

User guide - Hill's model optimal designs

1. Change the directory to the folder containing the p-codes, type "design_for_hill_model" in the command window. A graphical user interface pops up.
2. Select theta's from the "Theta value" menu.
3. Input lower limit and upper limit. (Caution: a too small design space may cause the algorithm to fail. Usually it fails when the mean function plot is not a complete "s" curve. We suggest a lower limit ≤ -4 , and an upper limit ≥ 4 .) Input delta for MED and compound.
4. For compound optimal designs, input the weights in q1 (D) and q2 (ED50) boxes. The weight for MED is $1 - q1 - q2$.
5. Choose a criterion from the "Optimality criterion" menu.
6. Choose an algorithm from the "Algorithm" menu. The number after "YBT" specifies how fine the design space is discretized.
7. Input the number of cuckoos (cuckoo search), swarms (PSO) or chromosomes (DE and GA) in the "Population size" box. Not applicable for V-algorithms.
8. Click "plot mean function" to see the mean function curve.
9. Click "Run", "Running..."s appear in the three bottom left boxes. For the metaheuristic algorithms, the number of iterations, current criterion value and current design are displayed in the command window. The optimization is done when the "Running..."s are replaced by numbers. Design, number of function evaluations, CPU time and optimal criterion value are displayed.

10. Click “Equivalence plot” to verify optimality.
11. Click “Clear” to clear the boxes and plot before a new session.

Guanghao Qi

11/2/2014