דוח תיאור של אלגוריתם גנטי

- מחשבים חסמים תחתונים – ולוקחים את המקסימלי
  - אם בשלב כלשהו בריצה השגנו tf=lowerBound עוצרים את הריצה.
- אנחנו מאתחלים את הדור הראשון שלנו בגנים(כרומוזומים) רנדומאלים לחלוטין.
  - מקבעים את הגן(כרומוזום) עם הTF הכי טוב להיות ה Best gene found
- מתחילים את הריצה על מספר הדורות
  - יוצרים דור חדש
    - בודקים אם השגנו tf=lowerBound
    - יוצרים מפת הסתברות: עבור כל גן:

geneFitness = (maximalTf-gene.Tf)/(maximalTf * genesNumber - tfSum);
- maximalTf := the highest TF of all the genes in this Genaraion
- tfSum:= the sum of all genes tf

- כדי לחשב את "ההשפעה" של גן עשינו שיקוף(כפילה במינוס אחד – בגלל שהיחס בין TF ל FITNESS הוא הפוך) ומרחק מ maximalTf (גם כפול מינוס אחד) ובסוף נרמול.
    - הגנים שנבחרים למוטציה:
- קבענו 20% להיות אחוז השינוי
- תגריל 20% אינדקסים שישונו
  - עבור כל אינקס שהוגרל: הגרל ערך בין 1-למספר המכונות – וזה הערך החדש.
    - הגנים שנבחרים ל XO:
- מגרילים אינקס לחתך ועושים XO לפי הגדרה. את שני הילדים שולחים ל NEXT GENERATION

- בהמשך נשלב 3 כרומוזומים התחלתיים לא רנדומיים (lpt, bestFit, sameMachine). לא עשינו אותם עדיין כדי שלא ישפיעו על התוצאות (כדי לבדוק את איכות ההיוריסטיקה עצמה ולא לקבל תמיד את LPT אם ההיוריסטיקה לא עשתה כלום)
  - נכון לעכשיו, נראה שהתוצאות טובות, אז נשקול אם יש טעם להוסיף אותם.

המשימה שלנו לדוח הראשון

- כרגע אנו מריצים סט קלטים באורך(40) עם הפרמטרים הבאים:
  - 1000 משימות
  - התפלגות יוניפורמית
  - מספר מכונות 5 או 10
  - בכל ריצה אנחנו רצים 3 פעמים עם הפרמטרים הבאים:
    - Attempt 1:
      - Population Size: 100
      - Number of generations: 100
    - Attempt 2:
      - Population Size: 50
      - Number of generations: 200
    - Attempt 3:
      - Population Size: 200
      - Number of generations: 50

  - לאחר סיום ריצת הניסיונות אנחנו משווים את התוצאה הטובה ביותר עם התוצאה של ה Benchmark.

ניתוח של הפלטים

- לא מגיעים לאופטימום אך נראה שהאלגוריתמים כן מתכנס לכיוון הפתרון האופטימלי.
- עשינו מאמצים שההתכנסות לא תהיה מהירה מידי ולראיה אנו מקבלים שהאלגוריתם מוצא פתרונות בדורות די גדולים. לכל פתרון בפלטים יש את מספר הדור האחרון שנמצא שיפור:
  **END On Gen=86
- סיכום הפלטים

  - "Correct (size-numberCorrect):" QMap()
  - "Mistakes(size-numberMistakes):" QMap((1000, 40))
  - "Avegare error: 85.4359"
  ○ ניתן לראות שהשגיאה הממוצעת היא 85 אך יש קלטים שגודל המשימות הוא בסדר גודל תלת או ארבע ספרתי.
- הרצנו 90 (אך סיימו ורצינו פידבק ראשוני40):

"number of input=90. distribution=U. range=all #jobs=1000. #machines=all"
"--------------------START 1 from 90------------------------------"
"1) U_1_1000_05_0.txt"
*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=**9990**
*Content of machines summed (9990, 9990, 9989, 9989, 9989)
input selected: size 1000 sum 49947
**END On Gen=62
**Best gene found: Gene id=68 TF=10019, #Machines=5, content:Very long..., Summed Machines(10000,9946,9998,10019,9984)
"Attempt 1(populationSize=100, genSize=100): TF=10019"
**END On Gen=174
**Best gene found: Gene id=29 TF=9995, #Machines=5, content:Very long..., Summed Machines(9989,9984,9989,9995,9990)
"Attempt 2(populationSize=50, genSize=200): TF=9995"
**END On Gen=40
**Best gene found: Gene id=138 TF=10016, #Machines=5, content:Very long..., Summed Machines(10008,10016,10011,10010,9902)
"Attempt 3(populationSize=200, genSize=50): TF=10016"
"----Comparison for the 0 example----"
"***BenchmarkTf=9990 ourGeneticTf=9995"
***RESULT IS Different 5
Run time: 73.387 seconds
"Correct (size-numberCorrect):" QMap()
"Mistakes(size-numberMistakes):" QMap((1000, 1))
"Avegare error: inf"
"-----------END 1 from 90---"
"--------------------START 2 from 90------------------------------"
"2) U_1_1000_05_1.txt"
*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=10263
*Content of machines summed (10263, 10263, 10263, 10262, 10262)
input selected: size 1000 sum 51313
**END On Gen=67
**Best gene found: Gene id=33 TF=10277, #Machines=5, content:Very long..., Summed Machines(10267,10277,10264,10276,10229)
"Attempt 1(populationSize=100, genSize=100): TF=10277"
**END On Gen=134

**Best gene found: Gene id=6 TF=10280, #Machines=5, content:Very long..., Summed Machines(10280,10269,10271,10271,10222)

"Attempt 2(populationSize=50, genSize=200): TF=10280"

**END On Gen=48

**Best gene found: Gene id=64 TF=10303, #Machines=5, content:Very long..., Summed Machines(10288,10294,10303,10283,10145)

"Attempt 3(populationSize=200, genSize=50): TF=10303"

"----Comparison for the 1 example----"

"***BenchmarkTf=10263 ourGeneticTf=10277"

***RESULT IS Different 14

Run time: 70.985 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 2))

"Avegare error: 19"

"-----------END 2 from 90--"

"-------------------START 3 from 90-------------------------------"

"3) U_1_1000_05_2.txt"

*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=10073

*Content of machines summed (10073, 10073, 10073, 10072, 10072)

input selected: size 1000 sum 50363

**END On Gen=85

**Best gene found: Gene id=1 TF=10091, #Machines=5, content:Very long..., Summed Machines(10068,10075,10076,10053,10091)

"Attempt 1(populationSize=100, genSize=100): TF=10091"

**END On Gen=182

**Best gene found: Gene id=7 TF=10095, #Machines=5, content:Very long..., Summed Machines(10095,10086,10042,10067,10073)

"Attempt 2(populationSize=50, genSize=200): TF=10095"

**END On Gen=21

**Best gene found: Gene id=94 TF=10113, #Machines=5, content:Very long..., Summed Machines(10075,10102,9977,10096,10113)

"Attempt 3(populationSize=200, genSize=50): TF=10113"

"----Comparison for the 2 example----"

"***BenchmarkTf=10073 ourGeneticTf=10091"

***RESULT IS Different 18

Run time: 70.598 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 3))

"Avegare error: 18.5"

"-----------END 3 from 90--"

"-------------------START 4 from 90-------------------------------"

"4) U_1_1000_05_3.txt"

*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=10106

*Content of machines summed (10106, 10106, 10105, 10105, 10105)

input selected: size 1000 sum 50527

**END On Gen=64

**Best gene found: Gene id=83 TF=10114, #Machines=5, content:Very long..., Summed Machines(10109,10107,10108,10089,10114)

"Attempt 1(populationSize=100, genSize=100): TF=10114"

**END On Gen=127

**Best gene found: Gene id=45 TF=10120, #Machines=5, content:Very long..., Summed Machines(10110,10097,10115,10120,10085)

"Attempt 2(populationSize=50, genSize=200): TF=10120"

**END On Gen=48

**Best gene found: Gene id=175 TF=10156, #Machines=5, content:Very long..., Summed Machines(10060,10156,10148,10086,10077)

"Attempt 3(populationSize=200, genSize=50): TF=10156"

"----Comparison for the 3 example----"

"***BenchmarkTf=10106 ourGeneticTf=10114"

***RESULT IS Different 8

Run time: 70.562 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 4))

"Avegare error: 15"

"-----------END 4 from 90--"

"--------------------START 5 from 90--------------------------------"

"5) U_1_1000_05_4.txt"

*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=9904

*Content of machines summed (9904, 9903, 9903, 9903, 9903)

input selected: size 1000 sum 49516

**END On Gen=91

**Best gene found: Gene id=59 TF=9924, #Machines=5, content:Very long..., Summed Machines(9866,9918,9893,9924,9915)

"Attempt 1(populationSize=100, genSize=100): TF=9924"

**END On Gen=169

**Best gene found: Gene id=25 TF=9915, #Machines=5, content:Very long..., Summed Machines(9888,9912,9907,9894,9915)

"Attempt 2(populationSize=50, genSize=200): TF=9915"

**END On Gen=37

**Best gene found: Gene id=134 TF=9942, #Machines=5, content:Very long..., Summed Machines(9936,9930,9819,9889,9942)

"Attempt 3(populationSize=200, genSize=50): TF=9942"

"----Comparison for the 4 example----"

"***BenchmarkTf=9904 ourGeneticTf=9915"

***RESULT IS Different 11

Run time: 70.844 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 5))

"Avegare error: 14"

"-----------END 5 from 90--"

"--------------------START 6 from 90--------------------------------"

"6) U_1_1000_05_5.txt"

*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=9783

*Content of machines summed (9783, 9783, 9782, 9782, 9782)

input selected: size 1000 sum 48912

**END On Gen=76

**Best gene found: Gene id=3 TF=9804, #Machines=5, content:Very long..., Summed Machines(9804,9774,9785,9777,9772)

"Attempt 1(populationSize=100, genSize=100): TF=9804"

**END On Gen=192

**Best gene found: Gene id=38 TF=9795, #Machines=5, content:Very long..., Summed Machines(9787,9759,9793,9795,9778)

"Attempt 2(populationSize=50, genSize=200): TF=9795"

**END On Gen=49

**Best gene found: Gene id=52 TF=9816, #Machines=5, content:Very long..., Summed Machines(9811,9691,9816,9785,9809)

"Attempt 3(populationSize=200, genSize=50): TF=9816"

"----Comparison for the 5 example----"

"***BenchmarkTf=9783 ourGeneticTf=9795"

***RESULT IS Different 12

Run time: 71.708 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 6))

"Avegare error: 13.6"

"-----------END 6 from 90--"

"--------------------START 7 from 90-------------------------------"

"7) U_1_1000_05_6.txt"

*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=10049

*Content of machines summed (10049, 10049, 10048, 10048, 10048)

input selected: size 1000 sum 50242

**END On Gen=78

**Best gene found: Gene id=22 TF=10071, #Machines=5, content:Very long..., Summed Machines(10038,10048,10071,10054,10031)

"Attempt 1(populationSize=100, genSize=100): TF=10071"

**END On Gen=179

**Best gene found: Gene id=17 TF=10059, #Machines=5, content:Very long..., Summed Machines(10033,10038,10056,10056,10059)

"Attempt 2(populationSize=50, genSize=200): TF=10059"

**END On Gen=44

**Best gene found: Gene id=156 TF=10104, #Machines=5, content:Very long..., Summed Machines(9991,10069,9994,10104,10084)

"Attempt 3(populationSize=200, genSize=50): TF=10104"

"----Comparison for the 6 example----"

"***BenchmarkTf=10049 ourGeneticTf=10059"

***RESULT IS Different 10

Run time: 75.914 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 7))

"Avegare error: 13"

"-----------END 7 from 90--"

"--------------------START 8 from 90-------------------------------"

"8) U_1_1000_05_7.txt"

*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=9861

*Content of machines summed (9861, 9861, 9861, 9861, 9860)

input selected: size 1000 sum 49304

**END On Gen=85

**Best gene found: Gene id=42 TF=9882, #Machines=5, content:Very long..., Summed Machines(9882,9830,9879,9861,9852)

"Attempt 1(populationSize=100, genSize=100): TF=9882"

**END On Gen=113

**Best gene found: Gene id=21 TF=9877, #Machines=5, content:Very long..., Summed Machines(9872,9842,9877,9847,9866)

"Attempt 2(populationSize=50, genSize=200): TF=9877"

**END On Gen=23

**Best gene found: Gene id=49 TF=9892, #Machines=5, content:Very long..., Summed Machines(9886,9832,9892,9811,9883)

"Attempt 3(populationSize=200, genSize=50): TF=9892"

"----Comparison for the 7 example----"

"***BenchmarkTf=9861 ourGeneticTf=9877"

***RESULT IS Different 16

Run time: 73.026 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 8))

"Avegare error: 13.4286"

"-----------END 8 from 90--"

"--------------------START 9 from 90-------------------------------"

"9) U_1_1000_05_8.txt"

*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=10064

*Content of machines summed (10064, 10064, 10064, 10064, 10064)

input selected: size 1000 sum 50320

**END On Gen=76

**Best gene found: Gene id=36 TF=10094, #Machines=5, content:Very long..., Summed Machines(10012,10094,10077,10066,10071)

"Attempt 1(populationSize=100, genSize=100): TF=10094"

**END On Gen=125

**Best gene found: Gene id=44 TF=10075, #Machines=5, content:Very long..., Summed Machines(10073,10068,10075,10039,10065)

"Attempt 2(populationSize=50, genSize=200): TF=10075"

**END On Gen=50

**Best gene found: Gene id=61 TF=10117, #Machines=5, content:Very long..., Summed Machines(10117,9997,10067,10072,10067)

"Attempt 3(populationSize=200, genSize=50): TF=10117"

"----Comparison for the 8 example----"

"***BenchmarkTf=10064 ourGeneticTf=10075"

***RESULT IS Different 11

Run time: 73.333 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 9))

"Avegare error: 13.125"

"-----------END 9 from 90--"

"--------------------START 10 from 90-------------------------------"

"10) U_1_1000_05_9.txt"

*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=9827

*Content of machines summed (9827, 9827, 9827, 9826, 9826)

input selected: size 1000 sum 49133

**END On Gen=65

**Best gene found: Gene id=40 TF=9851, #Machines=5, content:Very long..., Summed Machines(9771,9851,9849,9815,9847)

"Attempt 1(populationSize=100, genSize=100): TF=9851"

**END On Gen=85

**Best gene found: Gene id=12 TF=9836, #Machines=5, content:Very long..., Summed Machines(9835,9823,9829,9810,9836)
"Attempt 2(populationSize=50, genSize=200): TF=9836"
**END On Gen=29
**Best gene found: Gene id=49 TF=9885, #Machines=5, content:Very long..., Summed Machines(9885,9817,9752,9859,9820)
"Attempt 3(populationSize=200, genSize=50): TF=9885"
"----Comparison for the 9 example----"
"***BenchmarkTf=9827 ourGeneticTf=9836"
***RESULT IS Different 9
Run time: 72.411 seconds
"Correct (size-numberCorrect):" QMap()
"Mistakes(size-numberMistakes):" QMap((1000, 10))
"Avegare error: 12.6667"
"-----------END 10 from 90--"
"-------------------START 11 from 90------------------------------"
"11) U_1_1000_10_0.txt"
*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=4837
*Content of machines summed (4837, 4837, 4837, 4836, 4836, 4836, 4836, 4836, 4836, 4836)
input selected: size 1000 sum 48363
**END On Gen=92
**Best gene found: Gene id=73 TF=4937, #Machines=10, content:Very long..., Summed Machines(4842,4854,4922,4736,4934,4900,4937,4523,4900,4815)
"Attempt 1(populationSize=100, genSize=100): TF=4937"
**END On Gen=194
**Best gene found: Gene id=10 TF=4864, #Machines=10, content:Very long..., Summed Machines(4829,4829,4841,4864,4845,4852,4830,4820,4804,4849)
"Attempt 2(populationSize=50, genSize=200): TF=4864"
**END On Gen=50
**Best gene found: Gene id=16 TF=4957, #Machines=10, content:Very long..., Summed Machines(4797,4732,4843,4932,4706,4957,4923,4844,4957,4672)
"Attempt 3(populationSize=200, genSize=50): TF=4957"
"----Comparison for the 10 example----"
"***BenchmarkTf=4837 ourGeneticTf=4864"
***RESULT IS Different 27
Run time: 76.685 seconds
"Correct (size-numberCorrect):" QMap()
"Mistakes(size-numberMistakes):" QMap((1000, 11))
"Avegare error: 14.1"
"-----------END 11 from 90--"
"-------------------START 12 from 90------------------------------"
"12) U_1_1000_10_1.txt"
*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=5021
*Content of machines summed (5021, 5021, 5020, 5020, 5020, 5020, 5020, 5020, 5020, 5020)
input selected: size 1000 sum 50202
**END On Gen=97
**Best gene found: Gene id=77 TF=5107, #Machines=10, content:Very long..., Summed Machines(5104,5100,5065,4689,5063,4917,5107,5063,5031,5063)

"Attempt 1(populationSize=100, genSize=100): TF=5107"

**END On Gen=159

**Best gene found: Gene id=47 TF=5081, #Machines=10, content:Very long..., Summed Machines(5077,4991,4968,5077,5069,4929,5081,4947,4998,5065)

"Attempt 2(populationSize=50, genSize=200): TF=5081"

**END On Gen=49

**Best gene found: Gene id=159 TF=5160, #Machines=10, content:Very long..., Summed Machines(4899,5114,5025,5020,5160,5058,4988,4901,4930,5107)

"Attempt 3(populationSize=200, genSize=50): TF=5160"

"----Comparison for the 11 example----"

"***BenchmarkTf=5021 ourGeneticTf=5081"

***RESULT IS Different 60

Run time: 72.307 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 12))

"Avegare error: 18.2727"

"-----------END 12 from 90---------------------------------------"

"-------------------START 13 from 90-------------------------------"

"13) U_1_1000_10_2.txt"

*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=5110

*Content of machines summed (5110, 5110, 5110, 5110, 5110, 5110, 5110, 5109, 5109, 5109)

input selected: size 1000 sum 51097

**END On Gen=91

**Best gene found: Gene id=58 TF=5194, #Machines=10, content:Very long..., Summed Machines(5165,5111,5176,5189,5072,5006,5194,4969,5038,5177)

"Attempt 1(populationSize=100, genSize=100): TF=5194"

**END On Gen=197

**Best gene found: Gene id=40 TF=5204, #Machines=10, content:Very long..., Summed Machines(5082,5133,5180,5181,5112,4920,5204,5203,5176,4906)

"Attempt 2(populationSize=50, genSize=200): TF=5204"

**END On Gen=35

**Best gene found: Gene id=131 TF=5226, #Machines=10, content:Very long..., Summed Machines(4880,5131,5149,5174,5162,4960,5226,5144,5153,5118)

"Attempt 3(populationSize=200, genSize=50): TF=5226"

"----Comparison for the 12 example----"

"***BenchmarkTf=5110 ourGeneticTf=5194"

***RESULT IS Different 84

Run time: 72.481 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 13))

"Avegare error: 23.75"

"-----------END 13 from 90---------------------------------------"

"-------------------START 14 from 90-------------------------------"

"14) U_1_1000_10_3.txt"

*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=4926

*Content of machines summed (4926, 4926, 4926, 4926, 4926, 4925, 4925, 4925, 4925, 4925)

input selected: size 1000 sum 49255

**END On Gen=41

**Best gene found: Gene id=84 TF=4973, #Machines=10, content:Very long..., Summed Machines(4973,4933,4962,4924,4892,4941,4971,4926,4849,4884)

"Attempt 1(populationSize=100, genSize=100): TF=4973"

**END On Gen=157

**Best gene found: Gene id=10 TF=4970, #Machines=10, content:Very long..., Summed Machines(4970,4773,4959,4917,4949,4962,4968,4906,4924,4927)

"Attempt 2(populationSize=50, genSize=200): TF=4970"

**END On Gen=30

**Best gene found: Gene id=83 TF=5012, #Machines=10, content:Very long..., Summed Machines(4890,4927,4960,5012,4968,5000,4859,4844,4896,4899)

"Attempt 3(populationSize=200, genSize=50): TF=5012"

"----Comparison for the 13 example----"

"***BenchmarkTf=4926 ourGeneticTf=4970"

***RESULT IS Different 44

Run time: 73.405 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 14))

"Avegare error: 25.3077"

"-----------END 14 from 90--"

"--------------------START 15 from 90-------------------------------"

"15) U_1_1000_10_4.txt"

*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=5119

*Content of machines summed (5119, 5119, 5119, 5119, 5119, 5119, 5118, 5118, 5118, 5118)

input selected: size 1000 sum 51186

**END On Gen=100

**Best gene found: Gene id=7 TF=5178, #Machines=10, content:Very long..., Summed Machines(5094,5178,5154,5158,5122,5100,5105,5099,5131,5045)

"Attempt 1(populationSize=100, genSize=100): TF=5178"

**END On Gen=192

**Best gene found: Gene id=14 TF=5166, #Machines=10, content:Very long..., Summed Machines(4835,5165,5162,5152,5144,5141,5153,5164,5166,5104)

"Attempt 2(populationSize=50, genSize=200): TF=5166"

**END On Gen=49

**Best gene found: Gene id=191 TF=5268, #Machines=10, content:Very long..., Summed Machines(5096,4698,5256,5111,5259,5175,5100,5124,5099,5268)

"Attempt 3(populationSize=200, genSize=50): TF=5268"

"----Comparison for the 14 example----"

"***BenchmarkTf=5119 ourGeneticTf=5166"

***RESULT IS Different 47

Run time: 72.216 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 15))

"Avegare error: 26.8571"

"-----------END 15 from 90--"

"--------------------START 16 from 90-------------------------------"

"16) U_1_1000_10_5.txt"

*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=4885

*Content of machines summed (4885, 4885, 4884, 4884, 4884, 4884, 4884, 4884, 4884, 4884)

input selected: size 1000 sum 48842

**END On Gen=98

**Best gene found: Gene id=16 TF=4957, #Machines=10, content:Very long..., Summed Machines(4909,4938,4826,4899,4941,4742,4952,4957,4833,4845)

"Attempt 1(populationSize=100, genSize=100): TF=4957"

**END On Gen=174

**Best gene found: Gene id=23 TF=4932, #Machines=10, content:Very long..., Summed Machines(4931,4920,4907,4885,4907,4925,4684,4932,4825,4926)

"Attempt 2(populationSize=50, genSize=200): TF=4932"

**END On Gen=42

**Best gene found: Gene id=84 TF=4994, #Machines=10, content:Very long..., Summed Machines(4772,4952,4926,4733,4906,4994,4883,4823,4920,4933)

"Attempt 3(populationSize=200, genSize=50): TF=4994"

"----Comparison for the 15 example----"

"***BenchmarkTf=4885 ourGeneticTf=4932"

***RESULT IS Different 47

Run time: 72.125 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 16))

"Avegare error: 28.2"

"-----------END 16 from 90--"

"-------------------START 17 from 90-------------------------------"

"17) U_1_1000_10_6.txt"

*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=4954

*Content of machines summed (4954, 4954, 4954, 4954, 4954, 4954, 4954, 4954, 4954, 4954)

input selected: size 1000 sum 49540

**END On Gen=100

**Best gene found: Gene id=76 TF=5021, #Machines=10, content:Very long..., Summed Machines(4936,4987,4903,5021,4956,5017,4977,4964,4785,4994)

"Attempt 1(populationSize=100, genSize=100): TF=5021"

**END On Gen=174

**Best gene found: Gene id=23 TF=5038, #Machines=10, content:Very long..., Summed Machines(4995,4966,4954,5011,4837,4976,4884,4924,5038,4955)

"Attempt 2(populationSize=50, genSize=200): TF=5038"

**END On Gen=49

**Best gene found: Gene id=197 TF=5100, #Machines=10, content:Very long..., Summed Machines(4875,4867,4686,5021,5049,4948,5081,5100,4995,4918)

"Attempt 3(populationSize=200, genSize=50): TF=5100"

"----Comparison for the 16 example----"

"***BenchmarkTf=4954 ourGeneticTf=5021"

***RESULT IS Different 67

Run time: 72.94 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 17))

"Avegare error: 30.625"

"-----------END 17 from 90--"

"-------------------START 18 from 90-------------------------------"

"18) U_1_1000_10_7.txt"

*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=5153

*Content of machines summed (5153, 5153, 5153, 5153, 5152, 5152, 5152, 5152, 5152, 5152)
input selected: size 1000 sum 51524
**END On Gen=59
**Best gene found: Gene id=37 TF=5235, #Machines=10, content:Very long..., Summed Machines(5226,5045,5151,5068,5166,4992,5235,5192,5216,5233)
"Attempt 1(populationSize=100, genSize=100): TF=5235"
**END On Gen=168
**Best gene found: Gene id=28 TF=5199, #Machines=10, content:Very long..., Summed Machines(5121,5162,5105,5174,5181,5196,5199,5103,5086,5197)
"Attempt 2(populationSize=50, genSize=200): TF=5199"
**END On Gen=47
**Best gene found: Gene id=153 TF=5239, #Machines=10, content:Very long..., Summed Machines(5152,5144,5159,5196,5147,5148,5060,5153,5126,5239)
"Attempt 3(populationSize=200, genSize=50): TF=5239"
"----Comparison for the 17 example----"
"***BenchmarkTf=5153 ourGeneticTf=5199"
***RESULT IS Different 46
Run time: 73.007 seconds
"Correct (size-numberCorrect):" QMap()
"Mistakes(size-numberMistakes):" QMap((1000, 18))
"Avegare error: 31.5294"
"-----------END 18 from 90--"
"--------------------START 19 from 90------------------------------"
"19) U_1_1000_10_8.txt"
*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=4855
*Content of machines summed (4855, 4855, 4855, 4855, 4855, 4855, 4854, 4854, 4854, 4854)
input selected: size 1000 sum 48546
**END On Gen=83
**Best gene found: Gene id=18 TF=4909, #Machines=10, content:Very long..., Summed Machines(4845,4892,4845,4887,4849,4678,4898,4841,4902,4909)
"Attempt 1(populationSize=100, genSize=100): TF=4909"
**END On Gen=195
**Best gene found: Gene id=24 TF=4907, #Machines=10, content:Very long..., Summed Machines(4827,4907,4894,4849,4869,4703,4907,4872,4831,4887)
"Attempt 2(populationSize=50, genSize=200): TF=4907"
**END On Gen=39
**Best gene found: Gene id=86 TF=5000, #Machines=10, content:Very long..., Summed Machines(4982,4962,5000,4952,4606,4447,4754,4983,4924,4936)
"Attempt 3(populationSize=200, genSize=50): TF=5000"
"----Comparison for the 18 example----"
"***BenchmarkTf=4855 ourGeneticTf=4907"
***RESULT IS Different 52
Run time: 73.469 seconds
"Correct (size-numberCorrect):" QMap()
"Mistakes(size-numberMistakes):" QMap((1000, 19))
"Avegare error: 32.6667"
"-----------END 19 from 90--"
"--------------------START 20 from 90------------------------------"

"20) U_1_1000_10_9.txt"

*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=4886

*Content of machines summed (4886, 4886, 4886, 4886, 4886, 4886, 4886, 4886, 4885, 4885)

input selected: size 1000 sum 48858

**END On Gen=94

**Best gene found: Gene id=93 TF=4935, #Machines=10, content:Very long..., Summed Machines(4928,4722,4935,4921,4847,4926,4933,4807,4905,4934)

"Attempt 1(populationSize=100, genSize=100): TF=4935"

**END On Gen=138

**Best gene found: Gene id=7 TF=4954, #Machines=10, content:Very long..., Summed Machines(4835,4929,4847,4954,4925,4936,4653,4942,4928,4909)

"Attempt 2(populationSize=50, genSize=200): TF=4954"

**END On Gen=19

**Best gene found: Gene id=15 TF=5009, #Machines=10, content:Very long..., Summed Machines(4845,4953,4936,4649,4964,4796,4939,4769,4998,5009)

"Attempt 3(populationSize=200, genSize=50): TF=5009"

"----Comparison for the 19 example----"

"***BenchmarkTf=4886 ourGeneticTf=4935"

***RESULT IS Different 49

Run time: 73.125 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 20))

"Avegare error: 33.5263"

"-----------END 20 from 90--"

"--------------------START 21 from 90-------------------------------"

"21) U_1_1000_25_0.txt"

*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=2025

*Content of machines summed (2025, 2025, 2025, 2025, 2025, 2025, 2025, 2025, 2025, 2025, 2025, 2025, 2024, 2024, 2025, 2025, 2024, 2024, 2024, 2024, 2024, 2024, 2024, 2024, 2024)

input selected: size 1000 sum 50614

**END On Gen=81

**Best gene found: Gene id=5 TF=2172, #Machines=25, content:Very long..., Summed Machines(1902,2102,2007,2091,2146,1848,2125,2169,2092,1828,1775,2036,2063,2102,2172,1922,1873,2066,2129,2154,2140,2067,1851,2077,1877)

"Attempt 1(populationSize=100, genSize=100): TF=2172"

**END On Gen=146

**Best gene found: Gene id=35 TF=2154, #Machines=25, content:Very long..., Summed Machines(1634,2076,2024,2121,1952,2154,1673,2148,2114,2122,2129,2048,2135,2135,2138,1924,2152,2037,2141,2147,1421,1998,1994,2088,2109)

"Attempt 2(populationSize=50, genSize=200): TF=2154"

**END On Gen=41

**Best gene found: Gene id=153 TF=2264, #Machines=25, content:Very long..., Summed Machines(2165,2055,2192,1607,2098,2158,2146,1407,1900,2007,2142,1628,2264,1572,2173,2258,2101,1916,2015,2181,1920,2192,2122,2140,2255)

"Attempt 3(populationSize=200, genSize=50): TF=2264"

"----Comparison for the 20 example----"

"***BenchmarkTf=2025 ourGeneticTf=2154"

***RESULT IS Different 129

Run time: 74.908 seconds
"Correct (size-numberCorrect):" QMap()
"Mistakes(size-numberMistakes):" QMap((1000, 21))
"Avegare error: 38.3"
"-----------END 21 from 90--"
"-------------------START 22 from 90-------------------------------"
"22) U_1_1000_25_1.txt"
*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=1931
*Content of machines summed (1931, 1930, 1930, 1930, 1930)
input selected: size 1000 sum 48271
**END On Gen=96
**Best gene found: Gene id=67 TF=2080, #Machines=25, content:Very long..., Summed Machines(2044,1860,2029,1951,1565,1890,1877,1870,1777,1735,2053,1940,1938,1997,2024,2080,2037,1630,1933,1944,1984,2059,2022,2068,1964)
"Attempt 1(populationSize=100, genSize=100): TF=2080"
**END On Gen=198
**Best gene found: Gene id=30 TF=2039, #Machines=25, content:Very long..., Summed Machines(1969,2006,1996,1965,2037,2032,1807,1778,2026,2021,2034,1999,1993,1550,1987,1901,1480,1979,2013,1874,1899,1955,1904,2027,2039)
"Attempt 2(populationSize=50, genSize=200): TF=2039"
**END On Gen=47
**Best gene found: Gene id=163 TF=2086, #Machines=25, content:Very long..., Summed Machines(2079,2016,2079,1922,1803,1696,1936,1805,2065,2081,2031,1897,2018,1995,2018,1962,1999,1512,2003,1962,1882,2080,2086,1433,1911)
"Attempt 3(populationSize=200, genSize=50): TF=2086"
"----Comparison for the 21 example----"
"***BenchmarkTf=1931 ourGeneticTf=2039"
***RESULT IS Different 108
Run time: 74.782 seconds
"Correct (size-numberCorrect):" QMap()
"Mistakes(size-numberMistakes):" QMap((1000, 22))
"Avegare error: 41.619"
"-----------END 22 from 90--"
"-------------------START 23 from 90-------------------------------"
"23) U_1_1000_25_2.txt"
*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=2027
*Content of machines summed (2027, 2027, 2027, 2027, 2027, 2027, 2026, 2026, 2026, 2027, 2026, 2026, 2026, 2026, 2026, 2026, 2026, 2025, 2025, 2025, 2025, 2025, 2025, 2026, 2026)
input selected: size 1000 sum 50651
**END On Gen=50
**Best gene found: Gene id=40 TF=2224, #Machines=25, content:Very long..., Summed Machines(2202,2146,1437,1979,2063,1695,2173,2147,1953,1912,2184,2184,2153,2224,1786,2170,2219,2076,1896,2117,2065,1792,2062,2019,1997)
"Attempt 1(populationSize=100, genSize=100): TF=2224"
**END On Gen=144

**Best gene found: Gene id=9 TF=2249, #Machines=25, content:Very long..., Summed Machines(2181,1990,2179,1870,2081,1968,1904,2211,2099,2130,2140,2006,2103,1974,2180,1875,1772,2134,1573,1954,1661,2049,2249,2189,2179)

"Attempt 2(populationSize=50, genSize=200): TF=2249"

**END On Gen=44

**Best gene found: Gene id=116 TF=2240, #Machines=25, content:Very long..., Summed Machines(2240,1880,2120,1821,2127,2163,1999,2139,1917,1761,1826,2188,2048,2109,2131,1943,2070,2004,2146,1936,1943,2141,1876,2015,2108)

"Attempt 3(populationSize=200, genSize=50): TF=2240"

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

"***BenchmarkTf=2027 ourGeneticTf=2224"

***RESULT IS Different 197

Run time: 73.142 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 23))

"Avegare error: 48.6818"

"-----------END 23 from 90--"

"-------------------START 24 from 90-------------------------------"

"24) U_1_1000_25_3.txt"

*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=2024

*Content of machines summed (2024, 2023, 2023, 2023, 2023, 2023, 2024, 2024, 2024, 2023, 2023, 2023, 2023, 2023, 2023, 2023, 2023, 2023, 2022, 2024, 2024, 2024, 2024, 2023, 2023)

input selected: size 1000 sum 50582

**END On Gen=87

**Best gene found: Gene id=3 TF=2180, #Machines=25, content:Very long..., Summed Machines(2050,1890,1885,2006,2025,2078,2170,2041,2123,2180,1929,1962,2085,1812,2126,2002,2137,2096,2144,2144,2144,2119,1923,1422,2089)

"Attempt 1(populationSize=100, genSize=100): TF=2180"

**END On Gen=94

**Best gene found: Gene id=35 TF=2172, #Machines=25, content:Very long..., Summed Machines(1964,1873,2163,2136,1873,1921,2147,1736,2035,2006,2166,2022,2080,2003,2156,2172,1997,1962,1696,2114,2138,1943,1998,2128,2153)

"Attempt 2(populationSize=50, genSize=200): TF=2172"

**END On Gen=46

**Best gene found: Gene id=115 TF=2272, #Machines=25, content:Very long..., Summed Machines(2210,2182,2003,2205,1476,2065,2172,1620,2137,2216,1962,2095,1835,1937,2233,2050,1938,1959,2082,1603,2116,2162,2272,2217,1835)

"Attempt 3(populationSize=200, genSize=50): TF=2272"

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

"***BenchmarkTf=2024 ourGeneticTf=2172"

***RESULT IS Different 148

Run time: 72.399 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 24))

"Avegare error: 53"

"-----------END 24 from 90--"

"-------------------START 25 from 90-------------------------------"

"25) U_1_1000_25_4.txt"

*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=2008

*Content of machines summed (2008, 2007, 2007)

input selected: size 1000 sum 50198

**END On Gen=95

**Best gene found: Gene id=1 TF=2162, #Machines=25, content:Very long..., Summed Machines(1762,1999,2053,2104,2115,2150,2011,2001,2151,2151,1968,2064,2019,1712,2162,1615,1893,1928,2007,2076,1991,2154,2141,1923,2048)

"Attempt 1(populationSize=100, genSize=100): TF=2162"

**END On Gen=148

**Best gene found: Gene id=41 TF=2178, #Machines=25, content:Very long..., Summed Machines(2086,1660,1390,1822,1961,2165,2048,2040,2151,1637,2137,1998,2102,2168,2016,2036,2151,2137,2125,1918,1869,2163,2144,2178,2096)

"Attempt 2(populationSize=50, genSize=200): TF=2178"

**END On Gen=50

**Best gene found: Gene id=139 TF=2218, #Machines=25, content:Very long..., Summed Machines(1806,1946,2057,2020,1834,2045,2218,1985,2154,1796,2070,1823,2086,1646,2024,2143,2122,2065,2187,1861,2112,1851,2181,2131,2035)

"Attempt 3(populationSize=200, genSize=50): TF=2218"

"----Comparison for the 24 example----"

"***BenchmarkTf=2008 ourGeneticTf=2162"

***RESULT IS Different 154

Run time: 73.104 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 25))

"Avegare error: 57.2083"

"-----------END 25 from 90--"

"--------------------START 26 from 90--------------------------------"

"26) U_1_1000_25_5.txt"

*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=1959

*Content of machines summed (1958, 1958, 1958, 1958, 1958, 1958, 1958, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1958, 1958, 1958, 1958, 1958, 1958, 1958, 1958, 1958, 1959, 1959)

input selected: size 1000 sum 48959

**END On Gen=91

**Best gene found: Gene id=32 TF=2145, #Machines=25, content:Very long..., Summed Machines(1815,1870,2107,1619,2000,2105,2081,2145,1951,2104,1741,2120,1253,2121,2011,2100,2011,2141,1958,2091,1437,1921,2144,1974,2139)

"Attempt 1(populationSize=100, genSize=100): TF=2145"

**END On Gen=104

**Best gene found: Gene id=21 TF=2194, #Machines=25, content:Very long..., Summed Machines(2163,1965,2162,2194,2128,2004,1372,2068,2145,2018,2191,2156,2031,1195,2182,2187,1970,1234,1849,1853,1595,2182,1961,2154,2000)

"Attempt 2(populationSize=50, genSize=200): TF=2194"

**END On Gen=30

**Best gene found: Gene id=66 TF=2210, #Machines=25, content:Very long..., Summed Machines(1587,1648,1856,1701,1890,2083,2165,2142,2111,2166,2080,2167,1984,1768,1764,2200,1766,2210,2014,1891,1673,2172,2054,2119,1748)

"Attempt 3(populationSize=200, genSize=50): TF=2210"

"----Comparison for the 25 example----"

"***BenchmarkTf=1959 ourGeneticTf=2145"

***RESULT IS Different 186

Run time: 72.522 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 26))

"Avegare error: 62.36"

"-----------END 26 from 90--"

"--------------------START 27 from 90-------------------------------"

"27) U_1_1000_25_6.txt"

*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=2033

*Content of machines summed (2033, 2033, 2033, 2033, 2033, 2033, 2033, 2033, 2033, 2033, 2033, 2032, 2032, 2032, 2032, 2032, 2032, 2033, 2032, 2032, 2032, 2032, 2032, 2032, 2032)

input selected: size 1000 sum 50812

**END On Gen=76

**Best gene found: Gene id=32 TF=2172, #Machines=25, content:Very long..., Summed Machines(2144,2136,2107,1908,1466,2159,1891,2119,2123,1983,2164,2152,2119,1994,2036,1819,2172,2062,2077,1902,2071,1921,1988,2156,2143)

"Attempt 1(populationSize=100, genSize=100): TF=2172"

**END On Gen=162

**Best gene found: Gene id=5 TF=2247, #Machines=25, content:Very long..., Summed Machines(2166,2122,2126,1336,2015,2194,1863,1733,2134,1838,2178,2247,2202,2212,1789,1548,2237,2231,2171,2158,1737,2109,2247,2105,2114)

"Attempt 2(populationSize=50, genSize=200): TF=2247"

**END On Gen=47

**Best gene found: Gene id=116 TF=2239, #Machines=25, content:Very long..., Summed Machines(2129,2178,1876,2080,2084,2239,1860,2015,2220,2117,1974,2153,2023,2059,2202,2011,2234,2091,2187,1937,2017,1960,1575,1703,1888)

"Attempt 3(populationSize=200, genSize=50): TF=2239"

"----Comparison for the 26 example----"

"***BenchmarkTf=2033 ourGeneticTf=2172"

***RESULT IS Different 139

Run time: 72.682 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 27))

"Avegare error: 65.3077"

"-----------END 27 from 90--"

"--------------------START 28 from 90-------------------------------"

"28) U_1_1000_25_7.txt"

*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=1966

*Content of machines summed (1966, 1966, 1966, 1966, 1966, 1966, 1966, 1965, 1965, 1965, 1965, 1965, 1965, 1965, 1965, 1965, 1965, 1965, 1965, 1965, 1965, 1965, 1965, 1965, 1965)

input selected: size 1000 sum 49132

**END On Gen=82

**Best gene found: Gene id=27 TF=2093, #Machines=25, content:Very long..., Summed Machines(1910,1886,1974,1904,2082,2071,2011,1613,2054,2065,2034,1940,1795,1870,1972,2090,2063,1644,1939,2093,2062,2085,1970,2013,1992)

"Attempt 1(populationSize=100, genSize=100): TF=2093"

**END On Gen=184

**Best gene found: Gene id=23 TF=2111, #Machines=25, content:Very long..., Summed Machines(2068,1832,1849,2008,1952,2051,1636,2019,1950,2092,2073,1866,2109,1883,1877,2110,1992,2111,2068,1891,2076,1855,1586,2077,2101)

"Attempt 2(populationSize=50, genSize=200): TF=2111"

**END On Gen=25

**Best gene found: Gene id=*199 TF=2208, #Machines=25, content:Very long..., Summed Machines(1895,2042,2208,1923,2068,2064,1957,2202,1814,1908,1439,1966,1963,1884,1649,2136,2043,2146,2155,2092,1884,1707,2057,1908,2022)

"Attempt 3(populationSize=200, genSize=50): TF=2208"

"----Comparison for the 27 example----"

"***BenchmarkTf=1966 ourGeneticTf=2093"

***RESULT IS Different 127

Run time: 72.968 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 28))

"Avegare error: 67.5926"

"-----------END 28 from 90--"

"-------------------START 29 from 90-------------------------------"

"29) U_1_1000_25_8.txt"

*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=2025

*Content of machines summed (2024, 2024, 2024, 2024, 2025, 2025, 2025, 2025, 2024, 2024, 2024, 2024, 2024, 2024, 2024, 2024, 2024, 2024, 2024, 2024, 2024, 2024, 2024, 2023, 2023)

input selected: size 1000 sum 50602

**END On Gen=89

**Best gene found: Gene id=57 TF=2163, #Machines=25, content:Very long..., Summed Machines(1849,2158,2056,2103,2149,2121,1715,2131,1909,1942,2088,2156,2046,1632,1702,2145,2090,2083,2154,2133,2003,2017,2061,2163,1996)

"Attempt 1(populationSize=100, genSize=100): TF=2163"

**END On Gen=191

**Best gene found: Gene id=30 TF=2201, #Machines=25, content:Very long..., Summed Machines(1866,1540,2048,2165,2198,2119,1957,1982,2146,2194,1818,2116,2053,1851,2201,1569,2141,2106,1973,1938,2149,2116,2174,2197,1985)

"Attempt 2(populationSize=50, genSize=200): TF=2201"

**END On Gen=49

**Best gene found: Gene id=34 TF=2277, #Machines=25, content:Very long..., Summed Machines(2087,1438,1966,2124,1751,2015,1969,1986,2277,2263,2267,2023,1880,2277,2199,2049,2009,2051,2076,2089,1885,2051,1980,1864,2026)

"Attempt 3(populationSize=200, genSize=50): TF=2277"

"----Comparison for the 28 example----"

"***BenchmarkTf=2025 ourGeneticTf=2163"

***RESULT IS Different 138

Run time: 73.104 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 29))

"Avegare error: 70.1071"

"-----------END 29 from 90--"

"-------------------START 30 from 90-------------------------------"

"30) U_1_1000_25_9.txt"

*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=2048

*Content of machines summed (2048, 2048, 2048, 2048, 2048, 2048, 2048, 2048, 2048, 2048, 2047, 2047, 2047, 2047, 2047, 2047, 2047, 2047, 2047, 2047, 2047, 2047, 2047, 2047, 2047)

input selected: size 1000 sum 51185

**END On Gen=87

**Best gene found: Gene id=25 TF=2217, #Machines=25, content:Very long..., Summed Machines(1854,1656,2214,2117,2189,2086,2030,2217,2208,1809,1909,1779,2137,2200,2157,2070,2102,2086,2022,2077,1890,2147,1979,2099,2151)

"Attempt 1(populationSize=100, genSize=100): TF=2217"

**END On Gen=184

**Best gene found: Gene id=12 TF=2212, #Machines=25, content:Very long..., Summed Machines(1895,2142,2212,2057,2080,2186,2204,1978,2089,2107,1254,2132,2195,2084,1983,1879,2211,2120,2018,1959,2118,2039,2188,2195,1860)

"Attempt 2(populationSize=50, genSize=200): TF=2212"

**END On Gen=50

**Best gene found: Gene id=28 TF=2223, #Machines=25, content:Very long..., Summed Machines(2223,2092,2121,2116,2155,1674,2147,1953,2221,1786,1716,2208,2223,2033,2197,2201,2045,2107,1690,2093,1972,2158,1973,2111,1970)

"Attempt 3(populationSize=200, genSize=50): TF=2223"

"----Comparison for the 29 example----"

"***BenchmarkTf=2048 ourGeneticTf=2212"

***RESULT IS Different 164

Run time: 72.899 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 30))

"Avegare error: 73.3448"

"-----------END 30 from 90--"

"--------------------START 31 from 90-------------------------------"

"31) U_2_1000_05_0.txt"

*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=102391

*Content of machines summed (102391, 102391, 102391, 102391, 102391)

input selected: size 1000 sum 511955

**END On Gen=42

**Best gene found: Gene id=45 TF=102506, #Machines=5, content:Very long..., Summed Machines(102506,102209,102491,102375,102374)

"Attempt 1(populationSize=100, genSize=100): TF=102506"

**END On Gen=109

**Best gene found: Gene id=23 TF=102524, #Machines=5, content:Very long..., Summed Machines(102524,102370,102359,102340,102362)

"Attempt 2(populationSize=50, genSize=200): TF=102524"

**END On Gen=13

**Best gene found: Gene id=14 TF=102522, #Machines=5, content:Very long..., Summed Machines(102443,102460,102308,102522,102222)

"Attempt 3(populationSize=200, genSize=50): TF=102522"

"----Comparison for the 30 example----"

"***BenchmarkTf=102391 ourGeneticTf=102506"

***RESULT IS Different 115

Run time: 71.254 seconds

"Correct (size-numberCorrect):" QMap()

"Mistakes(size-numberMistakes):" QMap((1000, 31))

"Avegare error: 74.7333"
"-----------END 31 from 90--"
"--------------------START 32 from 90-------------------------------"
"32) U_2_1000_05_1.txt"
*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=98204
*Content of machines summed (98204, 98204, 98204, 98204, 98203)
input selected: size 1000 sum 491019
**END On Gen=82
**Best gene found: Gene id=57 TF=98418, #Machines=5, content:Very long..., Summed Machines(98418,98213,98264,98293,97831)
"Attempt 1(populationSize=100, genSize=100): TF=98418"
**END On Gen=187
**Best gene found: Gene id=13 TF=98349, #Machines=5, content:Very long..., Summed Machines(98349,98042,98268,98274,98086)
"Attempt 2(populationSize=50, genSize=200): TF=98349"
**END On Gen=29
**Best gene found: Gene id=25 TF=98757, #Machines=5, content:Very long..., Summed Machines(98017,97879,98757,97895,98471)
"Attempt 3(populationSize=200, genSize=50): TF=98757"
"----Comparison for the 31 example----"
"***BenchmarkTf=98204 ourGeneticTf=98349"
***RESULT IS Different 145
Run time: 71.406 seconds
"Correct (size-numberCorrect):" QMap()
"Mistakes(size-numberMistakes):" QMap((1000, 32))
"Avegare error: 77"
"-----------END 32 from 90--"
"--------------------START 33 from 90-------------------------------"
"33) U_2_1000_05_2.txt"
*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=98086
*Content of machines summed (98084, 98086, 98086, 98086, 98086)
input selected: size 1000 sum 490428
**END On Gen=100
**Best gene found: Gene id=13 TF=98316, #Machines=5, content:Very long..., Summed Machines(98316,98022,98265,97675,98150)
"Attempt 1(populationSize=100, genSize=100): TF=98316"
**END On Gen=104
**Best gene found: Gene id=23 TF=98202, #Machines=5, content:Very long..., Summed Machines(98202,98185,98041,98050,97950)
"Attempt 2(populationSize=50, genSize=200): TF=98202"
**END On Gen=15
**Best gene found: Gene id=172 TF=98515, #Machines=5, content:Very long..., Summed Machines(98515,98413,98078,97018,98404)
"Attempt 3(populationSize=200, genSize=50): TF=98515"
"----Comparison for the 32 example----"
"***BenchmarkTf=98086 ourGeneticTf=98202"
***RESULT IS Different 116
Run time: 71.335 seconds
"Correct (size-numberCorrect):" QMap()
"Mistakes(size-numberMistakes):" QMap((1000, 33))

"Avegare error: 78.2188"
"-----------END 33 from 90--"
"-------------------START 34 from 90------------------------------"
"34) U_2_1000_05_3.txt"
*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=101874
*Content of machines summed (101874, 101874, 101874, 101874, 101871)
input selected: size 1000 sum 509367
**END On Gen=92
**Best gene found: Gene id=51 TF=102031, #Machines=5, content:Very long..., Summed
Machines(101860,101433,102020,102023,102031)
"Attempt 1(populationSize=100, genSize=100): TF=102031"
**END On Gen=69
**Best gene found: Gene id=13 TF=101948, #Machines=5, content:Very long..., Summed
Machines(101948,101869,101848,101934,101768)
"Attempt 2(populationSize=50, genSize=200): TF=101948"
**END On Gen=48
**Best gene found: Gene id=80 TF=102098, #Machines=5, content:Very long..., Summed
Machines(102067,102098,101329,101906,101967)
"Attempt 3(populationSize=200, genSize=50): TF=102098"
"----Comparison for the 33 example----"
"***BenchmarkTf=101874 ourGeneticTf=101948"
***RESULT IS Different 74
Run time: 71.508 seconds
"Correct (size-numberCorrect):" QMap()
"Mistakes(size-numberMistakes):" QMap((1000, 34))
"Avegare error: 78.0909"
"-----------END 34 from 90--"
"-------------------START 35 from 90------------------------------"
"35) U_2_1000_05_4.txt"
*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=99749
*Content of machines summed (99749, 99749, 99749, 99749, 99749)
input selected: size 1000 sum 498745
**END On Gen=83
**Best gene found: Gene id=1 TF=99983, #Machines=5, content:Very long..., Summed
Machines(99843,99237,99983,99874,99808)
"Attempt 1(populationSize=100, genSize=100): TF=99983"
**END On Gen=106
**Best gene found: Gene id=35 TF=99884, #Machines=5, content:Very long..., Summed
Machines(99633,99791,99844,99884,99593)
"Attempt 2(populationSize=50, genSize=200): TF=99884"
**END On Gen=43
**Best gene found: Gene id=89 TF=100064, #Machines=5, content:Very long..., Summed
Machines(100064,99380,99964,99575,99762)
"Attempt 3(populationSize=200, genSize=50): TF=100064"
"----Comparison for the 34 example----"
"***BenchmarkTf=99749 ourGeneticTf=99884"
***RESULT IS Different 135
Run time: 70.808 seconds
"Correct (size-numberCorrect):" QMap()
"Mistakes(size-numberMistakes):" QMap((1000, 35))

"Avegare error: 79.7647"
"-----------END 35 from 90--"
"-------------------START 36 from 90------------------------------"
"36) U_2_1000_05_5.txt"
*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=100073
*Content of machines summed (100073, 100073, 100072, 100071, 100072)
input selected: size 1000 sum 500361
**END On Gen=87
**Best gene found: Gene id=17 TF=100317, #Machines=5, content:Very long..., Summed Machines(99381,100225,100160,100317,100278)
"Attempt 1(populationSize=100, genSize=100): TF=100317"
**END On Gen=159
**Best gene found: Gene id=39 TF=100254, #Machines=5, content:Very long..., Summed Machines(100254,100090,100232,99899,99886)
"Attempt 2(populationSize=50, genSize=200): TF=100254"
**END On Gen=30
**Best gene found: Gene id=103 TF=100503, #Machines=5, content:Very long..., Summed Machines(100482,100503,99854,100298,99224)
"Attempt 3(populationSize=200, genSize=50): TF=100503"
"----Comparison for the 35 example----"
"***BenchmarkTf=100073 ourGeneticTf=100254"
***RESULT IS Different 181
Run time: 70.988 seconds
"Correct (size-numberCorrect):" QMap()
"Mistakes(size-numberMistakes):" QMap((1000, 36))
"Avegare error: 82.6571"
"-----------END 36 from 90--"
"-------------------START 37 from 90------------------------------"
"37) U_2_1000_05_6.txt"
*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=98726
*Content of machines summed (98726, 98725, 98725, 98725, 98725)
input selected: size 1000 sum 493626
**END On Gen=59
**Best gene found: Gene id=29 TF=99019, #Machines=5, content:Very long..., Summed Machines(99019,98486,98583,98757,98781)
"Attempt 1(populationSize=100, genSize=100): TF=99019"
**END On Gen=136
**Best gene found: Gene id=46 TF=98916, #Machines=5, content:Very long..., Summed Machines(98798,98464,98679,98916,98769)
"Attempt 2(populationSize=50, genSize=200): TF=98916"
**END On Gen=48
**Best gene found: Gene id=50 TF=99057, #Machines=5, content:Very long..., Summed Machines(98788,98812,98394,98575,99057)
"Attempt 3(populationSize=200, genSize=50): TF=99057"
"----Comparison for the 36 example----"
"***BenchmarkTf=98726 ourGeneticTf=98916"
***RESULT IS Different 190
Run time: 70.818 seconds
"Correct (size-numberCorrect):" QMap()
"Mistakes(size-numberMistakes):" QMap((1000, 37))

"Avegare error: 85.6389"
"-----------END 37 from 90--"
"-------------------START 38 from 90------------------------------"
"38) U_2_1000_05_7.txt"
*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=99388
*Content of machines summed (99388, 99387, 99388, 99388, 99388)
input selected: size 1000 sum 496939
**END On Gen=80
**Best gene found: Gene id=54 TF=99555, #Machines=5, content:Very long..., Summed Machines(99215,99509,99201,99459,99555)
"Attempt 1(populationSize=100, genSize=100): TF=99555"
**END On Gen=116
**Best gene found: Gene id=22 TF=99459, #Machines=5, content:Very long..., Summed Machines(99459,99406,99438,99261,99375)
"Attempt 2(populationSize=50, genSize=200): TF=99459"
**END On Gen=21
**Best gene found: Gene id=151 TF=99864, #Machines=5, content:Very long..., Summed Machines(99461,98730,99864,99854,99030)
"Attempt 3(populationSize=200, genSize=50): TF=99864"
"----Comparison for the 37 example----"
"***BenchmarkTf=99388 ourGeneticTf=99459"
***RESULT IS Different 71
Run time: 71.403 seconds
"Correct (size-numberCorrect):" QMap()
"Mistakes(size-numberMistakes):" QMap((1000, 38))
"Avegare error: 85.2432"
"-----------END 38 from 90--"
"-------------------START 39 from 90------------------------------"
"39) U_2_1000_05_8.txt"
*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=101818
*Content of machines summed (101818, 101818, 101818, 101818, 101817)
input selected: size 1000 sum 509089
**END On Gen=86
**Best gene found: Gene id=42 TF=101981, #Machines=5, content:Very long..., Summed Machines(101865,101805,101981,101923,101515)
"Attempt 1(populationSize=100, genSize=100): TF=101981"
**END On Gen=173
**Best gene found: Gene id=30 TF=101931, #Machines=5, content:Very long..., Summed Machines(101931,101930,101878,101509,101841)
"Attempt 2(populationSize=50, genSize=200): TF=101931"
**END On Gen=9
**Best gene found: Gene id=109 TF=102223, #Machines=5, content:Very long..., Summed Machines(101897,102223,100750,102115,102104)
"Attempt 3(populationSize=200, genSize=50): TF=102223"
"----Comparison for the 38 example----"
"***BenchmarkTf=101818 ourGeneticTf=101931"
***RESULT IS Different 113
Run time: 71.419 seconds
"Correct (size-numberCorrect):" QMap()
"Mistakes(size-numberMistakes):" QMap((1000, 39))

"Avegare error: 85.9737"
"-----------END 39 from 90--"
"-------------------START 40 from 90------------------------------"
"40) U_2_1000_05_9.txt"
*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=99330
*Content of machines summed (99329, 99330, 99329, 99329, 99330)
input selected: size 1000 sum 496647
**END On Gen=84
**Best gene found: Gene id=40 TF=99523, #Machines=5, content:Very long..., Summed Machines(99353,99024,99523,99422,99325)
"Attempt 1(populationSize=100, genSize=100): TF=99523"
**END On Gen=81
**Best gene found: Gene id=22 TF=99395, #Machines=5, content:Very long..., Summed Machines(99356,99320,99395,99325,99251)
"Attempt 2(populationSize=50, genSize=200): TF=99395"
**END On Gen=17
**Best gene found: Gene id=83 TF=99856, #Machines=5, content:Very long..., Summed Machines(99808,99856,98784,99853,98346)
"Attempt 3(populationSize=200, genSize=50): TF=99856"
"----Comparison for the 39 example----"
"***BenchmarkTf=99330 ourGeneticTf=99395"
***RESULT IS Different 65
Run time: 72.144 seconds
"Correct (size-numberCorrect):" QMap()
"Mistakes(size-numberMistakes):" QMap((1000, 40))
"Avegare error: 85.4359"
"-----------END 40 from 90--"