Assignment 6

Reading

[Hufford et al 2012](#)

Data

Download the [annotation for version 1 of the maize genome](#).

Download `Hufford_et_al._2012_10kb_statistics.txt` statistics from [figshare](#). You will want the column `fst_teo_mz` representing F_{ST} between maize and *parviglumis*.

Questions

1. Use [bedtools](#) to find the list of genes in windows of high F_{ST} that are also "assimilation genes" (i.e. show differential expression in teosinte but not differential expression in maize from homwework 5). Are "assimilation genes" enriched for evidence of selection?

Hints 1) You may want to filter the F_{ST} windows by amount of data (bp or SNPs or both). 2) The easiest way to test for enrichment is a permutation test using e.g. `sample` in R. 3) Not all genes in your list will be in the gff because versions of the annotaiton have changed!