

```
106     if(!NEWPOP) {if(length(popmissing)!=0){respop <- (1:npops)[-popmissing]  
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] <- your_intern_function(bial,populations,...)  
115  
116  
117 }  
118 }  
119  
120 return(new.value)  
121 })
```