

Here are links to papers describing the methods I mentioned (or didn't have time to mention) during my lecture:

abcRF (demography): <https://academic.oup.com/bioinformatics/article/32/6/859/1744513> and <https://academic.oup.com/bioinformatics/advance-article-abstract/doi/10.1093/bioinformatics/bty867/5132692?redirectedFrom=fulltext> (extension for parameter inference)

evolBoosting (sweeps): <http://www.genetics.org/content/187/1/229>

evoNet (demography + sweeps):
<https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1004845>

FastEPRR (recombination): <http://www.g3journal.org/content/6/6/1563.short>

FILET (introgression):
<https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1007341>

Hierarchical boosting for sweeps:
<https://academic.oup.com/bioinformatics/article/31/24/3946/197410>

S/HIC (sweeps):
<https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1005928> and
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5982824/> (extension to unphased data with little/no loss in accuracy)

SFSelect (sweeps): <http://www.genetics.org/content/195/1/181.short>

SWIF(r) (sweeps): <https://www.nature.com/articles/s41467-018-03100-7>

Trendsetter (sweeps): <https://academic.oup.com/mbe/article/36/2/252/5162488>

And here is the paper describing our approach for doing deep learning directly on genotype/haplotype data, which I may have had time to give a brief overview of at the end of the lecture: <https://academic.oup.com/mbe/article/36/2/220/5229930>