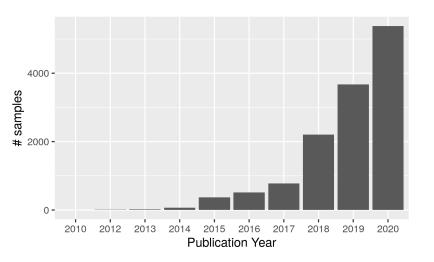
F-statistics and PCA

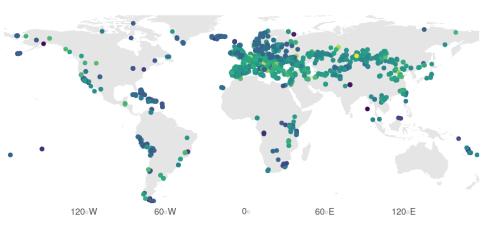
Benjamin Peter

April 22, 2021

Population structure and ancient DNA

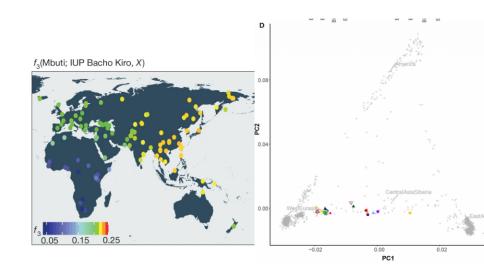


Population structure and ancient DNA



https://reich.hms.harvard.edu/

PCA and *F*-statistics



Goals of this talk

- Technical & Conceptual Background
- Establish conceptual links between frameworks
 - How can we interpret PCA in context of F-stats?
 - 4 How can we interpret F-stats in the context of PCA?
- (Use established links to improve data interpretation)

Goals of this talk

- Technical & Conceptual Background
- Establish conceptual links between frameworks
 - **1** How can we interpret PCA in context of *F*-stats?
 - We have a second to the context of PCA?
 Output
 Description:
- (Use established links to improve data interpretation)

Focus on intuition

Some details in terms of estimation, normalization, missing data will be glossed over

Definition	Branch length
$F_2(X_1, X_2) = \sum_{l} (X_{il} - X_{jl})^2 - H_1 - H_2$	$\begin{array}{cccc} A & P_0 \\ & & \\ P_1 & & P_2 \end{array}$

Definition

Branch length

$$F_2(X_1, X_2) = \sum_{l} (X_{il} - X_{jl})^2 - H_1 - H_2$$

$$F_3(X_x; X_1, X_2) = \sum_{I} (X_{xI} - X_{1I})(X_{xI} - X_{2I}) - H_X$$

$$F_3(X_x; X_1, X_2) = F_2(X_x, X_1) + F_2(X_x, X_2) - F_2(X_1, X_2)$$



Patterson et al. 2012; Peter 2016

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"Admixture"- F_3 -statistic: If data is generated by a tree-like relationship, $F_3(P_X; P_1, P_2) \ge 0$



atterson et al. 2012; Peter 2016

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Branch	
length	

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"Outgroup" - F_3 -statistic: Most similar pops have highest $F_3(P_2; P_X, P_1)$



Patterson et al. 2012; Peter 2016

D (.	
Defi	nition

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$$F_3(X_x; X_1, X_2) = F_2(X_x, X_1) + F_2(X_x, X_2) - F_2(X_1, X_2)$$

$$F_4^{(B)}(X_1; X_2; X_3, X_4) = \sum_{I} (X_{1I} - X_{3I})(X_{2I} - X_{4I})$$



Patierson et 4.22613: P4ter 2010

D (.		
Defi	nıt	ion
	• • • •	. •

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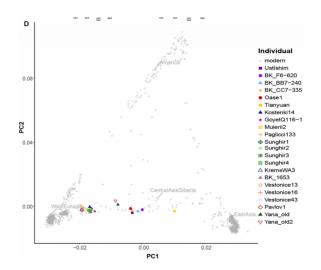
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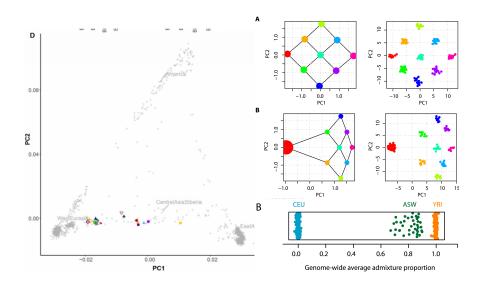
$$F_3(X_x; X_1, X_2) = F_2(X_x, X_1) + F_2(X_x, X_2) - F_2(X_1, X_2)$$

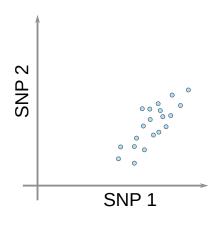
$$F_4^{(T)}(X_1; X_2; X_3, X_4) == \sum_{I} (X_{1I} - X_{2I})(X_{3I} - X_{4I})$$



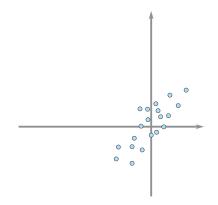
Patterson et 2.22613; Pater 2016



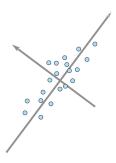




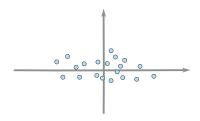
• Raw SNP data **X**; x_{ij}



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- Centering $\mathbf{Y} = \mathbf{CX}$; $y_{ij} = x_{ij} \mu_j$



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- Rotation $\mathbf{Y} = \underbrace{\mathbf{P}}_{\mathsf{PCs}} \underbrace{\mathbf{L}}_{\mathsf{Rotation}}$

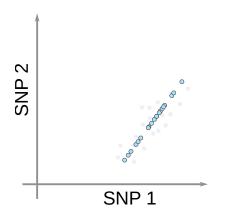


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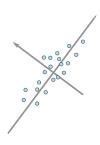
• Truncation
$$\hat{\mathbf{P}} = \begin{pmatrix} \mathbf{P}_1 \\ \mathbf{p}_2 \\ \vdots \\ \mathbf{p}_n \end{pmatrix}$$



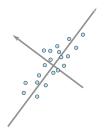
- Raw SNP data **X**; x_{ij}
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• Truncation
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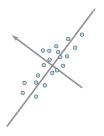
 \bullet Approximation $\hat{\boldsymbol{Y}}=\hat{\boldsymbol{P}}\hat{\boldsymbol{L}}$



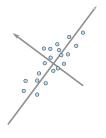
Singular Value Decomposition:Y = (UD)L = PL



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- Eigendecomposition of \mathbf{YY}^T : $\mathbf{YY}^T = \mathbf{UD}^2\mathbf{U}^T = \mathbf{PP}^T$

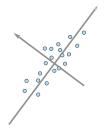


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- \bullet $(\mathbf{YY}^T)_{ij}$

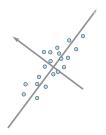


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•
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- $\bullet \ (\mathbf{YY}^T)_{ij} = F_3(\mu; \mathbf{X}_i, \mathbf{X}_j)$

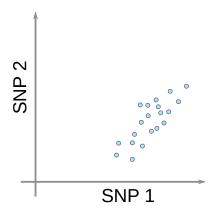


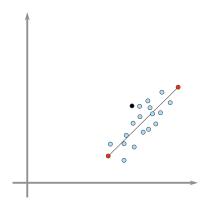
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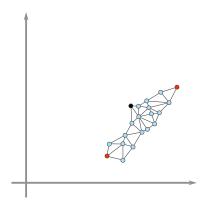
Observation

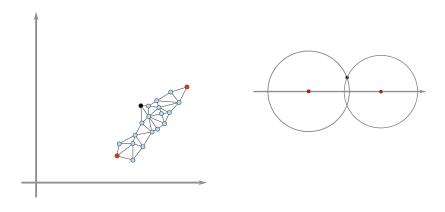
PCA is equivalent to outgroup- F_3 -analysis with sample mean as outgroup

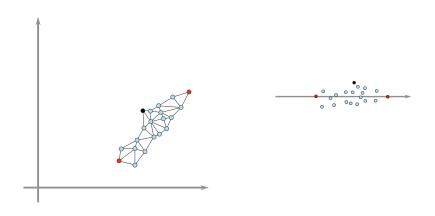


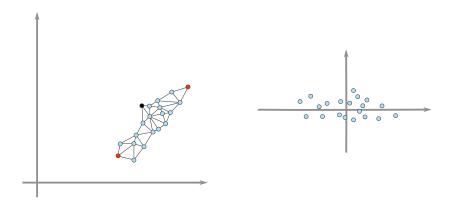


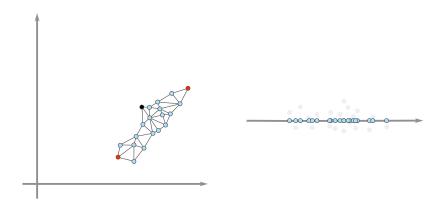












PCA is MDS on \mathbf{F}_2

ullet PCA is decomposition of Covariance matrix: $\mathbf{Y}\mathbf{Y}^T$

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•
$$\mathbf{CF_2C} = \underbrace{\mathbf{CX_i^2C}}_{0} + \underbrace{\mathbf{CX_i^2C}}_{0} - 2\underbrace{\mathbf{CXX^TC}}_{\mathbf{YY^T}}$$

PCA is MDS on \mathbf{F}_2

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Observation

PCA is equivalent to MDS on \mathbf{F}_2

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$$\mathbf{CF_3C} = \underbrace{\mathbf{CO^2C}}_0 - \underbrace{\mathbf{COX_iC}}_0 - \underbrace{\mathbf{COX_jC}}_0 + \underbrace{\mathbf{CXX^TC}}_{\mathbf{YY^T}}$$

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$$\bullet \ \, \mathbf{CF_3C} = \underbrace{\mathbf{C}\mathcal{O}^2\mathbf{C}}_0 - \underbrace{\mathbf{C}\mathcal{O}\mathbf{X_iC}}_0 - \underbrace{\mathbf{C}\mathcal{O}\mathbf{X_jC}}_0 + \underbrace{\mathbf{C}\mathbf{X}\mathbf{X}^T\mathbf{C}}_{\mathbf{YY}^T}$$

Observation

Decomposition of *any* centered F_3 -matrix is equivalent to PCA.

0-diagonal MDS

• Recall that PCA is just translation + rotation

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- Distances (such as F_2) are invariant to translation + rotation

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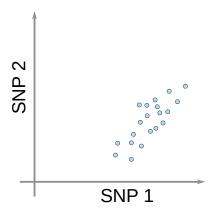
$$F_2(X_1, X_2) = \sum_{\text{loci}} (x_{1l} - x_{2l})^2$$

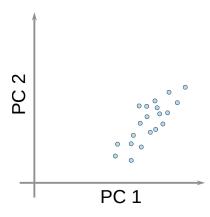
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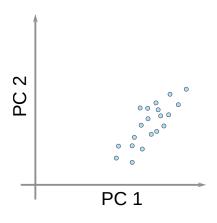
$$F_2(X_1, X_2) = \sum_{PCs} (x_{1p} - x_{2p})^2$$

Observation

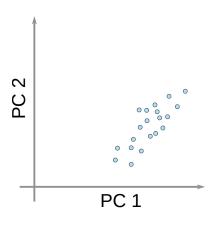
 F_2 can be decomposed in contributions of different principal components



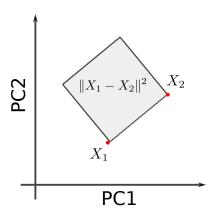




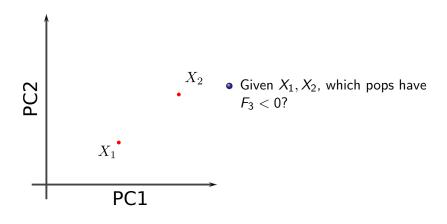
- F-statistics have a geometrical representation on PCA-plot
- Exact only if we use all PCs

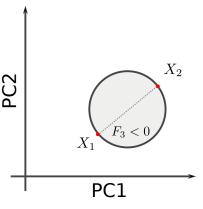


- F-statistics have a geometrical representation on PCA-plot
- Exact only if we use all PCs
- Good approximation for 2D-plot if first 2 PCs capture relevant population structure

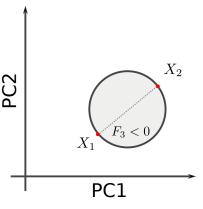


- $F_2(X_1, X_2) = \sum_{I} (X_{1I} X_{2I})^2$
- $F_2(X_1, X_2) = ||X_1, X_2||^2$

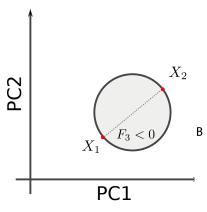




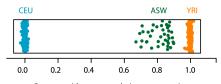
- Given X_1, X_2 , which pops have $F_3 < 0$?
- $F_3(Y; X_1, X_2) = 0$ is a circle!



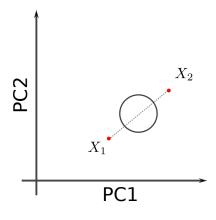
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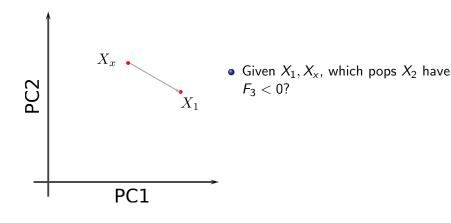


Genome-wide average admixture proportion

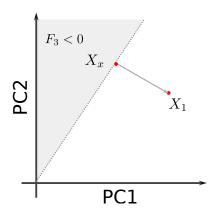


- Given X_1, X_2 , which pops have $F_3 < 0$?
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- $F_3(Y; X_1, X_2) = k < 0$ is smaller circle

Admixture F_3 -stats on PCA-plot

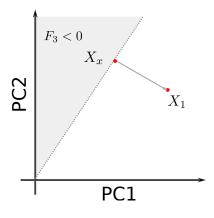


Admixture F_3 -stats on PCA-plot



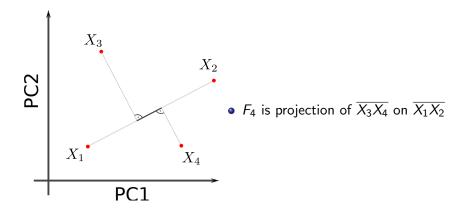
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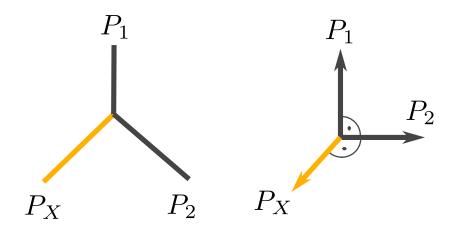


- Given X_1, X_x , which pops X_2 have $F_3 < 0$?
- F_3 is 0 if $(X_x; X_1), (X_x; X_2)$ form a right angle!
- Inner (dot) product: $F_3(X_x; X_1, X_2) = \langle X_x - X_1, X_x - X_2 \rangle$

F_4 -stats on PCA-plot



Where does Orthogonality come from?



- Better link F-stats and PCA results
 - \bullet use Dimensions / Orthogonality for useful data representations

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- ② Distinguish admixture events

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- Setter out-of-sample predictions
 - qpGraph and other tools fail with large samples

