DNA sequence alignment is expected to help in revealing important information related to the human body, disease, genetic and other biological upon discovery of the sequence alignment. Moreover, there have been intensive efforts in improving the performance of the sequence alignment process via hardware-based acceleration using the Field Programmable Gate Array (FPGA). This implementation is becoming popular due to the flexibility of the accelerator design, the ability to reduce the execution cycle, parallel computational solutions, and the ability to increase the performance of alignment at the same time. The performance of the DNA sequence alignment system strongly depends on the algorithm, design architecture and accelerator performance. This study proposed three new DNA sequence alignment accelerator system design and architecture named as the new Optimized SWA Linear Gap Penalty (OSL), Optimized SWA Affine Gap Penalty (OSA) and Optimized Recursive Variable Expansion SWA Linear Gap Penalty (ORSL). The OSL, OSA and ORSL proposed a new optimized two data representation format for DNA sequence characters, which is previously used in the eight bit ASCII 2 characters format. Moreover, the OSL, OSA and ORSL cell designs reduce the complexity of the DNA sequence alignment by rescheduling the process of alignment via a new parallel arrangement of the processing or computational element. On top of that, minimal stages of computation cycle were proposed and introduced in OSL cell design, with a reduction of 25% compared to the previous SWA linear gap penalty design. Next, the new OSL, OSA and ORSL also proposed a new optimized systolic array-based architecture for optimizing and accelerating the performance of the SWA cell design. In this study, the As Soon As Possible (ASAP) optimization has been adopted in the OSA, OSL and ORSL cell designs, which resulted in reducing the stages of the computational cycle. Moreover, the minimal size of the two bit data representation characters format used in the design has resulted in minimizing the temporary memory requirement in the cell design up to 75%. The proposed OSL, OSA and ORSL design code was developed, simulated and implemented using commercial design software, the Altera Quartus II version 12.1 and the NIOS II IDE. The design was targeted to the Altera FPGA platforms, specifically the Altera DE2-115. The performance of the system was characterized by referring to the logic function of the design or known as Logic Element (LE) and Cell Update (CU). The performance of OSL was improved as compared to the previous design with 3.2 GCUPS for single PE and 25.6 GCUPS for a complete architecture. While, the OSA was improved by 9.22% as compared to the previous design with 32.0 GCUPS. The ORSL has shown superior results compared to Recursive Variable Expansion (RVE) and Extended Recursive Variable Expansion (ERVE) techniques with 6.4 GCUPS. Again, the size is slightly bigger since the main target of the proposed design is to improve the design performance. Result attained has proven that, the proposed system produces better performance and design over previous work in accelerating the SWA DNA sequence alignment.

The welding and joining industry in the past few decades has witnessed a huge growth in pursuit of process optimization and design minimization due to the continued escalation of prices. A relatively typical new welding process that requires wide attention in process optimization for an ideal low defect joint and life cycle improvement is friction stir welding due to its advantage of having minimal parameters to be controlled during the process. However, despite its many advantages tensile residual stress in friction stir welded joints remains to be a significant concern due to its extensive clamping and stirring process causing a lower fatigue resistance particularly in structures subjected to fluctuating loads triggering a need for improvement by utilizing modern post-weld treatment processes. Aiming to apply the HFMI method of pneumatic impact treatment (PIT) to enhance the fatigue performance of a 6 mm thick AA6061-T651 FSW butt joint, this research consisted of three main phases. The initial phase focused on the optimization of the rotational and traverse speed based on multiple mechanical properties and quality features, which emphasized on the tensile strength, hardness and the weld quality class using the Multi-objective Taguchi Method (MTM). Furthermore, the first order model for predicting the mechanical properties and weld quality class was derived by applying Response Surface Methodology (RSM). The second phase dealt with determining the best governing process parameters of HFMI technique using a similar optimization approach for varied parameters centered on indenter diameter, air pressure and impact frequency. In the final phase, the nominal stress approach was employed to determine the fatigue class (FAT) enhancement values as well as S-N curves of HFMI/PIT treated, post weld heat treated (PHWT), as-welded and in-service HFMI/PIT treated FSW AA6061 joints. Subsequent sub-surface hardness measurements and static test evaluation with microstructure analysis was conducted to gain a better understanding of the fatigue behavior for each condition. Further analyses and measurements of the longitudinal and transverse residual stress for FSW AA6061 joints using the hole-drilling method with electronic speckle pattern interferometry (ESPI) for various conditions was conducted to establish the vicissitudes of residual stress with each as-welded and post weld treatment. It was found that the PIT treatment imparted significant amount of compressive residual stress to the FSW joint resulting in an enhanced fatigue life of FSW PIT treated condition. The FSW in-service PIT treated joints achieved marginally higher fatigue strength than the as-welded conditions although being pre-fatigued, thus giving a whole new meaning to asset integrity and management for in-service FSW aluminum alloy joints and structures.