BENCHMARK RESULTS OF A GENETIC ALGORITHM FOR NON-PERMUTATION FLOWSHOPS USING CONSTRAINED BUFFERS*

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ABSTRACT

This paper presents the performance study of a Genetic Algorithm, for the special case of a mixed model non-permutation flowshop production line, where resequencing is permitted when stations have access to intermittent or centralized resequencing buffers. The access to the buffers is restricted by the number of available buffer places and the physical size of the products. Results from other authors are compared which presented results on permutation sequences [1] or which treat a problem similar to the one studied in this work [2], based on the benchmark data provided by Taillard [3]. Improvements that come with the introduction of constrained resequencing buffers are highlighted.
Keywords: Genetic Algorithm, Non-Permutation Flowshop, Constrained Buffer

1. INTRODUCTION

Mixed model production lines consider that more than one model is being processed on the same production line in an arbitrary sequence. However, the majority of publications in this area are limited to solutions which determine the job sequence before the jobs enter the line and maintain it without interchanging jobs until the end of the production line, which is known as permutation flowshop. Exact approaches for makespan minimization can be found in [4, 5, 6], among others. In two recent reviews [7, 8] heuristic methods for sequencing problems are presented.

In the case of more than three stations and with the objective function to minimize the makespan, a unique permutation is no longer optimal. In [9] a study of the benefit of using non-permutation flowshops is presented. Furthermore, there exist various designs of production lines which permit resequencing of jobs: using large buffers (Automatic-Storage-and-Retrieval-System) which decouple one part of the line from the rest of the line [10]; buffers which are located off-line [11]; hybrid or flexible lines [12]; and more seldom, the interchange of job attributes instead of physically changing the position of a job within the sequence [13].

2. DESCRIPTION OF LINE

The present work considers a flowshop with the possibility to resequence jobs between consecutive stations. The buffers are located off-line either accessible from a single station (intermittent case) or from various stations (centralized case). In both cases, it is considered that a job may not be able to be stored in a buffer place, due to its extended physical size. The heuristic used here is a variation of the Genetic Algorithm explained in [14] and is explained in more detail in [15].

3. BENCHMARK COMPARISON

For the case of larger problem sizes it is more difficult to find adequate input data. This is contingent on the great variety of existent problems and the fact that many times only results are presented rather than input data. In [3] a widely used test-bed is presented. In what follows, an attempt is made to compare results for this test-bed from other authors which presented results on permutation sequences [1] or which treat a problem similar to the one studied in this work [2].

3.1. Watson, Barbulescu, Whitley, Howe

In the work of [1], upper bounds for different data sets for permutation flowshop instances are listed. In one of the sets, the operation durations are independently and uniformly sampled in the interval [1,99], following [3], and contains four different problem sizes: 20, 50, 100 and 200 jobs, each for a 20 station flowshop. For each problem size 100 samples are presented. Next to the sample data, if best solution, or in case that this is not known, the best known upper bounds are given, allowing only permutation sequences.

In what follows, the results of the Genetic Algorithm are compared to these data sets when resequencing is permitted within the production line. The study of only 20 of the 100 sample data gave meaningful results. In the case of 200 jobs only 5 sample data were studied. In the case *I3*, the 10th station has access to an intermittent resequencing buffer with three buffer places, for C33, the 4th and the 11th station have access to a centralized resequencing buffer with three buffer places. In (*lim*) the physical size of the buffer places is restricted and not all jobs can be stored in all buffer places.
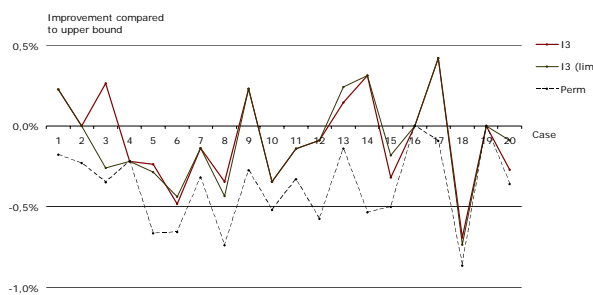

Figure 1. Comparison to the upper bound for permutation sequences (20 jobs and 20 stations).
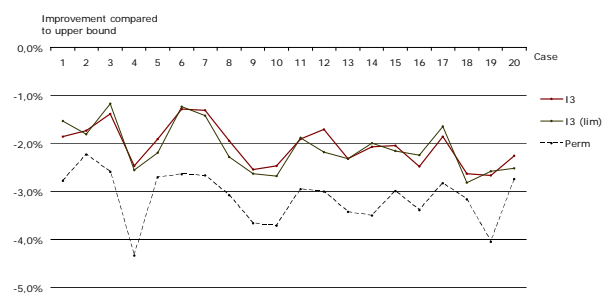

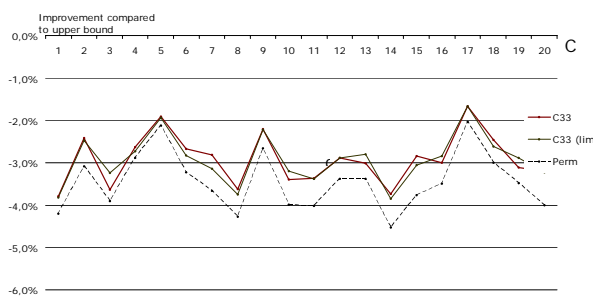*Figure 2. Comparison to the upper bound for permutation sequences (50 jobs and 20 stations).*

Figure 3. Comparison to the upper bound for permutation sequences (100 jobs and 20 stations).
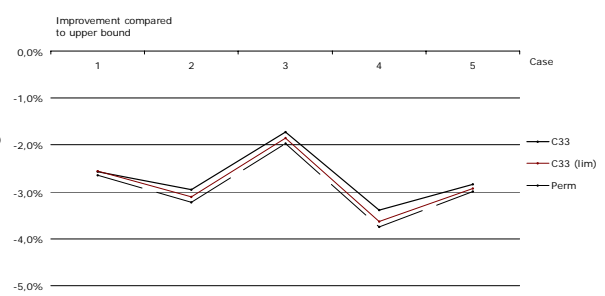
Figure 4. Comparison to the upper bound for permutation sequences (200 jobs and 20 stations).

Figure 1 shows that for the case of permutation sequences the Genetic Algorithm already achieves good results and when resequencing is permitted at one station, in some cases a considerable improvement can be achieved. In the case in which the physical size of the buffer places are limited, (*lim*), the solutions in general are similar to the previous ones and in all but three cases are better than the permutation sequences. In figure 2 to 4 the Genetic Algorithm performs better when resequencing is allowed. Limiting the physical size of the buffer places (*lim*) gives nearly as good results.

3.2. Brucker, Heitmann, Hurink

The work of [2], presents a Tabu search for a flowshop with the possibility of resequencing within the production line. They position a buffer between all consecutive stations with the possibility to resequence. The variable parameter is the number of buffer places which is 0, 1, 2, or n (infinite). The number of buffer places is the same for all resequencing buffer. The case of 0 buffer places does not allow resequencing and is equivalent to the permutation flowshop.

Table 1. Comparison of the solutions of the optimal solutions with the Tabu search and the Genetic Algorithm for the permutation case and for the introduction of resequencing buffers for the case of 20 jobs and 5 stations.

| Instance | Permutation | | | Non-Permutation | | | | | | | | | |
| | Opt. solution | Brucker b_i = 0 | Genetic Algorithm | Upper bound/ Opt. solution | Brucker | | | Genetic Algorithm | | | | | |
					b_i = 1	b_i = 2	b_i = n	I3	I3 (lim)	C3	C3 (lim)	I22	I22 (lim)
ta010	1108	1302	1108	1103	1134	1115	**1103**	**1103**	**1103**	1108	1108	1108	1108
ta009	1230	1433	1230	1210	1289	1249	**1210**	1230	1230	1230	1230	1230	1230
ta008	1206	1436	1206	1199	1227	1215	**1199**	**1199**	**1199**	1206	1206	1206	1206
ta007	1234	1436	1239	1234	1266	1251	1234	1239	1239	1239	1239	1239	1239
ta006	1195	1434	1195	1193	1268	1217	**1193**	**1193**	**1193**	1195	1195	1195	1195
ta005	1235	1370	1235	1231	1262	1250	**1231**	1235	1235	1235	1235	1235	1235
ta004	1293	1471	1300	1292	1329	1329	**1292**	1293	1293	1297	1297	1297	1297
ta003	1081	1353	1081	1073	1132	1098	**1073**	**1080**	**1080**	1081	1081	1081	1081
ta002	1359	1451	1359	1358	1365	1365	**1358**	1359	1359	1359	1359	1359	1359
ta001	1278	1437	1278	1278	1287	1287	1278	1278	1278	1278	1278	1278	1278

Table 2. Comparison of the solutions of the optimal solutions with the Tabu search and the Genetic Algorithm for the permutation case and for the introduction of resequencing buffers for the case of 20 jobs and 10 stations.

| Instance | Permutation | | | Non-Permutation | | | | | | | | | |
| | Opt. solution | Brucker b_i = 0 | Genetic Algorithm | Upper bound/ Opt. solution | Brucker | | | Genetic Algorithm | | | | | |
					b_i = 1	b_i = 2	b_i = n	I3	I3 (lim)	C3	C3 (lim)	I22	I22 (lim)
ta020	1591	1806	1608	1559	1632	1642	1642	1603	1603	1606	1603	1603	1603
ta019	1593	1772	1594	1586	1672	1628	1626	1594	1594	1594	1594	1594	1594
ta018	1538	1788	1558	1527	1582	1585	1580	**1538**	**1538**	1554	1554	1553	1554
ta017	1484	1673	1484	1428	1559	1521	1505	**1476**	**1479**	**1468**	**1468**	**1468**	**1479**
ta016	1397	1632	1401	1369	1424	1413	1419	1400	1397	1397	1400	1397	1397
ta015	1419	1678	1427	1413	1501	1476	1463	**1409**	**1409**	1419	1419	1419	1419
ta014	1377	1620	1383	1368	1433	1413	1402	1382	1382	1383	**1374**	**1374**	1383
ta013	1496	1755	1508	1486	1565	1544	1540	1508	1508	1501	1501	1501	1504
ta012	1659	1875	1678	1644	1763	1737	1737	1667	1664	1665	1665	1665	1665
ta011	1582	1758	1590	1560	1681	1659	1659	1583	1583	1586	1586	1586	1586

Table 3. Comparison of the solutions of the optimal solutions with the Tabu search and the Genetic Algorithm for the permutation case and for the introduction of resequencing buffers for the case of 50 jobs and 5 stations.

| Instance | Permutation | | | Non-Permutation | | | | | | | | | |
| | Opt. solution | Brucker b_i = 0 | Genetic Algorithm | Upper bound/ Opt. solution | Brucker | | | Genetic Algorithm | | | | | |
					b_i = 1	b_i = 2	b_i = n	I3	I3 (lim)	C3	C3 (lim)	I22	I22 (lim)
ta040	2782	3350	2782	2776	2856	**2776**	**2776**	2782	2782	**2776**	**2776**	**2776**	**2776**
ta039	2552	3045	2561	2545	2599	2558	2559	2557	2557	2561	2561	2561	2561
ta038	2683	3187	2683	2683	2769	2697	2688	2683	2683	2683	2683	2683	2683
ta037	2725	3166	2725	2716	2765	2843	2843	2725	2725	2725	**2717**	2725	2725
ta036	2829	3364	2829	2825	2916	2837	2829	**2828**	**2828**	2829	2829	2829	2829
ta035	2863	3350	2863	2853	2918	2871	2872	**2857**	**2857**	2853	2853	2853	2853
ta034	2751	3334	2751	2751	2888	2764	2782	2751	2751	2751	2751	2751	2751
ta033	2621	3265	2621	2612	2730	2632	2623	**2620**	**2620**	2615	2615	2615	2621
ta032	2834	3385	2838	2834	2913	2877	2882	2838	2838	2838	2838	2838	2838
ta031	2724	3238	2724	2724	2808	2729	2729	2724	2724	2724	2724	2724	2724

Table 4. Comparison of the solutions of the optimal solutions with the Tabu search and the Genetic Algorithm for the permutation case and for the introduction of resequencing buffers for the case of 50 jobs and 10 stations.

| Instance | Permutation | | | Non-Permutation | | | | | | | | | |
| | Opt. solution | Brucker b_i = 0 | Genetic Algorithm | Upper bound/ Opt. solution | Brucker | | | Genetic Algorithm | | | | | |
					b_i = 1	b_i = 2	b_i = n	I3	I3 (lim)	C3	C3 (lim)	I22	I22 (lim)
ta050	3065	3816	3146	3065	3273	3169	3201	3131	3131	3138	3138	3138	3138
ta049	2897	3771	2968	2887	3114	3049	3013	2952	2962	2962	2962	2958	2962
ta048	3037	3722	3079	3026	3183	3142	3150	3060	3074	3079	3079	3079	3079
ta047	3093	3789	3160	3093	3348	3234	3234	3156	3156	3156	3147	3147	3151
ta046	3006	3755	3075	2991	3177	3126	3119	3065	3075	3075	3075	3075	3075
ta045	2976	3838	3060	2976	3232	3141	3152	3037	3026	3040	3045	3043	3045
ta044	3063	3844	3090	3063	3242	3129	3146	3087	3087	3087	3085	3086	3085
ta043	2839	3658	2930	2832	3077	2925	2964	2926	2926	2926	2927	2929	2926
ta042	2867	3664	2972	2867	3111	3003	3031	2946	2932	2957	2957	2957	2957
ta041	2991	3806	3068	2970	3258	3179	3142	3063	3063	3062	3066	3062	3068

The presented results consider four instances of 20 and 50 Jobs for a 5- and a 10-station flowshop. Next to the results of the Tabu search, the optimal solution or the so far best upper bound is listed. In the case of 5 stations table 1 and 3 show that the Genetic Algorithm achieves the optimal solution in 8 out of 10 cases for the permutation case, as indicated by the cells with colored background. For the non-permutation case, the optimal solution on permutation sequences is surpassed in various cases by

the introduction of one buffer. The solutions achieved by the Tabu search show promising results mainly for *n* buffers. In the case of 10 stations, see table 2 and 4, the Genetic Algorithm outperforms the Tabu search for permutation sequences, as well as for non-permutation sequences. As in the previous benchmark comparison, limiting the physical size of the buffer places *(lim)* gives nearly as good results.

4. CONCLUSIONS

This paper presented the performance comparison of a Genetic Algorithm for benchmark data, based on the work by Taillard [3]. The considered case is a special case of a mixed model non-permutation flowshop production line, where resequencing is permitted when stations have access to intermittent or centralized resequencing buffers. The access to the buffers is restricted by the number of available buffer places and the physical size of the products. The Genetic Algorithm gives promising results for the comparison with [1] where only permutation sequences are considered and outperforms the Tabu search of [2] which presents a similar approach to resequencing of jobs within the production line as the one studied in this work.

5. REFERENCES

[1] Watson, J., Barbulescu, L., Whitley, L., Howe, A.: Contrasting structured and random permutation flow-shop scheduling problems: Search-space topology and algorithm performance. INFORMS Journal on Computing, 14(2):98–123, 2002.

[2] Brucker, P., Heitmann, S., Hurink, J.: Flow-shop problems with intermediate buffers. OR Spectrum, 25:549–574, 2003.

[3] Taillard, E.: Benchmarks for basic scheduling problems. European Journal of Operational Research, 64(2):278–285, 1993.

[4] Ignall, E., Schrage, L.: Application of the branch and bound technique to some flow-shop problems. Operations Research, 13(3):400–412, 1965.

[5] Potts, C.: An adaptive branching rule for the permutation flowshop problem. European Journal of Operational Research, 5(2):19–25: 1980.

[6] Carlier, J., Rebai, I.: Two branch and bound algorithms for the permutation flowshop problem. European Journal of Operational Research, 90(2):238–251, 1996.

[7] Framinan, J., Gupta, J., Leisten, R.: A review and classification of heuristics for permuation flowshop scheduling with makespan objective. Technical Report OI/PPC-2001/02. Vers.1.2, 2002.

[8] Framinan, J., Leisten, R.: Comparison of heuristics for flowtime minimisation in permuation flowshops. Technical Report IO-2003/01. Version 0.5., 2003.

[9] Potts C.N., Shmoys D.B., Williamson D.P.: Permutation vs. non-permutation flow shop schedules. Operations Res. Letters, 10(5):281–284, 1991.

[10] Lee H.F., Schaefer S.K.: Sequencing methods for automated storage and retrieval systems with dedicated storage. Computers and Industrial Engineering, 32(2):351–362, 1997.

[11] Lahmar M., Ergan H., Benjaafar S.: Resequencing and feature assignment on an automated assembly line. IEEE Transactions on Robotics and Automation, 19(1):89–102, 2003.

[12] Engstrõm T., Jonsson D., Johansson B.: Alternatives to line assembly: Some swedish examples. International Journal of Industrial Ergonomics, 17(3):235–245, 1996.

[13] Rachakonda P., Nagane S.: Simulation study of paint batching problem in automobile industry. http://sweb.uky.edy/˜pkrach0/Projects/ MFS605Project.pdf, 2000. consulted 14.07.2004.

[14] Michaelewicz, Z.: Gentic Algorithms + Data Structures = Evolution Programs. Springer Verlag, 3rd edition, 1996.

[15] Färber G., Coves A.M.: Genetic Algorithm for Sequencing in Mixed Model Non-Permutation Flowshops using Constrained Buffers., XXIX Congreso Nacional de la Sociedad de Estadística e Investigación Operativa (SEIO 2006), Tenerife, Spain, 2006