



Enabling Grids for E-scienceE

# Genetic Stellarator Optimisation in Grid

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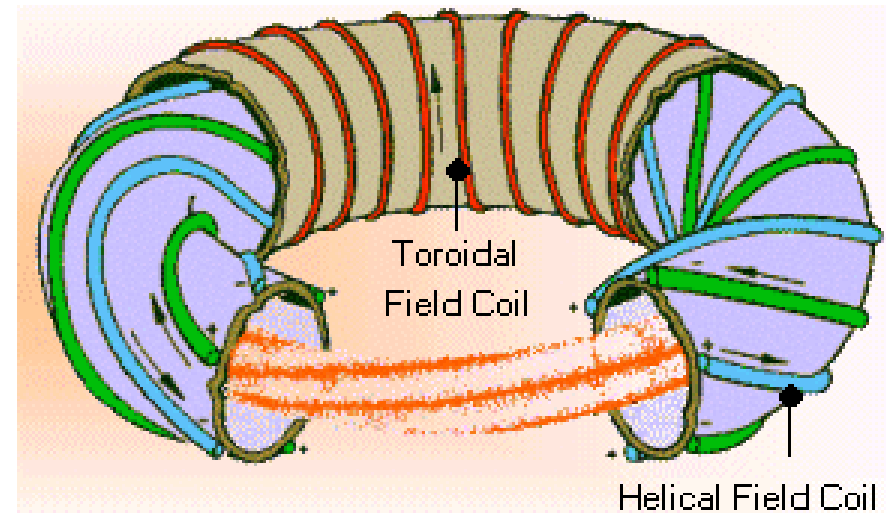
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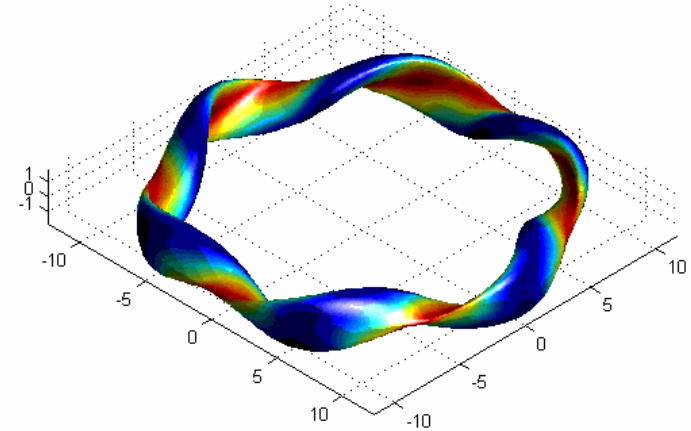
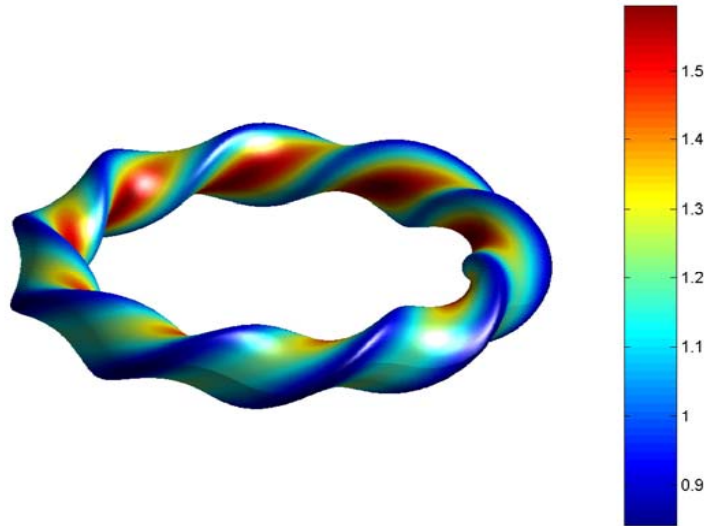


- **Devices, facilities, operational regimes, etc.**
- **Example: stellarator facilities for magnetic plasma confinement.**

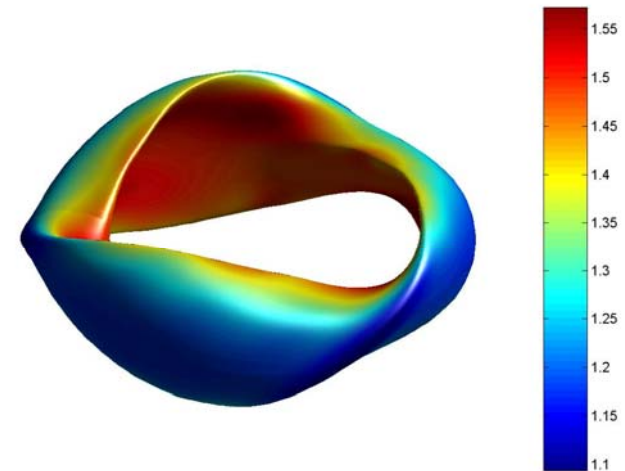
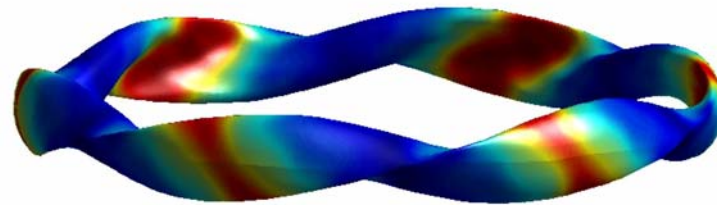


- The boundary plasma surface may be defined by several (100-150) Fourier coefficients, that are the *optimisation parameters*.
- The plasma equilibrium can be found if the boundary plasma surface and the radial profiles of plasma pressure and toroidal current are prescribed.
- So, several *quality parameters*: stability, fast particle confinement, transport coefficients, bootstrap current, etc. can be computed.
- *Target function* is usually a weighted sum of quality parameters.

*Magnetic field lines lie on the surfaces, colour shows its strength*



↑ Conventional: field maximums “mirror” some part of the ions, so they “shift out” of the surfaces  
 Optimisation: make magnetic field more symmetric ↓ → ↑



\* M.I.Mikhailov, A.A.Subbotin, et.al. Improved alpha-particle confinement in stellarators with poloidally closed contours of the magnetic field strength. // Nuclear Fusion 42 (2002) L23-L26

- **Optimisation parameters vector = “genome”.**
- **Initial genome pool is generated randomly in the optimisation domain.**
- **Iterational process implies three activities:**
  1. Random selection of “parents” among genome pool. Genomes with better target function values should have a preference. Selection should not hardly suppress bad but potentially fruitful genomes, i.e. should prevent “supergenome” to dominate initially.
  2. Breeding: generation of a new genome based on two selected parents genomes. There is no reason for shifting, convergence or scattering of the genome pool during the breeding, so breeding should not change statistical mean and dispersion of the pool.
  3. Computation of quality parameters and target function values.

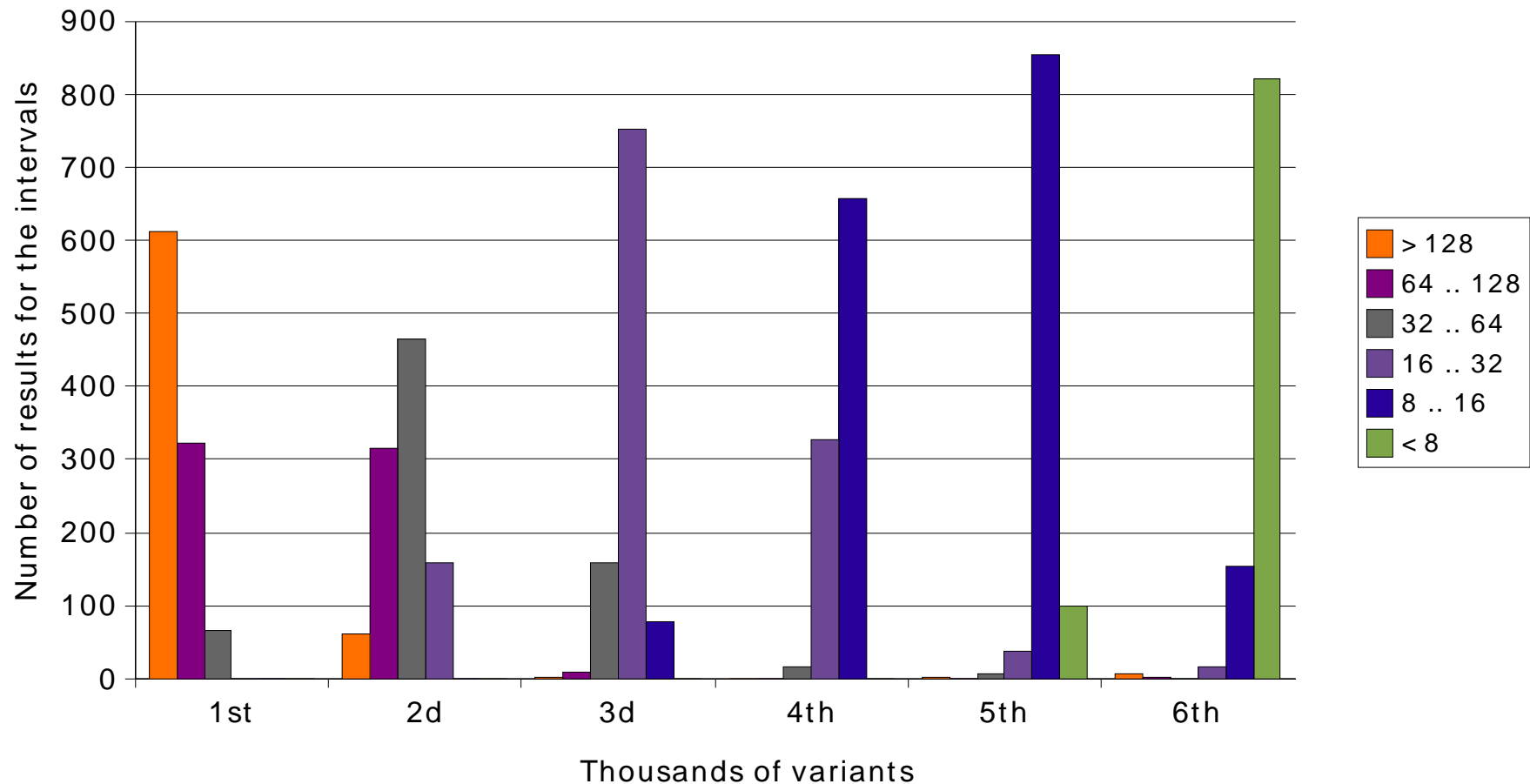
- **Medium-sized (several minutes) computation of quality parameters and target function value for a given optimisation parameters vector may be efficiently encapsulated into independent job**
- **Delaying and cancellation of several jobs in grid do not affect the overall GA-based optimisation process hardly**
- **Quality parameters of a stellarator variant may be computed in 15-40 min on a PC, so PC-based grid may be employed for such optimisation task**

- **Selection of “mother”:**
  - Genomes are sorted by target function values, best go first.
  - Loop: do iterate over genomes until a mother becomes chosen. On each step, mother is (or is not) chosen randomly with some probability (say, 2% or 3%).
- **“Farther” is selected the same way**
- **Breeding:**
  - Every parameter in new optimisation parameters vector is generated independently.
  - For a given parameter, its mother value  $f$  and farther value  $m$ , a new value is a random number of Gaussian distribution with mean  $(f+m)/2$  and standard deviation  $|f-m|/2$ .
- **Proposed GA conserves the pool mean and standard deviation and allows to respect weak genomes**

- **Set of scripts realising the technique has been developed in *Python*:**
  - Generate initial genome pool randomly
  - Spawn variant calculation jobs in grid
  - Gather completed results
  - Generate (i.e. select and breed) new variants
- ***Bash* script realises iteration which implies the last three scripts and scheduling of a new iteration using *at (1)* Unix command**
- **Scripts are intended to run under user's control commands on *LCG-2* user interface host**

## 6000 successful stellarator variants have been computed

Distribution of target function values by coloured intervals for the 1st, 2d, 3d, 4th, 5th and 6th thousands of variants in order of appearance





- **The proposed technique is based on the genetic algorithms approach and is suitable for a grid computing**
- **It works good for stellarators optimisation tasks**
- **It may also be employed in a wide spectrum of applications, both scientific and practical**