**Starting C:\algo\build-h-Desktop\_Qt\_5\_6\_0\_MinGW\_32bit-Debug\debug\h.exe...**

"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=0

\*\*Best gene found: Gene id=98 TF=9990, #Machines=5, content:Very long..., Summed Machines(9990,9990,9989,9989,9989)

"Attempt 1(populationSize=100, genSize=100): TF=9990; BenchMark=9990"

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

"\*\*\*BenchmarkTf=9990 ourGeneticTf=9990"

\*\*\*RESULT IS THE SAME

Run time: 0.031 seconds

"Correct (size-numberCorrect):" QMap((1000, 1))

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

"Avegare error: nan"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=10263, #Machines=5, content:Very long..., Summed Machines(10263,10263,10263,10262,10262)

"Attempt 1(populationSize=100, genSize=100): TF=10263; BenchMark=10263"

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

"\*\*\*BenchmarkTf=10263 ourGeneticTf=10263"

\*\*\*RESULT IS THE SAME

Run time: 0.016 seconds

"Correct (size-numberCorrect):" QMap((1000, 2))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=10073, #Machines=5, content:Very long..., Summed Machines(10073,10073,10073,10072,10072)

"Attempt 1(populationSize=100, genSize=100): TF=10073; BenchMark=10073"

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

"\*\*\*BenchmarkTf=10073 ourGeneticTf=10073"

\*\*\*RESULT IS THE SAME

Run time: 0.031 seconds

"Correct (size-numberCorrect):" QMap((1000, 3))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=10106, #Machines=5, content:Very long..., Summed Machines(10106,10106,10105,10105,10105)

"Attempt 1(populationSize=100, genSize=100): TF=10106; BenchMark=10106"

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

"\*\*\*BenchmarkTf=10106 ourGeneticTf=10106"

\*\*\*RESULT IS THE SAME

Run time: 0.016 seconds

"Correct (size-numberCorrect):" QMap((1000, 4))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=9904, #Machines=5, content:Very long..., Summed Machines(9904,9903,9903,9903,9903)

"Attempt 1(populationSize=100, genSize=100): TF=9904; BenchMark=9904"

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

"\*\*\*BenchmarkTf=9904 ourGeneticTf=9904"

\*\*\*RESULT IS THE SAME

Run time: 0.031 seconds

"Correct (size-numberCorrect):" QMap((1000, 5))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=9783, #Machines=5, content:Very long..., Summed Machines(9783,9783,9782,9782,9782)

"Attempt 1(populationSize=100, genSize=100): TF=9783; BenchMark=9783"

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

"\*\*\*BenchmarkTf=9783 ourGeneticTf=9783"

\*\*\*RESULT IS THE SAME

Run time: 0.015 seconds

"Correct (size-numberCorrect):" QMap((1000, 6))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=10049, #Machines=5, content:Very long..., Summed Machines(10049,10049,10048,10048,10048)

"Attempt 1(populationSize=100, genSize=100): TF=10049; BenchMark=10049"

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

"\*\*\*BenchmarkTf=10049 ourGeneticTf=10049"

\*\*\*RESULT IS THE SAME

Run time: 0.032 seconds

"Correct (size-numberCorrect):" QMap((1000, 7))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=9861, #Machines=5, content:Very long..., Summed Machines(9861,9861,9861,9861,9860)

"Attempt 1(populationSize=100, genSize=100): TF=9861; BenchMark=9861"

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

"\*\*\*BenchmarkTf=9861 ourGeneticTf=9861"

\*\*\*RESULT IS THE SAME

Run time: 0.015 seconds

"Correct (size-numberCorrect):" QMap((1000, 8))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=10064, #Machines=5, content:Very long..., Summed Machines(10064,10064,10064,10064,10064)

"Attempt 1(populationSize=100, genSize=100): TF=10064; BenchMark=10064"

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

"\*\*\*BenchmarkTf=10064 ourGeneticTf=10064"

\*\*\*RESULT IS THE SAME

Run time: 0.032 seconds

"Correct (size-numberCorrect):" QMap((1000, 9))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=9827, #Machines=5, content:Very long..., Summed Machines(9827,9827,9827,9826,9826)

"Attempt 1(populationSize=100, genSize=100): TF=9827; BenchMark=9827"

"----Comparison for the 9 example----"

"\*\*\*BenchmarkTf=9827 ourGeneticTf=9827"

\*\*\*RESULT IS THE SAME

Run time: 0.015 seconds

"Correct (size-numberCorrect):" QMap((1000, 10))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=4837, #Machines=10, content:Very long..., Summed Machines(4837,4837,4837,4836,4836,4836,4836,4836,4836,4836)

"Attempt 1(populationSize=100, genSize=100): TF=4837; BenchMark=4837"

"----Comparison for the 10 example----"

"\*\*\*BenchmarkTf=4837 ourGeneticTf=4837"

\*\*\*RESULT IS THE SAME

Run time: 0.031 seconds

"Correct (size-numberCorrect):" QMap((1000, 11))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=5021, #Machines=10, content:Very long..., Summed Machines(5021,5021,5021,5021,5021,5019,5019,5019,5020,5020)

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

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

"\*\*\*BenchmarkTf=5021 ourGeneticTf=5021"

\*\*\*RESULT IS THE SAME

Run time: 0.032 seconds

"Correct (size-numberCorrect):" QMap((1000, 12))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=5110, #Machines=10, content:Very long..., Summed Machines(5110,5110,5110,5110,5110,5110,5110,5109,5109,5109)

"Attempt 1(populationSize=100, genSize=100): TF=5110; BenchMark=5110"

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

"\*\*\*BenchmarkTf=5110 ourGeneticTf=5110"

\*\*\*RESULT IS THE SAME

Run time: 0.015 seconds

"Correct (size-numberCorrect):" QMap((1000, 13))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=4926, #Machines=10, content:Very long..., Summed Machines(4926,4926,4926,4926,4926,4925,4925,4925,4925,4925)

"Attempt 1(populationSize=100, genSize=100): TF=4926; BenchMark=4926"

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

"\*\*\*BenchmarkTf=4926 ourGeneticTf=4926"

\*\*\*RESULT IS THE SAME

Run time: 0.032 seconds

"Correct (size-numberCorrect):" QMap((1000, 14))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=5119, #Machines=10, content:Very long..., Summed Machines(5119,5119,5119,5119,5119,5119,5118,5118,5118,5118)

"Attempt 1(populationSize=100, genSize=100): TF=5119; BenchMark=5119"

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

"\*\*\*BenchmarkTf=5119 ourGeneticTf=5119"

\*\*\*RESULT IS THE SAME

Run time: 0.031 seconds

"Correct (size-numberCorrect):" QMap((1000, 15))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=4885, #Machines=10, content:Very long..., Summed Machines(4885,4885,4884,4884,4884,4884,4884,4884,4884,4884)

"Attempt 1(populationSize=100, genSize=100): TF=4885; BenchMark=4885"

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

"\*\*\*BenchmarkTf=4885 ourGeneticTf=4885"

\*\*\*RESULT IS THE SAME

Run time: 0.015 seconds

"Correct (size-numberCorrect):" QMap((1000, 16))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=4954, #Machines=10, content:Very long..., Summed Machines(4954,4954,4954,4954,4954,4954,4954,4954,4954,4954)

"Attempt 1(populationSize=100, genSize=100): TF=4954; BenchMark=4954"

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

"\*\*\*BenchmarkTf=4954 ourGeneticTf=4954"

\*\*\*RESULT IS THE SAME

Run time: 0.032 seconds

"Correct (size-numberCorrect):" QMap((1000, 17))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=5153, #Machines=10, content:Very long..., Summed Machines(5153,5153,5153,5153,5153,5153,5151,5151,5152,5152)

"Attempt 1(populationSize=100, genSize=100): TF=5153; BenchMark=5153"

"----Comparison for the 17 example----"

"\*\*\*BenchmarkTf=5153 ourGeneticTf=5153"

\*\*\*RESULT IS THE SAME

Run time: 0.031 seconds

"Correct (size-numberCorrect):" QMap((1000, 18))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=4855, #Machines=10, content:Very long..., Summed Machines(4855,4855,4855,4855,4855,4855,4854,4854,4854,4854)

"Attempt 1(populationSize=100, genSize=100): TF=4855; BenchMark=4855"

"----Comparison for the 18 example----"

"\*\*\*BenchmarkTf=4855 ourGeneticTf=4855"

\*\*\*RESULT IS THE SAME

Run time: 0.015 seconds

"Correct (size-numberCorrect):" QMap((1000, 19))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=4886, #Machines=10, content:Very long..., Summed Machines(4886,4886,4886,4886,4886,4886,4886,4886,4885,4885)

"Attempt 1(populationSize=100, genSize=100): TF=4886; BenchMark=4886"

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

"\*\*\*BenchmarkTf=4886 ourGeneticTf=4886"

\*\*\*RESULT IS THE SAME

Run time: 0.032 seconds

"Correct (size-numberCorrect):" QMap((1000, 20))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=2025, #Machines=25, content:Very long..., Summed Machines(2025,2025,2025,2025,2025,2025,2025,2025,2025,2025,2025,2025,2025,2025,2025,2025,2025,2025,2025,2023,2025,2022,2022,2024,2023)

"Attempt 1(populationSize=100, genSize=100): TF=2025; BenchMark=2025"

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

"\*\*\*BenchmarkTf=2025 ourGeneticTf=2025"

\*\*\*RESULT IS THE SAME

Run time: 0.049 seconds

"Correct (size-numberCorrect):" QMap((1000, 21))

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

"Avegare error: 0"

"-----------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, 1931, 1931, 1931, 1931, 1931, 1931, 1931, 1931, 1931, 1931, 1931, 1931, 1931, 1931, 1931, 1931, 1931, 1931, 1931, 1931, 1930, 1930, 1930, 1930)

input selected: size 1000 sum 48271

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=1931, #Machines=25, content:Very long..., Summed Machines(1931,1931,1931,1931,1931,1931,1931,1931,1931,1931,1931,1931,1931,1931,1931,1931,1931,1931,1931,1931,1931,1931,1931,1929,1929)

"Attempt 1(populationSize=100, genSize=100): TF=1931; BenchMark=1931"

"----Comparison for the 21 example----"

"\*\*\*BenchmarkTf=1931 ourGeneticTf=1931"

\*\*\*RESULT IS THE SAME

Run time: 0.042 seconds

"Correct (size-numberCorrect):" QMap((1000, 22))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=2027, #Machines=25, content:Very long..., Summed Machines(2027,2027,2027,2027,2027,2027,2027,2027,2027,2027,2027,2027,2027,2027,2027,2027,2027,2027,2025,2024,2023,2024,2023,2023,2023)

"Attempt 1(populationSize=100, genSize=100): TF=2027; BenchMark=2027"

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

"\*\*\*BenchmarkTf=2027 ourGeneticTf=2027"

\*\*\*RESULT IS THE SAME

Run time: 0.031 seconds

"Correct (size-numberCorrect):" QMap((1000, 23))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=2024, #Machines=25, content:Very long..., Summed Machines(2024,2024,2024,2024,2024,2024,2024,2024,2024,2024,2024,2024,2024,2024,2024,2024,2024,2024,2024,2024,2022,2020,2020,2020,2020)

"Attempt 1(populationSize=100, genSize=100): TF=2024; BenchMark=2024"

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

"\*\*\*BenchmarkTf=2024 ourGeneticTf=2024"

\*\*\*RESULT IS THE SAME

Run time: 0.047 seconds

"Correct (size-numberCorrect):" QMap((1000, 24))

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

"Avegare error: 0"

"-----------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, 2008, 2008, 2008, 2008, 2008, 2008, 2008, 2008, 2008, 2008, 2008, 2008, 2008, 2008, 2008, 2008, 2008, 2008, 2008, 2008, 2008, 2008, 2007, 2007)

input selected: size 1000 sum 50198

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=2008, #Machines=25, content:Very long..., Summed Machines(2008,2008,2008,2008,2008,2008,2008,2008,2008,2008,2008,2008,2008,2008,2008,2008,2008,2008,2008,2008,2008,2008,2008,2007,2007)

"Attempt 1(populationSize=100, genSize=100): TF=2008; BenchMark=2008"

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

"\*\*\*BenchmarkTf=2008 ourGeneticTf=2008"

\*\*\*RESULT IS THE SAME

Run time: 0.047 seconds

"Correct (size-numberCorrect):" QMap((1000, 25))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=1959, #Machines=25, content:Very long..., Summed Machines(1959,1959,1959,1959,1959,1959,1959,1959,1959,1959,1959,1959,1959,1958,1957,1959,1959,1959,1959,1959,1958,1959,1955,1955,1955)

"Attempt 1(populationSize=100, genSize=100): TF=1959; BenchMark=1959"

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

"\*\*\*BenchmarkTf=1959 ourGeneticTf=1959"

\*\*\*RESULT IS THE SAME

Run time: 0.031 seconds

"Correct (size-numberCorrect):" QMap((1000, 26))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=2033, #Machines=25, content:Very long..., Summed Machines(2033,2033,2033,2033,2033,2033,2033,2033,2033,2033,2033,2033,2032,2032,2032,2032,2032,2032,2032,2032,2032,2032,2032,2032,2032)

"Attempt 1(populationSize=100, genSize=100): TF=2033; BenchMark=2033"

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

"\*\*\*BenchmarkTf=2033 ourGeneticTf=2033"

\*\*\*RESULT IS THE SAME

Run time: 0.047 seconds

"Correct (size-numberCorrect):" QMap((1000, 27))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=1966, #Machines=25, content:Very long..., Summed Machines(1966,1966,1966,1966,1966,1966,1966,1966,1966,1966,1966,1966,1964,1964,1965,1965,1965,1964,1965,1965,1965,1965,1964,1964,1965)

"Attempt 1(populationSize=100, genSize=100): TF=1966; BenchMark=1966"

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

"\*\*\*BenchmarkTf=1966 ourGeneticTf=1966"

\*\*\*RESULT IS THE SAME

Run time: 0.049 seconds

"Correct (size-numberCorrect):" QMap((1000, 28))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=2025, #Machines=25, content:Very long..., Summed Machines(2025,2025,2025,2025,2025,2025,2025,2025,2025,2025,2023,2023,2023,2023,2024,2024,2024,2024,2024,2024,2024,2023,2023,2023,2023)

"Attempt 1(populationSize=100, genSize=100): TF=2025; BenchMark=2025"

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

"\*\*\*BenchmarkTf=2025 ourGeneticTf=2025"

\*\*\*RESULT IS THE SAME

Run time: 0.032 seconds

"Correct (size-numberCorrect):" QMap((1000, 29))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=2048, #Machines=25, content:Very long..., Summed Machines(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)

"Attempt 1(populationSize=100, genSize=100): TF=2048; BenchMark=2048"

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

"\*\*\*BenchmarkTf=2048 ourGeneticTf=2048"

\*\*\*RESULT IS THE SAME

Run time: 0.047 seconds

"Correct (size-numberCorrect):" QMap((1000, 30))

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

"Avegare error: 0"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=102392, #Machines=5, content:Very long..., Summed Machines(102392,102391,102391,102391,102390)

"Attempt 1(populationSize=100, genSize=100): TF=102392; BenchMark=102391"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=102392, #Machines=5, content:Very long..., Summed Machines(102392,102391,102391,102391,102390)

"Attempt 2(populationSize=50, genSize=200): TF=102392; BenchMark=102391"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=102392, #Machines=5, content:Very long..., Summed Machines(102392,102391,102391,102391,102390)

"Attempt 3(populationSize=200, genSize=50): TF=102392; BenchMark=102391"

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

"\*\*\*BenchmarkTf=102391 ourGeneticTf=102392"

\*\*\*RESULT IS Different 1

Run time: 60.944 seconds

"Correct (size-numberCorrect):" QMap((1000, 30))

"Mistakes(size-numberMistakes):" QMap((1000, 1))

"Avegare error: 0.0333333"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=98204, #Machines=5, content:Very long..., Summed Machines(98204,98204,98204,98203,98204)

"Attempt 1(populationSize=100, genSize=100): TF=98204; BenchMark=98204"

"----Comparison for the 31 example----"

"\*\*\*BenchmarkTf=98204 ourGeneticTf=98204"

\*\*\*RESULT IS THE SAME

Run time: 0.011 seconds

"Correct (size-numberCorrect):" QMap((1000, 31))

"Mistakes(size-numberMistakes):" QMap((1000, 1))

"Avegare error: 0.0322581"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=98087, #Machines=5, content:Very long..., Summed Machines(98087,98086,98086,98083,98086)

"Attempt 1(populationSize=100, genSize=100): TF=98087; BenchMark=98086"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=98087, #Machines=5, content:Very long..., Summed Machines(98087,98086,98086,98083,98086)

"Attempt 2(populationSize=50, genSize=200): TF=98087; BenchMark=98086"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=98087, #Machines=5, content:Very long..., Summed Machines(98087,98086,98086,98083,98086)

"Attempt 3(populationSize=200, genSize=50): TF=98087; BenchMark=98086"

"----Comparison for the 32 example----"

"\*\*\*BenchmarkTf=98086 ourGeneticTf=98087"

\*\*\*RESULT IS Different 1

Run time: 63.267 seconds

"Correct (size-numberCorrect):" QMap((1000, 31))

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

"Avegare error: 0.0625"

"-----------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=0

\*\*Best gene found: Gene id=99 TF=101874, #Machines=5, content:Very long..., Summed Machines(101874,101874,101873,101874,101872)

"Attempt 1(populationSize=100, genSize=100): TF=101874; BenchMark=101874"

"----Comparison for the 33 example----"

"\*\*\*BenchmarkTf=101874 ourGeneticTf=101874"

\*\*\*RESULT IS THE SAME

Run time: 0.016 seconds

"Correct (size-numberCorrect):" QMap((1000, 32))

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

"Avegare error: 0.0606061"

"-----------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=0

\*\*Best gene found: Gene id=99 TF=99749, #Machines=5, content:Very long..., Summed Machines(99749,99749,99749,99749,99749)

"Attempt 1(populationSize=100, genSize=100): TF=99749; BenchMark=99749"

"----Comparison for the 34 example----"

"\*\*\*BenchmarkTf=99749 ourGeneticTf=99749"

\*\*\*RESULT IS THE SAME

Run time: 0.031 seconds

"Correct (size-numberCorrect):" QMap((1000, 33))

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

"Avegare error: 0.0588235"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=100073, #Machines=5, content:Very long..., Summed Machines(100072,100073,100072,100072,100072)

"Attempt 1(populationSize=100, genSize=100): TF=100073; BenchMark=100073"

"----Comparison for the 35 example----"

"\*\*\*BenchmarkTf=100073 ourGeneticTf=100073"

\*\*\*RESULT IS THE SAME

Run time: 0.016 seconds

"Correct (size-numberCorrect):" QMap((1000, 34))

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

"Avegare error: 0.0571429"

"-----------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=0

\*\*Best gene found: Gene id=98 TF=98726, #Machines=5, content:Very long..., Summed Machines(98726,98725,98725,98725,98725)

"Attempt 1(populationSize=100, genSize=100): TF=98726; BenchMark=98726"

"----Comparison for the 36 example----"

"\*\*\*BenchmarkTf=98726 ourGeneticTf=98726"

\*\*\*RESULT IS THE SAME

Run time: 0.031 seconds

"Correct (size-numberCorrect):" QMap((1000, 35))

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

"Avegare error: 0.0555556"

"-----------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=0

\*\*Best gene found: Gene id=99 TF=99388, #Machines=5, content:Very long..., Summed Machines(99388,99388,99388,99388,99387)

"Attempt 1(populationSize=100, genSize=100): TF=99388; BenchMark=99388"

"----Comparison for the 37 example----"

"\*\*\*BenchmarkTf=99388 ourGeneticTf=99388"

\*\*\*RESULT IS THE SAME

Run time: 0.016 seconds

"Correct (size-numberCorrect):" QMap((1000, 36))

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

"Avegare error: 0.0540541"

"-----------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=0

\*\*Best gene found: Gene id=99 TF=101818, #Machines=5, content:Very long..., Summed Machines(101818,101818,101817,101818,101818)

"Attempt 1(populationSize=100, genSize=100): TF=101818; BenchMark=101818"

"----Comparison for the 38 example----"

"\*\*\*BenchmarkTf=101818 ourGeneticTf=101818"

\*\*\*RESULT IS THE SAME

Run time: 0.031 seconds

"Correct (size-numberCorrect):" QMap((1000, 37))

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

"Avegare error: 0.0526316"

"-----------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=0

\*\*Best gene found: Gene id=99 TF=99330, #Machines=5, content:Very long..., Summed Machines(99330,99329,99330,99330,99328)

"Attempt 1(populationSize=100, genSize=100): TF=99330; BenchMark=99330"

"----Comparison for the 39 example----"

"\*\*\*BenchmarkTf=99330 ourGeneticTf=99330"

\*\*\*RESULT IS THE SAME

Run time: 0.015 seconds

"Correct (size-numberCorrect):" QMap((1000, 38))

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

"Avegare error: 0.0512821"

"-----------END 40 from 90-----------------------------------------"

"--------------------START 41 from 90--------------------------------"

"41) U\_2\_1000\_10\_0.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=50318

\*Content of machines summed (50318, 50318, 50318, 50318, 50317, 50317, 50317, 50316, 50317, 50317)

input selected: size 1000 sum 503173

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=50318, #Machines=10, content:Very long..., Summed Machines(50318,50318,50317,50318,50318,50317,50318,50318,50318,50313)

"Attempt 1(populationSize=100, genSize=100): TF=50318; BenchMark=50318"

"----Comparison for the 40 example----"

"\*\*\*BenchmarkTf=50318 ourGeneticTf=50318"

\*\*\*RESULT IS THE SAME

Run time: 0.032 seconds

"Correct (size-numberCorrect):" QMap((1000, 39))

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

"Avegare error: 0.05"

"-----------END 41 from 90-----------------------------------------"

"--------------------START 42 from 90--------------------------------"

"42) U\_2\_1000\_10\_1.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=48374

\*Content of machines summed (48373, 48374, 48374, 48374, 48374, 48372, 48373, 48373, 48373, 48374)

input selected: size 1000 sum 483734

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=48374, #Machines=10, content:Very long..., Summed Machines(48374,48374,48374,48374,48374,48374,48373,48374,48374,48369)

"Attempt 1(populationSize=100, genSize=100): TF=48374; BenchMark=48374"

"----Comparison for the 41 example----"

"\*\*\*BenchmarkTf=48374 ourGeneticTf=48374"

\*\*\*RESULT IS THE SAME

Run time: 0.031 seconds

"Correct (size-numberCorrect):" QMap((1000, 40))

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

"Avegare error: 0.0487805"

"-----------END 42 from 90-----------------------------------------"

"--------------------START 43 from 90--------------------------------"

"43) U\_2\_1000\_10\_2.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=48583

\*Content of machines summed (48583, 48583, 48583, 48583, 48583, 48583, 48583, 48583, 48583, 48581)

input selected: size 1000 sum 485828

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=48583, #Machines=10, content:Very long..., Summed Machines(48583,48583,48583,48582,48583,48583,48583,48583,48582,48583)

"Attempt 1(populationSize=100, genSize=100): TF=48583; BenchMark=48583"

"----Comparison for the 42 example----"

"\*\*\*BenchmarkTf=48583 ourGeneticTf=48583"

\*\*\*RESULT IS THE SAME

Run time: 0.015 seconds

"Correct (size-numberCorrect):" QMap((1000, 41))

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

"Avegare error: 0.047619"

"-----------END 43 from 90-----------------------------------------"

"--------------------START 44 from 90--------------------------------"

"44) U\_2\_1000\_10\_3.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=50547

\*Content of machines summed (50547, 50547, 50547, 50547, 50547, 50547, 50547, 50547, 50547, 50540)

input selected: size 1000 sum 505463

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=50547, #Machines=10, content:Very long..., Summed Machines(50547,50547,50547,50547,50547,50547,50547,50546,50546,50542)

"Attempt 1(populationSize=100, genSize=100): TF=50547; BenchMark=50547"

"----Comparison for the 43 example----"

"\*\*\*BenchmarkTf=50547 ourGeneticTf=50547"

\*\*\*RESULT IS THE SAME

Run time: 0.032 seconds

"Correct (size-numberCorrect):" QMap((1000, 42))

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

"Avegare error: 0.0465116"

"-----------END 44 from 90-----------------------------------------"

"--------------------START 45 from 90--------------------------------"

"45) U\_2\_1000\_10\_4.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=50556

\*Content of machines summed (50556, 50556, 50556, 50556, 50556, 50556, 50556, 50556, 50556, 50553)

input selected: size 1000 sum 505557

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=50556, #Machines=10, content:Very long..., Summed Machines(50556,50556,50556,50556,50555,50556,50556,50556,50556,50554)

"Attempt 1(populationSize=100, genSize=100): TF=50556; BenchMark=50556"

"----Comparison for the 44 example----"

"\*\*\*BenchmarkTf=50556 ourGeneticTf=50556"

\*\*\*RESULT IS THE SAME

Run time: 0.031 seconds

"Correct (size-numberCorrect):" QMap((1000, 43))

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

"Avegare error: 0.0454545"

"-----------END 45 from 90-----------------------------------------"

"--------------------START 46 from 90--------------------------------"

"46) U\_2\_1000\_10\_5.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=49108

\*Content of machines summed (49108, 49108, 49108, 49108, 49108, 49108, 49108, 49108, 49108, 49103)

input selected: size 1000 sum 491075

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=49108, #Machines=10, content:Very long..., Summed Machines(49108,49108,49108,49108,49108,49108,49107,49108,49107,49105)

"Attempt 1(populationSize=100, genSize=100): TF=49108; BenchMark=49108"

"----Comparison for the 45 example----"

"\*\*\*BenchmarkTf=49108 ourGeneticTf=49108"

\*\*\*RESULT IS THE SAME

Run time: 0.016 seconds

"Correct (size-numberCorrect):" QMap((1000, 44))

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

"Avegare error: 0.0444444"

"-----------END 46 from 90-----------------------------------------"

"--------------------START 47 from 90--------------------------------"

"47) U\_2\_1000\_10\_6.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=49301

\*Content of machines summed (49301, 49301, 49301, 49301, 49301, 49301, 49301, 49301, 49301, 49296)

input selected: size 1000 sum 493005

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=49301, #Machines=10, content:Very long..., Summed Machines(49301,49301,49301,49301,49301,49299,49301,49301,49300,49299)

"Attempt 1(populationSize=100, genSize=100): TF=49301; BenchMark=49301"

"----Comparison for the 46 example----"

"\*\*\*BenchmarkTf=49301 ourGeneticTf=49301"

\*\*\*RESULT IS THE SAME

Run time: 0.016 seconds

"Correct (size-numberCorrect):" QMap((1000, 45))

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

"Avegare error: 0.0434783"

"-----------END 47 from 90-----------------------------------------"

"--------------------START 48 from 90--------------------------------"

"48) U\_2\_1000\_10\_7.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=50102

\*Content of machines summed (50102, 50102, 50102, 50102, 50102, 50102, 50102, 50102, 50102, 50100)

input selected: size 1000 sum 501018

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=50105, #Machines=10, content:Very long..., Summed Machines(50105,50101,50102,50100,50102,50102,50102,50100,50102,50102)

"Attempt 1(populationSize=100, genSize=100): TF=50105; BenchMark=50102"

\*\*END On Gen=0

\*\*Best gene found: Gene id=49 TF=50105, #Machines=10, content:Very long..., Summed Machines(50105,50101,50102,50100,50102,50102,50102,50100,50102,50102)

"Attempt 2(populationSize=50, genSize=200): TF=50105; BenchMark=50102"

\*\*END On Gen=0

\*\*Best gene found: Gene id=199 TF=50105, #Machines=10, content:Very long..., Summed Machines(50105,50101,50102,50100,50102,50102,50102,50100,50102,50102)

"Attempt 3(populationSize=200, genSize=50): TF=50105; BenchMark=50102"

"----Comparison for the 47 example----"

"\*\*\*BenchmarkTf=50102 ourGeneticTf=50105"

\*\*\*RESULT IS Different 3

Run time: 62.532 seconds

"Correct (size-numberCorrect):" QMap((1000, 45))

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

"Avegare error: 0.106383"

"-----------END 48 from 90-----------------------------------------"

"--------------------START 49 from 90--------------------------------"

"49) U\_2\_1000\_10\_8.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=50232

\*Content of machines summed (50232, 50232, 50232, 50232, 50232, 50232, 50232, 50232, 50232, 50232)

input selected: size 1000 sum 502320

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=50234, #Machines=10, content:Very long..., Summed Machines(50234,50234,50233,50232,50232,50232,50231,50234,50234,50224)

"Attempt 1(populationSize=100, genSize=100): TF=50234; BenchMark=50232"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=50234, #Machines=10, content:Very long..., Summed Machines(50234,50234,50233,50232,50232,50232,50231,50234,50234,50224)

"Attempt 2(populationSize=50, genSize=200): TF=50234; BenchMark=50232"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=50234, #Machines=10, content:Very long..., Summed Machines(50234,50234,50233,50232,50232,50232,50231,50234,50234,50224)

"Attempt 3(populationSize=200, genSize=50): TF=50234; BenchMark=50232"

"----Comparison for the 48 example----"

"\*\*\*BenchmarkTf=50232 ourGeneticTf=50234"

\*\*\*RESULT IS Different 2

Run time: 62.742 seconds

"Correct (size-numberCorrect):" QMap((1000, 45))

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

"Avegare error: 0.145833"

"-----------END 49 from 90-----------------------------------------"

"--------------------START 50 from 90--------------------------------"

"50) U\_2\_1000\_10\_9.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=49955

\*Content of machines summed (49955, 49955, 49955, 49953, 49955, 49955, 49955, 49954, 49955, 49954)

input selected: size 1000 sum 499546

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=49955, #Machines=10, content:Very long..., Summed Machines(49955,49954,49955,49955,49955,49955,49955,49955,49953,49954)

"Attempt 1(populationSize=100, genSize=100): TF=49955; BenchMark=49955"

"----Comparison for the 49 example----"

"\*\*\*BenchmarkTf=49955 ourGeneticTf=49955"

\*\*\*RESULT IS THE SAME

Run time: 0.028 seconds

"Correct (size-numberCorrect):" QMap((1000, 46))

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

"Avegare error: 0.142857"

"-----------END 50 from 90-----------------------------------------"

"--------------------START 51 from 90--------------------------------"

"51) U\_2\_1000\_25\_0.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=20306

\*Content of machines summed (20306, 20306, 20306, 20306, 20306, 20306, 20306, 20306, 20306, 20306, 20306, 20306, 20306, 20306, 20306, 20306, 20306, 20306, 20306, 20306, 20306, 20306, 20306, 20306, 20294)

input selected: size 1000 sum 507638

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=20306, #Machines=25, content:Very long..., Summed Machines(20306,20306,20306,20306,20306,20306,20306,20306,20306,20306,20306,20305,20306,20306,20306,20306,20306,20305,20305,20305,20306,20306,20305,20306,20299)

"Attempt 1(populationSize=100, genSize=100): TF=20306; BenchMark=20306"

"----Comparison for the 50 example----"

"\*\*\*BenchmarkTf=20306 ourGeneticTf=20306"

\*\*\*RESULT IS THE SAME

Run time: 0.043 seconds

"Correct (size-numberCorrect):" QMap((1000, 47))

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

"Avegare error: 0.14"

"-----------END 51 from 90-----------------------------------------"

"--------------------START 52 from 90--------------------------------"

"52) U\_2\_1000\_25\_1.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=20101

\*Content of machines summed (20101, 20101, 20101, 20101, 20101, 20101, 20101, 20101, 20101, 20101, 20101, 20101, 20101, 20101, 20101, 20101, 20101, 20101, 20101, 20101, 20101, 20101, 20101, 20101, 20080)

input selected: size 1000 sum 502504

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=20101, #Machines=25, content:Very long..., Summed Machines(20101,20101,20101,20101,20101,20101,20100,20101,20101,20101,20101,20100,20101,20101,20101,20100,20101,20101,20100,20101,20101,20101,20101,20101,20084)

"Attempt 1(populationSize=100, genSize=100): TF=20101; BenchMark=20101"

"----Comparison for the 51 example----"

"\*\*\*BenchmarkTf=20101 ourGeneticTf=20101"

\*\*\*RESULT IS THE SAME

Run time: 0.043 seconds

"Correct (size-numberCorrect):" QMap((1000, 48))

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

"Avegare error: 0.137255"

"-----------END 52 from 90-----------------------------------------"

"--------------------START 53 from 90--------------------------------"

"53) U\_2\_1000\_25\_2.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=19822

\*Content of machines summed (19822, 19822, 19822, 19822, 19822, 19822, 19822, 19822, 19822, 19822, 19822, 19822, 19822, 19822, 19822, 19822, 19822, 19822, 19822, 19822, 19822, 19822, 19822, 19822, 19819)

input selected: size 1000 sum 495547

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=19828, #Machines=25, content:Very long..., Summed Machines(19828,19826,19828,19827,19828,19828,19828,19828,19828,19827,19827,19827,19828,19824,19807,19808,19807,19825,19806,19827,19806,19824,19806,19823,19826)

"Attempt 1(populationSize=100, genSize=100): TF=19828; BenchMark=19822"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=19828, #Machines=25, content:Very long..., Summed Machines(19828,19826,19828,19827,19828,19828,19828,19828,19828,19827,19827,19827,19828,19824,19807,19808,19807,19825,19806,19827,19806,19824,19806,19823,19826)

"Attempt 2(populationSize=50, genSize=200): TF=19828; BenchMark=19822"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=19828, #Machines=25, content:Very long..., Summed Machines(19828,19826,19828,19827,19828,19828,19828,19828,19828,19827,19827,19827,19828,19824,19807,19808,19807,19825,19806,19827,19806,19824,19806,19823,19826)

"Attempt 3(populationSize=200, genSize=50): TF=19828; BenchMark=19822"

"----Comparison for the 52 example----"

"\*\*\*BenchmarkTf=19822 ourGeneticTf=19828"

\*\*\*RESULT IS Different 6

Run time: 61.691 seconds

"Correct (size-numberCorrect):" QMap((1000, 48))

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

"Avegare error: 0.25"

"-----------END 53 from 90-----------------------------------------"

"--------------------START 54 from 90--------------------------------"

"54) U\_2\_1000\_25\_3.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=20463

\*Content of machines summed (20463, 20463, 20463, 20463, 20463, 20463, 20463, 20463, 20463, 20463, 20463, 20463, 20463, 20463, 20463, 20463, 20463, 20463, 20463, 20463, 20463, 20463, 20463, 20463, 20444)

input selected: size 1000 sum 511556

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=20463, #Machines=25, content:Very long..., Summed Machines(20463,20463,20463,20463,20463,20462,20463,20463,20462,20463,20463,20462,20463,20463,20462,20463,20462,20463,20463,20463,20459,20463,20463,20461,20455)

"Attempt 1(populationSize=100, genSize=100): TF=20463; BenchMark=20463"

"----Comparison for the 53 example----"

"\*\*\*BenchmarkTf=20463 ourGeneticTf=20463"

\*\*\*RESULT IS THE SAME

Run time: 0.047 seconds

"Correct (size-numberCorrect):" QMap((1000, 49))

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

"Avegare error: 0.245283"

"-----------END 54 from 90-----------------------------------------"

"--------------------START 55 from 90--------------------------------"

"55) U\_2\_1000\_25\_4.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=19361

\*Content of machines summed (19361, 19361, 19361, 19361, 19361, 19361, 19361, 19361, 19361, 19361, 19361, 19361, 19361, 19361, 19361, 19361, 19361, 19361, 19361, 19361, 19361, 19361, 19361, 19361, 19339)

input selected: size 1000 sum 484003

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=19361, #Machines=25, content:Very long..., Summed Machines(19361,19361,19361,19361,19361,19361,19361,19361,19361,19361,19361,19361,19360,19361,19361,19361,19360,19361,19361,19360,19361,19360,19359,19361,19345)

"Attempt 1(populationSize=100, genSize=100): TF=19361; BenchMark=19361"

"----Comparison for the 54 example----"

"\*\*\*BenchmarkTf=19361 ourGeneticTf=19361"

\*\*\*RESULT IS THE SAME

Run time: 0.031 seconds

"Correct (size-numberCorrect):" QMap((1000, 50))

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

"Avegare error: 0.240741"

"-----------END 55 from 90-----------------------------------------"

"--------------------START 56 from 90--------------------------------"

"56) U\_2\_1000\_25\_5.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=20022

\*Content of machines summed (20022, 20022, 20022, 20022, 20022, 20022, 20022, 20022, 20022, 20022, 20022, 20022, 20022, 20022, 20022, 20022, 20022, 20022, 20022, 20022, 20022, 20022, 20022, 20022, 20010)

input selected: size 1000 sum 500538

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=20022, #Machines=25, content:Very long..., Summed Machines(20022,20021,20020,20021,20021,20022,20022,20022,20021,20022,20022,20022,20022,20022,20022,20022,20021,20022,20022,20022,20022,20022,20017,20022,20022)

"Attempt 1(populationSize=100, genSize=100): TF=20022; BenchMark=20022"

"----Comparison for the 55 example----"

"\*\*\*BenchmarkTf=20022 ourGeneticTf=20022"

\*\*\*RESULT IS THE SAME

Run time: 0.047 seconds

"Correct (size-numberCorrect):" QMap((1000, 51))

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

"Avegare error: 0.236364"

"-----------END 56 from 90-----------------------------------------"

"--------------------START 57 from 90--------------------------------"

"57) U\_2\_1000\_25\_6.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=20557

\*Content of machines summed (20557, 20557, 20557, 20557, 20557, 20557, 20557, 20557, 20557, 20557, 20557, 20557, 20557, 20557, 20557, 20557, 20557, 20557, 20557, 20557, 20557, 20557, 20557, 20557, 20536)

input selected: size 1000 sum 513904

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=20557, #Machines=25, content:Very long..., Summed Machines(20556,20557,20557,20556,20557,20557,20555,20557,20557,20557,20557,20557,20557,20557,20557,20557,20556,20556,20557,20556,20557,20556,20557,20556,20545)

"Attempt 1(populationSize=100, genSize=100): TF=20557; BenchMark=20557"

"----Comparison for the 56 example----"

"\*\*\*BenchmarkTf=20557 ourGeneticTf=20557"

\*\*\*RESULT IS THE SAME

Run time: 0.047 seconds

"Correct (size-numberCorrect):" QMap((1000, 52))

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

"Avegare error: 0.232143"

"-----------END 57 from 90-----------------------------------------"

"--------------------START 58 from 90--------------------------------"

"58) U\_2\_1000\_25\_7.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=20320

\*Content of machines summed (20320, 20320, 20320, 20320, 20320, 20320, 20320, 20320, 20320, 20320, 20320, 20320, 20320, 20320, 20320, 20320, 20320, 20320, 20320, 20320, 20320, 20320, 20320, 20320, 20302)

input selected: size 1000 sum 507982

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=20320, #Machines=25, content:Very long..., Summed Machines(20320,20320,20320,20320,20320,20320,20319,20320,20319,20320,20320,20320,20320,20319,20319,20320,20320,20319,20320,20320,20320,20320,20319,20320,20308)

"Attempt 1(populationSize=100, genSize=100): TF=20320; BenchMark=20320"

"----Comparison for the 57 example----"

"\*\*\*BenchmarkTf=20320 ourGeneticTf=20320"

\*\*\*RESULT IS THE SAME

Run time: 0.031 seconds

"Correct (size-numberCorrect):" QMap((1000, 53))

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

"Avegare error: 0.22807"

"-----------END 58 from 90-----------------------------------------"

"--------------------START 59 from 90--------------------------------"

"59) U\_2\_1000\_25\_8.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=20123

\*Content of machines summed (20123, 20123, 20123, 20123, 20123, 20123, 20123, 20123, 20123, 20123, 20123, 20123, 20123, 20123, 20123, 20123, 20123, 20123, 20123, 20123, 20123, 20123, 20123, 20123, 20102)

input selected: size 1000 sum 503054

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=20123, #Machines=25, content:Very long..., Summed Machines(20123,20123,20123,20123,20123,20123,20123,20121,20123,20123,20123,20123,20121,20123,20123,20123,20122,20122,20122,20123,20121,20123,20123,20123,20111)

"Attempt 1(populationSize=100, genSize=100): TF=20123; BenchMark=20123"

"----Comparison for the 58 example----"

"\*\*\*BenchmarkTf=20123 ourGeneticTf=20123"

\*\*\*RESULT IS THE SAME

Run time: 0.047 seconds

"Correct (size-numberCorrect):" QMap((1000, 54))

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

"Avegare error: 0.224138"

"-----------END 59 from 90-----------------------------------------"

"--------------------START 60 from 90--------------------------------"

"60) U\_2\_1000\_25\_9.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=19120

\*Content of machines summed (19120, 19120, 19120, 19120, 19120, 19120, 19120, 19120, 19120, 19120, 19120, 19120, 19120, 19120, 19120, 19120, 19120, 19120, 19120, 19120, 19120, 19120, 19120, 19120, 19109)

input selected: size 1000 sum 477989

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=19120, #Machines=25, content:Very long..., Summed Machines(19120,19120,19120,19120,19120,19120,19120,19120,19119,19119,19120,19120,19120,19120,19119,19120,19119,19120,19120,19120,19120,19120,19120,19120,19113)

"Attempt 1(populationSize=100, genSize=100): TF=19120; BenchMark=19120"

"----Comparison for the 59 example----"

"\*\*\*BenchmarkTf=19120 ourGeneticTf=19120"

\*\*\*RESULT IS THE SAME

Run time: 0.05 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 0.220339"

"-----------END 60 from 90-----------------------------------------"

"--------------------START 61 from 90--------------------------------"

"61) U\_3\_1000\_05\_0.txt"

\*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=1001419

\*Content of machines summed (1001419, 1001419, 1001419, 1001419, 1001416)

input selected: size 1000 sum 5.00709e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=1.00142e+06, #Machines=5, content:Very long..., Summed Machines(1001423,1001424,1001425,1001424,1001396)

"Attempt 1(populationSize=100, genSize=100): TF=1.00142e+06; BenchMark=1.00142e+06"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=1.00142e+06, #Machines=5, content:Very long..., Summed Machines(1001423,1001424,1001425,1001424,1001396)

"Attempt 2(populationSize=50, genSize=200): TF=1.00142e+06; BenchMark=1.00142e+06"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=1.00142e+06, #Machines=5, content:Very long..., Summed Machines(1001423,1001424,1001425,1001424,1001396)

"Attempt 3(populationSize=200, genSize=50): TF=1.00142e+06; BenchMark=1.00142e+06"

"----Comparison for the 60 example----"

"\*\*\*BenchmarkTf=1.00142e+06 ourGeneticTf=1.00142e+06"

\*\*\*RESULT IS Different 6

Run time: 62.098 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 0.316667"

"-----------END 61 from 90-----------------------------------------"

"--------------------START 62 from 90--------------------------------"

"62) U\_3\_1000\_05\_1.txt"

\*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=993454

\*Content of machines summed (993454, 993454, 993454, 993454, 993453)

input selected: size 1000 sum 4.96727e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=993458, #Machines=5, content:Very long..., Summed Machines(993456,993449,993451,993458,993455)

"Attempt 1(populationSize=100, genSize=100): TF=993458; BenchMark=993454"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=993458, #Machines=5, content:Very long..., Summed Machines(993456,993449,993451,993458,993455)

"Attempt 2(populationSize=50, genSize=200): TF=993458; BenchMark=993454"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=993458, #Machines=5, content:Very long..., Summed Machines(993456,993449,993451,993458,993455)

"Attempt 3(populationSize=200, genSize=50): TF=993458; BenchMark=993454"

"----Comparison for the 61 example----"

"\*\*\*BenchmarkTf=993454 ourGeneticTf=993458"

\*\*\*RESULT IS Different 4

Run time: 61.407 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 0.377049"

"-----------END 62 from 90-----------------------------------------"

"--------------------START 63 from 90--------------------------------"

"63) U\_3\_1000\_05\_2.txt"

\*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=1012869

\*Content of machines summed (1012869, 1012869, 1012869, 1012869, 1012868)

input selected: size 1000 sum 5.06434e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=1.01288e+06, #Machines=5, content:Very long..., Summed Machines(1012885,1012862,1012868,1012863,1012866)

"Attempt 1(populationSize=100, genSize=100): TF=1.01288e+06; BenchMark=1.01287e+06"

\*\*END On Gen=0

\*\*Best gene found: Gene id=49 TF=1.01288e+06, #Machines=5, content:Very long..., Summed Machines(1012885,1012862,1012868,1012863,1012866)

"Attempt 2(populationSize=50, genSize=200): TF=1.01288e+06; BenchMark=1.01287e+06"

\*\*END On Gen=0

\*\*Best gene found: Gene id=199 TF=1.01288e+06, #Machines=5, content:Very long..., Summed Machines(1012885,1012862,1012868,1012863,1012866)

"Attempt 3(populationSize=200, genSize=50): TF=1.01288e+06; BenchMark=1.01287e+06"

"----Comparison for the 62 example----"

"\*\*\*BenchmarkTf=1.01287e+06 ourGeneticTf=1.01288e+06"

\*\*\*RESULT IS Different 16

Run time: 63.2 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 0.629032"

"-----------END 63 from 90-----------------------------------------"

"--------------------START 64 from 90--------------------------------"

"64) U\_3\_1000\_05\_3.txt"

\*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=1011508

\*Content of machines summed (1011508, 1011508, 1011508, 1011508, 1011507)

input selected: size 1000 sum 5.05754e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=1.01151e+06, #Machines=5, content:Very long..., Summed Machines(1011508,1011513,1011495,1011511,1011512)

"Attempt 1(populationSize=100, genSize=100): TF=1.01151e+06; BenchMark=1.01151e+06"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=1.01151e+06, #Machines=5, content:Very long..., Summed Machines(1011508,1011513,1011495,1011511,1011512)

"Attempt 2(populationSize=50, genSize=200): TF=1.01151e+06; BenchMark=1.01151e+06"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=1.01151e+06, #Machines=5, content:Very long..., Summed Machines(1011508,1011513,1011495,1011511,1011512)

"Attempt 3(populationSize=200, genSize=50): TF=1.01151e+06; BenchMark=1.01151e+06"

"----Comparison for the 63 example----"

"\*\*\*BenchmarkTf=1.01151e+06 ourGeneticTf=1.01151e+06"

\*\*\*RESULT IS Different 5

Run time: 63.803 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 0.698413"

"-----------END 64 from 90-----------------------------------------"

"--------------------START 65 from 90--------------------------------"

"65) U\_3\_1000\_05\_4.txt"

\*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=988263

\*Content of machines summed (988263, 988263, 988263, 988263, 988261)

input selected: size 1000 sum 4.94131e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=988266, #Machines=5, content:Very long..., Summed Machines(988266,988262,988262,988260,988263)

"Attempt 1(populationSize=100, genSize=100): TF=988266; BenchMark=988263"

\*\*END On Gen=0

\*\*Best gene found: Gene id=49 TF=988266, #Machines=5, content:Very long..., Summed Machines(988266,988262,988262,988260,988263)

"Attempt 2(populationSize=50, genSize=200): TF=988266; BenchMark=988263"

\*\*END On Gen=0

\*\*Best gene found: Gene id=199 TF=988266, #Machines=5, content:Very long..., Summed Machines(988266,988262,988262,988260,988263)

"Attempt 3(populationSize=200, genSize=50): TF=988266; BenchMark=988263"

"----Comparison for the 64 example----"

"\*\*\*BenchmarkTf=988263 ourGeneticTf=988266"

\*\*\*RESULT IS Different 3

Run time: 60.111 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

"Mistakes(size-numberMistakes):" QMap((1000, 10))

"Avegare error: 0.734375"

"-----------END 65 from 90-----------------------------------------"

"--------------------START 66 from 90--------------------------------"

"66) U\_3\_1000\_05\_5.txt"

\*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=968879

\*Content of machines summed (968879, 968879, 968879, 968879, 968876)

input selected: size 1000 sum 4.84439e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=968882, #Machines=5, content:Very long..., Summed Machines(968882,968882,968877,968874,968877)

"Attempt 1(populationSize=100, genSize=100): TF=968882; BenchMark=968879"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=968882, #Machines=5, content:Very long..., Summed Machines(968882,968882,968877,968874,968877)

"Attempt 2(populationSize=50, genSize=200): TF=968882; BenchMark=968879"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=968882, #Machines=5, content:Very long..., Summed Machines(968882,968882,968877,968874,968877)

"Attempt 3(populationSize=200, genSize=50): TF=968882; BenchMark=968879"

"----Comparison for the 65 example----"

"\*\*\*BenchmarkTf=968879 ourGeneticTf=968882"

\*\*\*RESULT IS Different 3

Run time: 61.784 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

"Mistakes(size-numberMistakes):" QMap((1000, 11))

"Avegare error: 0.769231"

"-----------END 66 from 90-----------------------------------------"

"--------------------START 67 from 90--------------------------------"

"67) U\_3\_1000\_05\_6.txt"

\*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=996507

\*Content of machines summed (996507, 996507, 996507, 996507, 996505)

input selected: size 1000 sum 4.98253e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=996510, #Machines=5, content:Very long..., Summed Machines(996505,996509,996510,996499,996510)

"Attempt 1(populationSize=100, genSize=100): TF=996510; BenchMark=996507"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=996510, #Machines=5, content:Very long..., Summed Machines(996505,996509,996510,996499,996510)

"Attempt 2(populationSize=50, genSize=200): TF=996510; BenchMark=996507"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=996510, #Machines=5, content:Very long..., Summed Machines(996505,996509,996510,996499,996510)

"Attempt 3(populationSize=200, genSize=50): TF=996510; BenchMark=996507"

"----Comparison for the 66 example----"

"\*\*\*BenchmarkTf=996507 ourGeneticTf=996510"

\*\*\*RESULT IS Different 3

Run time: 62.907 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 0.80303"

"-----------END 67 from 90-----------------------------------------"

"--------------------START 68 from 90--------------------------------"

"68) U\_3\_1000\_05\_7.txt"

\*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=1006554

\*Content of machines summed (1006554, 1006554, 1006554, 1006554, 1006550)

input selected: size 1000 sum 5.03277e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=1.00658e+06, #Machines=5, content:Very long..., Summed Machines(1006577,1006552,1006551,1006549,1006537)

"Attempt 1(populationSize=100, genSize=100): TF=1.00658e+06; BenchMark=1.00655e+06"

\*\*END On Gen=0

\*\*Best gene found: Gene id=49 TF=1.00658e+06, #Machines=5, content:Very long..., Summed Machines(1006577,1006552,1006551,1006549,1006537)

"Attempt 2(populationSize=50, genSize=200): TF=1.00658e+06; BenchMark=1.00655e+06"

\*\*END On Gen=0

\*\*Best gene found: Gene id=199 TF=1.00658e+06, #Machines=5, content:Very long..., Summed Machines(1006577,1006552,1006551,1006549,1006537)

"Attempt 3(populationSize=200, genSize=50): TF=1.00658e+06; BenchMark=1.00655e+06"

"----Comparison for the 67 example----"

"\*\*\*BenchmarkTf=1.00655e+06 ourGeneticTf=1.00658e+06"

\*\*\*RESULT IS Different 23

Run time: 63.562 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 1.13433"

"-----------END 68 from 90-----------------------------------------"

"--------------------START 69 from 90--------------------------------"

"69) U\_3\_1000\_05\_8.txt"

\*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=999716

\*Content of machines summed (999716, 999716, 999716, 999716, 999716)

input selected: size 1000 sum 4.99858e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=999721, #Machines=5, content:Very long..., Summed Machines(999707,999720,999718,999714,999721)

"Attempt 1(populationSize=100, genSize=100): TF=999721; BenchMark=999716"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=999721, #Machines=5, content:Very long..., Summed Machines(999707,999720,999718,999714,999721)

"Attempt 2(populationSize=50, genSize=200): TF=999721; BenchMark=999716"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=999721, #Machines=5, content:Very long..., Summed Machines(999707,999720,999718,999714,999721)

"Attempt 3(populationSize=200, genSize=50): TF=999721; BenchMark=999716"

"----Comparison for the 68 example----"

"\*\*\*BenchmarkTf=999716 ourGeneticTf=999721"

\*\*\*RESULT IS Different 5

Run time: 61.333 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 1.19118"

"-----------END 69 from 90-----------------------------------------"

"--------------------START 70 from 90--------------------------------"

"70) U\_3\_1000\_05\_9.txt"

\*Data: machinesNum=5 jobsNum=1000 BenchMarkTf=1012238

\*Content of machines summed (1012238, 1012238, 1012238, 1012238, 1012238)

input selected: size 1000 sum 5.06119e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=1.01224e+06, #Machines=5, content:Very long..., Summed Machines(1012243,1012243,1012242,1012233,1012229)

"Attempt 1(populationSize=100, genSize=100): TF=1.01224e+06; BenchMark=1.01224e+06"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=1.01224e+06, #Machines=5, content:Very long..., Summed Machines(1012243,1012243,1012242,1012233,1012229)

"Attempt 2(populationSize=50, genSize=200): TF=1.01224e+06; BenchMark=1.01224e+06"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=1.01224e+06, #Machines=5, content:Very long..., Summed Machines(1012243,1012243,1012242,1012233,1012229)

"Attempt 3(populationSize=200, genSize=50): TF=1.01224e+06; BenchMark=1.01224e+06"

"----Comparison for the 69 example----"

"\*\*\*BenchmarkTf=1.01224e+06 ourGeneticTf=1.01224e+06"

\*\*\*RESULT IS Different 5

Run time: 62.098 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 1.24638"

"-----------END 70 from 90-----------------------------------------"

"--------------------START 71 from 90--------------------------------"

"71) U\_3\_1000\_10\_0.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=495463

\*Content of machines summed (495463, 495463, 495463, 495463, 495463, 495463, 495463, 495463, 495463, 495455)

input selected: size 1000 sum 4.95462e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=495477, #Machines=10, content:Very long..., Summed Machines(495477,495475,495471,495475,495473,495469,495458,495446,495440,495438)

"Attempt 1(populationSize=100, genSize=100): TF=495477; BenchMark=495463"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=495477, #Machines=10, content:Very long..., Summed Machines(495477,495475,495471,495475,495473,495469,495458,495446,495440,495438)

"Attempt 2(populationSize=50, genSize=200): TF=495477; BenchMark=495463"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=495477, #Machines=10, content:Very long..., Summed Machines(495477,495475,495471,495475,495473,495469,495458,495446,495440,495438)

"Attempt 3(populationSize=200, genSize=50): TF=495477; BenchMark=495463"

"----Comparison for the 70 example----"

"\*\*\*BenchmarkTf=495463 ourGeneticTf=495477"

\*\*\*RESULT IS Different 14

Run time: 60.821 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 1.42857"

"-----------END 71 from 90-----------------------------------------"

"--------------------START 72 from 90--------------------------------"

"72) U\_3\_1000\_10\_1.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=482122

\*Content of machines summed (482122, 482122, 482122, 482122, 482122, 482122, 482122, 482122, 482122, 482122)

input selected: size 1000 sum 4.82122e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=482153, #Machines=10, content:Very long..., Summed Machines(482144,482151,482152,482143,482119,482088,482071,482153,482061,482138)

"Attempt 1(populationSize=100, genSize=100): TF=482153; BenchMark=482122"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=482153, #Machines=10, content:Very long..., Summed Machines(482144,482151,482152,482143,482119,482088,482071,482153,482061,482138)

"Attempt 2(populationSize=50, genSize=200): TF=482153; BenchMark=482122"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=482153, #Machines=10, content:Very long..., Summed Machines(482144,482151,482152,482143,482119,482088,482071,482153,482061,482138)

"Attempt 3(populationSize=200, genSize=50): TF=482153; BenchMark=482122"

"----Comparison for the 71 example----"

"\*\*\*BenchmarkTf=482122 ourGeneticTf=482153"

\*\*\*RESULT IS Different 31

Run time: 61.367 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 1.84507"

"-----------END 72 from 90-----------------------------------------"

"--------------------START 73 from 90--------------------------------"

"73) U\_3\_1000\_10\_2.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=494774

\*Content of machines summed (494774, 494774, 494774, 494774, 494774, 494774, 494774, 494774, 494774, 494771)

input selected: size 1000 sum 4.94774e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=494806, #Machines=10, content:Very long..., Summed Machines(494806,494793,494792,494803,494781,494806,494779,494750,494742,494685)

"Attempt 1(populationSize=100, genSize=100): TF=494806; BenchMark=494774"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=494806, #Machines=10, content:Very long..., Summed Machines(494806,494793,494792,494803,494781,494806,494779,494750,494742,494685)

"Attempt 2(populationSize=50, genSize=200): TF=494806; BenchMark=494774"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=494806, #Machines=10, content:Very long..., Summed Machines(494806,494793,494792,494803,494781,494806,494779,494750,494742,494685)

"Attempt 3(populationSize=200, genSize=50): TF=494806; BenchMark=494774"

"----Comparison for the 72 example----"

"\*\*\*BenchmarkTf=494774 ourGeneticTf=494806"

\*\*\*RESULT IS Different 32

Run time: 62.287 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

"Mistakes(size-numberMistakes):" QMap((1000, 18))

"Avegare error: 2.26389"

"-----------END 73 from 90-----------------------------------------"

"--------------------START 74 from 90--------------------------------"

"74) U\_3\_1000\_10\_3.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=502896

\*Content of machines summed (502896, 502896, 502896, 502896, 502896, 502896, 502896, 502896, 502896, 502891)

input selected: size 1000 sum 5.02896e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=502938, #Machines=10, content:Very long..., Summed Machines(502937,502935,502932,502929,502924,502900,502846,502808,502938,502806)

"Attempt 1(populationSize=100, genSize=100): TF=502938; BenchMark=502896"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=502938, #Machines=10, content:Very long..., Summed Machines(502937,502935,502932,502929,502924,502900,502846,502808,502938,502806)

"Attempt 2(populationSize=50, genSize=200): TF=502938; BenchMark=502896"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=502938, #Machines=10, content:Very long..., Summed Machines(502937,502935,502932,502929,502924,502900,502846,502808,502938,502806)

"Attempt 3(populationSize=200, genSize=50): TF=502938; BenchMark=502896"

"----Comparison for the 73 example----"

"\*\*\*BenchmarkTf=502896 ourGeneticTf=502938"

\*\*\*RESULT IS Different 42

Run time: 61.039 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

"Mistakes(size-numberMistakes):" QMap((1000, 19))

"Avegare error: 2.80822"

"-----------END 74 from 90-----------------------------------------"

"--------------------START 75 from 90--------------------------------"

"75) U\_3\_1000\_10\_4.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=483591

\*Content of machines summed (483591, 483591, 483591, 483591, 483591, 483591, 483591, 483591, 483591, 483583)

input selected: size 1000 sum 4.8359e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=483626, #Machines=10, content:Very long..., Summed Machines(483619,483626,483622,483615,483548,483547,483543,483626,483530,483626)

"Attempt 1(populationSize=100, genSize=100): TF=483626; BenchMark=483591"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=483626, #Machines=10, content:Very long..., Summed Machines(483619,483626,483622,483615,483548,483547,483543,483626,483530,483626)

"Attempt 2(populationSize=50, genSize=200): TF=483626; BenchMark=483591"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=483626, #Machines=10, content:Very long..., Summed Machines(483619,483626,483622,483615,483548,483547,483543,483626,483530,483626)

"Attempt 3(populationSize=200, genSize=50): TF=483626; BenchMark=483591"

"----Comparison for the 74 example----"

"\*\*\*BenchmarkTf=483591 ourGeneticTf=483626"

\*\*\*RESULT IS Different 35

Run time: 63.354 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 3.24324"

"-----------END 75 from 90-----------------------------------------"

"--------------------START 76 from 90--------------------------------"

"76) U\_3\_1000\_10\_5.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=488311

\*Content of machines summed (488311, 488311, 488311, 488311, 488311, 488311, 488311, 488311, 488311, 488311)

input selected: size 1000 sum 4.88311e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=488322, #Machines=10, content:Very long..., Summed Machines(488319,488318,488305,488309,488296,488319,488318,488317,488322,488287)

"Attempt 1(populationSize=100, genSize=100): TF=488322; BenchMark=488311"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=488322, #Machines=10, content:Very long..., Summed Machines(488319,488318,488305,488309,488296,488319,488318,488317,488322,488287)

"Attempt 2(populationSize=50, genSize=200): TF=488322; BenchMark=488311"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=488322, #Machines=10, content:Very long..., Summed Machines(488319,488318,488305,488309,488296,488319,488318,488317,488322,488287)

"Attempt 3(populationSize=200, genSize=50): TF=488322; BenchMark=488311"

"----Comparison for the 75 example----"

"\*\*\*BenchmarkTf=488311 ourGeneticTf=488322"

\*\*\*RESULT IS Different 11

Run time: 63.18 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

"Mistakes(size-numberMistakes):" QMap((1000, 21))

"Avegare error: 3.34667"

"-----------END 76 from 90-----------------------------------------"

"--------------------START 77 from 90--------------------------------"

"77) U\_3\_1000\_10\_6.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=492997

\*Content of machines summed (492997, 492997, 492997, 492997, 492997, 492997, 492997, 492997, 492997, 492996)

input selected: size 1000 sum 4.92997e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=493014, #Machines=10, content:Very long..., Summed Machines(493012,493007,492986,493014,492986,492994,492993,492989,492993,492995)

"Attempt 1(populationSize=100, genSize=100): TF=493014; BenchMark=492997"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=493014, #Machines=10, content:Very long..., Summed Machines(493012,493007,492986,493014,492986,492994,492993,492989,492993,492995)

"Attempt 2(populationSize=50, genSize=200): TF=493014; BenchMark=492997"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=493014, #Machines=10, content:Very long..., Summed Machines(493012,493007,492986,493014,492986,492994,492993,492989,492993,492995)

"Attempt 3(populationSize=200, genSize=50): TF=493014; BenchMark=492997"

"----Comparison for the 76 example----"

"\*\*\*BenchmarkTf=492997 ourGeneticTf=493014"

\*\*\*RESULT IS Different 17

Run time: 62.122 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

"Mistakes(size-numberMistakes):" QMap((1000, 22))

"Avegare error: 3.52632"

"-----------END 77 from 90-----------------------------------------"

"--------------------START 78 from 90--------------------------------"

"78) U\_3\_1000\_10\_7.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=511506

\*Content of machines summed (511506, 511506, 511506, 511506, 511506, 511506, 511506, 511506, 511506, 511497)

input selected: size 1000 sum 5.11505e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=511530, #Machines=10, content:Very long..., Summed Machines(511520,511511,511528,511496,511530,511529,511445,511527,511526,511439)

"Attempt 1(populationSize=100, genSize=100): TF=511530; BenchMark=511506"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=511530, #Machines=10, content:Very long..., Summed Machines(511520,511511,511528,511496,511530,511529,511445,511527,511526,511439)

"Attempt 2(populationSize=50, genSize=200): TF=511530; BenchMark=511506"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=511530, #Machines=10, content:Very long..., Summed Machines(511520,511511,511528,511496,511530,511529,511445,511527,511526,511439)

"Attempt 3(populationSize=200, genSize=50): TF=511530; BenchMark=511506"

"----Comparison for the 77 example----"

"\*\*\*BenchmarkTf=511506 ourGeneticTf=511530"

\*\*\*RESULT IS Different 24

Run time: 60.642 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 3.79221"

"-----------END 78 from 90-----------------------------------------"

"--------------------START 79 from 90--------------------------------"

"79) U\_3\_1000\_10\_8.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=506910

\*Content of machines summed (506910, 506910, 506910, 506910, 506910, 506910, 506910, 506910, 506910, 506910)

input selected: size 1000 sum 5.0691e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=99 TF=506938, #Machines=10, content:Very long..., Summed Machines(506938,506910,506910,506904,506897,506909,506909,506909,506909,506905)

"Attempt 1(populationSize=100, genSize=100): TF=506938; BenchMark=506910"

\*\*END On Gen=0

\*\*Best gene found: Gene id=49 TF=506938, #Machines=10, content:Very long..., Summed Machines(506938,506910,506910,506904,506897,506909,506909,506909,506909,506905)

"Attempt 2(populationSize=50, genSize=200): TF=506938; BenchMark=506910"

\*\*END On Gen=0

\*\*Best gene found: Gene id=199 TF=506938, #Machines=10, content:Very long..., Summed Machines(506938,506910,506910,506904,506897,506909,506909,506909,506909,506905)

"Attempt 3(populationSize=200, genSize=50): TF=506938; BenchMark=506910"

"----Comparison for the 78 example----"

"\*\*\*BenchmarkTf=506910 ourGeneticTf=506938"

\*\*\*RESULT IS Different 28

Run time: 62.692 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 4.10256"

"-----------END 79 from 90-----------------------------------------"

"--------------------START 80 from 90--------------------------------"

"80) U\_3\_1000\_10\_9.txt"

\*Data: machinesNum=10 jobsNum=1000 BenchMarkTf=512239

\*Content of machines summed (512239, 512239, 512239, 512239, 512239, 512239, 512239, 512239, 512239, 512230)

input selected: size 1000 sum 5.12238e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=512264, #Machines=10, content:Very long..., Summed Machines(512257,512264,512264,512216,512264,512251,512226,512223,512191,512225)

"Attempt 1(populationSize=100, genSize=100): TF=512264; BenchMark=512239"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=512264, #Machines=10, content:Very long..., Summed Machines(512257,512264,512264,512216,512264,512251,512226,512223,512191,512225)

"Attempt 2(populationSize=50, genSize=200): TF=512264; BenchMark=512239"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=512264, #Machines=10, content:Very long..., Summed Machines(512257,512264,512264,512216,512264,512251,512226,512223,512191,512225)

"Attempt 3(populationSize=200, genSize=50): TF=512264; BenchMark=512239"

"----Comparison for the 79 example----"

"\*\*\*BenchmarkTf=512239 ourGeneticTf=512264"

\*\*\*RESULT IS Different 25

Run time: 62.232 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 4.36709"

"-----------END 80 from 90-----------------------------------------"

"--------------------START 81 from 90--------------------------------"

"81) U\_3\_1000\_25\_0.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=202498

\*Content of machines summed (202498, 202498, 202498, 202498, 202498, 202498, 202498, 202498, 202498, 202498, 202498, 202498, 202498, 202498, 202498, 202498, 202498, 202498, 202498, 202498, 202498, 202498, 202498, 202498, 202477)

input selected: size 1000 sum 5.06243e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=202568, #Machines=25, content:Very long..., Summed Machines(202567,202558,202564,202568,202551,202530,202552,202560,202531,202522,202534,202554,202560,202568,202349,202356,202339,202566,202506,202496,202518,202520,202352,202352,202356)

"Attempt 1(populationSize=100, genSize=100): TF=202568; BenchMark=202498"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=202568, #Machines=25, content:Very long..., Summed Machines(202567,202558,202564,202568,202551,202530,202552,202560,202531,202522,202534,202554,202560,202568,202349,202356,202339,202566,202506,202496,202518,202520,202352,202352,202356)

"Attempt 2(populationSize=50, genSize=200): TF=202568; BenchMark=202498"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=202568, #Machines=25, content:Very long..., Summed Machines(202567,202558,202564,202568,202551,202530,202552,202560,202531,202522,202534,202554,202560,202568,202349,202356,202339,202566,202506,202496,202518,202520,202352,202352,202356)

"Attempt 3(populationSize=200, genSize=50): TF=202568; BenchMark=202498"

"----Comparison for the 80 example----"

"\*\*\*BenchmarkTf=202498 ourGeneticTf=202568"

\*\*\*RESULT IS Different 70

Run time: 59.989 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 5.1875"

"-----------END 81 from 90-----------------------------------------"

"--------------------START 82 from 90--------------------------------"

"82) U\_3\_1000\_25\_1.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=198821

\*Content of machines summed (198821, 198821, 198821, 198821, 198821, 198821, 198821, 198821, 198821, 198821, 198821, 198821, 198821, 198821, 198821, 198821, 198821, 198821, 198821, 198821, 198821, 198821, 198821, 198821, 198817)

input selected: size 1000 sum 4.97052e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=198905, #Machines=25, content:Very long..., Summed Machines(198905,198903,198900,198876,198896,198896,198898,198898,198904,198805,198677,198719,198890,198885,198719,198835,198601,198715,198621,198715,198904,198905,198905,198904,198645)

"Attempt 1(populationSize=100, genSize=100): TF=198905; BenchMark=198821"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=198905, #Machines=25, content:Very long..., Summed Machines(198905,198903,198900,198876,198896,198896,198898,198898,198904,198805,198677,198719,198890,198885,198719,198835,198601,198715,198621,198715,198904,198905,198905,198904,198645)

"Attempt 2(populationSize=50, genSize=200): TF=198905; BenchMark=198821"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=198905, #Machines=25, content:Very long..., Summed Machines(198905,198903,198900,198876,198896,198896,198898,198898,198904,198805,198677,198719,198890,198885,198719,198835,198601,198715,198621,198715,198904,198905,198905,198904,198645)

"Attempt 3(populationSize=200, genSize=50): TF=198905; BenchMark=198821"

"----Comparison for the 81 example----"

"\*\*\*BenchmarkTf=198821 ourGeneticTf=198905"

\*\*\*RESULT IS Different 84

Run time: 60.166 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 6.16049"

"-----------END 82 from 90-----------------------------------------"

"--------------------START 83 from 90--------------------------------"

"83) U\_3\_1000\_25\_2.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=205821

\*Content of machines summed (205821, 205821, 205821, 205821, 205821, 205821, 205821, 205821, 205821, 205821, 205821, 205821, 205821, 205821, 205821, 205821, 205821, 205821, 205821, 205821, 205821, 205821, 205821, 205821, 205806)

input selected: size 1000 sum 5.14551e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=205852, #Machines=25, content:Very long..., Summed Machines(205851,205841,205848,205846,205835,205850,205840,205852,205837,205804,205815,205849,205812,205816,205830,205761,205799,205772,205851,205805,205799,205778,205821,205785,205813)

"Attempt 1(populationSize=100, genSize=100): TF=205852; BenchMark=205821"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=205852, #Machines=25, content:Very long..., Summed Machines(205851,205841,205848,205846,205835,205850,205840,205852,205837,205804,205815,205849,205812,205816,205830,205761,205799,205772,205851,205805,205799,205778,205821,205785,205813)

"Attempt 2(populationSize=50, genSize=200): TF=205852; BenchMark=205821"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=205852, #Machines=25, content:Very long..., Summed Machines(205851,205841,205848,205846,205835,205850,205840,205852,205837,205804,205815,205849,205812,205816,205830,205761,205799,205772,205851,205805,205799,205778,205821,205785,205813)

"Attempt 3(populationSize=200, genSize=50): TF=205852; BenchMark=205821"

"----Comparison for the 82 example----"

"\*\*\*BenchmarkTf=205821 ourGeneticTf=205852"

\*\*\*RESULT IS Different 31

Run time: 58.804 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 6.46341"

"-----------END 83 from 90-----------------------------------------"

"--------------------START 84 from 90--------------------------------"

"84) U\_3\_1000\_25\_3.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=202423

\*Content of machines summed (202423, 202423, 202423, 202423, 202423, 202423, 202423, 202423, 202423, 202423, 202423, 202423, 202423, 202423, 202423, 202423, 202423, 202423, 202423, 202423, 202423, 202423, 202423, 202423, 202416)

input selected: size 1000 sum 5.06057e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=202528, #Machines=25, content:Very long..., Summed Machines(202518,202522,202525,202524,202528,202521,202527,202524,202520,202518,202528,202502,202304,202298,202358,202341,202324,202280,202277,202341,202335,202341,202297,202528,202287)

"Attempt 1(populationSize=100, genSize=100): TF=202528; BenchMark=202423"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=202528, #Machines=25, content:Very long..., Summed Machines(202518,202522,202525,202524,202528,202521,202527,202524,202520,202518,202528,202502,202304,202298,202358,202341,202324,202280,202277,202341,202335,202341,202297,202528,202287)

"Attempt 2(populationSize=50, genSize=200): TF=202528; BenchMark=202423"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=202528, #Machines=25, content:Very long..., Summed Machines(202518,202522,202525,202524,202528,202521,202527,202524,202520,202518,202528,202502,202304,202298,202358,202341,202324,202280,202277,202341,202335,202341,202297,202528,202287)

"Attempt 3(populationSize=200, genSize=50): TF=202528; BenchMark=202423"

"----Comparison for the 83 example----"

"\*\*\*BenchmarkTf=202423 ourGeneticTf=202528"

\*\*\*RESULT IS Different 105

Run time: 61.088 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 7.6506"

"-----------END 84 from 90-----------------------------------------"

"--------------------START 85 from 90--------------------------------"

"85) U\_3\_1000\_25\_4.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=197546

\*Content of machines summed (197546, 197546, 197546, 197546, 197546, 197546, 197546, 197546, 197546, 197546, 197546, 197546, 197546, 197546, 197546, 197546, 197546, 197546, 197546, 197546, 197546, 197546, 197546, 197546, 197534)

input selected: size 1000 sum 4.93864e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=197612, #Machines=25, content:Very long..., Summed Machines(197609,197610,197597,197598,197609,197608,197581,197612,197604,197603,197612,197611,197602,197596,197603,197523,197411,197601,197396,197407,197413,197402,197415,197403,197612)

"Attempt 1(populationSize=100, genSize=100): TF=197612; BenchMark=197546"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=197612, #Machines=25, content:Very long..., Summed Machines(197609,197610,197597,197598,197609,197608,197581,197612,197604,197603,197612,197611,197602,197596,197603,197523,197411,197601,197396,197407,197413,197402,197415,197403,197612)

"Attempt 2(populationSize=50, genSize=200): TF=197612; BenchMark=197546"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=197612, #Machines=25, content:Very long..., Summed Machines(197609,197610,197597,197598,197609,197608,197581,197612,197604,197603,197612,197611,197602,197596,197603,197523,197411,197601,197396,197407,197413,197402,197415,197403,197612)

"Attempt 3(populationSize=200, genSize=50): TF=197612; BenchMark=197546"

"----Comparison for the 84 example----"

"\*\*\*BenchmarkTf=197546 ourGeneticTf=197612"

\*\*\*RESULT IS Different 66

Run time: 62.637 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 8.34524"

"-----------END 85 from 90-----------------------------------------"

"--------------------START 86 from 90--------------------------------"

"86) U\_3\_1000\_25\_5.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=203789

\*Content of machines summed (203789, 203789, 203789, 203789, 203789, 203789, 203789, 203789, 203789, 203789, 203789, 203789, 203789, 203789, 203789, 203789, 203789, 203789, 203789, 203789, 203789, 203789, 203789, 203789, 203778)

input selected: size 1000 sum 5.09471e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=203836, #Machines=25, content:Very long..., Summed Machines(203836,203812,203822,203827,203836,203831,203836,203815,203834,203798,203834,203786,203828,203830,203836,203810,203735,203815,203673,203695,203675,203826,203657,203664,203803)

"Attempt 1(populationSize=100, genSize=100): TF=203836; BenchMark=203789"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=203836, #Machines=25, content:Very long..., Summed Machines(203836,203812,203822,203827,203836,203831,203836,203815,203834,203798,203834,203786,203828,203830,203836,203810,203735,203815,203673,203695,203675,203826,203657,203664,203803)

"Attempt 2(populationSize=50, genSize=200): TF=203836; BenchMark=203789"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=203836, #Machines=25, content:Very long..., Summed Machines(203836,203812,203822,203827,203836,203831,203836,203815,203834,203798,203834,203786,203828,203830,203836,203810,203735,203815,203673,203695,203675,203826,203657,203664,203803)

"Attempt 3(populationSize=200, genSize=50): TF=203836; BenchMark=203789"

"----Comparison for the 85 example----"

"\*\*\*BenchmarkTf=203789 ourGeneticTf=203836"

\*\*\*RESULT IS Different 47

Run time: 60.87 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

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

"Avegare error: 8.8"

"-----------END 86 from 90-----------------------------------------"

"--------------------START 87 from 90--------------------------------"

"87) U\_3\_1000\_25\_6.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=195469

\*Content of machines summed (195469, 195469, 195469, 195469, 195469, 195469, 195469, 195469, 195469, 195469, 195469, 195469, 195469, 195469, 195469, 195469, 195469, 195469, 195469, 195469, 195469, 195469, 195469, 195469, 195447)

input selected: size 1000 sum 4.8867e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=195517, #Machines=25, content:Very long..., Summed Machines(195517,195515,195516,195401,195507,195363,195512,195510,195513,195359,195506,195480,195357,195512,195509,195495,195362,195517,195357,195511,195515,195478,195513,195515,195363)

"Attempt 1(populationSize=100, genSize=100): TF=195517; BenchMark=195469"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=195517, #Machines=25, content:Very long..., Summed Machines(195517,195515,195516,195401,195507,195363,195512,195510,195513,195359,195506,195480,195357,195512,195509,195495,195362,195517,195357,195511,195515,195478,195513,195515,195363)

"Attempt 2(populationSize=50, genSize=200): TF=195517; BenchMark=195469"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=195517, #Machines=25, content:Very long..., Summed Machines(195517,195515,195516,195401,195507,195363,195512,195510,195513,195359,195506,195480,195357,195512,195509,195495,195362,195517,195357,195511,195515,195478,195513,195515,195363)

"Attempt 3(populationSize=200, genSize=50): TF=195517; BenchMark=195469"

"----Comparison for the 86 example----"

"\*\*\*BenchmarkTf=195469 ourGeneticTf=195517"

\*\*\*RESULT IS Different 48

Run time: 64.946 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

"Mistakes(size-numberMistakes):" QMap((1000, 32))

"Avegare error: 9.25581"

"-----------END 87 from 90-----------------------------------------"

"--------------------START 88 from 90--------------------------------"

"88) U\_3\_1000\_25\_7.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=201133

\*Content of machines summed (201133, 201133, 201133, 201133, 201133, 201133, 201133, 201133, 201133, 201133, 201133, 201133, 201133, 201133, 201133, 201133, 201133, 201133, 201133, 201133, 201133, 201133, 201133, 201133, 201115)

input selected: size 1000 sum 5.02831e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=201175, #Machines=25, content:Very long..., Summed Machines(201164,201175,201170,201164,201166,201172,201173,201175,201174,201168,201174,201167,201144,201166,201126,201076,201066,201044,201127,201082,201081,201062,201114,201127,201050)

"Attempt 1(populationSize=100, genSize=100): TF=201175; BenchMark=201133"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=201175, #Machines=25, content:Very long..., Summed Machines(201164,201175,201170,201164,201166,201172,201173,201175,201174,201168,201174,201167,201144,201166,201126,201076,201066,201044,201127,201082,201081,201062,201114,201127,201050)

"Attempt 2(populationSize=50, genSize=200): TF=201175; BenchMark=201133"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=201175, #Machines=25, content:Very long..., Summed Machines(201164,201175,201170,201164,201166,201172,201173,201175,201174,201168,201174,201167,201144,201166,201126,201076,201066,201044,201127,201082,201081,201062,201114,201127,201050)

"Attempt 3(populationSize=200, genSize=50): TF=201175; BenchMark=201133"

"----Comparison for the 87 example----"

"\*\*\*BenchmarkTf=201133 ourGeneticTf=201175"

\*\*\*RESULT IS Different 42

Run time: 64.344 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

"Mistakes(size-numberMistakes):" QMap((1000, 33))

"Avegare error: 9.63218"

"-----------END 88 from 90-----------------------------------------"

"--------------------START 89 from 90--------------------------------"

"89) U\_3\_1000\_25\_8.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=202465

\*Content of machines summed (202465, 202465, 202465, 202465, 202465, 202465, 202465, 202465, 202465, 202465, 202465, 202465, 202465, 202465, 202465, 202465, 202465, 202465, 202465, 202465, 202465, 202465, 202465, 202465, 202463)

input selected: size 1000 sum 5.06162e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=202516, #Machines=25, content:Very long..., Summed Machines(202514,202509,202510,202513,202513,202514,202470,202399,202387,202516,202512,202398,202458,202428,202449,202430,202498,202505,202389,202405,202476,202455,202460,202463,202452)

"Attempt 1(populationSize=100, genSize=100): TF=202516; BenchMark=202465"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=202516, #Machines=25, content:Very long..., Summed Machines(202514,202509,202510,202513,202513,202514,202470,202399,202387,202516,202512,202398,202458,202428,202449,202430,202498,202505,202389,202405,202476,202455,202460,202463,202452)

"Attempt 2(populationSize=50, genSize=200): TF=202516; BenchMark=202465"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=202516, #Machines=25, content:Very long..., Summed Machines(202514,202509,202510,202513,202513,202514,202470,202399,202387,202516,202512,202398,202458,202428,202449,202430,202498,202505,202389,202405,202476,202455,202460,202463,202452)

"Attempt 3(populationSize=200, genSize=50): TF=202516; BenchMark=202465"

"----Comparison for the 88 example----"

"\*\*\*BenchmarkTf=202465 ourGeneticTf=202516"

\*\*\*RESULT IS Different 51

Run time: 66.958 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

"Mistakes(size-numberMistakes):" QMap((1000, 34))

"Avegare error: 10.1023"

"-----------END 89 from 90-----------------------------------------"

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

"90) U\_3\_1000\_25\_9.txt"

\*Data: machinesNum=25 jobsNum=1000 BenchMarkTf=200508

\*Content of machines summed (200508, 200508, 200508, 200508, 200508, 200508, 200508, 200508, 200508, 200508, 200508, 200508, 200508, 200508, 200508, 200508, 200508, 200508, 200508, 200508, 200508, 200508, 200508, 200508, 200496)

input selected: size 1000 sum 5.01269e+06

\*\*END On Gen=0

\*\*Best gene found: Gene id=98 TF=200552, #Machines=25, content:Very long..., Summed Machines(200552,200548,200536,200552,200548,200544,200547,200547,200542,200550,200545,200549,200546,200504,200543,200545,200543,200481,200411,200409,200402,200395,200412,200403,200534)

"Attempt 1(populationSize=100, genSize=100): TF=200552; BenchMark=200508"

\*\*END On Gen=0

\*\*Best gene found: Gene id=48 TF=200552, #Machines=25, content:Very long..., Summed Machines(200552,200548,200536,200552,200548,200544,200547,200547,200542,200550,200545,200549,200546,200504,200543,200545,200543,200481,200411,200409,200402,200395,200412,200403,200534)

"Attempt 2(populationSize=50, genSize=200): TF=200552; BenchMark=200508"

\*\*END On Gen=0

\*\*Best gene found: Gene id=198 TF=200552, #Machines=25, content:Very long..., Summed Machines(200552,200548,200536,200552,200548,200544,200547,200547,200542,200550,200545,200549,200546,200504,200543,200545,200543,200481,200411,200409,200402,200395,200412,200403,200534)

"Attempt 3(populationSize=200, genSize=50): TF=200552; BenchMark=200508"

"----Comparison for the 89 example----"

"\*\*\*BenchmarkTf=200508 ourGeneticTf=200552"

\*\*\*RESULT IS Different 44

Run time: 64.858 seconds

"Correct (size-numberCorrect):" QMap((1000, 55))

"Mistakes(size-numberMistakes):" QMap((1000, 35))

"Avegare error: 10.4831"

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

"Correct (size-numberCorrect):" QMap((1000, 55))

"Mistakes(size-numberMistakes):" QMap((1000, 35))

"Total Avegare error: 10.3667"

"Total time: 2179.58 seconds"

oldest Gen 0

**C:\algo\build-h-Desktop\_Qt\_5\_6\_0\_MinGW\_32bit-Debug\debug\h.exe exited with code 0**