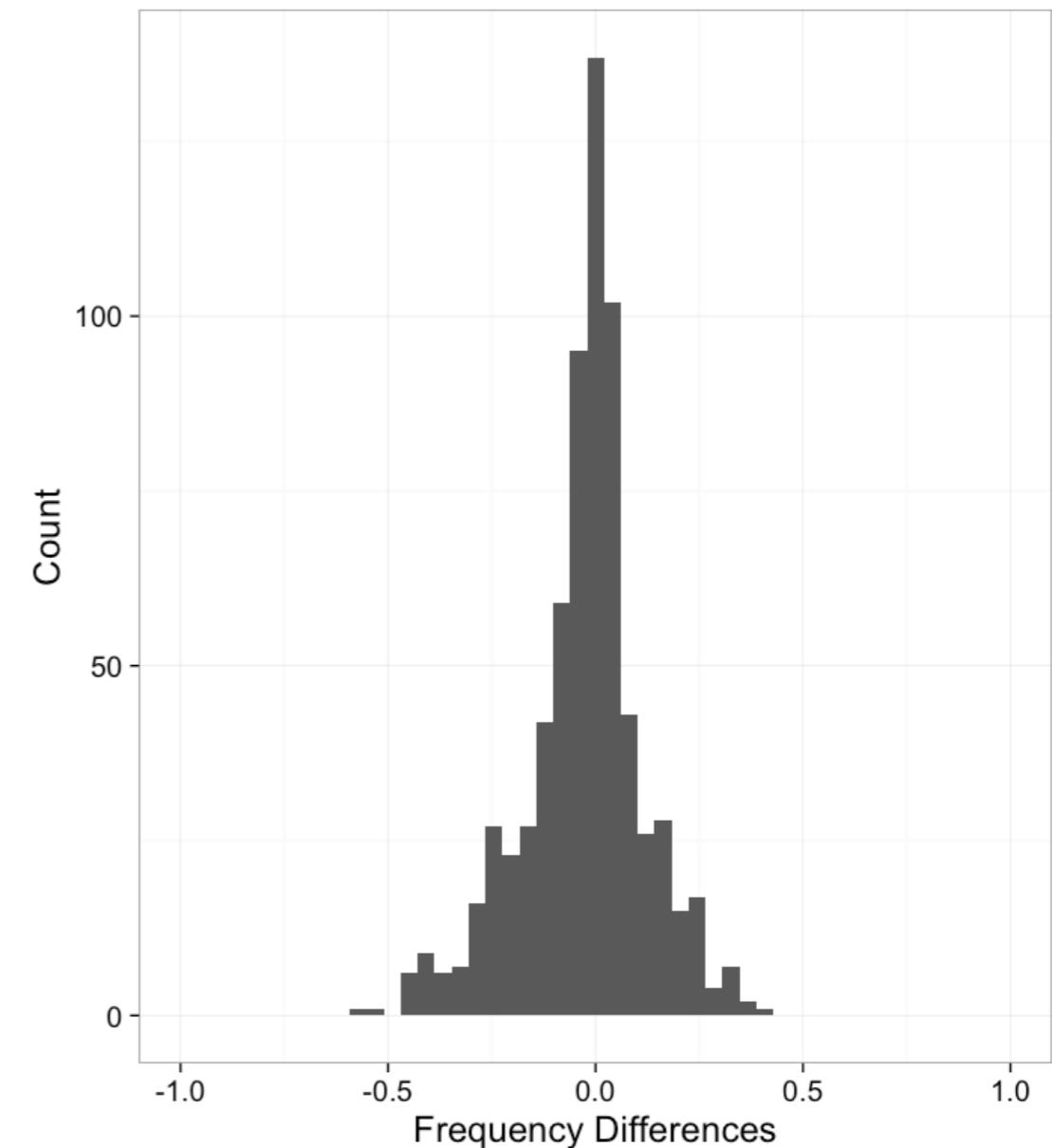
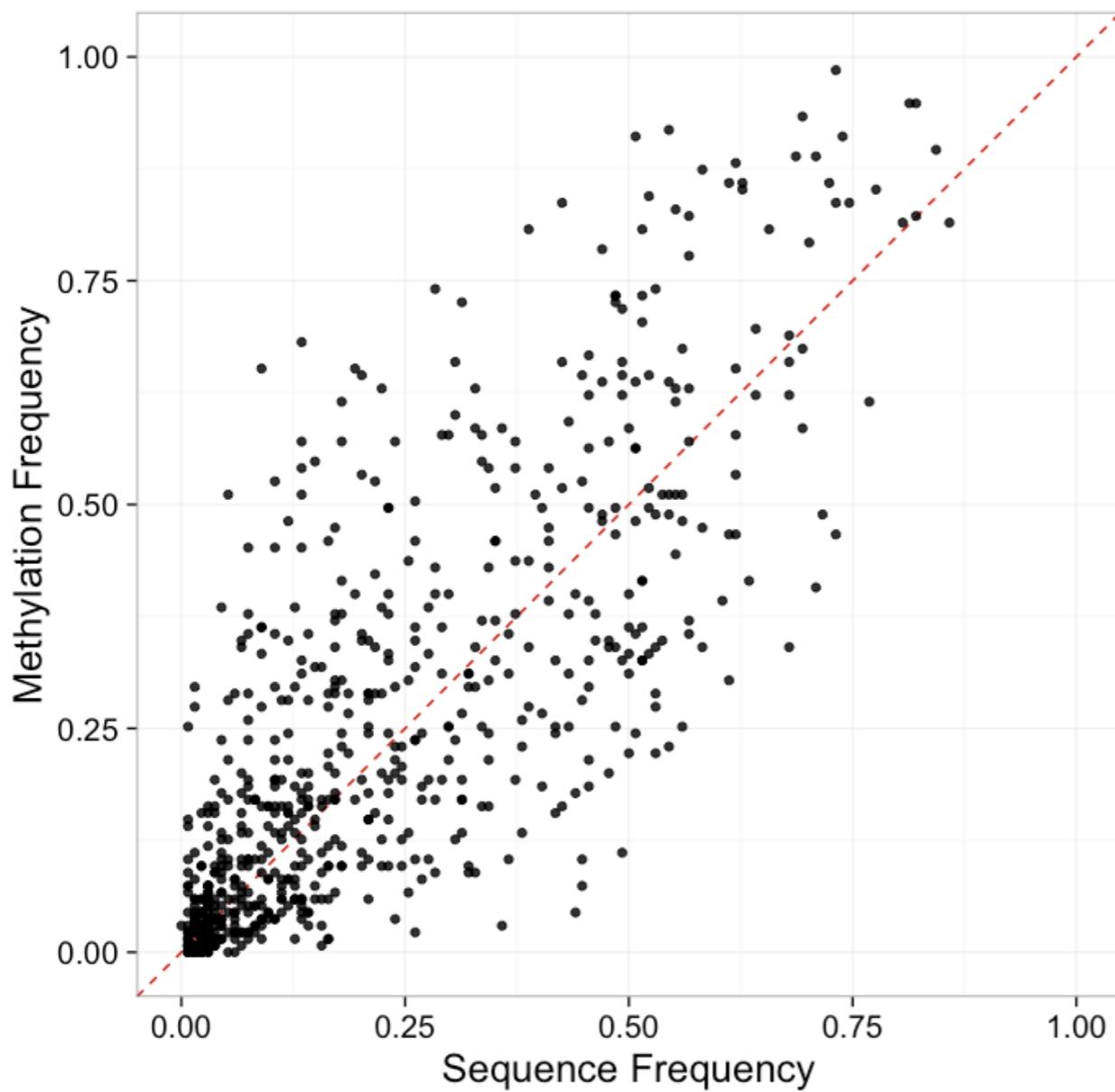
msAFLP Genome Scans

- Individuals from single clade, controlling for taxonomy & historical demography
- Paired ‘homologous’ sequence-based & methylation-based markers
- 702 paired SEQ/METH markers

		MspI	
		Band	No Band
HpaII	Band		
	No Band		

+ 6 more infrequent combinations

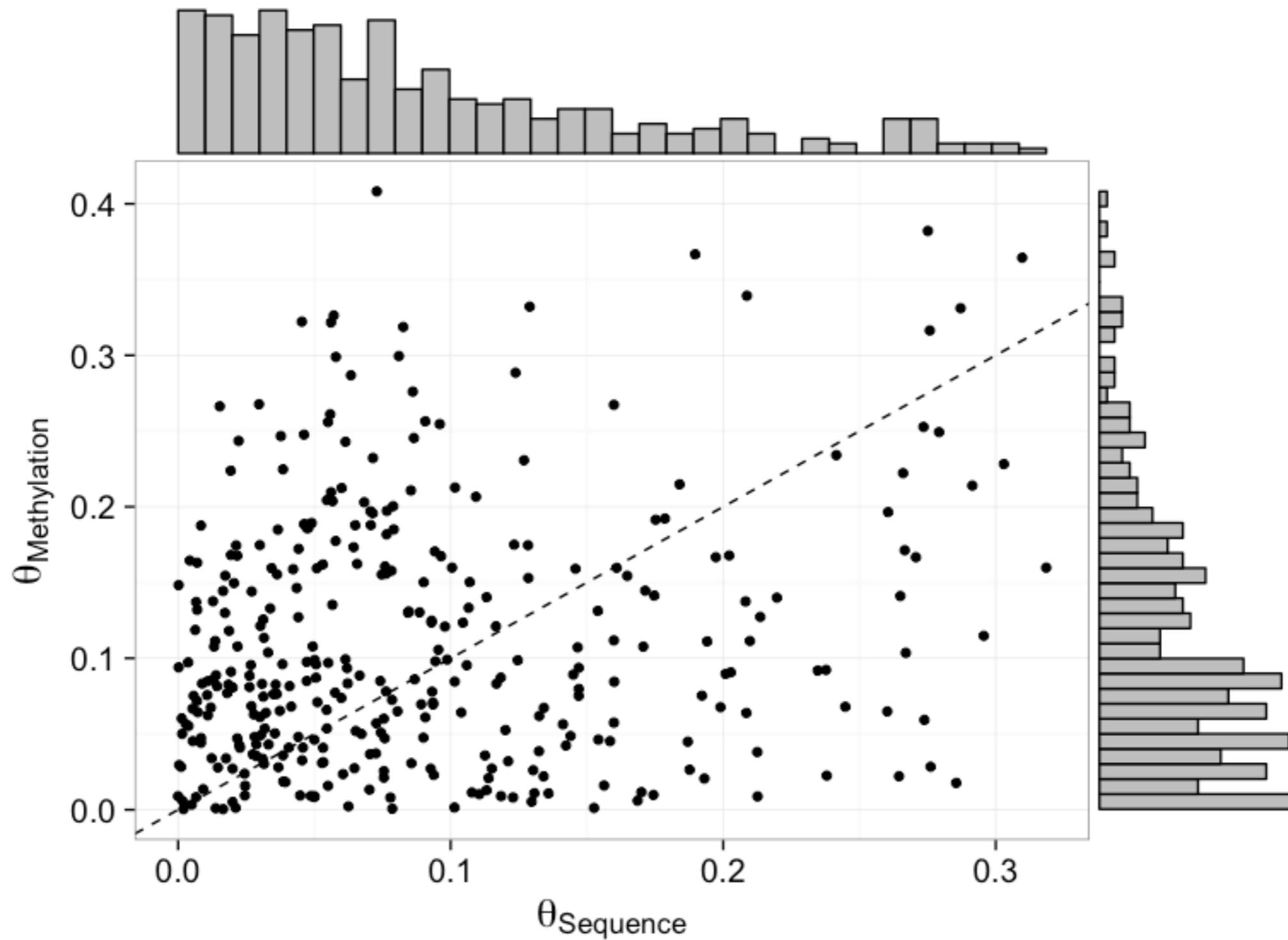
Overall Marker Frequency



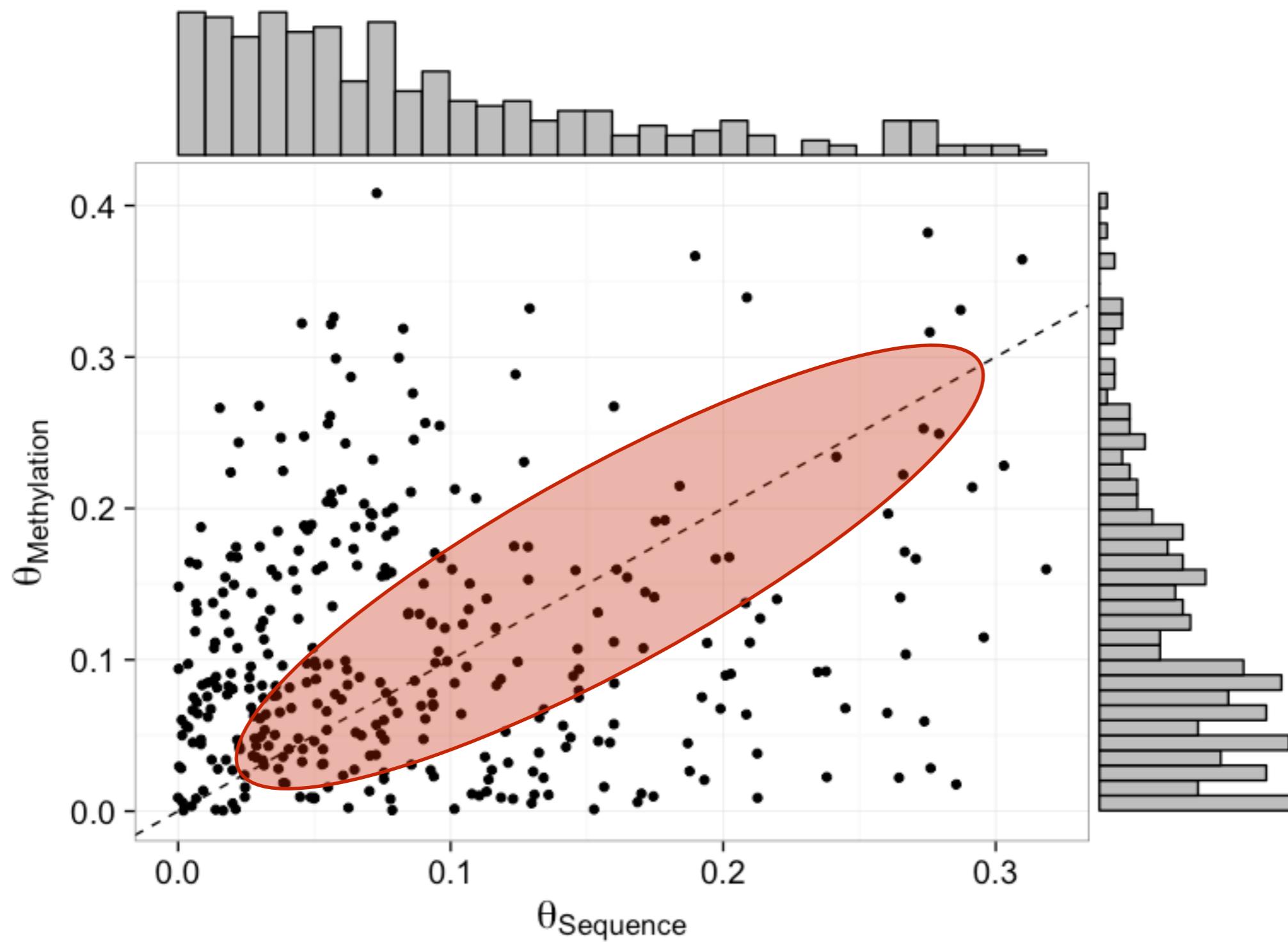
Wilcoxon signed rank test with continuity correction

data: frequency difference
V = 102870, p-value = 0.0001714
alternative hypothesis: true location is not equal to 0

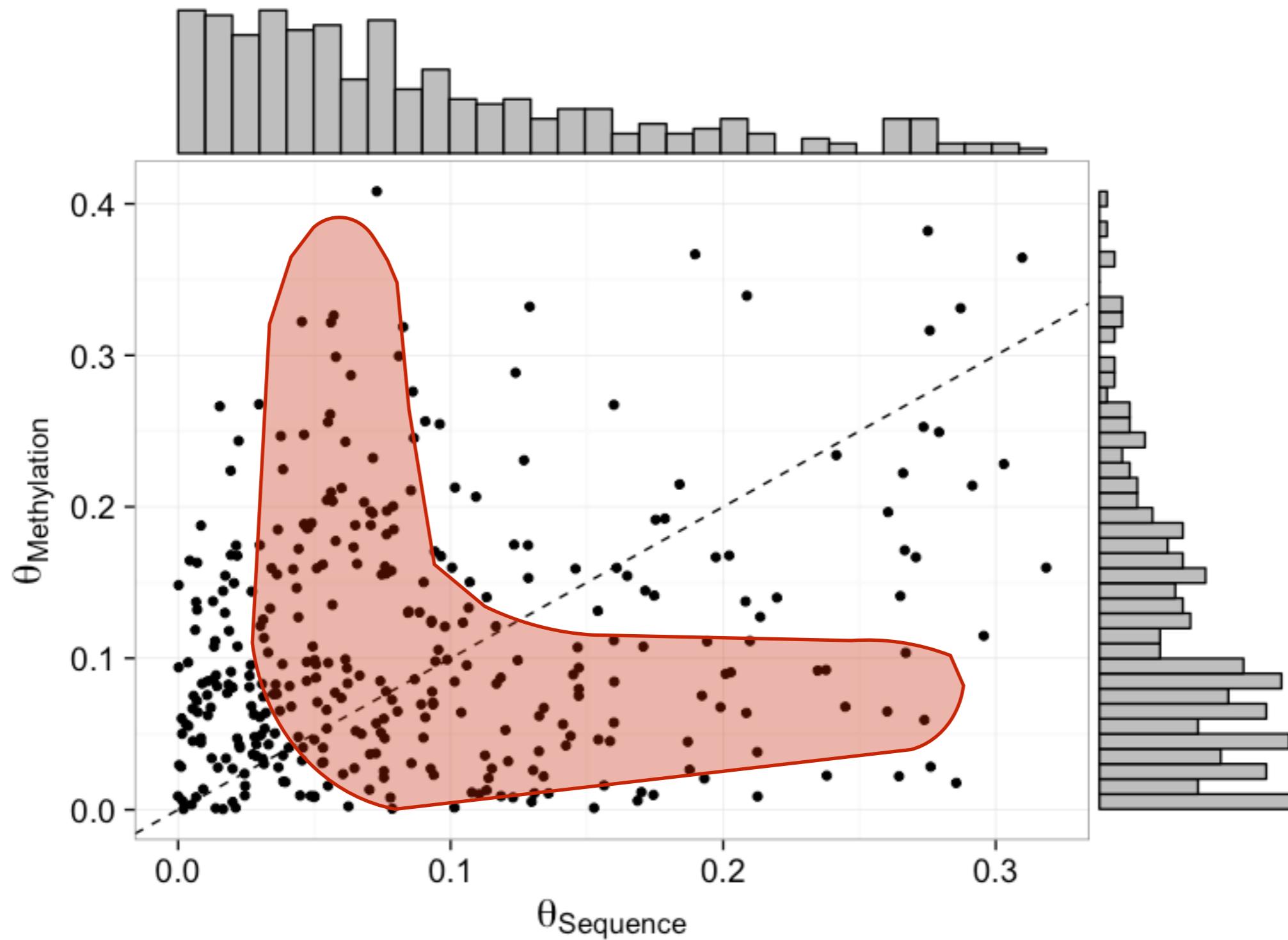
Population Structure



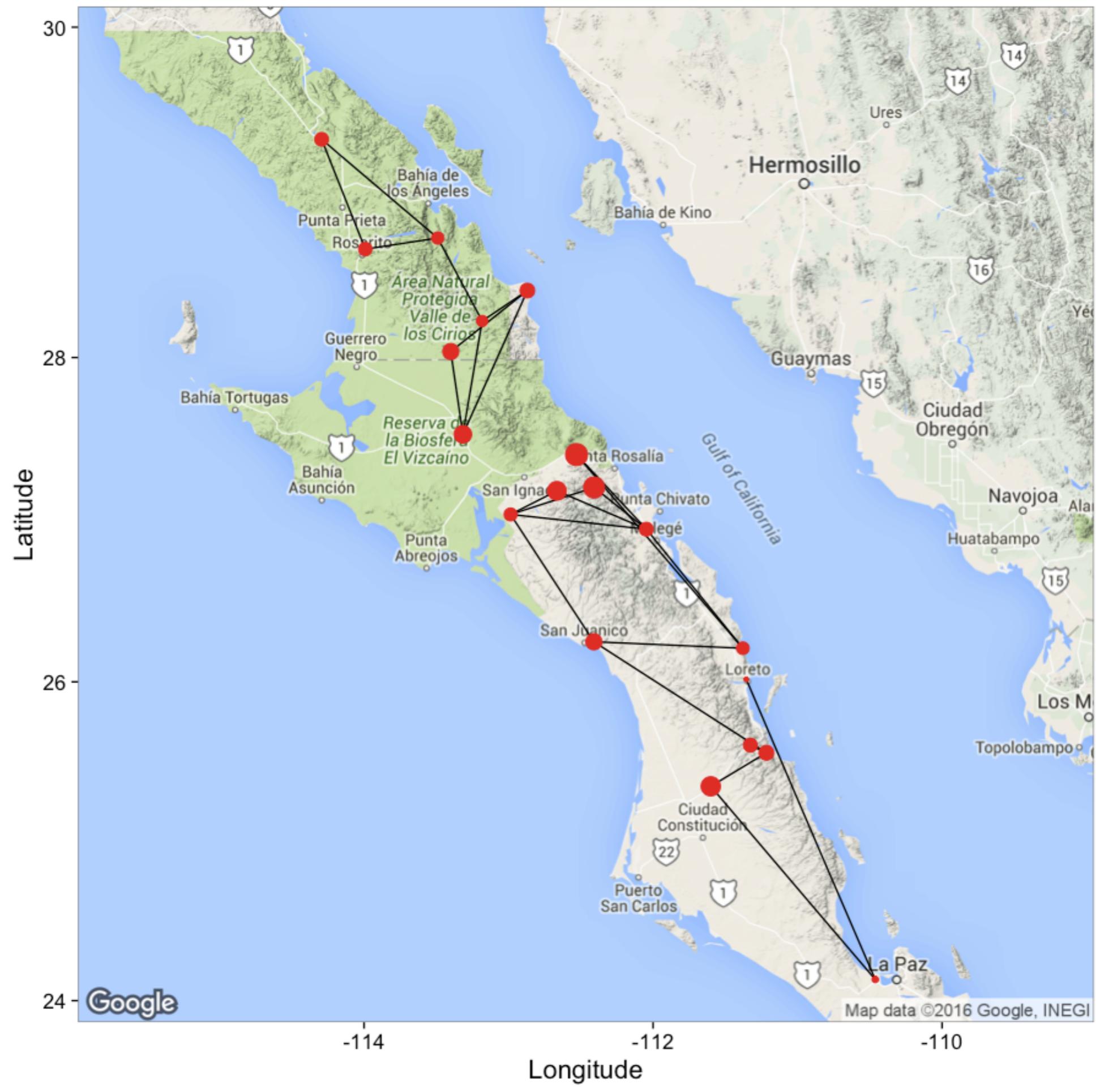
Population Structure

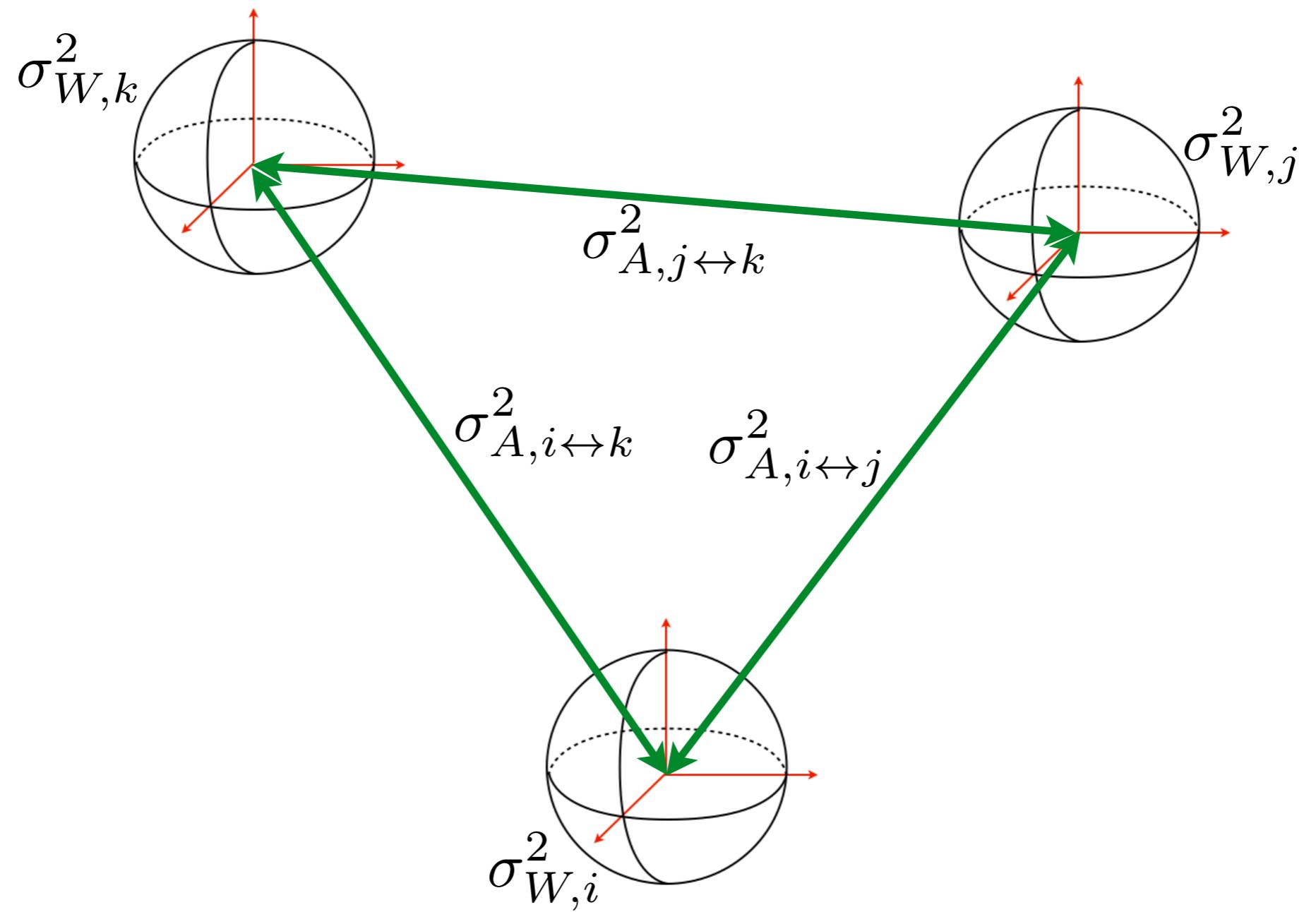


Population Structure



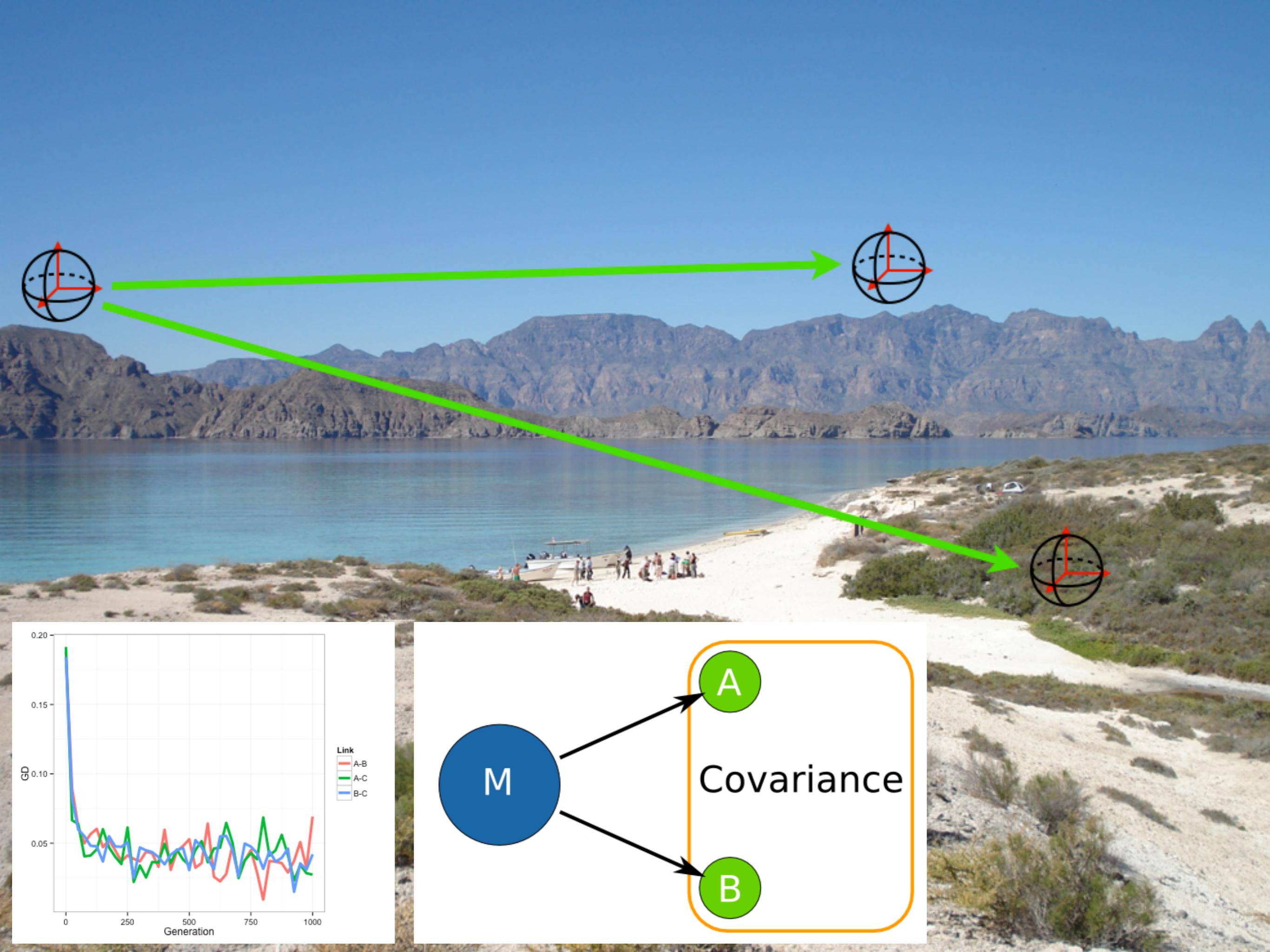
Spatial Congruence



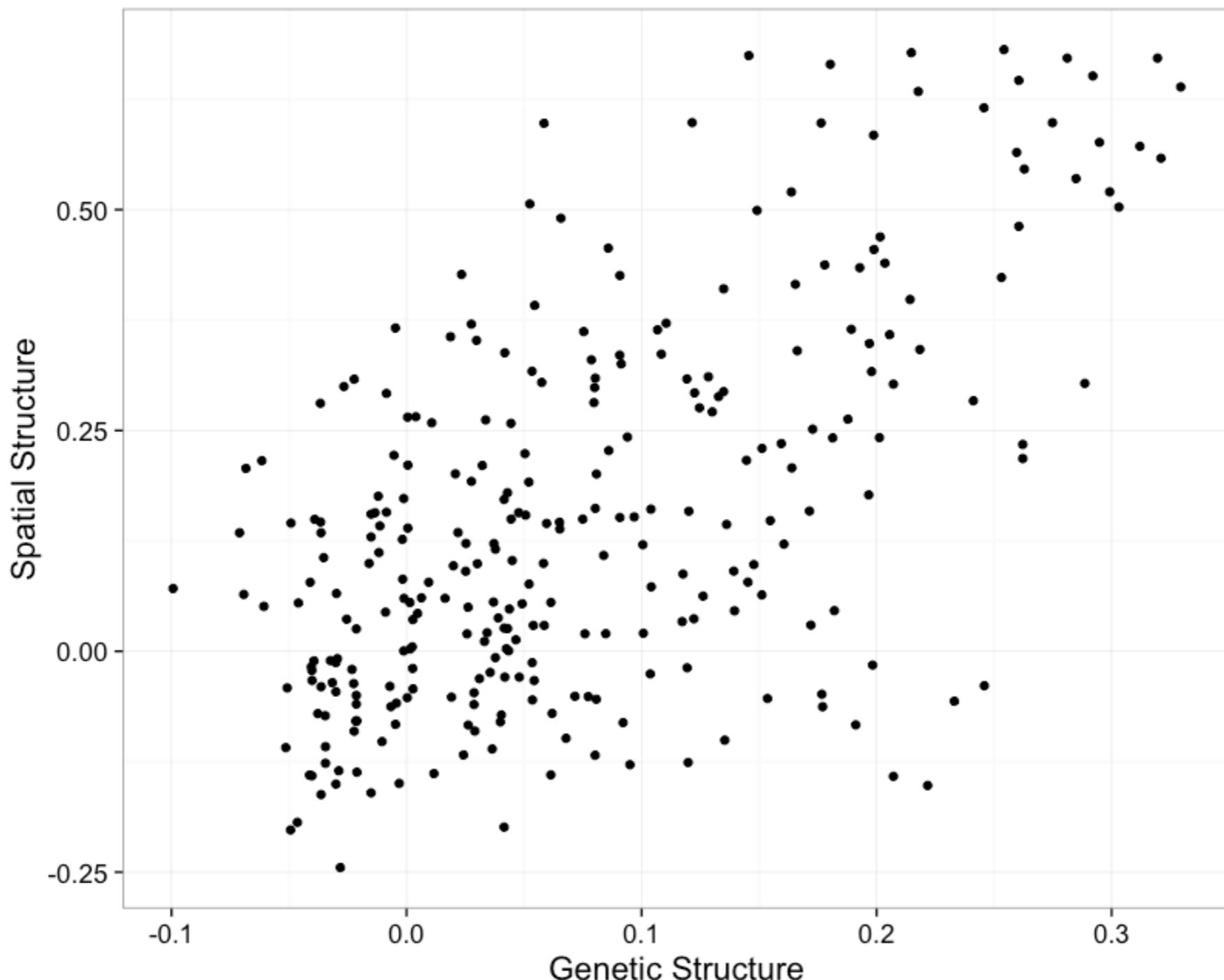


$$\sigma_W^2 = \sum_{\forall} \sigma_{W,n}^2$$

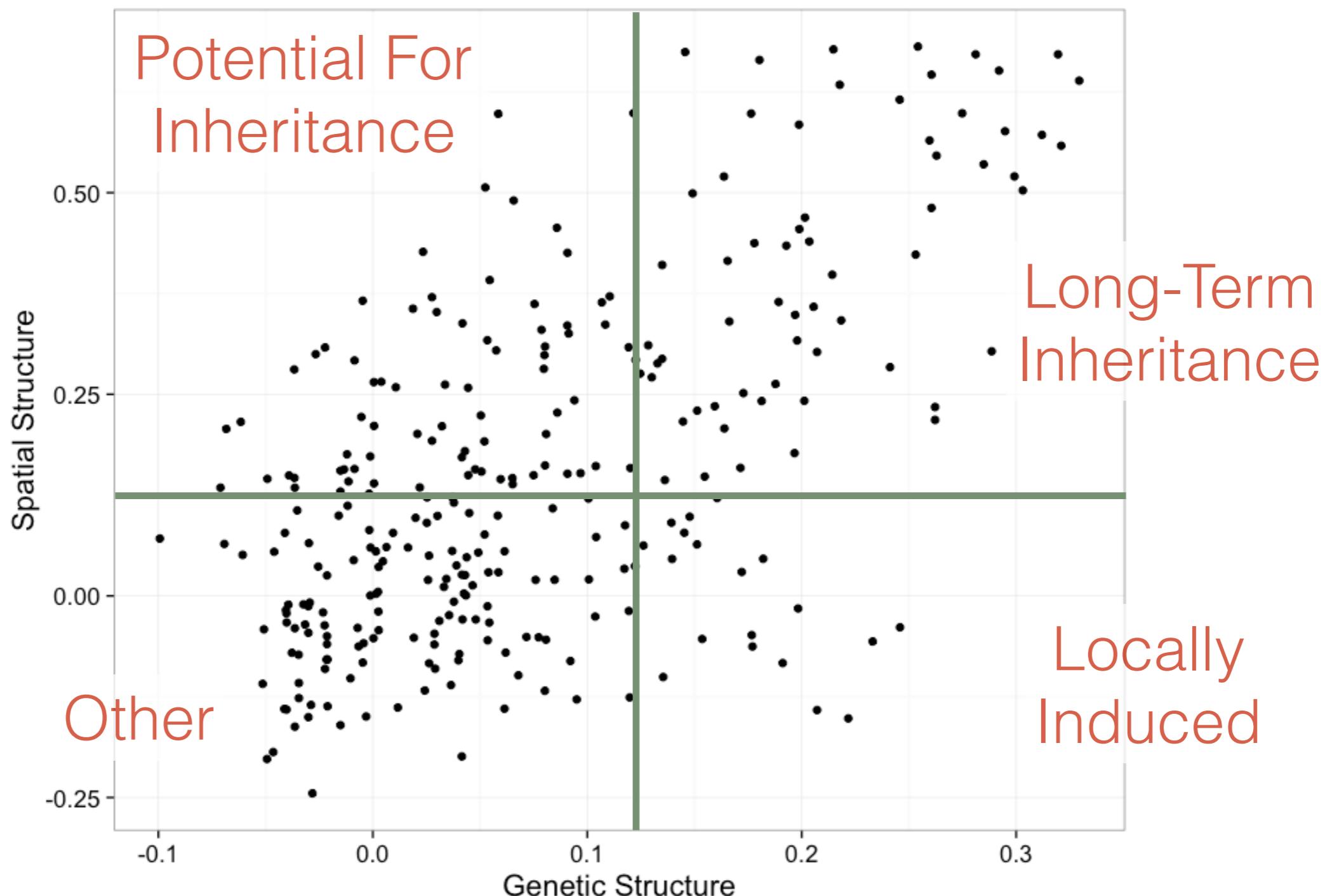
$$\sigma_A^2 = \sum_{m \neq n} \sigma_{A,m \leftrightarrow n}^2$$



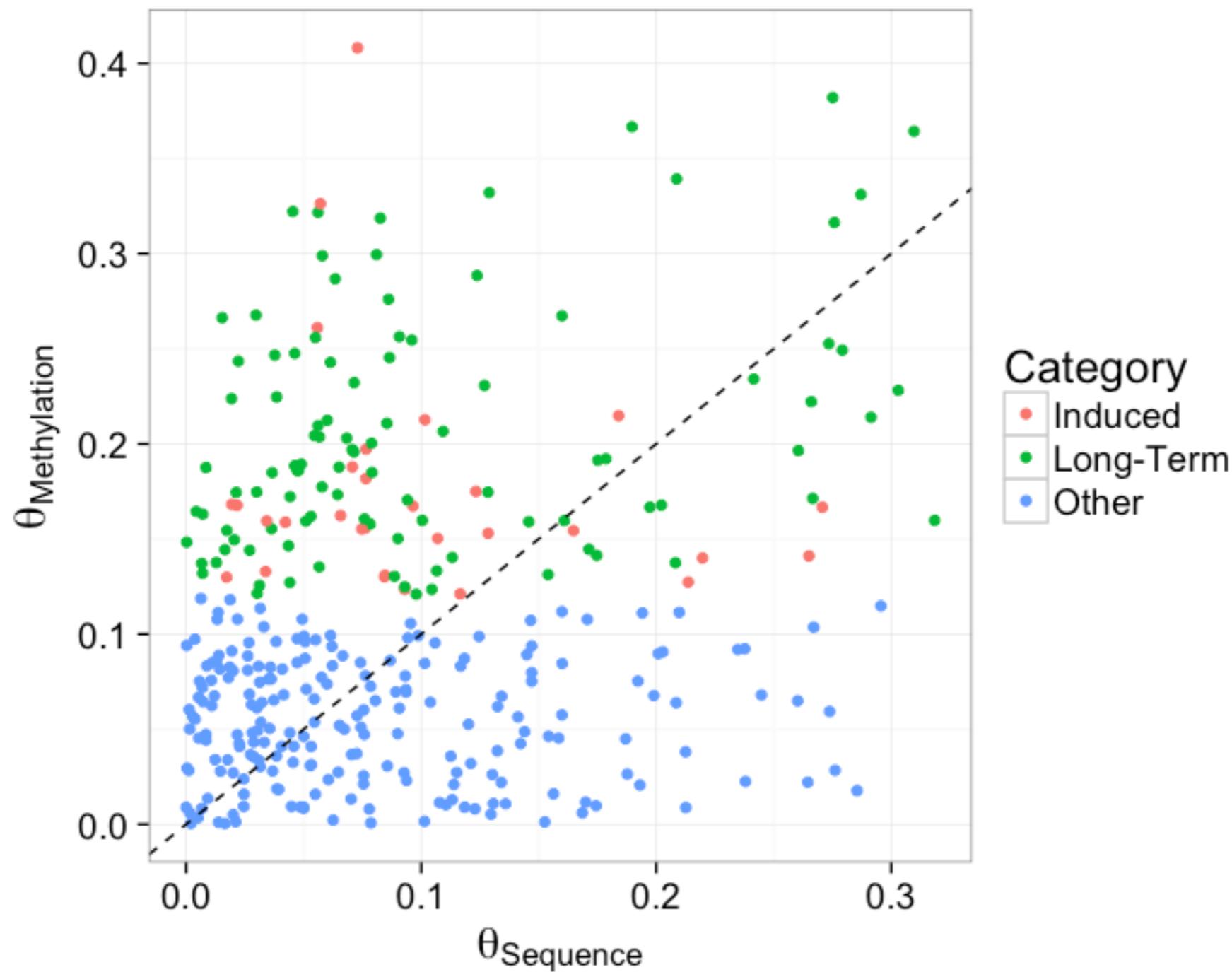
Spatial & Genetic Congruence



Epigenetic Categories



Population Structure



Conclusions

- Yet Another “Hidden Source of Adaptive Variation”
- Integrating spatial context differentiates long-term vs induced