Testing for Adaptive Divergence: Q_{ST}/F_{ST} Comparisons in Populations with Complicated Histories

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University of California, Davis

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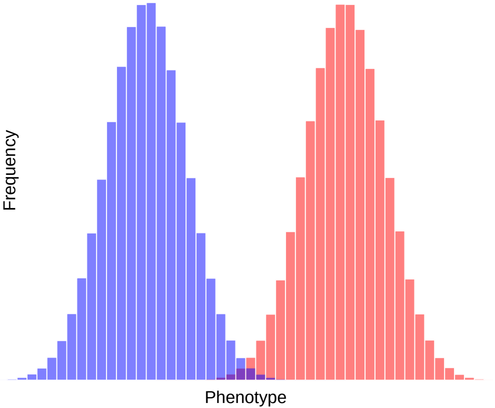
- Compute Q_{ST} and F_{ST}; compare them
- **What if the individuals in our sample can't be fit neatly into a discrete set of populations?**

The Standard Q_{ST}/F_{ST} Comparison



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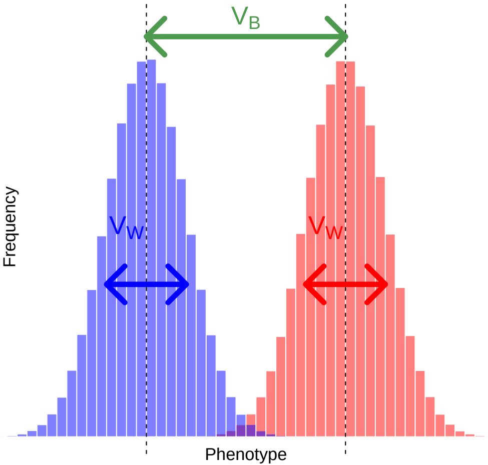

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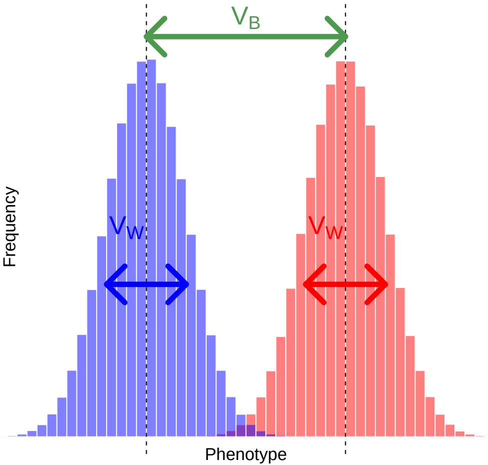

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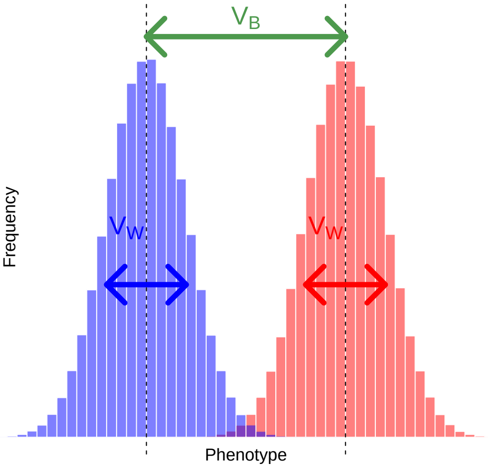

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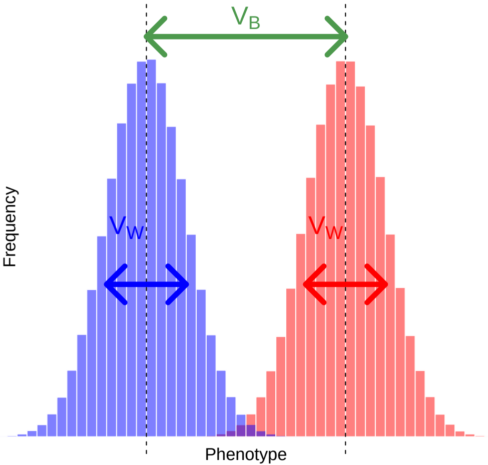

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$$\frac{Q_{ST}}{F_{ST}} = \frac{V_B}{\mathbb{E}[V_B]} \sim \chi^2$$

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

$$Z_k = \sum_{\ell=1}^{L} \alpha_\ell p_{k\ell}$$

$\alpha =$ effect size

$p =$ allele count

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]

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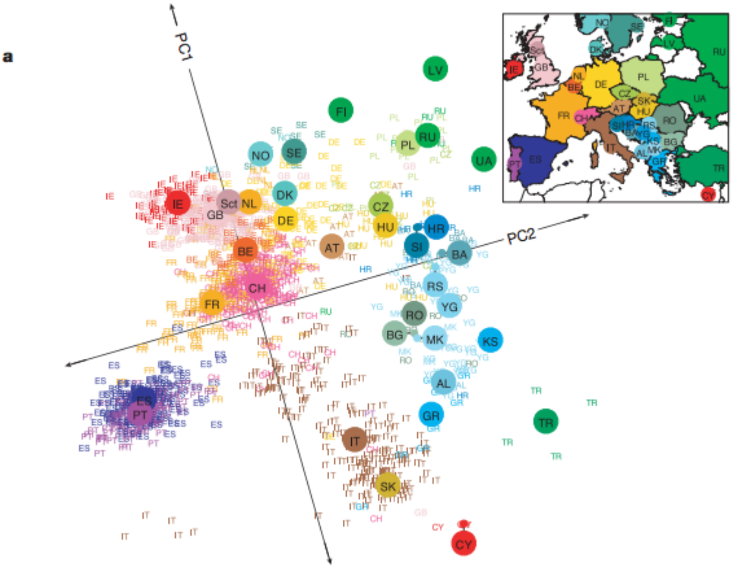
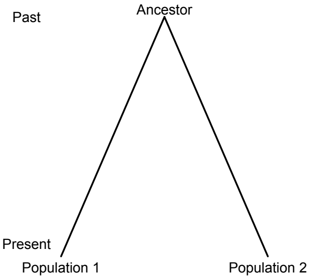
What about continuously sampled populations?



Q_{ST}/F_{ST} on a natural scale



Variance Partitions

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

$$F_{ST} = \mathbb{E}\left[Q_{ST}\right]$$

The Kinship Matrix

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

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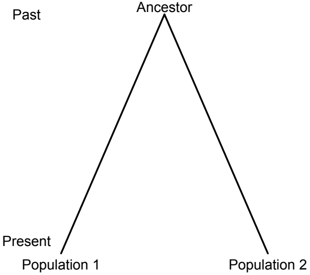

Variance Partitions

$$V_B = \left(\vec{U}_1 \cdot \vec{Z}\right)^2$$

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$$F_{ST} = \frac{\lambda_1}{\sum_{i=1}^{K-1} \lambda_i}$$

The Eigenvalue Decomposition (Principal Components)

$$\mathbf{F} = \begin{bmatrix} \vec{U}_1 & \vec{U}_2 & \dots & \vec{U}_{K-1} \end{bmatrix} \begin{bmatrix} \lambda_1 & 0 & 0 \\ 0 & \ddots & 0 \\ 0 & 0 & \lambda_{K-1} \end{bmatrix} \begin{bmatrix} \vec{U}_1^T \\ \vec{U}_2^T \\ \dots \\ \vec{U}_{K-1}^T \end{bmatrix}$$

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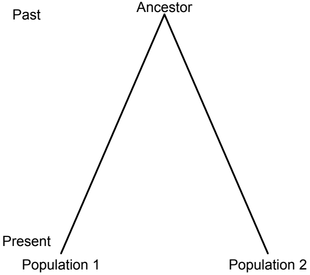

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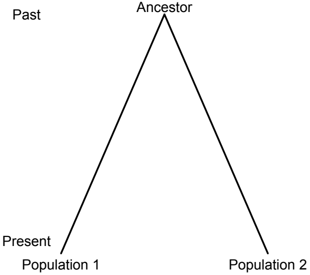

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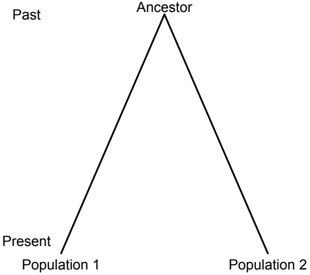

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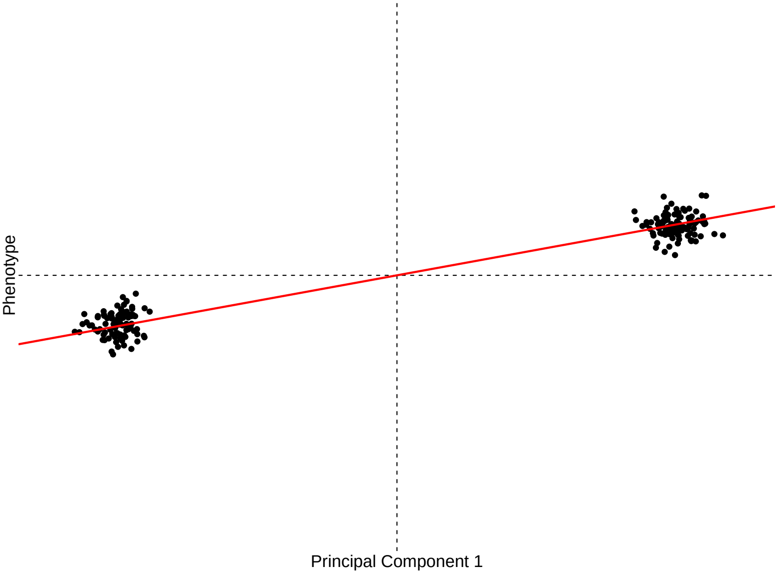

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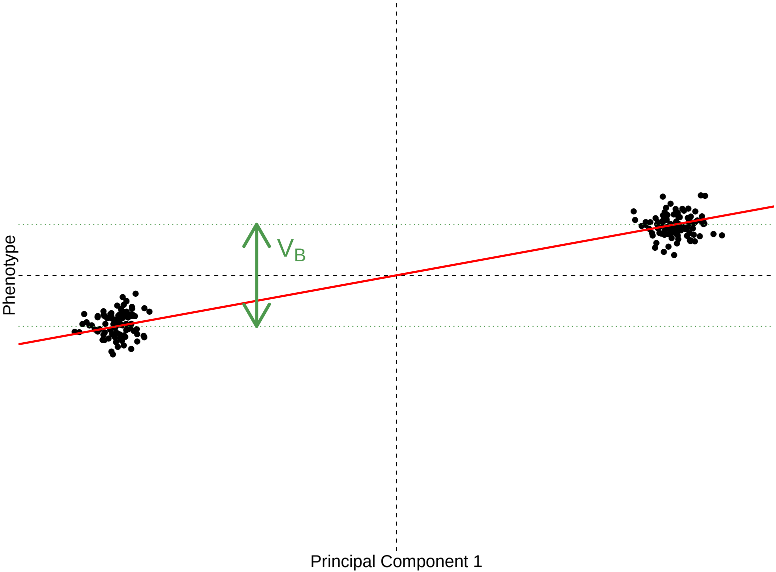

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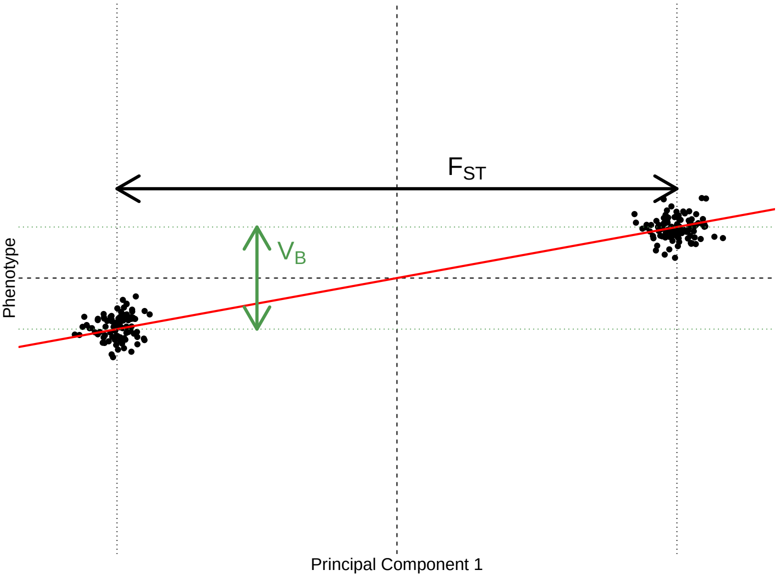

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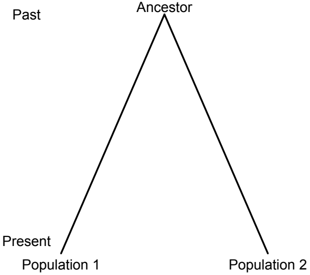

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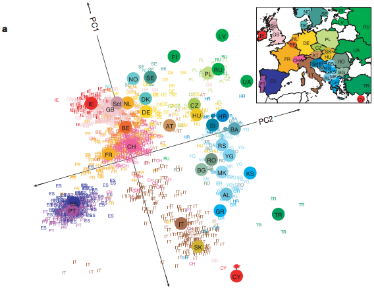

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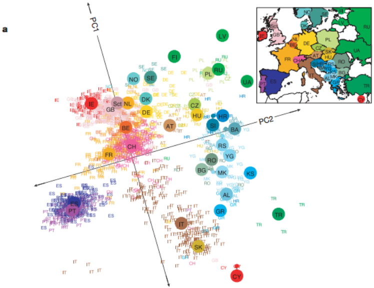

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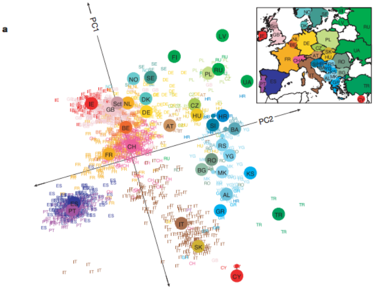

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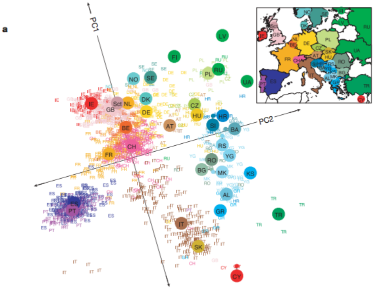

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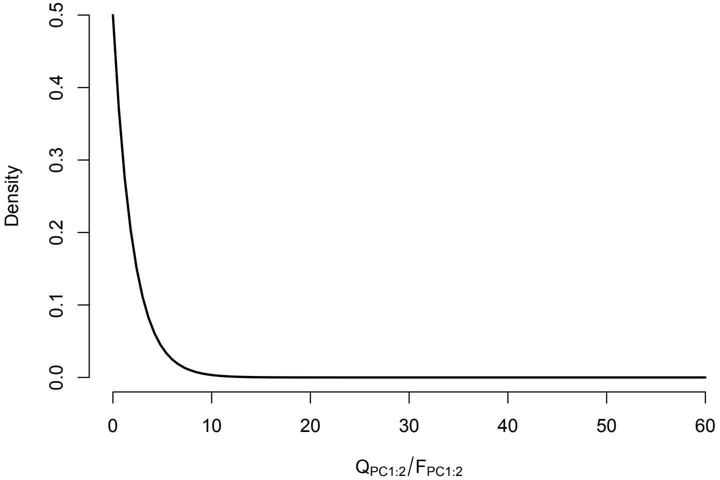
Genetic Divergence for Height in Europe



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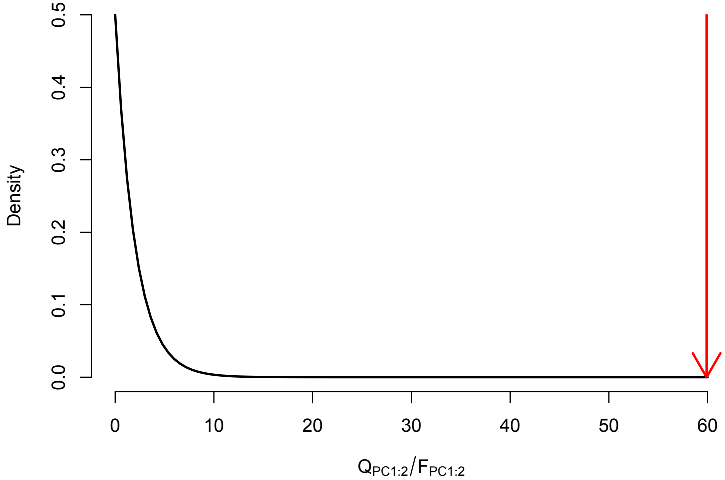

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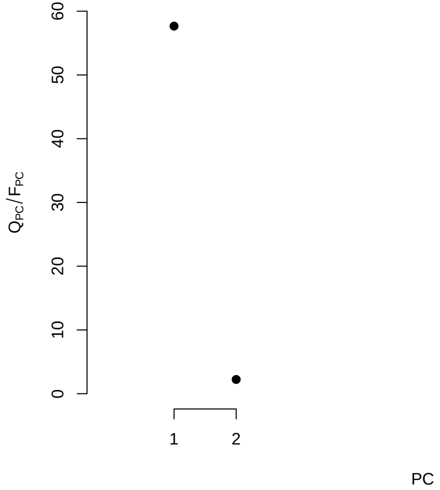

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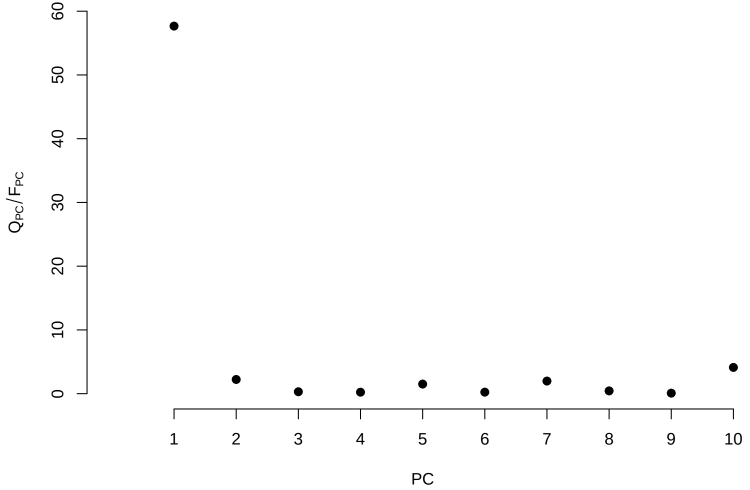

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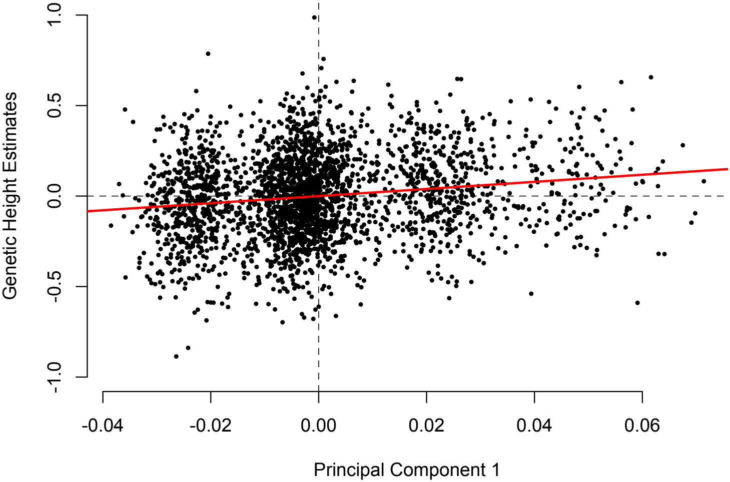

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- Q_{ST}/F_{ST} can be formulated in terms of projections onto reduced rank factorizations of the individual-by-individual kinship matrix
  - Relationship to PCA, *structure*, factor analysis in general
    - Engelhardt and Stephens 2010
  - Every word of caution applicable to PCA/*structure* etc. applies here as well

Things I Didn't Mention

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- Breeding designs easily be incorporated to help with estimation of genetic variance parameters

Thanks!

NSF Graduate Research Fellowship Program

The Center for Population Biology aims to advance understanding of the origins & maintenance of diversity in biological systems through ecological & evolutionary research.

- Coop Lab
  - Alisa
  - Gideon
  - Simon
  - Kristin
  - Chenling
  - Graham
- Annie Schmitt Lab
- Jeff Ross-Ibarra Lab
- Simon Myers