Evolution 2014

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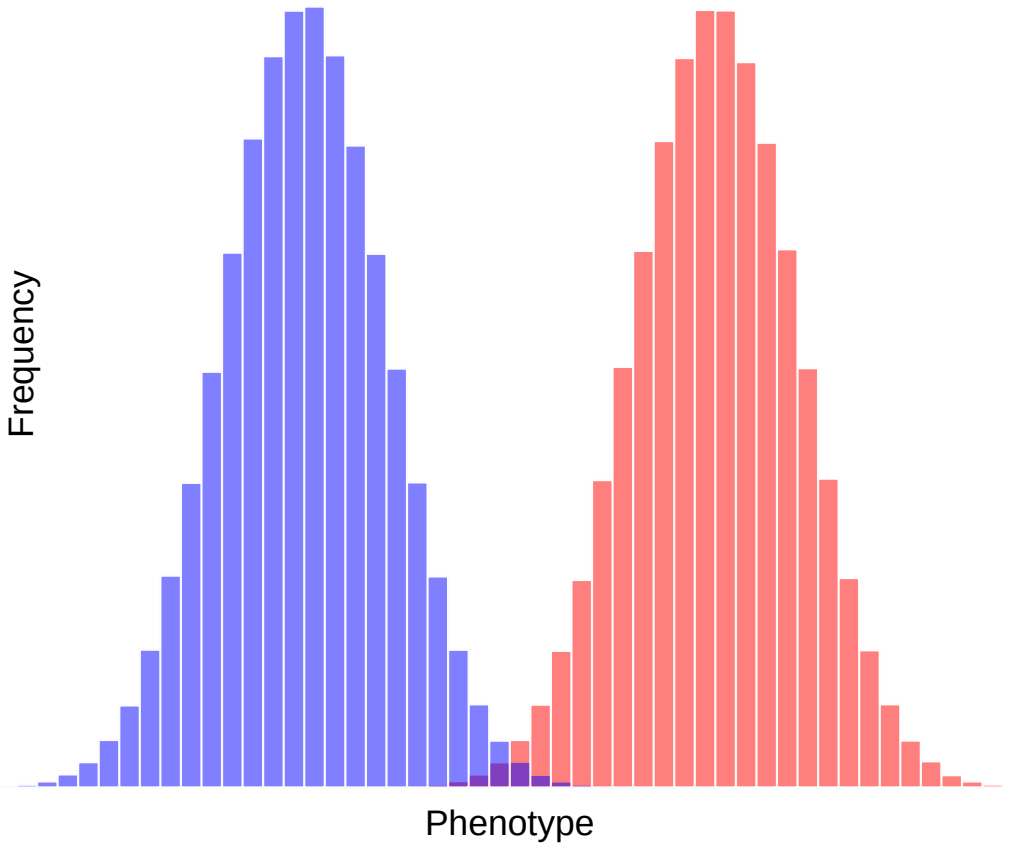
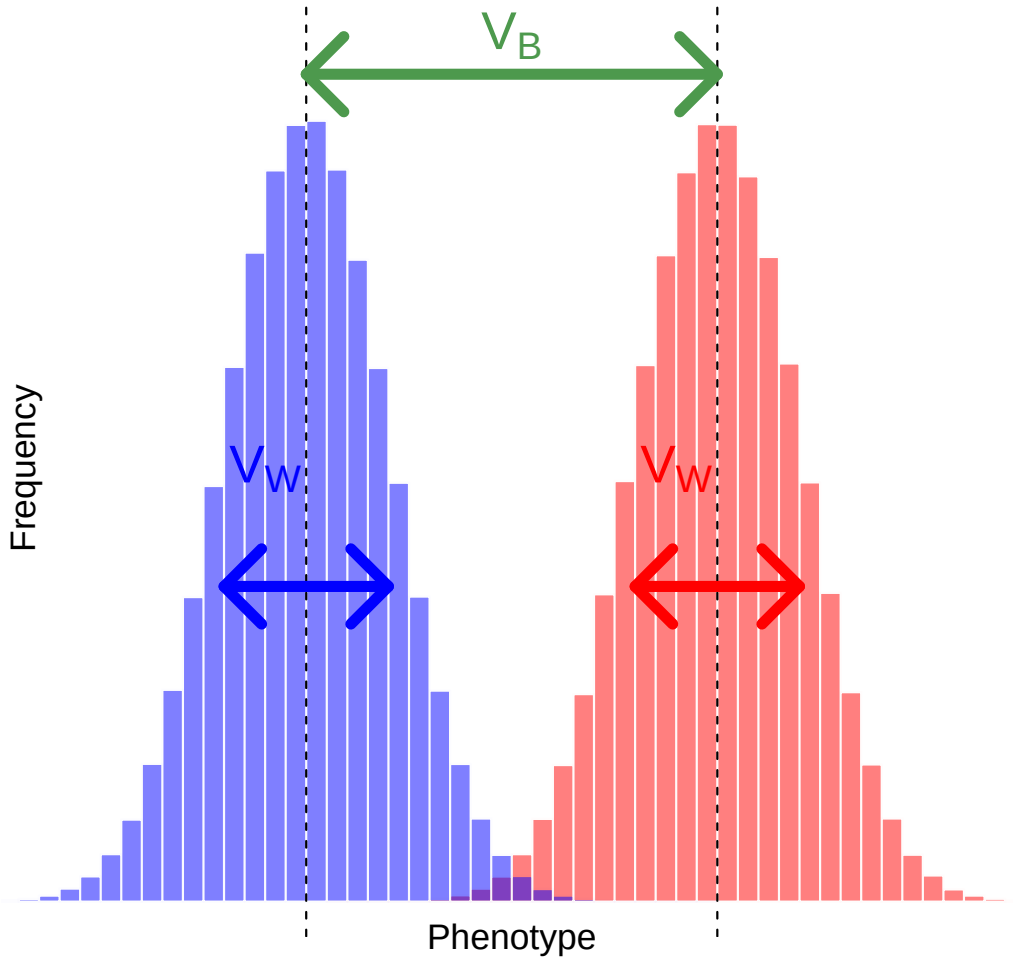
Background Slide(s)

- We want to know whether a particular trait is adaptively differentiated among populations

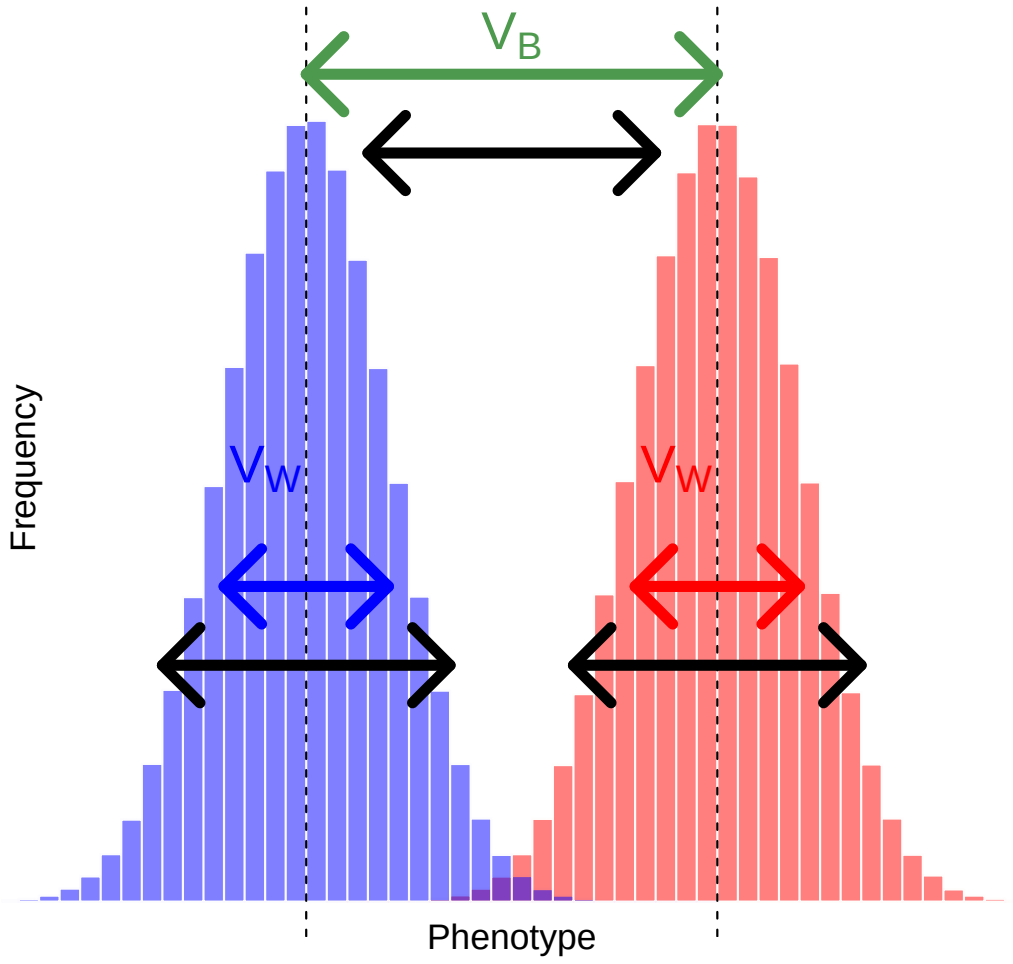
Background Slide(s)

- We want to know whether a particular trait is adaptively differentiated among populations
  - Put them in a common garden and measure them


Frequency
Phenotype

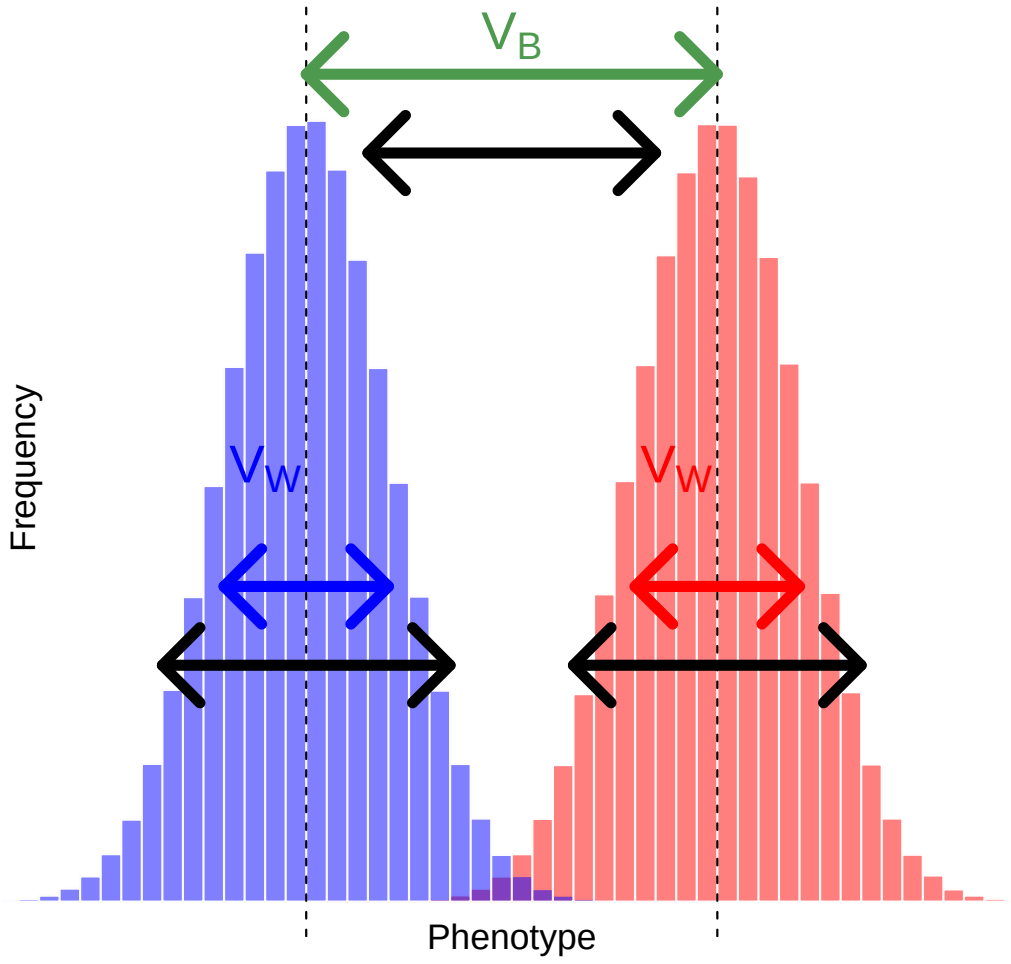


$$Q_{ST} = \frac{V_B}{V_B + V_W} = \frac{V_B}{V_T}$$



$$Q_{ST} = \frac{V_B}{V_B + V_W} = \frac{V_B}{V_T}$$

$$F_{ST} = \mathbb{E}\left[\frac{V_B}{V_B + V_W}\right]$$



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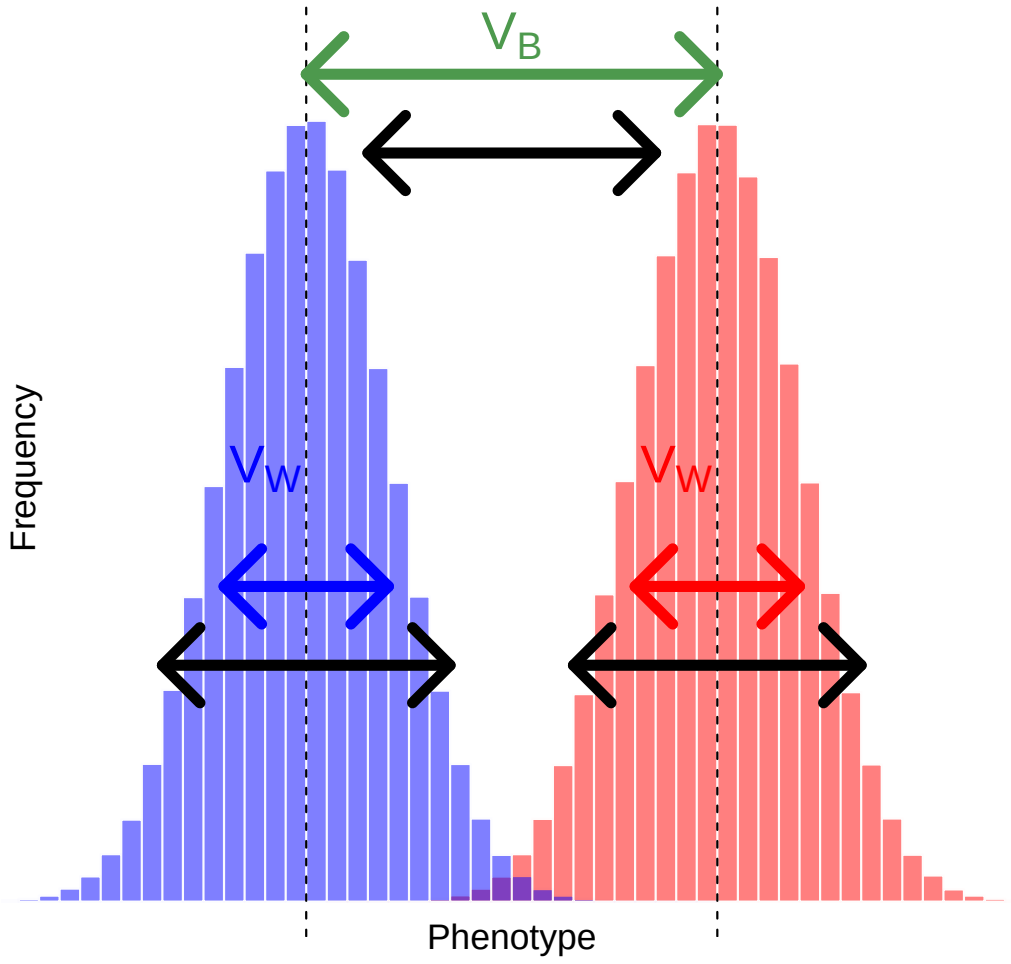

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$$\frac{Q_{ST}}{F_{ST}} = \frac{V_B}{\mathbb{E}[V_B]} \sim \chi^2$$

Generalizing Q_{ST}/F_{ST}

Q_{ST}/F_{ST} with hierarchical relatedness

$$\vec{Z} \sim MVN\left(\vec{\mu}, V_T \mathbf{F}\right)$$

$$\frac{\vec{Z}^T \mathbf{F}^{-1} \vec{Z}}{V_T} \sim \chi^2$$

- **Ovaskainen et al 2011**, Berg and Coop 2014
- $\propto$ to negative log likelihood of the data under the null model
- Reduces to $\frac{Q_{ST}}{F_{ST}}$ when all populations equally related

Using GWAS hits to estimate genetic values

LETTER

doi:10.1038/nature09410

Hundreds of variants clustered in genomic loci and biological pathways affect human height

$$Z_m = \sum_{\ell=1}^{L} \alpha_\ell p_{m\ell}$$

α = effect size

p = allele frequency

Using GWAS hits to estimate genetic values

Evidence of widespread selection on standing variation in Europe at height-associated SNPs

Michael C Turchin[1–5,8], Charleston WK Chiang[1–6,8], Cameron D Palmer[1–5], Sriram Sankararaman[5,6], David Reich[5,6], Genetic Investigation of ANthropometric Traits (GIANT) Consortium[7] & Joel N Hirschhorn[1–6]

$$Z_m = \sum_{\ell=1}^{L} \alpha_\ell p_{m\ell}$$

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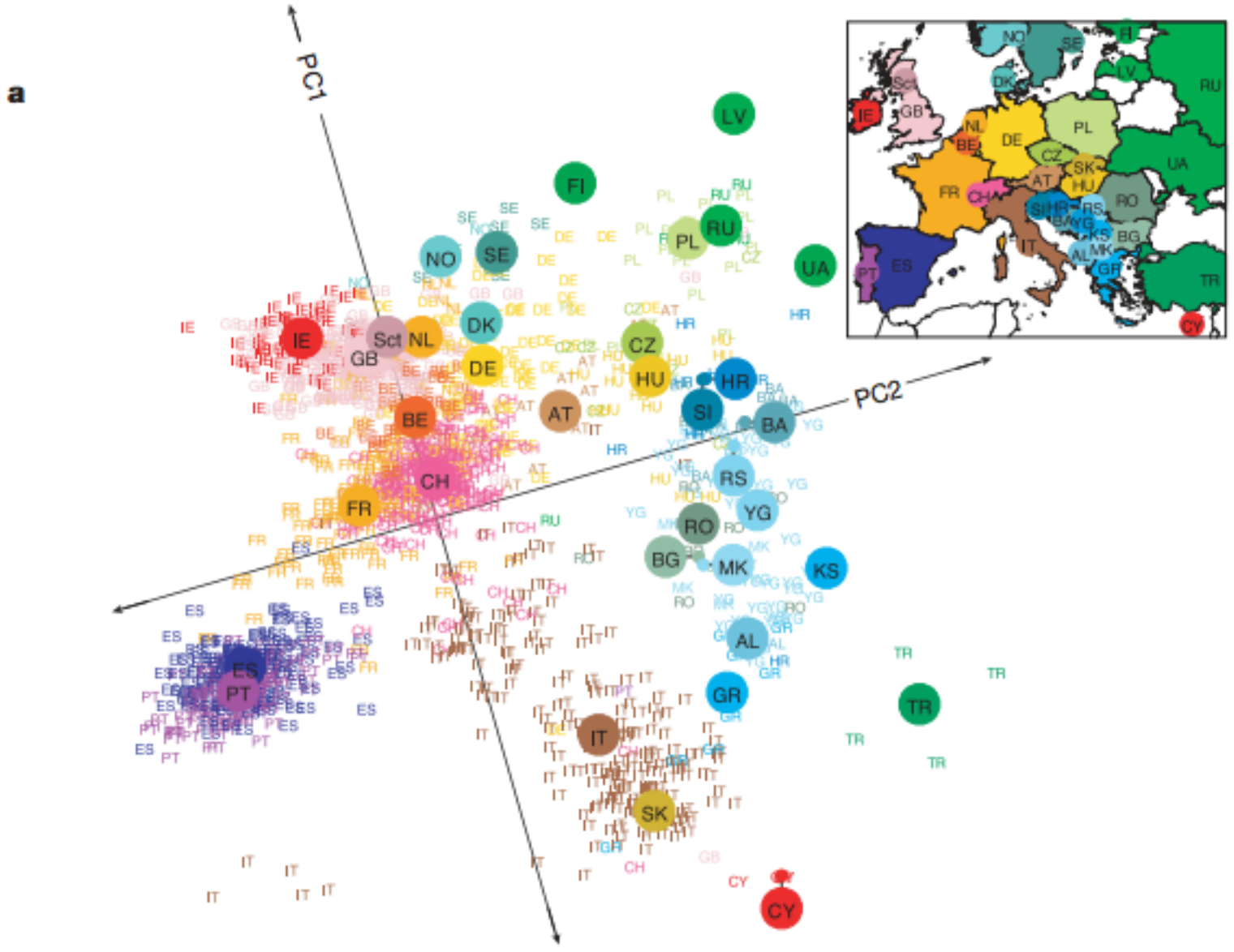
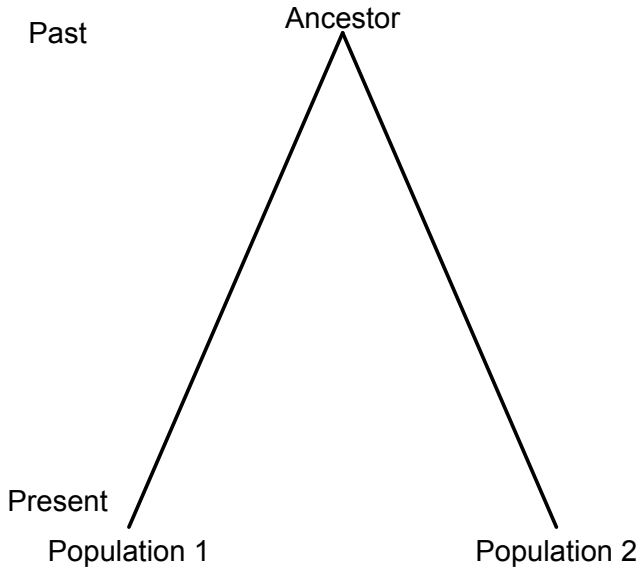
What about continuously sampled populations?



Q_{ST}/F_{ST} in continuously sampled populations



Q_{ST}

$$Q_{ST} = \frac{V_B}{V_B + V_W}$$

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The Principal Components View

$$\mathbf{F} = \begin{bmatrix} \mathbf{F_1} & \mathbf{0} \\ \mathbf{0} & \mathbf{F_2} \end{bmatrix}$$

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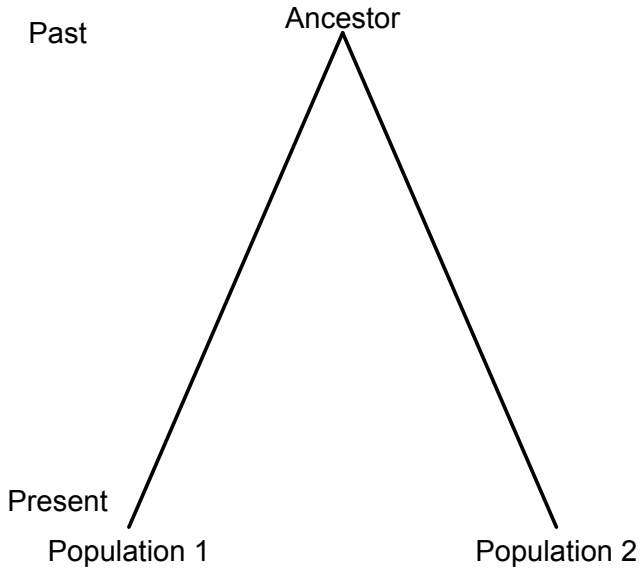

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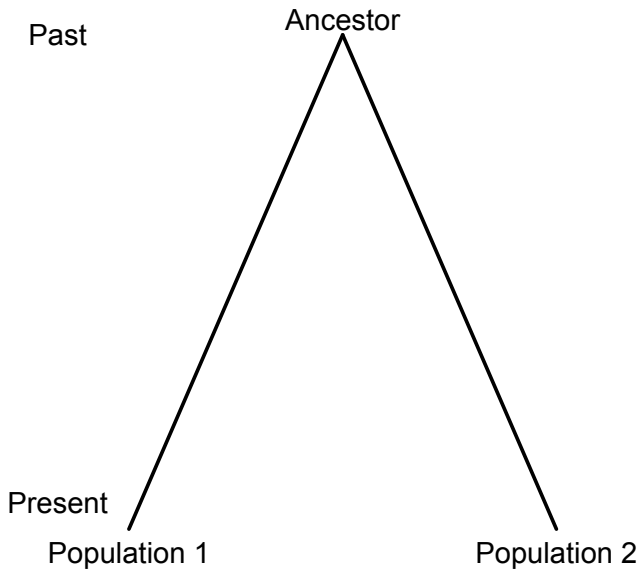

Q_{ST}

$$Q_{ST} = \frac{\left(\vec{U}_1 \cdot \vec{Z}\right)^2}{\left(\vec{U}_1 \cdot \vec{Z}\right)^2 + \sum_{j=2}^{K} \left(\vec{U}_j \cdot \vec{Z}\right)^2}$$

$$F_{ST} = \frac{\lambda_1}{\lambda_1 + \sum_{j=2}^{K} \lambda_j}$$

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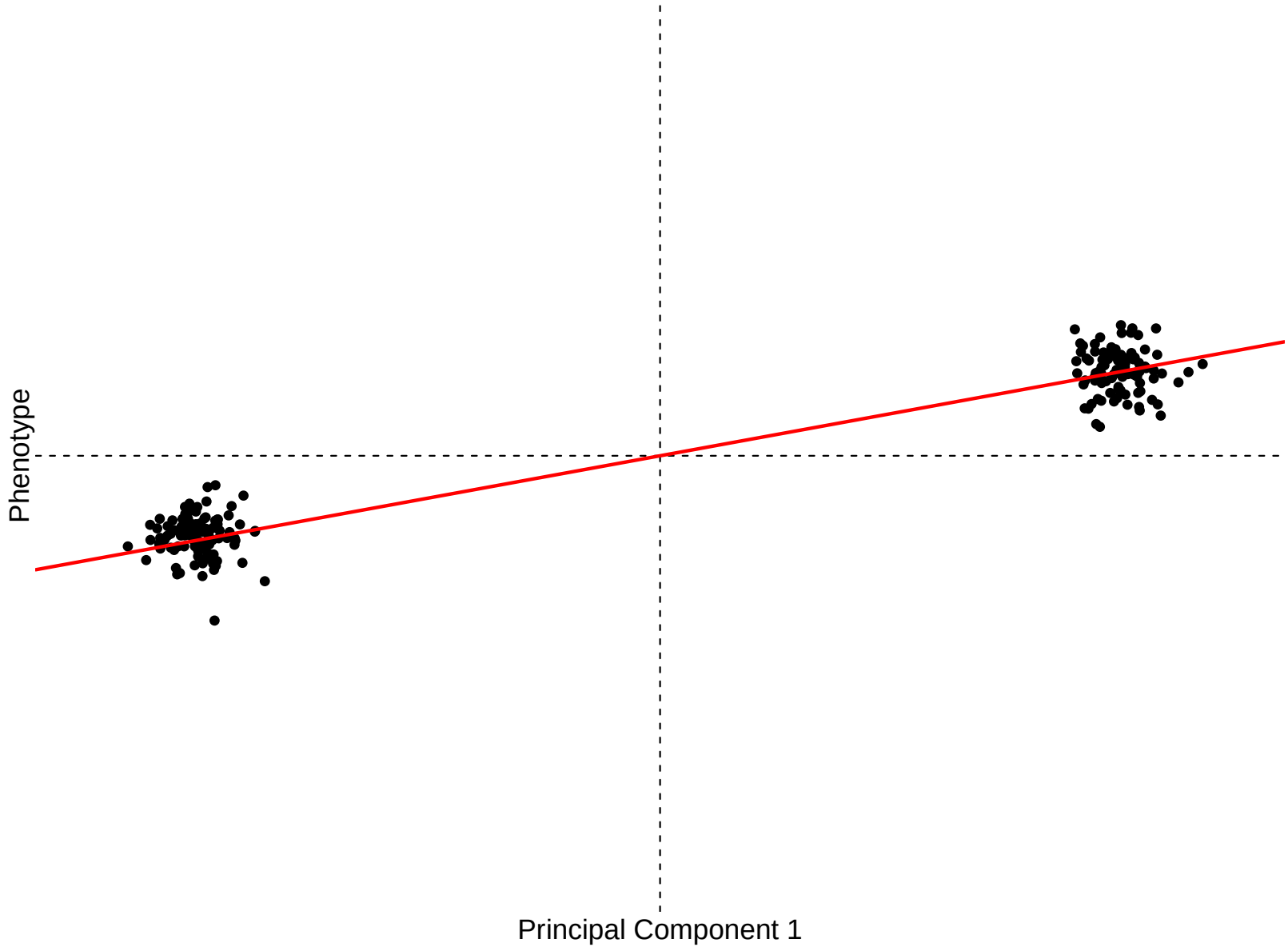
Positive result if population predicts phenotype better than expected



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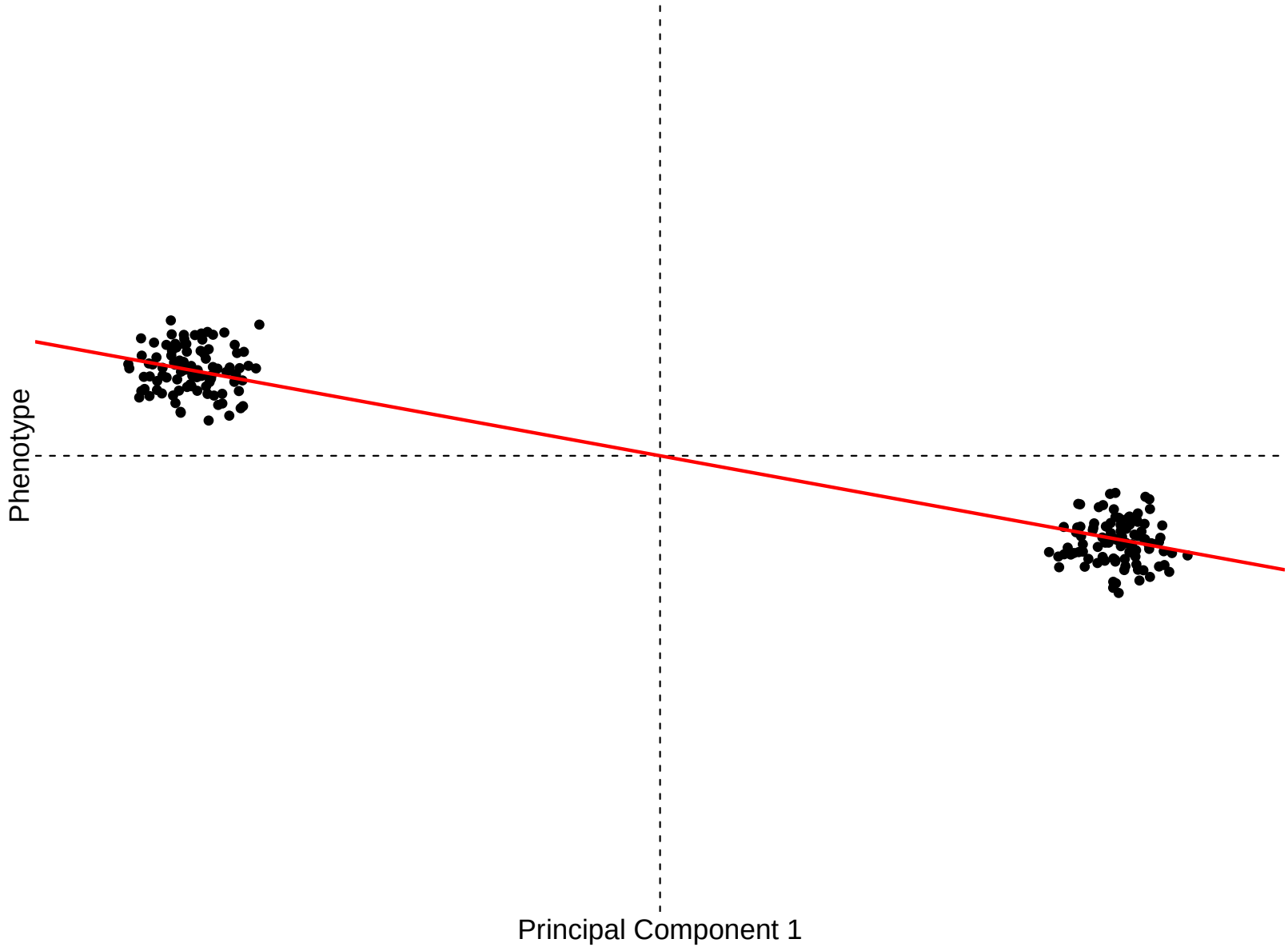

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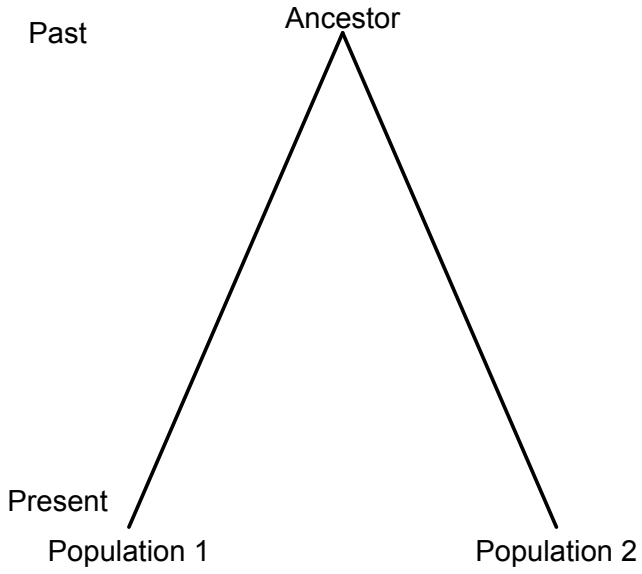

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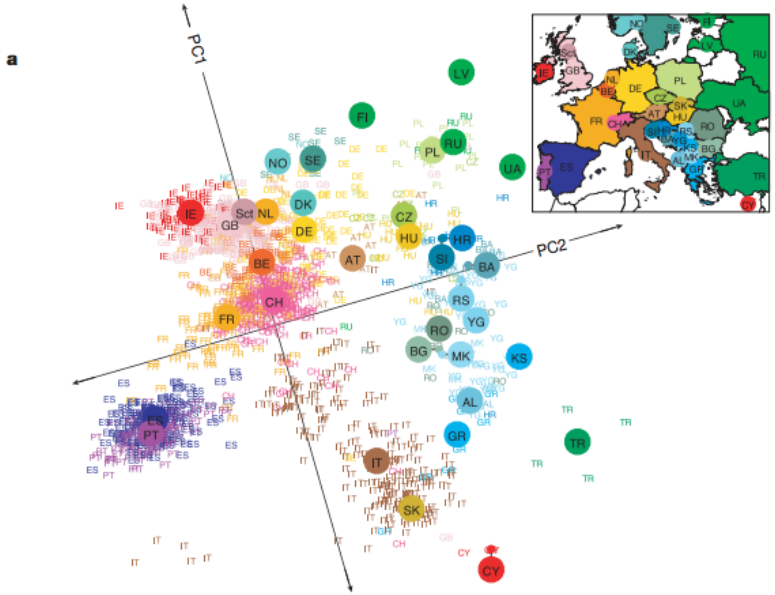
Q_{ST}/F_{ST} in continuously sampled populations



Q_{ST}

$$Q_{PC1:2} = \frac{V_{PC1:2}}{V_{PC1:2}+V_{PC3:K-1}}$$

$$F_{PC1:2} = \mathbb{E}\left[\frac{V_{PC1:2}}{V_{PC1:2}+V_{PC3:K-1}}\right]$$

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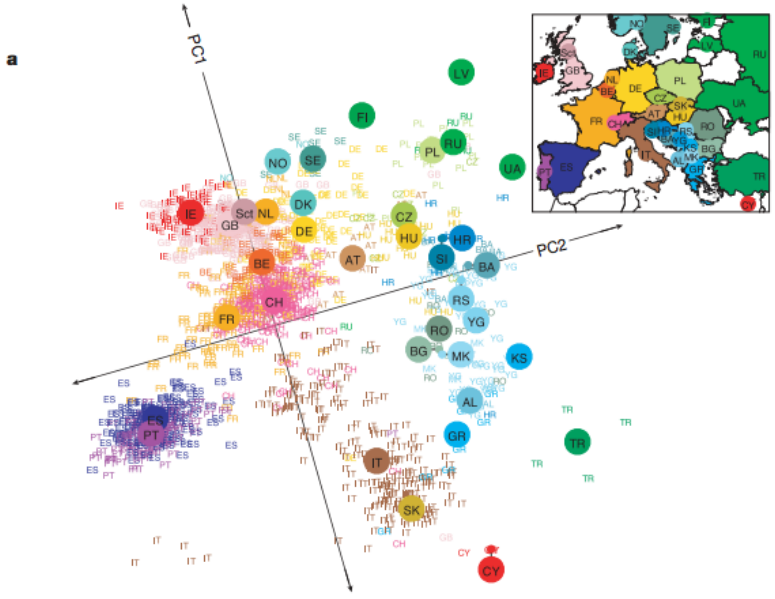

Q_{ST}

$$Q_{PC1} = \frac{\sum_{i=1}^{2} \left(\vec{U}_i \cdot \vec{Z}\right)^2}{\sum_{i=1}^{2} \left(\vec{U}_i \cdot \vec{Z}\right)^2 + \sum_{j=3}^{K-1} \left(\vec{U}_j \cdot \vec{Z}\right)^2}$$

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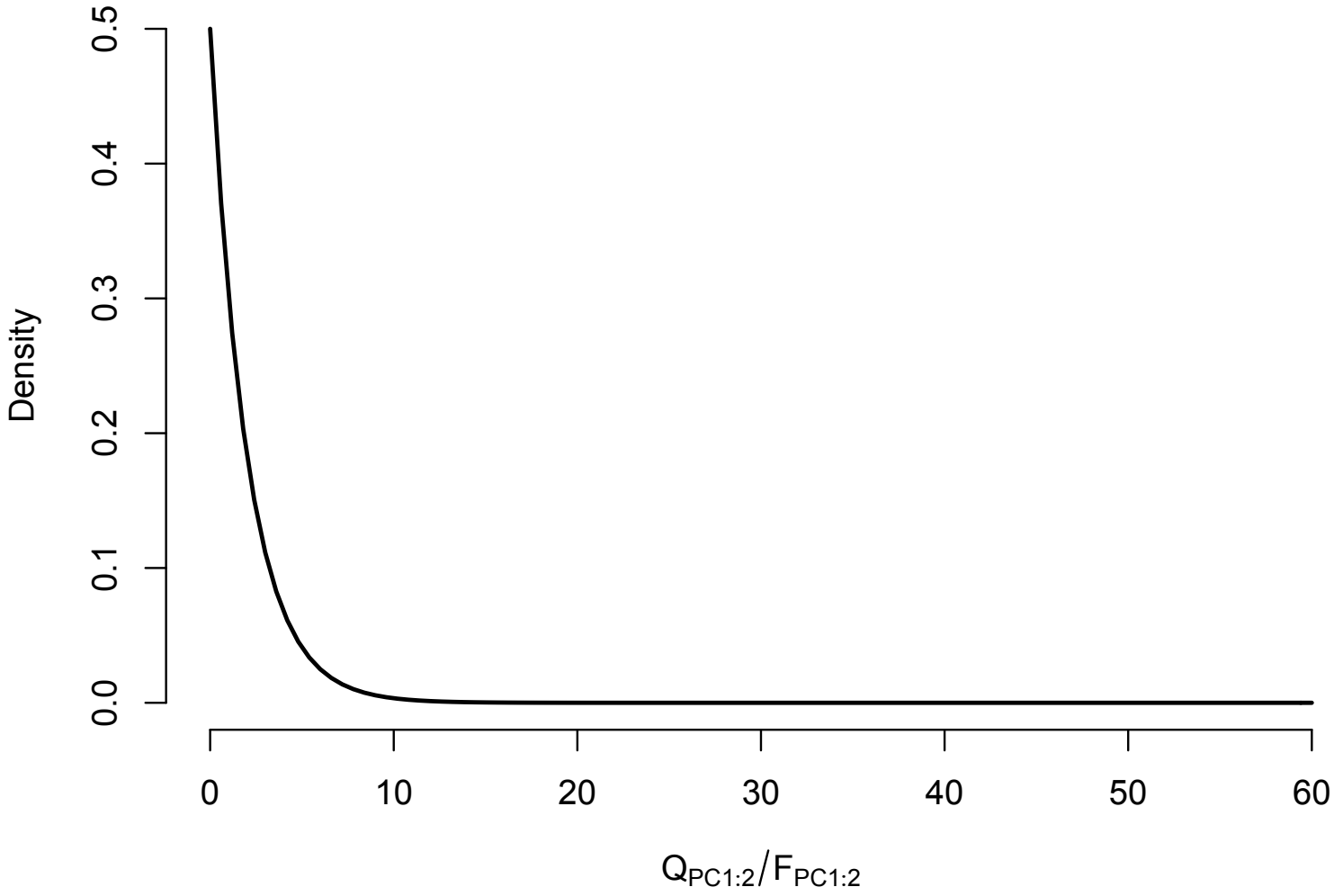
Genetic Divergence for Height in Europe



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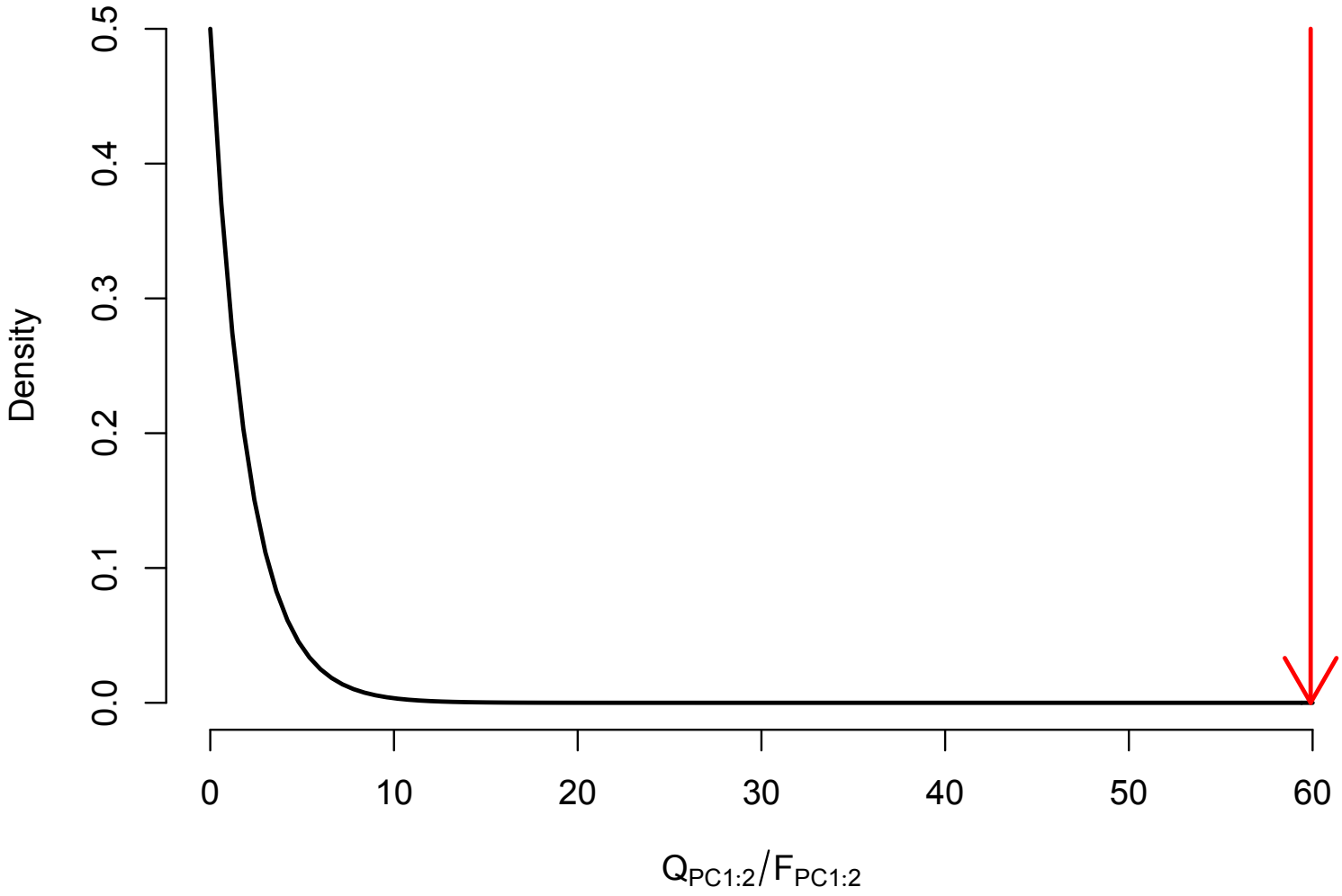
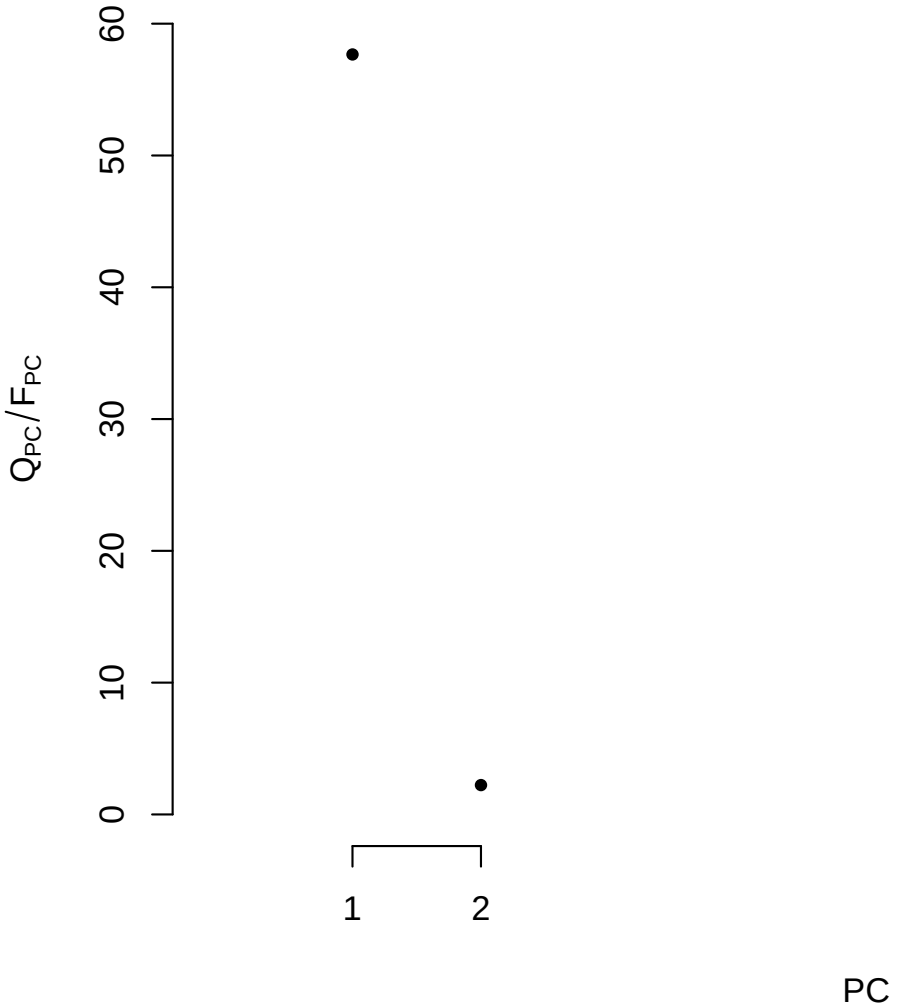


Genetic Divergence in Height Along PC1 in Europe



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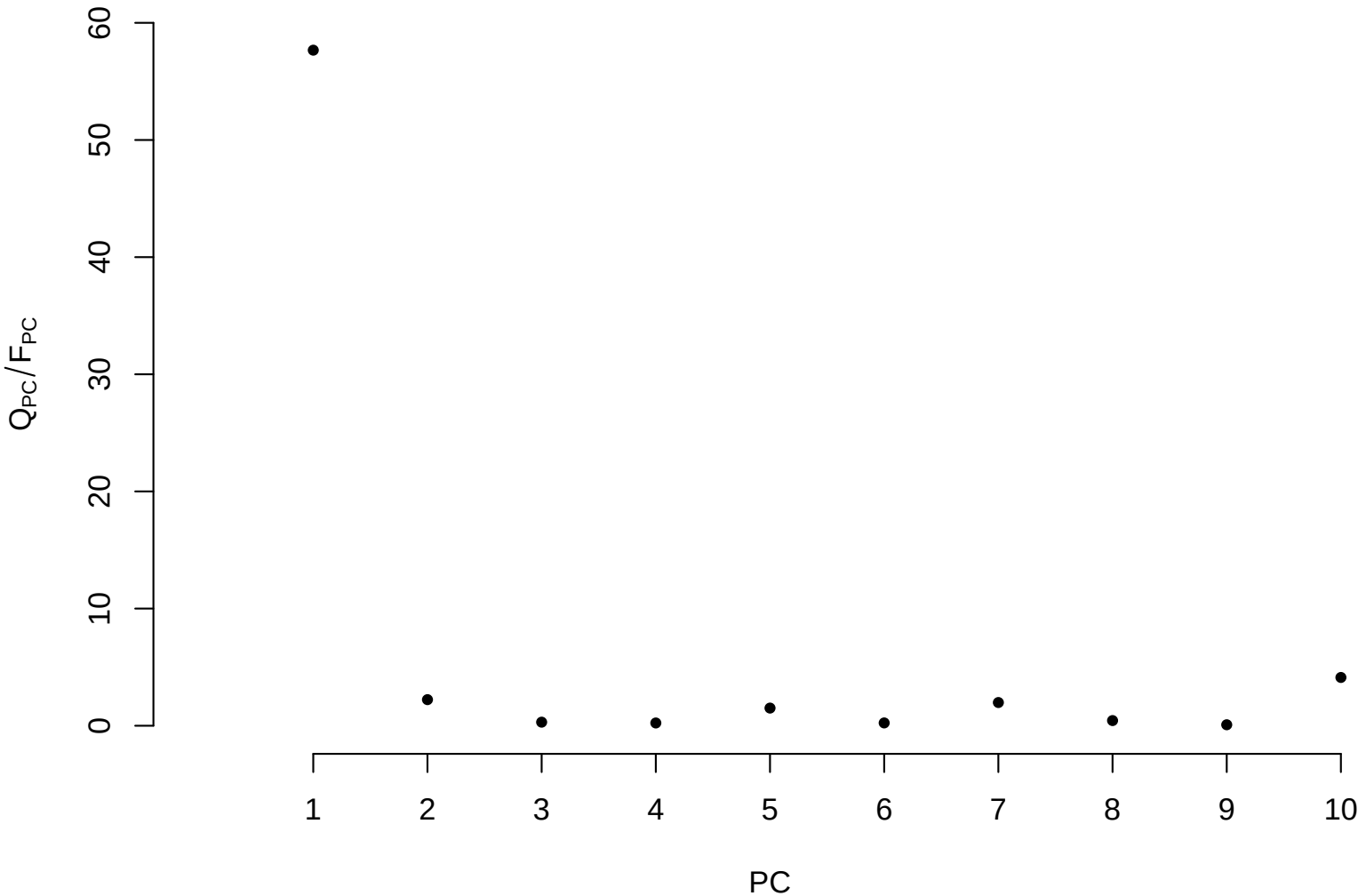

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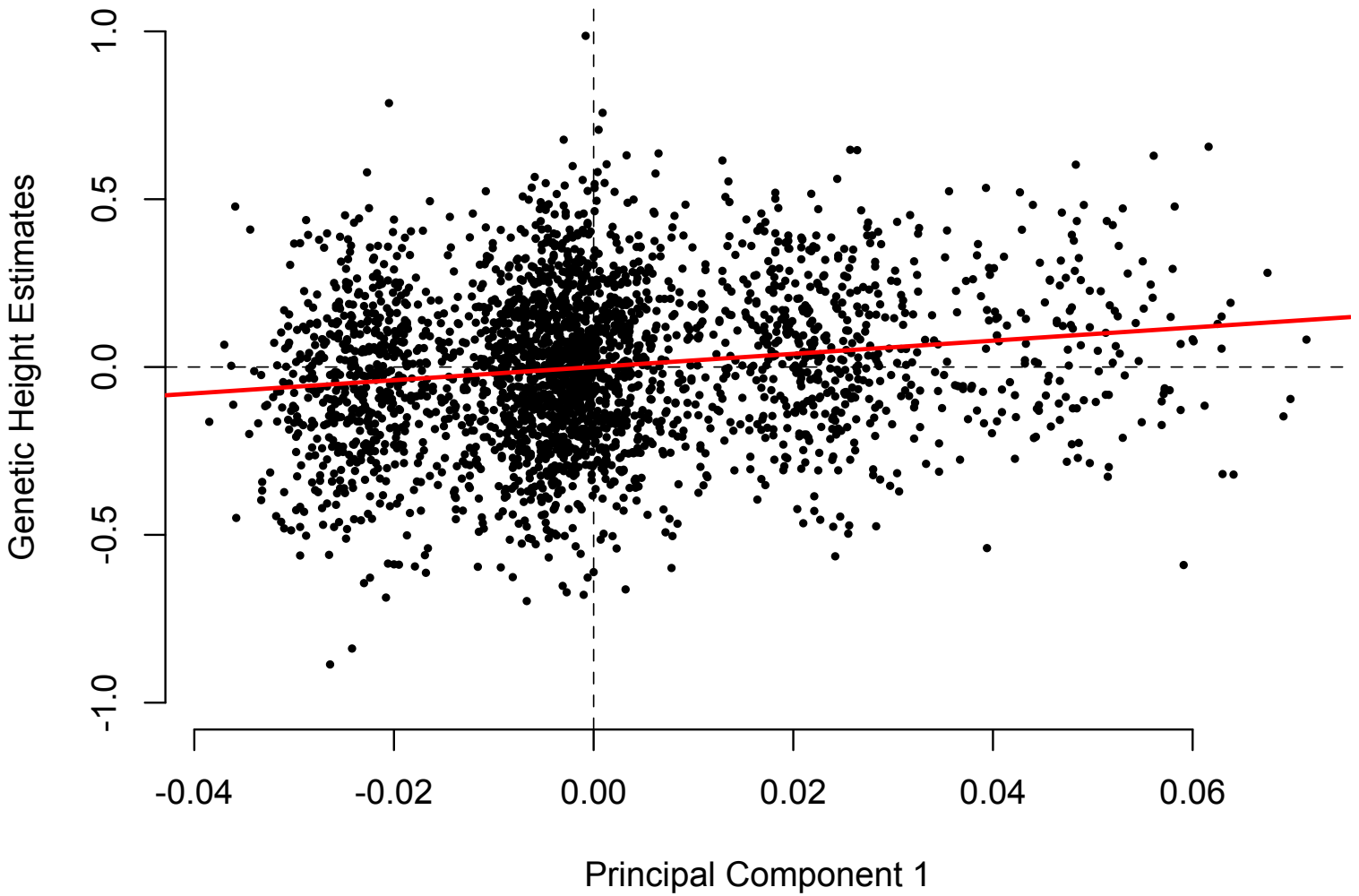

Take Aways

- Height associated SNPs significantly correlated with PC1/N-S axis in Europe (but we already knew that)

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- Q_{ST}/F_{ST} can be formulated in terms of reduced rank factorizations of the individual-by-individual kinship matrix
  - Direct relationship to PCA, *structure*, Sparse Factor Analysis
  - Engelhardt and Stephens 2010

Things I Didn't Mention

- Can add include multiple correlated traits, but interpretation potentially trickier
  - Chenoweth and Blows (2008)
  - Martin et al (2008)
- In species where it's possible to set up breeding designs, continuous sampling is not a barrier

Acknowledgements