**Global optimizer MATLAB code**

**23 test functions**

|  |  |
| --- | --- |
| **No.** | **fname** |
| 1 | 'rast' |
| 2 | 'rast' |
| 3 | 'griewank' |
| 4 | 'griewank2' |
| 5 | 'molefd' |
| 6 | 'molefd' |
| 7 | 'levy13' |
| 8 | 'michal' |
| 9 | 'shubert' |
| 10 | 'langer' |
| 11 | 'example3' |
| 12 | 'example4' |
| 13 | 'ackley' |
| 14 | 'booth' |
| 15 | 'drop' |
| 16 | 'molefd\_1f1d' |
| 17 | 'molefd\_1f2d' |
| 18 | 'molefd\_1f2d' |
| 19 | 'molefd\_1f3d' |
| 20 | mole\_pd |
| 21 | Dirichletfun |
| 22 | DirichletfunAD |
| 23 | heatfunAD |

**Remarks:**

1. The new test functions (DirichletfunAD and heatfunAD) are used to test ADMAT application in this global optimizer.
2. The derivatives of the first 21 test functions are computed by analytical form. The derivatives of the 22nd and 23rd test functions are computed by ADMAT software.
3. The details of the 23rd test function is attached as file heatfun\_docs.pdf

Main function

**run\_global\_RBF\_TRM.m ：**

basic code to apply global optimizer

phase 1 global\_RBF\_TRM,

pahse 2: Quasi-Newton

**(new) run\_global\_RBF\_TRM\_cost.m ：**

basic code to apply global optimizer

phase 1 global\_RBF\_TRM,

pahse 2: Quasi-Newton

**Remarks:**

1. This is the new main function of the global optimizer.
2. All the 23 test functions are updated with new 23 test functions with a smoothing method. (see fcost.m and fcostsmooth.m etc.)
3. The result could be got by running the test script file (smoothing\_test.m)
4. By the smoothing method, the optimal solution could be got by using less iterations.
5. A sample result is stored in the file (sample\_result.xls)

**output table – 11 columns**

No. Problem order

fname test function name

dim dimension of solution x

f\_init initial function value

f\_ph1 function value after phase 1 by Global RBF\_TRM method

f\_ph2 function value after phase 2 by Quasi-Newton

it\_ph1 number of computing function values in phase 1 by Global RBF\_TRM

it\_ph2 number of computing function values in phase 2 by Quasi-Newton

gNum number of gradient in phase 2

gNorm norm of gradient after phase2

f\_onlyph2 function value computed only by phase 2 from starting point

**Other run\_global functions**

**run\_global\_RBF\_FM.m:**

compare four methods in phase 2: Quasi-Newton, ADMAT forward mode, ADMAT reverse mode and MATLAB built-in "fminunc"

**run\_globalRBF\_reverseQN.m**

apply ADMAT reverse mode in phase 2

Some test functions can not be solved well by ADMAT reverse mode if they include gradient computing code. So we remove the gradient computing code in the test functions and then apply ADMAT reverse mode.

**run\_global\_RBF\_TRM\_tt.m**

1-D,2-D,3-D Atom function test with and without special structures

for problem 20 21 22 23, 24 25 need x0 and DM input

used in **test\_molefunc.m**

**Atom function （molecule problem）**

**1D**

make\_mole\_1d.m: %create a 1-D molecule problem

molefd.m MOLE Test function objective function is 2-norm

molefd\_1f1d.m 1-D , objective function is 1-norm

**2D**

make\_mole\_2d.m: create a 2-D molecule problem

mole\_2d\_case.m: generate DM for special structures

molefd2.m: MOLE Test function objective function is 2-norm

molefd\_1f2d.m 2-D , objective function is 1-norm

new2dmole.m % remove rotations, test function based on w not x

**3D**

make\_mole\_3d.m create a 3-D molecule problem

mole\_3d\_case.m: generate DM for special structures

molefd\_1f3d.m 3-D , objective function is 1-norm

new3dmole.m % 3D remove rotations, test function based on w not x

**p-Dimension**

make\_mole\_pd.m create a p-D molecule problem

mole\_pd.m MOLE Test function p-dimension,objective function is 1-norm

**Compare handmade gradient computing code with ADMAT**

test\_1dmole\_old.m 1-D molecule problem

test\_2dmole\_old.m 2-D molecule problem

test\_3dmole.m 3-D molecule problem

test\_pdmole.m p-D molecule problem

test\_gradient.m test gradient after phase 1

**Compare simulate Annealing with RBF**

compare\_SA\_RBF.m：

compare global\_RBF\_TRM and SA in phase 1, use Quasi-Newton in gr\_pahse2=1

**ADD Transaction Function**

In run\_global\_RBF\_TRM\_tt.m problem 19, not doing well.

**Experiments**

**Compare how phase 1 global\_RBF\_TRM works on all test functions**

File test20160106\_ph1\_.xls show relative change in phase 1, phase 2 and only phase 2.

**Special Structure of 2D and 3D Atom function**

All .doc file like figures1202.doc figures20151201.doc

**Compare simulate Annealing with RBF**

test20160113\_SA.xls

test20160120——SA.xls

test20160125\_SA\_Dirich.xls

**Different percentage in creating 3D molecule problem**

test20151216-3d.xls

**3D molecule problem with and without removing rotaions**

test20151218-3d\_old and new.xls

**Different atom number in 3D ordinary and special structures**

test20151215.xls

**2D molecule problem with and without removing rotaions**

test20151214.xls

test20151211.xls

test20151208.xls

test20151204.xls

**2D molecule problem Null space**

test20151202.xls

**Transaction cost smoothing function**

test20151201.xls

**Different atom number in 2D molecule problem special structures**

test20151130.xls

**Null space of 2D s molecule problem pecial structures with objective molefd\_1f2d.m**

test20151127.xls

**ADMAT Reverse mode for all test functions and new 1-norm 1D and 2D molecule problem**

test20151126.xls