

Package: xegaPopulation (via r-universe)

August 26, 2024

Title Genetic Population Level Functions

Version 1.0.0.4

Description This collection of gene representation-independent functions implements the population layer of extended evolutionary and genetic algorithms and its support. The population layer consists of functions for initializing, logging, observing, evaluating a population of genes, as well as of computing the next population. For parallel evaluation of a population of genes 4 execution models - named Sequential, MultiCore, FutureApply, and Cluster - are provided. They are implemented by configuring the lapply() function. The execution model FutureApply can be externally configured as recommended by Bengtsson (2021) <doi:10.32614/RJ-2021-048>. Configurable acceptance rules and cooling schedules (see Kirkpatrick, S., Gelatt, C. D. J, and Vecchi, M. P. (1983) <doi:10.1126/science.220.4598.671>, and Aarts, E., and Korst, J. (1989, ISBN:0-471-92146-7) offer simulated annealing or greedy randomized approximate search procedure elements. Adaptive crossover and mutation rates depending on population statistics generalize the approach of Stanhope, S. A. and Daida, J. M. (1996, ISBN:0-18-201-031-7).

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URL <<https://github.com/ageyerschulz/xegaPopulation>>

Encoding UTF-8

LazyData false

RoxygenNote 7.2.3

Depends R (>= 4.0.0), parallel, future.apply, utils, stats

Suggests testthat (>= 3.0.0), future, parallelly

Imports xegaGaGene, xegaSelectGene

Repository <https://ageyerschulz.r-universe.dev>

RemoteUrl <https://github.com/ageyerschulz/xegapopulation>

RemoteRef HEAD

RemoteSha 35868206c1c327a153382aec3fc0f0249a9b5eb0