

# Relatedness and differentiation in arbitrary population structures

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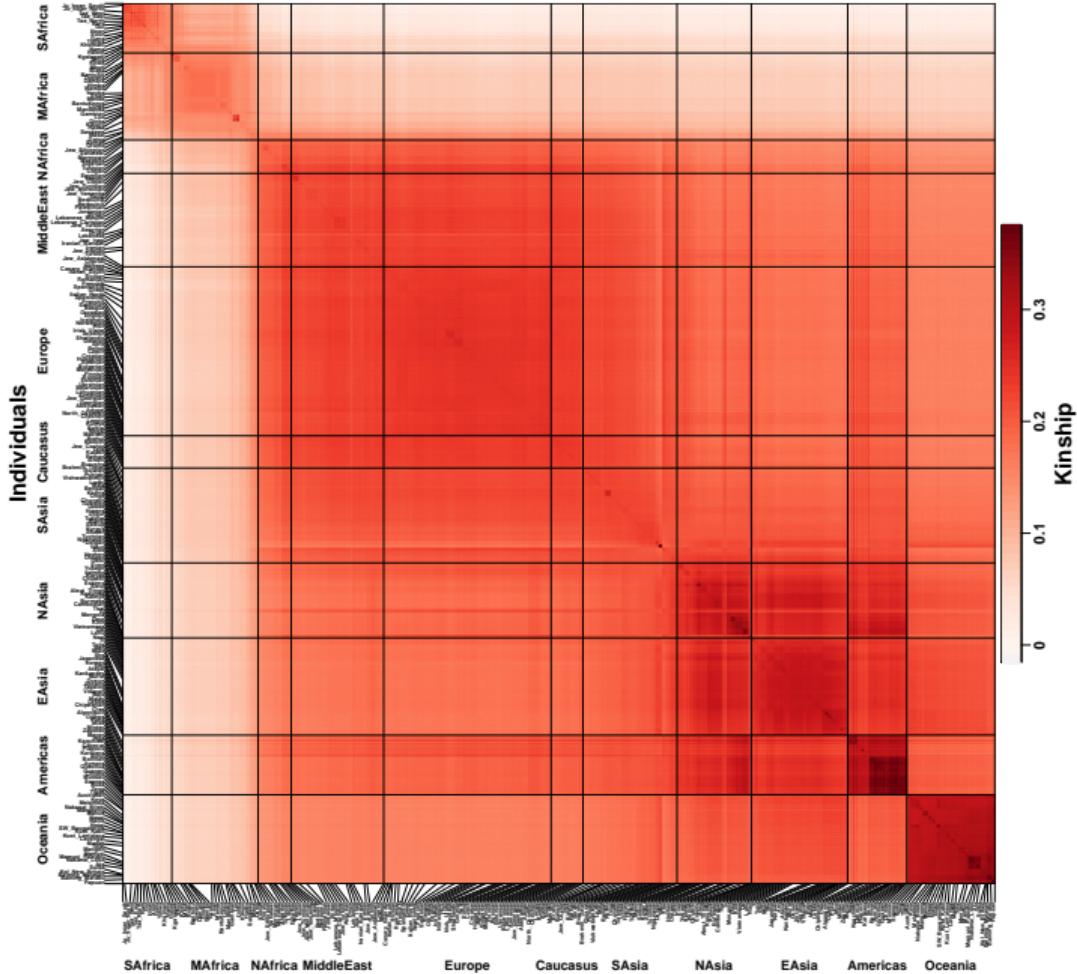
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[popkin](#): first unbiased kinship estimator! — R package on CRAN

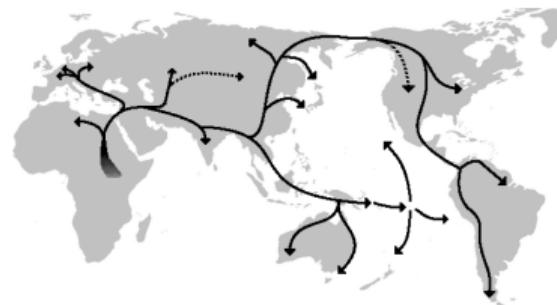
$$A_{jk} = \frac{1}{m} \sum_{i=1}^m (x_{ij} - 1)(x_{ik} - 1) - 1, \quad A_{\min} = \min_{u \neq v} \frac{1}{|S_u||S_v|} \sum_{j \in S_u} \sum_{k \in S_v} A_{jk},$$

$$\hat{\varphi}_{jk} = 1 - \frac{A_{jk}}{A_{\min}} \xrightarrow[m \rightarrow \infty]{\text{a.s.}} \varphi_{jk}.$$



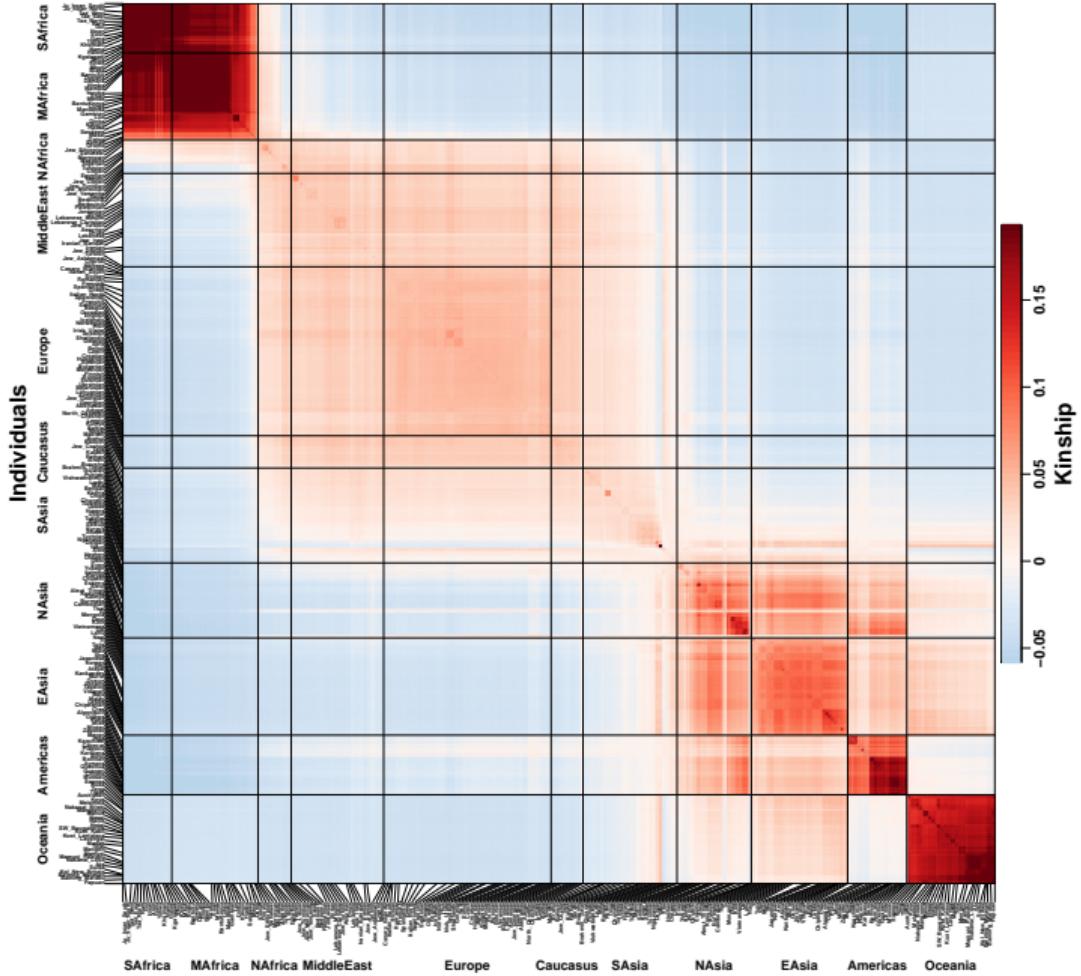
# Our new kinship estimates

Genotypes from "Human Origins"  
(Lazaridis et al. 2014, 2016;  
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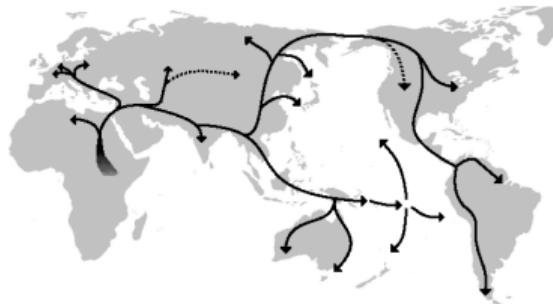
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\*Inbreeding coeffs. on diagonal

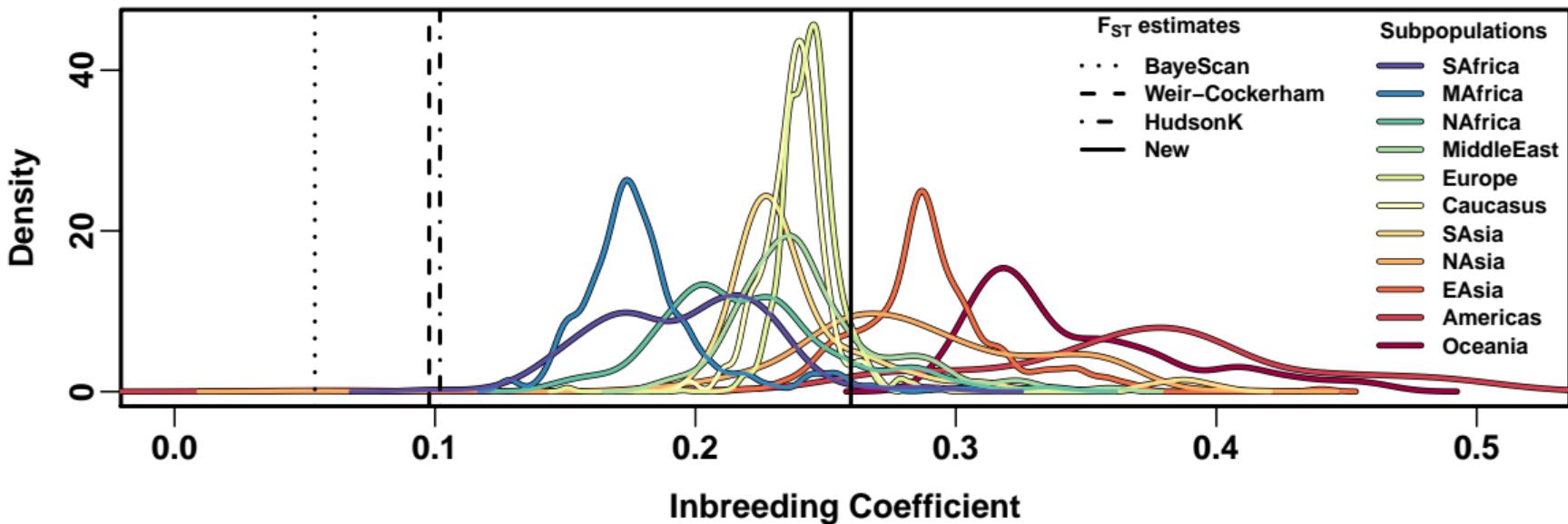


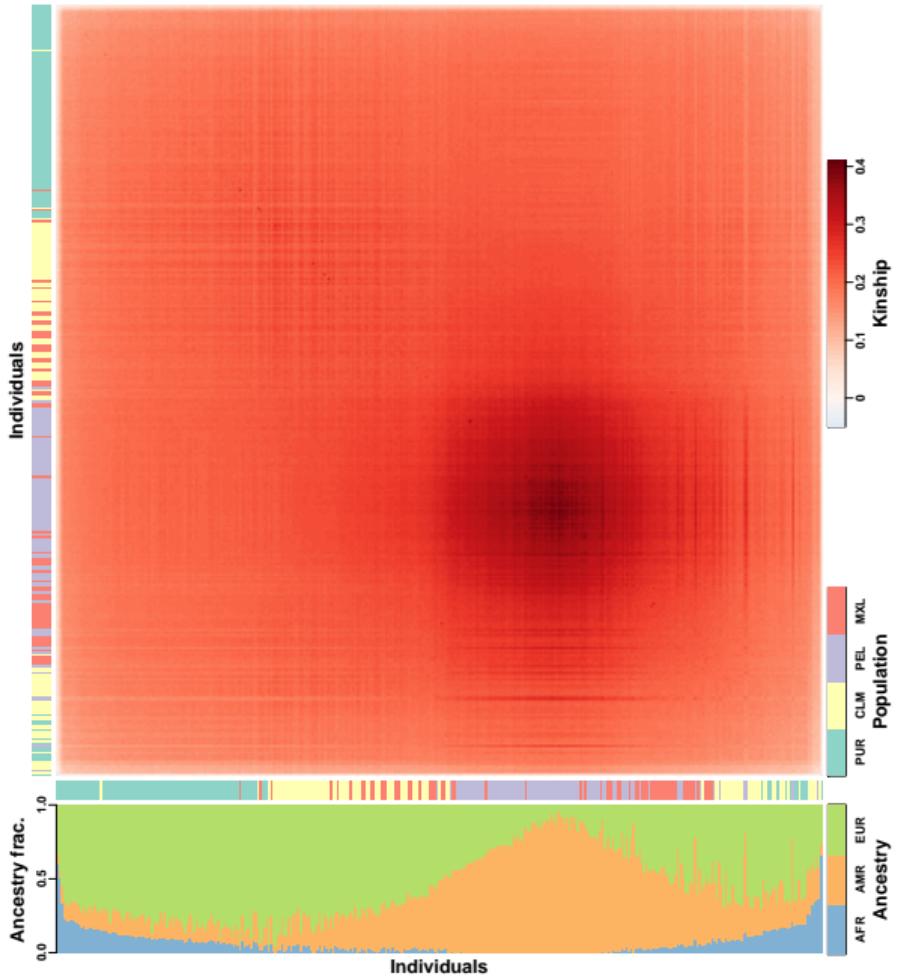
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# Differentiation ( $F_{ST}$ ) previously underestimated





Kinship driven by  
admixture in Hispanics

Our new kinship estimates

Genotypes from the 1000 Genomes Project (2013)

# Better kinship estimates will improve GWAS!

¡Muchas gracias!

Princeton University

**John D. Storey**

Wei Hao

University of Warsaw

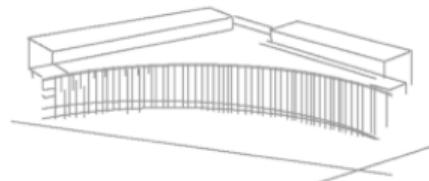
Neo Christopher Chung

Funding

National Institutes of Health

Otsuka Pharmaceutical

Duke StatGen Center  
Biostatistics & Bioinformatics



Lewis-Sigler Institute for Integrative Genomics