```
default:
  ploidy            : 4
  genotypeFile      : "example-genotype-tetra.csv"
  phenotypeFile     : "example-phenotype.csv"
  significanceLevel : 0.05
  correctionMethod  : "Bonferroni"
  gwasModel         : "Full"
  nBest             : 10
  filtering         : TRUE
  MAF               : 0.01
  MIND              : 0.1
  GENO              : 0.1
  HWE               : 1e-10
  tools             : "GWASpoly SHEsis PLINK TASSEL"
```