

## R Code

### 'GA' Package Modification

File: R\ga.R

Lines: 248-259

GA version 2.0 code:

```
# mutation
if(is.function(mutation) & pmutation > 0)
{ for(i in 1:popSize)
  { if(pmutation > runif(1))
    { Mutation <- mutation(object, i)
      Pop[i,] <- Mutation
      Fitness[i] <- NA
    }
  }
object@population <- Pop
object@fitness <- Fitness
}
```

Modified to:

#mutation – optionally return genome and fitness in a list to facilitate AGA

```
if(is.function(mutation) & pmutation > 0)
{ for(i in 1:popSize)
  { if(pmutation > runif(1))
    { Mutation <- mutation(object, i)
      if(is.list(Mutation)) {
        Pop[i,] <- Mutation$genome
        Fitness[i] <- Mutation$fitness
      } else {
        Pop[i,] <- Mutation
        Fitness[i] <- NA
      }
    }
  }
object@population <- Pop
object@fitness <- Fitness
}
```