

default:

```
genotypeFile      : "example-genotype.tbl"
phenotypeFile     : "example- phenotype.tbl"
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"
```