chem-bla-ics

An R-based genetic algorithm

Egon Willighagen

Published November 19, 2007

Citation
Willighagen, E. (n.d.). In *chem-bla-ics*. chem-bla-ics. https://doi.org/10.59350/hfw6p-d6p02

Keywords
Rstats, Chemometrics

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During my PhD I wrote a simple but effective genetic algorithm package for R. Because there was a bug recently found, and there is interest in extending the functionality, I have set up a SourceForge project called genalg.

The package provides GA support for binary and real-value chromosomes (and integer chromosomes is something that will be added soon), and allows to use custom evaluation functions. Here is some example code:

```
# optimize two values to match pi and sqrt(50)
evaluate <- function(string=c()) {
    returnVal = NA;
    if (length(string) == 2) {
        returnVal = abs(string[1]-pi) + abs(string[2]-sqrt(50));
    } else {
        stop("Expecting a chromosome of length 2!");
    }
    returnVal
}
monitor <- function(obj) {
    # plot the population
    xlim = c(obj$stringMin[1], obj$stringMax[1]);
    ylim = c(obj$stringMin[2], obj$stringMax[2]);
    plot(obj$population, xlim=xlim, ylim=ylim, xlab="pi", ylab="sqrt(50)");
}
rbga.results = rbga(c(1, 1), c(5, 10), monitorFunc=monitor,
    evalFunc=evaluate, verbose=TRUE, mutationChance=0.01)
plot(rbga.results)
plot(rbga.results, type="hist")
plot(rbga.results, type="vars")
```