```
default:
 ploidy
 genotypeFile
                    : "example-genotype-tetra.csv"
 phenotypeFile
                    : "example-phenotype.csv"
 significanceLevel: 0.05
 correctionMethod
                    : "Bonferroni"
 gwasModel
                    : "Full"
 nRest
                    : 10
 filtering
                    : TRUF
 MAF
                    . 0.01
MTND
                    · 0.1
 GFNO
                    · 0.1
HWF
                    : 1e-10
 tools
                    : "GWASpolv SHEsis PLINK TASSEL"
```