

```

105 if(NEWPOP) {if(length(popmissing)!=0){respop <- (1:npops)[!popmissing]
106 if(!NEWPOP) {if(length(object@region.data@popmissing[[xx]])!=0){popmiss
popmissing]]else{respop <- 1:npops}}
107
108 # END: DO NOT EDIT
109
110 # define here your own function in the PopGenome framework.
111 # default: bial (biallelic matrix), populations (the defined populations)
112 # ... choose here everthing you want from the GENOME class
113
114 new.value[xx,respop] <- EW_Test(bial,populations)
115
116
117 }
118 }
119
120 return(new.value)
121 })

```