

Starting C:\algo\build-h-Desktop_Qt_5_6_0_MinGW_32bit-Debug\debug\h.exe...

121 "number of input=30. distribution=U. range=all #jobs=10. #machines=all"

211 "-----START 1 from 30-----"

213 "input file number 1: inputName=C:/algo/h/docs/benchMark/all/U_1_0010_05_0.txt and
solutionName=C:/algo/h/docs/benchMark/all/SOL_U_1_05_0010_0.txt"

285 "***Data from file U_1_0010_05_0.txt: machinesNum=5 jobsNum=10"

328 "***SOLUTION Data from file SOL_U_1_05_0010_0.txt: machinesNum=5
jobsNum=10 lowerBound=101 upperBound=101 isOptimal=1"

332 Content of machines summed (92, 87, 94, 96, 101)

354 input selected: (92, 80, 68, 61, 53, 48, 35, 26, 5, 2) size 10 sum 470

starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5

LowerBounds calc: perfectSplit=94, pMax=92, pigeonholePrinciple=7 => lowerBound set to
94

**Best gene from 1st generation: Gene id=19 TF=115, #Machines=5,
content:<3,2,4,1,1,5,2,4,4,4>, Summed Machines(114,115,92,101,48)

**Best gene got replaced in generation 5. Gene details: Gene id=99 TF=114, #Machines=5,
content:<2,3,4,1,1,5,5,4,4,4>, Summed Machines(114,92,80,101,83)

**Best gene got replaced in generation 9. Gene details: Gene id=82 TF=103, #Machines=5,
content:<5,1,4,2,3,3,2,4,1,3>, Summed Machines(85,96,103,94,92)

**Best gene got replaced in generation 10. Gene details: Gene id=52 TF=101, #Machines=5,
content:<5,1,4,2,3,3,2,4,4,1>, Summed Machines(82,96,101,99,92)

**END oldes Gen=10

**Best gene found: Gene id=52 TF=101, #Machines=5, content:<5,1,4,2,3,3,2,4,4,1>,
Summed Machines(82,96,101,99,92)

219 "----Comparison for the 0 example----

220 "***tf from benchmark=101 target function from our Genetic=101"

223 ***RESULT IS THE SAME

230 Run time: 15.98 seconds

231 "Correct (size-numberCorrect):" QMap((10, 1))

231 "Mistakes(size-numberMistakes):" QMap()

231 "Avegare error: nan"

232 "-----END 1 from 30-----"

211 "-----START 2 from 30-----"

213 "input file number 2: inputName=C:/algo/h/docs/benchMark/all/U_1_0010_05_1.txt and
solutionName=C:/algo/h/docs/benchMark/all/SOL_U_1_05_0010_1.txt"

285 "***Data from file U_1_0010_05_1.txt: machinesNum=5 jobsNum=10"

328 "***SOLUTION Data from file SOL_U_1_05_0010_1.txt: machinesNum=5
jobsNum=10 lowerBound=86 upperBound=86 isOptimal=1"

332 Content of machines summed (86, 78, 76, 75, 77)

354 input selected: (86, 67, 52, 44, 40, 33, 31, 24, 11, 4) size 10 sum 392

starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5

LowerBounds calc: perfectSplit=78.4, pMax=86, pigeonholePrinciple=15 => lowerBound set
to 86

**Best gene from 1st generation: Gene id=65 TF=97, #Machines=5,
content:<5,3,2,1,4,1,2,3,5,1>, Summed Machines(81,83,91,40,97)

**Best gene got replaced in generation 7. Gene details: Gene id=66 TF=91, #Machines=5,
content:<3,2,5,4,1,1,5,2,4,3>, Summed Machines(73,91,90,55,83)

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**Best gene got replaced in generation 10. Gene details: Gene id=62 TF=90, #Machines=5,
content:<2,1,3,4,5,5,4,3,1,2>, Summed Machines(78,90,76,75,73)
**Best gene got replaced in generation 11. Gene details: Gene id=88 TF=86, #Machines=5,
content:<2,1,3,4,5,5,4,3,1,3>, Summed Machines(78,86,80,75,73)
Best gene target function value is equal to lower bound. stopping Genetic H
**END oldes Gen=11
**Best gene found: Gene id=88 TF=86, #Machines=5, content:<2,1,3,4,5,5,4,3,1,3>,
Summed Machines(78,86,80,75,73)
219 "----Comparison for the 1 example----"
220 "***tf from benchmark=86 target function from our Genetic=86"
223 ***RESULT IS THE SAME
230 Run time: 1.535 seconds
231 "Correct (size-numberCorrect):" QMap((10, 2))
231 "Mistakes(size-numberMistakes):" QMap()
231 "Avegare error: 0"
232 "-----END 2 from 30-----"
211 "-----START 3 from 30-----"
213 "input file number 3: inputName=C:/algo/h/docs/benchMark/all/U_1_0010_05_2.txt and
solutionName=C:/algo/h/docs/benchMark/all/SOL_U_1_05_0010_2.txt"
285 "***Data from file U_1_0010_05_2.txt: machinesNum=5 jobsNum=10"
328 "***SOLUTION Data from file SOL_U_1_05_0010_2.txt: machinesNum=5
jobsNum=10 lowerBound=116 upperBound=116 isOptimal=1"
332 Content of machines summed (111, 101, 116, 106, 116)
354 input selected: (81, 81, 72, 72, 63, 53, 44, 34, 30, 20) size 10 sum 550
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=110, pMax=81, pigeonholePrinciple=50 => lowerBound set
to 110
**Best gene from 1st generation: Gene id=31 TF=144, #Machines=5,
content:<1,3,5,2,1,3,2,5,4,2>, Summed Machines(144,136,134,30,106)
**Best gene got replaced in generation 2. Gene details: Gene id=84 TF=135, #Machines=5,
content:<2,1,3,5,5,1,4,2,4,4>, Summed Machines(134,115,72,94,135)
**Best gene got replaced in generation 3. Gene details: Gene id=85 TF=134, #Machines=5,
content:<5,3,4,2,1,3,4,2,1,2>, Summed Machines(93,126,134,116,81)
**Best gene got replaced in generation 7. Gene details: Gene id=73 TF=127, #Machines=5,
content:<1,2,4,5,3,4,5,3,3,2>, Summed Machines(81,101,127,125,116)
**Best gene got replaced in generation 8. Gene details: Gene id=9 TF=125, #Machines=5,
content:<1,5,3,4,2,3,1,5,2,4>, Summed Machines(125,93,125,92,115)
**END oldes Gen=11
**Best gene found: Gene id=9 TF=125, #Machines=5, content:<1,5,3,4,2,3,1,5,2,4>,
Summed Machines(125,93,125,92,115)
219 "----Comparison for the 2 example----"
220 "***tf from benchmark=116 target function from our Genetic=125"
228 ***Different 9
230 Run time: 15.715 seconds
231 "Correct (size-numberCorrect):" QMap((10, 2))
231 "Mistakes(size-numberMistakes):" QMap((10, 1))
231 "Avegare error: 4.5"
232 "-----END 3 from 30-----"
211 "-----START 4 from 30-----"

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213 "input file number 4: inputName=C:/algo/h/docs/benchMark/all/U_1_0010_05_3.txt and
solutionName=C:/algo/h/docs/benchMark/all/SOL_U_1_05_0010_3.txt"
285 "****Data from file U_1_0010_05_3.txt: machinesNum=5 jobsNum=10"
328 "****SOLUTION Data from file SOL_U_1_05_0010_3.txt: machinesNum=5
jobsNum=10 lowerBound=125 upperBound=125 isOptimal=1"
332 Content of machines summed (100, 125, 120, 112, 120)
354 input selected: (97, 85, 78, 68, 62, 58, 44, 42, 40, 3) size 10 sum 577
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=115.4, pMax=97, pigeonholePrinciple=43 => lowerBound
set to 116
**Best gene from 1st generation: Gene id=28 TF=149, #Machines=5,
content:<5,4,1,1,2,3,2,4,3,1>, Summed Machines(149,106,98,127,97)
**Best gene got replaced in generation 3. Gene details: Gene id=65 TF=147, #Machines=5,
content:<2,5,1,3,5,3,4,4,2,4>, Summed Machines(78,137,126,89,147)
**Best gene got replaced in generation 3. Gene details: Gene id=71 TF=125, #Machines=5,
content:<2,5,4,3,1,1,3,4,5,1>, Summed Machines(123,97,112,120,125)
**END oldes Gen=11
**Best gene found: Gene id=71 TF=125, #Machines=5, content:<2,5,4,3,1,1,3,4,5,1>,
Summed Machines(123,97,112,120,125)
219 "----Comparison for the 3 example----"
220 "****tf from benchmark=125 target function from our Genetic=125"
223 ***RESULT IS THE SAME
230 Run time: 15.271 seconds
231 "Correct (size-numberCorrect):" QMap((10, 3))
231 "Mistakes(size-numberMistakes):" QMap((10, 1))
231 "Avegare error: 3"
232 "-----END 4 from 30-----"
211 "-----START 5 from 30-----"
213 "input file number 5: inputName=C:/algo/h/docs/benchMark/all/U_1_0010_05_4.txt and
solutionName=C:/algo/h/docs/benchMark/all/SOL_U_1_05_0010_4.txt"
285 "****Data from file U_1_0010_05_4.txt: machinesNum=5 jobsNum=10"
328 "****SOLUTION Data from file SOL_U_1_05_0010_4.txt: machinesNum=5
jobsNum=10 lowerBound=89 upperBound=89 isOptimal=1"
332 Content of machines summed (69, 76, 68, 80, 89)
354 input selected: (65, 63, 54, 52, 50, 39, 28, 14, 13, 4) size 10 sum 382
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=76.4, pMax=65, pigeonholePrinciple=17 => lowerBound set
to 77
**Best gene from 1st generation: Gene id=38 TF=102, #Machines=5,
content:<2,4,1,3,5,5,1,3,5,2>, Summed Machines(82,69,66,63,102)
**Best gene got replaced in generation 2. Gene details: Gene id=61 TF=93, #Machines=5,
content:<2,4,1,3,5,5,1,2,3,5>, Summed Machines(82,79,65,63,93)
**Best gene got replaced in generation 3. Gene details: Gene id=97 TF=89, #Machines=5,
content:<2,4,1,3,5,5,1,2,3,1>, Summed Machines(86,79,65,63,89)
**END oldes Gen=11
**Best gene found: Gene id=97 TF=89, #Machines=5, content:<2,4,1,3,5,5,1,2,3,1>,
Summed Machines(86,79,65,63,89)
219 "----Comparison for the 4 example----"

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220 "***tf from benchmark=89 target function from our Genetic=89"
223 ***RESULT IS THE SAME
230 Run time: 15.246 seconds
231 "Correct (size-numberCorrect):" QMap((10, 4))
231 "Mistakes(size-numberMistakes):" QMap((10, 1))
231 "Avegare error: 2.25"
232 "-----END 5 from 30-----"
211 "-----START 6 from 30-----"
213 "input file number 6: inputName=C:/algo/h/docs/benchMark/all/U_1_0010_05_5.txt and
solutionName=C:/algo/h/docs/benchMark/all/SOL_U_1_05_0010_5.txt"
285 "***Data from file U_1_0010_05_5.txt: machinesNum=5 jobsNum=10"
328 "***SOLUTION Data from file SOL_U_1_05_0010_5.txt: machinesNum=5
jobsNum=10 lowerBound=121 upperBound=121 isOptimal=1"
332 Content of machines summed (95, 95, 109, 109, 121)
354 input selected: (95, 85, 79, 77, 69, 52, 32, 30, 6, 4) size 10 sum 529
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=105.8, pMax=95, pigeonholePrinciple=10 => lowerBound
set to 106
**Best gene from 1st generation: Gene id=64 TF=127, #Machines=5,
content:<2,5,1,3,4,4,2,1,1,3>, Summed Machines(115,127,81,121,85)
**Best gene got replaced in generation 3. Gene details: Gene id=32 TF=125, #Machines=5,
content:<2,5,1,3,4,4,1,2,5,1>, Summed Machines(115,125,77,121,91)
**Best gene got replaced in generation 16. Gene details: Gene id=43 TF=121, #Machines=5,
content:<3,4,5,1,2,2,4,1,3,4>, Summed Machines(107,121,101,121,79)
**END oldes Gen=16
**Best gene found: Gene id=43 TF=121, #Machines=5, content:<3,4,5,1,2,2,4,1,3,4>,
Summed Machines(107,121,101,121,79)
219 "----Comparison for the 5 example----"
220 "***tf from benchmark=121 target function from our Genetic=121"
223 ***RESULT IS THE SAME
230 Run time: 15.278 seconds
231 "Correct (size-numberCorrect):" QMap((10, 5))
231 "Mistakes(size-numberMistakes):" QMap((10, 1))
231 "Avegare error: 1.8"
232 "-----END 6 from 30-----"
211 "-----START 7 from 30-----"
213 "input file number 7: inputName=C:/algo/h/docs/benchMark/all/U_1_0010_05_6.txt and
solutionName=C:/algo/h/docs/benchMark/all/SOL_U_1_05_0010_6.txt"
285 "***Data from file U_1_0010_05_6.txt: machinesNum=5 jobsNum=10"
328 "***SOLUTION Data from file SOL_U_1_05_0010_6.txt: machinesNum=5
jobsNum=10 lowerBound=113 upperBound=113 isOptimal=1"
332 Content of machines summed (113, 113, 108, 92, 83)
354 input selected: (93, 92, 83, 67, 46, 40, 39, 34, 10, 5) size 10 sum 509
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=101.8, pMax=93, pigeonholePrinciple=15 => lowerBound
set to 102
**Best gene from 1st generation: Gene id=42 TF=122, #Machines=5,
content:<5,2,1,4,3,3,1,3,2,5>, Summed Machines(122,102,120,67,98)

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**Best gene got replaced in generation 2. Gene details: Gene id=88 TF=119, #Machines=5,
content:<4,3,1,2,5,2,5,5,3,4>, Summed Machines(83,107,102,98,119)
**Best gene got replaced in generation 13. Gene details: Gene id=69 TF=117, #Machines=5,
content:<5,3,2,4,1,4,1,2,3,4>, Summed Machines(85,117,102,112,93)
**END oldes Gen=16
**Best gene found: Gene id=69 TF=117, #Machines=5, content:<5,3,2,4,1,4,1,2,3,4>,
Summed Machines(85,117,102,112,93)
219 "----Comparison for the 6 example----"
220 "***tf from benchmark=113 target function from our Genetic=117"
228 ***Different 4
230 Run time: 15.238 seconds
231 "Correct (size-numberCorrect):" QMap((10, 5))
231 "Mistakes(size-numberMistakes):" QMap((10, 2))
231 "Avegare error: 2.16667"
232 "-----END 7 from 30-----"
211 "-----START 8 from 30-----"
213 "input file number 8: inputName=C:/algo/h/docs/benchMark/all/U_1_0010_05_7.txt and
solutionName=C:/algo/h/docs/benchMark/all/SOL_U_1_05_0010_7.txt"
285 "***Data from file U_1_0010_05_7.txt: machinesNum=5 jobsNum=10"
328 "***SOLUTION Data from file SOL_U_1_05_0010_7.txt: machinesNum=5
jobsNum=10 lowerBound=99 upperBound=99 isOptimal=1"
332 Content of machines summed (99, 90, 88, 93, 93)
354 input selected: (99, 90, 68, 63, 56, 26, 20, 20, 11, 10) size 10 sum 463
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=92.6, pMax=99, pigeonholePrinciple=21 => lowerBound set
to 99
**Best gene from 1st generation: Gene id=10 TF=119, #Machines=5,
content:<3,4,1,2,5,1,3,2,2,4>, Summed Machines(94,94,119,100,56)
**Best gene got replaced in generation 2. Gene details: Gene id=86 TF=103, #Machines=5,
content:<2,1,3,5,4,4,5,5,1,4>, Summed Machines(101,99,68,92,103)
**Best gene got replaced in generation 7. Gene details: Gene id=2 TF=100, #Machines=5,
content:<1,5,3,2,4,4,2,3,4,5>, Summed Machines(99,83,88,93,100)
**Best gene got replaced in generation 10. Gene details: Gene id=87 TF=99, #Machines=5,
content:<1,5,3,2,4,4,2,3,4,3>, Summed Machines(99,83,98,93,90)
Best gene target function value is equal to lower bound. stopping Genetic H
**END oldes Gen=16
**Best gene found: Gene id=87 TF=99, #Machines=5, content:<1,5,3,2,4,4,2,3,4,3>,
Summed Machines(99,83,98,93,90)
219 "----Comparison for the 7 example----"
220 "***tf from benchmark=99 target function from our Genetic=99"
223 ***RESULT IS THE SAME
230 Run time: 1.375 seconds
231 "Correct (size-numberCorrect):" QMap((10, 6))
231 "Mistakes(size-numberMistakes):" QMap((10, 2))
231 "Avegare error: 1.85714"
232 "-----END 8 from 30-----"
211 "-----START 9 from 30-----"
213 "input file number 9: inputName=C:/algo/h/docs/benchMark/all/U_1_0010_05_8.txt and
solutionName=C:/algo/h/docs/benchMark/all/SOL_U_1_05_0010_8.txt"

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285 "Data from file U_1_0010_05_8.txt: machinesNum=5 jobsNum=10"
328 "SOLUTION Data from file SOL_U_1_05_0010_8.txt: machinesNum=5
jobsNum=10 lowerBound=116 upperBound=116 isOptimal=1"
332 Content of machines summed (100, 106, 102, 112, 116)
354 input selected: (91, 90, 85, 69, 66, 50, 43, 17, 16, 9) size 10 sum 536
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=107.2, pMax=91, pigeonholePrinciple=25 => lowerBound
set to 108
**Best gene from 1st generation: Gene id=10 TF=151, #Machines=5,
content:<2,5,3,4,1,3,1,1,3,1>, Summed Machines(135,91,151,69,90)
**Best gene got replaced in generation 2. Gene details: Gene id=99 TF=140, #Machines=5,
content:<3,1,4,5,2,1,3,5,2,5>, Summed Machines(140,82,134,85,95)
**Best gene got replaced in generation 3. Gene details: Gene id=0 TF=135, #Machines=5,
content:<3,1,4,5,2,4,2,2,5,3>, Summed Machines(90,126,100,135,85)
**Best gene got replaced in generation 4. Gene details: Gene id=65 TF=134, #Machines=5,
content:<5,3,2,4,1,1,5,2,3,4>, Summed Machines(116,102,106,78,134)
**Best gene got replaced in generation 6. Gene details: Gene id=88 TF=132, #Machines=5,
content:<5,3,2,4,1,1,2,5,1,3>, Summed Machines(132,128,99,69,108)
**Best gene got replaced in generation 8. Gene details: Gene id=43 TF=128, #Machines=5,
content:<4,2,5,3,1,3,1,5,2,3>, Summed Machines(109,106,128,91,102)
**Best gene got replaced in generation 8. Gene details: Gene id=75 TF=116, #Machines=5,
content:<4,3,2,5,1,1,5,4,2,3>, Summed Machines(116,101,99,108,112)
**END oldes Gen=16
**Best gene found: Gene id=75 TF=116, #Machines=5, content:<4,3,2,5,1,1,5,4,2,3>,
Summed Machines(116,101,99,108,112)
219 "----Comparison for the 8 example----"
220 "tf from benchmark=116 target function from our Genetic=116"
223 ***RESULT IS THE SAME
230 Run time: 15.215 seconds
231 "Correct (size-numberCorrect):" QMap((10, 7))
231 "Mistakes(size-numberMistakes):" QMap((10, 2))
231 "Avegare error: 1.625"
232 "-----END 9 from 30-----"
211 "-----START 10 from 30-----"
213 "input file number 10: inputName=C:/algo/h/docs/benchMark/all/U_1_0010_05_9.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_1_05_0010_9.txt"
285 "Data from file U_1_0010_05_9.txt: machinesNum=5 jobsNum=10"
328 "SOLUTION Data from file SOL_U_1_05_0010_9.txt: machinesNum=5
jobsNum=10 lowerBound=104 upperBound=104 isOptimal=1"
332 Content of machines summed (85, 97, 104, 94, 86)
354 input selected: (80, 69, 68, 53, 43, 43, 41, 36, 28, 5) size 10 sum 466
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=93.2, pMax=80, pigeonholePrinciple=33 => lowerBound set
to 94
**Best gene from 1st generation: Gene id=49 TF=112, #Machines=5,
content:<3,1,4,2,5,1,5,2,4,3>, Summed Machines(112,89,85,96,84)
**Best gene got replaced in generation 7. Gene details: Gene id=83 TF=111, #Machines=5,
content:<2,1,3,4,5,3,1,4,5,4>, Summed Machines(110,80,111,94,71)

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**Best gene got replaced in generation 11. Gene details: Gene id=95 TF=110, #Machines=5,
content:<4,5,1,3,2,3,1,5,2,5>, Summed Machines(109,71,96,80,110)
**Best gene got replaced in generation 22. Gene details: Gene id=21 TF=109, #Machines=5,
content:<4,5,1,2,2,3,1,5,3,4>, Summed Machines(109,96,71,85,105)
**END oldes Gen=22
**Best gene found: Gene id=21 TF=109, #Machines=5, content:<4,5,1,2,2,3,1,5,3,4>,
Summed Machines(109,96,71,85,105)
219 "----Comparison for the 9 example----"
220 "***tf from benchmark=104 target function from our Genetic=109"
228 ***Different 5
230 Run time: 15.223 seconds
231 "Correct (size-numberCorrect):" QMap((10, 7))
231 "Mistakes(size-numberMistakes):" QMap((10, 3))
231 "Avegare error: 2"
232 "-----END 10 from 30-----"
211 "-----START 11 from 30-----"
213 "input file number 11: inputName=C:/algo/h/docs/benchMark/all/U_2_0010_05_0.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_2_05_0010_0.txt"
285 "***Data from file U_2_0010_05_0.txt: machinesNum=5 jobsNum=10"
328 "***SOLUTION Data from file SOL_U_2_05_0010_0.txt: machinesNum=5
jobsNum=10 lowerBound=1354 upperBound=1354 isOptimal=1"
332 Content of machines summed (1149, 1155, 1290, 1354, 1255)
354 input selected: (973, 925, 859, 837, 696, 559, 517, 431, 230, 176) size 10 sum 6203
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=1240.6, pMax=973, pigeonholePrinciple=406 =>
lowerBound set to 1241
**Best gene from 1st generation: Gene id=1 TF=1431, #Machines=5,
content:<2,5,1,4,3,3,4,5,1,3>, Summed Machines(1089,973,1431,1354,1356)
**Best gene got replaced in generation 2. Gene details: Gene id=82 TF=1356, #Machines=5,
content:<2,5,1,4,3,3,4,5,1,1>, Summed Machines(1265,973,1255,1354,1356)
**END oldes Gen=22
**Best gene found: Gene id=82 TF=1356, #Machines=5, content:<2,5,1,4,3,3,4,5,1,1>,
Summed Machines(1265,973,1255,1354,1356)
219 "----Comparison for the 10 example----"
220 "***tf from benchmark=1354 target function from our Genetic=1356"
228 ***Different 2
230 Run time: 15.262 seconds
231 "Correct (size-numberCorrect):" QMap((10, 7))
231 "Mistakes(size-numberMistakes):" QMap((10, 4))
231 "Avegare error: 2"
232 "-----END 11 from 30-----"
211 "-----START 12 from 30-----"
213 "input file number 12: inputName=C:/algo/h/docs/benchMark/all/U_2_0010_05_1.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_2_05_0010_1.txt"
285 "***Data from file U_2_0010_05_1.txt: machinesNum=5 jobsNum=10"
328 "***SOLUTION Data from file SOL_U_2_05_0010_1.txt: machinesNum=5
jobsNum=10 lowerBound=1108 upperBound=1108 isOptimal=1"
332 Content of machines summed (957, 905, 898, 1106, 1108)
354 input selected: (957, 858, 791, 620, 608, 500, 486, 107, 30, 17) size 10 sum 4974

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starting Genetic with args: generationsNumber=100, populationSize=100, machinesNumber=5
LowerBounds calc: perfectSplit=994.8, pMax=957, pigeonholePrinciple=47 => lowerBound set to 995
**Best gene from 1st generation: Gene id=64 TF=1291, #Machines=5, content:<4,3,2,1,5,2,1,1,4,1>, Summed Machines(1230,1291,858,987,608)
**Best gene got replaced in generation 7. Gene details: Gene id=24 TF=1227, #Machines=5, content:<5,1,3,2,4,2,4,2,1,3>, Summed Machines(888,1227,808,1094,957)
**Best gene got replaced in generation 8. Gene details: Gene id=57 TF=1120, #Machines=5, content:<5,1,3,2,4,2,4,5,5,3>, Summed Machines(858,1120,808,1094,1094)
**Best gene got replaced in generation 34. Gene details: Gene id=90 TF=1108, #Machines=5, content:<4,2,3,5,1,1,5,3,3,4>, Summed Machines(1108,858,928,974,1106)
**END oldes Gen=34
**Best gene found: Gene id=90 TF=1108, #Machines=5, content:<4,2,3,5,1,1,5,3,3,4>, Summed Machines(1108,858,928,974,1106)
219 "----Comparison for the 11 example----"
220 "***tf from benchmark=1108 target function from our Genetic=1108"
223 ***RESULT IS THE SAME
230 Run time: 15.19 seconds
231 "Correct (size-numberCorrect):" QMap((10, 8))
231 "Mistakes(size-numberMistakes):" QMap((10, 4))
231 "Avegare error: 1.81818"
232 "-----END 12 from 30-----"
211 "-----START 13 from 30-----"
213 "input file number 13: inputName=C:/algo/h/docs/benchMark/all/U_2_0010_05_2.txt and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_2_05_0010_2.txt"
285 "***Data from file U_2_0010_05_2.txt: machinesNum=5 jobsNum=10"
328 "***SOLUTION Data from file SOL_U_2_05_0010_2.txt: machinesNum=5 jobsNum=10 lowerBound=961 upperBound=961 isOptimal=1"
332 Content of machines summed (961, 953, 844, 932, 876)
354 input selected: (961, 953, 787, 542, 391, 292, 218, 193, 172, 57) size 10 sum 4566
starting Genetic with args: generationsNumber=100, populationSize=100, machinesNumber=5
LowerBounds calc: perfectSplit=913.2, pMax=961, pigeonholePrinciple=229 => lowerBound set to 961
**Best gene from 1st generation: Gene id=53 TF=1154, #Machines=5, content:<1,4,3,2,5,3,5,1,5,4>, Summed Machines(1154,542,1079,1010,781)
**Best gene got replaced in generation 2. Gene details: Gene id=63 TF=1133, #Machines=5, content:<1,3,2,4,4,5,5,2,1,5>, Summed Machines(1133,980,953,933,567)
**Best gene got replaced in generation 6. Gene details: Gene id=94 TF=1125, #Machines=5, content:<1,4,3,2,5,5,5,3,4,2>, Summed Machines(961,599,980,1125,901)
**Best gene got replaced in generation 8. Gene details: Gene id=1 TF=1010, #Machines=5, content:<1,4,3,2,5,5,2,5,3,4>, Summed Machines(961,760,959,1010,876)
**Best gene got replaced in generation 21. Gene details: Gene id=11 TF=1005, #Machines=5, content:<1,5,2,4,4,3,2,3,3,3>, Summed Machines(961,1005,714,933,953)
**Best gene got replaced in generation 32. Gene details: Gene id=22 TF=961, #Machines=5, content:<1,4,3,2,5,5,2,5,3,2>, Summed Machines(961,817,959,953,876)
Best gene target function value is equal to lower bound. stopping Genetic H
**END oldes Gen=34


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**Best gene found: Gene id=22 TF=961, #Machines=5, content:<1,4,3,2,5,5,2,5,3,2>,
Summed Machines(961,817,959,953,876)
219 "----Comparison for the 12 example----"
220 "****tf from benchmark=961 target function from our Genetic=961"
223 ***RESULT IS THE SAME
230 Run time: 4.734 seconds
231 "Correct (size-numberCorrect):" QMap((10, 9))
231 "Mistakes(size-numberMistakes):" QMap((10, 4))
231 "Avegare error: 1.66667"
232 "-----END 13 from 30-----"
211 "-----START 14 from 30-----"
213 "input file number 14: inputName=C:/algo/h/docs/benchMark/all/U_2_0010_05_3.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_2_05_0010_3.txt"
285 "****Data from file U_2_0010_05_3.txt: machinesNum=5 jobsNum=10"
328 "****SOLUTION Data from file SOL_U_2_05_0010_3.txt: machinesNum=5
jobsNum=10 lowerBound=1127 upperBound=1127 isOptimal=1"
332 Content of machines summed (1046, 1117, 1093, 1127, 1083)
354 input selected: (985, 825, 788, 656, 597, 486, 471, 305, 292, 61) size 10 sum 5466
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=1093.2, pMax=985, pigeonholePrinciple=353 =>
lowerBound set to 1094
**Best gene from 1st generation: Gene id=80 TF=1385, #Machines=5,
content:<4,5,2,3,2,1,5,1,3,5>, Summed Machines(791,1385,948,985,1357)
**Best gene got replaced in generation 2. Gene details: Gene id=24 TF=1357, #Machines=5,
content:<3,2,4,5,1,5,2,1,1,2>, Summed Machines(1194,1357,985,788,1142)
**Best gene got replaced in generation 4. Gene details: Gene id=62 TF=1290, #Machines=5,
content:<3,2,4,5,1,5,4,3,2,2>, Summed Machines(597,1178,1290,1259,1142)
**Best gene got replaced in generation 13. Gene details: Gene id=86 TF=1277,
#Machines=5, content:<2,3,4,5,1,5,4,1,2,5>, Summed Machines(902,1277,825,1259,1203)
**Best gene got replaced in generation 14. Gene details: Gene id=42 TF=1259,
#Machines=5, content:<2,3,4,5,1,5,4,1,1,2>, Summed Machines(1194,1046,825,1259,1142)
**END oldes Gen=34
**Best gene found: Gene id=42 TF=1259, #Machines=5, content:<2,3,4,5,1,5,4,1,1,2>,
Summed Machines(1194,1046,825,1259,1142)
219 "----Comparison for the 13 example----"
220 "****tf from benchmark=1127 target function from our Genetic=1259"
228 ***Different 132
230 Run time: 15.183 seconds
231 "Correct (size-numberCorrect):" QMap((10, 9))
231 "Mistakes(size-numberMistakes):" QMap((10, 5))
231 "Avegare error: 11.6923"
232 "-----END 14 from 30-----"
211 "-----START 15 from 30-----"
213 "input file number 15: inputName=C:/algo/h/docs/benchMark/all/U_2_0010_05_4.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_2_05_0010_4.txt"
285 "****Data from file U_2_0010_05_4.txt: machinesNum=5 jobsNum=10"
328 "****SOLUTION Data from file SOL_U_2_05_0010_4.txt: machinesNum=5
jobsNum=10 lowerBound=782 upperBound=782 isOptimal=1"
332 Content of machines summed (782, 631, 665, 657, 684)

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354 input selected: (782, 631, 629, 369, 279, 245, 185, 160, 103, 36) size 10 sum 3419
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=683.8, pMax=782, pigeonholePrinciple=139 =>
lowerBound set to 782
**Best gene from 1st generation: Gene id=45 TF=782, #Machines=5,
content:<1,3,2,4,5,5,4,5,3,4>, Summed Machines(782,629,734,590,684)
Best gene target function value is equal to lower bound. stopping Genetic H
**END oldes Gen=34
**Best gene found: Gene id=45 TF=782, #Machines=5, content:<1,3,2,4,5,5,4,5,3,4>,
Summed Machines(782,629,734,590,684)
219 "----Comparison for the 14 example----"
220 "****tf from benchmark=782 target function from our Genetic=782"
223 ***RESULT IS THE SAME
230 Run time: 0 seconds
231 "Correct (size-numberCorrect):" QMap((10, 10))
231 "Mistakes(size-numberMistakes):" QMap((10, 5))
231 "Avegare error: 10.8571"
232 "-----END 15 from 30-----"
211 "-----START 16 from 30-----"
213 "input file number 16: inputName=C:/algo/h/docs/benchMark/all/U_2_0010_05_5.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_2_05_0010_5.txt"
285 "****Data from file U_2_0010_05_5.txt: machinesNum=5 jobsNum=10"
328 "****SOLUTION Data from file SOL_U_2_05_0010_5.txt: machinesNum=5
jobsNum=10 lowerBound=939 upperBound=939 isOptimal=1"
332 Content of machines summed (916, 902, 812, 798, 939)
354 input selected: (916, 902, 556, 543, 515, 424, 249, 131, 125, 6) size 10 sum 4367
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=873.4, pMax=916, pigeonholePrinciple=131 =>
lowerBound set to 916
**Best gene from 1st generation: Gene id=93 TF=1070, #Machines=5,
content:<2,3,5,4,1,1,4,1,5,5>, Summed Machines(1070,916,902,792,687)
**Best gene got replaced in generation 2. Gene details: Gene id=1 TF=1033, #Machines=5,
content:<4,5,1,2,3,3,1,5,2,3>, Summed Machines(805,668,945,916,1033)
**Best gene got replaced in generation 6. Gene details: Gene id=22 TF=1027, #Machines=5,
content:<2,3,5,4,1,1,4,4,3,4>, Summed Machines(939,916,1027,929,556)
**Best gene got replaced in generation 6. Gene details: Gene id=90 TF=945, #Machines=5,
content:<2,3,5,4,1,1,4,4,5,1>, Summed Machines(945,916,902,923,681)
**Best gene got replaced in generation 13. Gene details: Gene id=56 TF=939, #Machines=5,
content:<2,3,5,4,1,1,4,4,5,4>, Summed Machines(939,916,902,929,681)
**END oldes Gen=34
**Best gene found: Gene id=56 TF=939, #Machines=5, content:<2,3,5,4,1,1,4,4,5,4>,
Summed Machines(939,916,902,929,681)
219 "----Comparison for the 15 example----"
220 "****tf from benchmark=939 target function from our Genetic=939"
223 ***RESULT IS THE SAME
230 Run time: 15.222 seconds
231 "Correct (size-numberCorrect):" QMap((10, 11))
231 "Mistakes(size-numberMistakes):" QMap((10, 5))

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231 "Avegare error: 10.1333"
232 "-----END 16 from 30-----"
211 "-----START 17 from 30-----"
213 "input file number 17: inputName=C:/algo/h/docs/benchMark/all/U_2_0010_05_6.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_2_05_0010_6.txt"
285 "***Data from file U_2_0010_05_6.txt: machinesNum=5 jobsNum=10"
328 "***SOLUTION Data from file SOL_U_2_05_0010_6.txt: machinesNum=5
jobsNum=10 lowerBound=760 upperBound=760 isOptimal=1"
332 Content of machines summed (760, 608, 559, 539, 569)
354 input selected: (760, 608, 453, 431, 429, 140, 62, 60, 46, 46) size 10 sum 3035
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=607, pMax=760, pigeonholePrinciple=92 => lowerBound
set to 760
**Best gene from 1st generation: Gene id=40 TF=760, #Machines=5,
content:<5,1,2,4,3,4,3,3,1>, Summed Machines(654,453,597,571,760)
Best gene target function value is equal to lower bound. stopping Genetic H
**END oldes Gen=34
**Best gene found: Gene id=40 TF=760, #Machines=5, content:<5,1,2,4,3,4,3,3,1>,
Summed Machines(654,453,597,571,760)
219 "----Comparison for the 16 example----"
220 "***tf from benchmark=760 target function from our Genetic=760"
223 ***RESULT IS THE SAME
230 Run time: 0 seconds
231 "Correct (size-numberCorrect):" QMap((10, 12))
231 "Mistakes(size-numberMistakes):" QMap((10, 5))
231 "Avegare error: 9.5"
232 "-----END 17 from 30-----"
211 "-----START 18 from 30-----"
213 "input file number 18: inputName=C:/algo/h/docs/benchMark/all/U_2_0010_05_7.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_2_05_0010_7.txt"
285 "***Data from file U_2_0010_05_7.txt: machinesNum=5 jobsNum=10"
328 "***SOLUTION Data from file SOL_U_2_05_0010_7.txt: machinesNum=5
jobsNum=10 lowerBound=1202 upperBound=1202 isOptimal=1"
332 Content of machines summed (1066, 1127, 1115, 1117, 1202)
354 input selected: (950, 932, 798, 637, 624, 578, 480, 317, 195, 116) size 10 sum 5627
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=1125.4, pMax=950, pigeonholePrinciple=311 =>
lowerBound set to 1126
**Best gene from 1st generation: Gene id=26 TF=1318, #Machines=5,
content:<3,4,1,5,2,2,5,1,3,2>, Summed Machines(1115,1318,1145,932,1117)
**Best gene got replaced in generation 2. Gene details: Gene id=82 TF=1233, #Machines=5,
content:<3,4,1,5,2,2,5,1,3,5>, Summed Machines(1115,1202,1145,932,1233)
**Best gene got replaced in generation 34. Gene details: Gene id=78 TF=1202,
#Machines=5, content:<2,5,1,4,3,3,4,1,2,5>, Summed Machines(1115,1145,1202,1117,1048)
**END oldes Gen=34
**Best gene found: Gene id=78 TF=1202, #Machines=5, content:<2,5,1,4,3,3,4,1,2,5>,
Summed Machines(1115,1145,1202,1117,1048)
219 "----Comparison for the 17 example----"

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220 "***tf from benchmark=1202 target function from our Genetic=1202"
223 ***RESULT IS THE SAME
230 Run time: 15.184 seconds
231 "Correct (size-numberCorrect):" QMap((10, 13))
231 "Mistakes(size-numberMistakes):" QMap((10, 5))
231 "Avegare error: 8.94118"
232 "-----END 18 from 30-----"
211 "-----START 19 from 30-----"
213 "input file number 19: inputName=C:/algo/h/docs/benchMark/all/U_2_0010_05_8.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_2_05_0010_8.txt"
285 "***Data from file U_2_0010_05_8.txt: machinesNum=5 jobsNum=10"
328 "***SOLUTION Data from file SOL_U_2_05_0010_8.txt: machinesNum=5
jobsNum=10 lowerBound=1390 upperBound=1390 isOptimal=1"
332 Content of machines summed (1112, 1390, 1307, 1316, 1240)
354 input selected: (999, 896, 792, 724, 623, 617, 592, 515, 494, 113) size 10 sum 6365
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=1273, pMax=999, pigeonholePrinciple=607 => lowerBound
set to 1273
**Best gene from 1st generation: Gene id=39 TF=1493, #Machines=5,
content:<1,3,5,2,4,2,4,5,1,4>, Summed Machines(1493,1341,896,1328,1307)
**Best gene got replaced in generation 2. Gene details: Gene id=84 TF=1411, #Machines=5,
content:<1,3,5,2,4,2,4,3,5,5>, Summed Machines(999,1341,1411,1215,1399)
**END oldes Gen=34
**Best gene found: Gene id=84 TF=1411, #Machines=5, content:<1,3,5,2,4,2,4,3,5,5>,
Summed Machines(999,1341,1411,1215,1399)
219 "----Comparison for the 18 example----"
220 "***tf from benchmark=1390 target function from our Genetic=1411"
228 ***Different 21
230 Run time: 15.175 seconds
231 "Correct (size-numberCorrect):" QMap((10, 13))
231 "Mistakes(size-numberMistakes):" QMap((10, 6))
231 "Avegare error: 9.61111"
232 "-----END 19 from 30-----"
211 "-----START 20 from 30-----"
213 "input file number 20: inputName=C:/algo/h/docs/benchMark/all/U_2_0010_05_9.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_2_05_0010_9.txt"
285 "***Data from file U_2_0010_05_9.txt: machinesNum=5 jobsNum=10"
328 "***SOLUTION Data from file SOL_U_2_05_0010_9.txt: machinesNum=5
jobsNum=10 lowerBound=1144 upperBound=1144 isOptimal=1"
332 Content of machines summed (957, 1018, 939, 1144, 1087)
354 input selected: (858, 841, 746, 728, 622, 465, 416, 193, 177, 99) size 10 sum 5145
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=1029, pMax=858, pigeonholePrinciple=276 => lowerBound
set to 1029
**Best gene from 1st generation: Gene id=26 TF=1350, #Machines=5,
content:<3,5,2,1,1,4,5,4,4,3>, Summed Machines(1350,746,957,835,1257)
**Best gene got replaced in generation 2. Gene details: Gene id=40 TF=1257, #Machines=5,
content:<5,4,1,3,2,3,4,1,2,1>, Summed Machines(1038,799,1193,1257,858)

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**Best gene got replaced in generation 2. Gene details: Gene id=60 TF=1243, #Machines=5,
content:<2,1,5,4,3,3,4,5,2,4>, Summed Machines(841,1035,1087,1243,939)
**Best gene got replaced in generation 3. Gene details: Gene id=39 TF=1186, #Machines=5,
content:<2,1,5,4,3,3,4,5,1,3>, Summed Machines(1018,858,1186,1144,939)
**Best gene got replaced in generation 15. Gene details: Gene id=42 TF=1162,
#Machines=5, content:<3,4,1,5,2,2,1,3,5,5>, Summed Machines(1162,1087,1051,841,1004)
**END oldes Gen=34
**Best gene found: Gene id=42 TF=1162, #Machines=5, content:<3,4,1,5,2,2,1,3,5,5>,
Summed Machines(1162,1087,1051,841,1004)
219 "----Comparison for the 19 example----"
220 "***tf from benchmark=1144 target function from our Genetic=1162"
228 ***Different 18
230 Run time: 15.284 seconds
231 "Correct (size-numberCorrect):" QMap((10, 13))
231 "Mistakes(size-numberMistakes):" QMap((10, 7))
231 "Avegare error: 10.0526"
232 "-----END 20 from 30-----"
211 "-----START 21 from 30-----"
213 "input file number 21: inputName=C:/algo/h/docs/benchMark/all/U_3_0010_05_0.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_3_05_0010_0.txt"
285 "***Data from file U_3_0010_05_0.txt: machinesNum=5 jobsNum=10"
328 "***SOLUTION Data from file SOL_U_3_05_0010_0.txt: machinesNum=5
jobsNum=10 lowerBound=13547 upperBound=13547 isOptimal=1"
332 Content of machines summed (11493, 11553, 12900, 13547, 12550)
354 input selected: (9731, 9250, 8593, 8377, 6957, 5593, 5170, 4307, 2303, 1762) size 10
sum 62043
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=12408.6, pMax=9731, pigeonholePrinciple=4065 =>
lowerBound set to 12409
**Best gene from 1st generation: Gene id=51 TF=15334, #Machines=5,
content:<2,1,5,3,3,4,1,5,4,2>, Summed Machines(14420,11493,15334,7896,12900)
**Best gene got replaced in generation 3. Gene details: Gene id=6 TF=15309, #Machines=5,
content:<5,2,1,3,4,4,3,2,1,3>, Summed Machines(10896,13557,15309,12550,9731)
**Best gene got replaced in generation 7. Gene details: Gene id=64 TF=14901,
#Machines=5, content:<4,3,5,2,1,5,4,2,1,1>, Summed
Machines(11022,12684,9250,14901,14186)
**Best gene got replaced in generation 9. Gene details: Gene id=91 TF=14420,
#Machines=5, content:<1,4,5,2,3,3,4,2,5,1>, Summed
Machines(11493,12684,12550,14420,10896)
**Best gene got replaced in generation 16. Gene details: Gene id=11 TF=14186,
#Machines=5, content:<3,4,2,5,1,2,5,4,1,1>, Summed
Machines(11022,14186,9731,13557,13547)
**Best gene got replaced in generation 21. Gene details: Gene id=85 TF=14038,
#Machines=5, content:<2,4,5,1,3,3,5,2,4,1>, Summed
Machines(10139,14038,12550,11553,13763)
**END oldes Gen=34
**Best gene found: Gene id=85 TF=14038, #Machines=5, content:<2,4,5,1,3,3,5,2,4,1>,
Summed Machines(10139,14038,12550,11553,13763)
219 "----Comparison for the 20 example----"

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220 "***tf from benchmark=13547 target function from our Genetic=14038"
228 ***Different 491
230 Run time: 15.2 seconds
231 "Correct (size-numberCorrect):" QMap((10, 13))
231 "Mistakes(size-numberMistakes):" QMap((10, 8))
231 "Avegare error: 34.1"
232 "-----END 21 from 30-----"
211 "-----START 22 from 30-----"
213 "input file number 22: inputName=C:/algo/h/docs/benchMark/all/U_3_0010_05_1.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_3_05_0010_1.txt"
285 "***Data from file U_3_0010_05_1.txt: machinesNum=5 jobsNum=10"
328 "***SOLUTION Data from file SOL_U_3_05_0010_1.txt: machinesNum=5
jobsNum=10 lowerBound=12344 upperBound=12344 isOptimal=1"
332 Content of machines summed (10634, 12344, 11737, 11805, 11984)
354 input selected: (8851, 8586, 7235, 6846, 6493, 5491, 4959, 4502, 3758, 1783) size 10
sum 58504
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=11700.8, pMax=8851, pigeonholePrinciple=5541 =>
lowerBound set to 11701
**Best gene from 1st generation: Gene id=97 TF=13810, #Machines=5,
content:<3,2,5,4,1,4,3,5,2,1>, Summed Machines(8276,12344,13810,12337,11737)
**Best gene got replaced in generation 4. Gene details: Gene id=72 TF=13767,
#Machines=5, content:<4,1,5,3,2,2,1,4,3,2>, Summed
Machines(13545,13767,10604,13353,7235)
**Best gene got replaced in generation 7. Gene details: Gene id=58 TF=12609,
#Machines=5, content:<2,1,3,5,4,5,3,4,2,1>, Summed
Machines(10369,12609,12194,10995,12337)
**END oldes Gen=34
**Best gene found: Gene id=58 TF=12609, #Machines=5, content:<2,1,3,5,4,5,3,4,2,1>,
Summed Machines(10369,12609,12194,10995,12337)
219 "----Comparison for the 21 example----"
220 "***tf from benchmark=12344 target function from our Genetic=12609"
228 ***Different 265
230 Run time: 15.236 seconds
231 "Correct (size-numberCorrect):" QMap((10, 13))
231 "Mistakes(size-numberMistakes):" QMap((10, 9))
231 "Avegare error: 45.0952"
232 "-----END 22 from 30-----"
211 "-----START 23 from 30-----"
213 "input file number 23: inputName=C:/algo/h/docs/benchMark/all/U_3_0010_05_2.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_3_05_0010_2.txt"
285 "***Data from file U_3_0010_05_2.txt: machinesNum=5 jobsNum=10"
328 "***SOLUTION Data from file SOL_U_3_05_0010_2.txt: machinesNum=5
jobsNum=10 lowerBound=10520 upperBound=10520 isOptimal=1"
332 Content of machines summed (9366, 9016, 8813, 8961, 10520)
354 input selected: (8447, 7959, 7625, 7475, 6696, 3824, 1486, 1188, 1057, 919) size 10 sum
46676
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5

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LowerBounds calc: perfectSplit=9335.2, pMax=8447, pigeonholePrinciple=1976 =>
lowerBound set to 9336

****Best gene from 1st generation: Gene id=77 TF=10520, #Machines=5,
content:<3,5,4,2,1,1,2,2,3,3>, Summed Machines(10520,10149,10423,7625,7959)**

****END oldes Gen=34**

****Best gene found: Gene id=77 TF=10520, #Machines=5, content:<3,5,4,2,1,1,2,2,3,3>,
Summed Machines(10520,10149,10423,7625,7959)**

219 "----Comparison for the 22 example----

220 "****tf from benchmark=10520 target function from our Genetic=10520"

223 *****RESULT IS THE SAME**

230 Run time: 15.231 seconds

231 "Correct (size-numberCorrect):" QMap((10, 14))

231 "Mistakes(size-numberMistakes):" QMap((10, 9))

231 "Avegare error: 43.0455"

232 "-----END 23 from 30-----"

211 "-----START 24 from 30-----"

213 "input file number 24: inputName=C:/algo/h/docs/benchMark/all/U_3_0010_05_3.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_3_05_0010_3.txt"

285 *****Data from file U_3_0010_05_3.txt: machinesNum=5 jobsNum=10"**

328 *****SOLUTION Data from file SOL_U_3_05_0010_3.txt: machinesNum=5
jobsNum=10 lowerBound=8513 upperBound=8513 isOptimal=1"**

332 Content of machines summed (8513, 7020, 7043, 6543, 8167)

354 input selected: (8513, 5858, 5107, 4887, 4096, 4071, 1656, 1315, 1162, 621) size 10 sum
37286

starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5

LowerBounds calc: perfectSplit=7457.2, pMax=8513, pigeonholePrinciple=1783 =>
lowerBound set to 8513

****Best gene from 1st generation: Gene id=6 TF=8513, #Machines=5,
content:<2,3,5,4,1,1,5,5,3,4>, Summed Machines(8167,8513,7020,5508,8078)**

Best gene target function value is equal to lower bound. stopping Genetic H

****END oldes Gen=34**

****Best gene found: Gene id=6 TF=8513, #Machines=5, content:<2,3,5,4,1,1,5,5,3,4>,
Summed Machines(8167,8513,7020,5508,8078)**

219 "----Comparison for the 23 example----

220 "****tf from benchmark=8513 target function from our Genetic=8513"

223 *****RESULT IS THE SAME**

230 Run time: 0 seconds

231 "Correct (size-numberCorrect):" QMap((10, 15))

231 "Mistakes(size-numberMistakes):" QMap((10, 9))

231 "Avegare error: 41.1739"

232 "-----END 24 from 30-----"

211 "-----START 25 from 30-----"

213 "input file number 25: inputName=C:/algo/h/docs/benchMark/all/U_3_0010_05_4.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_3_05_0010_4.txt"

285 *****Data from file U_3_0010_05_4.txt: machinesNum=5 jobsNum=10"**

328 *****SOLUTION Data from file SOL_U_3_05_0010_4.txt: machinesNum=5
jobsNum=10 lowerBound=10828 upperBound=10828 isOptimal=1"**

332 Content of machines summed (9454, 10633, 10828, 10091, 10419)

354 input selected: (9454, 8814, 7232, 5185, 4906, 3919, 3784, 3596, 2716, 1819) size 10
sum 51425
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=10285, pMax=9454, pigeonholePrinciple=4535 =>
lowerBound set to 10285
**Best gene from 1st generation: Gene id=47 TF=12598, #Machines=5,
content:<2,5,1,1,4,3,5,3,4,2>, Summed Machines(12417,11273,7515,7622,12598)
**Best gene got replaced in generation 3. Gene details: Gene id=60 TF=12421,
#Machines=5, content:<4,5,2,1,3,3,1,3,4,1>, Summed
Machines(10788,7232,12421,12170,8814)
**Best gene got replaced in generation 4. Gene details: Gene id=83 TF=12138,
#Machines=5, content:<5,2,1,3,1,4,4,3,3,4>, Summed
Machines(12138,8814,11497,9522,9454)
**Best gene got replaced in generation 8. Gene details: Gene id=97 TF=11910,
#Machines=5, content:<3,5,4,2,2,1,1,1,5,2>, Summed
Machines(11299,11910,9454,7232,11530)
**Best gene got replaced in generation 9. Gene details: Gene id=18 TF=11530,
#Machines=5, content:<4,3,5,2,2,1,1,1,3,4>, Summed
Machines(11299,10091,11530,11273,7232)
**END oldes Gen=34
**Best gene found: Gene id=18 TF=11530, #Machines=5, content:<4,3,5,2,2,1,1,1,3,4>,
Summed Machines(11299,10091,11530,11273,7232)
219 "----Comparison for the 24 example----"
220 "***tf from benchmark=10828 target function from our Genetic=11530"
228 ***Different 702
230 Run time: 15.22 seconds
231 "Correct (size-numberCorrect):" QMap((10, 15))
231 "Mistakes(size-numberMistakes):" QMap((10, 10))
231 "Avegare error: 68.7083"
232 "-----END 25 from 30-----"
211 "-----START 26 from 30-----"
213 "input file number 26: inputName=C:/algo/h/docs/benchMark/all/U_3_0010_05_5.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_3_05_0010_5.txt"
285 "***Data from file U_3_0010_05_5.txt: machinesNum=5 jobsNum=10"
328 "***SOLUTION Data from file SOL_U_3_05_0010_5.txt: machinesNum=5
jobsNum=10 lowerBound=11056 upperBound=11056 isOptimal=1"
332 Content of machines summed (10667, 10697, 8970, 9396, 11056)
354 input selected: (8956, 8547, 6675, 6360, 6324, 4732, 3036, 2295, 2150, 1711) size 10
sum 50786
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=10157.2, pMax=8956, pigeonholePrinciple=3861 =>
lowerBound set to 10158
**Best gene from 1st generation: Gene id=21 TF=13688, #Machines=5,
content:<4,3,1,5,2,4,3,2,2,3>, Summed Machines(6675,10769,13294,13688,6360)
**Best gene got replaced in generation 2. Gene details: Gene id=13 TF=11992,
#Machines=5, content:<3,1,4,5,2,4,3,1,5,5>, Summed
Machines(10842,6324,11992,11407,10221)

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**Best gene got replaced in generation 6. Gene details: Gene id=46 TF=11407,
#Machines=5, content:<3,1,4,5,2,4,2,5,3,5>, Summed
Machines(8547,9360,11106,11407,10366)
**END oldes Gen=34
**Best gene found: Gene id=46 TF=11407, #Machines=5, content:<3,1,4,5,2,4,2,5,3,5>,
Summed Machines(8547,9360,11106,11407,10366)
219 "----Comparison for the 25 example----"
220 "****tf from benchmark=11056 target function from our Genetic=11407"
228 ***Different 351
230 Run time: 15.247 seconds
231 "Correct (size-numberCorrect):" QMap((10, 15))
231 "Mistakes(size-numberMistakes):" QMap((10, 11))
231 "Avegare error: 80"
232 "-----END 26 from 30-----"
211 "-----START 27 from 30-----"
213 "input file number 27: inputName=C:/algo/h/docs/benchMark/all/U_3_0010_05_6.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_3_05_0010_6.txt"
285 "****Data from file U_3_0010_05_6.txt: machinesNum=5 jobsNum=10"
328 "****SOLUTION Data from file SOL_U_3_05_0010_6.txt: machinesNum=5
jobsNum=10 lowerBound=11575 upperBound=11575 isOptimal=1"
332 Content of machines summed (9943, 11426, 11575, 10166, 10923)
354 input selected: (9943, 9621, 9580, 8070, 5665, 4119, 2096, 1995, 1805, 1139) size 10
sum 54033
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=10806.6, pMax=9943, pigeonholePrinciple=2944 =>
lowerBound set to 10807
**Best gene from 1st generation: Gene id=83 TF=11676, #Machines=5,
content:<5,2,1,3,4,4,1,3,4,2>, Summed Machines(11676,10760,10065,11589,9943)
**END oldes Gen=34
**Best gene found: Gene id=83 TF=11676, #Machines=5, content:<5,2,1,3,4,4,1,3,4,2>,
Summed Machines(11676,10760,10065,11589,9943)
219 "----Comparison for the 26 example----"
220 "****tf from benchmark=11575 target function from our Genetic=11676"
228 ***Different 101
230 Run time: 18.157 seconds
231 "Correct (size-numberCorrect):" QMap((10, 15))
231 "Mistakes(size-numberMistakes):" QMap((10, 12))
231 "Avegare error: 80.8077"
232 "-----END 27 from 30-----"
211 "-----START 28 from 30-----"
213 "input file number 28: inputName=C:/algo/h/docs/benchMark/all/U_3_0010_05_7.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_3_05_0010_7.txt"
285 "****Data from file U_3_0010_05_7.txt: machinesNum=5 jobsNum=10"
328 "****SOLUTION Data from file SOL_U_3_05_0010_7.txt: machinesNum=5
jobsNum=10 lowerBound=14233 upperBound=14233 isOptimal=1"
332 Content of machines summed (10016, 12162, 14233, 14098, 13379)
354 input selected: (9965, 9512, 8770, 7785, 6981, 6398, 6313, 5463, 2650, 51) size 10 sum
63888

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starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=12777.6, pMax=9965, pigeonholePrinciple=2701 =>
lowerBound set to 12778
**Best gene from 1st generation: Gene id=74 TF=14975, #Machines=5,
content:<2,3,1,4,5,4,5,3,1,1>, Summed Machines(11471,9965,14975,14183,13294)
**Best gene got replaced in generation 21. Gene details: Gene id=79 TF=14233,
#Machines=5, content:<4,2,5,1,3,1,3,5,2,4>, Summed
Machines(14183,12162,13294,10016,14233)
**END oldes Gen=34
**Best gene found: Gene id=79 TF=14233, #Machines=5, content:<4,2,5,1,3,1,3,5,2,4>,
Summed Machines(14183,12162,13294,10016,14233)
219 "----Comparison for the 27 example----"
220 "***tf from benchmark=14233 target function from our Genetic=14233"
223 ***RESULT IS THE SAME
230 Run time: 15.885 seconds
231 "Correct (size-numberCorrect):" QMap((10, 16))
231 "Mistakes(size-numberMistakes):" QMap((10, 12))
231 "Avegare error: 77.8148"
232 "-----END 28 from 30-----"
211 "-----START 29 from 30-----"
213 "input file number 29: inputName=C:/algo/h/docs/benchMark/all/U_3_0010_05_8.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_3_05_0010_8.txt"
285 "***Data from file U_3_0010_05_8.txt: machinesNum=5 jobsNum=10"
328 "***SOLUTION Data from file SOL_U_3_05_0010_8.txt: machinesNum=5
jobsNum=10 lowerBound=12749 upperBound=12749 isOptimal=1"
332 Content of machines summed (9968, 10246, 12749, 12417, 12614)
354 input selected: (9347, 9336, 8314, 7863, 7643, 4971, 4554, 4435, 910, 621) size 10 sum
57994
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=11598.8, pMax=9347, pigeonholePrinciple=1531 =>
lowerBound set to 11599
**Best gene from 1st generation: Gene id=66 TF=14307, #Machines=5,
content:<4,2,3,1,5,2,5,3,1,1>, Summed Machines(9394,14307,12749,9347,12197)
**Best gene got replaced in generation 2. Gene details: Gene id=11 TF=12919,
#Machines=5, content:<2,5,1,3,4,4,1,3,5,3>, Summed
Machines(12868,9347,12919,12614,10246)
**END oldes Gen=34
**Best gene found: Gene id=11 TF=12919, #Machines=5, content:<2,5,1,3,4,4,1,3,5,3>,
Summed Machines(12868,9347,12919,12614,10246)
219 "----Comparison for the 28 example----"
220 "***tf from benchmark=12749 target function from our Genetic=12919"
228 ***Different 170
230 Run time: 15.596 seconds
231 "Correct (size-numberCorrect):" QMap((10, 16))
231 "Mistakes(size-numberMistakes):" QMap((10, 13))
231 "Avegare error: 81.1071"
232 "-----END 29 from 30-----"
211 "-----START 30 from 30-----"

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213 "input file number 30: inputName=C:/algo/h/docs/benchMark/all/U_3_0010_05_9.txt
and solutionName=C:/algo/h/docs/benchMark/all/SOL_U_3_05_0010_9.txt"
285 "****Data from file U_3_0010_05_9.txt: machinesNum=5 jobsNum=10"
328 "****SOLUTION Data from file SOL_U_3_05_0010_9.txt: machinesNum=5
jobsNum=10 lowerBound=13586 upperBound=13586 isOptimal=1"
332 Content of machines summed (10223, 10781, 10468, 12897, 13586)
354 input selected: (9743, 9731, 9092, 8389, 7662, 5924, 4508, 1376, 1050, 480) size 10 sum
57955
starting Genetic with args: generationsNumber=100, populationSize=100,
machinesNumber=5
LowerBounds calc: perfectSplit=11591, pMax=9743, pigeonholePrinciple=1530 =>
lowerBound set to 11591
**Best gene from 1st generation: Gene id=68 TF=14962, #Machines=5,
content:<2,3,1,4,5,5,3,5,1,2>, Summed Machines(10142,10223,14239,8389,14962)
**Best gene got replaced in generation 5. Gene details: Gene id=6 TF=14793, #Machines=5,
content:<4,1,2,3,5,3,4,2,2,3>, Summed Machines(9731,11518,14793,14251,7662)
**Best gene got replaced in generation 6. Gene details: Gene id=9 TF=14313, #Machines=5,
content:<4,1,2,3,5,3,4,2,2,2>, Summed Machines(9731,11998,14313,14251,7662)
**Best gene got replaced in generation 9. Gene details: Gene id=27 TF=14080,
#Machines=5, content:<4,1,2,5,3,3,2,1,1,2>, Summed
Machines(12157,14080,13586,9743,8389)
**Best gene got replaced in generation 10. Gene details: Gene id=98 TF=13600,
#Machines=5, content:<4,1,2,5,3,3,2,1,1,5>, Summed
Machines(12157,13600,13586,9743,8869)
**Best gene got replaced in generation 18. Gene details: Gene id=26 TF=13586,
#Machines=5, content:<5,1,4,2,3,3,2,1,4,2>, Summed
Machines(11107,13377,13586,10142,9743)
**END oldes Gen=34
**Best gene found: Gene id=26 TF=13586, #Machines=5, content:<5,1,4,2,3,3,2,1,4,2>,
Summed Machines(11107,13377,13586,10142,9743)
219 "----Comparison for the 29 example----"
220 "****tf from benchmark=13586 target function from our Genetic=13586"
223 ***RESULT IS THE SAME
230 Run time: 15.794 seconds
231 "Correct (size-numberCorrect):" QMap((10, 17))
231 "Mistakes(size-numberMistakes):" QMap((10, 13))
231 "Avegare error: 78.3103"
232 "-----END 30 from 30-----"
234 "Correct (size-numberCorrect):" QMap((10, 17))
235 "Mistakes(size-numberMistakes):" QMap((10, 13))
236 "Total Avegare error: 75.7"
237 "Total time: 378.877 seconds"
238 oldest Gen 34
C:\algo\build-h-Desktop_Qt_5_6_0_MinGW_32bit-Debug\debug\h.exe exited with code
0

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