Annotated bibliography for *Learning phylogeny through simple statistical genetics*

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1. We first introduce f-statistics, now a commonplace tool in population genetics, used to discover and test models for demographic history. We describe the theory and ADMIXTOOLS, a package that implements most of the tests used. We give a number of examples of discoveries about human history made using f-statistics.

2. *[Joint work with Priya Moorjani]*
   We describe DATES (an earlier version was called *rolloff*. This uses 2-point methods to date 'admixture events'. Simulations show remarkable accuracy.

We include a small annotated bibliography, and for convenience the papers can be downloaded at
`https://drive.google.com/drive/folders/1zxzOYpSh4Kxhrbovszl6-fLYmEYE2soQ?usp=sharing`
The last reference on Ancient Admixture is the most relevant to the talk.

References

[LWH+15] Stephen Leslie, Bruce Winney, Garrett Hellenthal, Dan Davison, Abdelhamid Boumertit, Tammy Day, Katarzyna Hutnik, Ellen C Royrvik, Barry Cunliffe, Daniel J Lawson, et al. The fine-scale genetic structure of the British population. *Nature*, 519(7543):309–314, 2015.

> An interesting example of how haplotype methods may add power to population analysis

[Nor01] M. Nordborg. Coalescent theory. In D.J. Balding, M. Bishop, and C. Cannings, editors, *Handbook of Statistical Genetics*, pages 179–212. John Wiley and Sons. New York., 2001.

A Primer on the Coalescent – a basic concept in modern
mathematical genetics

[PML+12] N. Patterson, P. Moorjani, Y. Luo, S. Mallick, N. Rohland, Y. Zhan, T. Genschoreck, T. Webster, and D. Reich. Ancient admixture in human history. *Genetics*, 192(3):1065–1093, Nov 2012.

A set of methods useful for recovering phylogeny from ge-
netic data – this is mostly what I will cover