The assessment of post-operative spine using computed tomography (CT) imaging is so challenging in the presence of metal artifacts induced by spinal implants. Metal artifacts can severely affect the quality of CT images, and mislead the diagnosis interpretation. The artifacts are due to the beam hardening, photon starvation effect, and inappropriate correction algorithm during image reconstruction. Knowledge on factors affecting the artifacts is crucially important to minimize these artifacts. The main aim of this study is to develop a novel technique for suppression of metal artifacts and this study generally consists of three main parts. The first part is the development of a simple phantom useful for metal streaking analysis performed in the second part of this work. A customized phantom was constructed with tissue-equivalent materials and various metal inserts to simulate the streaking artifacts similar to the clinical findings in post-operative spine imaging. In this work, a thorough study on factors influencing the magnitude of metal streak artifacts is presented. There are 3 different variables studied which were metal insert characteristics, exposure factors, and reconstruction parameters. The phantom was scanned using Siemens Definition AS+ CT scanner in Radiology Department, HUSM. All phantom images were acquired using standard field of view (FOV) of 230mm with various acquisition and reconstruction protocols depending on the parameters studied. Standardized regions of interest (ROIs) were defined within the streaking region to obtain 1625 attenuation measurements in Hounsfield units (HU). All data are displayed as mean ± standard deviation (SD). The severity of metal streak in each image was determined by CT fluctuation, and noise at each ROI. Results show similar degrees of streaking artifacts noted in phantom images compared with the clinical CT outcomes. From artifacts analysis, it is found that smaller size and low density metal implants produce less severe artifacts. The result shows increased kVp and mAs has reduced streak artifacts with reduction in image noise and enhanced signal-to-noise ratio (SNR) values. A sharper kernel reduces metal streaks, but produces significantly higher noise (P <0.05) in the images as compared to smooth kernel. Thicker slice also reduced metal artifacts and noise in image. The last part is the development of a metal artifact correction (MAC) algorithm and evaluation of the proposed algorithm in artifacts reduction in CT images. The MAC algorithm was developed in MATLAB environment and was applied on virtual sinogram which directly computed through forward projection of CT images. The missing projection data due to metal region is detected and extracted using an improved technique of dual-step adaptive thresholding. Then, the missing data are replaced by interpolated values by using the spline cubic interpolation. The interpolated and metal-only images were reconstructed and fused together to obtain the final corrected images. The corrected and non-corrected phantom images were compared to evaluate the performance of the proposed MAC. It is shown that the streaking region close to metal inserts was reduced after applying the MAC algorithm. The result also shows significant reduction in image noise, and SNR is enhanced in corrected images. As a conclusion, the fabricated phantom is useful for metal streak analysis with a broad range of parameters can be studied and cost effective. It is concluded that the proposed algorithm allows significant reduction of the streaking artifacts in both phantom and clinical CT images.

Motif Discovery (MD) is the process of identifying meaningful patterns in DNA, RNA, or protein sequences. In the field of bioinformatics, a pattern is also known as a motif. Numerous algorithms had been developed for MD, but most of these were not designed to discover species specific motifs used in identifying a specifically selected species where the exact location of these motifs also needs to be identified. Evaluation of these algorithms showed that the results are unsatisfactory due to the lower validity and accuracy of these algorithms. At present, DNA sequencing analysis is the most utilised technique for species identification where patterns of DNA sequences are determined by comparing the sequence to comprehensive databases. However, several false and gap sequences had been identified to be present in these databases which lead to false identification. Therefore, this study addresses these problems by introducing a hybrid algorithm for MD. In this study, the MD is a process to discover all possible motifs that existed in DNA sequences whereas Motif Identification (MI) is a process to identify the correct motif that can represent a selected species. Particle Swarm Optimisation (PSO) was selected as the base algorithm that needs improvement and integration with other techniques. The Linear-PSO algorithm was the first version of improvement. However due to the longer time required for complete execution of this algorithm, the Binary Search technique was integrated and a new version of the algorithm was developed, namely the Linear-PSO with Binary Search (LPBS) algorithm. A total of 11 experiments were conducted in this research, where the aim of the first four experiments was algorithm improvement; the next four experiments were for identifying suitable input data, while the final three experiments were for algorithm validation. Several DNA sequences from different species were collected from the GenBank and TRansCompel databases and used as input for the algorithm. The collected DNA sequences were from the Mitochondrial Cytochrome C Oxidase Subunit I (COX1) gene. Due to the limitation of available data, only four species were collected for Motif Discovery, namely pig, cow, yak, and chicken. Another five species were used for Motif Identification, which were human, sheep, dog, frog, and rat. The algorithm was run on an Intel(R) Core(TM) Duo CPU 1.73 GHz notebook with 3 GB RAM. The results showed that the LPBS algorithm was able to discover possible correct motifs that can represent a species with higher validity and accuracy as compared to previous algorithms. The motifs discovered were consistent for each execution with higher calculated fitness values.