Journal of Computer Engineering
ISSN 10003428

Original Research Article

Vol 8, Issue 4, 2019 | ISSN: 1000-3428

Evaluating Multi-Objective EEG Feature Selection Through Power-Performance Optimization on Heterogeneous Parallel Architectures

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Abstract

This paper provides an insight on the power-performance issues related with the CPU-GPU parallel implementations of problems that frequently appear in the context of applications on bioinformatics and biomedical engineering. More specifically, we analyse the power-performance behaviour of an evolutionary parallel multiobjective electroencephalogram (EEG) feature selection procedure that evolves subpopulations of solutions with time-demanding fitness evaluation. The procedure has been implemented in OpenMP to dynamically distribute either subpopulations or individuals among devices, and uses OpenCL to evaluate the fitness of the individuals. The development of parallel codes usually implies to maximize the code efficiency, thus optimizing the achieved speedups. To follow the same trend, this paper extends and provides a more complete analysis of our previous works about the power-performance characteristics in heterogeneous CPU-GPU platforms considering different operation frequencies and evolutionary parameters such as distribution of individuals, etc. This way, different experimental configurations of the proposed procedure have been evaluated and compared with respect to a master-worker approach, not only in runtime but also considering energy consumption. The experimental results show that lower operating frequencies does not necessarily mean lower energy consumptions since energy is the product of power and time. Thus, we have observed that parallel processing not only reduces the runtime but

Indexed keywords: Heterogeneous Parallelism, Energy-aware Computing, Dynamic Scheduling, EEG Classification, Multi-objective Feature Selection, Subpopulations.

Article History: Received: 20 January 2019 | Accepted: 21 March 2019 | Published: 12 April 2019

How to cite: Maria Rodriguez-Castillo, Carlos Sanchez-Lopez, Sofia Hernandez-Gonzalez, Elena Rivas-Martinez, Juan Carlos Navarro-Molina (2019). Evaluating Multi-Objective EEG Feature Selection Through Power-Performance Optimization on Heterogeneous Parallel Architectures. Journal of Computer Engineering, 8(4), 107–119. DOI: https://doi.org/10.5281/zenodo.19340105

also the energy consumed by the application despite a higher instantaneous power. Particularly, the workload distribution among both CPU and GPU cores provides the best runtime and very low energy consumption compared with the values achieved by the same alternatives executed by only CPU threads.

1. INTRODUCTION

EEG classification problems appear in many neurological and bioengineering applications such as diagnosis of sleep disorders, prediction of epileptic seizures, or Brain Computer Interfaces (BCI) tasks (Rupp et al., 2014). EEG classification involves some hard issues related with the unstable behaviour and non-linearity of the signals, the low signal to noise rate, and the high number of features required to represent the information included in the evolution of the signals with respect to time. Moreover, as the experimental work required to register EEG signals (or EEG patterns) for different subjects and situations is quite time consuming, the number of EEG patterns available to train the classifiers is much smaller than the number of features used to describe each EEG. Thus, a so-called curse-of-dimensionality problem (Duin, 2000) arises, unless a feature selection procedure to reduce the dimensionality of the EEG patterns is accomplished.

Nevertheless, finding the optimum set of features has proven to be a Non-deterministic Polynomial-time hard (NP-hard) problem, and thus metaheuristics such as simulated annealing, genetic algorithms, ant colony optimization, and particle swarm optimization constitute suitable approaches to tackle the problem (Marinaki and Marinakis, 2014). Thus, feature selection can take advantage of evolutionary algorithms. Although these algorithms could require a lot of runtime in high-dimensional problems, as they do not use explicit information about the problem to be solved, they can be accelerated by present parallel computer architectures in several ways. In our previous papers (Escobar et al., 2017a, 2016a,b, 2017c), we described the benefits of CPUs and GPU cores to accelerate EEG classification which, as many other bioinformatics applications, requires solving problems with different parallelism types. More specifically, in (Escobar et al., 2017a), we accelerated the EEG feature selection problem by a subpopulation-based evolutionary algorithm to take advantage of parallel architectures involving multicore CPUs and GPUs. Nevertheless, besides speed, energy consumption has become an important issue to evaluate the program efficiency, not only due to economic and environmental reasons, but also as a challenge for the High-Performance Computing (HPC) community to allow efficient use of future Exascale systems, and as a requirement for handheld and wearable devices.

Although the relevance of energy consumption in the context of evolutionary algorithms has been pointed out in (Cotta et al., 2015), and even taking into account that decreasing energy consumption should be considered at par with decreasing the running time, to the best of our knowledge, there is not any paper on parallel evolutionary algorithms that provides a detailed efficiency analysis from the power-performance approach. (Fern´andez-de-Vega et al., 2016) analyses the energy consumption in different platforms of a sequential evolutionary procedure, but deals more with the energy efficiency of different platforms than with the comparison of the energy consumption of different algorithms in the same heterogeneous platform.

In this paper we provide a detailed analysis of different parallel implementations of our subpopulation-based evolutionary algorithm for EEG feature selection, not only with respect to the quality of the obtained solutions and the speedup achieved by the alternative configurations of parallel platforms but also considering their energy consumption characteristics. This way, with respect to our previous paper (Escobar et al., 2017a), we analyze the quality of the solutions achieved (hypervolume indicator), the speedup, and the energy consumed by our parallel codes in a more complete set of experiments. These experiments correspond to different operating frequencies (1.2 and 2.1 GHz, and the alternative used by the runtime system), subpopulations and individuals per subpopulations, number of migrations, and platforms (heterogenous platforms including both CPU and GPU cores, or constituted by either CPU or GPU cores). We have also shown the evolution with time of the instantaneous power dissipated by different alternatives on operating frequency and subpopulations.

After this introduction, Section 2 briefly describes the parallel evolutionary multi-objective algorithm alternatives for feature selection in heterogeneous CPU-GPU architectures along with some details for their implementations. Then, Section 3 shows the related works in the literature, Section 4 describes and analyses the experimental setup and results, and finally, Section 5 summarises the conclusions.

2. A SUBPOPULATION-BASED MULTI-OBJECTIVE FEATURE SELECTION ON CPU-GPU PLATFORMS

A multi-objective evolutionary procedure, in our case the well-known NSGA-II algorithm (Deb et al., 2000), evolves subpopulations of individuals that codify different feature selections. Besides the mutation and crossover operators applied to some selected parent individuals, NSGA-II also includes the so-called Non-domination Sorting to rank the individuals into different levels of non-dominance: the first level (Pareto front) includes the individuals non-dominated by any other individual.

Given a feature selection (an individual in the subpopulation), the components of the N_P patterns included in the training dataset, *DS*, are determined and correspond to the selected features among the whole set of N_F features. In our approach, the fitness of each feature selection is obtained by applying the *K*-means algorithm to the N_P patterns $P_i = (p_i^1, ..., p_i^{N_F})(i = 1, ..., N_P)$ in order to determine the centroids $K^t(j)(j = 1,..,W)$ of the *W* possible clusters (*W* = 3 because it is equal to the number of classes in our BCI tasks). Once the clusters are built by including each pattern in its nearest centroid, the fitness of each individual in the subpopulation is evaluated by using two Clustering Validation Indices (CVIs), defined by the intraclass f_1 and the interclass f_2 distances, which are detailed in (Escobar et al., 2017c).

The parallel code has been implemented with OpenMP pragmas and OpenCL. OpenMP dynamically distributes the fitness evaluation of the individuals (the cost functions f_1 and f_2) launching OpenCL kernels among both CPU and GPU devices. As many CPU threads as available OpenCL devices, N_D, are created through the corresponding OpenMP pragma to parallelise the loop that iterates over all subpopulations, S_p. To evaluate the fitness in parallel, two dynamic scheduling alternatives can be applied, as the procedure distributes subpopulations or individuals when only one subpopulation is detected. Thus, according to the device, two parallelism levels can be achieved in a CPU, and up to three in a GPU, where the *K*-means data parallelism is also implemented. Algorithm 1 provides a detailed description of our parallel multi-objective evolutionary algorithm, named D2S_NSGAII (Dynamic Distribution of Subpopulations using NSGA-II), which also is summarised in Figure 1.

On the other hand, to execute a GPU kernel, the individuals must be transferred from the host memory to the GPU memory, and vice-versa. The required copies per generation between devices could constitute an important bottleneck, as was analysed in (Escobar et al., 2017b). Nevertheless, as the subpopulations are dynamically allocated to the devices available in the platform, the time required for transferring data can be overlapped.

A migration implies to build a new set of subpopulations. To define a new subpopulation, each subpopulation contributes with half of its solutions of its present Pareto front at most. Finally, the solutions obtained by different subpopulations are recombined by the main CPU thread, and returned at the end of the function. These steps are repeated according to the required number of subpopulation generations and migrations as Figure 1 shows.

3. RELATED WORKS

The use of multi-objective optimization in data mining applications has been shown in (Mukhopadhyay et al., 2014a,b), and its benefits in both supervised and unsupervised classification have been reported elsewhere (Handl and Knowles, 2006). As GPU architectures constitute one of the present mainstream approaches to take advantage of technology improvements (Collet, 2013), their use has been described in many previous papers involving the analysis of the acceleration rates attained by the GPUs with respect to a sequential implementation that only uses CPU cores (Luong et al., 2010). With respect to evolutionary algorithm implementations, it is

Algorithm 1: Subpopulations scheduler pseudocode. The evaluation of subpopulations is distributed among all OpenCL devices, where each of them is assigned to one OpenMP thread

1 **Function** D2S NSGAII(Sp,N_D,D,N_{Spop},M,DS,K,DS^t)

Input: The initial subpopulations, $Sp_i; \forall i = 1,...,N_{Spop}$

Input: Number of available OpenCL devices, N_D

Input: Object D_j containing the OpenCL devices, $\forall j = 1,...,N_D$

Input: Number of subpopulations N_{Spop} to be evolved

Input: Number of individuals in each subpopulation, M

Input: Dataset DS: N_P training patterns of N_F features

Input: Set K of W centroids randomly chosen from DS

Input: Dataset DS^t is DS in column-major order

Output: S, the new solution for the problem

repeat

return S

2

// OpenMP parallel section with N_D devices

3 **repeat**

// Start the evolution process

4**repeat**

5$Offspr \leftarrow$UniformCrossover(Sp_i)

6**if** D_j is a CPU **then**

7$Offspr \leftarrow$evaluationsCPU($Offspr,M,DS,K$)

8**else**

9$Offspr \leftarrow$evaluationsGPU($Offspr,M,DS,K,DS^t$)

10**end**

// Replacement process

11 $Aux \leftarrow$ Join Sp_i and $Offspr$ in one array

12 $Aux \leftarrow$ nonDominatedSorting(Aux,$M + N_{Offspr}$)

13 $Sp_i \leftarrow$ Copy the first M individuals from Aux

14 **until** the number of subpopulations generations is reached;

15 **until** all N_{Spop} subpopulations are evaluated; 16 $Sp \leftarrow$migration(Sp,N_{Spop},M)

17 **until** the number of desired migrations is reached;

// Recombination process

18 $Sp \leftarrow$nonDominatedSorting(Sp,$N_{Spop} \times M$)

19 $S \leftarrow$ Copy the first M individuals from Sp

20

21 **End**

possible to use the GPU only to evaluate the fitness of the individuals in the population, taking advantage of the data parallelism present in that fitness function. Another approach is to implement the whole evolutionary algorithm in the GPU (J¨ahne, 2016).

An alternative GPU implementation of the non-dominance rank used in NSGA-II, the Archived-based

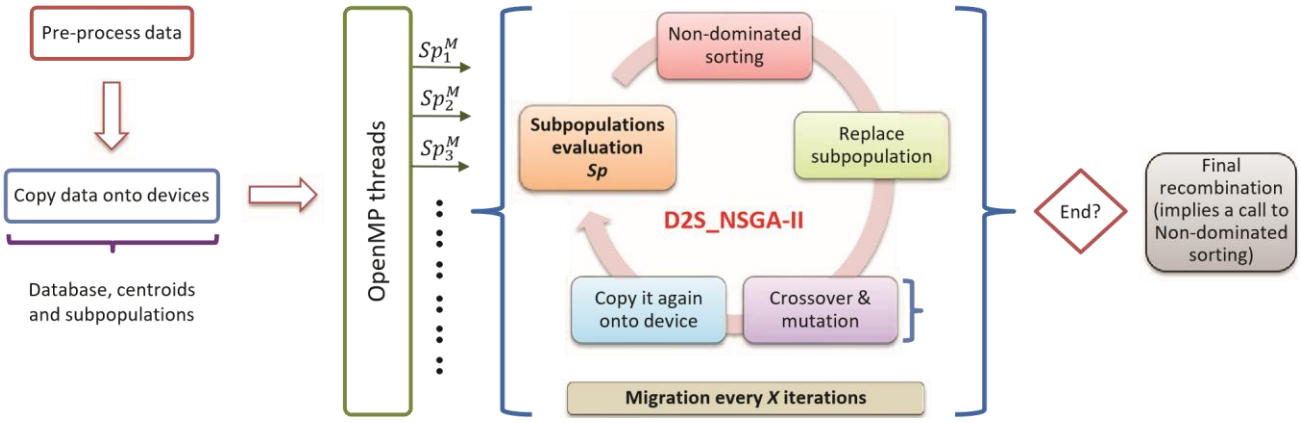


Figure 1. Scheme of the steps in the D2S_NSGAII procedure. Firstly, the algorithm receives all necessary parameters to perform the evolution of subpopulations. Then, each subpopulation $Sp^M{}_i$ (assigned to one CPU thread) is evaluated by one OpenCL device, which executes the cycle of steps inside of the blue brackets. If only one subpopulation is detected, all devices cooperate to perform the evaluation. The algorithm uses uniform crossover with a probability of 0.75, mutation by inversion of the selected bit with a probability of 0.025, and selection by binary tournament.

Stochastic Ranking Evolutionary Algorithm (ASREA), is provided in (Sharma and Collet, 2013). Paper (Wong and Cui, 2013) provides a parallel NSGA-II implementation for a data mining application that executes all steps of the algorithm in the GPU except for the non-dominated selection of a multi-objective evolutionary algorithm. Nevertheless, works analysing the effect in the parallel performance of heavy fitness functions requiring highvolume datasets and the parallelization on a heterogeneous platform of a whole data mining application with similar characteristics to our target application are less frequent. In our previous paper (Escobar et al., 2016a), we proposed a multi-objective feature selection that implements both functional and data parallelism

which can be executed either in a CPU or in a GPU. Moreover, in (Escobar et al., 2016b, 2017c), the effect of memory access optimization on GPU implementations has been demonstrated.

The main approaches to the development of energy-efficient parallel and distributed codes can be grouped into two alternatives. Several approaches propose scheduling procedures that take into account not only running time but also energy consumption of the program (Baskiyar and Abdel-Kader, 2010; Dorronsoro et al., 2014; Lee and Zomaya, 2011; Nesmachnow et al., 2013; Rotem et al., 2016; Zhang et al., 2002). Other approaches investigate the effect of different implementations for a specific application in energy consumption and try to derive energy-aware strategies and power models from the corresponding experimental results (Aliaga et al., 2014). Here, we follow this approach.

With respect to energy consumption efficiency of hybrid CPU-GPU platforms, papers (Allen and Ge, 2016;

Ma et al., 2012; Marowka, 2012) provide some results on this topic. For example, (Marowka, 2012) provides analytical models to get insight into performance gains and energy consumption and concludes that a greater parallelism allows opportunities for energy-saving parallel applications. We demonstrate this from the energy consumption we have measured in our computing node.

4. EXPERIMENTAL RESULTS AND DISCUSSION

In this section, we analyse the performance of our OpenMP-OpenCL codes running on Linux CentOS 6.7 operating system, in a node with two Intel Xeon E5-2620 v4 processors at 2.1 GHz including eight cores per socket with two Hyper-Threading threads per core, thus comprising 32 threads. The node also has a GPU Nvidia Tesla K40m with 288 GB/s as maximum memory bandwidth and 2,880 CUDA cores at 745 MHz. In our experiments, we have used three datasets from the BCI Laboratory at the University of Essex and described in (Asensio-Cubero et al., 2013). They correspond to subjects coded as 104, 107, and 110, and each includes 178 EEG patterns with 3,600 features per pattern. The measures have been obtained considering three different alternatives: two correspond to the use of fixed operation frequencies at 1.2 GHz and 2.1 GHz in CPU, and the third one is the so-called *Syst* alternative in which the runtime system modifies the operation frequency according to its strategy to optimize the code efficiency.

4.1 HYPERVOLUME RESULTS

The quality of the solution obtained by our procedure is evaluated thought their corresponding Pareto front hypervolume (Fonseca et al., 2018), computed here with (1,1) as reference point, and the minimum values of the cost functions f_1 and f_2 are respectively 0 and -1. Thus, the maximum value for the hypervolume is 2. We have made 10 repetitions of each experiment to analyse, through Kolmogorov-Smirnov and Kruskal-Wallis tests, the statistical significance of the observed differences among alternatives. Figure 2 shows hypervolume results for some of the parallel alternatives we have compared. They correspond to good enough solutions included in Pareto fronts with average hypervolumes between 1.881 and 1.978 and standard deviations among 0.007 and
0.03. The statistical analysis does not show significant hypervolume differences for any pair of alternatives. Thus, although our parallel algorithms are not equivalent to the corresponding sequential procedure with only one subpopulation, they provide solutions with similar classification quality.

4.2 RUNNING TIME PERFORMANCE

Figure 3 provides the averages of the speedups obtained for the dataset of subject 110 by different platform configurations using 32 CPU threads and/or GPU. In Figures 3.a, 3.b, and 3.c, a population of 480 individuals is distributed into 2, 4, 8, and 16 subpopulations of, respectively, 240, 120, 60, and 30 individuals. Each

subpopulation independently executes generations among migrations. The figures show results for 1 to 5 migrations and,

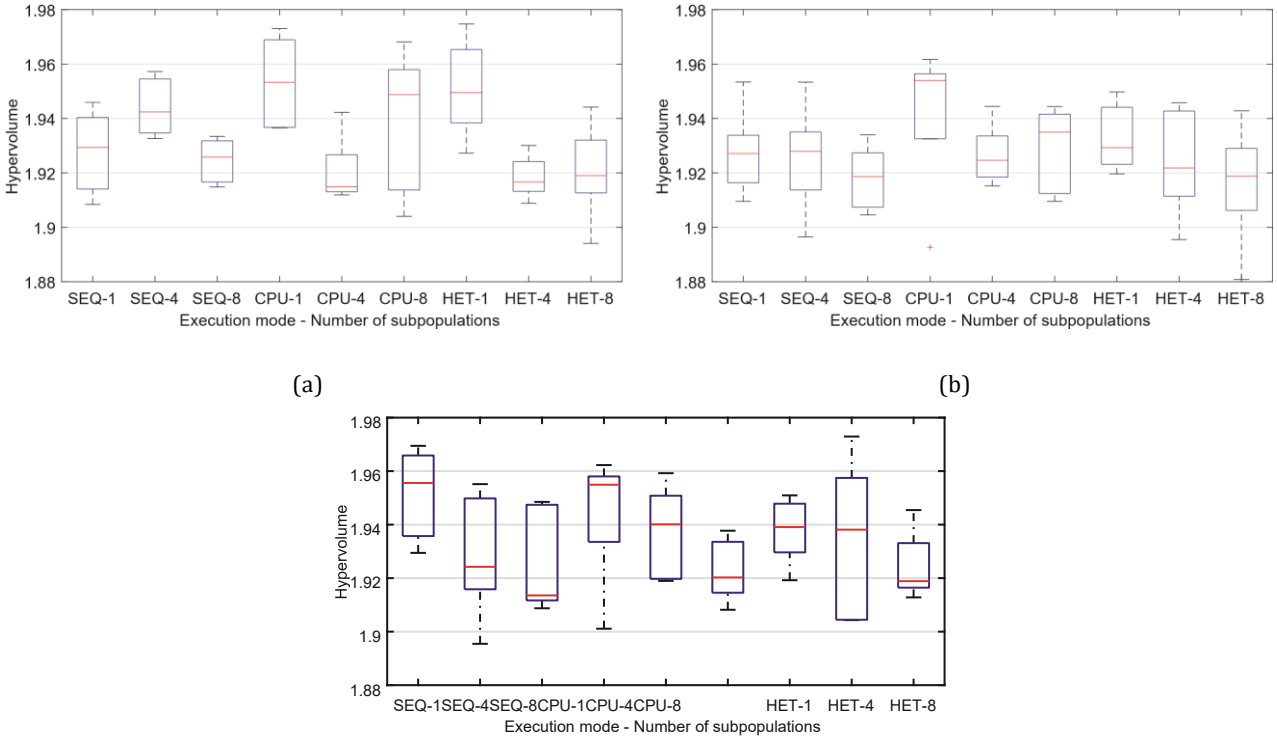


Figure 2. Hypervolumes obtained using multiple CPU frequencies, and different number of subpopulations and execution modes (SEQ: 1 thread; CPU: 32 threads; HET: CPU + GPU): (a) 1.2 GHz; (b) 2.1 GHz; (c) *Syst* alternative. We only show the results obtained for subject 110, as they are similar to those obtained for the rest of subjects.

as all algorithms execute 60 generations, respectively 60, 30, 20, 15, and 12 generations of independent evolutions are executed by each subpopulation between migrations, also showing improvements in the speedups as the number of subpopulations decreases, or as the number of individuals in the subpopulations increases (the same in all cases, i.e. 480). With respect to changes in the number of migrations, the speedups remain approximately constant. A migration implies send individuals and cost functions among subpopulations and thus, its cost increases with the number of subpopulations and individuals per subpopulation. Nevertheless, communications should not be more costly than the replacement process because communications are indeed done through the shared memory that stores the information about individuals and their fitness. The main changes shown in the speedups of Figures 3.a, 3.b, and 3.c seem to be determined by the number of subpopulations and their size (as more subpopulations mean less individuals per subpopulation). As the number of subpopulations grows, the number of calls to the CPU or GPU kernels that allocate a subpopulation to the corresponding device also grows, being costly because a call to the kernel implies to initialize it, and to copy the data to and from the device.

By comparing Figures 3.a, 3.b, and 3.c is apparent that the speedups obtained by using only 32 CPU threads

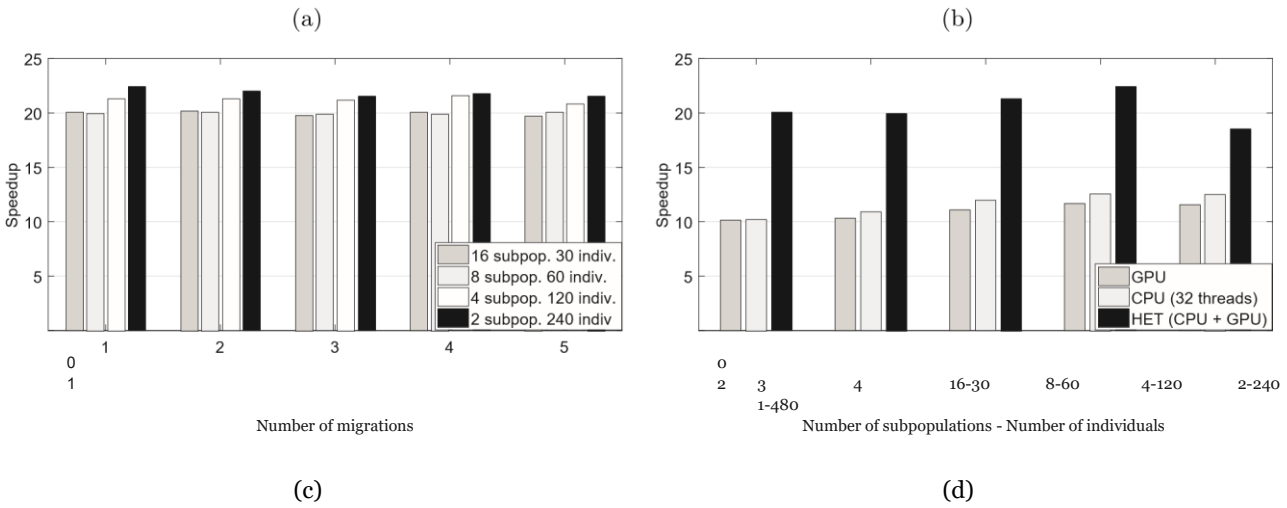


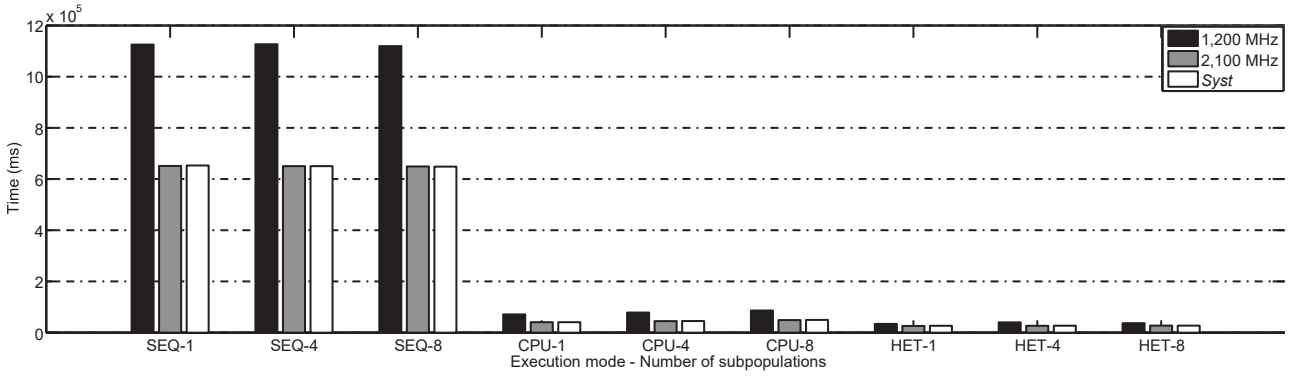
Figure 3. Averages of speedups achieved with different number of subpopulations and execution modes: (a) GPU; (b) CPU: 32 threads; (c) HET: CPU + GPU; (d) Comparison of platforms for different number of subpopulations and individuals per subpopulation. The speedup characteristics for subjects 104 and 107 are quite similar.

are quite similar to those obtained by the GPU. The effect of using both CPU and GPU cores is shown in Figures 3.c and 3.d. As Figure 3.d shows, the speedup grows as the number of subpopulations decreases, except in the case of using only one subpopulation. In this case, the CPU and GPU kernels respectively take 32 and 15 individuals and thus, (480/32 = 15) and (480/15 = 32) calls to the CPU or GPU kernels are required. Consequently, the number of calls is higher in the one subpopulation case than in the case of multiple subpopulations.

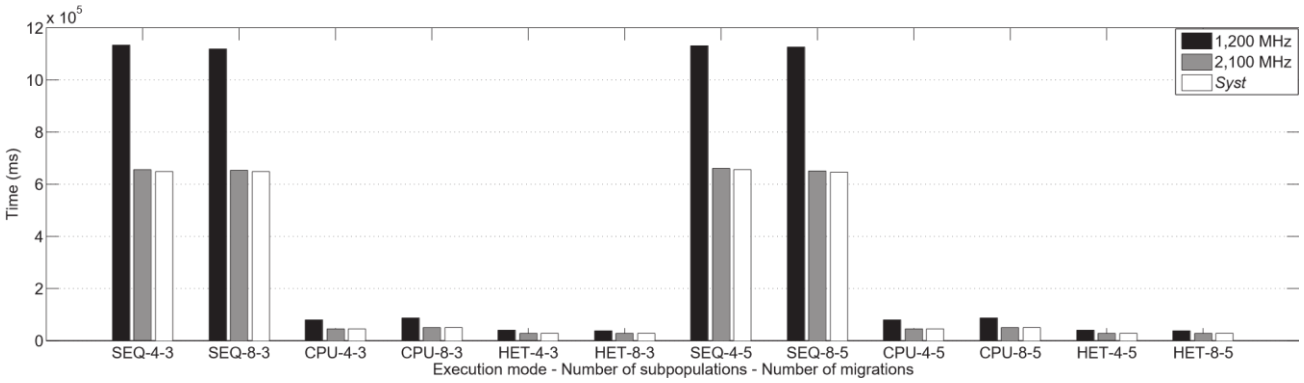
Figure 4 provides the average of the running time for alternatives corresponding to different values of subpopulations, number of migrations, operating frequencies, and platform configurations. The running time for the parallel alternatives are clearly lower than those corresponding to the sequential executions. It is also clear that the times also decrease in case of using an operating frequency of 2.1 GHz and the *Syst* strategy.

4.3 ENERGY CONSUMPTION BEHAVIOUR

The power and the energy consumption in the node has been measured by using a data acquisition system which we have devised, based on *Arduino Mega*, which gives four real-time measures per second of power and energy consumption. In what follows, we analyse the energy-power behaviour of our approach for frequencies of



(a)

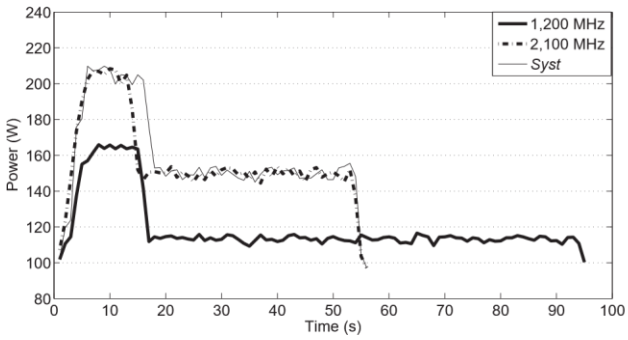


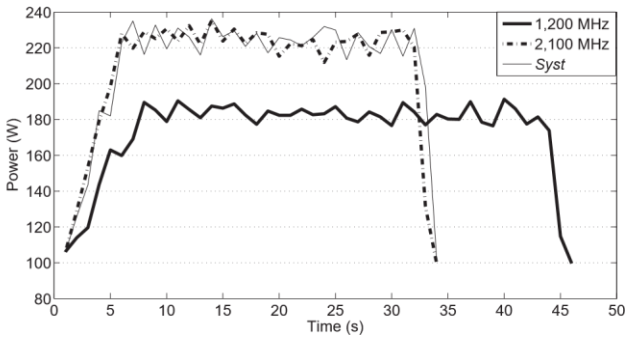
(b)

Figure 4. Running time for different parallel alternatives and operating frequencies, using 60 generations and 480 individuals distributed into multiple number of subpopulations: (a) 1 migration; (b) 3 and 5 migrations.

1.2 GHz and 2.1 GHz, and the *Syst* strategy, previously described. Figures 5.a and 5.b provide the evolution of the instantaneous power consumed along the execution of our procedure in two different parallel configurations: one running in the CPU and the other using the heterogenous mode (HET). These figures show that the lowest instantaneous power values correspond to the 1.2 GHz alternative. The 2.1 GHz and *Syst* alternatives present similar values. Figures 5.c and 5.d clearly show the advantage of using the HET mode instead of only CPU. In addition, it is also clear that the highest instantaneous power consumption corresponds to the HET mode, followed by the configuration which only includes CPU. Nevertheless, the energy consumption depends on the time required to complete the task.

The behaviour with respect to energy consumption for different alternatives is shown in Figure 6. From this figure, it is also clear that the parallel alternatives consume less energy. Although the instantaneous power consumed is higher, the achieved speedup allows better consumption figures. Moreover, the energy consumption is also less in case of an operating frequency of 2.1 GHz and in the *Syst* strategy. In those two last alternatives,





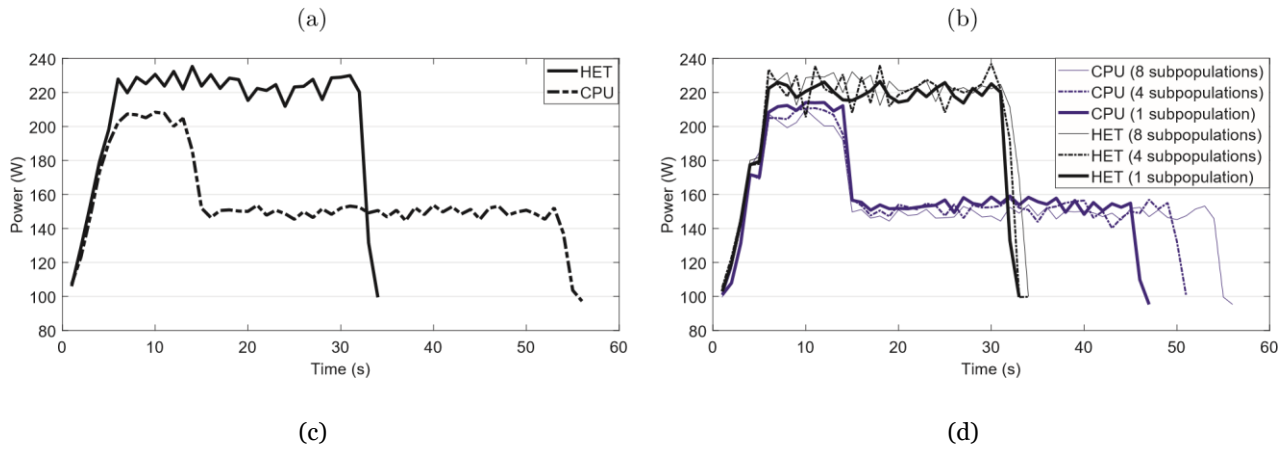
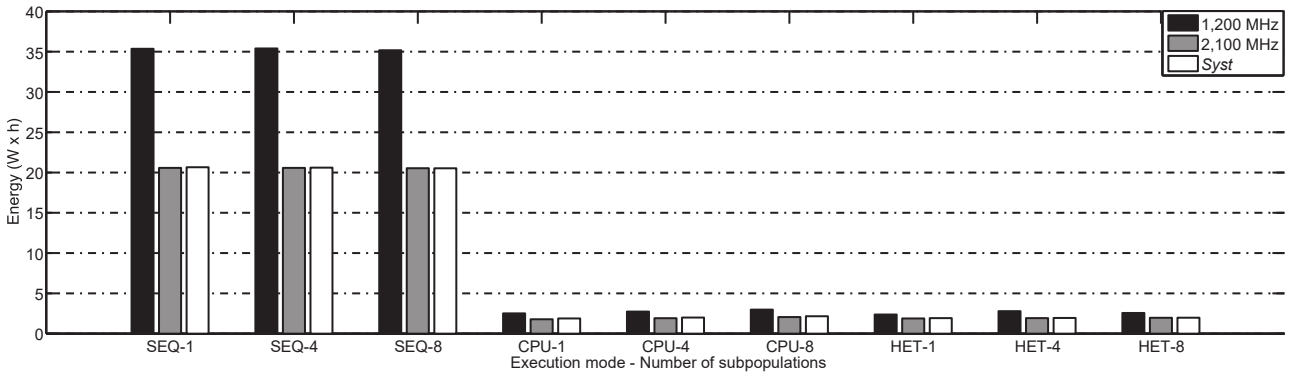


Figure 5. Power measured along the execution of different parallel alternatives with 60 generations and 480 individuals:

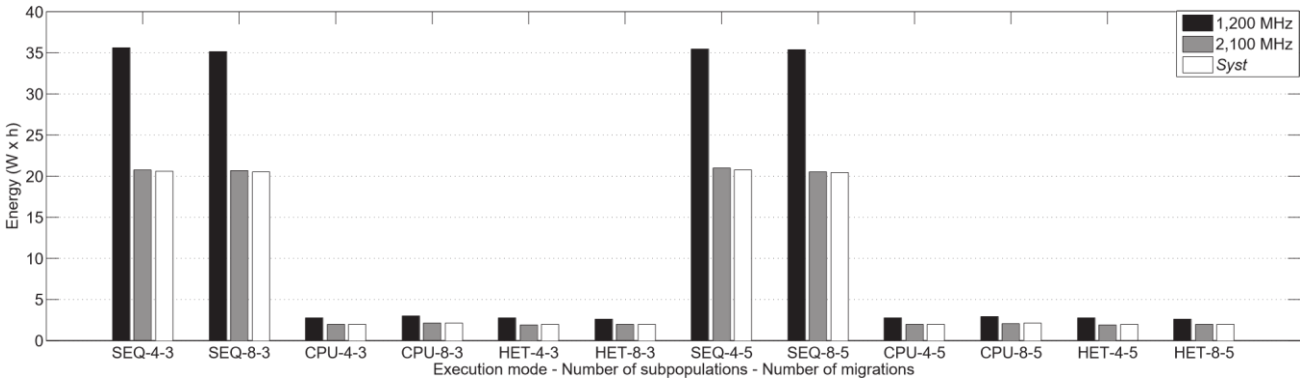
(a) CPU mode with 8 subpopulations, 5 migrations; (b) HET mode with 8 subpopulations, 5 migrations; (c) CPU and HET modes with 8 subpopulations, 5 migrations at 2,100 MHz; (d) CPU and HET modes with 1 migration at 2,100 MHz

the energy consumption is almost the same. It has to be noticed that the energy measures correspond to the energy consumed by the whole node including the consumption of buses and memories. Nevertheless, differences are still apparent for different processing architectures.

Figure 7 compares the energy consumption of the CPU mode with respect to the HET mode. It shows that the CPU alternative only implies less energy consumption in case of one subpopulation for both 2.1 GHz and *Syst* alternatives. The Kruskal-Wallis test shows statistically significant differences in these two cases. Instead, the application of the Kruskal-Wallis test does not detect statistically significant differences between CPU and HET alternatives in case of 4 subpopulations. Finally, the HET mode shows lower energy consumption than the CPU one in case of 8 subpopulations. In this case, the differences are statistically significant according to the Kruskal-Wallis test. Thus, although the HET mode shows higher instantaneous power consumptions than the CPU alternative, the lower execution time of the HET mode in conjunction with an increase in the energy consumed by the CPU alternative when more subpopulations are evolved would explain this behaviour. A similar behaviour can also be seen in Figure 8.



(a)



(b)

Figure 6. Energy consumption for different parallel alternatives and operating frequencies, using 60 generations and 480 individuals distributed into multiple number of subpopulations: (a) 1 migration; (b) 3 and 5 migrations.

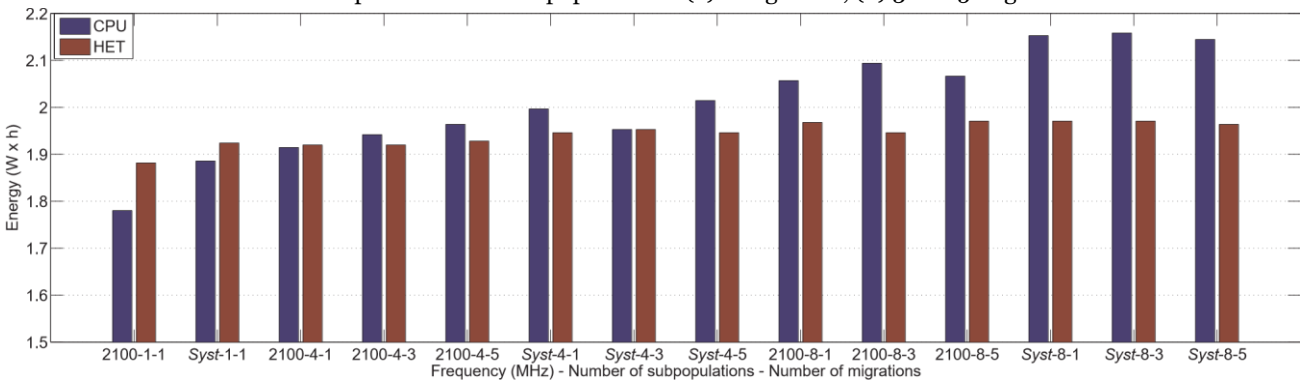


Figure 7. Comparison of energy consumption for configurations using only CPU threads and HET mode.

From Table 1, it can be seen that there are statistically significant differences in all cases considered when the parallel code is executed only by CPU threads. Instead, when the parallel code is executed by both, CPU threads and GPU, there are only statistically significant differences between 4 and 8 subpopulations in the 2.1 GHz case. Even in these cases with significant differences, the p-values are near (p = 0.05). In all cases, the

Table 1. p-values obtained from Kruskal-Wallis test to analyse the statistical significance of differences in the energy consumption for different parallel configurations with multiple number of subpopulations and migrations, N_M (p-value < 0.05 means statistically significance).

N_M	# Subpopulations	CPU (2.1 GHz)	CPU (*Syst*)	HET (2.1 GHz)	HET (*Syst*)
1	1 vs 4	0.005	0.008	**0.091**	**0.093**
	4 vs 8	0.007	0.008	0.030	**0.155**
3	4 vs 8	0.012	0.007	0.045	**0.282**
5	4 vs 8	0.007	0.008	0.045	**0.155**

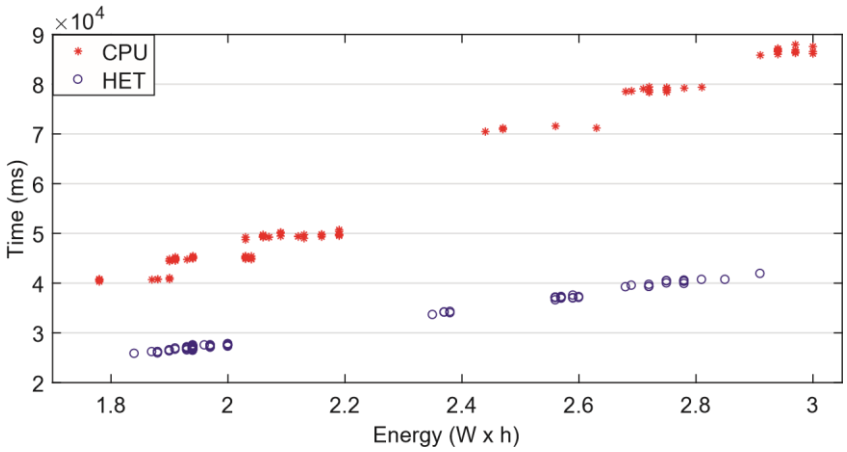


Figure 8. Time versus energy for different parallel configurations. The alternatives which uses CPU threads and GPU provide the lowest values of running time. One of the heterogeneous alternatives even shows a very low energy consumption, despite that the lowest energy consumption values correspond to parallel configurations that only involve CPU threads.

statistically significant differences correspond to increases with the number of subpopulations.

5. CONCLUSIONS

This paper proposes and analyses parallel heterogeneous implementations of a multi-objective feature selection procedure applied to EEG classification on BCI tasks, which take advantage of both CPU and GPU architectures. It uses OpenMP threads to distribute the workload and OpenCL kernels to perform the fitness evaluation of the individuals in each subpopulation. The *K*-means algorithm to evaluate the individual fitness is also parallelized through the GPU cores, with the objective of taking advantage of the data parallel GPU capabilities.

The experimental evaluation of our approach has been done in terms of speedup and energy consumption for different alternatives of subpopulations, migrations, and platform configurations. It has been shown that, for some subpopulation and migration alternatives, the configuration including both CPU and GPU devices provides not only better speedups results but also lower energy consumption than the corresponding alternatives. Compared with a master-worker parallel implementation (the alternative corresponding to only one subpopulation), the heterogeneous configuration still provides the highest speedups, and depending on their specific values, its energy consumption could be higher or lower than the corresponding CPU configuration. Moreover, although the instantaneous power is higher for HET configurations than for the corresponding ones using only CPU threads, the runtime are lower for the HET mode. On the other hand, the energy consumption measured for the HET configuration almost does not show any significant changes with the number of subpopulations. In this case, the energy consumed by components not included in the CPU (buses, RAM memory, etc.) could mask the differences in the energy consumption.

Among other approaches that should be explored to take advantage of both CPU and GPU architectures, a message-passing implementation could offer new insights about speed and energy behaviour of heterogeneous architectures for applications that demand a high amount of heterogeneous parallelism. Moreover, building accurate quantitative models for energy consumption will be also very useful to identify energy-performance efficient workload distributions.

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