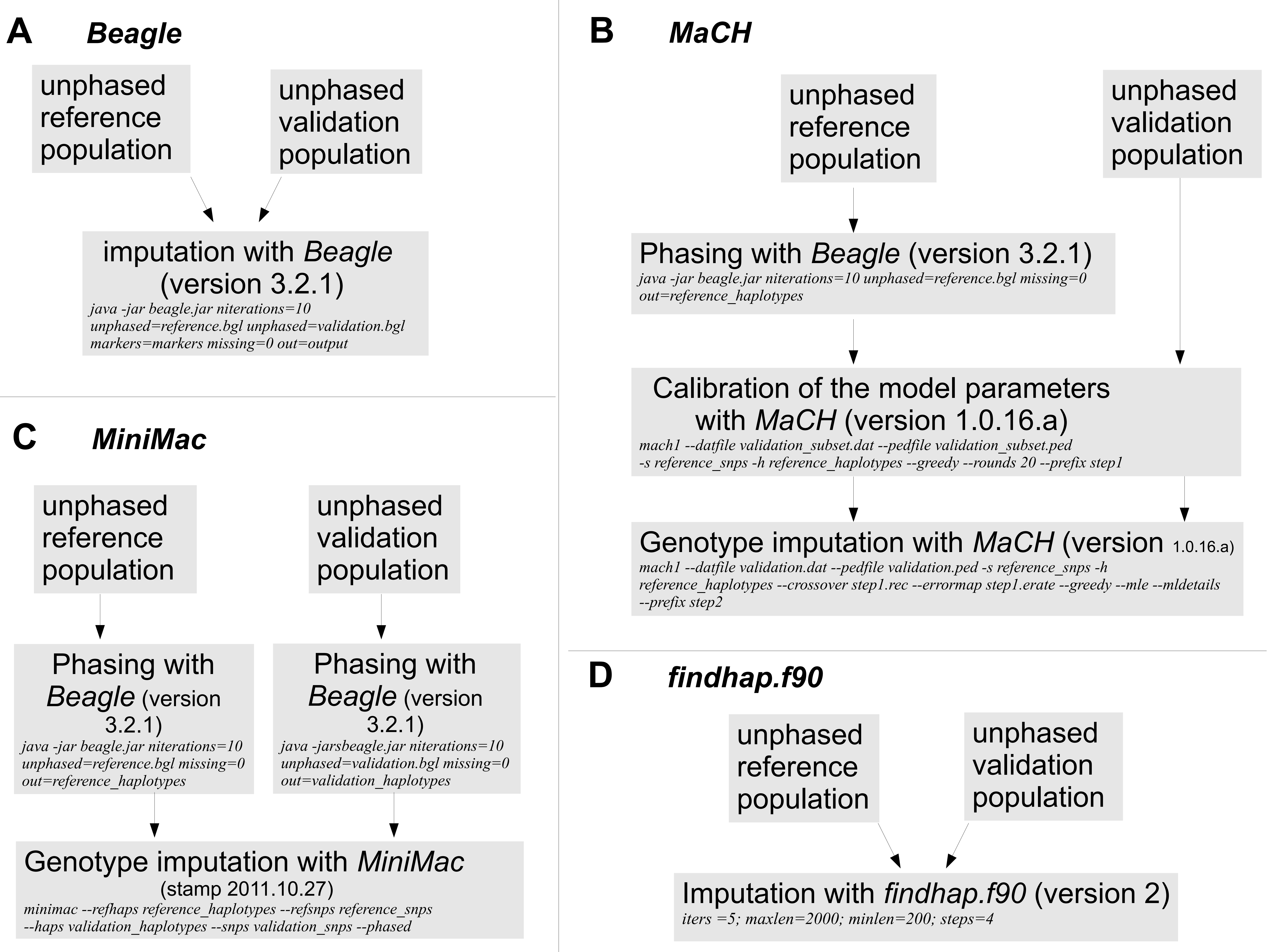

A *Beagle*: imputation with *Beagle* (version 3.2.1)

```
java -jar beagle.jar niterations=10
unphased=reference.bgl unphased=validation.bgl
markers=markers missing=0 out=output
```

B *MaCH*: Phasing with *Beagle* (version 3.2.1)

```
java -jar beagle.jar niterations=10 unphased=reference.bgl missing=0
out=reference_haplotypes
```

Calibration of the model parameters with *MaCH* (version 1.0.16.a)

```
mach1 --datfile validation_subset.dat --pedfile validation_subset.ped
-s reference_snps -h reference_haplotypes --greedy --rounds 20 --prefix step1
```

Genotype imputation with *MaCH* (version 1.0.16.a)

```
mach1 --datfile validation.dat --pedfile validation.ped -s reference_snps -h
reference_haplotypes --crossover step1.rec --errormap step1.erate --greedy --mle --mldetails
--prefix step2
```

C *MiniMac*: Phasing with *Beagle* (version 3.2.1)

```
java -jar beagle.jar niterations=10
unphased=reference.bgl missing=0
out=reference_haplotypes
```

Phasing with *Beagle* (version 3.2.1)

```
java -jarsbeagle.jar niterations=10
unphased=validation.bgl missing=0
out=validation_haplotypes
```

Genotype imputation with *MiniMac* (stamp 2011.10.27)

```
minimac --refhaps reference_haplotypes --refsnps reference_snps
--haps validation_haplotypes --snps validation_snps --phased
```

D *findhap.f90*: Imputation with *findhap.f90* (version 2)

```
iters =5; maxlen=2000; minlen=200; steps=4
```