Supporting Information – Table S1

Table S1. Data and parameters of the inference model implemented in Wilson and Rannala's [1] Bayesian assignment test.

	Variable	Set notation	Description
Observed variables (data)			
Source populations	**S**	$\{S_h\}$	S_h is the population from which individual h was sampled
Genotypes	**X**	$\{X_{hj}\}$	X_{hj} is the genotype of individual h at locus j
Unobserved variables (parameters)			
Migration rates	**m**	$\{m_{lq}\}$	m_{lq} is fraction of individuals in population q that migrated from population l
Migrant ancestry	**M**	$\{M_h\}$	M_h is the source of migrant ancestry of individual h
Time of migration	**t**	$\{t_h\}$	t_h is the generation at which a migrant ancestor of individual h arrived
Population allele frequencies	**P**	$\{p_{ijl}\}$	p_{ijl} is the frequency of allele i at locus j in population l
Inbreeding coefficient	**F**	$\{F_l\}$	F_l is the inbreeding coefficient for population l

1.   Wilson, G. and B. Rannala, *Bayesian Inference of Recent Migration Rates Using Multilocus Genotypes.* Genetics, 2003. **163**: p. 1177-1191.