**Notes on running our simulation model:**

Run the script in the file named “individualBasedSimModel\_HeredityInbreeding\_13Feb2015.r”. Carefully follow the directions given at the beginning of the script.

Several files are included in the output from the simulation:

* .ped and .map files (PLINK format) containing the simulated genotypes from all individuals in the last generation
* a pedigree record of all individuals simulated. Columns are:
1. gen: generation
2. Id: individual identification
3. Sex
4. par1: first parent
5. par2: second parent
6. immigrant: 1 if the individual is an immigrant or a founder, zero otherwise
7. FrohChrom: The realized proportion of the genome that is identical by descent
8. Several columns containing the pedigree inbreeding coefficient calculated using the numbers of generations specified in the simulation script (only for individuals in the last simulated generation)
9. Several columns with multiple locus heterozygosity at the numbers of loci specified in the simulation script (only for individuals in the last simulated generation)
* A file containing the genomic coordinates of identical by descent chromosome segments
	+ You need to run the script called “concatenateIBDTracts\_13Feb2015” to concatenate IBD chromosome segments that are directly adjacent (i.e., those IBD segments that are not separated by any base pairs)

After concatenating the IBD chromosome segments, you can uses these to calculate realized genomic inbreeding (e.g., considering IBD tracts in different length categories if you choose to take this approach).