*2021 International Nuclear Atlantic Conference – INAC 2021*
*Virtual meeting, Brazil, November 29 – December 2, 2021*

ISBN: 978-65-594-1256-3

# RELOAD OPTIMIZATION OF NUCLEAR POWER PLANTS USING GA TOTALLY DISCRET TOGETHER WITH THE GENES REACTOR PHYSICS CODE

De Lima, A. M. M.[1], Nicolau, A.S[2], and
Freire. F. S.[3]

[1] *alan@lmp.ufrj.br,*
[2] *andressa@lmp.ufrj.br,*
[3] *ffreire@eletronuclear.gov.br,*

## 1. Introduction

Nuclear Power Plants (NPP) reactor reload process occurs whenever it is no longer possible to maintain the critical reactor producing energy at the nominal power, since the burning of the Fuel Elements (FEs) in the reactor core reached a certain value and the reactor needs to be turned off to exchange the FEs. FEs are discharged from the core and stored in a used fuel pool. The FEs with very low concentrations of $U^{235}$ are kept permanently in the pool. On the other hand, FEs with higher concentrations of $U^{235}$ together with new FEs will form part of the next cycle arrangement.

Nuclear reactor reload optimization problem (NRP) consists in determining the positioning of new and used FEs in the reactor core in an optimized way. In other words, to minimize the Fes cost-effective, making maximum use of the FE burning guaranteeing the safety and symmetry constraints. As such, NRP is a complex problem, that its difficulty grows exponentially with the number of FEs in the reactor core.

In this work a computational modeling is presented to perform the NRP based on Genetic Algorithm (GA) totally discrete. A new reactor physics code called GENES, generating a system called GATD-GENES is used. GENES is able to calculate the value of the power mean in the FE with accuracy and the boron concentration with a margin of error of, less than 20 ppm.

The GATD-GENES was test using data from cycle 8 of Angra 1 NPP. The results were compared with the ELETRONUCLEAR (ETN) real results. With the methodology proposed is possible to obtain a new core configuration in 1,7 days, 30 times shorter than 52 days provide by ELETRONUCLEAR.

## 2. GENES Physics Reactors Code

The GENES code uses of the nodal expansion method (NEM) [1] to solve the neutron continuity equation for two energy groups. In general, in this methodology, the volume of the reactor core is subdivided into volume nodes, $V_n = a_x^n a_y^n a_z^n$; transforming the continuity equation into discrete classical form presented in the equation (1).

$$\sum_{u=x,y,z} (J_{gur}^n - J_{gul}^n)/a_u^n + \Sigma_{Rg}^n \phi_g^n = \frac{1}{k_{eff}} \chi_g \sum_{g'=1}^{2} \nu\Sigma_{fg'}^n \phi_{g'}^n + \sum_{\substack{g'=1 \\ g' \neq g}}^{2} \Sigma_{gg'}^n \phi_{g'}^n \tag{1}$$

where,

$$J_{gus}^{n} \equiv J_{gus}^{+n} - J_{gus}^{-n} = -D_{g}^{n} \frac{d}{du} \psi_{gu}^{n}(u) \Big|_{u=u_{s}^{n}} \tag{2}$$

and,

$$\phi_{g}^{n} \equiv \frac{1}{V_{n}} \int_{0}^{a_{x}^{n}} \int_{0}^{a_{y}^{n}} \int_{0}^{a_{z}^{n}} \phi_{g}(x,y,z) dx dy dz \tag{3}$$

$$J_{gus}^{\pm n} \equiv \frac{1}{a_{v}^{n} a_{w}^{n}} \int_{0}^{a_{v}^{n}} \int_{0}^{a_{w}^{n}} J_{gu}^{\pm}(u_{s}^{n}, v, w) dv dw \tag{4}$$

$$\psi_{gu}^{n}(u) \equiv \frac{1}{a_{v}^{n} a_{w}^{n}} \int_{0}^{a_{v}^{n}} \int_{0}^{a_{w}^{n}} \phi_{g}(u,v,w) dv dw \tag{5}$$

Nuclear data are considered to be $V_n = a_x^n a_y^n a_z^n$. After integrating the diffusion equation across the direction u (= x, y, z), we arrive at:

$$-D_{g}^{n} \frac{d^{2}}{du^{2}} \psi_{gu}^{n}(u) + \Sigma_{gu}^{n} \psi_{gu}^{n}(u) = \frac{1}{k_{eff}} \chi_{g} \sum_{g'=1}^{2} \nu \Sigma_{fg'}^{n} \psi_{g'u}^{n}(u) + \sum_{g'=1}^{2} \Sigma_{gg'}^{n} \psi_{g'u}^{n}(u) - L_{gu}^{n}(u) \tag{6}$$

where,

$$L_{gu}^{n}(u) \equiv -\frac{D_{g}^{n}}{a_{v}^{n} a_{w}^{n}} \int_{0}^{a_{v}^{n}} \int_{0}^{a_{w}^{n}} \left( \frac{\partial}{\partial v} \phi_{g}(u,v,w) + \frac{\partial}{\partial w} \phi_{g}(u,v,w) \right) dv dw \tag{7}$$

It is identified as the transverse leak direction u (= x, y, z).

The GENES code has an dynamic memory allocation; Thus allows a varied number of radial and axial nodes in the modeling. It contains classic features of a contemporary commercial depletion code. In general, the code contains properties suitable for modeling large commercial reactors.

## 3. GA Totally Discrete (GATD)

The GATD methodology proposed in this work is based on the standard GA [2] and Random Keys Methods (RKM) [3]. However, in this case the RKM is only used in the FEs that are repeated reducing the chance of confusion in algorithm learning, besides only having integer numbers. Here, a solution generator vector is composed of 20 numbers from 1 to 20, as presented in figure 2.

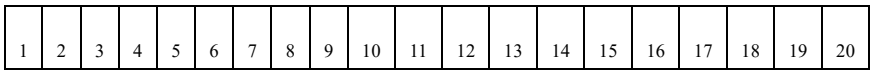


Figure 2: List 3: Solution generator vector

The GATD initial population is generated by making random changes in the solution vector. So, in the initial population we only have valid solutions. The mutation operator only generates valid solution since random changes are made to the solution vector according to the mutation rate. Is meant by random changes, simple exchanges of positions of the FEs. But when we apply the crossover operator we generate invalid solutions, as shown in figure 3.

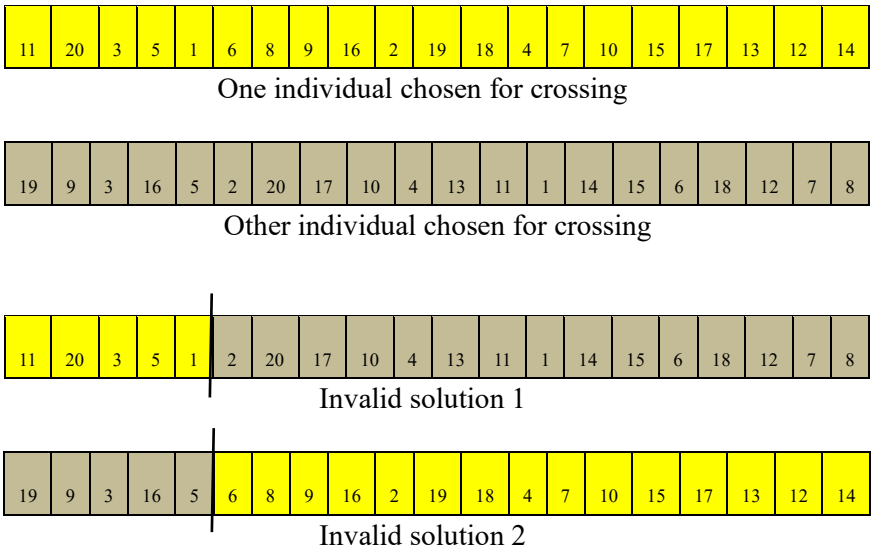


Figure 3: Crossover Process

In figure 3, we can note that the crossover point was chosen as the fifth position. After the crossover was generated two invalid solutions, it is called invalid because they repeat some numbers. In solution 1 the numbers 11, 20 and 1 are repeated, and in solution 2 the numbers 19, 9 and 16 are repeated. So, we only have 3 numbers repeated, in this case we just need to apply the random keys operator on the 3 repeated numbers and substitute them for the 3 missing numbers, different from traditional GA. In GATD the maximum number to which the RKM is apply is the half of the number of FEs, in this case 10.

## 4. Results and Discussion

The GATD-GENES was test using data from Angra 1 cycle 8 and the results was compared with the ETN real results, cycle 8 was chosen because this cycle is considered as an initial cycle due to internal events in Angra 1. For a low-leak strategy the objective function used in GATD was:

If peak factor > limit value then Objective function = peak factor
If no Objective function = 1 / Boron concentration

In this function, for peak values of radial power above the limit value of the technical specification, we want to minimize them, because with these values above the limit this core configuration becomes

invalid, and for values below this limit, where the configurations of core become valid, we want to maximize the critical concentration of soluble boron. With the use of this function we clearly realize that when we reach the limit value of the radial power peak of the technical specification (1,435), the value of boron tends to be stable or rise, and the value of the radial power peak oscillates below 1.435. Table 1 shows the 5 best results found by the GATD-GENES system and also executed in the licensed code to validate the results, and the actual result from Angra 1 cycle 8.

Table I: Results and Conclusions.

| Case | Peak Power Factor | Boron concentration (ppm) |
|---|---|---|
| Real cycle 8 | 1.362 | 1108 |
| Test 1 | 1.411 | 1208 |
| Test 2 | 1.427 | 1189 |
| Test 3 | 1.416 | 1250 |
| Test 4 | 1.390 | 1181 |
| Test 5 | 1.384 | 1210 |

## 5. Conclusion

This article presents a new physics reactors code (GENE) that works integrated with a GATD, called GATD - GENES system, in order to solve NRP. The results were compared with real data of a physic reactors code used by ETN. Each test run lasted approximately 24 hours. The GATD-GENES system runs in 5 seconds, while the licensed code runs in 30 seconds. Besides, the best result of Boron concentration found with GATD-GENES system was 1250 ppm, against 1108 ppm of the ETN real cycle. The 142 ppm of boron provide us approximately 38 more days of effective full power operation, which could have provided a larger revenue to the ETN.

The good results obtained with GATD-GENES system shows that the new methodology can help to find go core configurations in a few hours. So, we can say that the GATD_GENES is a good tool for solving this type of problem.

## References

[1] CHRISTENSE, B., 1985, Three-dimensional Static and Dynamic Reactor Calculations by the

Nodal Expansion Method, Riso National Laboratory, DK-4000 Roskilde, Denmark.

[2] A. HOLLAND, J.H., 1975, Adaptation In Natural and Artificial Systems, Ann Arbor,

University of Michigan Press.

[3] BEAN. J.C., 1994, Genetic Algorithms and Random Keys for Sequencing and Optimization,

ORSA Journal on Computing, vol. 6, n 2, Spring.