7.1 Background

Microarray technology might be characterized as a rapid evolution since its being constantly adopted by more and more researchers. Microarrays experimental procedure has been dramatically improved and with the chip prices being continuously reduced researchers use microarrays more frequently, and in greater number. Additionally, the great amount of information regarding genes, genomes and sequenced organisms that might be found, nowadays, in public databases renders microarray technology to be a powerful tool for a wide range of medical, biological and pharmaceutical applications.

7.2 Summary

In this thesis we have devised some novel methodologies for microarray image restoration presented in chapter 3. We have presented two novel techniques for restoration of microarray images. In the first technique a restoration system model is developed, which takes the noisy image as input, estimates the type of noise present in the image and appropriate filters are used to denoise the image. If the input image consists of mixture of noise sources, then bilateral filter is used to denoise the noisy image. After applying the filtering techniques, the denoised image becomes blurred. In that case blind deconvolution technique is used, which estimates both the true and the blurred image from degraded image characteristics, using partial information or no information about the image.

In the second technique Mathematical Morphology is used to denoise the image. The Top-hat and Bottom-hat transforms are used for restoring the degraded microarray images with appropriate structuring element. Both the transforms work well to remove artifacts in the noisy image, whereas to remove the insignificant spots, adaptive threshold concept is used. From the experimental results, it has been observed that most of the contaminated pixels have been removed from the noisy
image. The entire process is robust, in the presence of noise, artifacts and weakly expressed spots. The proposed work can be used at pre-processing stage, before using it in any of the stages of microarray image analysis, which then results in accurate gene expression profiling.

In chapter 4, three novel methods for automatic gridding of noisy, skewed microarray image is proposed. In the first method, spatial topology technique to automatically grid skewed noisy microarray images is discussed. The results of our experiment on skewed microarray images on SMD and UNC are encouraging. The skew correction algorithm depends on determination of coordinate addresses of just two positions in the image. The noise removal is done through adaptive threshold computation which makes processes effective. Finally the gridding is performed based on spatial topology of spots. In the second method, rectangular grid (Bounding box) on each spot to automatically grid noisy, skewed microarray images is discussed. The noise removal is performed through adaptive threshold computation and the entire process is robust, in the presence of noise, skew, artifacts and weakly expressed spots. Finally the gridding is performed by drawing Bounding Box on each spot in the subgrid. In the third method, the projection profiles of the binarized image are obtained, noise removed using morphological operations. The unduly non uniform distance between grid lines in noisy microarray images are corrected using coefficient of variation (CV) of the successive differences in the gridding locations.

In chapter 5, we proposed two techniques for automatic segmentation of noisy microarray image. The first method utilizes the segmentation results of K-Means and intensity information of neighboring pixels. Also the method, takes advantage of the spatial information around each spot of interest, calculating of the found foreground F through existing K-means method. Subsequently the method analyses the neighbors at the boundary of F carefully, before making the final decision of including some of the noisy pixels to F. The second method utilizes the segmentation results of existing K-Means method, refines it, by considering the pixels that are boundary pixels carefully for low SNR images to avoid misclassification of foreground/background pixels thus providing more reliable means of estimating gene expressions on microarray images. The proposed methods overcome the difficulties faced by existing segmentation techniques.
In chapter 6, an efficient quantification algorithm is proposed to validate the performance of segmentation. We demonstrate the success of the proposed method by measuring confidence interval of the proposed and the available existing segmentation methods. Also we, investigate the influence of noise on simulated images in the accuracy of segmentation performance. We show the results of image processing using the proposed quantification method on the simulated and real microarray images, which compare the robustness and accuracy against those obtained with GMM, K-means and Multi-feature methods. Twelve frameworks have been proposed using restoration, gridding, segmentation methods and shown that the proposed frameworks are superior than existing contemporary methods through extensive experimentation.

Finally, in this chapter, a brief summary of all the proposed models is presented. In the following section, the list of major contributions accomplished in this thesis is given.

7.3 Contributions

In this thesis, we have designed some novel approaches for microarray image analysis. The list of contributions made in this thesis is given below:

Restoration
- Restoration system model to automatically find the type of noise in the image and to denoise the image.
- Two stage morphological method to denoise the image.

Gridding
- Spatial topology technique to detect and correct skew followed by automatic gridding of noisy microarray images.
- Bounding box method to automatically grid noisy microarray images.
- Coefficient of variation method to automatically grid noisy microarray images.
Segmentation

- Refinement of K-means method to automatically segment spot’s foreground from background in noisy microarray images.
- Extended K-means method to automatically segment spot’s foreground from background in noisy microarray images.

Quantification

- A new metric based on confidence intervals to validate the performance of segmentation algorithms.
- Twelve frameworks using proposed restoration, gridding and segmentation methods are devised.

7.4 Scope for Future work

- Future perspective of this thesis would be the inclusion of wavelet theory in restoration and segmentation.

- Alternative soft computing tools like fuzzy theory can be explored in segmentation phase while deciding the pixel’s status (Foreground / Background) in a spot.

- Multilevel decomposition with automatic thresholding using wavelets may be useful at the preprocessing stage.
Publications based on this thesis

Journals


Conferences


