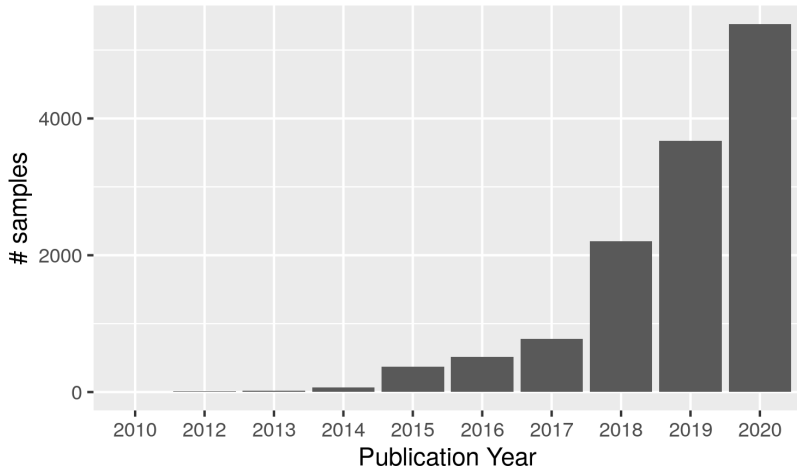


# F-statistics and PCA

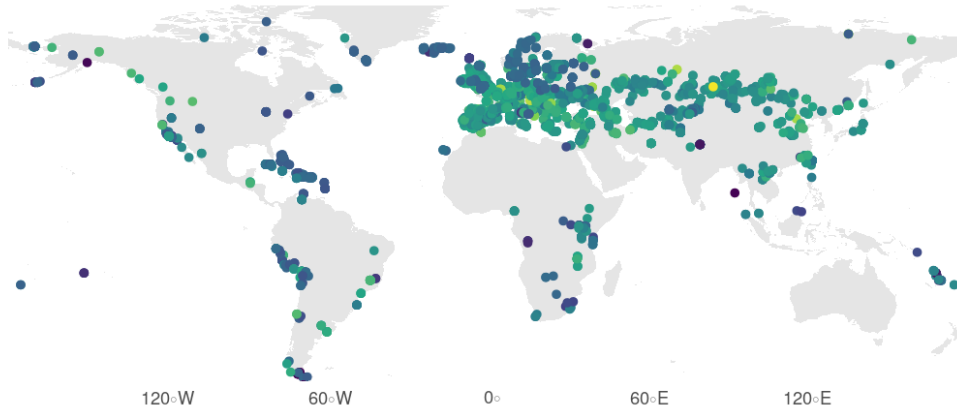
Benjamin Peter

April 21, 2021

# Population structure and ancient DNA



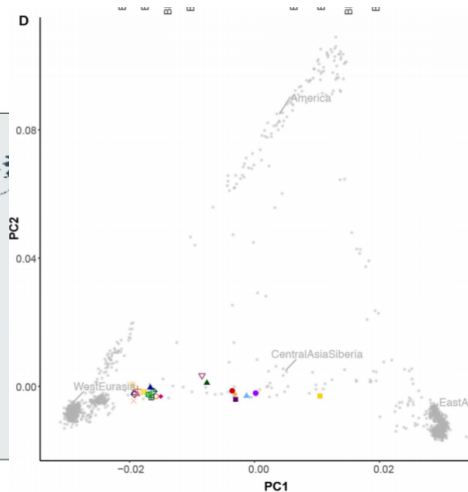
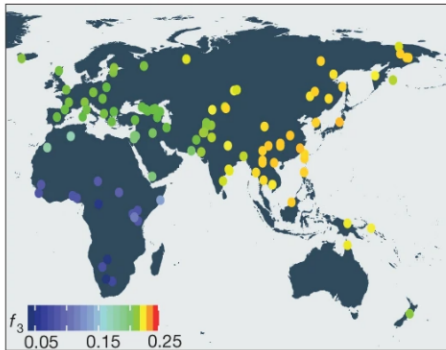
# Population structure and ancient DNA



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

# PCA and $F$ -statistics

$f_3(\text{Mbuti}; \text{IUP Bacho Kiro}, X)$



# Goals of this talk

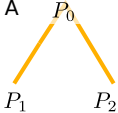
- Technical & Conceptual Background
- Establish conceptual links between frameworks
  - ① How can we interpret PCA in context of  $F$ -stats?
  - ② How can we interpret  $F$ -stats in the context of PCA?
- (Use established links to improve data interpretation)

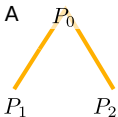
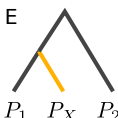
# Goals of this talk

- Technical & Conceptual Background
- Establish conceptual links between frameworks
  - ① How can we interpret PCA in context of  $F$ -stats?
  - ② How can we interpret  $F$ -stats in the context of PCA?
- (Use established links to improve data interpretation)

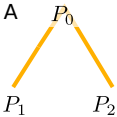
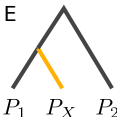
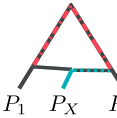
## Focus on intuition

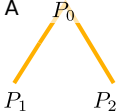


Some details in terms of estimation, normalization, missing data will be glossed over

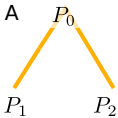


Definition	Branch length
$F_2(X_1, X_2) = \sum_l (X_{il} - X_{jl})^2 - H_1 - H_2$	<p>A</p>  <p><math>P_0</math></p> <p><math>P_1</math> <math>P_2</math></p>

Definition	Branch length
$F_2(X_1, X_2) = \sum_l (X_{1l} - X_{2l})^2 - H_1 - H_2$	<p>A</p> 
$F_3(X_x; X_1, X_2) = \sum_l (X_{xl} - X_{1l})(X_{xl} - X_{2l}) - H_x$ $F_3(X_x; X_1, X_2) = F_2(X_x, X_1) + F_2(X_x, X_2) - F_2(X_1, X_2)$	<p>E</p> 

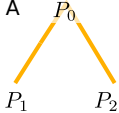




Definition	Branch length
$F_2(X_1, X_2) = \sum_l (X_{1l} - X_{2l})^2 - H_1 - H_2$	<p>A</p> 
$F_3(X_x; X_1, X_2) = \sum_l (X_{xl} - X_{1l})(X_{xl} - X_{2l}) - H_x$ $F_3(X_x; X_1, X_2) = F_2(X_x, X_1) + F_2(X_x, X_2) - F_2(X_1, X_2)$	<p>E</p> 
<p>“Admixture”-<math>F_3</math>-statistic: If data is generated by a tree-like relationship, <math>F_3(P_x; P_1, P_2) \geq 0</math></p>	

Definition	Branch length
$F_2(X_1, X_2) = \sum_i (X_{1i} - X_{2i})^2 - H_1 - H_2$	<p>A</p> 
$F_3(X_x; X_1, X_2) = \sum_i (X_{xi} - X_{1i})(X_{xi} - X_{2i}) - H_x$ $F_3(X_x; X_1, X_2) = F_2(X_x, X_1) + F_2(X_x, X_2) - F_2(X_1, X_2)$	<p>E</p> 
<p>“Outgroup”-<math>F_3</math>-statistic: Most similar pops have highest <math>F_3(P_2; P_x, P_1)</math></p>	

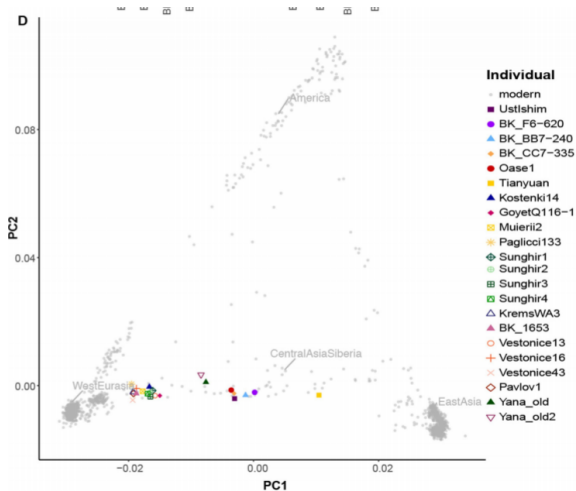
Definition	Branch length
$F_2(X_1, X_2) = \sum_l (X_{1l} - X_{2l})^2 - H_1 - H_2$	<p>A</p> 
$F_3(X_x; X_1, X_2) = \sum_l (X_{xl} - X_{1l})(X_{xl} - X_{2l}) - H_x$ $F_3(X_x; X_1, X_2) = F_2(X_x, X_1) + F_2(X_x, X_2) - F_2(X_1, X_2)$	<p>E</p> 
$F_4^{(B)}(X_1; X_2; X_3, X_4) = \sum_l (X_{1l} - X_{3l})(X_{2l} - X_{4l})$	<p>I</p> 

# F-statistics

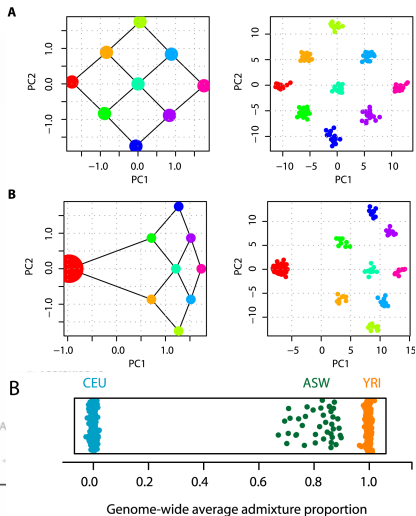
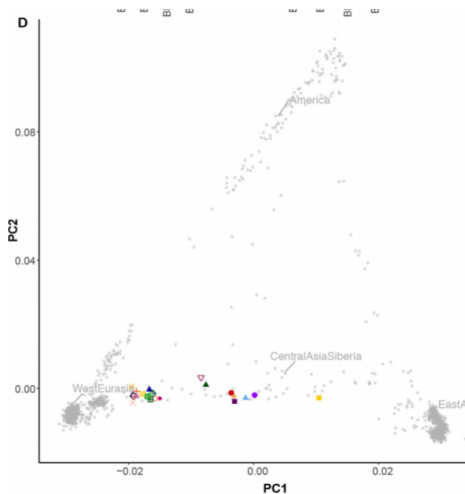
Definition	Branch length
$F_2(X_1, X_2) = \sum_l (X_{1l} - X_{2l})^2 - H_1 - H_2$	<p>A</p> 
$F_3(X_x; X_1, X_2) = \sum_l (X_{xl} - X_{1l})(X_{xl} - X_{2l}) - H_x$ $F_3(X_x; X_1, X_2) = F_2(X_x, X_1) + F_2(X_x, X_2) - F_2(X_1, X_2)$	<p>E</p> 
$F_4^{(T)}(X_1; X_2; X_3, X_4) = \sum_l (X_{1l} - X_{2l})(X_{3l} - X_{4l})$	<p>M</p> 

Patterson et al. 2012; Peter 2016

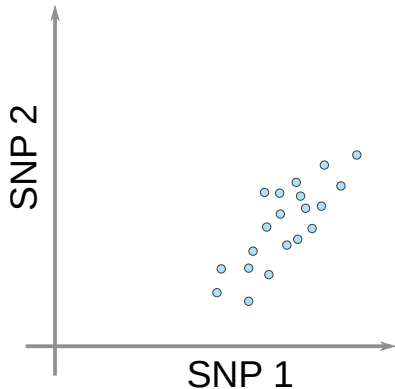
# Principal Component Analysis



# Principal Component Analysis

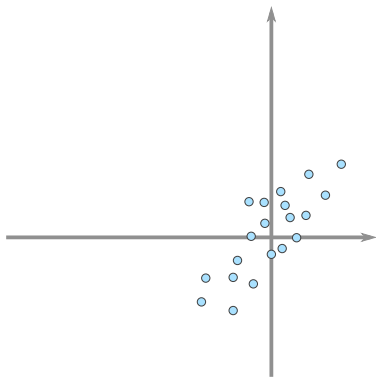


# Principal Component Analysis



- Raw SNP data  $\mathbf{X}$ ;  $x_{ij}$

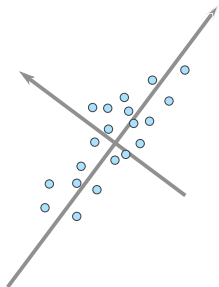
# Principal Component Analysis



- Raw SNP data  $\mathbf{X}$ ;  $x_{ij}$
- Centering  
 $\mathbf{Y} = \mathbf{C}\mathbf{X}$ ;  $y_{ij} = x_{ij} - \mu_j$



# Principal Component Analysis



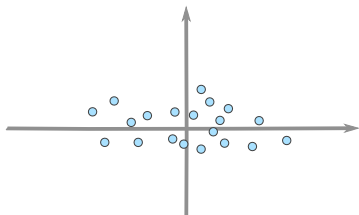
- Raw SNP data  $\mathbf{X}$ ;  $x_{ij}$

- Centering

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

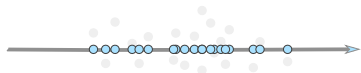
- Rotation  $\mathbf{Y} = \underbrace{\mathbf{P}}_{\text{PCs}} \underbrace{\mathbf{L}}_{\text{Rotation}}$

# Principal Component Analysis



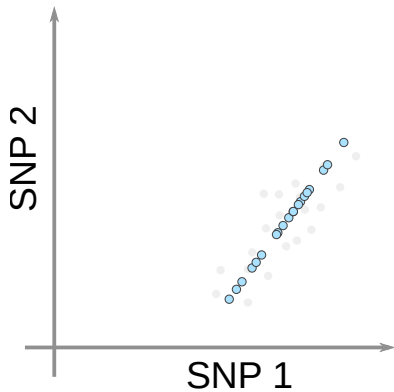
- Raw SNP data  $\mathbf{X}$ ;  $x_{ij}$
- Centering  
 $\mathbf{Y} = \mathbf{CX}$ ;  $y_{ij} = x_{ij} - \mu_j$
- Rotation  $\mathbf{Y} = \mathbf{PL}$

# Principal Component Analysis



- Raw SNP data  $\mathbf{X}$ ;  $x_{ij}$
- Centering  
 $\mathbf{Y} = \mathbf{CX}$ ;  $y_{ij} = x_{ij} - \mu_j$
- Rotation  $\mathbf{Y} = \mathbf{PL}$
- Truncation  $\hat{\mathbf{P}} = \begin{pmatrix} \mathbf{p}_1 \\ \mathbf{p}_2 \\ \vdots \\ \mathbf{p}_n \end{pmatrix}$

# Principal Component Analysis



- Raw SNP data  $\mathbf{X}$ ;  $x_{ij}$

- Centering

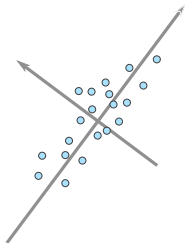
$$\mathbf{Y} = \mathbf{C}\mathbf{X}; y_{ij} = x_{ij} - \mu_j$$

- Rotation  $\mathbf{Y} = \mathbf{P}\mathbf{L}$

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

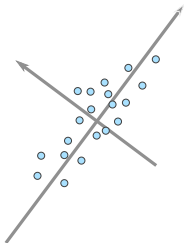
- Approximation  $\hat{\mathbf{Y}} = \hat{\mathbf{P}}\hat{\mathbf{L}}$

# How to find PCs



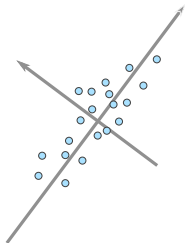
- Singular Value Decomposition:  
 $\mathbf{Y} = (\mathbf{UD})\mathbf{L} = \mathbf{PL}$

# How to find PCs



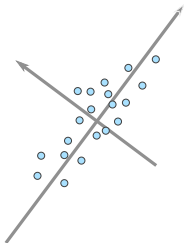
- Singular Value Decomposition:  
 $\mathbf{Y} = (\mathbf{UD})\mathbf{L} = \mathbf{PL}$
- Eigendecomposition of  $\mathbf{YY}^T$ :  
 $\mathbf{YY}^T = \mathbf{UD}^2\mathbf{U}^T = \mathbf{PP}^T$

# How to find PCs



- Singular Value Decomposition:  
 $\mathbf{Y} = (\mathbf{UD})\mathbf{L} = \mathbf{PL}$
- Eigendecomposition of  $\mathbf{YY}^T$ :  
 $\mathbf{YY}^T = \mathbf{UD}^2\mathbf{U}^T = \mathbf{PP}^T$
- $y_{ij}$

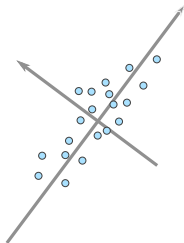
# How to find PCs



- Singular Value Decomposition:  
 $\mathbf{Y} = (\mathbf{UD})\mathbf{L} = \mathbf{PL}$
- Eigendecomposition of  $\mathbf{YY}^T$ :  
 $\mathbf{YY}^T = \mathbf{UD}^2\mathbf{U}^T = \mathbf{PP}^T$
- $y_{ij} = \sum_l (x_{il} - \mu_l)(x_{jl} - \mu_l)$

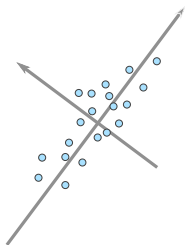


# How to find PCs



- Singular Value Decomposition:  
 $\mathbf{Y} = (\mathbf{UD})\mathbf{L} = \mathbf{PL}$
- Eigendecomposition of  $\mathbf{YY}^T$ :  
 $\mathbf{YY}^T = \mathbf{UD}^2\mathbf{U}^T = \mathbf{PP}^T$
- $y_{ij} = \sum_l (x_{il} - \mu_l)(x_{jl} - \mu_l)$
- $y_{ij} = F_3(\boldsymbol{\mu}; \mathbf{X}_i, \mathbf{X}_j)$

# How to find PCs

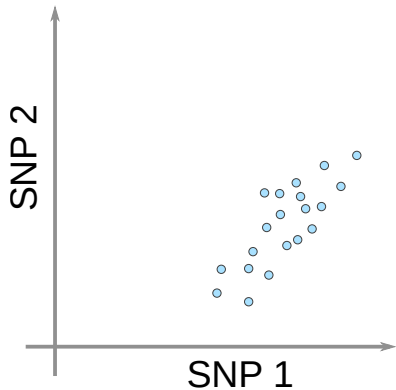


- Singular Value Decomposition:  
 $\mathbf{Y} = (\mathbf{UD})\mathbf{L} = \mathbf{PL}$
- Eigendecomposition of  $\mathbf{YY}^T$ :  
 $\mathbf{YY}^T = \mathbf{UD}^2\mathbf{U}^T = \mathbf{PP}^T$
- $y_{ij} = \sum_l (x_{il} - \mu_l)(x_{jl} - \mu_l)$
- $y_{ij} = F_3(\boldsymbol{\mu}; \mathbf{X}_i, \mathbf{X}_j)$

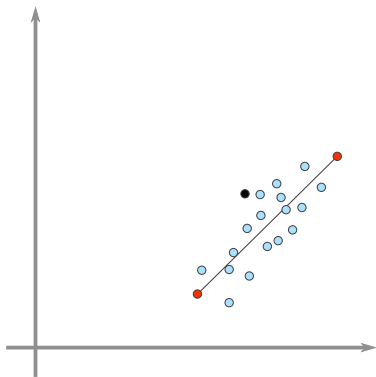
## Observation

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

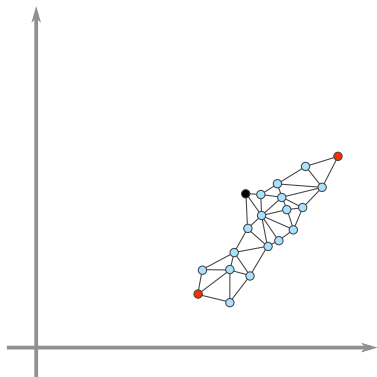
# (metric) Multi-Dimensional Scaling (MDS)



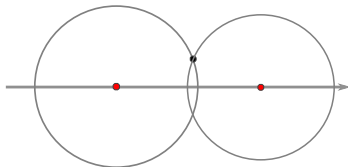
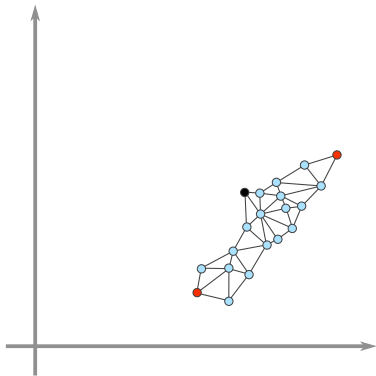
# (metric) Multi-Dimensional Scaling (MDS)



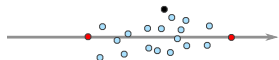
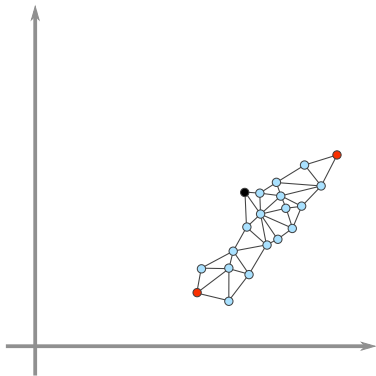
# (metric) Multi-Dimensional Scaling (MDS)



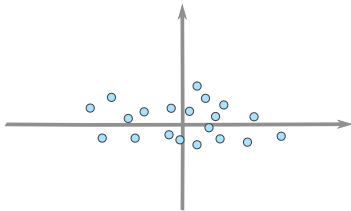
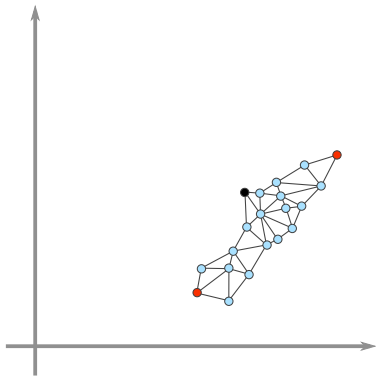
# (metric) Multi-Dimensional Scaling (MDS)



# (metric) Multi-Dimensional Scaling (MDS)

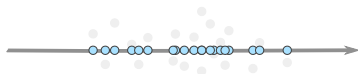
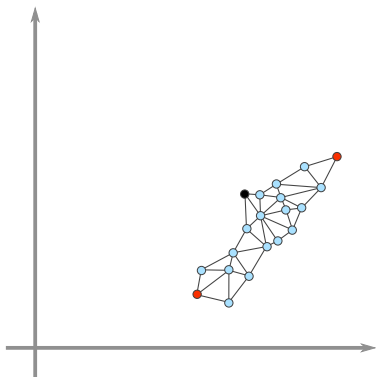


# (metric) Multi-Dimensional Scaling (MDS)





# (metric) Multi-Dimensional Scaling (MDS)



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

- PCA is decomposition of Covariance matrix:  $\mathbf{Y}\mathbf{Y}^T$
- Consider  $\mathbf{F}_2$ ;  $f_{ij} = F_2(X_i, X_j) = X_i^2 + X_j^2 - 2X_iX_j$

- PCA is decomposition of Covariance matrix:  $\mathbf{Y}\mathbf{Y}^T$
- Consider  $\mathbf{F}_2$ ;  $f_{ij} = F_2(X_i, X_j) = X_i^2 + X_j^2 - 2X_iX_j$
- MDS is Eigendecomposition of  $-\frac{1}{2}\mathbf{C}\mathbf{F}_2\mathbf{C}$

- PCA is decomposition of Covariance matrix:  $\mathbf{Y}\mathbf{Y}^T$
- Consider  $\mathbf{F}_2$ ;  $f_{ij} = F_2(X_i, X_j) = X_i^2 + X_j^2 - 2X_iX_j$
- MDS is Eigendecomposition of  $-\frac{1}{2}\mathbf{C}\mathbf{F}_2\mathbf{C}$
- $\mathbf{C}\mathbf{F}_2\mathbf{C} = \underbrace{\mathbf{C}\mathbf{X}_i^2\mathbf{C}}_0 + \underbrace{\mathbf{C}\mathbf{X}_j^2\mathbf{C}}_0 - 2\underbrace{\mathbf{C}\mathbf{X}\mathbf{X}^T\mathbf{C}}_{\mathbf{Y}\mathbf{Y}^T}$

- PCA is decomposition of Covariance matrix:  $\mathbf{Y}\mathbf{Y}^T$
- Consider  $\mathbf{F}_2$ ;  $f_{ij} = F_2(X_i, X_j) = X_i^2 + X_j^2 - 2X_iX_j$
- MDS is Eigendecomposition of  $-\frac{1}{2}\mathbf{C}\mathbf{F}_2\mathbf{C}$
- $\mathbf{C}\mathbf{F}_2\mathbf{C} = \underbrace{\mathbf{C}\mathbf{X}_i^2\mathbf{C}}_0 + \underbrace{\mathbf{C}\mathbf{X}_j^2\mathbf{C}}_0 - 2\underbrace{\mathbf{C}\mathbf{X}\mathbf{X}^T\mathbf{C}}_{\mathbf{Y}\mathbf{Y}^T}$

## Observation

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

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

# PCA is MDS on Outgroup $\mathbf{F}_3$

- PCA is decomposition of Covariance matrix:  $\mathbf{Y}\mathbf{Y}^T$
- Consider  $\mathbf{F}_3(O)$ ;  $f_{ij} = F_3(O; X_i, X_j) = O^2 - OX_i - OX_j + X_iX_j$



# PCA is MDS on Outgroup $\mathbf{F}_3$

- PCA is decomposition of Covariance matrix:  $\mathbf{Y}\mathbf{Y}^T$
- Consider  $\mathbf{F}_3(O)$ ;  $f_{ij} = F_3(O; X_i, X_j) = O^2 - OX_i - OX_j + X_iX_j$

# PCA is MDS on Outgroup $\mathbf{F}_3$

- PCA is decomposition of Covariance matrix:  $\mathbf{Y}\mathbf{Y}^T$
- Consider  $\mathbf{F}_3(O)$ ;  $f_{ij} = F_3(O; X_i, X_j) = O^2 - OX_i - OX_j + X_iX_j$
- $\mathbf{C}\mathbf{F}_3\mathbf{C} = \underbrace{\mathbf{C}O^2\mathbf{C}}_0 - \underbrace{\mathbf{C}OX_i\mathbf{C}}_0 - \underbrace{\mathbf{C}OX_j\mathbf{C}}_0 + \underbrace{\mathbf{C}\mathbf{X}\mathbf{X}^T\mathbf{C}}_{\mathbf{Y}\mathbf{Y}^T}$

# PCA is MDS on Outgroup $F_3$

- PCA is decomposition of Covariance matrix:  $\mathbf{Y}\mathbf{Y}^T$
- Consider  $\mathbf{F}_3(O)$ ;  $f_{ij} = F_3(O; X_i, X_j) = O^2 - OX_i - OX_j + X_iX_j$
- $\mathbf{C}\mathbf{F}_3\mathbf{C} = \underbrace{\mathbf{C}O^2\mathbf{C}}_0 - \underbrace{\mathbf{C}OX_i\mathbf{C}}_0 - \underbrace{\mathbf{C}OX_j\mathbf{C}}_0 + \underbrace{\mathbf{C}\mathbf{X}\mathbf{X}^T\mathbf{C}}_{\mathbf{Y}\mathbf{Y}^T}$

## Observation

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



- Recall that PCA is just translation + rotation

- Recall that PCA is just translation + rotation
- Distances (such as  $F_2$ ) are invariant to translation + rotation

- Recall that PCA is just translation + rotation
- Distances (such as  $F_2$ ) are invariant to translation + rotation
- 

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

- Recall that PCA is just translation + rotation
- Distances (such as  $F_2$ ) are invariant to translation + rotation

- 

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

- 

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



- Recall that PCA is just translation + rotation
- Distances (such as  $F_2$ ) are invariant to translation + rotation

- 

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

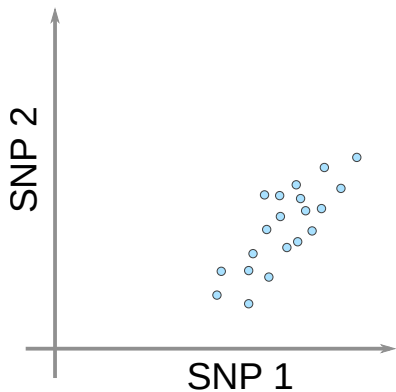
- 

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

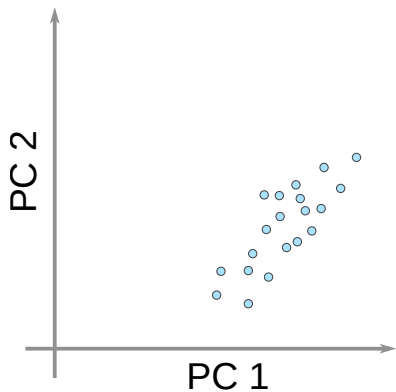
## Observation

$F_2$  can be decomposed in contributions of different principal components

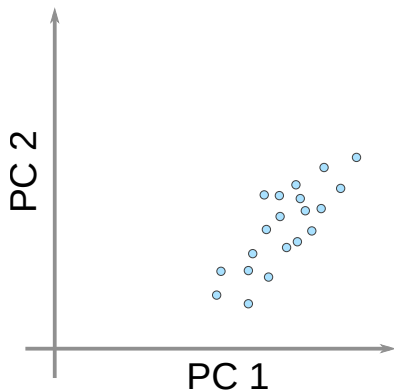
# F-statistics on PCA-plot



# F-statistics on PCA-plot

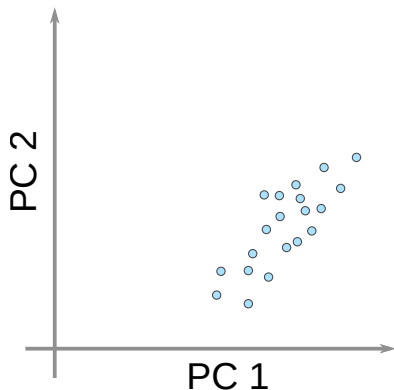


# F-statistics on PCA-plot



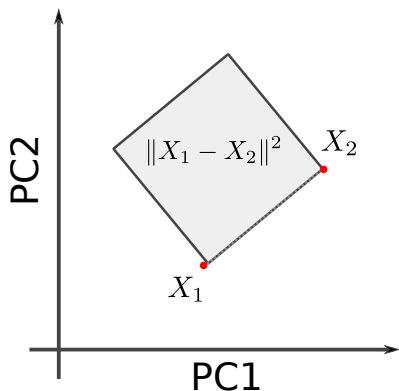
- $F$ -statistics have a geometrical representation on PCA-plot
- Exact only if we use *all* PCs

# F-statistics on PCA-plot



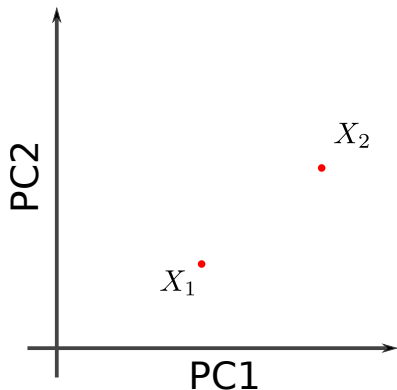
- $F$ -statistics have a geometrical representation on PCA-plot
- Exact only if we use *all* PCs
- Good approximation for 2D-plot if first 2 PCs capture relevant population structure

## $F_2$ -statistic on PCA-plot



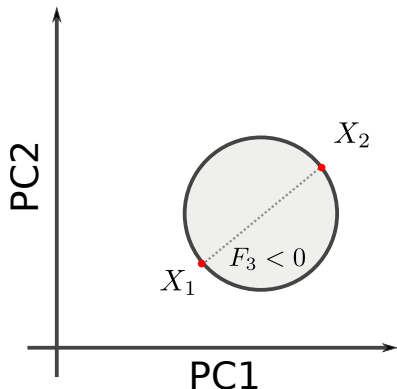
- $F_2(X_1, X_2) = \sum_l (X_{1l} - X_{2l})^2$
- $F_2(X_1, X_2) = \|X_1 - X_2\|^2$

# Admixed populations ( $F_3$ ) on PCA-plot



- Given  $X_1, X_2$ , which pops have  $F_3 < 0$ ?

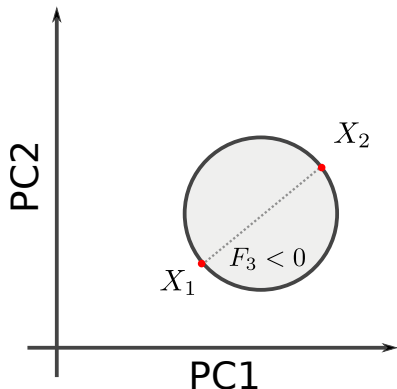
# Admixed populations ( $F_3$ ) on PCA-plot



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

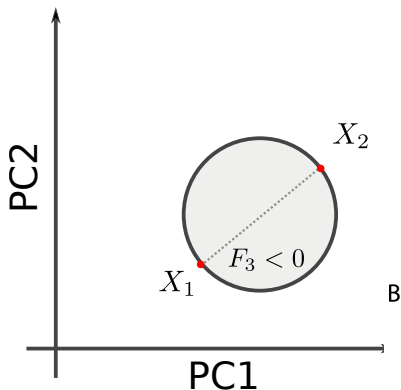


# Admixed populations ( $F_3$ ) on PCA-plot

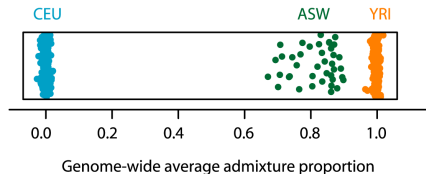


- Given  $X_1, X_2$ , which pops have  $F_3 < 0$ ?
- $F_3(Y; X_1, X_2) = 0$  is a circle!
- Samples outside circle will always have positive  $F_3$

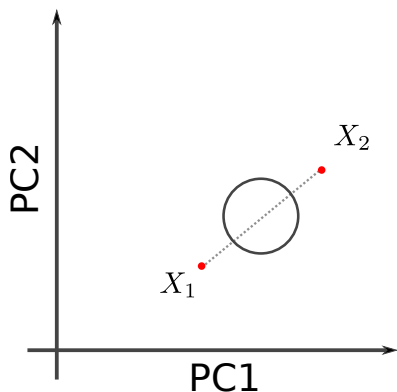
# Admixed populations ( $F_3$ ) on PCA-plot



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

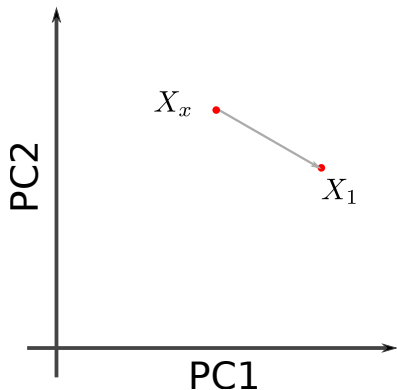


# Admixed populations ( $F_3$ ) on PCA-plot



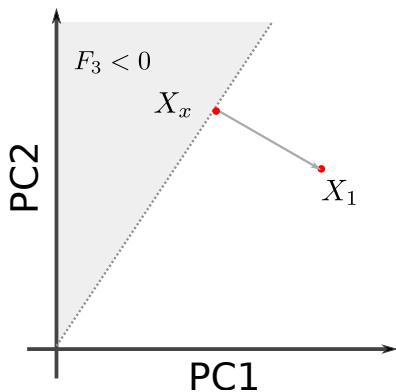
- Given  $X_1, X_2$ , which pops have  $F_3 < 0$ ?
- $F_3(Y; X_1, X_2) = 0$  is a circle!
- Samples outside circle will always have positive  $F_3$
- $F_3(Y; X_1, X_2) = k < 0$  is smaller circle

# Admixture $F_3$ -stats on PCA-plot



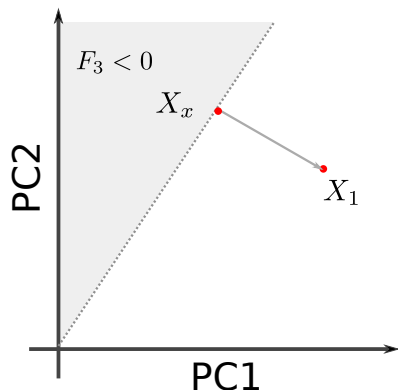
- Given  $X_1, X_x$ , which pops  $X_2$  have  $F_3 < 0$ ?

# Admixture $F_3$ -stats on PCA-plot



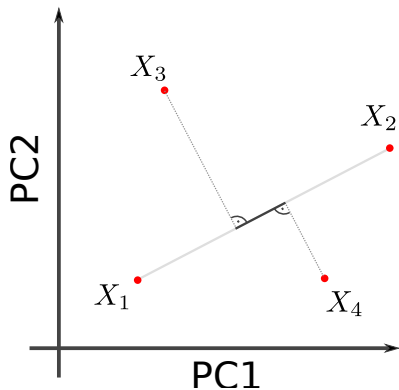
- Given  $X_1, X_x$ , which pops  $X_2$  have  $F_3 < 0$ ?
- $F_3$  is 0 if  $(X_x; X_1), (X_x; X_2)$  form a right angle!

# Admixture $F_3$ -stats on PCA-plot



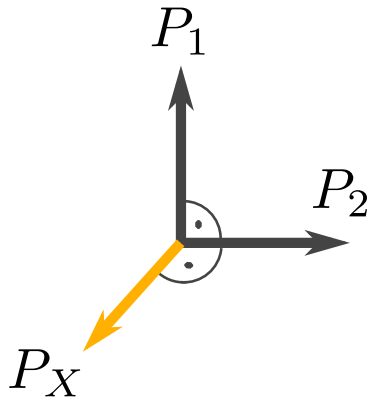
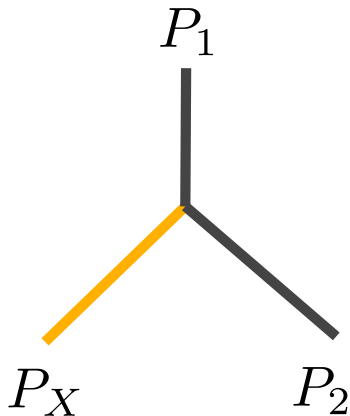
- Given  $X_1, X_x$ , which pops  $X_2$  have  $F_3 < 0$ ?
- $F_3$  is 0 if  $(X_x; X_1), (X_x; X_2)$  form a right angle!
- Inner (dot) product:  
$$F_3(X_x; X_1, X_2) = \langle X_x - X_1, X_x - X_2 \rangle$$

## $F_4$ -stats on PCA-plot



- $F_4$  is projection of  $\overline{X_3X_4}$  on  $\overline{X_1X_2}$

# Where does Orthogonality come from?





- ① Better link  $F$ -stats and PCA results
  - use Dimensions / Orthogonality for useful data representations

- ① Better link  $F$ -stats and PCA results
  - use Dimensions / Orthogonality for useful data representations
- ② Distinguish admixture events

- ① Better link  $F$ -stats and PCA results
  - use Dimensions / Orthogonality for useful data representations
- ② Distinguish admixture events
  - same  $F_3$  value may arise from distinct admixture events, PCs may point to differences

- ① Better link  $F$ -stats and PCA results
  - use Dimensions / Orthogonality for useful data representations
- ② Distinguish admixture events
  - same  $F_3$  value may arise from distinct admixture events, PCs may point to differences
- ③ Understand discrepancies
  - most likely due to data artifacts / higher PCs

- ① Better link  $F$ -stats and PCA results
  - use Dimensions / Orthogonality for useful data representations
- ② Distinguish admixture events
  - same  $F_3$  value may arise from distinct admixture events, PCs may point to differences
- ③ Understand discrepancies
  - most likely due to data artifacts / higher PCs
- ④ Standardize normalization
  - $F_2^{(\text{PCA})} = \frac{1}{\sigma} \sum (X_i - X_j)^2$
  - $F_2^{(\text{F-stats})} = \sum (X_i - X_j)^2$

- ① Better link  $F$ -stats and PCA results
  - use Dimensions / Orthogonality for useful data representations
- ② Distinguish admixture events
  - same  $F_3$  value may arise from distinct admixture events, PCs may point to differences
- ③ Understand discrepancies
  - most likely due to data artifacts / higher PCs
- ④ Standardize normalization
  - $F_2^{(\text{PCA})} = \frac{1}{\sigma} \sum (X_i - X_j)^2$
  - $F_2^{(\text{F-stats})} = \sum (X_i - X_j)^2$

- ① Better link  $F$ -stats and PCA results
  - use Dimensions / Orthogonality for useful data representations
- ② Distinguish admixture events
  - same  $F_3$  value may arise from distinct admixture events, PCs may point to differences
- ③ Understand discrepancies
  - most likely due to data artifacts / higher PCs
- ④ Standardize normalization
  - $F_2^{(\text{PCA})} = \frac{1}{\sigma} \sum (X_i - X_j)^2$
  - $F_2^{(\text{F-stats})} = \sum (X_i - X_j)^2$
- ⑤ Better out-of-sample predictions
  - qpGraph and other tools fail with large samples